Supplementary Table 8. Significantly perturbed genes after severe trauma injury.

						Shown are $\log_2$ transformed measured expression values							
						Control				Trauma			
Probeset ID	**Gene Symbol**	**Gene ID**	**Gene Name**	**q-value**	**Cluster**	**CTRL**	**day0**	**day1**	**day4**	**day7**	**day14**	**day21**	**day28**
TC1300271	ABHD13	84945	abhydrolase domain containing 13	4.33E-10	1	6.28	7.25	7.09	6.91	6.83	6.89	6.78	6.76
TC0103035	ABL2	27	v-abl Abelson murine leukemia viral on	1.34E-09	1	4.08	4.86	4.67	4.52	4.41	4.36	4.30	4.19
TC1001292	ABLIM1	3983	actin binding LIM protein 1 /// Actin-bi	0.000385	1	4.07	4.46	4.10	4.21	4.21	4.19	4.13	4.16
TC0301103	ACAA1	30	acetyl-Coenzyme A acyltransferase 1 (p	0.000181	1	5.99	6.08	6.12	6.26	6.15	6.10	6.07	5.86
TC1101017	ACAD8	27034	acyl-Coenzyme A dehydrogenase family	0.000394	1	4.96	5.28	5.15	5.18	5.27	5.06	5.09	5.06
TC0103283	ACBD3	64746	acyl-Coenzyme A binding domain conta	7.38E-07	1	6.31	6.88	6.82	6.89	6.79	6.84	6.87	6.90
TC0701489	ACHE	43	acetylcholinesterase (Yt blood group) //	0.000169	1	4.95	5.17	5.21	5.20	5.21	5.12	5.10	5.10
TC0700500	ACN9	57001	ACN9 homolog (S. cerevisiae)	1.28E-30	1	3.39	6.04	6.27	5.55	5.34	5.06	4.78	4.51
TC0X00816	ACOT9	23597	acyl-CoA thioesterase 9 /// Acyl-coenzy	0.000435	1	5.45	5.92	5.84	5.68	5.45	5.61	5.76	5.69
TC0102655	ACP6	51205	acid phosphatase 6, lysophosphatidic	1.79E-17	1	4.17	5.16	4.99	4.78	4.90	4.82	4.63	4.63
TC0401451	ACSL1	2180	acyl-CoA synthetase long-chain family m	2.54E-21	1	9.80	10.78	10.68	10.42	10.22	10.16	10.02	9.94
TC0201137	ACSL3	2181	acyl-CoA synthetase long-chain family m	2.80E-26	1	4.93	6.63	6.35	5.71	5.61	5.69	5.70	5.58
TC0X01151	ACSL4	2182	acyl-CoA synthetase long-chain family m	8.93E-16	1	7.15	8.54	8.36	8.13	7.82	7.81	7.82	7.86
TC0501266	ACSL6	23305	acyl-CoA synthetase long-chain family m	6.13E-05	1	3.35	3.47	3.48	3.45	3.47	3.41	3.35	3.41
TC0103331	ACTA1	58	actin, alpha 1, skeletal muscle /// Actin	0.000124	1	5.14	5.54	5.61	5.53	5.56	5.50	5.35	5.44
TC1500813	ACTC1	70	actin, alpha, cardiac muscle 1	6.04E-05	1	3.85	4.09	4.17	4.08	4.09	4.09	3.98	3.99
TC1701778	ACTG1	71	actin, gamma 1	3.07E-07	1	8.31	8.84	8.96	8.83	8.93	8.79	8.64	8.61
TC1400260	ACTR10	55860	actin-related protein 10 homolog (S. ce	8.95E-10	1	5.69	6.16	6.38	6.10	5.97	6.01	6.00	5.97
TC1001246	ACTR1A	10121	ARP1 actin-related protein 1 homolog A	6.44E-08	1	6.55	7.24	7.17	7.13	6.95	6.90	6.90	6.86
TC0200299	ACTR2	10097	ARP2 actin-related protein 2 homolog (	2.42E-12	1	10.51	10.81	10.89	10.82	10.76	10.75	10.72	10.70
TC0200608	ACTR3	10096	ARP3 actin-related protein 3 homolog (	1.97E-08	1	9.44	9.60	9.78	9.66	9.60	9.62	9.55	9.55
TC1200344	ACVR1B	91	activin A receptor, type IB	6.56E-20	1	4.48	5.65	5.56	5.33	5.26	5.05	5.03	4.92
TC0101110	ADAM15	8751	ADAM metallopeptidase domain 15 ///	3.29E-06	1	5.27	5.52	5.50	5.42	5.53	5.49	5.38	5.32
TC0800235	ADAM9	8754	ADAM metallopeptidase domain 9 (me	5.76E-31	1	4.65	6.67	6.90	6.44	6.36	5.86	5.75	5.35
TC0401025	ADAMTS3	9508	ADAM metallopeptidase with thrombo	2.70E-17	1	2.81	3.05	3.87	3.30	3.05	2.68	2.65	2.64
TC0201359	ADCY3	109	adenylate cyclase 3	5.67E-05	1	4.49	4.71	4.85	4.85	4.89	4.72	4.63	4.56
TC1000574	ADD3	120	adducin 3 (gamma)	7.15E-12	1	6.48	7.01	7.10	6.92	6.83	6.80	6.78	6.72
TC0401137	ADH5	647346 //	alcohol dehydrogenase 5 (class III), chi	8.12E-07	1	4.48	5.18	5.35	5.39	5.33	5.25	5.37	5.24
TC1100171	ADM	133	adrenomedullin	0.000304	1	5.09	5.35	5.37	5.54	5.45	5.39	5.27	5.19
TC2200138	ADORA2A	135	adenosine A2a receptor /// Adenosine	0.000446	1	5.33	5.56	5.58	5.55	5.58	5.53	5.45	5.47
TC1200179	AEBP2	121536	AE binding protein 2 /// AE binding pro	3.94E-06	1	4.64	5.16	5.02	5.20	5.29	5.02	5.08	4.99

TC0401422	AGA	175	aspartylglucosaminidase	5.72E-10	1	4.27	5.42	5.71	5.45	5.43	5.34	5.40	5.06
TC0500287	AGGF1	55109	angiogenic factor with G patch and FH	1.29E-10	1	5.20	5.89	6.16	6.22	5.98	5.99	6.10	5.96
TC0100762	AGL	178	amylo-1, 6-glucosidase, 4-alpha-glucan	1.39E-07	1	3.60	4.68	4.52	4.17	4.33	4.24	4.14	3.96
TC0901446	AGPAT2	10555	1-acylglycerol-3-phosphate O-acyltrans	1.60E-09	1	4.72	5.33	5.38	5.48	5.54	5.36	5.30	5.25
TC0601735	AGPAT4	56895	1-acylglycerol-3-phosphate O-acyltrans	8.12E-07	1	3.71	3.82	3.88	3.86	3.80	3.68	3.67	3.63
TC0800249	AGPAT6	137964	1-acylglycerol-3-phosphate O-acyltrans	2.54E-24	1	4.79	5.89	5.63	5.51	5.41	5.24	5.16	5.11
TC0400363	AGPAT9	84803	1-acylglycerol-3-phosphate O-acyltrans	8.29E-17	1	7.14	8.25	8.71	8.53	8.41	8.39	8.10	8.04
TC0901088	AGTPBP1	23287	ATP/GTP binding protein 1 /// ATP/GT	1.08E-20	1	8.26	8.92	9.12	8.79	8.69	8.60	8.41	8.35
TC0600601	AIM1	202	absent in melanoma 1 /// Absent in m	8.06E-09	1	6.31	6.85	7.25	6.97	6.74	6.70	6.74	6.63
TC1000734	AKR1C2	1646	aldo-keto reductase family 1, member	6.47E-05	1	2.88	3.07	3.26	3.20	3.14	3.15	3.09	3.04
TC1000027	AKR1C3	8644	aldo-keto reductase family 1, member	3.12E-14	1	2.96	3.38	3.80	3.63	3.24	3.29	3.37	3.28
TC0103415	AKT3	10000	v-akt murine thymoma viral oncogene	4.76E-10	1	3.97	4.58	4.77	5.01	4.79	4.56	4.51	4.43
TC0901044	ALDH1A1	216	aldehyde dehydrogenase 1 family, me	1.20E-09	1	3.20	4.20	3.89	4.08	3.82	3.55	3.41	3.56
TC1600328	ALDOA	226	aldolase A, fructose-bisphosphate	9.86E-07	1	6.95	7.45	7.39	7.49	7.45	7.29	7.21	7.22
TC1701169	ALDOC	230	aldolase C, fructose-bisphosphate	6.47E-07	1	5.09	5.03	4.89	5.48	5.14	4.93	4.98	5.00
TC1300065	ALOX5AP	241	arachidonate 5-lipoxygenase-activatin	6.40E-09	1	10.70	11.28	11.30	11.13	11.08	11.00	10.85	10.95
TC0100229	ALPL	249	alkaline phosphatase, liver/bone/kidne	3.82E-13	1	6.69	7.99	8.48	8.68	8.39	7.99	7.81	7.47
TC0401027	ANKRD17	26057	ankyrin repeat domain 17 /// ankyrin r	0.000361	1	6.66	7.02	6.86	6.73	6.65	6.66	6.77	6.64
TC1001140	ANKRD22	118932	ankyrin repeat domain 22	5.02E-16	1	4.62	8.05	8.00	7.13	7.09	6.99	6.92	6.76
TC0501109	ANKRD34B	340120	ankyrin repeat domain 34B	2.63E-12	1	4.27	4.65	5.15	5.89	5.53	4.60	4.53	4.45
TC0401242	ANKRD50	57182	ankyrin repeat domain 50	7.51E-17	1	4.05	4.96	5.08	5.06	4.75	4.47	4.51	4.27
TC0500991	ANKRD55	79722	ankyrin repeat domain 55	2.22E-18	1	3.97	4.95	5.15	5.63	5.41	4.85	4.82	4.66
TC0900293	ANXA1	301	annexin A1 /// Annexin A1 (Annexin-1)	2.42E-21	1	7.15	9.00	9.28	9.14	9.08	8.87	8.86	8.49
TC1501009	ANXA2	302	annexin A2	2.14E-06	1	4.12	4.64	4.82	5.19	4.64	4.48	4.59	4.62
TC0400340	ANXA3	306	annexin A3 /// Annexin A3 (Annexin-3)	3.19E-36	1	6.93	9.80	10.01	9.63	9.62	9.36	9.09	8.63
TC0401231	ANXA5	308	annexin A5	1.30E-17	1	7.04	8.14	8.40	8.37	8.18	8.03	7.99	7.80
TC0501418	ANXA6	309	annexin A6 /// Annexin A6 (Annexin-6)	7.37E-06	1	5.09	6.08	6.00	6.21	6.26	6.03	5.96	5.71
TC1001068	ANXA7	310	annexin A7	2.78E-05	1	6.91	7.34	7.29	7.25	7.14	7.15	7.22	7.16
TC1000941	ANXA8L1 /// A	728113 //	annexin A8-like 1 /// annexin A8 /// an	0.000793	1	3.91	3.95	3.99	3.91	4.07	4.03	3.92	3.88
TC1601236	AP1G1	164	adaptor-related protein complex 1, ga	1.30E-09	1	6.86	7.33	7.19	7.01	6.90	6.98	6.86	6.91
TC0X00787	AP1S2	654127 //	adaptor-related protein complex 1, sig	1.12E-13	1	5.37	6.07	6.12	5.91	5.97	5.99	5.82	5.82
TC1700374	AP2B1	163	adaptor-related protein complex 2, bet	1.45E-06	1	6.52	6.91	7.06	6.94	6.78	6.68	6.66	6.63
TC1501185	AP3B2	8120	adaptor-related protein complex 3, bet	1.10E-10	1	3.26	3.36	3.95	3.90	3.66	3.37	3.28	3.27
TC0500405	AP3S1	730730 //	adaptor-related protein complex 3, sig	1.05E-19	1	5.31	6.16	6.41	6.32	6.38	6.27	6.21	6.12

TC0102561	AP4B1	10717	adaptor-related protein complex 4, bet	0.000361	1	4.30	4.40	4.50	4.45	4.51	4.38	4.38	4.30
TC1000124	APBB1IP	54518	amyloid beta (A4) precursor protein-bi	0.000375	1	8.37	8.51	8.68	8.58	8.39	8.44	8.40	8.35
TC1800051	APCDD1	147495	adenomatosis polyposis coli down-regu	0.00011	1	4.63	4.91	4.95	4.95	4.92	4.88	4.73	4.81
TC1500397	APH1B	83464	anterior pharynx defective 1 homolog	3.59E-13	1	5.13	5.99	6.12	5.98	5.78	5.74	5.83	5.64
TC1100287	API5	8539	apoptosis inhibitor 5 /// Apoptosis inhi	0.000337	1	5.10	6.03	6.16	6.16	6.02	5.95	6.10	5.91
TC0102937	APOA2	336	apolipoprotein A-II	1.93E-12	1	5.12	6.04	5.89	5.79	5.78	5.74	5.46	5.31
TC2200285	APOBEC3H	164668	apolipoprotein B mRNA editing enzym	8.81E-05	1	3.89	4.13	3.98	4.01	4.20	4.04	3.76	3.82
TC0X00817	APOO	79135	apolipoprotein O /// Apolipoprotein O	1.34E-06	1	3.66	4.32	4.42	4.16	4.04	4.01	4.07	3.95
TC1100896	ARCN1	372	archain 1 /// Coatomer subunit delta (	1.54E-05	1	7.55	7.93	7.97	7.99	7.85	7.99	7.99	7.99
TC0301291	ARF4	378	ADP-ribosylation factor 4	1.14E-08	1	6.31	6.93	6.93	6.83	6.78	6.80	6.74	6.79
TC1400214	ARF6	382	ADP-ribosylation factor 6	1.11E-09	1	5.40	6.31	6.21	6.34	6.27	6.24	6.03	6.09
TC2200733	ARFGAP3	26286	ADP-ribosylation factor GTPase activati	7.31E-10	1	6.24	7.11	7.01	6.90	6.79	6.74	6.69	6.47
TC0800995	ARFGEF1	10565	ADP-ribosylation factor guanine nucleo	8.63E-06	1	6.66	7.26	7.17	7.17	7.31	7.25	7.18	7.01
TC0600720	ARG1	383	arginase, liver /// Arginase-1 (EC 3.5.3.	1.18E-24	1	5.96	9.50	9.48	9.36	9.37	8.84	8.45	7.73
TC0601593	ARHGAP18	93663	Rho GTPase activating protein 18 /// R	8.28E-10	1	4.71	6.17	6.24	6.13	6.11	6.20	6.20	5.95
TC0400368	ARHGAP24	83478	Rho GTPase activating protein 24 /// R	3.86E-13	1	4.34	5.69	5.65	5.73	5.72	5.48	5.43	5.07
TC0102459	ARHGAP29	9411	Rho GTPase activating protein 29 /// P	8.18E-11	1	2.44	2.70	2.75	2.58	2.54	2.48	2.46	2.44
TC0301281	ARHGEF3	50650	Rho guanine nucleotide exchange fact	4.15E-16	1	5.01	5.86	5.84	5.77	5.35	5.13	5.30	5.35
TC0700841	ARHGEF5	7984	Rho guanine nucleotide exchange fact	1.10E-07	1	4.73	5.30	4.93	4.86	5.11	5.10	5.06	4.90
TC1300279	ARHGEF7	8874	Rho guanine nucleotide exchange fact	7.27E-09	1	4.51	4.79	4.75	4.67	4.57	4.52	4.53	4.51
TC0200494	ARID5A	10865	AT rich interactive domain 5A (MRF1-li	1.38E-10	1	4.59	5.18	5.01	4.97	4.93	4.80	4.75	4.72
TC1000274	ARID5B	84159	AT rich interactive domain 5B (MRF1-li	7.64E-20	1	4.00	5.45	5.85	6.26	5.70	5.10	5.17	4.70
TC1500459	ARIH1	25820	ariadne homolog, ubiquitin-conjugatin	8.66E-05	1	6.91	7.19	6.99	7.02	6.92	7.05	7.06	7.08
TC1300146	ARL11	115761	ADP-ribosylation factor-like 11	5.02E-06	1	5.40	5.97	5.95	5.84	5.74	5.87	5.74	5.73
TC0300414	ARL13B	200894	ADP-ribosylation factor-like 13B	4.29E-08	1	4.32	5.17	5.04	4.92	4.81	4.84	5.05	4.92
TC1001248	ARL3	403	ADP-ribosylation factor-like 3	0.000127	1	6.53	6.59	6.96	7.07	6.78	6.79	6.71	6.70
TC1000091	ARL5B	221079	ADP-ribosylation factor-like 5B	9.26E-12	1	5.01	6.07	5.68	5.51	5.37	5.60	5.60	5.58
TC0103123	ARL8A	127829	ADP-ribosylation factor-like 8A	9.11E-08	1	6.50	7.24	7.26	7.20	7.06	6.87	6.74	6.71
TC0300013	ARL8B	55207	ADP-ribosylation factor-like 8B	2.03E-14	1	5.45	6.33	6.45	6.41	6.41	6.41	6.37	6.24
TC0300651	ARMC8	25852	armadillo repeat containing 8	2.05E-05	1	6.14	6.69	6.76	6.76	6.70	6.65	6.61	6.50
TC0X00430	ARMCX3	51566	armadillo repeat containing, X-linked 3	4.28E-08	1	4.21	4.65	4.66	4.51	4.56	4.48	4.47	4.40
TC0102732	ARNT	405	aryl hydrocarbon receptor nuclear tran	0.000652	1	6.90	7.36	7.28	7.33	7.20	7.14	7.21	7.13
TC0201090	ARPC2	10109	actin related protein 2/3 complex, sub	0.000876	1	10.28	10.34	10.43	10.32	10.27	10.31	10.31	10.29
TC0103062	ARPC5	10092	actin related protein 2/3 complex, sub	2.63E-15	1	9.45	9.78	9.92	9.82	9.76	9.75	9.71	9.69

TC0900560	ARPC5L	81873	actin related protein 2/3 complex, subu	1.30E-05	1	4.84	5.24	5.35	5.23	5.23	5.01	5.11	4.89
TC1700047	ARRB2	409	arrestin, beta 2 /// Beta-arrestin-2 (Arr	0.000114	1	8.95	9.42	9.41	9.40	9.30	9.10	8.95	9.06
TC0201228	ASB1	51665	ankyrin repeat and SOCS box-containin	4.32E-15	1	4.87	5.32	5.47	5.37	5.33	5.16	5.10	4.95
TC1500672	ASB7	140460	ankyrin repeat and SOCS box-containin	4.32E-08	1	6.41	7.07	7.12	7.11	6.90	6.99	6.87	6.87
TC1001055	ASCC1	51008	activating signal cointegrator 1 comple	9.77E-07	1	4.60	4.91	4.88	4.80	4.81	4.80	4.76	4.79
TC0701441	ASNS	440	asparagine synthetase	6.11E-16	1	3.85	4.66	4.55	4.37	4.44	4.28	4.18	4.09
TC0800969	ASPH	444	aspartate beta-hydroxylase /// Asparty	5.63E-15	1	6.47	7.25	7.84	7.59	7.43	7.28	7.27	6.84
TC2200156	ASPHD2	57168	aspartate beta-hydroxylase domain co	1.11E-05	1	5.42	5.97	5.87	5.95	5.83	5.96	5.92	6.02
TC0201369	ASXL2	55252	additional sex combs like 2 (Drosophila	4.09E-05	1	6.91	7.38	7.22	7.04	6.92	6.94	7.07	6.94
TC1001135	ATAD1	84896	ATPase family, AAA domain containing	1.81E-08	1	4.46	5.08	5.17	4.90	4.85	4.88	4.91	4.82
TC0201350	ATAD2B	54454	ATPase family, AAA domain containing	1.22E-06	1	5.23	5.62	5.51	5.39	5.21	5.27	5.29	5.21
TC1001321	ATE1	11101	arginyltransferase 1 /// Arginyl-tRNA--	5.22E-08	1	4.12	4.77	4.83	4.89	4.97	4.88	4.79	4.62
TC1201254	ATF7	11016	activating transcription factor 7 /// Cyc	1.90E-07	1	6.19	6.59	6.61	6.65	6.67	6.45	6.51	6.37
TC0500313	ATG10	83734	ATG10 autophagy related 10 homolog	8.28E-05	1	3.72	4.09	4.29	4.21	4.06	4.10	4.15	4.08
TC0301447	ATG3	64422	ATG3 autophagy related 3 homolog (S.	4.30E-05	1	9.24	9.62	9.62	9.57	9.48	9.67	9.66	9.67
TC0X00486	ATG4A	115201	ATG4 autophagy related 4 homolog A (	6.80E-06	1	4.05	4.48	4.68	4.51	4.34	4.43	4.51	4.38
TC1900176	ATG4D	84971	ATG4 autophagy related 4 homolog D (	0.000638	1	4.89	5.03	4.98	4.91	4.93	4.90	4.87	4.82
TC0601490	ATG5	9474	ATG5 autophagy related 5 homolog (S.	0.000862	1	5.36	5.82	5.96	5.88	5.81	5.88	5.96	5.87
TC0202331	ATG9A /// ABC	79065 ///	ATG9 autophagy related 9 homolog A (	2.21E-12	1	4.79	5.00	4.90	4.91	4.95	4.80	4.70	4.65
TC1101505	ATL3 /// ATLA3	25923	atlastin 3 /// Atlastin-3. [Source:Unipro	3.02E-23	1	3.80	4.95	5.15	5.04	4.90	4.66	4.54	4.29
TC0300836	ATP11B	23200	ATPase, class VI, type 11B	3.50E-29	1	7.54	9.00	9.18	8.83	8.56	8.33	8.30	8.06
TC0301867	ATP13A3	79572	ATPase type 13A3 /// Probable cation-	1.14E-17	1	4.38	6.35	6.43	6.58	6.37	5.95	5.77	5.13
TC0300675	ATP1B3	483	ATPase, Na+/K+ transporting, beta 3 p	4.30E-05	1	3.47	4.02	3.63	3.76	3.82	3.74	3.79	3.63
TC1200691	ATP2A2	488	ATPase, Ca++ transporting, cardiac mu	3.61E-14	1	4.86	5.64	5.81	5.72	5.71	5.36	5.42	5.13
TC0101436	ATP2B4	493	ATPase, Ca++ transporting, plasma me	1.50E-11	1	6.28	7.06	7.39	7.22	6.85	6.71	6.67	6.39
TC1600635	ATP2C2	9914	ATPase, Ca++ transporting, type 2C, m	8.38E-10	1	3.71	4.60	4.08	4.00	4.29	4.14	4.05	3.80
TC1000044	ATP5C1	509	ATP synthase, H+ transporting, mitoch	5.87E-15	1	5.63	6.43	6.78	6.80	6.69	6.67	6.69	6.62
TC0100835	ATP5F1	515	ATP synthase, H+ transporting, mitoch	4.59E-16	1	5.42	6.14	6.35	6.20	6.12	6.02	6.01	5.94
TC0202118	ATP5G3	518	ATP synthase, H+ transporting, mitoch	2.52E-13	1	3.47	4.32	4.58	4.60	4.57	4.52	4.52	4.37
TC2100318	ATP5O	539	ATP synthase, H+ transporting, mitoch	2.31E-10	1	6.01	6.53	6.70	6.63	6.68	6.64	6.67	6.60
TC0X00151	ATP6AP2	10159	ATPase, H+ transporting, lysosomal acc	2.30E-13	1	6.68	7.54	7.43	7.22	7.19	7.25	7.19	7.21
TC0800478	ATP6V1C1	528	ATPase, H+ transporting, lysosomal 42	9.67E-25	1	7.30	8.59	9.13	8.70	8.38	8.29	8.13	7.99
TC0201486	ATP6V1E2	90423	ATPase, H+ transporting, lysosomal 31	0.000977	1	3.29	3.42	3.53	3.59	3.53	3.43	3.50	3.40
TC0800935	ATP6V1H	51606	ATPase, H+ transporting, lysosomal 50/	1.20E-07	1	4.49	5.11	5.09	5.06	4.97	4.95	5.02	4.93

TC2000834	ATP9A	10079	ATPase, class II, type 9A /// Probable p	6.14E-26	1	3.57	5.62	5.93	5.38	5.12	4.54	4.24	3.88
TC0102227	ATPAF1	64756	ATP synthase mitochondrial F1 comple	1.86E-07	1	4.36	4.90	5.12	4.91	4.79	4.77	4.79	4.72
TC0600969	ATXN1 /// Q96	6310	ataxin 1 /// ATXN1 protein (Fragment).	7.49E-13	1	6.01	6.57	6.73	6.69	6.42	6.31	6.23	6.11
TC1401078	ATXN3	4287	ataxin 3 /// ataxin 3 isoform 2 [Source:	2.72E-05	1	6.63	7.14	7.27	7.10	6.98	7.13	7.17	7.05
TC0701537	ATXN7L1	222255	ataxin 7-like 1 /// Ataxin-7-like protein	0.000126	1	4.65	4.89	5.08	5.06	4.93	4.98	5.04	4.97
TC01r00008	AURKAIP1	54998	aurora kinase A interacting protein 1	1.36E-05	1	6.83	7.12	7.20	7.21	7.16	7.15	7.15	7.16
TC2000510	AVP	551	arginine vasopressin (neurophysin II, a	0.000455	1	3.94	4.16	4.20	4.16	4.16	4.22	3.94	4.07
TC0301116	AXUD1	64651	AXIN1 up-regulated 1 /// Axin-1 up-reg	1.83E-05	1	5.43	6.07	5.81	5.79	5.72	5.80	5.55	5.71
TC0301075	AZI2	64343	5-azacytidine induced 2 /// 5-azacytidi	2.78E-20	1	5.09	6.54	6.55	6.38	6.30	6.09	6.05	5.88
TC0801173	AZIN1	51582	antizyme inhibitor 1	4.01E-24	1	6.56	8.37	8.24	7.78	7.90	7.90	7.61	7.61
TC0301711	B3GALNT1	8706	beta-1,3-N-acetylgalactosaminyltransf	5.32E-07	1	3.52	3.85	3.83	3.66	3.71	3.78	3.64	3.61
TC0600308	B3GALT4	8705	UDP-Gal:betaGlcNAc beta 1,3-galactos	2.85E-12	1	6.01	6.70	6.83	6.80	6.79	6.63	6.57	6.53
TC0601378	B3GAT2	135152	beta-1,3-glucuronyltransferase 2 (gluc	7.59E-05	1	4.88	5.10	5.27	5.21	5.14	5.17	5.20	5.15
TC1101478	B3GAT3	26229	beta-1,3-glucuronyltransferase 3 (gluc	0.000335	1	5.73	5.80	6.00	5.86	5.85	5.79	5.78	5.79
TC0200277	B3GNT2	10678	UDP-GlcNAc:betaGal beta-1,3-N-acetyl	1.56E-21	1	6.18	7.23	7.64	7.54	7.40	7.39	7.18	7.11
TC1900308	B3GNT3	10331	UDP-GlcNAc:betaGal beta-1,3-N-acetyl	9.46E-06	1	3.76	4.17	4.05	4.18	4.10	3.99	3.96	3.99
TC0300837	B3GNT5	84002	UDP-GlcNAc:betaGal beta-1,3-N-acetyl	3.43E-18	1	5.10	6.44	5.99	5.76	5.60	5.58	5.56	5.55
TC0301472	B4GALT4	8702	UDP-Gal:betaGlcNAc beta 1,4- galactos	8.38E-13	1	3.66	4.39	4.27	4.12	4.15	4.03	4.08	3.91
TC2000820	B4GALT5	9334	UDP-Gal:betaGlcNAc beta 1,4- galactos	1.02E-21	1	8.67	9.74	9.58	9.76	9.77	9.69	9.55	9.39
TC0800228	BAG4	9530	BCL2-associated athanogene 4	1.17E-08	1	4.37	4.92	5.17	5.16	5.11	5.05	5.06	4.89
TC0701446	BAIAP2L1	55971	BAI1-associated protein 2-like 1	0.000425	1	3.79	3.82	3.90	3.95	3.93	3.84	3.78	3.76
TC0202292	BARD1	580	BRCA1 associated RING domain 1	1.42E-06	1	3.92	4.55	4.86	4.91	5.11	4.98	4.75	4.42
TC0500061	BASP1	10409	brain abundant, membrane attached si	1.44E-08	1	8.96	9.41	9.47	9.40	9.31	9.32	9.26	9.21
TC1400380	BATF	10538	basic leucine zipper transcription facto	4.70E-22	1	5.83	7.73	7.74	7.74	7.64	7.15	7.05	6.66
TC1400784	BAZ1A	11177	bromodomain adjacent to zinc finger d	0.000562	1	9.17	9.50	9.45	9.30	9.19	9.11	9.23	9.09
TC0401234	BBS7	55212	Bardet-Biedl syndrome 7	0.000913	1	3.24	3.54	3.65	3.61	3.57	3.56	3.69	3.58
TC0X01369	BCAP31	10134	B-cell receptor-associated protein 31	6.75E-07	1	5.86	6.28	6.44	6.40	6.36	6.22	6.12	6.12
TC1501158	BCL2A1	597	BCL2-related protein A1 /// Bcl-2-relate	7.26E-22	1	8.24	9.33	9.42	9.08	8.93	8.92	8.88	8.95
TC1400099	BCL2L2	599	BCL2-like 2	0.000574	1	5.20	5.45	5.43	5.46	5.48	5.44	5.41	5.35
TC1900615	BCL3	602	B-cell CLL/lymphoma 3	6.89E-11	1	6.12	7.00	6.56	6.53	6.50	6.51	6.35	6.42
TC0701318	BCL7B	9275	B-cell CLL/lymphoma 7B	0.000547	1	5.32	5.71	5.72	5.70	5.77	5.76	5.68	5.66
TC0100953	BCL9	607	B-cell CLL/lymphoma 9	1.17E-05	1	4.34	4.70	4.67	4.59	4.61	4.44	4.50	4.44
TC0X00560	BCORL1	63035	BCL6 co-repressor-like 1 /// BCL6 co-re	3.26E-05	1	5.51	5.99	5.97	5.97	5.96	5.79	5.81	5.72
TC1600193	BFAR	51283	bifunctional apoptosis regulator	3.47E-07	1	5.26	6.02	5.96	6.01	5.99	6.01	5.96	5.85

TC2000895	BHLHB4	128408	basic helix-loop-helix domain containin	0.000907	1	5.18	5.52	5.49	5.52	5.46	5.43	5.36	5.42
TC2200338	BIK	638	BCL2-interacting killer (apoptosis-induc	5.81E-09	1	4.42	5.01	4.88	4.86	4.93	4.81	4.81	4.75
TC0201011	BMPR2	659	bone morphogenetic protein receptor,	4.76E-07	1	4.86	5.69	5.59	5.69	5.35	5.48	5.78	5.77
TC0X00059	BMX	660	BMX non-receptor tyrosine kinase	1.96E-23	1	4.26	7.18	6.82	6.29	6.09	5.92	5.67	5.41
TC1501008	BNIP2	663	BCL2/adenovirus E1B 19kDa interactin	8.32E-27	1	7.54	8.48	8.53	8.33	8.17	8.14	8.01	7.96
TC0103241	BPNT1	10380	3'(2'), 5'-bisphosphate nucleotidase 1 /	3.40E-05	1	3.74	4.20	4.32	4.25	4.34	4.14	4.22	4.08
TC0701689	BRAF	673	v-raf murine sarcoma viral oncogene h	3.34E-06	1	6.83	7.31	7.00	6.89	6.93	6.99	6.89	6.96
TC0200138	BRE	9577	brain and reproductive organ-expresse	2.36E-07	1	5.57	5.97	5.99	5.88	5.80	5.76	5.72	5.67
TC1900072	BRUNOL5	60680	bruno-like 5, RNA binding protein (Dro	0.000136	1	4.36	4.44	4.47	4.38	4.44	4.43	4.26	4.36
TC1000639	BRWD2	55717	bromodomain and WD repeat domain	0.000872	1	3.62	4.28	4.22	4.21	4.19	4.10	4.22	4.10
TC0400114	BST1	683	bone marrow stromal cell antigen 1 ///	5.64E-12	1	7.53	8.29	8.39	8.37	8.22	8.04	7.86	7.90
TC1101215	BTBD10	84280	BTB (POZ) domain containing 10	3.28E-05	1	6.97	7.47	7.78	7.58	7.48	7.62	7.50	7.47
TC1900228	BTBD14B	112939	BTB (POZ) domain containing 14B	7.23E-09	1	5.91	6.53	6.41	6.54	6.43	6.36	6.23	6.27
TC2000079	BTBD3	22903	BTB (POZ) domain containing 3	6.04E-09	1	3.61	3.99	3.93	3.93	3.97	3.86	3.87	3.81
TC0100721	BTBD8	284697	BTB (POZ) domain containing 8 /// BTB	1.16E-05	1	2.31	2.47	2.71	2.57	2.41	2.44	2.42	2.43
TC0200982	BZW1	9689	basic leucine zipper and W2 domains 1	5.46E-05	1	6.83	7.37	7.24	7.29	7.24	7.30	7.28	7.29
TC1001315	C10orf119	79892	chromosome 10 open reading frame 1	5.73E-14	1	6.50	7.28	7.40	7.46	7.36	7.34	7.23	7.16
TC1000055	C10orf47	254427	chromosome 10 open reading frame 4	0.00066	1	4.80	5.02	5.00	5.02	5.05	5.07	4.99	4.97
TC1000381	C10orf57	80195	chromosome 10 open reading frame 5	4.36E-06	1	3.38	3.73	3.85	3.73	3.80	3.69	3.72	3.59
TC1000514	C10orf6	55719	chromosome 10 open reading frame 6	1.46E-05	1	3.96	4.49	4.73	4.53	4.44	4.42	4.52	4.24
TC1001240	C10orf76	79591	chromosome 10 open reading frame 7	0.00076	1	4.61	5.02	5.10	5.02	5.01	4.89	4.95	4.81
TC1101637	C11orf51	25906	chromosome 11 open reading frame 5	3.08E-19	1	6.14	7.67	7.70	7.81	7.84	7.59	7.40	7.07
TC1100198	C11orf58	651744 //	chromosome 11 open reading frame 5	7.71E-08	1	6.13	6.85	6.82	6.62	6.53	6.59	6.64	6.61
TC1101848	C11orf71	54494	chromosome 11 open reading frame 7	2.18E-07	1	4.90	5.37	5.55	5.52	5.44	5.41	5.22	5.16
TC1100725	C11orf73	51501	chromosome 11 open reading frame 7	8.91E-06	1	3.90	4.60	4.75	4.51	4.58	4.54	4.63	4.39
TC1100712	C11orf82	220042	chromosome 11 open reading frame 8	5.13E-10	1	3.87	4.39	4.81	4.75	4.68	4.56	4.40	4.24
TC1200031	C12orf5	57103	chromosome 12 open reading frame 5	0.000752	1	2.75	3.05	3.12	3.17	2.98	3.03	2.97	3.14
TC1300414	C13orf23	80209	chromosome 13 open reading frame 2	2.92E-15	1	4.38	6.80	6.67	6.17	6.07	5.82	5.88	5.45
TC1400272	C14orf100	51528	chromosome 14 open reading frame 1	7.30E-06	1	5.45	5.52	5.93	5.83	5.64	5.68	5.76	5.75
TC1400253	C14orf101	54916	chromosome 14 open reading frame 1	6.84E-21	1	4.95	6.11	6.41	5.88	5.58	5.44	5.44	5.20
TC1400257	C14orf108	55745	chromosome 14 open reading frame 1	1.59E-10	1	3.95	4.44	4.79	4.60	4.41	4.46	4.53	4.47
TC1400095	C14orf119	55017	chromosome 14 open reading frame 1	1.15E-09	1	4.81	5.38	5.65	5.74	5.65	5.61	5.60	5.47
TC1400478	C14orf129	51527	chromosome 14 open reading frame 1	1.12E-08	1	4.86	5.78	5.97	5.78	5.66	5.69	5.59	5.55
TC1400778	C14orf147	171546	chromosome 14 open reading frame 1	7.35E-18	1	4.88	6.19	6.58	7.08	7.09	6.55	6.26	5.87

TC1400394	C14orf174	161394	chromosome 14 open reading frame 1	0.000107	1	2.96	3.19	3.34	3.30	3.16	3.00	3.21	3.02
TC1401151	C14orf2	9556	chromosome 14 open reading frame 2	3.48E-26	1	7.66	8.45	8.67	8.59	8.62	8.51	8.46	8.33
TC1400167	C14orf24	283635	chromosome 14 open reading frame 2	2.49E-10	1	5.48	6.41	6.24	6.01	6.09	6.05	6.04	5.88
TC1401103	C14orf49	161176	chromosome 14 open reading frame 4	2.79E-05	1	4.92	5.11	5.16	5.02	4.98	4.95	4.94	4.93
TC1400709	C14orf94	54930	chromosome 14 open reading frame 9	3.00E-08	1	7.18	7.57	8.23	8.03	7.70	7.76	7.83	7.47
TC1500970	C15orf15	730628 //	chromosome 15 open reading frame 1	2.54E-26	1	5.87	7.59	7.71	7.52	7.74	7.61	7.46	7.27
TC1500538	C15orf37	283687	chromosome 15 open reading frame 3	1.11E-10	1	6.40	7.52	7.20	6.71	6.62	6.61	6.60	6.83
TC1501235	C15orf38 /// A	348110 //	chromosome 15 open reading frame 3	5.35E-14	1	5.24	5.60	5.80	5.87	5.79	5.57	5.53	5.43
TC1600320	C16orf53	79447	chromosome 16 open reading frame 5	1.55E-13	1	6.61	7.22	7.36	7.31	7.31	7.32	7.31	7.26
TC1600484	C16orf57	79650	chromosome 16 open reading frame 5	4.63E-11	1	6.31	7.16	7.30	7.37	7.12	7.01	6.86	6.75
TC1600229	C16orf62	57020	chromosome 16 open reading frame 6	5.72E-09	1	4.48	4.87	5.12	5.15	5.08	4.90	4.99	4.81
TC1601352	C16orf7	9605	chromosome 16 open reading frame 7	1.49E-07	1	4.80	5.17	5.06	4.97	4.96	4.91	4.81	4.86
TC1600511	C16orf70	80262	chromosome 16 open reading frame 7	7.24E-20	1	5.05	5.40	5.88	6.05	5.87	5.64	5.47	5.33
TC1600163	C16orf72	29035	chromosome 16 open reading frame 7	5.59E-05	1	8.70	9.01	9.08	9.11	8.96	8.99	8.81	8.85
TC1601074	C16orf87	388272	chromosome 16 open reading frame 8	1.38E-09	1	3.80	5.26	5.00	4.95	4.71	4.78	5.03	4.75
TC1701207	C17orf42	79736	chromosome 17 open reading frame 4	1.66E-05	1	3.41	3.55	3.82	3.67	3.61	3.57	3.65	3.48
TC1700159	C17orf45 /// S	125144	chromosome 17 open reading frame 4	1.87E-06	1	4.16	5.00	4.68	4.64	4.96	4.84	4.72	4.46
TC1700689	C17orf60	284021	chromosome 17 open reading frame 6	8.25E-07	1	4.91	6.44	6.68	6.33	6.07	6.04	6.12	5.84
TC1701180	C17orf63	55731	chromosome 17 open reading frame 6	1.06E-08	1	5.23	5.92	5.42	5.45	5.43	5.44	5.45	5.40
TC1701217	C17orf75	64149	chromosome 17 open reading frame 7	9.87E-05	1	3.42	3.79	3.99	3.91	3.98	3.87	3.96	3.81
TC1701214	C17orf79	55352	chromosome 17 open reading frame 7	6.18E-07	1	4.56	4.91	4.94	4.92	5.05	4.93	4.95	4.86
TC1701782	C17orf90	339229	chromosome 17 open reading frame 9	4.42E-06	1	5.88	6.22	6.27	6.29	6.39	6.24	6.17	6.13
TC1800072	C18orf1	753	chromosome 18 open reading frame 1	7.51E-14	1	4.46	4.64	4.81	4.59	4.60	4.54	4.44	4.46
TC1800142	C18orf21	83608	chromosome 18 open reading frame 2	9.00E-10	1	5.57	6.00	6.37	6.30	6.22	6.19	6.23	6.19
TC1800375	C18orf45	85019	chromosome 18 open reading frame 4	1.34E-06	1	3.20	3.43	3.44	3.31	3.44	3.39	3.27	3.26
TC1900037	C19orf24	55009	chromosome 19 open reading frame 2	0.000153	1	6.21	6.53	6.56	6.50	6.58	6.52	6.46	6.45
TC1901018	C19orf35	374872	chromosome 19 open reading frame 3	0.000168	1	5.80	6.33	6.22	6.12	6.14	6.08	6.03	6.03
TC1900135	C19orf59	199675	chromosome 19 open reading frame 5	1.57E-40	1	5.45	9.72	10.04	9.46	9.16	8.28	7.74	7.14
TC0201582	C1D	647375 //	nuclear DNA-binding protein	2.94E-09	1	5.07	5.89	6.13	6.01	5.80	5.92	5.90	5.94
TC0700064	C1GALT1	56913	core 1 synthase, glycoprotein-N-acetyl	6.72E-09	1	5.50	6.48	6.53	6.31	6.29	6.37	6.37	6.37
TC0X01202	C1GALT1C1	29071	C1GALT1-specific chaperone 1	9.57E-15	1	5.33	5.89	6.26	6.03	5.95	5.95	5.84	5.93
TC0100412	C1orf108	79647	chromosome 1 open reading frame 10	0.000244	1	6.76	7.03	6.96	6.96	6.90	7.06	6.92	7.00
TC0101528	C1orf115	79762	chromosome 1 open reading frame 11	3.28E-05	1	3.92	4.14	4.05	4.05	4.03	3.97	3.82	3.99
TC0102005	C1orf135	79000	chromosome 1 open reading frame 13	7.03E-12	1	4.44	4.98	4.95	5.04	5.10	5.01	4.99	4.93

TC0100836	C1orf162	128346	chromosome 1 open reading frame 16	2.20E-31	1	5.98	7.85	8.14	7.88	7.62	7.19	7.19	6.94
TC0102941	C1orf192	257177	chromosome 1 open reading frame 19	5.54E-05	1	4.17	4.36	4.39	4.51	4.29	4.21	4.16	4.04
TC0102098	C1orf212	113444	chromosome 1 open reading frame 21	4.76E-06	1	6.12	6.46	6.57	6.48	6.40	6.36	6.29	6.40
TC0103070	C1orf25	81627	chromosome 1 open reading frame 25	5.39E-06	1	5.38	5.85	6.09	6.00	5.77	5.86	5.87	5.89
TC0102506	C1orf59	113802	chromosome 1 open reading frame 59	1.25E-09	1	4.92	5.27	5.60	5.35	5.21	5.15	5.14	5.01
TC0101494	C1orf97	84791	chromosome 1 open reading frame 97	0.000105	1	3.51	4.09	4.08	3.93	3.80	3.99	3.97	3.97
TC2000299	C20orf121	79183	chromosome 20 open reading frame 1	3.22E-09	1	4.84	5.63	5.52	5.53	5.56	5.46	5.38	5.24
TC2000419	C20orf177	63939	chromosome 20 open reading frame 1	9.42E-19	1	6.16	7.40	7.37	7.01	6.96	6.85	6.71	6.61
TC2000057	C20orf196	149840	chromosome 20 open reading frame 1	0.000106	1	4.73	5.46	5.39	5.29	5.41	5.37	5.45	5.21
TC2000633	C20orf3	57136	chromosome 20 open reading frame 3	6.51E-14	1	7.58	8.95	8.71	8.92	8.97	8.70	8.43	8.18
TC2000226	C20orf52	140823	chromosome 20 open reading frame 5	1.92E-16	1	6.75	7.94	8.04	7.98	8.11	7.89	7.66	7.51
TC2000600	C20orf74	57186	chromosome 20 open reading frame 7	6.91E-14	1	6.75	7.47	7.41	7.27	7.17	6.97	6.86	6.74
TC2100187	C21orf70	85395	chromosome 21 open reading frame 7	0.000878	1	4.63	4.82	4.82	4.88	4.96	4.78	4.74	4.76
TC2100233	C21orf91	54149	chromosome 21 open reading frame 9	2.22E-11	1	6.70	7.51	7.70	7.73	7.42	7.52	7.44	7.60
TC2200610	C22orf28	51493	chromosome 22 open reading frame 2	2.43E-05	1	4.49	5.44	5.41	5.32	5.35	5.32	5.43	5.10
TC2200750	C22orf9	23313	chromosome 22 open reading frame 9	1.44E-18	1	5.31	6.15	6.60	6.70	6.47	6.07	5.99	5.88
TC0202043	C2orf12	---	Uncharacterized protein C2orf12 (Cervi	5.44E-07	1	6.84	7.57	7.54	7.42	7.19	7.23	7.20	7.08
TC0201995	C2orf25	27249	chromosome 2 open reading frame 25	6.90E-22	1	6.59	7.53	7.83	7.41	7.29	7.26	7.09	7.09
TC0200241	C2orf30	27248	chromosome 2 open reading frame 30	1.70E-09	1	4.11	4.84	5.10	5.13	4.93	4.99	5.07	4.98
TC0200970	C2orf47	79568	chromosome 2 open reading frame 47	1.53E-19	1	3.65	4.91	5.28	5.12	4.95	4.54	4.55	4.34
TC0200183	C2orf58	285154	chromosome 2 open reading frame 58	4.97E-05	1	3.59	3.81	4.09	4.18	3.96	3.85	3.82	3.80
TC0202208	C2orf60	129450	chromosome 2 open reading frame 60	4.12E-19	1	4.12	5.05	5.18	4.95	4.82	4.42	4.43	4.30
TC1200936	C3AR1	719	complement component 3a receptor 1	3.35E-08	1	2.88	4.25	4.43	4.79	4.70	4.18	4.12	4.05
TC0300041	C3orf10	55845	chromosome 3 open reading frame 10	0.000501	1	7.16	7.76	7.81	7.90	7.86	7.81	7.79	7.79
TC0300211	C3orf23	285343	chromosome 3 open reading frame 23	6.04E-17	1	4.86	5.69	5.70	5.39	5.29	5.05	5.02	4.78
TC0300404	C3orf38	285237	chromosome 3 open reading frame 38	1.76E-05	1	4.86	5.69	5.78	5.65	5.40	5.60	5.69	5.65
TC0301280	C3orf63	23272	chromosome 3 open reading frame 63	6.56E-08	1	5.30	5.79	6.20	6.12	5.95	5.88	5.96	5.71
TC0400465	C4orf16	55435	chromosome 4 open reading frame 16	8.28E-10	1	3.81	4.73	4.61	4.71	4.45	4.32	4.45	4.30
TC0401359	C4orf18	51313	chromosome 4 open reading frame 18	5.01E-07	1	3.05	3.82	3.98	4.05	3.59	3.45	3.47	3.42
TC0401396	C4orf27	54969	chromosome 4 open reading frame 27	4.07E-13	1	4.62	5.67	6.01	5.77	5.70	5.59	5.61	5.48
TC0400126	C4orf28	133015	chromosome 4 open reading frame 28	7.38E-05	1	3.06	3.33	3.42	3.36	3.30	3.24	3.38	3.26
TC0400464	C4orf32	132720	chromosome 4 open reading frame 32	4.80E-09	1	5.19	6.19	6.40	6.56	6.34	6.35	6.33	6.35
TC0400890	C4orf34	201895	chromosome 4 open reading frame 34	2.99E-14	1	5.51	6.25	6.41	6.45	6.21	6.21	6.24	6.21
TC0501284	C5orf15	56951	chromosome 5 open reading frame 15	0.000274	1	5.23	5.57	5.59	5.54	5.56	5.54	5.52	5.53

TC0500096	C5orf22	55322	chromosome 5 open reading frame 22	8.24E-07	1	4.35	5.07	5.21	5.07	5.00	5.02	5.14	5.00
TC0500378	C5orf30	90355	chromosome 5 open reading frame 30	9.43E-08	1	3.87	4.31	4.33	4.43	4.48	4.38	4.25	4.18
TC0500528	C5orf32	84418	chromosome 5 open reading frame 32	2.77E-28	1	7.82	10.07	10.44	9.82	9.66	9.30	9.01	8.73
TC0501010	C5orf43	643155	chromosome 5 open reading frame 43	1.27E-11	1	4.87	5.74	5.91	5.87	5.98	5.70	5.73	5.54
TC0600886	C6orf120	387263	chromosome 6 open reading frame 12(	1.82E-05	1	4.59	5.04	5.32	5.22	5.15	5.17	5.11	5.10
TC0601392	C6orf150	115004	chromosome 6 open reading frame 15(	7.02E-20	1	4.75	6.10	6.15	5.84	5.66	5.47	5.57	5.35
TC0601441	C6orf166	55122	chromosome 6 open reading frame 16(	1.47E-10	1	7.34	7.93	7.98	7.99	7.96	8.05	7.88	7.95
TC0600901	C6orf195	154386	chromosome 6 open reading frame 19!	0.000304	1	3.47	3.67	3.60	3.47	3.64	3.51	3.45	3.45
TC0601519	C6orf199	221264	chromosome 6 open reading frame 19(	1.63E-05	1	3.78	4.10	4.44	4.41	4.22	4.18	4.27	4.22
TC0600415	C6orf206	221421	chromosome 6 open reading frame 20(	2.38E-07	1	4.34	4.85	4.94	5.12	5.00	4.85	4.85	4.71
TC0601126	C6orf47	57827	chromosome 6 open reading frame 47	0.000129	1	5.12	5.52	5.50	5.48	5.44	5.38	5.39	5.47
TC0601230	C6orf64	55776	chromosome 6 open reading frame 64	9.76E-05	1	3.60	3.91	3.97	3.96	3.90	3.94	4.01	3.91
TC0601693	C6orf98	387079	chromosome 6 open reading frame 98	6.63E-05	1	3.34	3.59	3.57	3.51	3.43	3.36	3.31	3.28
TC0700114	C7orf30	115416	chromosome 7 open reading frame 30	1.63E-13	1	6.38	7.32	7.56	7.41	7.21	7.39	7.38	7.29
TC0701561	C7orf60 /// NP	154743	chromosome 7 open reading frame 60	1.03E-06	1	6.54	7.01	7.21	7.34	7.16	7.21	7.12	7.14
TC0800257	C8orf40	114926	chromosome 8 open reading frame 40	3.97E-10	1	4.86	5.59	5.67	5.55	5.65	5.57	5.47	5.36
TC0800643	C8orf77	---	Uncharacterized protein C8orf77. [Sou	0.00042	1	3.73	4.14	4.00	3.93	3.89	3.91	3.97	3.93
TC0900412	C9orf102 /// N	375748 //	chromosome 9 open reading frame 10:	5.22E-07	1	4.42	4.56	4.84	4.78	4.48	4.40	4.51	4.42
TC0900334	C9orf103	414328	chromosome 9 open reading frame 10:	3.33E-25	1	4.89	5.94	7.11	7.20	6.64	5.93	5.86	5.45
TC0901329	C9orf126	286205	chromosome 9 open reading frame 12(	1.38E-06	1	3.32	3.42	3.69	3.39	3.34	3.38	3.38	3.37
TC0900590	C9orf16	79095	chromosome 9 open reading frame 16	4.84E-08	1	4.71	5.21	5.14	5.14	5.22	5.22	5.07	5.14
TC0900727	C9orf167	54863	chromosome 9 open reading frame 16;	4.54E-07	1	5.77	6.25	6.23	6.19	6.11	6.11	6.16	6.02
TC0900172	C9orf19	152007	chromosome 9 open reading frame 19	0.000827	1	8.06	8.54	8.52	8.63	8.52	8.56	8.38	8.49
TC0900767	C9orf46	55848	chromosome 9 open reading frame 46	4.55E-14	1	4.39	5.22	5.58	5.54	5.30	5.30	5.29	5.15
TC0900475	C9orf6	54942	chromosome 9 open reading frame 6 /,	0.000121	1	3.75	4.13	4.30	4.16	4.09	4.08	4.00	4.03
TC0901081	C9orf64	84267	chromosome 9 open reading frame 64	5.28E-06	1	4.62	4.91	5.11	4.97	4.88	4.88	5.00	4.95
TC0901255	C9orf80	58493	chromosome 9 open reading frame 80	8.13E-05	1	5.17	5.51	5.44	5.36	5.35	5.47	5.49	5.52
TC0901051	C9orf95	54981	chromosome 9 open reading frame 95	2.69E-05	1	4.32	4.84	4.99	5.00	4.85	4.86	4.84	4.68
TC1700651	CA4	762	carbonic anhydrase IV	6.02E-12	1	5.43	6.27	6.57	6.30	6.37	6.07	5.83	5.69
TC0X00060	CA5BL	---	Carbonic anhydrase VB-like protein (Fr	0.000241	1	4.61	4.86	4.76	4.68	4.75	4.73	4.63	4.63
TC0900163	CA9	768	carbonic anhydrase IX	0.000595	1	4.22	4.39	4.33	4.26	4.34	4.31	4.18	4.20
TC0201163	CAB39	51719	calcium binding protein 39	1.18E-19	1	7.17	7.89	8.07	7.91	7.76	7.62	7.46	7.48
TC1101594	CABP2	51475	calcium binding protein 2	0.000479	1	5.13	5.26	5.23	5.22	5.19	5.15	5.04	5.15
TC0101337	CACNA1E	777	calcium channel, voltage-dependent, R	5.42E-06	1	4.36	4.54	4.77	4.64	4.37	4.37	4.31	4.27

TC1200296	CACNB3	784	calcium channel, voltage-dependent, b	0.000718	1	4.04	4.13	4.16	4.03	4.10	4.08	4.03	4.01
TC0701592	CADPS2	93664	Ca2+-dependent activator protein for s	0.000777	1	2.49	2.59	2.62	2.53	2.57	2.53	2.50	2.51
TC1400439	CALM3 /// CAL	808 /// 8	calmodulin 3 (phosphorylase kinase, de	1.47E-18	1	9.07	9.76	9.90	9.87	9.92	9.78	9.71	9.66
TC0100422	CAP1	10487	CAP, adenylate cyclase-associated prot	1.81E-07	1	10.27	10.54	10.59	10.57	10.47	10.43	10.36	10.37
TC0201673	CAPG	822	capping protein (actin filament), gelsoli	7.50E-29	1	5.46	6.88	7.03	6.81	6.68	6.44	6.34	6.12
TC1100534	CAPN1	823	calpain 1, (mu/I) large subunit	4.20E-06	1	5.65	6.13	6.14	6.15	6.09	5.88	5.80	5.79
TC1900470	CAPNS1	826	calpain, small subunit 1	5.44E-08	1	7.64	8.63	8.66	8.78	8.66	8.37	8.29	8.23
TC0100846	CAPZA1	829	capping protein (actin filament) muscle	6.66E-05	1	8.40	8.69	8.77	8.69	8.61	8.63	8.52	8.57
TC0700630	CAPZA2	830	capping protein (actin filament) muscle	2.33E-09	1	8.67	9.07	9.38	9.33	9.23	9.24	9.17	9.19
TC0500143	CARD6	84674	caspase recruitment domain family, me	1.05E-27	1	5.55	6.98	7.33	7.14	6.86	6.49	6.47	6.22
TC1101082	CARS	833	cysteinyl-tRNA synthetase	0.000269	1	5.75	6.06	5.93	5.91	5.82	5.84	5.82	5.78
TC0500354	CAST	831	calpastatin /// Calpastatin (Calpain inhi	4.03E-13	1	6.83	8.27	8.34	8.24	8.10	7.78	7.95	7.54
TC1101559	CATSPER1	117144	cation channel, sperm associated 1	5.32E-14	1	4.18	4.55	4.79	4.98	4.69	4.54	4.41	4.34
TC1600510	CBFB	865	core-binding factor, beta subunit	3.08E-06	1	6.64	7.33	7.32	7.27	7.17	7.27	7.29	7.20
TC0102412	CCBL2 /// NP_	56267	cysteine conjugate-beta lyase 2 /// Kyn	6.37E-07	1	5.24	5.79	5.65	5.41	5.29	5.36	5.39	5.33
TC1600294	CCDC101	112869	coiled-coil domain containing 101	6.96E-08	1	4.86	5.13	5.39	5.42	5.33	5.19	5.15	5.12
TC2200169	CCDC117	150275	coiled-coil domain containing 117	5.74E-09	1	5.76	6.46	6.70	6.39	6.29	6.31	6.29	6.20
TC0301162	CCDC12	151903	coiled-coil domain containing 12	5.19E-08	1	6.65	7.30	7.26	7.27	7.34	7.27	7.23	7.15
TC0700117	CCDC126	90693	coiled-coil domain containing 126	1.53E-07	1	3.30	4.22	4.32	4.13	4.11	4.24	4.13	4.03
TC0X00221	CCDC22	28952	coiled-coil domain containing 22	0.00024	1	4.67	4.85	4.83	4.82	4.92	4.83	4.77	4.69
TC1101270	CCDC34	91057	coiled-coil domain containing 34 /// co	0.000178	1	3.44	3.87	4.27	3.88	4.07	3.94	3.97	3.74
TC1701605	CCDC47	57003	coiled-coil domain containing 47	2.51E-05	1	7.37	7.90	7.82	7.74	7.65	7.58	7.58	7.57
TC1201503	CCDC53	51019	coiled-coil domain containing 53	9.06E-18	1	6.21	7.03	7.52	7.36	7.13	7.05	7.09	7.01
TC1100747	CCDC67	159989	coiled-coil domain containing 67	2.79E-05	1	1.97	2.07	2.16	2.07	2.11	2.03	2.05	2.03
TC1101708	CCDC90B	60492	coiled-coil domain containing 90B	9.35E-10	1	5.00	5.87	6.05	5.85	5.81	5.89	5.92	5.86
TC1200221	CCDC91	55297	coiled-coil domain containing 91 /// Co	2.29E-07	1	4.76	5.34	5.49	5.41	5.29	5.25	5.33	5.30
TC0400808	CCDC96	257236	coiled-coil domain containing 96	7.47E-05	1	3.23	3.68	3.47	3.48	3.21	3.57	3.61	3.54
TC1300086	CCNA1	8900	cyclin A1	2.07E-05	1	2.55	2.93	3.13	3.34	3.17	3.04	2.86	2.82
TC0601478	CCNC	892	cyclin C /// Cyclin-C. [Source:Uniprot/S	5.14E-12	1	3.50	4.24	4.24	4.07	4.05	3.98	3.92	3.82
TC0601260	CCND3	896	cyclin D3 /// G1/S-specific cyclin-D3. [S	1.39E-11	1	5.45	6.13	6.05	6.03	6.07	5.89	5.81	5.76
TC0500672	CCNG1	900	cyclin G1 /// Cyclin-G1 (Cyclin-G). [Sour	5.14E-07	1	4.79	5.72	5.79	5.66	5.62	5.55	5.55	5.42
TC0501129	CCNH	902	cyclin H	4.11E-05	1	6.15	6.55	6.28	6.21	6.14	6.27	6.31	6.28
TC0301152	CCR1	1230	chemokine (C-C motif) receptor 1	0.000453	1	8.76	9.29	9.37	9.44	9.03	9.23	9.14	9.30
TC1100029	CD151	977	CD151 molecule (Raph blood group)	1.39E-05	1	4.73	4.99	4.96	5.09	5.13	5.03	4.92	4.92

TC1200923	CD163	9332	CD163 molecule	4.93E-10	1	3.58	4.84	4.94	4.37	3.91	3.72	3.86	3.75
TC0601512	CD164	8763	CD164 molecule, sialomucin /// Putativ	8.12E-20	1	8.36	9.55	9.77	9.65	9.53	9.44	9.26	9.20
TC1601006	CD2BP2	10421	CD2 (cytoplasmic tail) binding protein	1.54E-05	1	5.93	6.53	6.41	6.47	6.35	6.39	6.26	6.30
TC0700443	CD36	948	CD36 molecule (thrombospondin recep	0.000892	1	3.64	4.52	4.75	4.97	4.59	4.51	4.37	4.40
TC1100275	CD44	960	CD44 molecule (Indian blood group) //,	4.71E-29	1	6.36	8.35	8.33	8.15	7.77	7.37	7.17	6.95
TC0102924	CD48	962	CD48 molecule /// CD48 antigen precu	1.42E-19	1	6.20	7.51	8.13	7.90	7.52	7.49	7.48	7.28
TC0101473	CD55	1604	CD55 molecule, decay accelerating fact	4.67E-22	1	9.22	10.01	9.91	9.69	9.61	9.47	9.36	9.35
TC0102581	CD58	965	CD58 molecule /// Lymphocyte functio	1.62E-06	1	6.88	7.49	7.59	7.31	7.24	7.34	7.32	7.32
TC1101298	CD59 /// Q3C1	966	CD59 molecule, complement regulator	6.85E-20	1	5.13	6.25	6.24	6.17	5.99	5.83	5.76	5.76
TC1201280	CD63	967	CD63 molecule	2.76E-20	1	6.61	7.15	7.26	7.33	7.27	7.20	7.11	7.04
TC1100299	CD82	3732	CD82 molecule	5.64E-05	1	5.91	6.20	6.34	6.29	6.19	5.98	5.96	5.89
TC0X01344	CD99L2	83692	CD99 molecule-like 2 /// CD99 antigen-	4.74E-12	1	4.90	5.00	5.26	5.32	5.24	5.14	5.04	4.91
TC0100221	CDA	978	cytidine deaminase	2.32E-05	1	7.46	8.30	8.15	8.33	8.47	8.31	7.97	8.02
TC1300142	CDADC1	81602	cytidine and dCMP deaminase domain	5.84E-20	1	4.29	6.67	6.10	5.57	5.63	5.39	5.28	5.00
TC1901162	CDC37	11140	cell division cycle 37 homolog (S. cerevi	0.000128	1	6.86	7.01	7.20	7.39	7.15	6.95	6.97	6.88
TC0600636	CDC40	51362	cell division cycle 40 homolog (S. cerevi	3.35E-07	1	6.06	6.70	6.96	6.89	6.59	6.65	6.76	6.59
TC0100238	CDC42	998	cell division cycle 42 (GTP binding prote	0.00068	1	8.71	8.93	9.01	8.93	8.89	8.93	8.87	8.89
TC0201437	CDC42EP3	10602	CDC42 effector protein (Rho GTPase bi	4.51E-13	1	7.11	7.74	7.82	7.79	7.68	7.54	7.37	7.36
TC0101378	CDC73	79577	cell division cycle 73, Paf1/RNA polyme	1.58E-11	1	7.98	8.74	8.67	8.46	8.37	8.41	8.41	8.36
TC1200416	CDK2	1017	cyclin-dependent kinase 2	9.24E-06	1	4.40	5.32	4.84	4.84	5.16	5.02	4.84	4.71
TC0701759	CDK5	1020	cyclin-dependent kinase 5	1.80E-08	1	4.80	5.11	5.42	5.53	5.49	5.26	5.26	5.01
TC0901293	CDK5RAP2	55755	CDK5 regulatory subunit associated pr	8.76E-09	1	5.21	5.73	5.86	5.92	5.95	5.75	5.85	5.53
TC1901167	CDKN2D	1032	cyclin-dependent kinase inhibitor 2D (	8.57E-09	1	5.93	6.17	6.25	6.17	6.19	6.20	6.01	6.10
TC1601280	CDYL2	124359	chromodomain protein, Y-like 2	0.000111	1	4.54	4.75	4.69	4.77	4.78	4.66	4.64	4.60
TC1901553	CEACAM1	634	carcinoembryonic antigen-related cell	1.27E-13	1	7.71	9.82	9.46	9.09	9.11	8.88	8.57	8.40
TC1901393	CEBPA /// NM_	1050	CCAAT/enhancer binding protein (C/EB	2.00E-11	1	4.65	4.99	5.08	5.04	5.01	4.95	4.85	4.84
TC2000365	CEBPB	1051	CCAAT/enhancer binding protein (C/EB	1.82E-17	1	6.21	6.96	7.00	6.82	6.62	6.71	6.63	6.67
TC0800919	CEBPD	1052	CCAAT/enhancer binding protein (C/EB	1.10E-09	1	5.48	6.06	6.03	5.98	5.99	5.92	5.84	5.89
TC0201433	CEBPZ	10153	CCAAT/enhancer binding protein zeta	5.80E-19	1	4.77	7.08	6.92	6.43	6.46	6.25	6.28	5.93
TC2000521	CENPB	1059	centromere protein B, 80kDa	8.36E-07	1	5.17	5.69	5.70	5.84	5.77	5.74	5.64	5.59
TC1700336	CENTA2	55803	centaurin, alpha 2	9.60E-05	1	3.86	4.15	4.10	4.24	4.03	3.99	4.07	3.99
TC0400873	CENTD1	116984	centaurin, delta 1	2.74E-17	1	4.41	6.29	5.85	5.20	5.17	5.32	5.35	5.13
TC1201326	CENTG1	116986	centaurin, gamma 1 /// Centaurin-gam	1.95E-09	1	5.53	6.23	5.88	5.88	5.93	5.83	5.75	5.66
TC0400243	CEP135	9662	centrosomal protein 135kDa	1.72E-07	1	4.83	5.85	5.74	5.43	5.19	5.17	5.33	5.14

TC0100829	CEPT1	10390	choline/ethanolamine phosphotransfe	1.37E-08	1	4.83	5.55	5.67	5.47	5.32	5.35	5.36	5.24
TC1101553	CFL1	1072	cofilin 1 (non-muscle)	4.18E-08	1	5.58	6.10	6.14	6.15	6.12	5.98	5.84	5.84
TC1400237	CGRRF1	10668	cell growth regulator with ring finger d	3.10E-06	1	3.92	4.48	4.55	4.56	4.47	4.45	4.46	4.40
TC0800312	CHCHD7	79145	coiled-coil-helix-coiled-coil-helix domai	2.81E-19	1	4.85	6.52	6.75	6.13	6.02	5.83	5.87	5.60
TC0900319	CHCHD9	645345	coiled-coil-helix-coiled-coil-helix domai	0.000694	1	4.21	4.60	4.78	4.53	4.55	4.59	4.59	4.64
TC0400954	CHIC2	26511	cysteine-rich hydrophobic domain 2	7.81E-11	1	7.53	8.18	8.35	8.34	8.24	8.27	8.16	8.22
TC0X01071	CHM	1121	choroideremia (Rab escort protein 1) /,	5.53E-11	1	3.65	4.13	4.23	4.04	3.86	3.82	3.85	3.81
TC0300399	CHMP2B	25978	chromatin modifying protein 2B	5.15E-15	1	7.37	8.36	8.46	8.19	8.00	8.19	8.15	8.13
TC2000206	CHMP4B	128866	chromatin modifying protein 4B	3.00E-11	1	8.31	9.00	8.85	8.89	8.86	8.81	8.80	8.75
TC1101740	CHORDC1	26973	cysteine and histidine-rich domain (CH	1.60E-09	1	4.42	5.03	5.41	5.10	5.01	4.86	4.88	4.74
TC1500250	CHP	11261	calcium binding protein P22	7.71E-07	1	7.85	8.60	8.57	8.50	8.40	8.35	8.22	8.26
TC1200634	CHPT1	56994	choline phosphotransferase 1	2.08E-16	1	7.06	8.07	8.40	8.33	8.16	8.10	8.08	8.02
TC0300685	CHST2	9435	carbohydrate (N-acetylglucosamine-6-(	2.65E-11	1	4.44	5.35	5.25	5.22	5.15	5.11	4.94	4.87
TC1501279	CHSY1	651391 //	chondroitin sulfate synthase 1	1.46E-19	1	7.30	8.72	8.28	8.01	7.93	8.06	7.95	7.86
TC1000262	CISD1	55847	CDGSH iron sulfur domain 1	8.06E-06	1	3.10	3.53	3.92	3.75	3.80	3.75	3.79	3.65
TC1201527	CKAP4	10970	cytoskeleton-associated protein 4 /// C	2.54E-20	1	6.71	7.44	7.42	7.36	7.43	7.36	7.26	7.18
TC0301847	CLDN1	9076	claudin 1	0.000303	1	2.91	3.22	3.24	3.08	3.15	3.18	3.09	3.13
TC0301393	CLDND1	56650	claudin domain containing 1	1.67E-08	1	6.22	6.77	6.83	6.60	6.53	6.55	6.55	6.53
TC1200101	CLEC4D	338339	C-type lectin domain family 4, member	1.17E-32	1	5.84	9.38	9.16	8.33	8.24	7.87	7.54	7.32
TC1200943	CLEC4E	26253	C-type lectin domain family 4, member	8.20E-06	1	10.30	10.85	10.63	10.49	10.42	10.38	10.41	10.53
TC0701699	CLEC5A	23601	C-type lectin domain family 5, member	2.92E-19	1	3.30	6.48	6.32	5.77	6.20	5.98	5.50	4.76
TC1200099	CLEC6A	93978	C-type lectin domain family 6, member	1.18E-23	1	3.58	5.35	5.48	4.75	4.48	4.29	4.16	4.12
TC0501453	CLINT1 /// Q14	9685	clathrin interactor 1 /// EPN4_HUMAN	7.91E-05	1	7.77	8.81	8.72	8.69	8.73	8.67	8.62	8.44
TC0400961	CLOCK	9575	clock homolog (mouse)	1.75E-09	1	3.49	3.71	3.81	3.78	3.69	3.57	3.63	3.57
TC0301665	CLRN1	7401	clarin 1 /// Clarin-1 (Usher syndrome ty	5.02E-09	1	2.65	2.79	2.88	3.12	3.03	2.78	2.78	2.64
TC1700646	CLTC	1213	clathrin, heavy chain (Hc)	3.88E-11	1	7.05	7.52	7.61	7.41	7.24	7.13	7.05	7.03
TC0300116	CMC1	152100	COX assembly mitochondrial protein h	1.85E-08	1	3.75	4.12	4.25	4.28	4.20	4.09	4.17	4.03
TC1600501	CMTM1 /// CKI	113540 //	CKLF-like MARVEL transmembrane don	1.38E-06	1	6.85	7.28	7.38	7.36	7.25	7.24	7.14	7.18
TC1600503	CMTM3	123920	CKLF-like MARVEL transmembrane don	1.21E-11	1	5.02	5.49	5.50	5.60	5.46	5.44	5.37	5.44
TC1601159	CMTM4	146223	CKLF-like MARVEL transmembrane don	6.33E-06	1	3.95	4.15	4.23	4.04	4.04	4.02	3.94	3.88
TC0301081	CMTM6	54918	CKLF-like MARVEL transmembrane don	9.54E-08	1	7.07	7.42	7.58	7.46	7.35	7.50	7.46	7.47
TC1400868	CNIH	10175	cornichon homolog (Drosophila)	5.23E-10	1	3.50	3.97	4.17	4.28	4.31	4.06	3.92	3.89
TC0101551	CNIH4	29097	cornichon homolog 4 (Drosophila) /// (	2.74E-35	1	6.59	8.99	9.24	8.92	8.74	8.66	8.49	8.33
TC0701655	CNOT4	4850	CCR4-NOT transcription complex, subu	3.46E-05	1	5.62	6.04	6.08	5.95	5.84	5.92	6.03	5.95

TC0900075	CNTLN /// C9or	54875	centlein, centrosomal protein /// Unch	4.64E-11	1	3.50	4.23	4.39	4.49	4.47	4.45	4.34	4.15
TC1400142	COCH	1690	coagulation factor C homolog, cochlin (	6.37E-05	1	3.40	3.60	3.71	3.62	3.61	3.56	3.54	3.49
TC0501073	COL4A3BP	10087	collagen, type IV, alpha 3 (Goodpasture	7.75E-12	1	7.09	7.72	7.89	7.86	7.69	7.59	7.55	7.40
TC0200276	COMMD1	150684	copper metabolism (Murr1) domain co	3.50E-10	1	4.86	6.24	6.39	6.39	6.42	6.38	6.34	5.97
TC1500494	COMMD4	54939	COMM domain containing 4 /// COMM	1.82E-05	1	5.01	5.49	5.20	5.18	5.27	5.29	5.27	5.12
TC1001085	COMTD1	118881	catechol-O-methyltransferase domain	5.70E-06	1	5.17	5.39	5.42	5.40	5.50	5.46	5.33	5.34
TC0102918	COPA	1314	coatomer protein complex, subunit alp	1.93E-13	1	6.60	7.55	7.39	7.25	7.06	6.90	6.82	6.70
TC1101220	COPB1	1315	coatomer protein complex, subunit bet	4.41E-09	1	6.53	7.23	7.31	7.21	7.05	7.06	7.09	6.97
TC0301609	COPB2	9276	coatomer protein complex, subunit bet	3.34E-10	1	7.54	8.07	8.16	8.10	7.93	7.93	7.91	7.88
TC0400360	COPS4	51138	COP9 constitutive photomorphogenic	8.03E-07	1	3.99	4.88	4.90	4.83	4.94	4.89	4.83	4.70
TC0201215	COPS8	10920	COP9 constitutive photomorphogenic	0.000124	1	3.58	3.88	4.10	4.03	4.00	3.91	3.99	3.92
TC1200388	COPZ1	22818	coatomer protein complex, subunit zet	9.03E-06	1	5.70	6.62	6.43	6.46	6.52	6.37	6.36	6.33
TC0401089	COQ2	27235	coenzyme Q2 homolog, prenyltransfer	6.15E-10	1	5.52	6.28	6.31	6.12	6.05	6.11	6.10	5.85
TC1201630	COQ5	84274	coenzyme Q5 homolog, methyltransfer	1.17E-07	1	4.49	5.39	5.22	5.38	5.53	5.40	5.30	5.05
TC1600222	COQ7	10229	coenzyme Q7 homolog, ubiquinone (ye	1.15E-08	1	4.88	5.67	5.64	5.55	5.42	5.48	5.37	5.40
TC1001213	COX15	1355	COX15 homolog, cytochrome c oxidase	3.09E-14	1	5.56	6.16	6.40	6.24	6.04	5.92	5.93	5.79
TC0801150	COX6C	1345	cytochrome c oxidase subunit VIc	3.00E-08	1	3.96	4.36	4.61	4.50	4.60	4.54	4.52	4.46
TC0601397	COX7A2	1347	cytochrome c oxidase subunit VIIa poly	1.14E-09	1	4.29	4.85	4.91	4.77	4.76	4.78	4.75	4.73
TC0201459	COX7A2L	9167	cytochrome c oxidase subunit VIIa poly	1.28E-16	1	5.19	6.63	6.53	6.40	6.64	6.53	6.29	6.08
TC0500326	COX7C	1350	cytochrome c oxidase subunit VIIc	3.77E-17	1	5.52	6.74	6.80	6.65	6.71	6.73	6.61	6.52
TC1100501	COX8A	1351	cytochrome c oxidase subunit 8A (ubiq	1.10E-11	1	7.31	8.35	8.46	8.50	8.62	8.44	8.41	8.24
TC1600228	CP110 /// CE11	9738	CP110 protein /// Centrosomal protein	1.19E-05	1	4.56	5.23	5.09	4.94	4.79	4.82	4.97	4.90
TC0500719	CPEB4	80315	cytoplasmic polyadenylation element	1.52E-10	1	7.94	8.55	8.27	8.18	8.08	7.98	7.90	7.80
TC0601216	CPNE5	57699	copine V	1.27E-19	1	3.62	4.36	4.27	3.92	3.84	3.81	3.72	3.66
TC1201104	CPNE8	144402	copine VIII /// Copine-8 (Copine VIII). [	9.56E-06	1	2.97	3.20	3.29	3.33	3.16	3.06	3.15	3.06
TC0200026	CPSF3	51692	cleavage and polyadenylation specific f	6.95E-14	1	4.31	5.24	5.49	5.50	5.54	5.44	5.44	5.18
TC1101613	CPT1A	1374	carnitine palmitoyltransferase 1A (liver	0.000272	1	4.91	5.26	5.44	5.44	5.50	5.25	5.41	5.25
TC0101475	CR1	1378	complement component (3b/4b) recep	2.25E-15	1	8.82	9.60	9.82	9.82	9.47	9.15	9.03	8.87
TC0101476	CR1L /// CR1	1379 /// 1	complement component (3b/4b) recep	1.66E-14	1	4.23	4.72	4.94	4.85	4.63	4.50	4.46	4.37
TC0300962	CRBN	51185	cereblon	5.49E-16	1	5.97	7.09	7.37	7.09	6.90	6.89	6.81	6.66
TC1000157	CREM	1390	cAMP responsive element modulator /	1.87E-16	1	3.50	4.61	4.15	3.99	3.93	3.89	3.83	3.81
TC1400637	CRIP2	1397	cysteine-rich protein 2	1.49E-05	1	4.84	5.10	5.08	5.04	5.09	5.07	4.98	5.00
TC0601314	CRISP3	10321	cysteine-rich secretory protein 3	1.86E-17	1	4.00	8.91	7.29	7.33	8.18	8.40	7.71	6.83
TC2000063	CRLS1	54675	cardiolipin synthase 1 /// Cardiolipin sy	9.46E-11	1	4.15	5.31	5.60	5.38	5.58	5.29	5.06	4.81

TC0700452	CROT	54677	carnitine O-octanoyltransferase	0.000382	1	2.67	2.68	2.80	2.78	2.69	2.64	2.75	2.73
TC1500627	CRTC3	64784	CREB regulated transcription coactivat	7.08E-16	1	4.48	5.47	5.14	4.80	4.65	4.61	4.64	4.61
TC0800779	CSGALNACT1 /	55790	chondroitin sulfate N-acetylgalactosam	1.69E-06	1	4.86	5.64	5.54	5.62	5.75	5.61	5.49	5.20
TC0501395	CSNK1A1	1452	casein kinase 1, alpha 1	2.43E-06	1	6.63	7.19	7.05	7.09	6.93	7.17	7.04	7.05
TC1300405	CSNK1A1L	122011	casein kinase 1, alpha 1-like	2.48E-09	1	5.44	5.88	6.01	5.62	5.39	5.50	5.36	5.21
TC1601134	CSNK2A2	1459	casein kinase 2, alpha prime polypepti	7.86E-19	1	4.97	6.66	6.53	6.55	6.43	6.22	6.26	6.03
TC2000142	CST7	8530	cystatin F (leukocystatin)	6.83E-36	1	7.50	10.33	10.75	10.69	10.49	10.07	9.94	9.37
TC1000987	CSTF2T	23283	cleavage stimulation factor, 3' pre-RNA	3.96E-09	1	3.79	4.36	4.08	3.95	3.83	3.79	3.83	3.91
TC1800278	CTDP1	9150	CTD (carboxy-terminal domain, RNA p	2.23E-08	1	5.28	5.75	5.58	5.50	5.45	5.36	5.35	5.33
TC0500512	CTNNA1	1495	catenin (cadherin-associated protein),	4.21E-05	1	5.46	6.09	5.87	5.86	5.68	5.66	5.70	5.59
TC0300189	CTNNB1	1499	catenin (cadherin-associated protein),	1.94E-06	1	6.68	6.99	7.07	7.01	6.85	6.79	6.77	6.72
TC2000246	CTNNBL1	56259	catenin, beta like 1 /// Beta-catenin-lik	0.000394	1	5.14	5.73	5.67	5.61	5.55	5.54	5.59	5.60
TC1100176	CTR9	9646	Ctr9, Paf1/RNA polymerase II complex	6.37E-05	1	5.91	6.55	6.55	6.42	6.22	6.28	6.42	6.33
TC0800746	CTSB	1508	cathepsin B	0.000688	1	5.20	5.69	5.69	5.93	5.72	5.53	5.61	5.59
TC1101065	CTSD	1509	cathepsin D	1.36E-07	1	6.21	7.07	7.00	7.38	7.48	7.14	6.92	6.86
TC1501149	CTSH	1512	cathepsin H	1.64E-28	1	4.32	6.08	5.44	5.31	5.27	4.78	4.59	4.45
TC0900351	CTSL1	1514	cathepsin L1 /// Cathepsin L precursor	4.41E-05	1	4.35	4.59	4.68	4.73	4.57	4.44	4.43	4.29
TC1001244	CUEDC2	79004	CUE domain containing 2	5.06E-06	1	4.78	5.05	5.22	5.29	5.21	5.10	5.19	5.08
TC1000882	CUL2	8453	cullin 2 /// Cullin-2 (CUL-2). [Source:Un	2.36E-05	1	4.53	5.07	5.11	5.08	5.04	5.07	5.07	5.01
TC1000503	CUTC	51076	cutC copper transporter homolog (E. c	1.58E-10	1	6.40	6.96	7.20	7.11	6.87	6.75	6.74	6.68
TC0700570	CUX1 /// CUTL	1523	cut-like homeobox 1 /// Protein CASP.	3.06E-07	1	5.95	6.54	6.46	6.48	6.47	6.33	6.30	6.20
TC1001219	CWF19L1	55280	CWF19-like 1, cell cycle control (S. pom	0.000349	1	5.19	5.60	5.69	5.58	5.46	5.32	5.44	5.33
TC1700939	CXCL16	58191	chemokine (C-X-C motif) ligand 16	8.91E-07	1	6.89	7.92	7.62	7.76	7.68	7.68	7.39	7.55
TC0X00094	CXorf58	254158	chromosome X open reading frame 58	8.63E-08	1	2.09	2.35	2.31	2.22	2.15	2.10	2.12	2.12
TC0103136	CYB5R1	51706	cytochrome b5 reductase 1	3.75E-12	1	4.88	5.10	5.52	5.46	5.35	5.15	5.05	4.98
TC2200728	CYB5R3	1727	cytochrome b5 reductase 3	2.16E-09	1	5.57	6.26	6.24	6.29	6.29	6.08	6.01	5.97
TC0X00142	CYBB	1536	cytochrome b-245, beta polypeptide (c	2.20E-09	1	8.02	9.83	9.55	9.53	9.74	9.68	9.37	9.18
TC0800619	CYC1	1537	cytochrome c-1	2.00E-08	1	4.49	4.99	5.11	5.04	5.02	4.85	4.77	4.68
TC1500019	CYFIP1	23191	cytoplasmic FMR1 interacting protein 1	0.000795	1	3.73	3.91	3.86	4.00	3.89	3.80	3.83	3.74
TC0500643	CYFIP2	26999	cytoplasmic FMR1 interacting protein	1.24E-05	1	7.16	7.97	7.64	7.73	7.72	7.63	7.54	7.46
TC1500957	CYP19A1	1588	cytochrome P450, family 19, subfamily	4.14E-13	1	2.54	2.59	2.95	2.76	2.68	2.55	2.51	2.50
TC0201439	CYP1B1	1545	cytochrome P450, family 1, subfamily	6.71E-20	1	3.35	4.54	4.99	5.25	4.67	4.02	3.84	3.75
TC0201304	CYS1	192668	cystin 1	0.000392	1	5.38	5.69	5.70	5.68	5.70	5.61	5.52	5.59
TC2100251	CYYR1	116159	cysteine/tyrosine-rich 1	7.23E-05	1	4.18	4.55	4.75	4.63	4.76	4.75	4.69	4.44

TC1300539	DACH1	1602	dachshund homolog 1 (Drosophila) ///	1.28E-16	1	4.87	6.23	6.37	6.70	6.50	6.17	6.13	5.78
TC1100462	DAGLA	747	diacylglycerol lipase, alpha	0.000534	1	4.40	4.54	4.57	4.45	4.51	4.47	4.46	4.45
TC0201959	DARS	1615	aspartyl-tRNA synthetase	8.07E-15	1	5.16	6.63	6.58	6.53	6.64	6.64	6.49	6.33
TC0700218	DBNL	28988	drebrin-like	3.02E-06	1	6.33	6.75	6.63	6.54	6.48	6.38	6.25	6.32
TC0500398	DCP2	167227	DCP2 decapping enzyme homolog (S. c	0.000146	1	7.99	8.30	8.48	8.41	8.26	8.32	8.20	8.20
TC1100989	DCPS	28960	decapping enzyme, scavenger	9.90E-05	1	4.85	5.26	5.27	5.21	5.34	5.28	5.28	5.09
TC1201324	DCTN2	10540	dynactin 2 (p50)	8.10E-07	1	6.53	7.07	7.11	7.13	7.05	6.97	6.88	6.80
TC0800185	DCTN6	10671	dynactin 6	2.21E-13	1	4.56	5.91	5.42	5.35	5.32	5.22	5.22	5.22
TC1600925	DCUN1D3	123879	DCN1, defective in cullin neddylation 1,	1.55E-07	1	4.47	5.35	5.06	5.10	4.88	4.82	4.75	4.87
TC0601132	DDAH2 /// CLI	23564 ///	dimethylarginine dimethylaminohydrol	6.01E-08	1	5.87	6.34	6.39	6.42	6.33	6.16	6.00	6.01
TC1000328	DDIT4	54541	DNA-damage-inducible transcript 4	5.40E-05	1	3.86	4.35	4.17	4.14	4.12	4.13	4.02	4.08
TC1600564	DDX19A /// DD	55308 ///	DEAD (Asp-Glu-Ala-As) box polypeptide	0.000139	1	4.70	5.14	4.91	4.91	4.99	4.94	5.02	4.90
TC1700681	DDX42	11325	DEAD (Asp-Glu-Ala-Asp) box polypeptic	5.49E-09	1	6.05	6.79	6.57	6.37	6.26	6.24	6.31	6.19
TC0103110	DDX59	83479	DEAD (Asp-Glu-Ala-Asp) box polypeptic	3.73E-08	1	5.95	6.26	6.57	6.48	6.36	6.38	6.40	6.27
TC0102933	DEDD	9191	death effector domain containing /// D	9.46E-06	1	5.82	6.22	6.16	6.16	6.01	6.00	5.89	5.95
TC0800676	DEFA5	1670	defensin, alpha 5, Paneth cell-specific	3.43E-05	1	4.55	4.82	4.73	4.63	4.64	4.61	4.56	4.47
TC2000653	DEFB121	245934	defensin, beta 121 /// Beta-defensin 1	5.06E-05	1	2.44	2.96	2.89	2.68	2.76	2.68	2.64	2.83
TC0101547	DEGS1	8560	degenerative spermatocyte homolog 1,	2.82E-14	1	6.10	6.77	6.80	6.59	6.69	6.72	6.65	6.65
TC0103098	DENND1B	163486 //	DENN/MADD domain containing 1B ///	5.02E-10	1	4.08	4.86	4.77	4.87	4.64	4.65	4.73	4.70
TC0102537	DENND2D	79961	DENN/MADD domain containing 2D //	6.03E-11	1	4.86	5.33	5.26	5.00	5.12	5.04	5.00	4.96
TC1200170	DERA	51071	2-deoxyribose-5-phosphate aldolase h	1.31E-10	1	4.00	4.50	4.75	4.80	4.66	4.60	4.66	4.49
TC1700957	DERL2	51009	Der1-like domain family, member 2	9.07E-05	1	5.61	5.86	6.05	5.90	5.85	5.94	6.01	5.97
TC1100678	DGAT2	84649	diacylglycerol O-acyltransferase homol	8.13E-06	1	6.35	6.92	6.92	6.81	6.64	6.64	6.49	6.50
TC0201200	DGKD	8527	diacylglycerol kinase, delta 130kDa	2.21E-10	1	5.64	6.43	6.35	6.39	6.42	6.15	6.19	5.99
TC0200350	DGUOK	1716	deoxyguanosine kinase /// Deoxyguan	5.76E-05	1	5.81	6.29	6.23	6.22	6.14	6.11	6.19	6.15
TC1101627	DHCR7	1717	7-dehydrocholesterol reductase	1.52E-11	1	4.40	5.53	5.08	4.88	5.06	4.84	4.59	4.52
TC0301384	DHFRL1	200895	dihydrofolate reductase-like 1	4.76E-07	1	3.61	3.70	3.93	3.97	3.90	3.76	3.72	3.82
TC1400895	DHRS7	51635	dehydrogenase/reductase (SDR family)	4.38E-09	1	8.31	8.43	8.77	8.69	8.63	8.58	8.55	8.55
TC1700252	DHRS7B	25979	dehydrogenase/reductase (SDR family)	0.000197	1	4.62	4.98	5.05	4.95	4.90	4.86	4.88	4.84
TC0200838	DHRS9	10170	dehydrogenase/reductase (SDR family)	0.000102	1	5.40	5.68	6.16	5.51	5.33	5.31	5.48	5.60
TC0Y00113	DHRSX /// ZBE	207063 //	dehydrogenase/reductase (SDR family)	0.000198	1	6.44	6.72	6.56	6.51	6.47	6.51	6.49	6.60
TC0X00733	DHRSX /// ZBE	207063 //	dehydrogenase/reductase (SDR family)	0.000768	1	6.08	6.38	6.25	6.21	6.18	6.21	6.19	6.28
TC0301682	DHX36	170506	DEAH (Asp-Glu-Ala-His) box polypeptid	9.22E-10	1	5.36	6.55	6.43	6.26	6.11	6.13	6.23	6.04
TC0501360	DIAPH1	1729	diaphanous homolog 1 (Drosophila) ///	0.000284	1	7.01	7.39	7.14	7.14	7.07	7.01	6.97	6.96

TC0X00410	DIAPH2	1730	diaphanous homolog 2 (Drosophila) ///	4.65E-12	1	3.72	5.05	5.03	5.27	5.20	5.00	5.00	4.68
TC0300558	DIRC2	84925	disrupted in renal carcinoma 2 /// Disru	2.06E-13	1	6.59	7.44	7.44	7.31	7.14	7.00	6.80	6.66
TC1101551	DKFZp761E198	91056	DKFZp761E198 protein	3.94E-05	1	5.77	6.19	6.08	6.03	6.07	6.08	6.03	6.05
TC0800765	DLC1	10395	deleted in liver cancer 1	3.11E-14	1	3.07	3.13	3.46	3.18	3.12	3.06	3.02	3.03
TC0700612	DLD	1738	dihydrolipoamide dehydrogenase	2.66E-08	1	6.41	7.20	7.21	7.02	6.98	6.98	6.96	6.83
TC2000234	DLGAP4	22839	discs, large (Drosophila) homolog-asso	0.000703	1	5.44	5.61	5.57	5.56	5.51	5.45	5.45	5.46
TC0900122	DNAJA1	3301	DnaJ (Hsp40) homolog, subfamily A, me	1.30E-05	1	8.29	8.74	8.76	8.70	8.54	8.69	8.70	8.77
TC1601076	DNAJA2	10294	DnaJ (Hsp40) homolog, subfamily A, me	6.56E-20	1	6.42	7.07	7.17	7.19	7.07	7.00	6.91	6.95
TC0300871	DNAJB11	51726	DnaJ (Hsp40) homolog, subfamily B, me	5.33E-07	1	6.40	7.44	7.08	7.00	6.98	6.97	7.12	6.98
TC0300627	DNAJC13	23317	DnaJ (Hsp40) homolog, subfamily C, me	3.88E-09	1	5.69	6.60	6.94	6.82	6.87	6.65	6.65	6.22
TC0100166	DNAJC16	23341	DnaJ (Hsp40) homolog, subfamily C, me	3.98E-05	1	4.41	4.82	4.79	4.73	4.70	4.64	4.63	4.58
TC1100508	DNAJC4	3338	DnaJ (Hsp40) homolog, subfamily C, me	9.10E-20	1	4.51	4.92	4.96	5.01	4.91	4.69	4.63	4.61
TC2000468	DNAJC5	80331	DnaJ (Hsp40) homolog, subfamily C, me	1.47E-13	1	6.08	6.76	6.63	6.64	6.68	6.53	6.38	6.30
TC0X01383	DNASE1L1	1774	deoxyribonuclease I-like 1	3.18E-06	1	5.30	5.42	5.55	5.50	5.46	5.41	5.33	5.32
TC1001215	DNMBP	23268	dynamin binding protein /// Dynamin-	7.05E-05	1	4.06	4.68	4.17	4.22	4.38	4.34	4.33	4.17
TC0102451	DNTTIP2	30836	deoxynucleotidyltransferase, terminal,	5.94E-11	1	5.68	6.82	6.70	6.53	6.38	6.29	6.38	6.28
TC1300609	DOCK9	23348	dedicator of cytokinesis 9 /// Dedicato	2.36E-06	1	3.23	3.64	3.57	3.38	3.41	3.30	3.29	3.21
TC1900052	DOT1L	84444	DOT1-like, histone H3 methyltransferas	4.86E-06	1	4.74	5.18	4.98	4.96	5.06	4.94	4.92	4.86
TC0102487	DPH5	51611	DPH5 homolog (S. cerevisiae) /// Proba	9.45E-22	1	3.76	4.74	4.91	4.50	4.32	4.13	4.12	3.93
TC0301434	DPPA2	151871	developmental pluripotency associate	0.000401	1	2.29	2.39	2.46	2.31	2.33	2.30	2.25	2.29
TC1900402	DPY19L3	147991	dpy-19-like 3 (C. elegans) /// dpy-19-lik	4.90E-17	1	4.37	5.19	5.82	5.24	5.07	4.89	4.79	4.55
TC0201416	DPY30 /// ME	732129 //	dpy-30 homolog (C. elegans) /// media	2.89E-08	1	5.61	5.97	6.05	6.03	6.00	5.96	5.94	5.93
TC0102472	DPYD	1806	dihydropyrimidine dehydrogenase ///	1.26E-12	1	6.92	7.39	7.55	7.31	7.05	7.00	6.96	6.85
TC0100736	DR1	1810	down-regulator of transcription 1, TBP-	5.83E-22	1	5.79	6.69	6.91	6.81	6.75	6.64	6.57	6.54
TC1200639	DRAM	55332	damage-regulated autophagy modulat	1.97E-21	1	5.24	6.52	6.93	6.82	6.57	6.35	6.25	6.10
TC0600661	DSE	29940	dermatan sulfate epimerase	1.44E-17	1	5.34	6.28	6.47	6.30	6.04	5.91	5.76	5.56
TC0600966	DTNBP1	84062	dystrobrevin binding protein 1 /// Dys	4.06E-07	1	5.37	6.08	6.06	5.89	5.65	5.79	5.86	5.79
TC1200998	DUSP16	80824	dual specificity phosphatase 16 /// Dua	2.46E-06	1	6.05	6.63	6.66	6.73	6.60	6.48	6.30	6.26
TC0600002	DUSP22	56940	dual specificity phosphatase 22	1.05E-09	1	6.47	6.88	6.85	6.84	6.74	6.66	6.60	6.52
TC1701408	DUSP3	1845	dual specificity phosphatase 3	2.89E-05	1	4.57	5.34	5.27	5.41	5.24	5.28	5.30	5.26
TC1800465	DYM	54808	dymeclin	4.94E-11	1	5.61	6.22	6.26	6.05	6.02	5.90	5.89	5.85
TC0200859	DYNC1I2	1781	dynein, cytoplasmic 1, intermediate ch	1.12E-18	1	4.42	6.65	6.59	6.10	6.21	6.05	5.98	5.60
TC0200208	DYNC2LI1	51626	dynein, cytoplasmic 2, light intermedia	2.00E-12	1	2.37	2.88	3.19	2.96	2.85	2.53	2.53	2.44
TC0X00845	DYNLT3	6990	dynein, light chain, Tctex-type 3 /// Dy	7.22E-24	1	4.49	6.24	5.68	5.36	5.35	5.24	5.22	5.23

TC1200034	DYRK4	8798	dual-specificity tyrosine-(Y)-phosphoryl	6.15E-05	1	2.92	3.18	3.28	3.04	3.14	3.15	3.06	2.99
TC0200337	DYSF	8291	dysferlin, limb girdle muscular dystroph	3.56E-12	1	7.56	8.45	8.51	8.42	8.23	7.86	7.71	7.58
TC0300483	DZIP3	9666	DAZ interacting protein 3, zinc finger	5.85E-06	1	2.92	3.01	3.20	3.11	3.01	2.95	2.98	2.99
TC0101979	E2F2	1870	E2F transcription factor 2	1.32E-08	1	4.91	5.53	5.33	5.23	5.31	5.20	5.06	4.92
TC0600112	E2F3	1871	E2F transcription factor 3 /// Transcript	5.25E-05	1	6.60	7.20	7.16	7.20	7.13	7.12	6.91	6.86
TC0300546	EAF2	55840	ELL associated factor 2	6.82E-10	1	4.98	5.90	6.30	6.27	6.22	6.18	6.15	5.92
TC2000029	EBF4	57593	early B-cell factor 4 /// early B-cell fact	0.000986	1	4.52	4.70	4.68	4.65	4.68	4.65	4.57	4.61
TC1300482	EBPL	84650	emopamil binding protein-like /// Emo	7.41E-17	1	4.36	4.99	5.32	5.09	4.98	4.92	4.93	4.67
TC1000054	ECHDC3	79746	enoyl Coenzyme A hydratase domain c	0.000347	1	4.31	4.65	4.57	4.46	4.43	4.42	4.41	4.39
TC0701215	ECOP /// NM_	81552	EGFR-coamplified and overexpressed p	4.96E-12	1	5.31	5.69	5.80	5.82	5.70	5.58	5.58	5.56
TC1201448	EEA1	8411	early endosome antigen 1	8.30E-09	1	4.31	5.26	5.48	5.37	5.28	5.18	5.42	5.11
TC1100724	EED	8726	embryonic ectoderm development ///	9.16E-05	1	3.84	4.22	4.38	4.30	4.34	4.35	4.39	4.19
TC0801314	EEF1D	1936	eukaryotic translation elongation facto	7.10E-07	1	6.08	6.42	6.32	6.25	6.29	6.30	6.25	6.24
TC0100614	EFCAB7	84455	EF-hand calcium binding domain 7	0.00087	1	2.96	3.31	3.29	3.40	3.38	3.32	3.23	3.19
TC1300334	EFHA1	221154	EF-hand domain family, member A1	8.71E-06	1	4.78	5.28	5.30	5.17	4.96	5.07	5.19	5.16
TC0X00869	EFHC2	80258	EF-hand domain (C-terminal) containin	0.000279	1	3.19	3.59	3.25	2.99	3.25	3.42	3.36	3.32
TC0100163	EFHD2	79180	EF-hand domain family, member D2 //	7.65E-06	1	7.45	7.91	8.01	8.11	8.01	8.03	7.92	7.94
TC0500509	EGR1	1958	early growth response 1	2.11E-05	1	5.03	6.80	6.31	6.46	6.82	6.81	6.48	6.53
TC0300181	EIF1B	10289	eukaryotic translation initiation factor	1.70E-08	1	7.08	7.83	8.00	7.82	7.67	7.72	7.72	7.70
TC0201431	EIF2AK2	5610	eukaryotic translation initiation factor	4.45E-08	1	6.52	7.81	7.38	7.09	7.14	7.45	7.66	7.61
TC1400374	EIF2B2	8892	eukaryotic translation initiation factor	2.90E-06	1	4.43	4.91	4.97	5.03	4.98	4.88	4.85	4.77
TC2000676	EIF2S2	8894	eukaryotic translation initiation factor	1.96E-05	1	6.42	7.01	6.93	6.94	6.91	6.93	7.01	6.87
TC1100149	EIF3F	8665	eukaryotic translation initiation factor	4.36E-08	1	5.26	6.19	6.11	6.21	6.23	6.18	6.24	6.04
TC0100357	EIF3I	8668	eukaryotic translation initiation factor	1.30E-09	1	4.89	6.04	5.71	5.65	5.90	5.65	5.59	5.32
TC0301340	EIF4E3	317649	eukaryotic translation initiation factor	7.02E-09	1	7.29	7.89	7.91	7.95	7.84	7.78	7.62	7.64
TC1101206	EIF4G2	1982	eukaryotic translation initiation factor	0.000867	1	8.30	8.48	8.57	8.59	8.53	8.52	8.51	8.50
TC0101960	EIF4G3	8672	eukaryotic translation initiation factor	6.34E-07	1	6.59	7.49	7.25	7.12	7.15	7.09	7.19	6.98
TC2000693	EIF6	3692	eukaryotic translation initiation factor	5.97E-08	1	4.56	5.11	5.20	5.12	5.08	5.02	5.00	4.99
TC2000798	ELMO2	63916	engulfment and cell motility 2 /// Engu	1.12E-06	1	6.00	6.73	6.74	6.64	6.39	6.32	6.41	6.25
TC0500969	EMB	133418	embigin homolog (mouse)	1.35E-31	1	5.62	7.75	7.89	7.79	7.85	7.63	7.33	6.99
TC1800015	EMILIN2	84034	elastin microfibril interfacer 2 /// EMIL	7.65E-19	1	5.16	5.70	5.99	6.08	5.96	5.74	5.65	5.49
TC1901600	EML2	24139	echinoderm microtubule associated pr	0.000281	1	4.81	4.99	4.99	4.94	4.93	4.91	4.88	4.85
TC1900120	EMR1	2015	egf-like module containing, mucin-like,	4.05E-05	1	7.05	8.05	7.98	8.15	7.69	7.32	7.54	7.39
TC0101830	ENO1	2023	enolase 1, (alpha)	6.09E-24	1	6.70	8.48	8.72	8.81	8.69	8.21	7.96	7.56

TC0600431	ENPP4	22875	ectonucleotide pyrophosphatase/phos	6.34E-08	1	3.70	5.21	4.87	4.81	5.32	5.06	4.87	4.37
TC0102725	ENSA	2029	endosulfine alpha /// Alpha-endosulfin	2.38E-07	1	5.88	6.37	6.24	6.19	6.22	6.19	6.29	6.19
TC1000502	ENTPD7	57089	ectonucleoside triphosphate diphosph	1.25E-24	1	4.58	6.90	7.31	6.32	6.05	5.44	5.27	4.98
TC0800500	ENY2	56943	enhancer of yellow 2 homolog (Drosop	2.17E-12	1	7.01	7.94	8.07	7.79	7.86	7.82	7.74	7.63
TC0102250	EPS15	2060	epidermal growth factor receptor path	1.86E-10	1	6.78	7.37	7.38	7.25	7.17	7.19	7.20	7.16
TC0700234	EPS15L2	---	---	0.000534	1	2.26	2.68	2.78	2.56	2.63	2.63	2.70	2.72
TC1700631	EPX	8288	eosinophil peroxidase	3.07E-05	1	3.79	4.13	3.88	3.86	3.97	3.86	3.80	3.84
TC1200008	ERC1	23085	ELKS/RAB6-interacting/CAST family me	9.65E-05	1	5.36	5.72	5.60	5.85	5.80	5.60	5.74	5.54
TC1201070	ERGIC2	51290	ERGIC and golgi 2 /// Endoplasmic retic	4.71E-09	1	6.82	7.73	7.78	7.64	7.52	7.67	7.49	7.37
TC1400950	ERH	2079	enhancer of rudimentary homolog (Dro	4.80E-09	1	6.02	6.45	7.00	6.79	6.70	6.53	6.60	6.43
TC1001218	ERLIN1 /// CHU	10613 ///	ER lipid raft associated 1 /// conserved	9.65E-14	1	5.79	6.91	6.80	6.64	6.51	6.53	6.54	6.39
TC0800220	ERLIN2	11160	ER lipid raft associated 2	5.12E-08	1	4.63	5.06	5.53	5.20	5.16	5.10	5.15	5.01
TC0100454	ERMAP	114625	erythroblast membrane-associated pro	2.99E-06	1	3.91	4.00	4.07	4.09	4.11	3.99	4.00	3.89
TC1400862	ERO1L	30001	ERO1-like (S. cerevisiae)	0.000137	1	6.97	7.66	7.82	7.61	7.52	7.62	7.53	7.38
TC1300464	ESD	2098	esterase D/formylglutathione hydrolas	4.67E-23	1	4.21	5.61	5.92	5.87	5.88	5.69	5.64	5.42
TC0501324	ETF1	2107	eukaryotic translation termination fact	2.73E-10	1	6.10	7.01	6.68	6.64	6.65	6.57	6.49	6.48
TC0400640	ETFDH	2110	electron-transferring-flavoprotein deh	0.000704	1	4.31	4.64	4.75	4.65	4.69	4.52	4.58	4.44
TC1200192	ETNK1	55500	ethanolamine kinase 1 /// Ethanolamir	7.23E-09	1	4.58	5.09	5.11	5.00	4.83	4.83	4.83	4.82
TC2100125	ETS2	2114	v-ets erythroblastosis virus E26 oncoge	3.94E-24	1	6.86	8.40	8.14	8.15	7.92	7.68	7.49	7.29
TC0600894	EXOC2	55770	exocyst complex component 2	3.68E-06	1	3.99	4.53	4.43	4.50	4.40	4.29	4.32	4.13
TC1400882	EXOC5	648110 //	exocyst complex component 5	4.82E-14	1	5.13	6.27	6.34	6.30	6.22	6.21	6.24	6.02
TC1000449	EXOC6 /// Q6Z	54536	exocyst complex component 6 /// Exoc	1.03E-19	1	6.45	7.34	7.74	7.54	7.25	7.17	7.10	6.96
TC0900917	EXOSC3	51010	exosome component 3	8.82E-11	1	5.43	6.42	6.37	6.28	6.43	6.52	6.43	6.28
TC0800617	EXOSC4	54512	exosome component 4	4.86E-23	1	5.40	6.96	7.16	6.83	6.68	6.13	5.84	5.66
TC0801208	EXT1	2131	exostoses (multiple) 1	4.42E-21	1	4.83	6.56	6.82	6.64	5.94	5.92	5.88	5.56
TC0601718	EZR /// VIL2	7430	ezrin /// Ezrin (p81) (Cytovillin) (Villin-2	2.78E-10	1	5.84	6.84	6.60	6.73	6.75	6.72	6.70	6.52
TC0102460	F3	2152	coagulation factor III (thromboplastin,	8.15E-05	1	3.33	3.60	3.56	3.44	3.51	3.45	3.34	3.47
TC0102980	F5	2153	coagulation factor V (proaccelerin, labi	5.86E-08	1	6.74	8.03	7.91	7.99	7.65	7.39	7.35	7.15
TC0X01399	F8	2157	coagulation factor VIII, procoagulant c	2.86E-08	1	2.94	2.98	3.14	3.03	2.99	2.97	2.88	2.95
TC0X01404	F8A1	8263	coagulation factor VIII-associated (intr	1.63E-14	1	7.21	7.87	8.09	8.01	8.03	7.96	8.04	7.93
TC0X00721	F8A1	8263	coagulation factor VIII-associated (intr	5.84E-07	1	7.61	8.00	8.30	8.17	8.22	8.15	8.20	8.12
TC0401217	FABP2	2169	fatty acid binding protein 2, intestinal	2.60E-05	1	2.46	3.08	3.58	3.41	3.22	2.80	2.84	2.65
TC0300655	FAIM	55179	Fas apoptotic inhibitory molecule	0.000511	1	2.64	2.73	2.83	2.79	2.84	2.75	2.74	2.71
TC1700875	FAM101B	359845	family with sequence similarity 101, m	4.48E-09	1	5.89	7.20	6.69	7.01	7.36	7.14	6.82	6.73

TC0100788	FAM102B	284611	family with sequence similarity 102, me	5.41E-14	1	4.24	5.83	5.52	5.72	5.67	5.31	5.28	5.00
TC0X00961	FAM104B	90736	family with sequence similarity 104, me	1.40E-05	1	4.96	5.24	5.32	5.34	5.31	5.32	5.30	5.27
TC0500055	FAM105A	54491	family with sequence similarity 105, me	5.87E-21	1	5.15	6.72	7.00	6.55	6.62	6.17	5.96	5.65
TC1000778	FAM107B	83641	family with sequence similarity 107, me	5.36E-10	1	5.72	6.26	6.32	6.34	6.40	6.26	6.18	6.08
TC1500544	FAM108C1	58489	family with sequence similarity 108, me	6.66E-08	1	3.43	4.73	4.30	4.31	4.43	4.44	4.38	4.01
TC0800323	FAM110B	90362	family with sequence similarity 110, me	2.93E-06	1	4.17	4.53	4.50	4.45	4.44	4.42	4.31	4.38
TC1200275	FAM113B	91523	family with sequence similarity 113, me	1.40E-08	1	3.72	3.99	4.08	3.82	3.84	3.86	3.82	3.78
TC0501435	FAM114A2	10827	family with sequence similarity 114, me	1.48E-09	1	4.00	4.90	4.93	4.67	4.62	4.62	4.66	4.58
TC0700825	FAM115C	285966	family with sequence similarity 115, me	3.32E-09	1	5.11	5.49	5.43	5.41	5.16	5.17	5.16	5.15
TC0900281	FAM122A	116224	family with sequence similarity 122A	4.13E-05	1	5.00	5.44	5.63	5.54	5.50	5.57	5.46	5.39
TC0900567	FAM125B	89853	family with sequence similarity 125, me	3.11E-14	1	4.06	4.89	4.86	4.90	5.02	4.81	4.74	4.46
TC0202217	FAM126B	285172	family with sequence similarity 126, me	4.35E-05	1	8.10	8.44	8.47	8.56	8.39	8.29	8.18	8.16
TC0X00579	FAM127A	8933	family with sequence similarity 127, me	1.98E-08	1	4.48	5.78	5.85	5.77	5.75	5.46	5.73	5.44
TC0X01274	FAM127B	26071	family with sequence similarity 127, me	0.000577	1	4.21	4.41	4.53	4.48	4.57	4.48	4.52	4.39
TC1201207	FAM130A1	81566	family with sequence similarity 130, me	0.000722	1	4.91	5.09	5.14	5.15	5.07	5.04	5.10	5.07
TC0500867	FAM134B	54463	family with sequence similarity 134, me	4.83E-08	1	3.64	4.02	4.13	4.19	4.08	3.79	3.76	3.80
TC1701384	FAM134C	162427	family with sequence similarity 134, me	2.39E-07	1	5.70	6.16	6.13	6.11	6.07	6.01	5.91	5.89
TC1401091	FAM14A	83982	family with sequence similarity 14, mer	8.22E-08	1	5.57	5.97	5.98	6.06	6.21	5.97	5.96	5.94
TC0201265	FAM150B /// N	285016	family with sequence similarity 150, me	7.32E-05	1	4.08	4.31	4.33	4.29	4.31	4.25	4.21	4.23
TC0500308	FAM151B	167555	family with sequence similarity 151, me	2.73E-07	1	4.74	5.11	5.49	5.55	5.62	5.18	5.21	4.93
TC1101150	FAM160A2	84067	family with sequence similarity 160, me	1.15E-10	1	5.72	6.09	6.11	6.03	6.09	5.81	5.74	5.65
TC1000604	FAM160B1 ///	57700	family with sequence similarity 160, me	7.28E-06	1	6.84	7.30	7.40	7.39	7.20	7.21	7.14	7.15
TC0501144	FAM172A	83989	family with sequence similarity 172, me	1.18E-15	1	5.18	6.05	6.24	6.08	5.79	5.72	5.72	5.47
TC1600032	FAM173A	65990	family with sequence similarity 173, me	5.30E-05	1	5.37	5.60	5.70	5.64	5.62	5.61	5.60	5.60
TC1700196	FAM18B	51030	family with sequence similarity 18, mer	0.00084	1	5.11	5.43	5.63	5.57	5.42	5.45	5.54	5.63
TC0X00564	FAM45B	55855	family with sequence similarity 45, mer	7.79E-06	1	5.14	5.69	5.92	5.75	5.46	5.56	5.67	5.70
TC0300462	FAM55C	91775	family with sequence similarity 55, mer	3.33E-08	1	4.81	5.54	5.64	5.45	5.47	5.36	5.22	5.17
TC1700006	FAM57A	79850	family with sequence similarity 57, mer	1.24E-05	1	4.25	4.55	4.57	4.63	4.63	4.66	4.52	4.51
TC1500370	FAM63B	54629	family with sequence similarity 63, mer	6.39E-08	1	4.67	5.42	5.83	5.72	5.46	5.34	5.36	5.14
TC1300671	FAM70B	348013	family with sequence similarity 70, mer	1.30E-05	1	4.91	5.17	5.17	5.04	5.09	5.05	5.02	4.97
TC0801095	FAM82B	51115	family with sequence similarity 82, mer	2.17E-10	1	5.02	5.99	6.19	5.95	5.88	5.85	5.95	5.79
TC1600829	FAM86B2 /// F	653333 //	family with sequence similarity 86, mer	0.000303	1	4.72	5.09	5.04	5.04	5.02	5.04	4.97	5.02
TC0103344	FAM89A	375061	family with sequence similarity 89, mer	2.86E-08	1	2.63	3.00	3.70	3.47	3.29	2.90	2.79	2.80
TC1100548	FAM89B	23625	family with sequence similarity 89, mer	3.35E-05	1	4.84	5.14	5.24	5.26	5.26	5.20	5.13	5.17

TC1100190	FAR1 /// MLST	84188	fatty acyl CoA reductase 1 /// Fatty acy	3.52E-12	1	7.23	7.76	7.95	7.83	7.71	7.62	7.53	7.41
TC0500843	FASTKD3	79072	FAST kinase domains 3 /// FAST kinase	3.10E-17	1	3.74	4.68	5.16	4.90	4.67	4.42	4.35	4.16
TC0501259	FBN2	2201	fibrillin 2 (congenital contractural arac	4.12E-07	1	3.48	4.09	3.88	3.94	3.99	3.79	3.73	3.55
TC0501198	FBXL17	64839	F-box and leucine-rich repeat protein 1	8.72E-05	1	4.26	4.60	4.61	4.57	4.50	4.48	4.49	4.45
TC0400830	FBXL5	26234	F-box and leucine-rich repeat protein 5	3.03E-08	1	8.15	8.68	8.67	8.60	8.47	8.54	8.38	8.42
TC0101546	FBXO28	23219	F-box protein 28	1.91E-11	1	4.76	5.55	5.41	5.18	5.12	5.46	5.58	5.51
TC0601667	FBXO30	84085	F-box protein 30	1.16E-21	1	6.10	7.11	7.50	7.22	6.90	6.86	6.75	6.73
TC1400245	FBXO34	55030	F-box protein 34	1.45E-13	1	5.49	6.15	6.04	6.20	5.97	5.83	5.76	5.63
TC0401414	FBXO8	26269	F-box protein 8 /// F-box only protein	3.35E-05	1	4.78	5.34	5.40	5.20	5.16	5.21	5.22	5.26
TC0600463	FBXO9	26268	F-box protein 9	5.14E-09	1	5.20	6.09	6.10	5.99	6.13	5.88	5.77	5.41
TC0501487	FBXW11	23291	F-box and WD repeat domain containi	5.96E-06	1	5.73	6.23	6.17	6.20	6.16	6.08	6.06	6.02
TC0901295	FBXW2	26190	F-box and WD repeat domain containi	2.93E-18	1	6.33	7.23	7.19	7.22	7.13	6.75	6.60	6.44
TC0901455	FBXW5	54461	F-box and WD repeat domain containi	1.16E-05	1	5.49	5.75	5.73	5.77	5.79	5.74	5.67	5.68
TC1900873	FCAR	2204	Fc fragment of IgA, receptor for	2.80E-26	1	6.88	9.01	8.63	8.30	8.33	8.02	7.72	7.57
TC0101207	FCER1G	2207	Fc fragment of IgE, high affinity I, recep	2.72E-28	1	9.64	11.31	11.48	11.33	11.15	11.07	10.95	10.74
TC0100997	FCGR1A	2209	Fc fragment of IgG, high affinity Ia, rece	2.89E-05	1	6.20	7.71	7.95	7.94	7.59	7.97	7.87	7.70
TC0102609	FCGR1B	2210	Fc fragment of IgG, high affinity Ib, rece	1.47E-05	1	7.24	8.54	8.81	8.75	8.38	8.73	8.65	8.54
TC0901425	FCN1	2219	ficolin (collagen/fibrinogen domain co	4.02E-08	1	8.94	10.46	10.10	10.38	10.46	10.28	9.79	9.77
TC0900684	FCN2	2220	ficolin (collagen/fibrinogen domain co	2.91E-06	1	5.80	6.16	6.05	6.07	6.12	6.11	5.92	5.92
TC0102032	FCN3	8547	ficolin (collagen/fibrinogen domain co	0.000842	1	4.52	4.68	4.63	4.54	4.62	4.57	4.54	4.54
TC0102877	FCRL1	115350	Fc receptor-like 1 /// Fc receptor-like 1	2.55E-23	1	4.56	6.01	6.19	5.60	5.27	4.88	4.74	4.58
TC1500430	FEM1B	10116	fem-1 homolog b (C. elegans)	7.03E-08	1	5.23	5.60	5.94	5.92	5.91	5.85	5.84	5.70
TC0501222	FEM1C	56929	fem-1 homolog c (C. elegans)	5.59E-28	1	5.57	6.90	7.02	6.77	6.56	6.50	6.35	6.27
TC1100506	FERMT3	83706	fermitin family homolog 3 (Drosophila)	7.98E-10	1	6.11	6.89	6.90	6.96	6.99	6.62	6.47	6.36
TC1500631	FES	2242	feline sarcoma oncogene	0.000849	1	5.63	5.83	5.76	5.79	5.73	5.67	5.66	5.59
TC0201426	FEZ2	9637	fasciculation and elongation protein ze	0.000381	1	4.62	5.01	4.98	5.03	4.96	4.98	4.98	4.91
TC1900440	FFAR3	731823 //	free fatty acid receptor 3	4.82E-06	1	4.21	4.92	4.73	4.81	4.66	4.43	4.59	4.40
TC1200240	FGD4	121512	FYVE, RhoGEF and PH domain containi	2.15E-25	1	6.07	7.83	7.58	7.20	7.03	6.94	6.90	6.84
TC0X01298	FGF13	2258	fibroblast growth factor 13 /// Fibrobla	9.51E-08	1	3.94	4.36	4.60	4.56	4.36	4.29	4.18	4.07
TC1900013	FGF22	27006	fibroblast growth factor 22 /// Fibrobla	0.000202	1	4.81	5.15	5.18	5.12	5.08	5.10	5.07	5.04
TC1200209	FGFR1OP2	26127	FGFR1 oncogene partner 2 /// FGFR1 o	6.44E-07	1	6.04	6.35	6.55	6.69	6.47	6.34	6.36	6.32
TC0102036	FGR	2268	Gardner-Rasheed feline sarcoma viral (	3.95E-07	1	8.10	8.49	8.61	8.50	8.38	8.24	8.10	8.01
TC1101555	FIBP	9158	fibroblast growth factor (acidic) intrace	3.81E-08	1	5.31	5.90	5.94	6.02	5.94	5.73	5.75	5.67
TC0600483	FKBP1C	---	Peptidyl-prolyl cis-trans isomerase. [So	0.000249	1	4.57	4.90	5.04	4.95	4.95	4.90	4.77	4.81

TC0601203	FKBP5	2289	FK506 binding protein 5 /// FK506-bind	3.01E-23	1	5.64	7.30	7.53	7.27	7.04	6.47	6.58	6.33
TC0700170	FKBP9	11328	FK506 binding protein 9, 63 kDa	1.45E-11	1	4.07	5.06	4.91	4.70	4.87	4.65	4.52	4.34
TC0701217	FKBP9L	360132	FK506 binding protein 9-like	3.20E-05	1	3.46	3.81	3.76	3.61	3.69	3.62	3.59	3.52
TC0101227	FLJ13137 /// N	400793 //	hypothetical gene supported by AK125	0.000752	1	4.59	4.72	4.69	4.61	4.69	4.67	4.60	4.59
TC0700065	FLJ20323	54468	hypothetical protein FLJ20323	1.61E-10	1	4.05	5.15	5.12	4.86	4.77	4.71	4.85	4.69
TC1201011	FLJ22662	79887	hypothetical protein FLJ22662	1.42E-15	1	8.75	9.81	9.83	9.75	9.68	9.40	9.27	9.13
TC0200094	FLJ30851	653140	hypothetical LOC653140	1.76E-07	1	4.38	4.66	4.78	4.73	4.70	4.61	4.58	4.57
TC1101670	FLJ33790	283212	hypothetical protein FLJ33790	0.000215	1	4.06	4.23	4.32	4.24	4.23	4.24	4.17	4.13
TC0701541	FLJ36031 /// N	168455	hypothetical protein FLJ36031	2.22E-09	1	5.24	5.97	5.83	5.98	6.02	5.87	5.73	5.79
TC0200969	FLJ38973	205327	hypothetical protein FLJ38973	2.83E-19	1	4.07	5.40	5.52	5.31	5.28	5.08	5.15	4.97
TC0701722	FLJ43692 /// O	730347 //	ARHGEF5-like /// olfactory receptor, fa	5.43E-08	1	5.00	5.34	5.13	5.07	5.21	5.24	5.14	5.07
TC0601105	FLOT1	10211	flotillin 1 /// Flotillin-1. [Source:Uniprot	3.81E-15	1	6.39	7.10	7.11	6.92	6.92	6.82	6.76	6.66
TC1701183	FLOT2 /// DHR	147015 //	dehydrogenase/reductase (SDR family)	1.98E-09	1	7.59	8.53	8.68	8.59	8.45	8.29	8.08	7.97
TC1400381	FLVCR2	55640	feline leukemia virus subgroup C cellul	0.000208	1	4.37	4.57	4.82	4.77	4.46	4.42	4.47	4.37
TC1300138	FNDC3A	22862	fibronectin type III domain containing	1.38E-20	1	5.71	7.10	6.77	6.90	6.74	6.52	6.40	6.37
TC0300791	FNDC3B	64778	fibronectin type III domain containing	3.61E-05	1	8.27	8.59	8.56	8.48	8.30	8.31	8.17	8.23
TC1100648	FOLR2	2350	folate receptor 2 (fetal) /// Folate rece	6.11E-06	1	4.12	4.33	4.48	4.43	4.43	4.43	4.21	4.22
TC0200139	FOSL2	2355	FOS-like antigen 2 /// Fos-related antig	5.92E-08	1	6.46	6.90	6.72	6.79	6.64	6.57	6.39	6.46
TC0600013	FOXC1	2296	forkhead box C1	9.30E-05	1	3.71	4.19	4.16	4.23	4.17	4.07	3.94	3.98
TC0900423	FOXE1 /// NDU	2304	forkhead box E1 (thyroid transcription	1.18E-10	1	4.90	5.30	5.33	5.28	5.31	5.27	5.21	5.20
TC0700030	FOXK1	221937	forkhead box K1	8.48E-05	1	4.55	4.72	4.69	4.61	4.64	4.56	4.59	4.56
TC0200233	FOXN2	3344	forkhead box N2 /// Forkhead box prot	7.21E-21	1	6.75	7.58	8.04	7.92	7.80	7.72	7.67	7.57
TC1201546	FOXN4	121643	forkhead box N4 /// Forkhead box prot	0.000135	1	4.83	5.05	5.02	4.97	4.94	4.98	4.93	4.92
TC1901751	FPR1	2357	formyl peptide receptor 1	2.84E-05	1	10.36	10.82	10.62	10.73	10.52	10.52	10.39	10.38
TC1900768	FPR2	2358	formyl peptide receptor 2	2.67E-07	1	7.74	8.57	8.27	8.20	8.05	8.06	7.82	8.00
TC0301336	FRMD4B	23150	FERM domain containing 4B	1.95E-30	1	3.54	5.67	5.21	4.80	4.65	4.33	4.20	4.09
TC0900183	FRMPD1	22844	FERM and PDZ domain containing 1	0.000244	1	3.11	3.22	3.23	3.23	3.24	3.16	3.15	3.13
TC0900459	FSD1L	83856	fibronectin type III and SPRY domain c	5.26E-06	1	2.27	2.74	2.96	2.75	2.74	2.58	2.55	2.49
TC1900014	FSTL3	10272	follistatin-like 3 (secreted glycoprotein)	0.000381	1	4.86	5.04	5.01	5.11	5.08	5.08	5.02	4.97
TC0501282	FSTL4	23105	follistatin-like 4 /// Follistatin-related p	3.97E-07	1	3.94	3.97	4.07	4.17	4.24	4.06	3.89	3.94
TC0901458	FUT7	2529	fucosyltransferase 7 (alpha (1,3) fucosy	2.97E-05	1	5.19	5.51	5.64	5.46	5.43	5.37	5.15	5.22
TC0300829	FXR1	8087	fragile X mental retardation, autosoma	0.000444	1	7.18	7.66	7.67	7.65	7.63	7.67	7.73	7.57
TC1900434	FXYD5	53827	FXYD domain containing ion transport	1.24E-10	1	6.27	6.92	7.21	7.27	7.23	7.00	6.89	6.85
TC0101483	G0S2	50486	G0/G1switch 2	3.80E-06	1	5.57	6.44	6.03	5.81	5.90	6.06	5.72	5.94

TC1600598	GABARAPL2	11345	GABA(A) receptor-associated protein-li	2.07E-09	1	8.89	9.28	9.39	9.48	9.42	9.38	9.30	9.30
TC0601083	GABBR1 /// N	2550	gamma-aminobutyric acid (GABA) B re	5.47E-08	1	5.57	5.93	5.84	5.82	5.94	5.92	5.80	5.73
TC0100637	GADD45A	1647	growth arrest and DNA-damage-induci	2.02E-38	1	5.10	7.54	7.94	7.33	7.20	6.63	6.55	6.22
TC1100611	GAL	51083	galanin prepropeptide	6.44E-07	1	4.93	5.28	5.27	5.27	5.31	5.30	5.24	5.14
TC1401045	GALC	2581	galactosylceramidase	0.00026	1	5.39	5.86	5.55	5.53	5.42	5.52	5.70	5.67
TC1701697	GALK1	2584	galactokinase 1 /// Galactokinase (EC 2	5.64E-06	1	5.31	5.43	5.56	5.64	5.58	5.52	5.49	5.45
TC1800141	GALNT1	2589	UDP-N-acetyl-alpha-D-galactosamine:p	8.70E-13	1	6.10	7.33	7.42	7.03	6.82	6.79	6.85	6.72
TC0201409	GALNT14	79623	UDP-N-acetyl-alpha-D-galactosamine:p	3.46E-14	1	4.61	5.15	5.54	5.82	5.77	5.52	5.36	5.06
TC0101601	GALNT2	2590	UDP-N-acetyl-alpha-D-galactosamine:p	6.08E-21	1	4.56	5.34	6.15	5.72	5.28	4.78	4.79	4.66
TC0202064	GALNT3	2591	UDP-N-acetyl-alpha-D-galactosamine:p	8.84E-11	1	5.51	6.13	6.84	6.65	6.35	6.60	6.52	6.48
TC1500264	GANC /// CAP	2595 ///	glucosidase, alpha; neutral C /// calpai	2.81E-06	1	4.64	5.11	5.02	4.93	5.01	4.91	4.88	4.60
TC1200055	GAPDH	2597	glyceraldehyde-3-phosphate dehydrog	2.33E-20	1	8.91	10.32	10.49	10.56	10.59	10.18	9.90	9.67
TC1400791	GARNL1	253959	GTPase activating Rap/RanGAP domain	0.000257	1	3.90	4.30	4.07	4.09	4.10	4.08	4.13	4.04
TC1701025	GAS7	8522	growth arrest-specific 7	1.32E-16	1	5.52	6.65	7.01	6.85	6.60	6.28	6.24	6.04
TC0102826	GBA /// GBAP	2629	glucosidase, beta; acid (includes glucos	9.97E-08	1	5.62	6.09	6.15	6.28	6.33	6.16	6.00	5.89
TC0700268	GBAS	2631	glioblastoma amplified sequence	5.25E-11	1	3.80	4.26	4.49	4.55	4.37	4.27	4.29	4.15
TC0301369	GBE1	2632	glucan (1,4-alpha-), branching enzyme	3.75E-13	1	5.57	6.82	6.64	6.58	6.74	6.55	6.30	6.11
TC0X01155	GBG5L_HUMA	---	Guanine nucleotide-binding protein G(	6.36E-20	1	6.98	7.81	8.15	8.10	8.04	7.92	7.76	7.73
TC0901407	GBGT1	26301	globoside alpha-1,3-N-acetylgalactosa	0.000414	1	4.93	5.09	5.20	5.08	5.04	5.02	4.93	4.97
TC0200821	GCA	25801	grancalcin, EF-hand calcium binding pr	1.02E-19	1	9.91	10.51	10.68	10.31	10.27	10.27	10.17	10.14
TC1400872	GCH1	2643	GTP cyclohydrolase 1 (dopa-responsive	3.28E-09	1	3.47	5.76	5.85	5.59	5.40	5.43	5.37	5.03
TC0102452	GCLM	2730	glutamate-cysteine ligase, modifier sub	4.78E-24	1	3.78	5.49	5.80	5.47	5.44	5.16	4.97	4.69
TC0102591	GDAP2	54834	ganglioside induced differentiation ass	0.000783	1	6.20	6.32	6.37	6.26	6.06	6.26	6.25	6.34
TC1000951	GDF10	2662	growth differentiation factor 10 /// Bo	0.000537	1	4.15	4.33	4.40	4.33	4.29	4.29	4.22	4.27
TC1000744	GDI2	2665	GDP dissociation inhibitor 2 /// Rab GD	2.62E-06	1	7.55	7.81	8.04	7.94	7.88	7.89	7.86	7.85
TC1601183	GFOD2	81577	glucose-fructose oxidoreductase doma	2.44E-08	1	5.50	5.83	5.90	5.73	5.82	5.69	5.58	5.48
TC2200141	GGT1	2678	gamma-glutamyltransferase 1	8.14E-09	1	5.47	5.66	5.66	5.70	5.67	5.52	5.42	5.45
TC2200426	GGT2	728441	gamma-glutamyltransferase 2	2.80E-07	1	5.37	5.64	5.67	5.65	5.63	5.53	5.41	5.39
TC2200471	GGT2	---	Gamma-glutamyltransferase-like prote	5.06E-07	1	4.96	5.09	5.09	5.07	5.11	4.97	4.89	4.88
TC2000631	GGTLC1	92086	gamma-glutamyltransferase light chain	3.56E-06	1	5.19	5.31	5.34	5.27	5.25	5.18	5.10	5.13
TC2200106	GGTLC2 /// GG	91227	gamma-glutamyltransferase light chain	7.63E-13	1	4.81	5.24	5.25	5.19	5.19	5.03	4.88	4.94
TC2200449	GGTLC3	728226	gamma-glutamyltransferase light chain	3.03E-06	1	6.25	6.58	6.61	6.59	6.54	6.50	6.37	6.36
TC1000393	GHITM	27069	growth hormone inducible transmemb	2.81E-05	1	6.92	7.28	7.37	7.30	7.21	7.22	7.22	7.23
TC0700881	GIMAP8	155038	GTPase, IMAP family member 8	1.46E-05	1	5.08	5.37	5.77	5.87	5.07	4.89	5.43	5.37

TC1300319	GJB6	10804	gap junction protein, beta 6, 30kDa	2.93E-10	1	3.89	4.69	4.26	4.17	4.30	4.29	4.09	4.08
TC1701432	GJC1	10052	gap junction protein, gamma 1, 45kDa	3.59E-05	1	3.24	3.46	3.58	3.50	3.43	3.37	3.34	3.36
TC0301620	GK5	256356	glycerol kinase 5 (putative) /// glycerol	3.90E-22	1	3.21	5.12	4.24	3.66	3.74	3.56	3.47	3.35
TC0700066	GLCCI1	113263	glucocorticoid induced transcript 1	3.42E-05	1	6.31	6.84	6.71	6.61	6.60	6.62	6.56	6.57
TC1500434	GLCE	26035	glucuronic acid epimerase	1.83E-05	1	3.59	3.76	3.89	3.88	3.81	3.74	3.70	3.69
TC0501156	GLRX	2745	glutaredoxin (thioltransferase)	2.83E-07	1	6.90	7.36	7.69	7.60	7.50	7.53	7.53	7.60
TC0103088	GLRX2	51022	glutaredoxin 2	2.12E-12	1	5.23	5.94	6.04	6.07	6.15	6.05	6.02	5.96
TC1900305	GLT25D1	79709	glycosyltransferase 25 domain containi	1.68E-11	1	5.20	5.69	6.06	6.04	5.77	5.53	5.49	5.39
TC1201555	GLTPP1 /// GLT	645312 //	glycolipid transfer protein pseudogene	3.87E-15	1	5.02	6.19	6.16	6.19	6.09	5.82	5.80	5.72
TC1001131	GLUD1	2746	glutamate dehydrogenase 1	4.38E-12	1	4.82	5.20	5.46	5.52	5.39	5.28	5.37	5.23
TC0500618	GM2A	2760	GM2 ganglioside activator	5.87E-05	1	5.48	6.14	6.34	6.42	6.12	5.95	5.82	5.71
TC0600897	GMDS	2762	GDP-mannose 4,6-dehydratase /// GDP	0.000174	1	4.25	4.47	4.27	4.41	4.46	4.33	4.31	4.27
TC1400869	GMFB	2764	glia maturation factor, beta /// Glia ma	8.54E-15	1	5.60	6.33	6.68	6.57	6.47	6.39	6.24	6.20
TC0100804	GNAI3	2773	guanine nucleotide binding protein (G	1.61E-08	1	9.01	9.38	9.46	9.34	9.17	9.24	9.13	9.19
TC0901061	GNAQ	2776	guanine nucleotide binding protein (G	1.43E-12	1	8.13	8.56	8.74	8.58	8.37	8.38	8.27	8.30
TC1400227	GNG2	54331	guanine nucleotide binding protein (G	1.36E-09	1	6.13	6.97	6.82	6.64	6.64	6.59	6.41	6.50
TC1201358	GNS	2799	glucosamine (N-acetyl)-6-sulfatase (Sar	5.87E-14	1	7.43	8.34	8.36	8.32	8.10	7.98	7.89	7.86
TC0500897	GOLPH3	64083	golgi phosphoprotein 3 (coat-protein)	7.01E-07	1	7.13	7.43	7.52	7.63	7.46	7.45	7.33	7.38
TC1200189	GOLT1B	51026	golgi transport 1 homolog B (S. cerevisi	0.000171	1	3.84	4.17	4.32	4.23	4.23	4.25	4.30	4.23
TC1700541	GOSR2	9570	golgi SNAP receptor complex member	2.90E-06	1	4.48	4.90	5.20	5.26	5.04	4.88	4.90	4.71
TC0800618	GPAA1	8733	glycosylphosphatidylinositol anchor att	3.95E-07	1	4.83	4.97	4.99	4.92	4.97	4.86	4.83	4.82
TC0103233	GPATCH2	55105	G patch domain containing 2 /// G patc	5.49E-05	1	3.55	3.66	3.80	3.72	3.64	3.61	3.64	3.56
TC1401164	GPR132	29933	G protein-coupled receptor 132	2.39E-08	1	4.90	5.57	5.28	5.23	5.18	5.06	5.12	5.06
TC0700191	GPR141	353345	G protein-coupled receptor 141	7.43E-21	1	5.66	7.79	7.59	7.61	7.79	7.11	6.75	6.64
TC0700010	GPR146	115330	G protein-coupled receptor 146	0.000785	1	4.78	5.07	5.10	5.03	4.99	5.08	4.96	5.03
TC0300779	GPR160	26996	G protein-coupled receptor 160	2.27E-21	1	5.47	7.35	7.62	7.12	7.09	6.97	6.71	6.71
TC0300367	GPR27	2850	G protein-coupled receptor 27	0.000449	1	4.81	5.41	5.42	5.36	5.33	5.42	5.29	5.18
TC1900441	GPR42P	2866	G protein-coupled receptor 42 pseudog	6.78E-05	1	5.57	6.00	5.92	6.13	5.87	5.81	5.76	5.75
TC1400419	GPR65	8477	G protein-coupled receptor 65	1.66E-14	1	7.32	8.78	8.41	7.88	7.73	8.22	8.34	8.51
TC1201264	GPR84	53831	G protein-coupled receptor 84	7.24E-27	1	3.99	7.67	7.40	6.52	6.49	5.82	5.26	4.94
TC1600479	GPR97	222487	G protein-coupled receptor 97 /// Prob	1.28E-12	1	8.16	9.36	9.10	8.81	8.67	8.46	8.16	8.13
TC1900426	GRAMD1A	57655	GRAM domain containing 1A	1.27E-08	1	5.77	6.24	6.24	6.09	6.09	5.89	5.81	5.76
TC2200365	GRAMD4	23151	GRAM domain containing 4	0.00021	1	4.40	4.59	4.64	4.53	4.52	4.47	4.42	4.42
TC0701202	GRB10	2887	growth factor receptor-bound protein	2.19E-15	1	4.33	4.89	5.39	5.32	5.16	4.80	4.80	4.59

TC1500187	GREM1	26585	gremlin 1, cysteine knot superfamily, h	0.000859	1	3.37	3.54	3.44	3.44	3.51	3.37	3.38	3.45
TC0800614	GRINA	2907	glutamate receptor, ionotropic, N-metl	3.00E-16	1	6.23	7.80	7.98	7.88	7.74	7.20	7.08	6.93
TC0500751	GRK6	2870	G protein-coupled receptor kinase 6	3.85E-13	1	6.22	7.17	6.97	6.86	6.91	6.69	6.56	6.51
TC1700507	GRN	2896	granulin /// Granulins precursor (Proep	4.46E-05	1	6.99	7.75	7.77	7.95	8.04	7.82	7.59	7.49
TC0400809	GRPEL1	80273	GrpE-like 1, mitochondrial (E. coli)	2.82E-15	1	5.45	6.62	6.69	6.41	6.36	6.20	6.24	5.92
TC0800847	GSR	2936	glutathione reductase	1.36E-14	1	7.33	7.96	8.21	8.47	8.34	8.08	8.17	7.97
TC0700810	GSTK1	373156	glutathione S-transferase kappa 1 /// G	0.000233	1	5.64	5.61	6.05	6.11	5.85	5.78	5.95	5.85
TC1000562	GSTO1	9446	glutathione S-transferase omega 1 /// (	2.84E-13	1	4.92	5.39	5.65	5.85	5.74	5.66	5.56	5.46
TC0201985	GTDC1	79712	glycosyltransferase-like domain contair	1.67E-14	1	5.33	6.06	6.20	5.79	5.66	5.46	5.32	5.32
TC1501007	GTF2A2	2958	general transcription factor IIA, 2, 12kD	9.78E-15	1	6.06	7.20	7.39	7.23	7.16	7.17	7.19	7.00
TC1300121	GTF2F2	2963	general transcription factor IIF, polypep	1.91E-07	1	6.24	7.03	7.32	7.02	6.79	6.82	6.92	6.74
TC0600845	GTF2H5	404672	general transcription factor IIH, polype	6.80E-14	1	4.22	5.20	5.71	5.64	5.61	5.51	5.58	5.27
TC0701333	GTF2IRD2	651101 //	GTF2I repeat domain containing 2	0.000746	1	5.02	5.26	5.24	5.18	5.27	5.25	5.24	5.13
TC0700397	GTF2IRD2B	651101 //	GTF2I repeat domain containing 2B	5.26E-05	1	5.13	5.51	5.49	5.46	5.48	5.48	5.42	5.34
TC0Xr00003	GTPBP6	8225	GTP binding protein 6 (putative)	0.000522	1	4.65	5.03	4.89	5.00	4.98	4.90	4.86	4.87
TC0300698	GYG1	2992	glycogenin 1 /// Glycogenin-1 (EC 2.4.1	0	1	5.87	8.96	9.10	8.71	8.60	8.18	7.84	7.47
TC1901674	GYS1	2997	glycogen synthase 1 (muscle) /// Glyco	7.02E-06	1	4.36	5.10	4.85	4.77	5.04	4.79	4.71	4.53
TC0X00464	H2BFM /// H2E	286436	H2B histone family, member M /// Hist	0.000384	1	2.46	2.50	2.66	2.47	2.53	2.44	2.43	2.48
TC0100095	H6PD	9563	hexose-6-phosphate dehydrogenase (g	3.22E-09	1	4.89	5.69	5.44	5.46	5.52	5.42	5.23	5.19
TC0201372	HADHA	3030	hydroxyacyl-Coenzyme A dehydrogena	1.87E-08	1	6.87	7.52	7.54	7.69	7.59	7.49	7.48	7.27
TC0200108	HADHB	3032	hydroxyacyl-Coenzyme A dehydrogena	2.00E-11	1	6.22	6.62	6.77	6.59	6.43	6.38	6.44	6.31
TC1600033	HAGHL	84264	hydroxyacylglutathione hydrolase-like	0.000761	1	5.07	5.25	5.27	5.23	5.26	5.25	5.13	5.18
TC0200860	HAT1	8520	histone acetyltransferase 1	1.73E-10	1	5.93	6.90	7.03	6.78	6.61	6.59	6.60	6.54
TC0501447	HAVCR2	84868	hepatitis A virus cellular receptor 2	7.67E-07	1	4.02	4.18	4.36	4.40	4.24	4.05	4.15	4.10
TC0601624	HBS1L	10767	HBS1-like (S. cerevisiae) /// HBS1-like p	1.55E-12	1	4.86	5.51	5.66	5.61	5.54	5.37	5.38	5.22
TC0102530	HBXIP	10542	hepatitis B virus x interacting protein //	8.59E-21	1	6.44	7.45	7.56	7.31	7.18	7.07	6.93	6.88
TC0X00037	HCCS	3052	holocytochrome c synthase (cytochrom	3.34E-13	1	4.94	5.69	5.75	5.69	5.65	5.71	5.70	5.66
TC0X00322	hCG_1642624 ,	645545 //	similar to immunoglobulin binding prot	7.33E-10	1	5.71	6.11	6.19	6.26	6.15	6.11	6.21	6.21
TC0501078	hCG_1757335	643752	hCG1757335	3.23E-06	1	4.95	5.49	5.56	5.48	5.56	5.50	5.45	5.41
TC1500965	hCG_18385 ///	646227 //	similar to cAMP-regulated phosphopro	0.000829	1	6.29	6.54	6.61	6.46	6.36	6.50	6.44	6.59
TC0100258	hCG_2003956 ,	388499 //	hCG2003956 /// lysophospholipase II /,	2.59E-05	1	5.99	6.33	6.35	6.32	6.32	6.33	6.24	6.24
TC1000484	hCG_2015138 ,	642969 //	phosphoglycerate mutase 1 pseudoger	4.04E-05	1	6.92	7.35	7.35	7.59	7.46	7.27	7.12	7.21
TC1800346	hCG_2025063 ,	646981 //	protein tyrosine phosphatase, non-rece	1.00E-10	1	4.52	5.56	5.51	5.32	5.10	5.00	5.19	4.99
TC1900462	HCST	10870	hematopoietic cell signal transducer	1.33E-19	1	5.45	6.98	6.68	6.69	6.84	6.73	6.63	6.31

TC0601544	HDAC2	3066	histone deacetylase 2 /// Histone deac	1.02E-16	1	6.04	7.09	6.86	6.82	6.86	6.93	6.91	6.75
TC0202430	HDAC4	9759	histone deacetylase 4	1.71E-08	1	5.67	6.12	6.04	6.15	6.05	5.97	5.91	5.87
TC0601579	HDDC2	51020	HD domain containing 2 /// HD domair	1.03E-06	1	5.51	5.86	6.05	5.68	5.77	5.76	5.83	5.69
TC1900093	HDGF2	84717	hepatoma-derived growth factor-relate	6.83E-05	1	5.17	5.51	5.43	5.48	5.48	5.44	5.41	5.40
TC0X00757	HDHD1A	8226	haloacid dehalogenase-like hydrolase c	6.52E-06	1	4.92	5.09	5.24	5.31	5.26	5.09	5.18	5.08
TC1800451	HDHD2	84064	haloacid dehalogenase-like hydrolase c	8.09E-12	1	4.55	5.73	5.97	5.75	5.80	5.50	5.43	5.15
TC1600418	HEATR3	55027	HEAT repeat containing 3 /// HEAT rep	0.000367	1	4.10	4.09	4.31	4.33	4.22	4.17	4.29	4.13
TC0600757	HEBP2	23593	heme binding protein 2 /// Heme-bindi	7.50E-16	1	7.21	8.13	8.31	8.07	8.00	8.02	8.01	7.98
TC1200494	HELB	92797	helicase (DNA) B	6.26E-06	1	5.05	6.32	5.76	5.93	5.64	5.52	5.69	5.52
TC0102149	HEYL	26508	hairy/enhancer-of-split related with YR	0.000987	1	3.53	3.68	3.62	3.52	3.67	3.61	3.47	3.58
TC0701381	HGF	3082	hepatocyte growth factor (hepapoietin	1.10E-25	1	3.15	5.42	5.41	4.90	4.47	3.85	3.59	3.47
TC1000448	HHEX	3087	hematopoietically expressed homeobo	7.62E-13	1	7.60	8.10	8.64	8.56	8.30	8.14	7.94	8.00
TC0100765	HIAT1	64645	hippocampus abundant transcript 1	1.54E-05	1	6.55	7.22	7.06	7.04	6.97	7.10	7.04	7.08
TC0900402	HIATL1	84641	hippocampus abundant transcript-like	1.26E-16	1	6.17	7.51	7.49	7.34	7.41	7.24	7.13	7.02
TC0901168	HIATL2	---	Hippocampus abundant transcript-like	8.47E-05	1	5.36	5.65	5.66	5.60	5.66	5.60	5.54	5.46
TC0202177	HIBCH	26275	3-hydroxyisobutyryl-Coenzyme A hydr	1.54E-05	1	4.22	4.50	4.78	4.63	4.47	4.41	4.49	4.39
TC1400283	HIF1A	3091	hypoxia-inducible factor 1, alpha subur	8.40E-16	1	9.22	10.01	9.57	9.49	9.30	9.32	9.27	9.40
TC1000512	HIF1AN	55662	hypoxia-inducible factor 1, alpha subur	0.000391	1	5.19	5.72	5.59	5.59	5.44	5.29	5.39	5.26
TC0301134	HIGD1A	25994	HIG1 domain family, member 1A	1.68E-12	1	7.44	7.96	8.40	8.16	7.96	8.05	7.94	7.94
TC0701351	HIP1	3092	huntingtin interacting protein 1	5.66E-08	1	6.23	6.95	6.90	6.74	6.46	6.28	6.25	6.22
TC0100859	HIPK1	204851	homeodomain interacting protein kina	2.35E-05	1	7.87	7.99	8.02	8.06	7.91	7.80	7.77	7.76
TC1100263	HIPK3	10114	homeodomain interacting protein kina	5.11E-05	1	9.10	9.30	9.36	9.32	9.14	9.14	9.03	9.02
TC1000304	HK1	3098	hexokinase 1	3.98E-12	1	5.24	5.98	5.79	5.83	5.76	5.64	5.58	5.58
TC0200364	HK2	3099	hexokinase 2	0.000965	1	6.28	6.95	6.82	6.86	6.77	6.69	6.64	6.59
TC0501523	HK3	3101	hexokinase 3 (white cell)	2.82E-25	1	5.27	6.56	6.69	6.45	6.35	5.92	5.74	5.50
TC0401406	HMGB2	3148	high-mobility group box 2	4.29E-27	1	6.11	7.37	7.34	7.25	7.33	7.19	6.99	6.92
TC1701687	HN1	51155	hematological and neurological expres	1.86E-09	1	7.78	8.30	8.48	8.39	8.18	8.24	8.17	8.11
TC0701077	HNRNPA2B1	3181	heterogeneous nuclear ribonucleoprot	0.000755	1	8.82	9.10	9.10	8.88	8.91	8.92	8.97	8.87
TC0200893	HNRNPA3 /// H	220988	heterogeneous nuclear ribonucleoprot	4.12E-09	1	8.16	8.93	8.81	8.54	8.56	8.59	8.67	8.52
TC1000911	HNRNPF	3185	heterogeneous nuclear ribonucleoprot	2.16E-10	1	5.25	5.79	5.65	5.58	5.64	5.68	5.62	5.58
TC1900151	HNRNPM	4670	heterogeneous nuclear ribonucleoprot	4.67E-06	1	7.67	8.60	8.46	8.25	8.39	8.29	8.30	8.09
TC1901311	HOMER3	9454	homer homolog 3 (Drosophila) /// Hom	9.79E-09	1	5.30	5.62	5.63	5.65	5.70	5.57	5.52	5.47
TC0800261	HOOK3	84376	hook homolog 3 (Drosophila)	9.88E-05	1	6.80	7.29	7.23	7.18	7.05	7.07	7.18	7.02
TC0200887	HOXD1	3231	homeobox D1 /// Homeobox protein H	0.000269	1	4.29	4.52	4.54	4.51	4.59	4.56	4.44	4.47

TC1600582	HP	3240	haptoglobin /// Haptoglobin precursor	3.40E-28	1	4.31	8.46	8.43	8.18	8.48	8.06	7.34	6.48
TC0401415	HPGD	3248	hydroxyprostaglandin dehydrogenase	3.06E-23	1	3.96	5.59	6.81	6.04	5.28	4.56	4.39	4.31
TC1600583	HPR	3250	haptoglobin-related protein /// Haptog	6.97E-27	1	4.52	5.86	5.88	5.77	5.82	5.72	5.56	5.28
TC0X00575	HPRT1	3251	hypoxanthine phosphoribosyltransfera	4.12E-11	1	4.42	5.28	5.79	5.38	5.40	5.32	5.22	5.10
TC1101243	HPS5	11234	Hermansky-Pudlak syndrome 5	3.56E-07	1	3.83	4.50	4.16	4.01	4.04	4.06	4.03	4.03
TC0201148	HRB	3267	HIV-1 Rev binding protein /// Nucleop	1.39E-38	1	6.75	9.12	9.32	8.62	8.43	7.88	7.64	7.41
TC0500726	HRH2	3274	histamine receptor H2	2.39E-06	1	5.87	6.55	6.32	6.26	6.15	6.06	6.06	5.87
TC2000880	HRH3	11255	histamine receptor H3 /// Histamine H	0.000923	1	4.81	5.01	5.01	4.95	4.95	4.95	4.93	4.89
TC1700144	HS3ST3B1	9953	heparan sulfate (glucosamine) 3-O-sulf	1.63E-25	1	4.72	6.19	6.72	5.84	5.79	5.45	5.33	5.08
TC1600628	HSBP1	3281	heat shock factor binding protein 1	1.08E-05	1	8.93	9.16	9.52	9.45	9.28	9.35	9.31	9.40
TC2200168	HSCB	150274	HscB iron-sulfur cluster co-chaperone	1.05E-17	1	3.29	4.56	5.08	4.15	4.02	3.75	3.77	3.61
TC1100292	HSD17B12	51144	hydroxysteroid (17-beta) dehydrogena	4.37E-10	1	6.08	7.44	7.07	7.06	7.36	7.24	6.98	6.83
TC0900489	HSDL2	84263	hydroxysteroid dehydrogenase like 2 /	1.05E-05	1	7.60	7.92	8.13	7.86	7.61	7.76	7.66	7.76
TC1401135	HSP90AA1	3320	heat shock protein 90kDa alpha (cytos	8.64E-06	1	8.65	9.23	9.10	9.00	9.09	9.10	9.16	9.04
TC0600280	HSPA1B	3304	heat shock 70kDa protein 1B	5.72E-16	1	5.82	6.82	7.00	6.91	6.79	6.58	6.56	6.54
TC0600279	HSPA1B /// HS	3304 ///	heat shock 70kDa protein 1B /// heat s	4.53E-14	1	7.85	8.56	8.75	8.52	8.54	8.35	8.24	8.30
TC0601137	HSPA1L	3305	heat shock 70kDa protein 1-like /// He	6.72E-05	1	5.57	6.10	6.14	6.10	6.13	5.98	6.04	5.90
TC1100226	HTATIP2	10553	HIV-1 Tat interactive protein 2, 30kDa	6.79E-11	1	6.59	7.07	7.38	7.38	7.24	7.25	7.24	7.19
TC0400075	HTRA3	94031	HtrA serine peptidase 3 /// Probable s	0.000114	1	4.22	4.42	4.31	4.33	4.50	4.48	4.30	4.26
TC0400036	HTT	3064	huntingtin	6.54E-08	1	4.39	5.07	4.94	4.75	4.77	4.58	4.63	4.50
TC0701196	HUS1	3364	HUS1 checkpoint homolog (S. pombe)	1.30E-06	1	4.52	5.02	5.10	4.97	4.93	4.75	4.82	4.73
TC1500285	HYPK /// SERF2	25764 ///	Huntingtin interacting protein K /// sm	2.48E-06	1	5.72	5.99	6.09	6.14	6.22	6.09	5.99	5.93
TC0200027	IAH1	285148	isoamyl acetate-hydrolyzing esterase 1	6.74E-08	1	6.00	6.09	6.39	6.30	6.29	6.21	6.19	6.06
TC0101525	IARS2	55699	isoleucyl-tRNA synthetase 2, mitochon	1.10E-14	1	3.83	4.73	5.08	4.95	4.83	4.66	4.66	4.41
TC0101982	ID3	3399	inhibitor of DNA binding 3, dominant n	1.73E-09	1	2.85	3.36	3.14	2.96	3.02	3.10	2.99	3.03
TC1000724	IDI1	3422	isopentenyl-diphosphate delta isomera	8.47E-24	1	4.79	6.28	6.31	5.67	5.43	5.34	5.31	5.26
TC0601107	IER3 /// NP_00	8870	immediate early response 3 /// immedi	6.94E-08	1	5.83	6.31	6.19	6.11	6.20	6.11	5.79	5.92
TC2100086	IFNAR1	3454	interferon (alpha, beta and omega) rec	8.73E-05	1	8.11	8.70	8.69	8.54	8.34	8.45	8.41	8.40
TC0601636	IFNGR1	3459	interferon gamma receptor 1 /// Interf	1.72E-11	1	6.83	7.22	7.31	7.05	6.94	6.97	6.84	6.92
TC1701160	IFT20	90410	intraflagellar transport 20 homolog (Ch	1.05E-15	1	5.58	6.43	6.39	6.13	6.16	6.05	5.97	5.91
TC2000287	IFT52	51098	intraflagellar transport 52 homolog (Ch	0.000365	1	4.74	4.99	5.04	4.92	4.96	4.85	5.00	4.93
TC0301427	IFT57	55081	intraflagellar transport 57 homolog (Ch	8.71E-05	1	4.91	5.85	5.72	5.68	5.80	5.77	5.78	5.52
TC0701189	IGFBP3	3486	insulin-like growth factor binding prote	0.000629	1	4.62	4.74	4.80	4.66	4.74	4.76	4.69	4.70
TC0103182	IL10	3586	interleukin 10	1.57E-12	1	2.79	3.08	3.74	3.24	3.09	2.84	2.71	2.77

TC1100885	IL10RA	3587	interleukin 10 receptor, alpha	5.98E-11	1	4.88	6.02	5.41	5.37	5.15	5.10	5.05	5.12
TC2100085	IL10RB	3588	interleukin 10 receptor, beta	4.04E-06	1	7.47	8.03	8.05	8.00	7.86	7.88	7.72	7.74
TC2200011	IL17RA	23765	interleukin 17 receptor A	5.59E-05	1	8.80	9.19	9.09	9.20	9.11	8.99	8.95	8.91
TC0200538	IL18R1	8809	interleukin 18 receptor 1 /// Interleukir	2.45E-23	1	5.06	8.23	8.02	7.55	7.16	6.66	6.46	6.11
TC0200539	IL18RAP	8807	interleukin 18 receptor accessory prote	1.77E-14	1	6.38	8.50	8.47	7.90	7.63	7.63	7.33	7.01
TC0200533	IL1R2	7850	interleukin 1 receptor, type II	1.40E-12	1	8.76	9.53	9.46	9.41	9.21	8.59	8.55	8.49
TC0200595	IL1RN	3557	interleukin 1 receptor antagonist	9.51E-08	1	5.24	6.17	6.02	6.13	5.96	5.95	5.84	5.90
TC1600284	IL4R	3566	interleukin 4 receptor /// Interleukin-4	1.72E-19	1	6.77	8.38	8.18	7.91	7.83	7.54	7.38	7.07
TC0500989	IL6ST	649891 //	interleukin 6 signal transducer (gp130,	1.61E-23	1	4.73	6.87	6.96	6.84	6.42	6.10	5.88	5.68
TC0102793	ILF2	3608	interleukin enhancer binding factor 2,	5.73E-05	1	4.40	5.08	5.04	5.06	5.20	5.12	5.14	4.92
TC1800058	IMPA2	3613	inositol(myo)-1(or 4)-monophosphatas	4.66E-05	1	7.16	7.06	7.46	7.44	7.21	7.19	7.10	7.15
TC0200624	INSIG2	51141	insulin induced gene 2 /// Insulin-induc	1.06E-11	1	5.98	6.78	7.05	6.83	6.75	6.57	6.70	6.51
TC0401168	INTS12	57117	integrator complex subunit 12	2.37E-06	1	5.28	5.93	5.90	5.79	5.61	5.72	5.87	5.74
TC1300499	INTS6	26512	integrator complex subunit 6	1.44E-12	1	6.17	6.84	6.81	6.56	6.47	6.46	6.35	6.39
TC1000995	IPMK	253430	inositol polyphosphate multikinase	8.13E-05	1	7.45	8.10	8.19	8.17	7.94	8.21	8.01	8.10
TC1201075	IPO8	10526	importin 8	2.08E-05	1	5.32	5.79	6.07	5.86	5.68	5.71	5.80	5.68
TC0101264	IQWD1	648494 //	IQ motif and WD repeats 1 /// IQ motif	2.17E-06	1	5.42	5.92	5.88	5.83	5.82	5.74	5.78	5.72
TC0300047	IRAK2	3656	interleukin-1 receptor-associated kinas	3.14E-08	1	4.25	4.75	4.58	4.73	4.83	4.58	4.52	4.44
TC1200492	IRAK3	11213	interleukin-1 receptor-associated kinas	2.47E-37	1	6.58	8.88	9.03	8.87	8.68	8.09	7.93	7.66
TC1200266	IRAK4	51135	interleukin-1 receptor-associated kinas	3.17E-06	1	6.32	6.43	6.68	6.57	6.26	6.23	6.39	6.18
TC1600359	ITGAM	3684	integrin, alpha M (complement compo	1.28E-22	1	7.71	8.93	8.97	8.96	8.92	8.50	8.28	8.11
TC0201298	ITGB1BP1	9270	integrin beta 1 binding protein 1 /// Int	1.48E-06	1	4.37	4.69	4.88	4.83	4.84	4.74	4.76	4.70
TC0103072	IVNS1ABP	10625	influenza virus NS1A binding protein //	2.50E-17	1	7.80	9.05	8.37	8.17	8.38	8.38	8.11	8.13
TC0900025	JAK2	3717	Janus kinase 2 (a protein tyrosine kinas	1.98E-18	1	6.60	7.84	7.96	7.80	7.57	7.58	7.52	7.41
TC1701722	JMJD6	23210	jumonji domain containing 6 /// JmjC d	2.92E-13	1	6.26	7.50	7.18	6.92	6.94	6.85	6.73	6.61
TC2200668	JOSD1	9929	Josephin domain containing 1	2.14E-19	1	4.98	6.81	6.32	6.14	6.03	5.84	5.69	5.53
TC1100775	JRKL	8690	jerky homolog-like (mouse)	5.03E-07	1	3.70	4.64	4.84	4.72	4.73	4.64	4.55	4.33
TC0X00760	KAL1	3730	Kallmann syndrome 1 sequence	1.57E-05	1	3.03	3.03	3.17	3.25	3.12	3.06	3.08	3.05
TC0601674	KATNA1	11104	katanin p60 (ATPase-containing) subun	4.14E-10	1	4.40	4.98	5.18	5.15	5.06	4.99	5.04	4.90
TC0701115	KBTBD2	25948	kelch repeat and BTB (POZ) domain cor	0.000661	1	7.55	7.81	7.71	7.61	7.50	7.68	7.65	7.71
TC1300427	KBTBD6	89890	kelch repeat and BTB (POZ) domain cor	2.91E-08	1	3.87	5.06	4.57	4.42	4.76	4.57	4.29	4.17
TC1300429	KBTBD7	84078	kelch repeat and BTB (POZ) domain cor	2.16E-07	1	6.23	7.17	7.36	7.27	7.20	7.04	6.94	6.88
TC0200401	KCMF1	56888	potassium channel modulatory factor 1	0.000102	1	7.82	8.12	8.22	8.19	8.05	8.07	8.00	7.99
TC0100819	KCNC4	3749	potassium voltage-gated channel, Shav	6.29E-06	1	4.05	4.27	4.18	4.08	4.11	4.09	4.03	4.00

TC2100322	KCNE1	3753	potassium voltage-gated channel, Isk-r	5.34E-14	1	4.70	5.26	5.58	5.52	5.26	4.86	4.93	4.74
TC0201460	KCNG3	170850	potassium voltage-gated channel, subf	0.000314	1	3.76	4.09	4.10	4.08	4.02	3.95	3.90	3.99
TC1200306	KCNH3	23416	potassium voltage-gated channel, subf	0.000345	1	4.76	4.82	4.85	4.93	4.88	4.82	4.73	4.75
TC0202053	KCNH7	90134	potassium voltage-gated channel, subf	2.04E-12	1	3.39	3.41	3.75	3.97	3.68	3.41	3.40	3.28
TC1001090	KCNMA1	3778	potassium large conductance calcium-a	1.22E-11	1	2.97	3.13	3.50	3.45	3.21	3.02	2.96	3.00
TC0100438	KCNQ4	9132	potassium voltage-gated channel, KQT-	0.000127	1	4.57	4.70	4.77	4.62	4.67	4.67	4.61	4.60
TC1700088	KCTD11 /// CE	147040 //	potassium channel tetramerisation dor	5.13E-15	1	6.41	7.18	7.11	6.89	6.87	6.58	6.56	6.40
TC0700346	KCTD7 /// RAB	154881 //	potassium channel tetramerisation dor	2.20E-31	1	5.15	6.13	5.90	5.84	5.89	5.65	5.46	5.35
TC1901654	KDELR1	10945	KDEL (Lys-Asp-Glu-Leu) endoplasmic re	2.94E-08	1	4.67	5.39	5.23	5.32	5.36	5.28	5.28	5.12
TC1800523	KDSR	2531	3-ketodihydrosphingosine reductase	0.000171	1	3.96	4.34	4.10	3.99	4.04	4.11	4.11	4.11
TC1500937	KIAA0256 /// K	9728	KIAA0256 gene product /// Uncharacte	0.000952	1	6.17	6.62	6.40	6.28	6.12	6.28	6.41	6.45
TC0700701	KIAA0265 /// N	23008	KIAA0265 protein	1.75E-10	1	5.57	5.84	6.02	6.01	5.89	5.80	5.84	5.80
TC0901245	KIAA0368	23392	KIAA0368 /// Proteasome-associated p	3.15E-11	1	4.85	5.55	5.69	5.49	5.39	5.27	5.32	5.07
TC1300436	KIAA0564 /// N	23078	KIAA0564 /// OTTHUMP00000018323.	8.22E-10	1	3.57	4.42	4.26	4.10	4.06	3.86	3.82	3.69
TC1400266	KIAA0586	9786	KIAA0586 /// Uncharacterized protein	2.30E-07	1	4.30	4.84	4.87	4.62	4.57	4.48	4.53	4.34
TC0400865	KIAA0746	23231	KIAA0746 protein	1.62E-21	1	3.95	5.15	5.98	5.81	5.43	4.65	4.55	4.29
TC0600577	KIAA0776	23376	KIAA0776	1.11E-05	1	3.89	4.85	4.90	4.66	4.71	4.63	4.73	4.54
TC1000335	KIAA0974	---	---	5.81E-11	1	4.08	4.56	4.69	4.74	4.60	4.50	4.51	4.39
TC0100722	KIAA1107	---	---	5.05E-08	1	2.85	3.05	3.62	3.52	2.99	3.10	3.12	3.01
TC1000856	KIAA1462	57608	KIAA1462	7.81E-08	1	3.02	3.31	3.27	3.21	3.21	3.18	3.13	3.15
TC1201179	KIAA1602	57701	KIAA1602 /// Uncharacterized protein	1.26E-06	1	4.80	5.02	4.97	4.92	4.95	4.87	4.79	4.79
TC1300118	KIAA1704	55425	KIAA1704 /// KIAA1704 (Novel protein)	0.00027	1	4.09	4.55	4.55	4.61	4.64	4.53	4.58	4.49
TC0202119	KIAA1715	80856	KIAA1715	4.64E-15	1	5.03	6.27	6.65	6.54	6.70	6.50	6.34	6.18
TC0900490	KIAA1958	158405	KIAA1958 /// Uncharacterized protein	0.000429	1	3.63	4.01	4.01	4.01	3.96	3.95	3.92	3.91
TC2000572	KIF16B /// C20	55614	kinesin family member 16B /// Kinesin-	0.000495	1	3.49	3.81	3.94	3.78	3.72	3.64	3.76	3.62
TC0100106	KIF1B	23095	kinesin family member 1B /// Kinesin-li	1.82E-23	1	6.35	8.00	7.77	7.60	7.52	7.16	7.02	6.78
TC0201370	KIF3C	3797	kinesin family member 3C	7.43E-21	1	5.17	6.28	6.39	6.16	6.08	5.76	5.61	5.48
TC1000869	KIF5B	3799	kinesin family member 5B	0.000282	1	8.00	8.55	8.51	8.46	8.42	8.45	8.49	8.40
TC19r00004	KIR2DL4	3805	killer cell immunoglobulin-like receptor	1.25E-05	1	3.86	4.15	4.16	4.03	4.08	4.04	3.88	3.95
TC1300077	KL	9365	klotho	1.79E-24	1	3.26	4.91	4.71	4.17	4.01	3.81	3.58	3.53
TC1500169	KLF13	51621	Kruppel-like factor 13	9.50E-05	1	5.00	5.27	5.31	5.28	5.28	5.11	5.10	5.11
TC0701637	KLF14	136259	Kruppel-like factor 14	0.00071	1	3.77	3.98	4.02	4.00	3.96	3.71	3.73	3.84
TC1901008	KLF16	83855	Kruppel-like factor 16	6.49E-05	1	5.57	5.99	6.07	6.05	6.07	6.02	5.97	5.96
TC0901030	KLF9	687	Kruppel-like factor 9	7.04E-08	1	3.67	4.36	4.45	4.17	3.97	3.87	3.88	3.79

TC1400210	KLHDC1	122773	kelch domain containing 1	0.000129	1	3.52	3.96	4.20	4.20	4.07	4.15	4.06	4.06
TC0103133	KLHL12	59349	kelch-like 12 (Drosophila) /// Kelch-like	2.91E-06	1	5.25	5.55	5.71	5.56	5.36	5.43	5.44	5.33
TC0X00819	KLHL15	80311	kelch-like 15 (Drosophila)	7.50E-14	1	4.37	5.64	5.24	4.90	4.80	4.81	4.78	4.70
TC0400660	KLHL2	11275	kelch-like 2, Mayven (Drosophila)	1.79E-27	1	8.15	9.46	9.68	9.44	9.20	8.98	8.77	8.65
TC0400166	KLHL5	51088	kelch-like 5 (Drosophila) /// Kelch-like	5.72E-07	1	4.98	5.50	5.58	5.71	5.28	5.06	5.31	5.21
TC0401105	KLHL8	57563	kelch-like 8 (Drosophila)	1.86E-06	1	6.86	7.44	7.64	7.75	7.56	7.43	7.43	7.49
TC0101665	KMO	8564	kynurenine 3-monooxygenase (kynure	6.90E-08	1	2.37	2.66	2.70	2.51	2.46	2.39	2.44	2.42
TC1300486	KPNA3	3839	karyopherin alpha 3 (importin alpha 4)	3.94E-11	1	4.18	4.70	4.88	4.99	4.87	4.89	4.81	4.75
TC0301709	KPNA4	3840	karyopherin alpha 4 (importin alpha 3)	6.16E-10	1	6.66	7.21	7.44	7.03	6.94	7.01	6.91	6.98
TC1201049	KRAS	3845	v-Ki-ras2 Kirsten rat sarcoma viral onco	1.13E-09	1	6.90	7.87	7.79	7.70	7.61	7.73	7.62	7.56
TC0201700	KRCC1	51315	lysine-rich coiled-coil 1	3.70E-07	1	6.92	7.42	7.65	7.54	7.46	7.59	7.62	7.52
TC2200172	KREMEN1	83999	kringle containing transmembrane pro	3.57E-10	1	5.32	6.66	6.79	7.14	6.93	6.99	6.68	6.34
TC1701319	KRT10	3858	keratin 10 (epidermolytic hyperkeratos	1.18E-06	1	3.51	3.77	3.79	3.82	3.82	3.80	3.81	3.74
TC1201223	KRT82	3888	keratin 82	9.38E-05	1	3.88	4.12	4.09	4.00	4.02	4.05	3.99	4.02
TC2100281	KRTAP19-5 ///	337972 //	keratin associated protein 19-5 /// ker	1.76E-06	1	5.01	5.88	6.00	6.03	6.01	5.90	5.68	5.70
TC1101628	KRTAP5-11	---	Keratin-associated protein 5-11 (Kerat	0.000597	1	5.30	5.71	5.71	5.51	5.52	5.66	5.56	5.68
TC0600716	L3MBTL3	84456	l(3)mbt-like 3 (Drosophila)	9.31E-11	1	5.01	5.44	5.67	5.57	5.18	5.20	5.23	5.21
TC1500395	LACTB	114294	lactamase, beta	7.22E-09	1	5.99	7.21	7.17	7.37	7.05	7.10	7.20	7.05
TC1901803	LAIR1	3903	leukocyte-associated immunoglobulin-	3.41E-06	1	4.69	4.92	5.22	5.44	5.38	5.12	5.14	4.95
TC0101348	LAMC1	3915	laminin, gamma 1 (formerly LAMB2)	1.56E-08	1	3.67	3.88	3.76	3.99	4.08	3.84	3.82	3.71
TC1300293	LAMP1	3916	lysosomal-associated membrane prote	1.41E-05	1	6.14	6.61	6.60	6.61	6.62	6.57	6.44	6.45
TC0201341	LAPTM4A	9741	lysosomal-associated protein transmen	1.47E-17	1	8.57	9.18	9.47	9.25	8.96	9.11	9.05	9.06
TC1000721	LARP5	23185	La ribonucleoprotein domain family, m	2.88E-05	1	6.26	6.60	6.62	6.39	6.39	6.34	6.28	6.23
TC1300324	LATS2	26524	LATS, large tumor suppressor, homolo	8.98E-08	1	5.48	5.99	5.80	6.07	5.90	5.78	5.78	5.76
TC0103276	LBR	3930	lamin B receptor	1.49E-06	1	8.51	8.99	8.96	8.79	8.78	8.87	8.65	8.73
TC1001229	LBX1	10660	ladybird homeobox 1	0.000136	1	4.95	5.24	5.24	5.18	5.24	5.23	5.12	5.15
TC0900589	LCN2	3934	lipocalin 2 /// Neutrophil gelatinase-as	1.45E-20	1	5.96	8.59	8.16	8.28	8.76	8.77	8.39	7.93
TC1100219	LDHA	3939	lactate dehydrogenase A /// L-lactate	4.44E-34	1	6.98	9.84	9.77	9.34	9.38	8.89	8.64	8.22
TC1900186	LDLR	3949	low density lipoprotein receptor (famili	9.56E-09	1	4.60	5.05	4.93	5.16	5.25	4.83	4.75	4.62
TC1200487	LEMD3	23592	LEM domain containing 3	9.39E-08	1	6.51	7.35	7.35	7.24	7.11	7.25	7.18	7.07
TC2200258	LGALS1	3956	lectin, galactoside-binding, soluble, 1 (	8.09E-30	1	5.06	8.35	8.18	8.48	7.92	6.84	6.48	6.29
TC1400243	LGALS3	3958	lectin, galactoside-binding, soluble, 3	1.84E-07	1	6.25	7.01	6.97	6.99	7.21	6.95	6.80	6.63
TC0101642	LGALS8	3964	lectin, galactoside-binding, soluble, 8 (	5.02E-15	1	5.39	6.41	6.27	6.11	5.86	5.77	5.78	5.62
TC1300646	LIG4	3981	ligase IV, DNA, ATP-dependent	6.50E-16	1	4.61	5.30	4.96	4.86	4.78	4.71	4.65	4.60

TC1901801	LILRA5	353514	leukocyte immunoglobulin-like receptc	1.84E-28	1	6.44	8.41	8.52	8.38	8.12	7.79	7.52	7.30
TC1901797	LILRA6 /// LILR	79168 ///	leukocyte immunoglobulin-like receptc	5.76E-06	1	7.73	7.99	8.02	8.01	7.91	7.77	7.68	7.70
TC1900867	LILRB4	11006	leukocyte immunoglobulin-like receptc	0.000166	1	5.71	5.82	5.85	5.78	5.74	5.70	5.67	5.63
TC0200570	LIMS3	96626	LIM and senescent cell antigen-like dor	2.01E-12	1	4.18	5.34	5.19	5.17	5.28	5.19	5.00	4.92
TC0401086	LIN54	132660	lin-54 homolog (C. elegans)	7.07E-14	1	5.75	6.63	6.55	6.35	6.17	6.22	6.23	6.20
TC1201419	LIN7A	8825	lin-7 homolog A (C. elegans)	3.18E-07	1	8.41	8.80	8.95	8.88	8.80	8.76	8.66	8.55
TC1900707	LIN7B	64130	lin-7 homolog B (C. elegans)	5.65E-05	1	5.02	5.33	5.29	5.34	5.34	5.37	5.34	5.25
TC1101272	LIN7C	55327	lin-7 homolog C (C. elegans)	2.75E-06	1	5.97	6.80	6.86	6.84	6.83	6.84	6.78	6.73
TC1000422	LIPM	340654	lipase, family member M	0.000598	1	3.23	3.81	3.83	3.48	3.48	3.50	3.57	3.50
TC1000421	LIPN	643418	lipase, family member N	1.47E-12	1	5.24	7.70	7.26	6.62	5.88	6.40	6.09	6.23
TC0501526	LMAN2	10960	lectin, mannose-binding 2	0.00039	1	7.73	8.13	8.12	8.31	8.20	8.17	8.10	8.08
TC0701796	LMBR1	64327	limb region 1 homolog (mouse) /// Lim	6.20E-08	1	5.30	6.05	5.88	5.69	5.80	5.72	5.62	5.58
TC0500441	LMNB1	4001	lamin B1	6.18E-23	1	6.31	7.74	7.61	7.63	7.59	7.55	7.50	7.33
TC0700505	LMTK2	22853	lemur tyrosine kinase 2	2.64E-07	1	7.14	7.96	7.52	7.41	7.35	7.43	7.30	7.35
TC1700783	LOC124512	124512	hypothetical protein LOC124512	0.000103	1	4.98	5.39	5.35	5.31	5.45	5.38	5.35	5.22
TC1701075	LOC201164	201164	similar to CG12314 gene product	0.000233	1	4.31	4.50	4.48	4.22	4.68	4.61	4.47	4.14
TC0X00664	LOC203547 ///	203547	hypothetical protein LOC203547	4.76E-09	1	3.87	4.51	4.64	4.56	4.62	4.54	4.59	4.33
TC0400025	LOC401115	401115	hypothetical LOC401115	6.61E-11	1	6.58	6.92	6.93	7.01	7.02	6.96	6.86	6.89
TC0401216	LOC401152	401152	HCV F-transactivated protein 1	2.05E-22	1	5.98	6.88	7.00	6.79	6.66	6.69	6.61	6.60
TC0400196	LOC402175	402175	hypothetical gene supported by AF044	5.89E-05	1	4.60	5.43	5.61	5.44	5.48	5.50	5.38	5.37
TC1800018	LOC642076 ///	642076 //	similar to myosin regulatory light chain	3.31E-23	1	8.20	8.71	8.89	8.80	8.75	8.75	8.68	8.63
TC0701222	LOC645317 ///	645317 //	similar to 16.7Kd protein /// coiled-coil	3.45E-06	1	6.15	6.87	7.04	6.86	6.91	6.96	6.98	6.92
TC0700048	LOC652200 ///	652200 //	similar to CG14980-PB /// chromosome	2.64E-14	1	6.57	7.24	7.47	7.31	7.24	7.23	7.20	7.14
TC0701004	LOC652200 ///	652200 //	similar to CG14980-PB /// chromosome	9.81E-15	1	5.75	6.34	6.56	6.34	6.32	6.33	6.31	6.26
TC1700340	LOC652330 ///	652330 //	similar to neurofibromin /// neurofibro	6.49E-17	1	5.34	6.16	5.93	5.59	5.45	5.41	5.41	5.37
TC0801324	LOC652460 ///	652460 //	similar to Plectin 1 (PLTN) (PCN) (Hemi	1.12E-11	1	5.07	5.54	5.47	5.38	5.40	5.26	5.17	5.17
TC0700824	LOC652795 ///	652795 //	similar to hypothetical protein FLJ4072	2.61E-09	1	5.05	5.35	5.30	5.25	5.09	5.08	5.06	5.04
TC0701679	LOC653052 ///	653052 //	hypothetical LOC653052 /// homeodor	9.32E-18	1	5.77	7.08	6.56	6.46	6.60	6.34	6.29	6.10
TC1001378	LOC653419	653419	similar to preproneuropeptide B	9.71E-11	1	6.05	6.62	6.76	6.72	6.70	6.64	6.61	6.57
TC1700847	LOC653419 ///	653419 //	similar to preproneuropeptide B /// ne	0.000473	1	6.55	6.87	6.91	6.75	6.87	6.88	6.68	6.79
TC0700516	LOC653888 ///	653888 //	similar to Actin-related protein 2/3 con	5.63E-09	1	6.99	7.33	7.59	7.67	7.56	7.40	7.24	7.24
TC0700127	LOC653972 ///	653972 //	similar to chromobox homolog 3 /// ch	9.55E-16	1	6.98	7.51	7.64	7.74	7.70	7.57	7.60	7.45
TC1300308	LOC654264 ///	654264 //	similar to Tubulin alpha-3 chain (Alpha-	0.0009	1	4.83	5.11	5.09	5.05	5.05	5.05	4.97	5.05
TC0200715	LOC654264 ///	654264 //	similar to Tubulin alpha-3 chain (Alpha-	0.000167	1	5.24	5.51	5.52	5.48	5.53	5.50	5.41	5.47

TC2200341	LOC727731	727731	similar to metallophosphoesterase don	0.00062	1	4.75	4.81	4.85	4.79	4.80	4.72	4.69	4.68
TC0400321	LOC727738	727738	similar to Amphiregulin precursor (AR)	0.000254	1	3.65	4.52	3.86	3.88	3.90	3.81	4.02	3.87
TC0400320	LOC727738 ///	727738 //	similar to Amphiregulin precursor (AR)	0.000188	1	2.89	4.00	3.10	3.20	3.15	3.07	3.39	3.20
TC0300538	LOC727762 ///	727762 //	similar to NADH:ubiquinone oxidoredu	3.24E-06	1	3.67	4.06	4.16	4.02	4.11	4.08	4.02	4.06
TC0X01056	LOC728188 ///	728188 //	similar to phosphoglycerate mutase pr	8.39E-13	1	5.98	6.62	6.76	6.84	6.65	6.57	6.54	6.51
TC0501046	LOC728401	728401	hypothetical LOC728401	7.59E-06	1	2.91	3.60	4.07	3.69	3.57	3.33	3.48	2.91
TC0500245	LOC728401	728401	hypothetical LOC728401	0.000193	1	5.76	6.10	6.75	6.48	6.20	5.87	5.90	5.42
TC0501043	LOC728535 ///	728535 //	NLR family, apoptosis inhibitory protei	3.80E-08	1	5.93	6.38	6.59	6.38	6.29	6.25	6.26	6.02
TC0501047	LOC728535 ///	728535 //	NLR family, apoptosis inhibitory protei	5.52E-14	1	6.02	6.99	7.67	7.29	6.85	6.59	6.52	6.11
TC0200564	LOC729260 ///	729260 //	similar to LIM and senescent cell antige	3.58E-13	1	5.37	6.73	6.48	6.54	6.67	6.58	6.33	6.23
TC0600892	LOC729891	729891	hypothetical LOC729891	2.52E-05	1	4.97	4.82	5.28	5.38	5.19	5.01	4.94	4.71
TC0500242	LOC730394 ///	730394 //	general transcription factor IIH, polype	5.30E-05	1	5.53	5.85	5.99	5.78	5.76	5.77	5.81	5.59
TC0701442	LOC730919 ///	730919	hypothetical protein LOC730919 /// M	5.50E-05	1	5.24	5.52	5.51	5.45	5.39	5.42	5.35	5.37
TC1000417	LOC731292 ///	731292 //	similar to Phosphatidylinositol-3,4,5-tri	1.06E-08	1	8.51	8.87	8.99	8.69	8.54	8.76	8.64	8.78
TC1100953	LOH11CR2A	4013	loss of heterozygosity, 11, chromosom	5.68E-07	1	3.59	3.69	3.88	4.12	3.81	3.71	3.68	3.71
TC1200143	LOH12CR1	118426	loss of heterozygosity, 12, chromosom	1.36E-06	1	4.83	5.15	5.07	4.94	5.07	5.06	4.76	4.80
TC1800443	LOXHD1	125336	lipoxygenase homology domains 1 /// l	1.39E-16	1	4.36	5.29	4.73	4.85	4.84	4.33	4.40	4.46
TC1600442	LPCAT2	54947	lysophosphatidylcholine acyltransferas	7.50E-07	1	8.75	9.14	9.38	9.14	8.98	9.17	9.19	9.20
TC1300130	LRCH1	23143	leucine-rich repeats and calponin hom	0.000154	1	3.95	4.29	4.29	4.27	4.14	4.10	4.17	4.06
TC0400782	LRPAP1	4043	low density lipoprotein receptor-relate	8.66E-14	1	6.72	7.54	7.77	7.93	7.71	7.34	7.33	7.18
TC0102351	LRRC40	55631	leucine rich repeat containing 40	9.66E-08	1	3.29	3.94	4.03	3.97	3.90	3.86	3.91	3.76
TC0100570	LRRC42	115353	leucine rich repeat containing 42 /// Le	3.58E-08	1	4.96	5.51	5.37	5.22	5.30	5.26	5.31	5.17
TC0100712	LRRC8C	84230	leucine rich repeat containing 8 family,	1.43E-08	1	4.51	4.75	5.21	5.24	4.96	4.73	4.74	4.69
TC0301097	LRRFIP2	9209	leucine rich repeat (in FLII) interacting	3.46E-17	1	5.30	6.36	6.50	6.28	6.13	6.03	6.07	5.89
TC0300009	LRRN1	57633	leucine rich repeat neuronal 1	2.18E-14	1	5.01	6.33	6.26	6.06	5.91	5.73	5.58	5.43
TC0800882	LSM1	27257	LSM1 homolog, U6 small nuclear RNA	3.98E-06	1	5.09	5.56	5.78	5.69	5.65	5.66	5.67	5.67
TC0400579	LSM6	11157	LSM6 homolog, U6 small nuclear RNA	2.29E-21	1	5.26	6.74	7.16	7.08	7.00	6.68	6.52	6.43
TC0801305	LY6H	4062	lymphocyte antigen 6 complex, locus H	0.000925	1	4.94	5.04	5.08	5.04	5.01	5.05	4.88	4.98
TC0800937	LYPLA1	10434	lysophospholipase I /// Acyl-protein thi	2.61E-14	1	5.07	5.78	6.28	6.18	6.07	5.95	5.83	5.72
TC1600238	LYRM1	57149	LYR motif containing 1	1.07E-08	1	6.06	6.67	6.86	6.70	6.49	6.55	6.56	6.63
TC1901064	M6PRBP1	10226	mannose-6-phosphate receptor bindin	9.55E-10	1	5.05	5.83	5.82	5.76	5.67	5.54	5.38	5.38
TC0100415	MACF1	23499	microtubule-actin crosslinking factor 1	2.24E-10	1	5.84	6.23	6.90	6.82	6.28	5.81	6.10	5.66
TC0101859	MAD2L2	10459	MAD2 mitotic arrest deficient-like 2 (ye	1.86E-19	1	5.50	6.20	6.28	6.20	6.14	6.06	5.96	5.88
TC0400018	MAEA	730744 //	macrophage erythroblast attacher	0.000536	1	5.68	6.05	5.89	5.95	5.86	5.78	5.67	5.69

TC0801310	MAFA	389692	v-maf musculoaponeurotic fibrosarcom	2.56E-06	1	5.18	5.75	5.60	5.70	5.52	5.53	5.49	5.47
TC1701790	MAFG	4097	v-maf musculoaponeurotic fibrosarcom	5.92E-22	1	5.62	6.57	6.47	6.36	6.44	6.27	6.08	6.01
TC17r00054	MAFG	4097	v-maf musculoaponeurotic fibrosarcom	3.65E-20	1	5.29	6.27	6.30	5.93	6.19	5.92	5.77	5.61
TC1600813	Magmas	51025	mitochondria-associated protein involv	1.62E-06	1	5.48	5.79	5.78	5.89	6.02	5.87	5.76	5.64
TC0X01055	MAGT1 /// IAG	84061	magnesium transporter 1 /// Implantat	6.76E-11	1	5.88	6.73	6.59	6.37	6.39	6.33	6.45	6.39
TC0800521	MAL2	114569	mal, T-cell differentiation protein 2	2.68E-05	1	3.65	3.94	3.92	3.89	3.89	3.93	3.87	3.82
TC0100880	MAN1A2	10905	mannosidase, alpha, class 1A, member	7.71E-11	1	5.47	6.08	6.12	6.19	6.23	6.11	6.14	6.04
TC1901205	MAN2B1	4125	mannosidase, alpha, class 2B, member	0.000775	1	5.69	5.71	5.71	5.86	5.78	5.60	5.68	5.57
TC1200996	MANSC1	54682	MANSC domain containing 1 /// MANS	5.56E-10	1	7.44	8.28	8.50	8.52	8.43	8.27	8.02	8.02
TC1600655	MAP1LC3B	81631	microtubule-associated protein 1 light	0.000401	1	6.02	6.37	6.36	6.35	6.30	6.29	6.29	6.35
TC1500420	MAP2K1	5604	mitogen-activated protein kinase kinas	9.56E-13	1	5.58	6.47	6.04	6.08	6.15	6.05	6.00	5.90
TC1700717	MAP2K6	5608	mitogen-activated protein kinase kinas	6.77E-34	1	4.64	7.45	7.88	7.66	7.16	6.62	6.57	6.09
TC0500191	MAP3K1	---	Mitogen-activated protein kinase kinas	2.10E-06	1	8.29	8.82	8.61	8.68	8.36	8.48	8.42	8.43
TC0300865	MAP3K13	9175	mitogen-activated protein kinase kinas	2.83E-07	1	3.26	3.52	3.46	3.33	3.30	3.27	3.36	3.42
TC0301171	MAP4	732227 //	microtubule-associated protein 4 /// M	3.53E-05	1	4.48	4.63	4.81	4.77	4.74	4.57	4.64	4.56
TC0200531	MAP4K4	9448	mitogen-activated protein kinase kinas	6.30E-05	1	8.92	9.41	9.20	9.22	9.16	9.12	9.03	9.03
TC2200779	MAPK11	5600	mitogen-activated protein kinase 11	0.000741	1	4.09	4.27	4.26	4.21	4.23	4.16	4.15	4.13
TC0600339	MAPK14	1432	mitogen-activated protein kinase 14	3.40E-28	1	7.68	9.12	9.31	9.09	8.92	8.67	8.49	8.26
TC1400242	MAPK1IP1L	93487	mitogen-activated protein kinase 1 inte	9.83E-18	1	5.95	7.18	7.03	7.02	6.99	7.02	6.98	6.88
TC1500343	MAPK6	5597	mitogen-activated protein kinase 6	1.18E-13	1	3.90	4.65	5.27	5.20	4.99	4.60	4.47	4.29
TC0901334	MAPKAP1	79109	mitogen-activated protein kinase assoc	2.26E-08	1	5.39	5.70	5.89	5.93	5.78	5.79	5.89	5.79
TC0101465	MAPKAPK2	9261	mitogen-activated protein kinase-activ	2.13E-05	1	7.96	8.65	8.42	8.38	8.31	8.29	8.13	8.24
TC2000184	MAPRE1	22919	microtubule-associated protein, RP/EB	4.41E-20	1	7.13	8.08	8.16	7.93	7.80	7.62	7.54	7.61
TC1900150	MAR2	51257	membrane-associated ring finger (C3H	2.25E-05	1	5.12	5.52	5.62	5.56	5.62	5.49	5.43	5.36
TC0501256	MAR3	648089 //	membrane-associated ring finger (C3H	1.62E-06	1	5.02	5.54	5.31	5.55	5.53	5.29	5.27	5.15
TC1000445	MAR5	54708	membrane-associated ring finger (C3H	5.03E-11	1	5.27	6.12	6.20	6.02	5.84	5.81	5.76	5.72
TC0600655	MARCKS	4082	myristoylated alanine-rich protein kina	2.61E-17	1	6.36	7.33	7.25	7.03	7.11	7.20	7.01	6.99
TC0500227	MAST4	375449	microtubule associated serine/threonir	1.55E-12	1	4.05	4.32	4.91	4.92	4.68	4.46	4.38	4.23
TC1800485	MBD2	8932	methyl-CpG binding domain protein 2	1.15E-18	1	8.88	9.60	9.58	9.42	9.33	9.28	9.29	9.24
TC0600990	MBOAT1	154141	membrane bound O-acyltransferase dc	0.000165	1	6.14	6.61	6.82	6.73	6.53	6.58	6.55	6.58
TC0201297	MBOAT2	129642	membrane bound O-acyltransferase dc	1.37E-10	1	6.11	6.77	7.03	6.89	6.84	6.82	6.73	6.61
TC1200918	MBOAT5	10162	membrane bound O-acyltransferase dc	1.14E-11	1	5.86	6.85	6.93	6.69	6.52	6.48	6.40	6.23
TC0900919	MCART1	92014	mitochondrial carrier triple repeat 1	5.13E-11	1	3.68	4.29	4.02	3.96	4.15	4.07	4.07	3.98
TC1800403	MCART2	147407	mitochondrial carrier triple repeat 2	0.000414	1	3.07	3.57	3.37	3.26	3.46	3.36	3.45	3.32

TC1900129	MCOLN1	57192	mucolipin 1	5.87E-06	1	5.59	6.09	5.95	5.85	5.75	5.85	5.74	5.77
TC0501153	MCTP1	79772	multiple C2 domains, transmembrane	4.97E-20	1	6.77	7.83	8.04	8.01	7.84	7.82	7.67	7.58
TC1500650	MCTP2	55784	multiple C2 domains, transmembrane	1.79E-16	1	7.75	8.39	8.39	8.06	7.92	7.82	7.62	7.49
TC0X00540	MCTS1	28985	malignant T cell amplified sequence 1 /	3.63E-17	1	3.12	3.72	3.97	3.86	3.82	3.77	3.72	3.66
TC0600381	MDFI	4188	MyoD family inhibitor /// MyoD family	0.000861	1	5.49	5.70	5.73	5.69	5.69	5.68	5.61	5.64
TC1400738	MDP-1 /// CH	145553 //	magnesium-dependent phosphatase 1	4.48E-05	1	5.50	5.90	5.96	5.96	5.89	5.95	6.02	5.91
TC1800183	ME2	4200	malic enzyme 2, NAD(+)-dependent, m	1.09E-07	1	7.91	8.30	8.53	8.28	8.21	8.27	8.16	8.11
TC0601598	MED23	9439	mediator complex subunit 23 /// CRSP	1.68E-05	1	5.35	5.55	5.74	5.58	5.47	5.40	5.40	5.31
TC1400960	MED6	10001	mediator complex subunit 6	8.30E-06	1	5.12	5.32	5.41	5.20	5.01	5.25	5.46	5.40
TC0501448	MED7	9443	mediator complex subunit 7	7.42E-07	1	4.63	4.96	5.01	4.79	4.78	4.86	4.77	4.81
TC1500668	MEF2A	4205	myocyte enhancer factor 2A /// Myocy	9.25E-21	1	6.12	7.45	7.79	7.53	7.04	6.92	6.90	6.64
TC1101522	MEN1	4221	multiple endocrine neoplasia I /// Men	0.000889	1	4.86	5.02	4.97	4.97	5.04	4.98	4.93	4.95
TC0200578	MERTK	10461	c-mer proto-oncogene tyrosine kinase	7.93E-10	1	3.39	4.28	5.00	4.27	4.10	3.71	3.59	3.50
TC1500546	MESDC1	59274	mesoderm development candidate 1	7.69E-12	1	5.91	6.61	6.76	6.62	6.54	6.68	6.71	6.71
TC1700870	METRNL	284207	meteorin, glial cell differentiation regul	7.38E-05	1	5.43	5.97	5.97	5.91	5.78	5.98	5.88	5.87
TC1200409	METTL7B	196410	methyltransferase like 7B	1.55E-08	1	4.43	4.63	4.72	5.21	5.06	4.44	4.50	4.45
TC1600245	METTL9	51108	methyltransferase like 9	3.24E-37	1	6.49	8.61	8.82	8.57	8.36	7.95	7.57	7.33
TC1800480	MEX3C	51320	mex-3 homolog C (C. elegans)	1.01E-10	1	4.72	5.40	5.41	5.41	5.35	5.31	5.36	5.29
TC0500625	MFAP3	4238	microfibrillar-associated protein 3	2.54E-08	1	5.43	6.20	6.17	6.12	6.14	6.11	6.03	5.97
TC0201147	MFF /// C2orf3	56947	mitochondrial fission factor /// Unchar	1.19E-22	1	5.04	5.85	6.23	5.92	5.76	5.64	5.64	5.50
TC0100129	MFN2	9927	mitofusin 2 /// Mitofusin-2 (EC 3.6.5.-)	2.91E-12	1	6.51	7.62	7.52	7.70	7.65	7.46	7.29	7.24
TC0300749	MFSD1	64747	major facilitator superfamily domain c	1.35E-07	1	7.03	7.74	8.04	7.83	7.77	7.80	7.75	7.57
TC1700784	MFSD11	79157	major facilitator superfamily domain c	0.000148	1	3.74	3.90	3.99	3.91	3.87	3.79	3.86	3.80
TC0700767	MGAM	8972	maltase-glucoamylase (alpha-glucosida	8.30E-10	1	9.39	9.70	9.91	9.69	9.53	9.26	9.12	8.99
TC0401170	MGC16169 ///	93627	hypothetical protein MGC16169 /// TB	1.91E-09	1	3.90	4.23	4.57	4.59	4.53	4.43	4.42	4.32
TC1701136	MGC33894	256302	transcript expressed during hematopoi	0.00023	1	5.09	5.39	5.41	5.43	5.49	5.42	5.31	5.30
TC0100631	MIER1	57708	mesoderm induction early response 1	4.28E-05	1	7.16	7.57	7.74	7.66	7.56	7.68	7.62	7.64
TC2200121	MIF	4282	macrophage migration inhibitory facto	9.46E-07	1	5.10	5.52	5.51	5.69	5.64	5.50	5.51	5.39
TC2000552	MKKS	8195	McKusick-Kaufman syndrome	1.14E-07	1	4.60	5.07	5.22	5.22	5.16	5.21	5.19	5.12
TC1901083	MLLT1	4298	myeloid/lymphoid or mixed-lineage leu	3.07E-09	1	5.54	6.31	6.30	6.04	5.92	5.73	5.61	5.65
TC1101772	MMP27	64066	matrix metallopeptidase 27	0.000176	1	2.61	3.03	2.91	2.81	2.90	2.88	2.78	2.72
TC1101773	MMP8	4317	matrix metallopeptidase 8 (neutrophil	3.88E-31	1	3.88	10.08	9.69	9.67	10.24	9.99	9.08	8.08
TC2000330	MMP9	4318	matrix metallopeptidase 9 (gelatinase	1.93E-22	1	7.11	10.29	9.95	9.64	9.77	9.05	8.41	8.20
TC0701797	MNX1	3110	motor neuron and pancreas homeobo	6.93E-06	1	4.06	4.39	4.33	4.38	4.34	4.30	4.15	4.32

TC0201631	MOBKL1B	55233	MOB1, Mps One Binder kinase activato	0.000443	1	8.46	8.70	8.85	8.81	8.71	8.75	8.69	8.75
TC0102226	MOBKL2C	148932	MOB1, Mps One Binder kinase activato	1.72E-09	1	4.62	5.17	4.92	4.87	4.75	4.74	4.74	4.67
TC0401411	MORF4	10934	mortality factor 4	0.000159	1	3.36	3.83	3.86	3.75	3.67	3.68	3.72	3.72
TC1500531	MORF4 /// MO	10934 ///	mortality factor 4 /// mortality factor 4	1.23E-08	1	9.08	9.43	9.43	9.37	9.28	9.26	9.26	9.27
TC0101530	MOSC1	64757	MOCO sulphurase C-terminal domain c	1.39E-05	1	6.59	7.05	7.12	7.32	7.34	7.13	6.91	6.94
TC0700548	MOSPD3	64598	motile sperm domain containing 3	1.15E-13	1	4.97	5.81	6.01	5.66	5.64	5.46	5.34	5.32
TC0X01396	MPP1	4354	membrane protein, palmitoylated 1, 55	1.92E-08	1	8.00	8.41	8.48	8.54	8.37	8.09	8.05	7.94
TC1000847	MPP7	143098	membrane protein, palmitoylated 7 (M	1.85E-18	1	5.08	6.20	6.58	6.65	6.51	6.34	6.36	6.16
TC0101333	MR1	3140	major histocompatibility complex, class	1.17E-07	1	5.60	6.45	6.36	6.16	5.95	6.09	6.21	6.13
TC0202298	MREG	55686	melanoregulin	9.77E-06	1	3.00	3.13	3.19	3.19	3.21	3.05	2.93	2.92
TC0400059	MRFAP1	93621	Mof4 family associated protein 1	2.15E-05	1	4.99	5.35	5.39	5.30	5.21	5.29	5.29	5.34
TC1600712	MRPL28	10573	mitochondrial ribosomal protein L28	1.80E-07	1	6.07	6.57	6.44	6.58	6.55	6.49	6.41	6.40
TC0200137	MRPL33	9553	mitochondrial ribosomal protein L33 //	1.28E-07	1	6.54	7.00	7.18	7.15	7.09	7.08	7.05	7.01
TC0500827	MRPL36	64979	mitochondrial ribosomal protein L36	0.000982	1	5.79	6.18	6.19	6.15	6.24	6.20	6.08	6.09
TC0301785	MRPL47	57129	mitochondrial ribosomal protein L47	1.33E-06	1	5.13	6.03	5.98	5.97	6.00	6.02	6.08	6.02
TC0201637	MRPL53	116540	mitochondrial ribosomal protein L53	2.41E-06	1	5.52	5.95	6.19	6.22	6.21	6.12	6.14	6.03
TC0900689	MRPS2	51116	mitochondrial ribosomal protein S2	6.14E-05	1	5.00	5.25	5.29	5.19	5.24	5.20	5.13	5.15
TC0300660	MRPS22	56945	mitochondrial ribosomal protein S22	4.29E-08	1	4.58	5.27	5.46	5.35	5.27	5.20	5.21	5.13
TC1300424	MRPS31	10240	mitochondrial ribosomal protein S31	1.05E-13	1	5.50	6.65	6.79	6.52	6.26	6.22	6.35	6.11
TC0600126	MRS2 /// MRS2	57380	MRS2 magnesium homeostasis factor h	0.000403	1	3.77	3.97	4.11	4.07	4.12	4.05	4.10	3.99
TC1100433	MS4A4A	51338	membrane-spanning 4-domains, subfam	2.94E-08	1	3.05	3.73	4.25	4.64	4.34	3.43	3.50	3.12
TC1101453	MS4A6A	64231	membrane-spanning 4-domains, subfam	4.52E-22	1	5.22	6.99	7.55	7.30	7.00	6.75	6.66	6.21
TC0500309	MSH3	4437	mutS homolog 3 (E. coli)	2.40E-08	1	4.84	5.58	5.88	5.94	5.83	5.59	5.62	5.42
TC0X00040	MSL3L1	10943	male-specific lethal 3-like 1 (Drosophila	3.69E-30	1	6.45	8.14	8.43	8.09	7.84	7.60	7.50	7.15
TC0800060	MSRA	4482	methionine sulfoxide reductase A /// P	5.84E-20	1	5.46	7.06	6.81	6.55	6.66	6.37	6.22	6.02
TC0500723	MSX2	4488	msh homeobox 2	7.93E-05	1	2.66	2.87	3.05	2.84	3.02	2.94	2.69	3.00
TC1101476	MTA2	9219	metastasis associated 1 family, membe	1.42E-05	1	5.13	5.78	5.53	5.76	5.80	5.70	5.67	5.51
TC0800449	MTDH	92140	metadherin	1.22E-17	1	6.17	7.73	7.80	8.01	8.10	7.93	7.93	7.53
TC0102133	MTF1 /// MGA	4520 ///	metal-regulatory transcription factor 1	2.48E-19	1	7.52	8.56	8.76	8.83	8.61	8.33	8.18	8.10
TC0100734	MTF2	22823	metal response element binding transc	8.12E-07	1	5.07	5.94	5.85	5.65	5.67	5.80	5.91	5.79
TC0200355	MTHFD2	10797	methylenetetrahydrofolate dehydroge	4.34E-09	1	4.04	5.25	5.39	5.77	5.59	5.51	5.45	5.22
TC1501155	MTHFS	10588	5,10-methenyltetrahydrofolate synthet	1.97E-14	1	6.51	7.24	7.18	6.85	6.64	6.64	6.57	6.73
TC1300351	MTMR6	9107	myotubularin related protein 6 /// Myo	2.08E-07	1	6.28	7.05	6.95	6.84	6.77	6.87	6.73	6.77
TC0800067	MTMR9	66036	myotubularin related protein 9	0.00026	1	4.14	4.56	4.62	4.44	4.37	4.39	4.40	4.36

TC0600506	MTO1	25821	mitochondrial translation optimization	2.17E-05	1	4.69	5.00	5.06	5.06	5.17	5.03	5.05	4.89
TC0701659	MTPN	136319	myotrophin	1.96E-11	1	9.38	9.83	9.99	9.96	9.90	9.98	9.90	9.91
TC0601697	MTRF1L	54516	mitochondrial translational release fact	0.000893	1	5.17	5.71	5.64	5.67	5.56	5.68	5.72	5.56
TC0500036	MTRR	4552	5-methyltetrahydrofolate-homocystein	7.75E-23	1	4.28	5.55	6.29	6.10	5.59	5.03	4.94	4.72
TC1100555	MUS81	80198	MUS81 endonuclease homolog (S. cere	1.65E-05	1	4.90	5.01	5.08	5.02	5.03	4.96	4.96	4.91
TC0601311	MUT	4594	methylmalonyl Coenzyme A mutase	9.68E-12	1	4.51	5.29	5.36	5.22	5.16	5.02	5.07	4.97
TC1701720	MXRA7	439921	matrix-remodelling associated 7 /// Ma	4.46E-05	1	3.68	4.60	4.72	4.83	4.85	4.57	4.50	4.25
TC0300159	MYD88	4615	myeloid differentiation primary respon	2.77E-08	1	7.99	8.77	8.73	8.92	8.83	8.81	8.54	8.53
TC0202435	MYEOV2	150678	myeloma overexpressed 2	8.52E-09	1	4.94	5.44	5.69	5.69	5.70	5.56	5.51	5.49
TC1200426	MYL6B /// MYL	140465 //	myosin, light chain 6B, alkali, smooth m	1.65E-15	1	6.60	7.03	7.09	7.05	7.04	7.01	6.94	6.91
TC0300775	MYNN	55892	myoneurin /// Myoneurin (Zinc finger a	3.20E-06	1	5.12	5.61	5.51	5.35	5.24	5.47	5.39	5.51
TC0500869	MYO10	4651	myosin X	0.000923	1	3.61	3.93	4.21	4.10	4.13	4.17	3.99	3.78
TC1501002	MYO1E	4643	myosin IE	0.000183	1	3.09	3.24	3.17	3.13	3.09	3.11	3.12	3.10
TC0701181	MYO1G	64005	myosin IG	9.20E-06	1	5.46	5.86	5.70	5.58	5.54	5.50	5.54	5.50
TC1701588	NACA2	342538	nascent polypeptide-associated comple	0.00035	1	2.38	2.59	2.76	2.69	2.74	2.69	2.68	2.69
TC0900427	NANS	54187	N-acetylneuraminic acid synthase (siali	1.97E-10	1	5.40	5.95	6.17	5.97	5.89	5.91	5.85	5.61
TC0801313	NAPRT1	93100	nicotinate phosphoribosyltransferase d	2.68E-05	1	5.50	5.77	5.78	5.66	5.74	5.63	5.55	5.53
TC1700863	NARF	26502	nuclear prelamin A recognition factor	1.69E-05	1	7.38	7.73	7.57	7.70	7.59	7.52	7.46	7.34
TC1300101	NARG1L	79612	NMDA receptor regulated 1-like /// NM	0.000123	1	3.81	4.14	4.24	4.16	4.12	4.18	4.11	4.07
TC0100499	NASP	4678	nuclear autoantigenic sperm protein (h	0.000284	1	5.37	6.32	6.08	6.05	6.00	6.06	6.31	6.03
TC1100225	NAV2	89797	neuron navigator 2 /// Neuron navigato	1.70E-05	1	3.17	3.36	3.26	3.20	3.34	3.32	3.21	3.21
TC0200550	NCK2	8440	NCK adaptor protein 2	6.04E-05	1	5.61	6.13	5.91	5.92	6.02	5.92	5.94	5.85
TC1200390	NCKAP1L	3071	NCK-associated protein 1-like	6.22E-12	1	7.48	8.05	8.42	8.22	7.94	7.77	7.79	7.62
TC0600702	NCOA7	135112	nuclear receptor coactivator 7 /// Nucl	2.35E-14	1	4.47	5.76	5.73	5.77	5.85	5.73	5.74	5.40
TC0500565	NDFIP1	80762	Nedd4 family interacting protein 1 /// I	1.90E-15	1	5.75	6.41	6.70	6.53	6.34	6.41	6.43	6.34
TC0801264	NDRG1	10397	N-myc downstream regulated gene 1 /,	1.42E-05	1	6.84	7.25	7.17	7.27	7.14	6.96	6.82	6.73
TC1001078	NDST2	8509	N-deacetylase/N-sulfotransferase (hep	1.86E-17	1	5.63	6.65	6.45	6.03	5.89	5.60	5.52	5.39
TC0X00533	NDUFA1	4694	NADH dehydrogenase (ubiquinone) 1 a	1.38E-20	1	9.41	10.00	10.20	10.11	10.09	10.08	10.05	10.05
TC0701014	NDUFA4	4697	NADH dehydrogenase (ubiquinone) 1 a	7.88E-13	1	6.26	7.28	7.59	7.47	7.47	7.38	7.34	7.21
TC0901305	NDUFA8	4702	NADH dehydrogenase (ubiquinone) 1 a	1.18E-13	1	4.52	6.24	6.37	6.51	6.47	6.17	6.30	5.85
TC1200035	NDUFA9	4704	NADH dehydrogenase (ubiquinone) 1 a	4.64E-07	1	3.33	4.48	4.49	4.42	4.52	4.48	4.43	4.16
TC1500862	NDUFAF1	51103	NADH dehydrogenase (ubiquinone) 1 a	1.88E-19	1	4.45	5.78	6.31	5.97	5.80	5.59	5.49	5.33
TC0200986	NDUFB3	4709	NADH dehydrogenase (ubiquinone) 1 b	1.46E-19	1	8.52	9.49	9.87	9.78	9.63	9.58	9.51	9.47
TC03r00006	NDUFB4	4710	NADH dehydrogenase (ubiquinone) 1 b	3.67E-06	1	3.64	4.04	4.22	4.16	4.18	4.14	4.15	4.12

TC0800545	NDUFB9	4715	NADH dehydrogenase (ubiquinone) 1 b	5.82E-21	1	5.72	7.58	7.87	7.69	7.76	7.49	7.22	6.95
TC0401272	NDUFC1	4717	NADH dehydrogenase (ubiquinone) 1,	1.67E-07	1	4.03	4.62	4.61	4.54	4.64	4.60	4.55	4.56
TC1101690	NDUFC2	4718	NADH dehydrogenase (ubiquinone) 1,	1.85E-17	1	4.41	5.42	5.99	5.87	5.76	5.52	5.57	5.35
TC0500175	NDUFS4	4724	NADH dehydrogenase (ubiquinone) Fe-	3.61E-11	1	3.83	5.08	5.29	5.02	5.17	4.99	4.77	4.59
TC0100413	NDUFS5	4725	NADH dehydrogenase (ubiquinone) Fe-	1.36E-23	1	7.18	8.75	9.10	9.14	9.25	9.14	9.02	8.63
TC1800041	NDUFV2	4729	NADH dehydrogenase (ubiquinone) fla	4.57E-12	1	5.25	6.15	6.25	6.25	6.07	6.15	6.19	6.00
TC0800425	NECAB1	64168	N-terminal EF-hand calcium binding pr	1.35E-22	1	2.91	3.32	4.31	4.63	4.06	3.30	3.12	3.06
TC0100181	NECAP2	55707	NECAP endocytosis associated 2 /// Ad	0.000159	1	6.02	6.42	6.36	6.48	6.36	6.31	6.36	6.36
TC1200610	NEDD1	121441	neural precursor cell expressed, develo	0.000193	1	4.13	4.75	4.91	4.66	4.66	4.53	4.63	4.57
TC1500976	NEDD4	4734	neural precursor cell expressed, develo	1.03E-19	1	3.58	5.54	5.81	5.24	5.23	4.83	4.50	4.12
TC1400739	NEDD8	4738	neural precursor cell expressed, develo	1.86E-05	1	7.42	7.91	8.01	8.01	7.87	7.86	7.89	7.82
TC1500495	NEIL1	79661	nei endonuclease VIII-like 1 (E. coli) ///	3.52E-09	1	4.44	4.71	4.58	4.51	4.54	4.49	4.44	4.43
TC1401001	NEK9	91754	NIMA (never in mitosis gene a)- related	7.11E-13	1	4.95	5.64	5.48	5.33	5.19	5.00	4.98	4.97
TC1601077	NETO2	81831	neuropilin (NRP) and tolloid (TLL)-like 2	1.83E-08	1	3.57	3.68	3.70	3.95	3.91	3.68	3.65	3.64
TC1201262	NFE2	4778	nuclear factor (erythroid-derived 2), 45	3.27E-05	1	7.62	8.24	8.16	8.26	8.05	7.91	7.62	7.66
TC0400429	NFKB1	4790	nuclear factor of kappa light polypepti	8.83E-14	1	6.82	7.56	7.74	7.76	7.53	7.39	7.40	7.24
TC1400790	NFKBIA	4792	nuclear factor of kappa light polypepti	6.80E-06	1	7.26	7.65	7.64	7.83	7.74	7.49	7.40	7.41
TC0300463	NFKBIZ	64332	nuclear factor of kappa light polypepti	1.12E-06	1	7.53	8.17	8.01	8.03	7.86	7.91	7.73	7.65
TC0201590	NFU1	27247	NFU1 iron-sulfur cluster scaffold homo	2.71E-14	1	4.51	5.61	5.76	5.49	5.68	5.68	5.58	5.52
TC1300094	NHLRC3	387921	NHL repeat containing 3	5.26E-09	1	3.64	4.81	4.80	4.48	4.55	4.40	4.37	4.07
TC2200569	NIPSNAP1	8508	nipsnap homolog 1 (C. elegans)	6.74E-05	1	4.23	4.31	4.46	4.54	4.41	4.41	4.31	4.30
TC0X01193	NKAP	79576	NFKB activating protein	4.07E-06	1	6.33	7.11	7.14	7.15	6.99	7.03	7.26	7.18
TC1901740	NKG7	4818	natural killer cell group 7 sequence	8.26E-11	1	5.65	7.90	7.82	7.88	8.60	8.33	7.82	7.11
TC1700276	NLK	51701	nemo-like kinase	5.82E-20	1	4.93	6.25	6.35	6.39	6.34	6.24	5.99	5.85
TC0201419	NLRC4	58484	NLR family, CARD domain containing 4	3.76E-31	1	5.29	7.37	7.77	7.55	7.39	7.02	6.81	6.32
TC1901788	NLRP12	91662	NLR family, pyrin domain containing 12	0.000161	1	6.91	7.09	7.20	7.00	6.90	6.92	6.82	6.81
TC0101693	NLRP3	114548	NLR family, pyrin domain containing 3 ,	2.17E-10	1	4.87	6.61	5.84	6.01	5.73	5.50	5.43	5.22
TC1901200	NM_00108082	---	zinc finger protein 799 (ZNF799), mRN	1.94E-06	1	3.60	3.99	3.94	3.94	3.67	3.68	3.76	3.78
TC1300072	NM_145293	---	---	3.22E-09	1	4.35	4.68	4.65	4.60	4.56	4.45	4.33	4.37
TC1600746	NME3	4832	non-metastatic cells 3, protein express	0.000146	1	5.01	5.24	5.29	5.25	5.34	5.27	5.21	5.21
TC1600016	NME4	4833	non-metastatic cells 4, protein express	3.32E-05	1	5.19	5.39	5.37	5.45	5.51	5.43	5.34	5.29
TC0103058	NMNAT2	23057	nicotinamide nucleotide adenylyltrans	2.16E-12	1	4.21	4.40	4.45	4.28	4.25	4.23	4.14	4.14
TC1700516	NMT1	4836	N-myristoyltransferase 1	9.12E-08	1	5.72	6.17	6.41	6.51	6.42	6.12	6.18	6.00
TC0600085	NOL7	51406	nucleolar protein 7, 27kDa	5.19E-21	1	6.88	8.57	8.68	8.39	8.35	8.25	8.28	7.98

TC1701780	NPLOC4	55666	nuclear protein localization 4 homolog	0.000347	1	5.94	6.08	6.01	6.02	6.00	5.94	5.86	5.83
TC0600022	NQO2 /// NM_	4835	NAD(P)H dehydrogenase, quinone 2 //	0.000135	1	5.96	6.02	6.21	6.19	6.17	6.07	6.04	5.90
TC1700149	NR_002211.1	---	Meis homeobox 3 pseudogene 1 (MEIS	4.88E-06	1	3.74	4.30	4.24	4.35	4.38	4.31	4.30	4.24
TC1001171	NR_002319.1	---	PIP5K1A and PSMD4-like (PIPSL) on chr	8.62E-07	1	4.71	5.13	5.31	5.30	5.12	5.27	5.24	5.30
TC0900896	NR_003051.1	---	RNA component of mitochondrial RNA	5.48E-06	1	3.86	5.74	5.94	5.59	5.83	5.59	5.05	5.15
TC0102938	NR1I3	9970	nuclear receptor subfamily 1, group I, r	0.000171	1	3.63	3.86	3.78	3.68	3.77	3.73	3.60	3.64
TC0600616	NR2E1	7101	nuclear receptor subfamily 2, group E,	2.77E-13	1	3.22	3.64	3.67	3.54	3.48	3.38	3.30	3.21
TC1600954	NSMCE1	197370	non-SMC element 1 homolog (S. cerevi	5.49E-16	1	4.68	5.56	5.78	5.79	5.70	5.52	5.51	5.39
TC0800549	NSMCE2	286053	non-SMC element 2, MMS21 homolog	1.43E-10	1	4.51	5.75	5.48	5.39	5.44	5.51	5.56	5.28
TC0300415	NSUN3	63899	NOL1/NOP2/Sun domain family, mem	4.73E-11	1	5.89	6.15	6.51	6.76	6.39	6.26	6.25	6.26
TC0400184	NSUN7	79730	NOL1/NOP2/Sun domain family, mem	6.74E-16	1	4.26	4.75	5.26	4.86	4.41	4.06	3.93	3.71
TC1201514	NT5DC3	51559	5'-nucleotidase domain containing 3	6.09E-11	1	3.22	4.02	3.79	3.67	3.91	3.79	3.65	3.54
TC1100507	NUDT22	84304	nudix (nucleoside diphosphate linked	7.54E-08	1	4.96	5.36	5.28	5.34	5.29	5.14	5.16	5.06
TC0X00491	NXT2	55916	nuclear transport factor 2-like export f	7.20E-15	1	4.19	4.94	5.27	5.11	5.11	5.02	4.92	4.76
TC1001330	OAT	648399 //	ornithine aminotransferase (gyrate atr	1.21E-26	1	4.64	5.90	6.21	5.77	5.62	5.27	5.12	4.95
TC0400212	OCIAD1	54940	OCIA domain containing 1	8.03E-05	1	5.62	5.87	5.93	5.72	5.71	5.69	5.73	5.74
TC0X00556	OCRL	4952	oculocerebrorenal syndrome of Lowe /	5.02E-05	1	2.97	3.40	3.36	3.28	3.56	3.44	3.32	3.18
TC0X01219	ODZ1	10178	odz, odd Oz/ten-m homolog 1(Drosop	1.98E-14	1	3.99	5.05	4.79	4.40	4.16	3.99	3.96	3.81
TC1000071	OLAH	55301	oleoyl-ACP hydrolase /// S-acyl fatty ac	1.90E-13	1	2.46	3.63	4.25	4.03	3.82	2.88	2.80	2.71
TC1300171	OLFM4	10562	olfactomedin 4	9.56E-10	1	3.87	7.71	6.86	7.93	8.41	7.75	7.08	6.05
TC0801326	OPLAH	26873	5-oxoprolinase (ATP-hydrolysing)	1.48E-06	1	5.30	5.41	5.42	5.37	5.38	5.33	5.21	5.25
TC2000475	OPRL1	652222 //	opiate receptor-like 1	0.000147	1	4.60	4.82	4.93	4.92	4.82	4.85	4.71	4.74
TC0700826	OR2F2	135948	olfactory receptor, family 2, subfamily	8.94E-07	1	2.56	2.98	3.21	2.93	2.88	2.91	2.55	2.74
TC1200766	ORAI1	84876	ORAI calcium release-activated calcium	5.23E-07	1	4.57	5.02	5.04	4.98	5.02	4.83	4.76	4.77
TC0600549	ORC3L	23595	origin recognition complex, subunit 3-li	0.00013	1	3.81	4.01	4.09	3.90	3.86	4.07	4.07	4.08
TC0900504	ORM2 /// OR	5005 ///	orosomucoid 2 /// orosomucoid 1	3.61E-07	1	6.72	7.99	7.32	7.15	7.78	7.73	7.28	6.95
TC1200412	ORMDL2	29095	ORM1-like 2 (S. cerevisiae)	2.04E-06	1	7.22	7.92	7.96	7.84	7.89	7.85	7.77	7.74
TC1800380	OSBPL1A	114876	oxysterol binding protein-like 1A	8.19E-08	1	4.23	5.02	5.20	5.03	5.13	5.07	5.03	4.79
TC0100545	OSBPL9	114883	oxysterol binding protein-like 9 /// Oxy	6.93E-18	1	5.70	6.58	6.44	6.22	6.08	5.90	5.87	5.78
TC1901790	OSCAR	126014	osteoclast associated, immunoglobulin	8.39E-13	1	4.55	5.06	5.17	4.98	4.95	4.81	4.80	4.74
TC0300933	OSTalpha	200931	organic solute transporter alpha	2.57E-14	1	4.67	5.46	5.53	5.06	5.04	4.93	4.84	4.73
TC0900300	OSTF1	26578	osteoclast stimulating factor 1	2.21E-07	1	9.28	9.69	9.84	9.75	9.59	9.68	9.63	9.66
TC1000115	OTUD1	220213	OTU domain containing 1	5.77E-06	1	6.59	6.69	7.19	7.30	7.08	7.04	6.96	6.96
TC0300160	OXSR1	9943	oxidative-stress responsive 1	9.82E-09	1	6.53	7.48	7.26	7.18	7.29	7.27	7.16	6.97

TC1001060	P4HA1	5033	procollagen-proline, 2-oxoglutarate 4-c	2.96E-07	1	5.30	5.95	5.72	6.13	5.86	5.67	5.69	5.67
TC0600865	PACRG	135138	PARK2 co-regulated	5.06E-05	1	3.52	3.68	3.67	3.54	3.59	3.58	3.51	3.56
TC0100197	PADI4	23569	peptidyl arginine deiminase, type IV ///	1.50E-08	1	7.55	8.68	8.19	8.06	8.32	8.05	7.58	7.51
TC1700024	PAFAH1B1	5048	platelet-activating factor acetylhydrola	0.000219	1	8.38	8.70	8.71	8.68	8.57	8.64	8.60	8.58
TC0801063	PAG1	55824	phosphoprotein associated with glycos	6.10E-24	1	5.79	7.54	7.56	7.35	7.25	7.12	7.01	6.70
TC0501478	PANK3	79646	pantothenate kinase 3	1.74E-13	1	4.56	5.79	5.70	5.44	5.43	5.36	5.34	5.12
TC0500303	PAPD4	167153	PAP associated domain containing 4	3.55E-10	1	7.72	8.22	8.41	8.23	8.08	8.06	7.98	7.98
TC1000415	PAPSS2	9060	3'-phosphoadenosine 5'-phosphosulfat	2.81E-05	1	4.51	5.05	4.86	4.86	4.94	4.92	4.82	4.74
TC0301808	PARL	55486	presenilin associated, rhomboid-like	0.000179	1	5.60	5.87	6.40	5.94	5.76	5.72	5.89	5.73
TC0600806	PCMT1	5110	protein-L-isoaspartate (D-aspartate) O-	1.57E-40	1	6.55	8.11	8.23	7.99	7.98	7.72	7.56	7.46
TC1700611	PCTP	58488	phosphatidylcholine transfer protein	0.000619	1	4.87	5.25	5.28	5.17	5.02	5.07	5.04	5.07
TC0301733	PDCD10	11235	programmed cell death 10	9.67E-10	1	8.12	8.59	8.80	8.58	8.47	8.55	8.52	8.51
TC0501002	PDE4D	5144	phosphodiesterase 4D, cAMP-specific (	5.19E-10	1	4.13	5.14	5.02	4.81	4.85	4.70	4.63	4.46
TC0401355	PDGFC	56034	platelet derived growth factor C	1.18E-23	1	3.30	4.13	5.58	5.53	4.75	3.84	3.62	3.55
TC0301297	PDHB	5162	pyruvate dehydrogenase (lipoamide) b	0.000473	1	5.23	5.64	5.68	5.70	5.64	5.66	5.73	5.58
TC0X00099	PDK3	5165	pyruvate dehydrogenase kinase, isozyn	0.00055	1	6.17	6.54	6.67	6.74	6.60	6.65	6.55	6.58
TC1000128	PDSS1	23590	prenyl (decaprenyl) diphosphate synth	4.30E-16	1	4.55	5.71	6.07	5.46	5.17	4.89	4.84	4.72
TC2100163	PDXK	8566	pyridoxal (pyridoxine, vitamin B6) kinas	3.34E-12	1	5.62	6.53	6.24	6.41	6.63	6.52	6.32	6.19
TC1001299	PDZD8	118987	PDZ domain containing 8	1.49E-08	1	7.50	8.32	8.29	8.05	8.11	8.11	7.99	7.78
TC0202299	PECR	55825	peroxisomal trans-2-enoyl-CoA reducta	2.13E-30	1	3.99	6.38	6.84	6.69	6.54	5.80	5.42	4.90
TC0102070	PEF1	553115	penta-EF-hand domain containing 1	3.08E-09	1	5.32	5.79	5.69	5.70	5.66	5.61	5.52	5.49
TC0202428	PER2	8864	period homolog 2 (Drosophila) /// Peri	1.70E-07	1	4.60	5.06	4.91	5.03	5.10	4.98	4.85	4.84
TC0601640	PERP	64065	PERP, TP53 apoptosis effector	0.000181	1	4.76	5.06	4.97	4.98	5.04	4.94	4.88	4.86
TC0200271	PEX13	5194	peroxisome biogenesis factor 13	0.000136	1	4.79	5.15	5.18	5.11	5.13	5.16	5.20	5.13
TC0501344	PFDN1	5201	prefoldin subunit 1	2.43E-09	1	4.88	5.91	5.58	5.57	5.55	5.53	5.53	5.30
TC0101469	PFKFB2	5208	6-phosphofructo-2-kinase/fructose-2,6	4.97E-29	1	5.35	8.43	8.37	7.26	6.93	6.25	6.18	5.93
TC1000036	PFKFB3	5209	6-phosphofructo-2-kinase/fructose-2,6	6.51E-27	1	6.16	8.71	8.37	7.94	7.74	7.23	6.86	6.64
TC1700945	PFN1	5216	profilin 1	1.09E-07	1	6.75	7.12	7.26	7.27	7.32	7.16	7.05	7.01
TC0Xr00014	PGAM4	441531	phosphoglycerate mutase family memb	1.39E-09	1	7.03	7.71	7.84	7.82	7.75	7.59	7.64	7.62
TC0100108	PGD	5226	phosphogluconate dehydrogenase	2.91E-24	1	8.77	9.98	10.06	10.08	9.92	9.62	9.48	9.36
TC0X00377	PGK1	5230	phosphoglycerate kinase 1	6.97E-31	1	6.76	7.78	7.89	7.65	7.48	7.36	7.26	7.17
TC1901615	PGLYRP1	8993	peptidoglycan recognition protein 1	3.11E-18	1	6.65	9.16	8.84	9.05	9.63	9.20	8.78	8.34
TC1901263	PGLYRP2	114770	peptidoglycan recognition protein 2 //	0.000468	1	4.41	4.58	4.58	4.52	4.46	4.47	4.39	4.40
TC0100616	PGM1	5236	phosphoglucomutase 1 /// Phosphoglu	3.01E-18	1	4.58	5.80	5.81	5.95	5.89	5.65	5.45	5.32

TC0400161	PGM2	55276	phosphoglucomutase 2	4.95E-10	1	6.98	6.98	7.69	7.62	7.35	7.28	7.28	7.22
TC1101658	PGM2L1	283209	phosphoglucomutase 2-like 1	2.24E-14	1	3.81	4.89	5.37	4.88	4.69	4.55	4.56	4.29
TC0600777	PHACTR2	9749	phosphatase and actin regulator 2 ///	6.86E-28	1	4.86	7.05	7.00	6.63	6.65	6.41	6.37	6.06
TC0301742	PHC3	80012	polyhomeotic homolog 3 (Drosophila)	0.00088	1	7.09	7.54	7.60	7.52	7.36	7.45	7.41	7.49
TC1100684	PHCA	55331	phytoceramidase, alkaline	1.16E-21	1	4.16	5.31	6.14	5.57	5.29	4.82	4.75	4.60
TC0X00574	PHF6	84295	PHD finger protein 6 /// PHD finger pro	0.000304	1	4.17	4.66	4.76	4.67	4.68	4.67	4.69	4.54
TC1201403	PHLDA1	22822	pleckstrin homology-like domain, famil	0.000331	1	3.34	3.55	3.53	3.57	3.66	3.60	3.44	3.43
TC1101079	PHLDA2	7262	pleckstrin homology-like domain, famil	6.57E-05	1	5.85	6.09	6.16	6.16	6.23	6.13	6.04	6.06
TC1800232	PHLPP	23239	PH domain and leucine rich repeat pro	5.27E-06	1	5.23	5.92	5.82	5.95	5.88	5.76	5.62	5.61
TC0102557	PHTF1	10745	putative homeodomain transcription f	1.07E-21	1	5.45	7.16	7.17	6.87	6.67	6.37	6.36	5.98
TC0102373	PIGK	10026	phosphatidylinositol glycan anchor bio	6.36E-14	1	4.15	5.08	5.60	5.28	5.19	5.03	5.06	4.83
TC1001191	PIK3AP1	118788	phosphoinositide-3-kinase adaptor pro	8.81E-09	1	8.28	9.15	9.20	9.21	8.97	8.81	8.78	8.74
TC0301603	PIK3CB	5291	phosphoinositide-3-kinase, catalytic, b	2.66E-16	1	6.02	6.65	6.80	6.93	6.87	6.66	6.57	6.38
TC0700604	PIK3CG	5294	phosphoinositide-3-kinase, catalytic, g	4.30E-05	1	8.29	8.81	8.59	8.61	8.53	8.54	8.40	8.46
TC0500229	PIK3R1	5295	phosphoinositide-3-kinase, regulatory	2.88E-08	1	6.36	6.68	6.87	7.02	6.76	6.75	6.90	6.81
TC0600357	PIM1	5292	pim-1 oncogene	6.45E-06	1	5.57	6.28	6.10	6.00	5.80	5.87	5.87	5.84
TC0X00348	PIN4	731103 //	protein (peptidylprolyl cis/trans isome	1.07E-08	1	4.88	5.30	5.51	5.42	5.53	5.42	5.49	5.31
TC0101030	PIP5K1A	8394	phosphatidylinositol-4-phosphate 5-ki	5.52E-05	1	6.61	7.12	6.96	6.88	6.74	6.86	6.78	6.76
TC1000727	PITRM1	10531	pitrilysin metallopeptidase 1 /// Preseq	0.000557	1	4.54	4.80	4.84	4.81	4.85	4.70	4.80	4.61
TC0501204	PJA2	9867	praja 2, RING-H2 motif containing	1.61E-06	1	9.34	9.65	9.62	9.47	9.31	9.41	9.29	9.35
TC1501082	PKM2	5315	pyruvate kinase, muscle /// Pyruvate ki	2.50E-35	1	5.81	8.35	8.18	8.65	8.67	7.94	7.56	7.18
TC1900248	PKN1	5585	protein kinase N1	7.68E-05	1	5.36	5.77	5.66	5.64	5.60	5.61	5.61	5.62
TC0101366	PLA2G4A	5321	phospholipase A2, group IVA (cytosolic	1.02E-06	1	2.93	3.79	3.44	3.62	3.76	3.57	3.59	3.42
TC0601304	PLA2G7	7941	phospholipase A2, group VII (platelet-a	2.46E-08	1	3.08	3.61	3.38	3.23	3.26	3.22	3.27	3.32
TC0900834	PLAA	9373	phospholipase A2-activating protein	2.09E-09	1	5.23	5.94	5.99	5.72	5.61	5.61	5.60	5.50
TC0401088	PLAC8	51316	placenta-specific 8	3.71E-31	1	3.98	7.28	8.43	8.00	7.88	7.21	6.77	6.06
TC0800949	PLAG1	5324	pleiomorphic adenoma gene 1	7.55E-11	1	3.39	3.90	3.94	3.68	3.61	3.62	3.64	3.62
TC0200140	PLB1	151056	phospholipase B1 /// phospholipase B1	6.46E-08	1	5.35	5.63	5.89	5.79	5.68	5.41	5.22	5.09
TC0301752	PLD1	5337	phospholipase D1, phosphatidylcholin	5.45E-08	1	4.38	5.17	5.09	5.13	5.32	5.18	4.98	4.81
TC0200903	PLEKHA3	65977	pleckstrin homology domain containin	0.000513	1	5.76	6.24	6.14	6.15	6.10	6.22	6.25	6.17
TC0800441	PLEKHF2	79666	pleckstrin homology domain containin	7.91E-08	1	6.78	7.19	7.45	7.30	7.17	7.25	7.22	7.26
TC0600815	PLEKHG1	57480	pleckstrin homology domain containin	6.97E-13	1	2.98	3.15	3.57	3.75	3.49	3.18	3.07	3.01
TC0100128	PLOD1	5351	procollagen-lysine 1, 2-oxoglutarate 5-	2.62E-05	1	5.75	6.09	6.15	6.39	6.29	6.19	5.95	6.01
TC0X00220	PLP2	5355	proteolipid protein 2 (colonic epitheliu	2.26E-13	1	7.67	9.12	9.36	9.29	9.24	8.88	8.66	8.55

TC0301639	PLSCR1	5359	phospholipid scramblase 1	1.40E-28	1	5.27	8.03	7.90	7.42	7.32	7.34	7.14	6.99
TC0600342	PNPLA1	285848	patatin-like phospholipase domain con	2.14E-09	1	5.01	5.58	5.85	5.93	5.86	5.67	5.52	5.41
TC1100027	PNPLA2	57104	patatin-like phospholipase domain con	3.90E-05	1	5.70	6.10	5.98	5.97	6.03	5.91	5.84	5.83
TC0701551	PNPLA8	50640	patatin-like phospholipase domain con	1.75E-07	1	5.27	6.08	5.91	5.78	5.66	5.81	5.83	5.81
TC1100664	POLD3	10714	polymerase (DNA-directed), delta 3, ac	0.00038	1	7.28	7.31	7.61	7.66	7.20	7.16	7.40	7.26
TC0200366	POLE4	56655	polymerase (DNA-directed), epsilon 4 (	9.90E-16	1	5.34	7.12	7.29	7.19	7.33	7.18	7.16	6.83
TC1800190	POLI	11201	polymerase (DNA directed) iota	0.000556	1	4.80	4.88	5.19	5.15	5.05	4.94	4.96	4.93
TC0500275	POLK /// CACN	51426	polymerase (DNA directed) kappa /// V	2.31E-16	1	4.59	5.36	5.71	5.65	5.40	5.14	5.19	5.07
TC1300059	POMP	51371	proteasome maturation protein	1.22E-16	1	9.44	10.12	10.27	10.17	10.06	10.12	10.04	10.01
TC1900388	POP4	10775	processing of precursor 4, ribonuclease	0.000434	1	4.91	5.43	5.56	5.53	5.35	5.35	5.50	5.38
TC0700410	POR	5447	P450 (cytochrome) oxidoreductase ///	1.07E-14	1	5.87	6.77	6.77	6.58	6.39	6.13	5.91	5.93
TC0701607	POT1	25913	POT1 protection of telomeres 1 homol	7.44E-12	1	3.48	4.12	4.17	3.82	3.72	3.74	3.83	3.75
TC0102137	POU3F1	5453	POU class 3 homeobox 1	7.78E-05	1	4.48	4.74	4.74	4.83	4.79	4.73	4.75	4.69
TC0401166	PPA2	27068	pyrophosphatase (inorganic) 2 /// Inor	1.20E-11	1	3.60	4.51	4.66	4.55	4.56	4.48	4.36	4.16
TC0300061	PPARG	5468	peroxisome proliferator-activated rece	4.92E-07	1	3.40	3.59	3.68	3.76	3.66	3.55	3.48	3.49
TC0100446	PPCS	79717	phosphopantothenoylcysteine synthet	7.74E-09	1	4.68	4.84	5.06	4.93	4.87	4.90	4.92	4.92
TC0401362	PPID	5481	peptidylprolyl isomerase D (cyclophilin	2.71E-08	1	6.75	7.01	7.54	7.23	7.04	7.13	7.24	7.21
TC0601673	PPIL4	85313	peptidylprolyl isomerase (cyclophilin)-li	2.51E-05	1	6.35	6.61	6.73	6.55	6.42	6.63	6.68	6.74
TC0200211	PPM1B	5495	protein phosphatase 1B (formerly 2C),	0.000201	1	6.35	6.73	6.72	6.69	6.62	6.64	6.64	6.63
TC0300305	PPM1M	132160	protein phosphatase 1M (PP2C domain	1.34E-14	1	6.56	6.83	7.38	7.31	6.98	6.71	6.59	6.47
TC0301876	PPP1R2	5504	protein phosphatase 1, regulatory (inhi	6.04E-07	1	6.81	7.39	7.24	7.07	7.02	7.14	7.11	7.21
TC0800724	PPP1R3B	79660	protein phosphatase 1, regulatory (inhi	6.27E-06	1	7.15	7.69	7.59	7.59	7.48	7.61	7.37	7.35
TC2000875	PPP1R3D	5509	protein phosphatase 1, regulatory (inhi	1.58E-19	1	5.59	6.63	6.76	6.53	6.37	6.27	6.16	6.12
TC0501288	PPP2CA	5515	protein phosphatase 2 (formerly 2A), c	5.48E-06	1	7.49	7.89	7.92	7.94	7.78	7.81	7.78	7.87
TC0400802	PPP2R2C	5522	protein phosphatase 2 (formerly 2A), r	0.000433	1	4.14	4.25	4.27	4.19	4.25	4.22	4.12	4.14
TC1100524	PPP2R5B	5526	protein phosphatase 2, regulatory subu	1.39E-06	1	4.97	5.35	5.09	5.00	5.06	4.99	5.01	5.07
TC1400907	PPP2R5E	5529	protein phosphatase 2, regulatory subu	4.43E-06	1	4.81	5.44	5.45	5.43	5.37	5.38	5.47	5.36
TC1001070	PPP3CB	5532	protein phosphatase 3 (formerly 2B), c	4.82E-15	1	6.04	6.98	7.25	7.00	6.78	6.78	6.84	6.62
TC0300372	PPP4R2	151987	protein phosphatase 4, regulatory subu	1.90E-25	1	7.01	8.56	8.47	8.46	8.40	8.22	7.98	7.84
TC0901331	PPP6C	5537	protein phosphatase 6, catalytic subun	6.15E-10	1	6.62	7.18	7.23	7.10	7.02	7.11	7.06	7.09
TC1101704	PRCP	5547	prolylcarboxypeptidase (angiotensinas	3.45E-09	1	6.60	6.90	7.24	7.24	7.09	7.04	6.93	6.89
TC0401224	PRDM5	11107	PR domain containing 5	4.68E-08	1	4.94	5.65	5.92	5.72	5.36	5.29	5.23	5.26
TC0102213	PRDX1	5052	peroxiredoxin 1 /// Peroxiredoxin-1 (E	1.35E-07	1	5.23	5.96	6.08	6.28	6.00	5.79	5.94	5.87
TC1001311	PRDX3	10935	peroxiredoxin 3	1.43E-08	1	6.62	7.11	7.45	7.44	7.27	7.10	7.12	7.07

TC0101293	PRDX6	9588	peroxiredoxin 6	3.52E-14	1	6.58	7.64	7.83	7.65	7.71	7.61	7.41	7.35
TC1101411	PRG2	5553	proteoglycan 2, bone marrow (natural	0.000271	1	3.06	3.71	3.37	3.42	3.48	3.35	3.32	3.19
TC0500939	PRKAA1	5562	protein kinase, AMP-activated, alpha 1	1.56E-07	1	6.90	7.25	7.36	7.50	7.52	7.34	7.21	7.10
TC1200745	PRKAB1	5564	protein kinase, AMP-activated, beta 1 r	0.000536	1	5.36	5.77	5.53	5.50	5.39	5.50	5.42	5.47
TC1201163	PRKAG1	5571	protein kinase, AMP-activated, gamma	6.76E-07	1	5.96	6.46	6.53	6.44	6.42	6.40	6.40	6.40
TC0301190	PRKAR2A	5576	protein kinase, cAMP-dependent, regu	2.64E-24	1	5.32	6.87	6.99	6.77	6.61	6.16	6.19	5.95
TC1700697	PRKCA	5578	protein kinase C, alpha	0.000888	1	3.84	4.11	4.34	4.43	4.39	4.13	4.09	3.99
TC0300783	PRKCI	5584	protein kinase C, iota /// Protein kinase	6.49E-10	1	3.66	4.66	4.61	4.68	4.68	4.55	4.49	4.31
TC0201434	PRKD3	23683	protein kinase D3	3.59E-08	1	4.19	4.97	4.69	4.82	4.79	4.71	4.69	4.60
TC0600994	PRL	5617	prolactin	0.000139	1	2.71	2.73	2.87	2.93	2.79	2.73	2.76	2.64
TC2100205	PRMT2	3275	protein arginine methyltransferase 2 //	6.03E-13	1	6.69	7.29	7.36	7.30	7.25	7.10	7.12	6.94
TC1400708	PRMT5	10419	protein arginine methyltransferase 5 //	0.000559	1	5.41	5.51	5.92	6.00	5.78	5.78	5.78	5.51
TC2000052	PRNP	5621	prion protein (p27-30) (Creutzfeldt-Jak	2.94E-12	1	5.89	6.59	6.59	6.55	6.68	6.59	6.42	6.39
TC0301341	PROK2	60675	prokineticin 2 /// Prokineticin-2 precur	7.00E-18	1	9.15	10.25	10.37	9.97	9.89	9.93	9.69	9.73
TC0800221	PROSC	11212	proline synthetase co-transcribed hom	1.04E-07	1	5.07	5.36	5.74	5.63	5.52	5.52	5.54	5.45
TC0100553	PRPF38A	84950	PRP38 pre-mRNA processing factor 38	2.41E-05	1	5.65	6.33	6.29	6.13	6.11	6.16	6.13	6.10
TC0901056	PRUNE2 /// BN	158471	prune homolog 2 (Drosophila) /// BNIP	0.000182	1	2.92	3.68	3.59	3.37	3.40	3.29	3.18	3.17
TC0700995	PSCD3	9265	pleckstrin homology, Sec7 and coiled-c	3.33E-06	1	3.95	4.18	4.14	4.14	4.05	4.04	3.97	3.95
TC1101221	PSMA1	5682	proteasome (prosome, macropain) sub	1.41E-07	1	4.88	5.28	5.46	5.30	5.26	5.08	5.11	5.01
TC1400169	PSMA6	5687	proteasome (prosome, macropain) sub	1.59E-17	1	6.87	8.30	8.37	8.19	8.04	7.95	7.97	7.95
TC1700052	PSMB6	5694	proteasome (prosome, macropain) sub	0.000122	1	5.61	6.36	6.38	6.35	6.25	6.17	6.09	6.05
TC0700590	PSMC2	5701	proteasome (prosome, macropain) 26S	3.46E-10	1	4.79	5.74	5.95	5.71	5.72	5.67	5.64	5.56
TC1101350	PSMC3	5702	proteasome (prosome, macropain) 26S	1.14E-05	1	5.42	6.24	6.17	6.11	6.20	6.19	6.16	6.03
TC1400232	PSMC6	5706	proteasome (prosome, macropain) 26S	1.63E-08	1	5.82	6.25	6.44	6.22	5.99	6.10	6.04	5.98
TC0201169	PSMD1	5707	proteasome (prosome, macropain) 26S	5.16E-11	1	5.57	6.40	6.78	6.52	6.33	6.20	6.31	6.08
TC0X01145	PSMD10	5716	proteasome (prosome, macropain) 26S	3.27E-09	1	5.43	6.23	6.51	6.27	6.03	6.05	6.03	6.13
TC1700354	PSMD11	5717	proteasome (prosome, macropain) 26S	0.000679	1	5.01	5.39	5.43	5.28	5.28	5.24	5.30	5.23
TC1701634	PSMD12	5718	proteasome (prosome, macropain) 26S	1.32E-06	1	6.39	7.09	7.05	6.95	6.87	6.83	6.90	6.80
TC0300856	PSMD2	5708	proteasome (prosome, macropain) 26S	2.22E-06	1	6.09	6.57	6.63	6.50	6.43	6.39	6.45	6.37
TC0901296	PSMD5	5711	proteasome (prosome, macropain) 26S	0.000498	1	3.52	3.87	3.92	3.87	3.77	3.68	3.76	3.74
TC0301315	PSMD6	9861	proteasome (prosome, macropain) 26S	2.22E-08	1	6.86	7.20	7.37	7.28	7.13	7.11	7.17	7.09
TC1600590	PSMD7	5713	proteasome (prosome, macropain) 26S	0.000373	1	7.71	8.11	8.25	8.08	7.98	8.05	8.09	7.93
TC1200771	PSMD9	5715	proteasome (prosome, macropain) 26S	1.63E-16	1	5.20	5.87	6.04	5.87	5.83	5.73	5.68	5.60
TC1800438	PSTPIP2	9050	proline-serine-threonine phosphatase i	1.21E-13	1	6.52	8.57	8.65	8.31	8.19	7.88	7.74	7.74

TC0100755	PTBP2	58155	polypyrimidine tract binding protein 2 ,	1.20E-06	1	3.71	4.27	4.25	4.20	4.28	4.19	4.18	3.94
TC1400230	PTGER2	5732	prostaglandin E receptor 2 (subtype EP	8.34E-14	1	4.27	4.82	5.17	5.48	5.31	4.99	4.95	4.64
TC0901382	PTGES	9536	prostaglandin E synthase	4.04E-05	1	5.27	5.58	5.50	5.27	5.37	5.41	5.22	5.27
TC0901247	PTGR1 /// LTB4	22949	prostaglandin reductase 1 /// NADP-de	9.46E-08	1	3.35	3.62	3.87	3.98	3.96	3.81	3.65	3.52
TC0600484	PTP4A1	7803	protein tyrosine phosphatase type IVA,	4.55E-14	1	6.46	7.53	7.26	6.97	6.90	7.16	7.05	7.15
TC2000369	PTPN1	5770	protein tyrosine phosphatase, non-rec	9.42E-11	1	6.72	7.71	7.68	7.71	7.45	7.30	7.36	7.25
TC0102558	PTPN22	26191	protein tyrosine phosphatase, non-rec	8.57E-20	1	5.43	7.06	7.05	6.81	6.88	6.75	6.58	6.49
TC1501115	PTPN9	5780	protein tyrosine phosphatase, non-rec	0.000466	1	4.07	4.48	4.53	4.49	4.45	4.40	4.41	4.30
TC1101949	PUS3	83480	pseudouridylate synthase 3	5.75E-16	1	4.51	5.97	6.16	5.86	5.56	5.57	5.54	5.41
TC0300337	PXK	54899	PX domain containing serine/threonine	1.42E-25	1	6.28	7.54	7.82	7.79	7.74	7.42	7.29	7.15
TC0801047	PXMP3	5828	peroxisomal membrane protein 3, 35k	6.85E-17	1	4.59	5.55	5.78	5.43	5.17	5.23	5.22	5.26
TC1400850	PYGL	5836	phosphorylase, glycogen; liver (Hers di	6.90E-23	1	9.22	10.20	10.30	10.27	10.15	9.91	9.79	9.63
TC1200188	PYROXD1	79912	pyridine nucleotide-disulphide oxidore	2.75E-07	1	4.56	5.35	5.37	5.17	5.12	5.01	5.07	5.00
TC1800354	Q14179_HUM	---	H.sapiens NF1 gene homologue (2) clo	3.71E-09	1	3.50	4.57	4.15	3.83	3.76	3.66	3.74	3.48
TC2100010	Q14179_HUM	---	H.sapiens NF1 gene homologue (2) clo	2.07E-08	1	3.01	3.92	3.59	3.39	3.34	3.15	3.02	3.06
TC0X01082	Q14236_HUM	---	Early lymphoid activation protein (Frag	1.11E-07	1	4.03	5.49	5.56	5.75	5.71	5.57	5.50	5.36
TC1700899	Q3C259_HUM	---	Succinate dehydrogenase complex, su	2.89E-11	1	3.81	5.68	6.01	5.87	5.56	5.28	5.01	4.91
TC2000120	Q4VXU4_HUM	---	OTTHUMP00000030388 (Fragment). [S	0.000507	1	5.01	5.69	5.68	5.38	5.35	4.93	5.28	4.92
TC1300129	Q5W0Q5_HU	---	OTTHUMP00000018371. [Source:Unipr	6.00E-15	1	5.86	7.09	7.06	7.02	7.04	7.01	6.91	6.85
TC0801119	Q629K1_HUM	---	---	2.70E-25	1	4.55	6.40	6.36	6.10	6.23	6.10	5.83	5.62
TC0202408	Q6NSB1_HUM	---	SRP9 protein (Fragment). [Source:Unip	1.56E-13	1	3.79	4.64	4.77	4.71	4.63	4.53	4.47	4.29
TC1900637	Q6P662_HUM	---	---	5.44E-16	1	4.06	4.39	4.93	5.36	5.08	4.30	4.27	4.20
TC0301140	Q6ZMS4_HUM	---	CDNA FLJ16720 fis, clone UTERU30010	2.64E-08	1	4.70	5.39	4.98	4.92	4.83	4.79	4.78	4.67
TC0700770	Q6ZN80_HUM	---	CDNA FLJ16351 fis, clone TESTI203906	3.76E-08	1	5.61	5.20	6.00	6.16	6.04	5.47	5.32	5.07
TC0501044	Q6ZNT7_HUM	---	CDNA FLJ27195 fis, clone SYN02786. [S	5.33E-07	1	6.32	6.95	7.78	7.22	6.98	6.69	6.81	6.31
TC0103006	Q6ZNX2_HUM	---	CDNA FLJ26950 fis, clone RCT08544. [S	1.08E-06	1	4.54	4.87	4.92	4.78	4.57	4.67	4.40	4.39
TC2000793	Q6ZWG0_HU	---	CDNA FLJ41161 fis, clone BRACE20394	2.14E-06	1	4.12	4.56	4.47	4.36	4.37	4.36	4.13	4.10
TC0401429	Q8N0S5_HUM	---	MGC45800 protein. [Source:Uniprot/S	3.03E-05	1	3.53	3.74	3.81	3.71	3.76	3.73	3.68	3.62
TC0400366	Q8N507_HUM	---	Putative uncharacterized protein C4orf	2.56E-05	1	3.43	3.76	3.75	3.61	3.77	3.74	3.61	3.59
TC1900584	Q8N6Q3-3	---	CD177_HUMAN Isoform 3 of Q8N6Q3 -	5.64E-27	1	4.53	9.21	9.57	9.28	9.10	7.51	7.03	6.07
TC1100174	Q8N6V7_HUM	---	---	1.32E-08	1	7.24	7.60	8.54	7.80	7.49	7.76	7.37	7.51
TC0201823	Q96C48_HUM	---	LOC541471 protein (Hypothetical prot	0.00015	1	5.74	6.07	6.23	6.16	5.95	6.08	6.14	6.02
TC0102969	Q96IX9_HUMA	---	MGC12538 protein (Novel protein). [So	1.08E-08	1	6.02	7.25	7.18	6.78	6.51	6.62	6.58	6.44
TC0800326	Q96QE0_HUM	---	---	6.99E-05	1	4.73	5.09	5.09	5.15	5.14	5.10	5.11	5.07

TC1400858	Q9H373_HUM	---	---	2.37E-10	1	7.28	8.44	8.48	8.19	8.12	8.20	7.93	8.15
TC0X00373	Q9H375_HUM	---	---	1.40E-06	1	7.38	8.46	8.39	8.14	7.93	8.06	8.32	8.31
TC2100210	Q9NSJ1_HUM	---	---	7.84E-05	1	2.13	2.38	2.43	2.40	2.37	2.37	2.42	2.45
TC0301543	Q9P156_HUM	---	---	8.64E-06	1	8.91	9.08	9.43	9.27	9.26	9.31	9.24	9.28
TC0500373	Q9P181_HUM	---	---	2.80E-15	1	5.71	7.66	7.85	7.56	7.54	7.33	7.17	7.17
TC1501256	Q9P1I3_HUMA	---	---	4.01E-08	1	6.06	6.94	6.74	6.23	6.22	6.07	5.94	5.72
TC0400323	Q9UHS6_HUM	---	---	2.34E-15	1	5.84	7.76	7.87	7.61	7.28	7.29	7.14	6.94
TC0200181	QPCT	25797	glutaminyl-peptide cyclotransferase (gl	7.54E-07	1	8.11	8.92	8.93	8.97	8.99	8.94	8.65	8.68
TC0101325	QSOX1	5768	quiescin Q6 sulfhydryl oxidase 1	2.33E-18	1	4.92	6.01	5.84	5.71	5.70	5.41	5.26	5.13
TC0800152	R3HCC1	203069	R3H domain and coiled-coil containing	7.26E-05	1	5.63	5.98	5.89	5.97	5.97	5.94	5.93	5.91
TC0200105	RAB10	10890	RAB10, member RAS oncogene family	5.82E-21	1	7.37	8.01	8.26	8.23	8.22	8.14	8.02	7.97
TC1500417	RAB11A	8766	RAB11A, member RAS oncogene family	1.97E-05	1	8.31	8.74	8.88	8.91	8.77	8.87	8.83	8.88
TC1000134	RAB18	22931	RAB18, member RAS oncogene family /	0.000691	1	7.94	7.97	8.26	8.14	7.99	8.03	7.93	8.09
TC0700746	RAB19	401409	RAB19, member RAS oncogene family /	1.13E-08	1	3.54	4.13	3.80	3.74	4.02	3.81	3.65	3.57
TC1300653	RAB20	55647	RAB20, member RAS oncogene family	3.00E-08	1	5.71	6.55	6.35	6.43	6.35	6.40	6.26	6.11
TC1200521	RAB21	23011	RAB21, member RAS oncogene family	3.78E-09	1	7.53	8.37	8.17	8.19	8.13	8.25	8.14	8.18
TC1500971	RAB27A	5873	RAB27A, member RAS oncogene family	7.44E-19	1	7.41	8.35	8.29	8.26	8.22	8.02	7.88	7.81
TC0400823	RAB28	9364	RAB28, member RAS oncogene family /	0.000653	1	4.85	5.32	5.31	5.12	5.13	5.13	5.11	5.17
TC0800328	RAB2A	5862	RAB2A, member RAS oncogene family	1.93E-05	1	7.71	8.02	8.17	8.19	8.05	8.07	8.03	8.06
TC1800047	RAB31	11031	RAB31, member RAS oncogene family	1.04E-22	1	8.59	9.49	9.55	9.59	9.51	9.38	9.23	9.15
TC0600786	RAB32	10981	RAB32, member RAS oncogene family	4.02E-34	1	5.75	7.58	7.80	7.56	7.44	7.23	7.06	6.85
TC0X00561	RAB33A	9363	RAB33A, member RAS oncogene family	1.51E-05	1	4.21	4.73	4.85	4.80	4.84	4.74	4.79	4.73
TC0400554	RAB33B	83452	RAB33B, member RAS oncogene family	3.22E-12	1	6.15	7.29	7.50	7.33	7.24	7.43	7.24	7.30
TC1901296	RAB3A	5864	RAB3A, member RAS oncogene family	4.68E-05	1	4.10	4.39	4.56	4.53	4.53	4.40	4.28	4.31
TC0200736	RAB3GAP1	22930	RAB3 GTPase activating protein subuni	4.71E-10	1	4.77	5.55	5.51	5.23	5.09	5.13	5.23	5.11
TC0103244	RAB3GAP2	25782	RAB3 GTPase activating protein subuni	1.06E-11	1	5.53	6.40	6.41	6.28	6.12	6.06	6.06	5.96
TC1200511	RAB3IP	117177	RAB3A interacting protein (rabin3) ///	2.00E-08	1	4.54	5.37	5.27	5.30	5.48	5.31	5.30	5.03
TC0301546	RAB43 /// ISY1	339122 //	RAB43, member RAS oncogene family /	1.37E-11	1	6.58	7.11	7.10	7.13	7.02	7.03	7.02	7.00
TC0300099	RAB5A	5868	RAB5A, member RAS oncogene family	0.000548	1	7.54	7.95	7.79	7.72	7.55	7.65	7.65	7.65
TC0200676	RAB6C /// NM_	84084	RAB6C, member RAS oncogene family /	4.71E-05	1	3.65	4.12	4.27	4.11	4.09	4.06	4.13	4.04
TC1101648	RAB6C /// RAB	84084 ///	RAB6C, member RAS oncogene family /	1.10E-16	1	6.44	7.12	7.30	7.19	7.15	7.07	7.05	6.95
TC0103170	RAB7L1	8934	RAB7, member RAS oncogene family-li	1.95E-15	1	5.03	6.13	6.28	5.94	5.64	5.66	5.71	5.67
TC1500396	RAB8B	51762	RAB8B, member RAS oncogene family	9.97E-06	1	8.49	8.89	8.92	8.98	8.86	8.89	8.75	8.80
TC1901542	RABAC1	10567	Rab acceptor 1 (prenylated)	3.86E-18	1	6.79	7.62	7.73	7.90	7.71	7.49	7.48	7.38

TC0103132	RABIF	5877	RAB interacting factor	1.53E-07	1	6.20	6.61	6.83	6.85	6.81	6.76	6.73	6.65
TC0900472	RAD23B	5887	RAD23 homolog B (S. cerevisiae) /// UV	3.74E-18	1	7.34	8.13	8.22	8.29	8.15	8.03	7.85	7.78
TC1400318	RAD51L1	5890	RAD51-like 1 (S. cerevisiae)	0.000154	1	3.81	4.13	4.28	4.19	4.23	4.14	4.16	3.97
TC2000404	RAE1	8480	RAE1 RNA export 1 homolog (S. pombe	0.000114	1	4.71	4.90	4.99	4.92	4.94	4.92	5.00	4.90
TC0200642	RALB	5899	v-ral simian leukemia viral oncogene h	7.77E-05	1	8.16	8.65	8.68	8.72	8.56	8.51	8.44	8.44
TC0101313	RALGPS2	55103	Ral GEF with PH domain and SH3 bindi	3.07E-11	1	5.28	6.12	6.02	5.58	5.45	5.63	5.67	5.61
TC0200565	RANBP2	5903	RAN binding protein 2	4.48E-05	1	5.99	6.81	6.56	6.46	6.31	6.25	6.42	6.22
TC0600960	RANBP9	10048	RAN binding protein 9 /// Ran-binding	6.93E-25	1	7.09	8.04	8.23	8.12	8.00	7.93	7.85	7.75
TC1200499	RAP1B	5908	RAP1B, member of RAS oncogene fami	3.66E-08	1	7.51	8.05	8.10	8.05	8.12	8.07	8.00	7.94
TC0300725	RAP2B	5912	RAP2B, member of RAS oncogene fami	1.13E-16	1	4.63	5.20	5.57	5.60	5.61	5.47	5.42	5.31
TC0X01245	RAP2C	57826	RAP2C, member of RAS oncogene fami	1.80E-06	1	7.01	7.44	7.43	7.39	7.40	7.43	7.25	7.30
TC0300672	RASA2	5922	RAS p21 protein activator 2	6.54E-24	1	6.16	7.77	7.39	7.05	6.95	6.91	6.76	6.66
TC0401076	RASGEF1B	153020	RasGEF domain family, member 1B	0.000129	1	2.77	2.97	3.24	3.20	3.03	2.80	2.83	2.83
TC1300133	RB1	5925	retinoblastoma 1 (including osteosarco	9.46E-16	1	5.80	6.79	6.78	6.58	6.44	6.41	6.38	6.30
TC0201360	RBJ	51277	rab and DnaJ domain containing /// ra	0.000337	1	3.54	3.82	3.81	3.72	3.68	3.67	3.70	3.59
TC0201399	RBKS	64080	ribokinase	6.98E-06	1	3.59	4.29	3.98	3.90	3.97	3.86	3.80	3.80
TC1600437	RBL2	5934	retinoblastoma-like 2 (p130) /// Retino	0.000352	1	7.87	8.06	8.05	8.00	7.84	7.86	7.84	7.82
TC2100014	RBM11	54033	RNA binding motif protein 11	9.74E-05	1	2.53	3.29	3.22	3.13	3.38	3.15	3.11	2.98
TC1000035	RBM17	84991	RNA binding motif protein 17	1.87E-05	1	4.84	5.46	5.35	5.32	5.39	5.28	5.31	5.15
TC2000405	RBM38	55544	RNA binding motif protein 38 /// RNA-	3.82E-05	1	5.31	5.72	5.62	5.71	5.78	5.58	5.49	5.42
TC0X01139	RBM41	55285	RNA binding motif protein 41 /// RNA-	4.26E-06	1	3.97	4.50	4.25	4.06	4.11	4.11	4.30	4.17
TC1900448	RBM42	79171	RNA binding motif protein 42 /// RNA	0.000131	1	5.48	5.82	5.76	5.76	5.70	5.78	5.74	5.75
TC1100865	RBM7	10179	RNA binding motif protein 7 /// RNA-bi	0.000539	1	6.33	7.04	7.04	6.91	6.71	6.99	6.92	6.94
TC0202044	RBMS1	5937	RNA binding motif, single stranded inte	2.75E-15	1	7.89	8.48	8.54	8.39	8.23	8.17	8.11	8.04
TC0400143	RBPJ	3516	recombination signal binding protein f	8.38E-13	1	8.15	8.70	8.76	8.54	8.43	8.49	8.37	8.29
TC2000311	RBPJL	11317	recombination signal binding protein f	0.000368	1	4.15	4.25	4.29	4.20	4.24	4.17	4.11	4.18
TC2200309	RBX1	9978	ring-box 1	1.10E-11	1	6.44	7.30	7.46	7.52	7.57	7.44	7.36	7.21
TC2100323	RCAN1	1827	regulator of calcineurin 1	2.47E-06	1	4.45	4.73	4.79	4.77	4.76	4.64	4.72	4.60
TC0401046	RCHY1	25898	ring finger and CHY zinc finger domain	8.26E-22	1	5.07	6.70	6.74	6.51	6.35	6.21	5.94	5.80
TC0900023	RCL1	10171	RNA terminal phosphate cyclase-like 1	6.49E-09	1	3.39	3.80	3.71	3.75	3.80	3.75	3.71	3.57
TC1200410	RDH5 /// BLOC	5959 /// 2	retinol dehydrogenase 5 (11-cis/9-cis) /	3.68E-09	1	5.50	5.87	5.99	6.09	6.05	5.88	5.78	5.71
TC0801341	RECQL4	9401	RecQ protein-like 4	8.72E-05	1	4.76	4.97	4.98	4.94	4.99	5.00	4.91	4.92
TC0501214	REEP5	7905	receptor accessory protein 5 /// Recep	8.92E-10	1	7.40	8.15	8.33	8.16	8.07	8.09	8.05	8.03
TC0200268	REL	5966	v-rel reticuloendotheliosis viral oncoge	9.05E-10	1	7.86	8.22	8.25	8.03	7.87	7.95	7.93	7.95

TC1900134	RETN	56729	resistin /// Resistin precursor (Cysteine	3.35E-16	1	4.59	8.41	8.77	8.36	9.17	8.63	7.79	6.73
TC0201672	RETSAT	54884	retinol saturase (all-trans-retinol 13,14	6.00E-05	1	4.58	4.61	4.80	4.86	4.77	4.69	4.68	4.69
TC0400886	RFC1	5981	replication factor C (activator 1) 1, 145	0.000105	1	4.56	5.46	5.09	5.08	5.05	5.00	5.31	5.04
TC0301265	RFT1	91869	RFT1 homolog (S. cerevisiae)	4.06E-19	1	4.70	5.08	5.47	5.54	5.45	5.26	5.16	5.07
TC0900750	RFX3	5991	regulatory factor X, 3 (influences HLA c	2.64E-12	1	4.71	5.08	5.25	4.81	4.62	4.76	4.72	4.66
TC2200120	RGL4 /// RGDS	266747	ral guanine nucleotide dissociation sti	1.13E-17	1	6.10	6.77	6.70	6.53	6.56	6.47	6.39	6.29
TC0900165	RGP1	9827	RGP1 retrograde golgi transport homol	9.33E-06	1	5.27	5.54	5.51	5.42	5.42	5.29	5.17	5.20
TC2000917	RGS19	10287	regulator of G-protein signaling 19	5.35E-07	1	6.11	6.51	6.53	6.54	6.54	6.50	6.38	6.41
TC0700409	RHBDD2	57414	rhomboid domain containing 2	3.72E-09	1	5.73	6.27	6.24	6.31	6.16	5.98	5.92	5.99
TC0301206	RHOA	387	ras homolog gene family, member A	4.79E-05	1	10.99	11.21	11.31	11.26	11.19	11.23	11.16	11.17
TC1101098	RHOG	391	ras homolog gene family, member G (r	5.72E-09	1	8.61	9.43	9.35	9.35	9.36	9.12	8.98	9.02
TC1700351	RHOT1	55288	ras homolog gene family, member T1 /	4.02E-10	1	6.36	6.94	7.13	7.25	7.12	7.09	7.08	7.06
TC0101590	RHOU	58480	ras homolog gene family, member U	5.55E-14	1	5.41	6.21	6.20	5.88	5.73	5.64	5.66	5.57
TC1400452	RIN3	79890	Ras and Rab interactor 3	3.64E-07	1	5.91	6.51	6.44	6.56	6.44	6.24	6.19	6.09
TC1800105	RIOK3	8780	RIO kinase 3 (yeast)	6.72E-06	1	7.70	8.01	7.78	7.89	7.92	7.81	7.67	7.47
TC0102839	RIT1	6016	Ras-like without CAAX 1	0.000512	1	8.25	8.33	8.54	8.51	8.33	8.40	8.30	8.33
TC0500763	RMND5B	64777	required for meiotic nuclear division 5	0.000559	1	4.92	5.10	5.07	4.96	5.00	4.96	4.96	4.97
TC1200754	RNF10	9921	ring finger protein 10	2.12E-24	1	6.70	7.97	8.10	7.92	7.65	7.31	7.19	6.99
TC0100543	RNF11	26994	ring finger protein 11	2.92E-10	1	5.46	5.99	6.03	6.02	6.05	6.04	5.85	5.90
TC0X01045	RNF12	51132	ring finger protein 12	7.84E-20	1	5.98	7.07	6.94	6.67	6.38	6.44	6.29	6.29
TC1700338	RNF135	84282	ring finger protein 135	0.000274	1	5.44	5.41	5.62	5.68	5.61	5.52	5.53	5.51
TC1800132	RNF138	51444	ring finger protein 138	1.00E-08	1	4.99	5.80	5.89	5.93	5.86	5.90	5.76	5.84
TC0800544	RNF139	11236	ring finger protein 139	2.70E-07	1	5.35	5.76	5.87	5.67	5.64	5.79	5.77	5.84
TC0600709	RNF146	81847	ring finger protein 146	1.15E-10	1	6.20	6.51	6.76	6.50	6.25	6.38	6.37	6.24
TC0800909	RNF170	81790	ring finger protein 170 /// RING finger	7.71E-14	1	4.60	4.93	5.19	5.01	4.87	4.84	4.96	4.76
TC0101357	RNF2	6045	ring finger protein 2 /// E3 ubiquitin-pr	2.61E-14	1	5.10	5.72	6.00	5.95	5.70	5.64	5.57	5.62
TC0900910	RNF38	152006	ring finger protein 38 /// RING finger p	0.000395	1	6.66	6.98	7.09	7.09	6.98	6.99	6.91	6.92
TC0300673	RNF7	9616	ring finger protein 7	8.26E-24	1	5.30	6.43	6.88	6.71	6.58	6.38	6.44	6.32
TC1701573	RNFT1 /// NP_	51136	ring finger protein, transmembrane 1 /	0.000104	1	5.91	6.19	6.48	6.16	6.18	6.21	6.24	6.10
TC0601444	RNGTT	8732	RNA guanylyltransferase and 5'-phosp	8.49E-07	1	5.07	5.74	5.85	5.67	5.57	5.46	5.57	5.35
TC1600823	ROGDI	79641	rogdi homolog (Drosophila)	3.25E-11	1	5.12	5.49	5.61	5.67	5.71	5.47	5.39	5.27
TC1100479	ROM1	6094	retinal outer segment membrane prot	4.29E-08	1	4.69	4.99	5.19	5.07	4.91	4.71	4.79	4.74
TC0500050	ROPN1L	83853	ropporin 1-like	3.71E-11	1	6.12	7.17	7.16	7.05	6.88	6.67	6.60	6.54
TC1000185	RP1-19N1.1 ///	644504 //	novel protein similar to chondroitin sul	1.93E-26	1	6.70	8.36	8.44	8.18	8.09	7.79	7.67	7.52

TC0X00177	RP2	6102	retinitis pigmentosa 2 (X-linked recessi	0.000405	1	8.42	8.76	8.93	8.91	8.76	8.80	8.65	8.77
TC0102570	RP5-1000E10.4	80143	suppressor of IKK epsilon /// suppresso	7.99E-09	1	5.17	5.65	5.86	5.86	5.78	5.72	5.75	5.77
TC0100130	RP5-1077B9.4	60672	invasion inhibitory protein 45	4.95E-08	1	5.02	5.39	5.37	5.37	5.39	5.36	5.32	5.29
TC1700482	RPL27	6155	ribosomal protein L27	3.01E-18	1	8.84	10.06	10.03	10.13	10.24	10.03	9.89	9.72
TC0200528	RPL31	732015 //	ribosomal protein L31	5.55E-13	1	6.21	7.04	7.03	7.14	7.18	7.12	7.05	6.79
TC0X00811	RPS6KA3	6197	ribosomal protein S6 kinase, 90kDa, po	5.01E-10	1	7.11	7.48	7.86	7.61	7.24	7.24	7.30	7.25
TC0900081	RRAGA	10670	Ras-related GTP binding A	5.93E-10	1	6.43	7.25	7.49	7.52	7.18	7.26	7.34	7.24
TC0X00286	RRAGB	10325	Ras-related GTP binding B	6.81E-05	1	3.65	4.08	4.10	4.01	3.93	3.86	4.02	3.81
TC2000577	RRBP1	6238	ribosome binding protein 1 homolog 1	4.95E-05	1	5.64	6.07	6.01	5.92	5.81	5.73	5.82	5.76
TC0102559	RSBN1	54665	round spermatid basic protein 1 /// rou	2.87E-33	1	5.56	7.45	7.41	7.26	7.06	6.79	6.68	6.44
TC0300744	RSRC1	51319	arginine/serine-rich coiled-coil 1 /// Ar	3.61E-05	1	5.05	5.76	5.97	5.77	5.71	5.87	5.88	5.72
TC0100767	RTCD1	8634	RNA terminal phosphate cyclase domai	6.03E-06	1	5.70	5.84	6.22	6.04	5.92	5.91	5.97	5.82
TC1901597	RTN2	6253	reticulon 2	1.20E-05	1	4.16	4.37	4.35	4.42	4.42	4.29	4.15	4.24
TC0201520	RTN4	57142	reticulon 4 /// Reticulon-4 (Neurite out	7.92E-18	1	5.54	5.86	6.04	5.95	5.95	5.87	5.83	5.77
TC0300235	RTP3	83597	receptor (chemosensory) transporter p	0.000932	1	2.94	3.40	3.29	3.16	3.40	3.27	3.24	3.34
TC0700454	RUNDC3B	154661	RUN domain containing 3B /// RUN do	0.000194	1	2.74	2.90	2.97	2.85	2.87	2.79	2.80	2.79
TC2100324	RUNX1	861	runt-related transcription factor 1 (acu	2.59E-12	1	5.47	5.82	6.05	6.11	6.01	5.80	5.81	5.70
TC0600666	RWDD1	51389	RWD domain containing 1	6.68E-11	1	4.59	5.55	5.82	5.76	5.78	5.66	5.74	5.54
TC0200320	RY1	11017	putative nucleic acid binding protein R	1.35E-19	1	5.64	7.14	7.26	6.79	6.77	6.75	6.82	6.75
TC0102761	S100A11	730558 //	S100 calcium binding protein A11	1.70E-13	1	10.27	10.80	10.99	11.12	10.97	10.90	10.84	10.84
TC0102779	S100A12	6283	S100 calcium binding protein A12 /// P	3.19E-36	1	10.27	11.59	11.77	11.59	11.57	11.39	11.24	11.08
TC0102789	S100A2	6273	S100 calcium binding protein A2 /// Pr	0.000638	1	5.41	5.51	5.61	5.56	5.52	5.56	5.44	5.45
TC0102785	S100A6	6277	S100 calcium binding protein A6	5.90E-16	1	6.49	6.96	7.18	7.22	7.18	7.02	6.96	6.91
TC0102782	S100A7L2	645922	S100 calcium binding protein A7-like 2	0.000503	1	2.63	2.84	2.97	2.75	2.76	2.73	2.80	2.75
TC0102780	S100A8	6279	S100 calcium binding protein A8	4.07E-18	1	11.15	11.61	11.65	11.66	11.64	11.59	11.50	11.44
TC0101079	S100A9	6280	S100 calcium binding protein A9	1.65E-17	1	11.95	12.39	12.49	12.50	12.46	12.38	12.29	12.20
TC0400061	S100P	6286	S100 calcium binding protein P	1.46E-06	1	8.22	9.02	9.01	8.90	8.94	8.83	8.68	8.75
TC0100775	S1PR1	1901	sphingosine-1-phosphate receptor 1	6.61E-23	1	4.97	6.69	7.46	6.38	5.53	5.25	5.30	5.16
TC1900070	S1PR4	8698	sphingosine-1-phosphate receptor 4	0.000483	1	5.18	5.80	5.86	5.81	5.78	5.73	5.55	5.73
TC1901235	SAMD1	90378	sterile alpha motif domain containing 1	0.000614	1	4.83	5.04	5.08	5.07	5.15	5.06	5.07	4.93
TC1000353	SAMD8	142891	sterile alpha motif domain containing	6.23E-05	1	6.31	6.72	6.53	6.42	6.35	6.49	6.42	6.41
TC2100221	SAMSN1	64092	SAM domain, SH3 domain and nuclear	9.51E-40	1	6.71	9.74	9.56	9.12	8.94	8.51	8.42	8.17
TC0400681	SAP30	8819	Sin3A-associated protein, 30kDa	7.71E-07	1	5.42	7.00	6.62	6.80	6.82	6.68	6.81	6.63
TC0501291	SAR1B	51128	SAR1 gene homolog B (S. cerevisiae)	2.93E-20	1	5.74	6.52	7.02	6.89	6.72	6.38	6.38	6.31

TC1100560	SART1	9092	squamous cell carcinoma antigen recog	3.85E-10	1	5.77	6.41	6.37	6.53	6.33	6.20	6.29	6.18
TC1700993	SAT2	112483	spermidine/spermine N1-acetyltransfe	0.000722	1	4.77	5.30	5.22	5.31	5.31	5.19	5.17	5.00
TC0301049	SATB1	6304	SATB homeobox 1 /// DNA-binding pro	3.80E-08	1	6.04	6.51	6.18	6.16	6.04	6.02	6.09	5.98
TC1201660	SBNO1	55206	strawberry notch homolog 1 (Drosophi	2.33E-05	1	6.89	7.37	7.34	7.39	7.31	7.16	7.19	7.11
TC0400662	SC4MOL	6307	sterol-C4-methyl oxidase-like	2.36E-14	1	4.96	5.83	5.81	5.78	5.90	5.65	5.49	5.25
TC1100933	SC5DL	6309	sterol-C5-desaturase (ERG3 delta-5-des	2.62E-07	1	3.81	4.29	4.11	4.13	4.28	4.23	4.22	4.15
TC1501106	SCAMP2	10066	secretory carrier membrane protein 2	0.000635	1	5.97	6.26	6.29	6.33	6.31	6.32	6.25	6.20
TC1100751	SCARNA9	---	small Cajal body-specific RNA 9 (SCARN	0.000429	1	7.83	8.50	8.73	8.77	8.76	8.66	8.51	8.44
TC0101689	SCCPDH	51097	saccharopine dehydrogenase (putative	3.17E-11	1	3.79	5.38	5.00	4.71	4.76	4.97	4.84	4.68
TC1400141	SCFD1	23256	sec1 family domain containing 1	3.14E-12	1	4.93	5.83	6.06	5.79	5.62	5.65	5.68	5.50
TC0501564	SCGB3A1	92304	secretoglobin, family 3A, member 1	2.59E-06	1	4.87	5.28	5.28	5.20	5.29	5.28	5.16	5.13
TC1200342	SCN8A	6334	sodium channel, voltage gated, type VI	2.25E-06	1	2.67	2.77	2.84	2.92	2.95	2.81	2.77	2.69
TC0202070	SCN9A	6335	sodium channel, voltage-gated, type IX	0.000901	1	2.64	3.29	3.23	3.36	3.40	3.27	3.17	2.99
TC0100561	SCP2	6342	sterol carrier protein 2	4.88E-06	1	3.99	4.78	4.94	4.90	5.04	4.91	4.89	4.69
TC1700617	SCPEP1	59342	serine carboxypeptidase 1	3.06E-08	1	6.31	6.92	6.98	7.19	7.12	6.73	6.71	6.61
TC1200621	SCYL2	55681	SCY1-like 2 (S. cerevisiae) /// SCY1-like	9.45E-08	1	7.00	7.53	7.51	7.46	7.37	7.38	7.33	7.34
TC0102060	SDC3	9672	syndecan 3 /// Syndecan-3 (SYND3). [S	0.000826	1	4.29	4.52	4.47	4.46	4.50	4.50	4.41	4.43
TC2000492	SDCBP2 /// FKE	27111 ///	syndecan binding protein (syntenin) 2 /	2.64E-09	1	5.38	5.68	5.77	5.68	5.66	5.63	5.50	5.54
TC0500215	SDCCAG10	10283	serologically defined colon cancer antig	5.46E-12	1	4.03	5.41	5.33	5.38	5.51	5.45	5.50	5.13
TC0101211	SDHC	6391	succinate dehydrogenase complex, sub	1.41E-21	1	5.40	6.46	6.79	6.70	6.49	6.27	6.06	5.95
TC0901442	SEC16A	9919	SEC16 homolog A (S. cerevisiae) /// Un	1.11E-05	1	5.56	5.98	5.72	5.65	5.69	5.59	5.53	5.51
TC0300561	SEC22A	26984	SEC22 vesicle trafficking protein homol	9.75E-06	1	3.43	3.86	3.82	3.75	3.88	3.74	3.82	3.74
TC0100924	SEC22B	9554	SEC22 vesicle trafficking protein homol	1.80E-08	1	7.83	8.47	8.57	8.38	8.24	8.32	8.23	8.25
TC0301130	SEC22C	9117	SEC22 vesicle trafficking protein homol	5.44E-19	1	4.40	4.91	5.21	5.05	4.93	4.75	4.75	4.67
TC1400807	SEC23A	10484	Sec23 homolog A (S. cerevisiae)	5.09E-11	1	5.06	5.76	5.75	5.60	5.54	5.53	5.48	5.34
TC2000109	SEC23B	10483	Sec23 homolog B (S. cerevisiae) /// Pro	1.59E-13	1	5.60	6.45	6.48	6.49	6.40	6.36	6.32	6.20
TC0500483	SEC24A	---	Protein transport protein Sec24A (SEC2	1.92E-27	1	4.94	5.99	6.62	6.42	6.11	5.74	5.73	5.50
TC0701212	SEC61G	23480	Sec61 gamma subunit	5.07E-21	1	5.80	6.81	6.97	6.85	6.85	6.78	6.70	6.65
TC0300778	SEC62	7095	SEC62 homolog (S. cerevisiae)	1.17E-18	1	7.93	8.78	8.87	8.77	8.71	8.68	8.65	8.59
TC0601504	SEC63	11231	SEC63 homolog (S. cerevisiae)	1.33E-08	1	5.94	6.84	6.71	6.66	6.94	6.87	6.90	6.55
TC0300709	SELT /// SELT_	51714	selenoprotein T /// Selenoprotein T pre	2.18E-19	1	8.06	8.58	8.95	8.84	8.72	8.59	8.47	8.52
TC0101138	SEMA4A	64218	sema domain, immunoglobulin domain	2.73E-05	1	6.64	6.93	7.13	7.14	7.07	6.89	6.88	6.72
TC1901058	SEMA6B	10501	sema domain, transmembrane domain	3.16E-14	1	4.54	4.87	4.86	4.62	4.64	4.56	4.51	4.51
TC0300867	SENP2	59343	SUMO1/sentrin/SMT3 specific peptidas	5.40E-06	1	6.05	6.66	6.45	6.38	6.34	6.47	6.38	6.39

TC0102404	SEP15 /// SEP1	9403	15 kDa selenoprotein /// 15 kDa selen	1.70E-09	1	6.59	6.80	7.19	7.16	7.03	7.03	7.00	6.97
TC1601011	SEPHS2	22928	selenophosphate synthetase 2	7.37E-15	1	5.71	6.45	6.46	6.49	6.44	6.34	6.37	6.28
TC0601714	SERAC1	84947	serine active site containing 1 /// Prote	0.000468	1	3.05	3.08	3.11	3.18	3.04	3.00	3.05	3.00
TC0100343	SERINC2	347735	serine incorporator 2 /// Serine incorp	9.21E-07	1	4.88	5.10	5.03	5.15	5.14	5.01	4.97	4.95
TC0301660	SERP1	27230	stress-associated endoplasmic reticulu	5.80E-14	1	3.95	4.52	4.71	4.68	4.60	4.54	4.64	4.63
TC0600903	SERPINB1	1992	serpin peptidase inhibitor, clade B (ova	1.61E-27	1	7.66	9.16	9.18	8.83	8.60	8.46	8.37	8.15
TC1800239	SERPINB2	5055	serpin peptidase inhibitor, clade B (ova	0.000129	1	3.17	3.74	3.68	4.03	3.97	3.76	3.75	3.65
TC1800242	SERPINB8	5271	serpin peptidase inhibitor, clade B (ova	2.24E-23	1	4.53	5.38	5.36	5.44	5.33	5.06	4.92	4.87
TC0600905	SERPINB9	5272	serpin peptidase inhibitor, clade B (ova	0.00029	1	4.81	5.56	5.45	5.08	4.94	5.06	5.20	5.12
TC0601509	SESN1	27244	sestrin 1 /// Sestrin-1 (p53-regulated p	7.81E-05	1	4.59	4.54	4.76	4.84	4.80	4.61	4.55	4.53
TC0100321	SESN2	83667	sestrin 2	1.07E-08	1	5.02	5.65	5.29	5.19	5.21	5.10	5.10	5.06
TC0202143	SESTD1	91404	SEC14 and spectrin domains 1	0.000189	1	4.75	5.79	5.73	5.74	5.66	5.67	5.72	5.62
TC1401118	SETD3	84193	SET domain containing 3 /// SET domai	1.86E-07	1	5.54	6.09	6.27	6.24	6.15	6.04	6.10	6.07
TC1200789	SETD8	387893	SET domain containing (lysine methyltr	5.48E-07	1	5.34	5.87	5.90	5.94	5.98	5.86	5.86	5.66
TC0201353	SF3B14	51639	splicing factor 3B, 14 kDa subunit	6.60E-07	1	7.54	8.24	8.36	8.31	8.22	8.31	8.22	8.29
TC0501024	SFRS12IP1	285672	SFRS12-interacting protein 1	2.12E-23	1	5.00	6.91	6.64	6.50	6.72	6.63	6.51	6.22
TC1201627	SFRS9	8683	splicing factor, arginine/serine-rich 9	3.59E-10	1	6.66	7.23	7.18	7.10	7.12	7.10	7.06	7.01
TC0601752	SFT2D1	113402	SFT2 domain containing 1 /// Vesicle tr	1.34E-11	1	6.76	7.43	7.55	7.40	7.33	7.41	7.34	7.34
TC0101266	SFT2D2 /// TBX	375035 //	SFT2 domain containing 2 /// T-box 19	5.15E-11	1	4.57	5.04	5.13	4.81	4.69	4.63	4.56	4.60
TC0500724	SFXN1	94081	sideroflexin 1	1.33E-08	1	4.18	5.27	4.97	4.79	5.00	4.75	4.76	4.46
TC0201619	SFXN5	94097	sideroflexin 5	8.76E-05	1	5.05	5.20	5.24	5.14	5.19	5.08	5.04	5.02
TC1501128	SGK269	79834	NKF3 kinase family member	4.02E-10	1	4.17	5.83	5.39	5.18	5.17	4.95	4.69	4.48
TC0400446	SGMS2	166929	sphingomyelin synthase 2	1.72E-17	1	3.81	4.55	4.75	4.77	4.63	4.28	4.27	4.14
TC1400910	SGPP1	81537	sphingosine-1-phosphate phosphatase	8.09E-06	1	4.36	4.79	4.94	5.22	5.04	4.80	4.81	4.99
TC1701764	SGSH	6448	N-sulfoglucosamine sulfohydrolase (sul	8.06E-07	1	4.62	4.81	4.86	4.94	4.88	4.82	4.71	4.69
TC0501029	SGTB	54557	small glutamine-rich tetratricopeptide	4.93E-13	1	6.05	6.87	7.17	7.02	6.72	6.60	6.63	6.50
TC0X00387	SH3BGRL	6451	SH3 domain binding glutamic acid-rich	4.44E-05	1	6.66	6.96	7.45	7.32	7.02	7.14	7.12	7.09
TC0301037	SH3BP5	9467	SH3-domain binding protein 5 (BTK-ass	8.49E-28	1	6.34	7.87	7.51	7.19	7.02	6.83	6.58	6.57
TC0100702	SH3GLB1	51100	SH3-domain GRB2-like endophilin B1 /	6.63E-18	1	8.12	8.86	9.13	9.05	8.97	8.95	8.82	8.76
TC0401394	SH3RF1	57630	SH3 domain containing ring finger 1	0.000132	1	3.60	3.82	3.90	3.87	3.99	3.90	3.79	3.73
TC0900920	SHB	6461	Src homology 2 domain containing ada	2.47E-12	1	4.44	4.98	4.82	4.73	4.74	4.67	4.66	4.58
TC1000584	SHOC2	8036	soc-2 suppressor of clear homolog (C.	4.75E-05	1	8.45	8.79	8.76	8.71	8.59	8.68	8.55	8.64
TC0X00924	SHROOM4	57477	shroom family member 4	0.000176	1	3.34	3.53	3.46	3.46	3.55	3.51	3.53	3.34
TC1900754	SIGLEC9	27180	sialic acid binding Ig-like lectin 9	9.59E-07	1	7.75	8.13	8.27	8.23	8.04	7.74	7.63	7.54

TC0501330	SIL1	64374	SIL1 homolog, endoplasmic reticulum c	1.51E-14	1	4.92	5.38	5.63	5.49	5.41	5.26	5.22	5.13
TC0103353	SIPA1L2	57568	signal-induced proliferation-associated	2.62E-12	1	5.92	7.18	6.87	6.73	6.50	6.38	6.29	6.16
TC0600084	SIRT5	23408	sirtuin (silent mating type information	1.16E-14	1	5.11	5.82	6.11	6.08	5.91	5.63	5.53	5.46
TC0701079	SKAP2	8935	src kinase associated phosphoprotein 2	6.15E-06	1	9.15	9.35	9.55	9.21	9.12	9.18	9.12	9.18
TC0300785	SKIL	6498	SKI-like oncogene	2.39E-20	1	5.84	7.52	7.16	6.89	6.79	6.86	6.63	6.58
TC0501287	SKP1	6500	S-phase kinase-associated protein 1	2.54E-05	1	7.86	8.17	8.28	8.19	8.13	8.21	8.21	8.23
TC0801263	SLA	6503	Src-like-adaptor	2.14E-10	1	6.99	7.62	7.56	7.13	6.93	7.07	6.97	6.99
TC1300211	SLAIN1	122060	SLAIN motif family, member 1 /// SLAIN	9.06E-07	1	4.67	5.54	5.66	5.50	5.53	5.53	5.40	5.41
TC1700855	SLC16A3	9123	solute carrier family 16, member 3 (mo	0.000743	1	5.85	6.12	6.07	6.13	6.08	6.03	5.94	5.98
TC0601395	SLC17A5	26503	solute carrier family 17 (anion/sugar tr	1.11E-10	1	4.86	5.50	5.60	5.58	5.65	5.60	5.62	5.49
TC0500125	SLC1A3	6507	solute carrier family 1 (glial high affinity	2.68E-18	1	3.24	4.40	4.57	3.75	3.55	3.40	3.36	3.24
TC0800906	SLC20A2	6575	solute carrier family 20 (phosphate tra	0.00057	1	4.16	4.32	4.34	4.30	4.34	4.28	4.25	4.24
TC0500462	SLC22A4	6583	solute carrier family 22 (organic cation/	1.86E-16	1	5.90	6.77	7.29	7.35	6.79	6.69	6.69	6.54
TC2000114	SLC24A3	57419	solute carrier family 24 (sodium/potass	4.57E-08	1	4.61	4.98	4.73	4.68	4.73	4.77	4.69	4.70
TC0202095	SLC25A12	8604	solute carrier family 25 (mitochondrial	3.54E-09	1	3.65	3.92	4.22	3.99	3.89	3.90	3.85	3.76
TC0102502	SLC25A24	29957	solute carrier family 25 (mitochondrial	3.50E-29	1	4.58	6.11	6.45	6.07	5.89	5.58	5.48	5.35
TC0701398	SLC25A40	55972	solute carrier family 25, member 40	3.16E-26	1	4.81	6.93	7.05	6.59	6.59	6.21	5.95	5.74
TC0601207	SLC26A8	116369	solute carrier family 26, member 8 /// s	3.12E-12	1	4.26	5.43	5.55	5.41	5.31	5.16	5.06	4.75
TC0102181	SLC2A1	6513	solute carrier family 2 (facilitated gluco	6.31E-13	1	5.01	5.34	5.47	5.67	5.59	5.44	5.33	5.10
TC1200933	SLC2A14 /// SL	144195 //	solute carrier family 2 (facilitated gluco	4.01E-24	1	6.64	7.49	7.46	7.38	7.22	7.10	6.90	6.83
TC0100771	SLC30A7	148867	solute carrier family 30 (zinc transporte	1.13E-11	1	5.02	6.04	5.80	5.59	5.38	5.45	5.53	5.42
TC0400192	SLC30A9	10463	solute carrier family 30 (zinc transporte	0.000159	1	4.88	5.29	5.41	5.34	5.18	5.15	5.21	5.15
TC0600940	SLC35B3	51000	solute carrier family 35, member B3 ///	4.29E-06	1	4.82	4.90	5.12	5.06	4.96	4.96	4.99	4.93
TC0500619	SLC36A1	206358	solute carrier family 36 (proton/amino	2.67E-08	1	5.79	5.84	6.15	6.09	5.93	5.81	5.74	5.67
TC1101742	SLC36A4	120103	solute carrier family 36 (proton/amino	1.81E-17	1	4.39	6.66	5.87	5.43	5.62	5.50	5.30	5.01
TC0701684	SLC37A3	84255	solute carrier family 37 (glycerol-3-pho	2.43E-20	1	5.74	7.34	6.98	6.73	6.65	6.36	6.11	5.82
TC1201129	SLC38A2	54407	solute carrier family 38, member 2	1.57E-15	1	8.28	9.21	9.28	9.19	9.13	8.94	8.90	8.78
TC0500988	SLC38A9	153129	solute carrier family 38, member 9	6.58E-06	1	3.49	3.87	4.01	3.84	3.79	3.81	3.93	3.78
TC0401154	SLC39A8	64116	solute carrier family 39 (zinc transporte	3.29E-11	1	3.64	4.34	4.50	4.74	4.72	4.40	4.38	4.17
TC0202172	SLC40A1	30061	solute carrier family 40 (iron-regulated	2.22E-13	1	6.75	7.36	7.79	7.74	7.64	7.52	7.34	7.37
TC0100747	SLC44A3	126969	solute carrier family 44, member 3	5.29E-08	1	3.01	3.06	3.21	2.99	3.06	3.03	2.97	2.99
TC1300370	SLC46A3	283537	solute carrier family 46, member 3	7.02E-10	1	4.68	5.50	5.84	5.33	5.17	5.28	5.24	5.04
TC0200136	SLC4A1AP	22950	solute carrier family 4 (anion exchange	2.38E-06	1	6.52	7.59	7.61	7.42	7.23	7.27	7.41	7.21
TC0700890	SLC4A2	6522	solute carrier family 4, anion exchange	0.000299	1	4.59	4.72	4.70	4.63	4.66	4.64	4.62	4.60

TC1601328	SLC7A5	8140	solute carrier family 7 (cationic amino a	4.49E-05	1	4.35	4.88	4.53	4.49	4.55	4.44	4.49	4.36
TC0200540	SLC9A4	389015	solute carrier family 9 (sodium/hydroge	2.33E-07	1	2.51	3.01	2.83	2.74	2.78	2.64	2.46	2.56
TC0X00590	SLC9A6	10479	solute carrier family 9 (sodium/hydroge	1.15E-20	1	4.37	5.29	5.42	5.14	5.04	4.90	4.84	4.70
TC2000360	SLC9A8	23315	solute carrier family 9 (sodium/hydroge	1.43E-06	1	6.98	7.29	7.08	7.08	7.07	6.97	6.94	6.78
TC0501184	SLCO4C1	353189	solute carrier organic anion transporter	5.36E-14	1	6.77	8.12	8.20	7.98	7.87	7.73	7.47	7.50
TC0400575	SMAD1	4086	SMAD family member 1	4.80E-07	1	3.78	4.07	4.14	4.04	4.05	3.87	3.91	3.83
TC0600497	SMAP1	60682	stromal membrane-associated GTPase-	1.28E-08	1	5.63	6.02	6.12	6.03	5.94	5.98	6.01	5.98
TC2200124	SMARCB1	6598	SWI/SNF related, matrix associated, act	0.00024	1	5.10	5.65	5.40	5.40	5.49	5.43	5.47	5.32
TC1700903	SMG6	23293	Smg-6 homolog, nonsense mediated m	0.000923	1	4.54	4.67	4.61	4.56	4.62	4.53	4.52	4.44
TC0600694	SMPDL3A	10924	sphingomyelin phosphodiesterase, aci	6.73E-16	1	3.66	5.41	5.81	5.56	5.21	4.61	4.37	4.03
TC0900851	SMU1	55234	smu-1 suppressor of mec-8 and unc-52	0.00024	1	6.25	6.78	6.69	6.71	6.58	6.59	6.58	6.55
TC0101084	SNAPIN	23557	SNAP-associated protein	1.32E-10	1	5.05	6.11	6.25	6.01	5.83	5.76	5.72	5.66
TC1701494	SNF8	11267	SNF8, ESCRT-II complex subunit, homol	3.60E-05	1	5.73	6.25	6.35	6.34	6.28	6.28	6.29	6.22
TC0700411	SNORA14A	---	small nucleolar RNA, H/ACA box 14A (S	3.05E-09	1	4.26	5.41	5.12	4.79	4.72	4.62	4.37	4.52
TC1300450	SNORA31	---	small nucleolar RNA, H/ACA box 31 (SN	5.69E-05	1	6.53	7.46	7.53	7.15	7.25	7.27	7.11	7.08
TC2000090	SNRPB2	6629	small nuclear ribonucleoprotein polype	1.31E-12	1	5.32	6.40	6.61	6.38	6.30	6.38	6.47	6.31
TC1600551	SNTB2	6645	syntrophin, beta 2 (dystrophin-associat	6.39E-10	1	5.08	5.88	5.88	5.68	5.70	5.58	5.49	5.31
TC1500400	SNX1	6642	sorting nexin 1	5.00E-06	1	7.00	7.47	7.48	7.44	7.24	7.21	7.23	7.20
TC0X01006	SNX12	29934	sorting nexin 12 /// Sorting nexin-12. [S	3.03E-15	1	5.89	6.39	6.57	6.46	6.50	6.40	6.29	6.28
TC0801073	SNX16	64089	sorting nexin 16	8.46E-05	1	4.41	4.95	5.11	5.13	4.89	4.95	4.99	4.89
TC0500179	SNX18 /// SNA	112574	sorting nexin 18 /// Sorting nexin-18 (S	1.99E-10	1	6.62	7.16	7.07	6.88	6.68	6.68	6.55	6.54
TC0601507	SNX3	8724	sorting nexin 3 /// Sorting nexin-3 (Pro	5.15E-40	1	6.03	7.64	7.95	7.64	7.52	7.17	7.02	6.81
TC0301511	SNX4	8723	sorting nexin 4	7.31E-13	1	4.19	5.46	5.54	5.45	5.47	5.40	5.46	5.25
TC1701740	SOCS3	9021	suppressor of cytokine signaling 3	9.83E-18	1	6.08	7.94	7.83	7.58	7.31	7.29	7.10	6.97
TC0102517	SORT1	6272	sortilin 1	1.49E-21	1	5.21	7.51	7.64	7.09	6.93	6.59	6.50	6.27
TC1400842	SOS2	6655	son of sevenless homolog 2 (Drosophila	4.81E-11	1	8.04	8.46	8.54	8.44	8.31	8.25	8.14	8.06
TC0701044	SP8	221833	Sp8 transcription factor /// Transcriptio	0.000145	1	3.81	4.03	3.99	3.84	3.95	3.91	3.80	3.91
TC1100964	SPA17	53340	sperm autoantigenic protein 17	4.50E-08	1	4.22	4.65	4.81	4.79	4.71	4.71	4.75	4.58
TC1300029	SPATA13 /// Q	221178	spermatogenesis associated 13 /// Sper	1.34E-11	1	5.50	6.18	6.03	5.91	5.64	5.67	5.66	5.68
TC0800615	SPATC1	375686	spermatogenesis and centriole associat	5.19E-09	1	4.46	4.90	4.86	4.76	4.70	4.58	4.60	4.57
TC0400691	SPCS3	60559	signal peptidase complex subunit 3 hor	1.55E-10	1	6.30	6.97	7.17	7.03	7.02	7.04	7.04	6.92
TC0200141	SPDYA /// PPP1	245711 //	speedy homolog A (Drosophila) /// pro	7.37E-14	1	6.20	6.76	6.76	6.62	6.46	6.43	6.34	6.33
TC2200137	SPECC1L	23384	SPECC1-like	2.14E-08	1	5.44	6.45	6.01	5.93	5.82	5.58	5.72	5.50
TC1300400	SPG20	23111	spastic paraplegia 20 (Troyer syndrome	2.04E-06	1	5.25	5.93	5.71	5.55	5.68	5.76	5.84	5.82

TC1900498	SPINT2	10653	serine peptidase inhibitor, Kunitz type,	1.83E-14	1	5.68	6.84	6.56	6.31	6.49	6.45	6.38	6.31
TC1500954	SPPL2A	84888	signal peptide peptidase-like 2A	5.14E-12	1	6.91	7.64	7.93	7.88	7.63	7.51	7.62	7.49
TC0201578	SPRED2	200734	sprouty-related, EVH1 domain containi	2.07E-15	1	4.01	5.20	4.67	4.54	4.72	4.46	4.43	4.37
TC0101072	SPRR1A	6698	small proline-rich protein 1A	0.000511	1	6.11	6.54	6.37	6.33	6.23	6.28	6.30	6.27
TC0901126	SPTLC1	731770 //	serine palmitoyltransferase, long chain	4.74E-05	1	6.12	6.49	6.56	6.55	6.45	6.39	6.33	6.32
TC1401023	SPTLC2	9517	serine palmitoyltransferase, long chain	1.19E-16	1	7.43	8.45	8.45	8.42	8.12	7.93	7.95	7.83
TC1500312	SQRDL /// PLDI	58472 ///	sulfide quinone reductase-like (yeast) /	2.59E-12	1	6.42	7.02	7.14	7.05	6.99	6.99	6.96	6.88
TC0500031	SRD5A1	6715	steroid-5-alpha-reductase, alpha polyp	1.66E-07	1	3.76	4.13	4.37	4.24	4.21	4.06	4.09	4.06
TC0400236	SRD5A3	79644	steroid 5 alpha-reductase 3	6.07E-05	1	2.96	2.94	3.31	3.16	3.05	2.93	3.04	3.00
TC0600403	SRF	6722	serum response factor (c-fos serum res	1.30E-09	1	6.17	6.76	6.86	6.74	6.66	6.64	6.54	6.53
TC0701399	SRI	6717	sorcin	1.74E-13	1	7.42	8.42	8.44	8.29	8.16	8.18	8.20	8.13
TC1500832	SRP14	6727	signal recognition particle 14kDa (hom	5.08E-16	1	8.04	8.51	8.67	8.66	8.59	8.57	8.60	8.55
TC1400166	SRP54	6729	signal recognition particle 54kDa	7.50E-06	1	5.62	6.38	6.15	6.03	5.95	5.96	6.01	5.90
TC0101560	SRP9	6726	signal recognition particle 9kDa /// Sigr	1.57E-11	1	7.18	7.81	7.93	7.88	7.98	7.90	7.87	7.76
TC1001159	SRP9	6726	signal recognition particle 9kDa	2.06E-07	1	6.45	7.48	7.48	7.45	7.68	7.51	7.48	7.27
TC0601206	SRPK1	6732	SFRS protein kinase 1 /// Serine/threor	1.12E-24	1	7.10	8.42	8.36	8.23	8.18	8.09	7.98	7.74
TC1800386	SS18	6760	synovial sarcoma translocation, chrom	1.28E-06	1	3.99	4.23	4.32	4.49	4.32	4.27	4.32	4.23
TC1900321	SSBP4	170463	single stranded DNA binding protein 4	0.000407	1	5.72	5.90	5.90	5.86	5.88	5.89	5.83	5.79
TC0200909	SSFA2	6744	sperm specific antigen 2 /// Sperm-spe	0.000391	1	6.81	7.09	7.30	7.14	6.90	7.04	7.06	7.08
TC1201541	SSH1	54434	slingshot homolog 1 (Drosophila) /// Pr	1.20E-17	1	4.32	4.90	5.10	5.12	4.92	4.60	4.59	4.46
TC1100990	ST3GAL4	6484	ST3 beta-galactoside alpha-2,3-sialyltra	8.06E-11	1	5.26	5.92	5.92	5.83	5.73	5.64	5.48	5.40
TC0100662	ST6GALNAC3	256435	ST6 (alpha-N-acetyl-neuraminyl-2,3-be	2.26E-24	1	3.39	4.98	5.39	4.63	4.46	4.28	4.06	3.84
TC0102549	ST7L	54879	suppression of tumorigenicity 7 like ///	2.51E-16	1	3.95	4.19	4.64	4.69	4.60	4.38	4.26	4.22
TC1000080	STAM	8027	signal transducing adaptor molecule (S	1.45E-08	1	5.95	6.68	6.46	6.56	6.55	6.51	6.45	6.36
TC0700194	STARD3NL	83930	STARD3 N-terminal like	1.50E-05	1	5.33	5.70	6.01	5.69	5.57	5.72	5.75	5.89
TC0801034	STAU2	27067	staufen, RNA binding protein, homolog	5.87E-17	1	5.87	6.60	6.74	6.65	6.60	6.52	6.48	6.41
TC1100072	STIM1	6786	stromal interaction molecule 1	7.10E-06	1	5.76	5.96	5.93	6.19	6.15	5.94	5.90	5.88
TC0201115	STK16	8576	serine/threonine kinase 16 /// Serine/t	4.56E-11	1	4.78	5.35	5.35	5.15	5.21	5.03	4.96	4.93
TC0700213	STK17A	9263	serine/threonine kinase 17a	4.11E-05	1	6.58	6.97	7.00	6.67	6.66	6.82	6.76	6.85
TC0202190	STK17B	9262	serine/threonine kinase 17b	2.63E-08	1	9.07	9.64	9.55	9.38	9.27	9.36	9.26	9.37
TC0202448	STK25	10494	serine/threonine kinase 25 (STE20 hom	0.000527	1	5.13	5.35	5.36	5.35	5.38	5.36	5.34	5.30
TC0801145	STK3	6788	serine/threonine kinase 3 (STE20 homo	1.52E-11	1	4.51	5.30	5.65	5.30	4.99	5.10	5.10	4.95
TC0601214	STK38	11329	serine/threonine kinase 38	1.06E-09	1	8.34	8.67	8.70	8.47	8.33	8.38	8.34	8.32
TC0901302	STOM	2040	stomatin	1.44E-37	1	5.73	9.61	9.62	9.41	9.65	9.05	8.61	7.92

TC1200169	STRAP	11171	serine/threonine kinase receptor assoc	3.60E-09	1	4.88	5.82	5.75	5.65	5.71	5.69	5.62	5.52
TC0201428	STRN	6801	striatin, calmodulin binding protein ///	4.06E-06	1	7.21	7.70	7.60	7.42	7.36	7.50	7.45	7.38
TC1400766	STRN3	29966	striatin, calmodulin binding protein 3	5.56E-10	1	5.80	6.46	6.42	6.33	6.19	6.13	6.10	6.00
TC0600780	STX11	8676	syntaxin 11	7.74E-06	1	5.89	6.65	6.58	6.72	6.49	6.46	6.34	6.43
TC0100312	STX12	23673	syntaxin 12 /// Syntaxin-12. [Source:Ur	2.78E-05	1	6.81	7.21	7.27	7.21	7.04	7.14	7.04	7.10
TC0400790	STX18	53407	syntaxin 18	5.52E-06	1	4.48	5.13	5.28	5.13	5.24	5.10	5.13	4.98
TC0103044	STX6	10228	syntaxin 6	0.000782	1	5.64	6.04	6.08	6.18	5.98	6.08	6.03	6.04
TC1701022	STX8	9482	syntaxin 8	2.59E-09	1	4.08	4.80	4.86	4.90	4.88	4.78	4.79	4.63
TC0701356	STYXL1	51657	serine/threonine/tyrosine interacting-l	2.50E-06	1	5.87	6.51	6.76	6.58	6.42	6.54	6.48	6.42
TC0500104	SUB1	730602 //	SUB1 homolog (S. cerevisiae)	2.53E-19	1	6.08	7.22	7.31	7.01	6.79	6.86	6.88	6.82
TC0201667	SUCLG1	8802	succinate-CoA ligase, alpha subunit ///	5.68E-17	1	5.33	6.32	6.49	6.47	6.47	6.24	6.13	5.93
TC0401016	SULT1B1	27284	sulfotransferase family, cytosolic, 1B, n	4.82E-14	1	7.59	8.46	8.96	8.68	8.43	8.39	8.11	8.05
TC0201432	SULT6B1	391365	sulfotransferase family, cytosolic, 6B, n	8.62E-06	1	2.42	2.56	2.64	2.44	2.46	2.46	2.35	2.38
TC0300965	SUMF1	285362	sulfatase modifying factor 1 /// Sulfata	7.95E-16	1	4.75	5.37	5.76	5.49	5.33	5.10	5.04	4.88
TC0202233	SUMO1	7341	SMT3 suppressor of mif two 3 homolog	7.84E-12	1	8.11	8.83	8.89	8.81	8.72	8.76	8.69	8.72
TC1701688	SUMO2	6613	SMT3 suppressor of mif two 3 homolog	1.59E-08	1	8.54	9.06	9.18	9.22	9.20	9.10	9.09	9.08
TC0X01171	SUMO2	730776 //	SMT3 suppressor of mif two 3 homolog	2.04E-05	1	8.60	9.05	9.16	9.19	9.14	9.07	9.06	9.05
TC2100404	SUMO3	6612	SMT3 suppressor of mif two 3 homolog	1.33E-13	1	4.90	5.98	5.93	5.98	6.09	5.93	5.89	5.72
TC1101263	SVIP_HUMAN	---	Small VCP/p97-interacting protein. [Sou	7.24E-18	1	4.52	6.72	6.70	6.70	7.06	7.01	6.75	6.35
TC0X00067	SYAP1	94056	synapse associated protein 1, SAP47 hc	1.81E-08	1	6.10	6.76	6.21	6.17	6.11	6.19	6.26	6.28
TC2000874	SYCP2	10388	synaptonemal complex protein 2	1.93E-11	1	2.81	3.08	3.53	3.61	3.25	2.98	3.00	2.80
TC1700806	SYNGR2	9144	synaptogyrin 2	2.26E-07	1	5.22	6.11	5.99	5.86	5.85	5.80	5.71	5.69
TC0701538	SYPL1	6856	synaptophysin-like 1	3.31E-17	1	5.33	6.26	6.23	6.24	6.38	6.37	6.31	6.14
TC0101131	SYT11	23208	synaptotagmin XI	1.71E-08	1	4.41	4.62	4.94	5.21	5.00	4.61	4.76	4.71
TC0300993	TADA3L	10474	transcriptional adaptor 3 (NGG1 homol	0.000793	1	5.38	5.52	5.51	5.58	5.45	5.39	5.35	5.38
TC0102512	TAF13	6884	TAF13 RNA polymerase II, TATA box bir	1.58E-09	1	6.08	7.10	7.22	7.26	7.26	7.02	7.10	6.90
TC0500108	TARS	6897	threonyl-tRNA synthetase	6.67E-05	1	3.92	5.10	4.92	5.04	5.08	4.93	4.90	4.73
TC0700809	TAS2R40	259286	taste receptor, type 2, member 40	1.58E-07	1	5.50	6.01	6.43	6.39	5.87	5.93	5.74	5.33
TC1200522	TBC1D15	64786	TBC1 domain family, member 15	2.65E-05	1	7.05	7.67	7.31	7.17	7.16	7.34	7.23	7.20
TC0600956	TBC1D7	51256	TBC1 domain family, member 7 /// TBC	4.71E-09	1	5.07	5.74	5.79	5.61	5.67	5.51	5.44	5.39
TC0201785	TBC1D8	11138	TBC1 domain family, member 8 (with G	2.18E-24	1	3.93	6.07	6.22	5.73	5.56	5.04	4.84	4.50
TC0X00476	TBC1D8B	54885	TBC1 domain family, member 8B (with	6.18E-17	1	2.21	2.72	2.72	2.25	2.31	2.32	2.32	2.27
TC0501086	TBCA	6902	tubulin folding cofactor A	8.90E-22	1	6.19	7.27	7.55	7.56	7.57	7.37	7.32	7.21
TC1900469	TBCB	1155	tubulin folding cofactor B	1.34E-10	1	5.62	6.11	6.29	6.15	6.09	5.92	5.94	5.77

TC0301770	TBL1XR1	79718	transducin (beta)-like 1 X-linked recept	7.75E-09	1	7.89	8.29	8.31	8.01	8.02	8.02	7.78	7.84
TC0701319	TBL2	26608	transducin (beta)-like 2	0.000259	1	4.69	4.78	4.85	4.84	4.88	4.77	4.73	4.74
TC0701370	tcag7.1314 ///	54103	hypothetical protein LOC54103	4.86E-07	1	3.70	4.07	4.30	4.16	4.11	3.83	3.82	3.68
TC0801037	TCEB1	6921	transcription elongation factor B (SIII),	9.27E-10	1	7.01	7.51	7.48	7.39	7.38	7.36	7.37	7.31
TC1500358	TCF12	6938	transcription factor 12 (HTF4, helix-loo	2.35E-10	1	4.36	5.24	5.22	5.37	5.44	5.31	5.34	5.09
TC1800490	TCF4	6925	transcription factor 4	6.28E-06	1	3.70	3.89	4.10	3.98	3.84	3.80	3.84	3.79
TC1200688	TCHP	84260	trichoplein, keratin filament binding	8.80E-06	1	5.92	6.10	6.28	6.29	6.23	6.08	6.07	6.00
TC0601726	TCP1	6950	t-complex 1	1.64E-06	1	6.66	7.38	7.46	7.31	7.27	7.27	7.20	7.11
TC0301893	TCTEX1D2 /// T	255758 //	Tctex1 domain containing 2 /// transm	2.01E-10	1	4.07	4.37	4.66	4.43	4.34	4.23	4.10	4.12
TC1200648	TDG	6996	thymine-DNA glycosylase	0.000113	1	4.59	4.92	4.95	4.98	4.91	4.92	4.97	4.88
TC1400616	TDRD9	122402	tudor domain containing 9 /// tudor d	4.87E-18	1	3.65	4.73	6.20	5.77	5.37	4.53	4.45	3.87
TC1600483	TEPP	374739	testis/prostate/placenta-expressed pro	0.000454	1	4.38	4.42	4.49	4.42	4.46	4.42	4.27	4.35
TC0700626	TES	26136	testis derived transcript (3 LIM domain	1.79E-29	1	7.06	8.61	8.62	8.60	8.37	8.21	8.14	8.05
TC1201605	TESC	54997	tescalcin /// Tescalcin (TSC). [Source:Ur	7.93E-18	1	4.96	6.67	6.82	6.47	6.55	6.15	5.93	5.73
TC1300295	TFDP1	7027	transcription factor Dp-1	2.37E-22	1	5.81	7.89	7.20	6.81	7.08	6.98	6.77	6.61
TC0301618	TFDP2	7029	transcription factor Dp-2 (E2F dimeriza	2.65E-10	1	5.07	6.57	5.78	5.78	6.02	5.98	5.97	5.78
TC2100366	TFF3	7033	trefoil factor 3 (intestinal) /// Trefoil fa	5.09E-07	1	4.30	5.05	4.83	4.80	4.93	4.80	4.73	4.70
TC0300447	TFG	10342	TRK-fused gene	2.93E-10	1	5.53	6.18	5.98	5.84	5.73	5.79	5.76	5.75
TC0301890	TFRC	7037	transferrin receptor (p90, CD71)	9.02E-05	1	4.37	5.18	4.54	4.55	4.60	4.51	4.57	4.37
TC0201606	TGFA	7039	transforming growth factor, alpha	7.64E-10	1	5.57	5.95	6.21	6.13	5.89	5.91	5.78	5.83
TC0900430	TGFBR1	7046	transforming growth factor, beta recep	5.22E-21	1	6.62	7.73	7.95	7.73	7.49	7.55	7.35	7.34
TC2000236	TGIF2 /// C20o	60436 ///	TGFB-induced factor homeobox 2 /// cl	1.30E-05	1	5.67	5.97	6.08	6.00	5.93	5.95	5.85	5.92
TC1200519	THAP2	83591	THAP domain containing, apoptosis ass	9.18E-10	1	3.42	3.99	4.38	4.33	4.30	4.08	4.06	3.88
TC0800053	THEX1	90459	three prime histone mRNA exonucleas	1.02E-14	1	4.91	7.03	6.83	6.42	6.16	6.12	6.01	5.83
TC1901063	TICAM1	148022	toll-like receptor adaptor molecule 1 //	1.63E-05	1	4.83	5.17	5.13	5.13	5.09	5.00	5.04	5.01
TC0401194	TIFA	92610	TRAF-interacting protein with forkhead	4.97E-10	1	4.88	6.56	6.78	6.88	6.53	6.38	6.31	6.33
TC1901120	TIMM44	10469	translocase of inner mitochondrial mer	0.00019	1	3.73	3.93	3.96	3.94	3.91	3.89	3.87	3.89
TC1101834	TIMM8B	26521	translocase of inner mitochondrial mer	9.24E-12	1	6.73	7.57	7.84	7.78	7.75	7.80	7.77	7.64
TC0X00192	TIMP1	7076	TIMP metallopeptidase inhibitor 1 ///	1.23E-09	1	5.94	6.71	6.79	7.02	6.97	6.67	6.39	6.42
TC1400740	TINF2	26277	TERF1 (TRF1)-interacting nuclear factor	2.10E-09	1	6.59	7.18	7.16	6.93	6.80	6.92	6.80	6.86
TC0300736	TIPARP	25976	TCDD-inducible poly(ADP-ribose) polym	5.63E-15	1	6.02	7.15	7.33	7.07	6.63	6.52	6.44	6.39
TC0101265	TIPRL	261726	TIP41, TOR signaling pathway regulator	6.30E-14	1	6.14	6.93	7.03	6.87	6.80	6.96	6.94	6.92
TC1100988	TIRAP	114609	toll-interleukin 1 receptor (TIR) domain	0.000349	1	4.68	5.08	5.00	4.83	4.91	4.85	4.88	4.82
TC1601158	TK2	7084	thymidine kinase 2, mitochondrial	5.94E-07	1	5.67	6.12	6.04	6.16	5.97	5.82	5.72	5.69

TC0901068	TLE1	7088	transducin-like enhancer of split 1 (E(sp	3.50E-05	1	3.43	3.74	3.77	3.70	3.66	3.60	3.61	3.61
TC0900518	TLR4	7099	toll-like receptor 4	2.64E-07	1	9.74	10.35	10.12	10.02	9.80	9.94	9.87	9.93
TC0103261	TLR5	7100	toll-like receptor 5	1.60E-21	1	5.03	6.64	7.38	7.25	6.86	6.63	6.51	6.06
TC0X00045	TLR8	51311	toll-like receptor 8 /// Toll-like recepto	2.51E-06	1	9.22	9.49	9.74	9.63	9.25	9.21	9.18	9.23
TC0102310	TM2D1	83941	TM2 domain containing 1 /// beta-amy	0.00027	1	4.86	5.12	5.32	5.07	5.10	5.10	5.16	5.03
TC0800890	TM2D2	83877	TM2 domain containing 2	0.00064	1	4.27	4.44	4.69	4.53	4.56	4.51	4.57	4.52
TC0202314	TMBIM1	64114	transmembrane BAX inhibitor motif co	0.000176	1	8.03	8.39	8.39	8.53	8.44	8.39	8.29	8.33
TC1201367	TMBIM4	51643	transmembrane BAX inhibitor motif co	8.28E-06	1	7.82	8.10	8.34	8.15	8.12	8.24	8.25	8.27
TC1300294	TMCO3	55002	transmembrane and coiled-coil domai	5.69E-19	1	5.85	6.57	6.78	6.66	6.51	6.29	6.25	6.08
TC0102446	TMED5	50999	transmembrane emp24 protein transp	8.26E-22	1	5.05	5.86	6.03	5.80	5.74	5.65	5.61	5.60
TC1401018	TMED8	283578	transmembrane emp24 protein transp	1.15E-19	1	4.59	5.85	5.91	5.64	5.53	5.29	5.28	5.14
TC0701355	TMEM120A	83862	transmembrane protein 120A	2.07E-10	1	6.00	6.69	6.73	6.45	6.40	6.30	6.15	6.21
TC1400640	TMEM121	80757	transmembrane protein 121	0.000108	1	3.50	3.98	3.98	4.04	4.05	3.93	3.95	3.94
TC1100719	TMEM126B	55863	transmembrane protein 126B /// Trans	1.72E-06	1	4.42	5.32	5.49	5.31	5.15	5.29	5.46	5.30
TC0201771	TMEM131	23505	transmembrane protein 131	1.24E-05	1	6.34	6.92	6.90	6.74	6.51	6.38	6.53	6.47
TC0400237	TMEM165	55858	transmembrane protein 165	7.56E-16	1	5.66	6.16	6.64	6.45	6.09	5.99	5.97	5.84
TC0501119	TMEM167A	153339	transmembrane protein 167A	1.29E-16	1	7.04	7.90	8.25	8.08	7.83	7.83	7.83	7.77
TC0701560	TMEM168	64418	transmembrane protein 168	0.000938	1	4.15	4.40	4.50	4.27	4.19	4.23	4.21	4.09
TC0201080	TMEM169	92691	transmembrane protein 169	8.96E-13	1	5.03	5.36	5.65	5.63	5.70	5.50	5.31	5.36
TC0301138	TMEM16K	55129	transmembrane protein 16K /// Transn	3.27E-19	1	4.42	5.45	5.50	5.50	5.60	5.13	4.97	4.81
TC0600075	TMEM170B	1E+08	transmembrane protein 170B	4.52E-22	1	5.37	7.32	7.00	7.00	7.07	7.01	6.81	6.55
TC0501339	TMEM173	340061	transmembrane protein 173	0.000145	1	4.60	4.88	4.90	4.88	4.96	4.81	4.86	4.70
TC0700886	TMEM176A	55365	transmembrane protein 176A	1.48E-05	1	4.70	5.06	5.08	5.18	5.07	5.07	5.09	5.03
TC0200195	TMEM178	130733	transmembrane protein 178 /// Transn	6.53E-09	1	4.95	5.35	5.35	5.34	5.35	5.36	5.30	5.22
TC1000540	TMEM180	79847	transmembrane protein 180 /// Transn	2.19E-07	1	4.36	4.84	4.61	4.61	4.69	4.61	4.60	4.48
TC0101429	TMEM183A	92703	transmembrane protein 183A	1.05E-09	1	6.18	6.40	6.61	6.65	6.62	6.54	6.52	6.52
TC0201861	TMEM185B	---	Transmembrane protein 185B (Protein	2.57E-07	1	4.29	5.37	5.25	5.10	5.15	4.91	4.96	4.64
TC0X00694	TMEM187	8269	transmembrane protein 187	0.000641	1	4.92	5.22	5.33	5.30	5.32	5.20	5.10	5.13
TC0401379	TMEM192	201931	transmembrane protein 192	0.000362	1	4.10	4.28	4.36	4.40	4.28	4.36	4.38	4.22
TC0901035	TMEM2	23670	transmembrane protein 2 /// Transmer	4.01E-10	1	7.36	7.82	7.94	7.87	7.54	7.49	7.50	7.44
TC0601398	TMEM30A	55754	transmembrane protein 30A /// Cell cy	8.16E-09	1	6.15	6.75	6.79	6.54	6.51	6.58	6.48	6.52
TC0X01284	TMEM32	93380	transmembrane protein 32	2.62E-20	1	5.12	6.56	6.70	6.24	6.22	6.26	6.07	6.02
TC0400190	TMEM33	55161	transmembrane protein 33	2.16E-10	1	7.58	7.61	8.10	8.10	7.89	7.85	7.73	7.81
TC1900287	TMEM38A	79041	transmembrane protein 38A	0.000107	1	4.15	4.60	4.40	4.43	4.49	4.50	4.34	4.35

TC0100351	TMEM39B	55116	transmembrane protein 39B /// Transn	1.54E-08	1	4.68	5.00	4.97	5.05	5.01	5.01	4.97	4.96
TC1101195	TMEM41B	440026	transmembrane protein 41B	0.000331	1	4.31	4.77	4.90	4.63	4.50	4.60	4.61	4.53
TC1200476	TMEM5	10329	transmembrane protein 5	1.13E-05	1	3.35	3.66	3.81	3.77	3.74	3.64	3.70	3.62
TC0801109	TMEM64	169200	transmembrane protein 64	2.65E-08	1	4.14	4.37	4.52	4.58	4.50	4.37	4.28	4.32
TC0800381	TMEM70	54968	transmembrane protein 70	1.42E-10	1	5.02	5.75	5.73	5.69	5.60	5.48	5.44	5.43
TC0102536	TMEM77	128338	transmembrane protein 77	1.18E-07	1	4.22	4.79	5.01	4.64	4.52	4.60	4.63	4.53
TC1500873	TMEM87A	25963	transmembrane protein 87A /// Transn	5.16E-13	1	5.12	6.15	6.21	6.09	6.04	6.03	6.09	5.87
TC0200580	TMEM87B	84910	transmembrane protein 87B	1.74E-13	1	4.16	5.00	5.34	5.30	5.24	5.06	4.93	4.89
TC1700439	TMEM99	147184	transmembrane protein 99	3.67E-06	1	2.76	3.12	3.18	3.12	3.16	3.09	3.20	3.13
TC1500339	TMOD3	29766	tropomodulin 3 (ubiquitous)	3.99E-15	1	7.68	8.24	8.41	8.47	8.25	8.16	8.10	8.01
TC1201072	TMTC1	83857	transmembrane and tetratricopeptide	0.000105	1	3.79	4.83	5.12	5.27	4.72	4.29	4.02	4.22
TC1200554	TMTC2	160335	transmembrane and tetratricopeptide	5.58E-07	1	3.07	3.30	3.33	3.41	3.20	3.22	3.19	3.10
TC0200784	TNFAIP6	7130	tumor necrosis factor, alpha-induced p	1.92E-08	1	7.04	8.77	8.37	8.83	8.69	8.64	8.61	8.75
TC1500956	TNFAIP8L3	388121	tumor necrosis factor, alpha-induced p	0.000829	1	3.87	4.00	4.10	3.92	3.96	3.88	3.77	3.80
TC0800801	TNFRSF10A	8797	tumor necrosis factor receptor superfa	3.52E-07	1	4.61	5.08	4.93	4.71	4.79	4.67	4.70	4.56
TC0800800	TNFRSF10D	8793	tumor necrosis factor receptor superfa	1.86E-16	1	4.97	6.13	5.53	5.30	5.28	5.14	5.06	5.04
TC2200714	TNFRSF13C	115650	tumor necrosis factor receptor superfa	8.06E-05	1	5.42	5.75	5.74	5.78	5.73	5.83	5.73	5.66
TC1700099	TNFSF12-TNFSI	407977 //	TNFSF12-TNFSF13 /// tumor necrosis fa	2.70E-07	1	5.79	6.27	6.22	6.25	6.18	6.19	6.21	6.20
TC1300272	TNFSF13B	10673	tumor necrosis factor (ligand) superfan	2.41E-14	1	8.20	9.76	9.52	9.20	8.88	9.05	9.00	9.02
TC0901278	TNFSF8	944	tumor necrosis factor (ligand) superfan	7.75E-09	1	4.71	5.76	4.88	4.62	4.79	5.16	5.21	5.29
TC0400778	TNIP2	79155	TNFAIP3 interacting protein 2	6.75E-08	1	5.89	6.38	6.34	6.30	6.18	6.25	6.28	6.17
TC0100653	TNNI3K /// FPG	51086 ///	TNNI3 interacting kinase /// fucose-1-p	6.48E-13	1	2.56	2.70	2.85	2.71	2.67	2.66	2.64	2.63
TC0701622	TNPO3	23534	transportin 3 /// Transportin-3 (Transp	1.94E-15	1	6.13	7.16	7.18	6.91	6.83	6.72	6.64	6.39
TC1101055	TOLLIP	54472	toll interacting protein /// Toll-interact	1.60E-09	1	5.45	5.79	5.94	5.92	5.92	5.85	5.78	5.77
TC0101208	TOMM40L	84134	translocase of outer mitochondrial mer	3.58E-12	1	4.17	4.85	4.70	4.60	4.72	4.63	4.41	4.32
TC0701055	TOMM7	54543	translocase of outer mitochondrial mer	1.27E-07	1	8.27	8.90	9.04	9.04	8.97	8.95	9.01	9.01
TC0101322	TOR1AIP1	26092	torsin A interacting protein 1 /// Torsin	0.000969	1	7.57	7.95	8.06	8.01	7.96	8.01	7.92	8.01
TC0103037	TOR1AIP2 /// II	163590 //	torsin A interacting protein 2 /// interfe	4.08E-10	1	6.38	6.97	6.99	7.12	6.92	6.94	6.77	6.80
TC1601101	TOX3	27324	TOX high mobility group box family me	0.00013	1	3.06	3.14	3.23	3.11	3.15	2.98	3.05	3.01
TC0103265	TP53BP2	7159	tumor protein p53 binding protein, 2	4.25E-06	1	5.76	6.25	6.22	6.38	6.29	6.21	6.24	6.09
TC1101326	TP53I11	9537	tumor protein p53 inducible protein 11	4.94E-16	1	5.38	6.03	6.01	5.84	5.89	5.76	5.63	5.63
TC1700320	TP53I13	90313	tumor protein p53 inducible protein 13	6.53E-06	1	4.97	5.18	5.24	5.23	5.19	5.20	5.14	5.15
TC0201354	TP53I3	9540	tumor protein p53 inducible protein 3 ,	1.35E-20	1	4.59	5.42	5.52	5.36	5.40	5.12	4.96	4.84
TC1200065	TPI1	732165 //	triosephosphate isomerase 1 /// Triose	1.06E-11	1	7.12	7.94	7.82	8.17	7.99	7.68	7.73	7.67

TC0701727	TPK1	27010	thiamin pyrophosphokinase 1 /// Thian	1.09E-15	1	4.12	4.97	5.23	4.85	4.41	4.16	4.19	4.17
TC0102808	TPM3	7170	tropomyosin 3 /// Tropomyosin alpha-	5.58E-09	1	7.11	7.39	7.40	7.33	7.31	7.31	7.29	7.27
TC1900280	TPM4	7171	tropomyosin 4 /// Tropomyosin alpha-	1.05E-10	1	8.57	9.33	9.29	9.13	9.02	8.91	8.72	8.70
TC0600981	TPMT	7172	thiopurine S-methyltransferase	9.52E-09	1	3.68	4.54	4.52	4.43	4.45	4.40	4.39	4.11
TC2200548	TPST2	8459	tyrosylprotein sulfotransferase 2	2.60E-18	1	6.36	6.90	7.57	7.48	7.35	7.10	6.94	6.83
TC1300448	TPT1	7178	tumor protein, translationally-controlle	4.09E-12	1	7.15	7.60	7.70	7.57	7.64	7.61	7.52	7.51
TC0101485	TRAF3IP3	80342	TRAF3 interacting protein 3 /// TRAF3-i	1.52E-08	1	6.47	7.18	6.90	6.60	6.53	6.58	6.46	6.56
TC1600075	TRAF7	84231	TNF receptor-associated factor 7	0.000461	1	4.89	5.10	5.02	4.96	4.95	4.96	4.92	4.94
TC0300190	TRAK1	22906	trafficking protein, kinesin binding 1	6.53E-05	1	5.19	5.57	5.40	5.43	5.28	5.29	5.29	5.22
TC1400808	TRAPPC6B	122553	trafficking protein particle complex 6B	5.72E-12	1	6.63	7.15	7.30	7.07	7.02	7.01	6.91	6.88
TC1000797	TRDMT1	1787	tRNA aspartic acid methyltransferase 1	1.61E-06	1	3.99	4.24	4.48	4.66	4.46	4.36	4.30	4.34
TC0601247	TREML2	79865	triggering receptor expressed on myel	0.000847	1	6.23	6.88	6.40	6.30	6.21	6.39	6.33	6.40
TC0800551	TRIB1	10221	tribbles homolog 1 (Drosophila)	5.56E-07	1	6.75	7.86	7.44	7.42	7.42	7.42	7.27	7.29
TC1701537	TRIM25	7706	tripartite motif-containing 25	1.82E-07	1	8.88	9.25	9.14	9.13	8.98	8.86	8.86	8.75
TC2000540	TRMT6	51605	tRNA methyltransferase 6 homolog (S.	4.18E-12	1	3.85	5.53	5.41	4.93	5.20	4.84	4.71	4.40
TC0101377	TROVE2	6738	TROVE domain family, member 2 /// 6	1.88E-07	1	5.85	6.56	6.47	6.35	6.33	6.41	6.38	6.36
TC2100172	TRPM2	7226	transient receptor potential cation cha	2.36E-15	1	4.59	5.16	5.12	5.01	5.07	4.93	4.81	4.76
TC0801204	TRPS1	7227	trichorhinophalangeal syndrome I /// Z	3.90E-31	1	3.90	6.95	6.83	6.10	5.80	5.23	4.93	4.47
TC1101510	TRPT1	83707	tRNA phosphotransferase 1	0.0005	1	4.99	5.31	5.27	5.26	5.31	5.27	5.27	5.22
TC1700158	TRPV2	51393	transient receptor potential cation cha	9.37E-22	1	4.88	6.08	5.93	5.56	5.50	5.25	5.28	5.17
TC0100328	TRSPAP1	54952	tRNA selenocysteine associated protei	2.79E-11	1	4.72	5.35	5.42	5.16	5.15	5.09	5.09	4.98
TC0300707	TSC22D2	9819	TSC22 domain family, member 2 /// TS	0.000604	1	4.54	4.82	4.65	4.78	4.61	4.71	4.75	4.86
TC0201775	TSGA10	80705	testis specific, 10	0.000421	1	2.77	2.82	2.86	2.91	2.90	2.78	2.79	2.77
TC0701636	TSGA13 /// CO	114960 //	testis specific, 13 /// coatomer protein	1.27E-08	1	3.22	3.21	3.42	3.42	3.23	3.17	3.26	3.19
TC1100683	TSKU	25987	tsukushin	0.000121	1	4.84	5.01	5.04	5.06	5.01	4.98	4.89	4.91
TC0101612	TSNAX	7257	translin-associated factor X /// Translin	1.79E-09	1	5.40	6.26	6.13	6.05	5.99	5.91	5.88	5.85
TC1000387	TSPAN14	81619	tetraspanin 14 /// Tetraspanin-14 (Tsp	6.57E-10	1	5.98	6.71	6.62	6.53	6.46	6.33	6.29	6.25
TC2200339	TSPO	706	translocator protein (18kDa) /// Transl	4.77E-22	1	5.98	7.31	7.62	7.60	7.54	7.17	6.94	6.77
TC0601551	TSPYL4	23270	TSPY-like 4	4.78E-06	1	4.21	4.74	4.75	4.74	4.72	4.62	4.55	4.50
TC1500881	TTBK2	146057	tau tubulin kinase 2 /// Tau-tubulin kin	3.16E-10	1	4.68	5.12	4.91	4.75	4.71	4.76	4.75	4.75
TC0103343	TTC13	79573	tetratricopeptide repeat domain 13 ///	6.96E-07	1	4.69	4.79	4.99	4.84	4.74	4.54	4.67	4.52
TC0500938	TTC33	23548	tetratricopeptide repeat domain 33	1.08E-07	1	4.89	5.58	5.62	5.51	5.46	5.46	5.39	5.32
TC0800498	TTC35	9694	tetratricopeptide repeat domain 35	8.67E-13	1	5.81	7.10	7.25	7.02	6.75	6.74	6.72	6.55
TC1400426	TTC8	123016	tetratricopeptide repeat domain 8 ///	4.63E-05	1	2.37	2.51	2.60	2.49	2.51	2.42	2.44	2.39

TC2200738	TTLL12	23170	tubulin tyrosine ligase-like family, mem	5.58E-07	1	4.82	5.14	5.14	5.15	5.12	5.03	4.99	4.95
TC0202333	TUBA4A	7277	tubulin, alpha 4a /// Tubulin alpha-4A	1.49E-08	1	7.52	8.34	8.12	8.10	8.14	7.98	7.79	7.85
TC0900724	TUBB2C	10383	tubulin, beta 2C	2.04E-05	1	5.66	5.97	5.92	5.97	6.01	5.98	5.89	5.84
TC1700466	TUBG2 /// TUB	27175 ///	tubulin, gamma 2 /// tubulin, gamma 1	5.07E-06	1	4.16	4.40	4.32	4.28	4.43	4.34	4.27	4.18
TC1201120	TWF1	5756	twinfilin, actin-binding protein, homol	1.20E-14	1	5.38	6.08	6.12	6.02	5.85	5.78	5.73	5.71
TC0901237	TXN	7295	thioredoxin /// Thioredoxin (Trx) (ATL-	2.19E-26	1	8.86	9.79	10.00	9.99	9.92	9.87	9.78	9.73
TC1800533	TXNDC10	54495	thioredoxin domain containing 10	0.00089	1	4.17	4.71	4.98	4.83	4.76	4.74	4.85	4.70
TC1600860	TXNDC11	51061	thioredoxin domain containing 11 /// T	2.97E-05	1	5.21	5.77	5.49	5.47	5.45	5.51	5.58	5.46
TC0700192	TXNDC3	51314	thioredoxin domain containing 3 (sper	1.57E-07	1	4.26	4.98	5.03	4.62	4.69	4.69	4.51	4.33
TC1800496	TXNL1	9352	thioredoxin-like 1	9.91E-12	1	5.56	6.09	6.27	6.14	6.10	6.14	6.08	6.10
TC0301334	UBA3	9039	ubiquitin-like modifier activating enzy	8.89E-05	1	7.41	7.40	7.78	7.81	7.51	7.49	7.55	7.53
TC0400995	UBA6	55236	ubiquitin-like modifier activating enzy	7.12E-14	1	4.86	6.42	6.17	5.63	5.46	5.48	5.54	5.34
TC0900143	UBAP1	51271	ubiquitin associated protein 1 /// Ubiq	3.95E-14	1	7.55	8.02	7.94	7.87	7.81	7.67	7.50	7.44
TC1000263	UBE2D1	7321	ubiquitin-conjugating enzyme E2D 1 (U	0.000106	1	7.93	8.29	8.48	8.57	8.43	8.50	8.39	8.40
TC0500521	UBE2D2	7322	ubiquitin-conjugating enzyme E2D 2 (U	0.000138	1	7.83	8.13	8.21	8.17	8.14	8.21	8.18	8.20
TC2000534	UBE2D3	7323	ubiquitin-conjugating enzyme E2D 3 (U	2.51E-06	1	7.74	8.10	8.28	8.06	8.00	8.15	8.07	8.12
TC0201222	UBE2F /// SCLY	140739 //	ubiquitin-conjugating enzyme E2F (put	2.33E-32	1	4.52	5.29	5.35	5.22	5.17	5.00	4.94	4.87
TC0701628	UBE2H	7328	ubiquitin-conjugating enzyme E2H (UB	5.21E-20	1	6.37	7.34	7.37	6.85	6.63	6.43	6.36	6.32
TC0601451	UBE2J1	51465	ubiquitin-conjugating enzyme E2, J1 (U	3.82E-17	1	7.23	7.87	8.41	8.08	7.88	7.90	7.85	7.69
TC0400176	UBE2K /// HIP2	3093	ubiquitin-conjugating enzyme E2K (UB	2.71E-22	1	8.06	8.85	9.08	9.10	8.97	8.93	8.92	8.86
TC1400244	UBE2L3	7332	ubiquitin-conjugating enzyme E2L 3	1.59E-09	1	7.25	8.00	8.05	8.08	8.09	8.09	8.03	8.01
TC2200078	UBE2L3	7332	ubiquitin-conjugating enzyme E2L 3	1.07E-05	1	8.08	8.47	8.48	8.56	8.55	8.50	8.49	8.48
TC0800282	UBE2V2	7336	ubiquitin-conjugating enzyme E2 varia	4.24E-05	1	6.36	6.71	6.70	6.73	6.70	6.75	6.70	6.70
TC1500738	UBE3A	7337	ubiquitin protein ligase E3A (human pa	0.000451	1	4.06	4.65	4.67	4.63	4.66	4.58	4.66	4.56
TC1300374	UBL3	5412	ubiquitin-like 3 /// Ubiquitin-like prote	7.24E-11	1	6.06	6.76	6.91	6.72	6.57	6.73	6.77	6.72
TC0X01386	UBL4A	8266	ubiquitin-like 4A /// Ubiquitin-like prot	0.000572	1	4.27	4.50	4.49	4.56	4.52	4.41	4.39	4.37
TC1900164	UBL5	59286	ubiquitin-like 5	3.72E-06	1	8.90	9.21	9.42	9.46	9.36	9.35	9.26	9.24
TC0500655	UBLCP1	134510	ubiquitin-like domain containing CTD p	5.55E-09	1	7.28	8.10	8.29	8.08	7.93	8.11	8.08	8.06
TC0901077	UBQLN1	29979	ubiquilin 1	0.000324	1	7.53	7.74	7.87	7.86	7.80	7.73	7.64	7.68
TC0X00290	UBQLN2	29978	ubiquilin 2	1.23E-13	1	5.15	6.27	6.72	6.55	6.18	6.17	6.23	6.13
TC0102845	UBQLN4	56893	ubiquilin 4 /// Ubiquilin-4 (Ataxin-1 ubi	0.000372	1	4.79	4.88	4.92	4.90	4.88	4.81	4.77	4.79
TC1500882	UBR1	197131	ubiquitin protein ligase E3 component	1.22E-09	1	4.43	5.34	5.01	4.83	4.73	4.78	4.88	4.73
TC1000486	UBTD1	80019	ubiquitin domain containing 1	2.55E-05	1	5.11	5.49	5.50	5.50	5.53	5.48	5.32	5.40
TC0501489	UBTD2	92181	ubiquitin domain containing 2 /// Ubiq	1.04E-12	1	4.95	5.28	5.28	5.33	5.25	5.20	5.11	5.09

TC0200740	UBXD2	23190	UBX domain containing 2	0.000525	1	7.56	7.95	8.00	7.99	7.85	7.88	7.87	7.85
TC1101245	UEVLD	55293	UEV and lactate/malate dehyrogenase	3.40E-11	1	4.83	5.48	5.65	5.31	5.13	5.13	5.09	4.98
TC1300091	UFM1	51569	ubiquitin-fold modifier 1 /// Ubiquitin-	0.000399	1	3.71	4.21	4.29	4.11	4.10	4.18	4.24	4.13
TC0900485	UGCG	7357	UDP-glucose ceramide glucosyltransfer	1.57E-26	1	5.15	8.45	8.30	7.83	8.10	7.72	7.22	6.62
TC0200285	UGP2	7360	UDP-glucose pyrophosphorylase 2	2.73E-20	1	6.20	7.03	7.09	7.03	6.97	6.88	6.81	6.73
TC0101228	UHMK1	127933	U2AF homology motif (UHM) kinase 1	1.16E-15	1	6.23	7.15	7.18	7.09	6.92	6.86	6.79	6.71
TC0200517	UNC50	25972	unc-50 homolog (C. elegans)	2.39E-06	1	6.35	6.86	7.06	6.93	6.90	6.96	6.95	6.93
TC2200671	UNC84B	25777	unc-84 homolog B (C. elegans)	2.14E-06	1	5.53	5.75	5.69	5.69	5.73	5.61	5.52	5.49
TC2200139	UPB1	51733	ureidopropionase, beta /// Beta-ureid	2.67E-06	1	3.73	3.79	4.00	3.93	3.85	3.70	3.66	3.60
TC0700239	UPP1	7378	uridine phosphorylase 1	2.83E-40	1	5.10	7.42	7.62	7.50	7.18	6.65	6.45	6.06
TC0801135	UQCRB	7381	ubiquinol-cytochrome c reductase bin	1.23E-14	1	5.55	6.35	6.56	6.47	6.37	6.34	6.36	6.24
TC0301184	UQCRC1	7384	ubiquinol-cytochrome c reductase core	3.06E-10	1	4.68	5.23	5.18	5.28	5.29	5.06	5.02	4.94
TC1901375	UQCRFS1	7386	ubiquinol-cytochrome c reductase, Rie	9.42E-12	1	5.90	6.75	6.81	6.70	6.81	6.59	6.44	6.37
TC1001255	USMG5	84833	up-regulated during skeletal muscle gr	2.85E-10	1	7.30	7.77	8.11	8.05	8.06	8.00	7.99	7.92
TC1800004	USP14	9097	ubiquitin specific peptidase 14 (tRNA-g	2.72E-08	1	3.70	4.41	4.50	4.42	4.56	4.32	4.36	4.17
TC1200678	USP30	84749	ubiquitin specific peptidase 30	5.70E-06	1	4.80	5.46	5.30	5.21	5.14	5.26	5.40	5.45
TC0400563	USP38	84640	ubiquitin specific peptidase 38	1.50E-07	1	6.18	6.83	6.80	6.78	6.49	6.56	6.47	6.49
TC1100178	USP47	55031	ubiquitin specific peptidase 47 /// Ubiq	3.61E-12	1	4.98	6.21	6.01	5.86	5.78	5.71	5.78	5.56
TC0400497	USP53	54532	ubiquitin specific peptidase 53	6.46E-15	1	3.60	4.62	3.90	3.77	3.71	3.75	3.83	3.74
TC0Y00051	USP9Y	8287	ubiquitin specific peptidase 9, Y-linked	3.85E-05	1	2.68	3.04	3.03	2.86	2.70	2.71	2.81	2.70
TC1700601	UTP18	51096	UTP18, small subunit (SSU) processom	0.000183	1	4.05	4.77	4.86	4.87	4.78	4.77	4.85	4.68
TC0100085	VAMP3	9341	vesicle-associated membrane protein 3	4.72E-12	1	8.10	8.94	8.91	8.68	8.73	8.76	8.61	8.65
TC0102998	VAMP4	8674	vesicle-associated membrane protein 4	9.14E-10	1	4.14	4.80	5.07	4.90	4.79	4.58	4.59	4.48
TC0Y00104	VAMP7	6845	vesicle-associated membrane protein 7	1.21E-14	1	5.33	6.29	6.37	6.24	6.16	6.18	6.06	6.07
TC0X00724	VAMP7 /// SYB	6845	vesicle-associated membrane protein 7	2.36E-15	1	5.76	6.75	6.81	6.70	6.63	6.64	6.56	6.54
TC1800049	VAPA	9218	VAMP (vesicle-associated membrane p	6.93E-18	1	7.04	8.06	8.03	7.97	7.88	7.84	7.64	7.63
TC0601134	VARS	7407	valyl-tRNA synthetase	1.60E-07	1	5.51	5.76	5.82	5.73	5.77	5.70	5.62	5.60
TC0102501	VAV3	10451	vav 3 guanine nucleotide exchange fac	2.62E-09	1	6.44	7.01	7.28	7.13	6.94	6.97	6.97	6.80
TC0X00717	VBP1	7411	von Hippel-Lindau binding protein 1	1.26E-20	1	5.69	6.81	7.15	7.06	7.02	7.01	6.86	6.80
TC0500318	VCAN	1462	versican /// Versican core protein prec	2.23E-13	1	3.90	6.96	6.55	6.93	6.16	5.58	5.44	5.53
TC0900887	VCP	7415	valosin-containing protein /// Transitio	0.000743	1	6.29	6.66	6.59	6.54	6.45	6.41	6.38	6.37
TC0301014	VGLL4	9686	vestigial like 4 (Drosophila)	2.67E-07	1	5.28	5.55	5.47	5.52	5.50	5.44	5.31	5.36
TC1000077	VIM	7431	vimentin	1.40E-15	1	8.51	9.15	9.37	9.39	9.34	9.10	8.98	8.87
TC2000045	VISA /// C20or	57506 ///	virus-induced signaling adapter /// chr	6.29E-06	1	4.93	5.10	5.04	4.94	5.01	5.01	4.95	4.92

TC0601610	VNN1	8876	vanin 1	6.74E-22	1	6.34	8.87	9.09	8.97	8.80	7.81	7.30	6.88
TC1601072	VPS35	55737	vacuolar protein sorting 35 homolog (S	1.82E-19	1	6.11	7.34	7.29	6.88	6.79	6.76	6.72	6.60
TC1300511	VPS36	51028	vacuolar protein sorting 36 homolog (S	0.000789	1	5.46	5.88	6.03	5.99	5.93	5.92	6.03	5.87
TC0800105	VPS37A	137492	vacuolar protein sorting 37 homolog A	3.22E-10	1	5.46	5.97	6.15	6.13	6.11	6.09	6.05	6.00
TC0201565	VPS54	51542	vacuolar protein sorting 54 homolog (S	3.32E-14	1	3.81	4.97	5.07	4.76	4.91	4.70	4.57	4.30
TC1400482	VRK1	7443	vaccinia related kinase 1	3.27E-16	1	6.37	7.58	7.97	8.16	8.18	7.92	7.60	7.34
TC1900387	VSTM2B	342865	V-set and transmembrane domain cont	2.02E-05	1	4.69	5.00	5.02	4.93	4.92	4.94	4.79	4.86
TC0600771	VTA1	51534	Vps20-associated 1 homolog (S. cerevis	4.16E-19	1	6.15	7.08	7.28	7.32	7.18	7.14	7.13	7.11
TC1001125	WAPAL	23063	wings apart-like homolog (Drosophila) /	0.000432	1	7.61	7.93	7.81	7.76	7.62	7.73	7.77	7.75
TC0601521	WASF1	8936	WAS protein family, member 1 /// Wisl	5.27E-07	1	3.47	3.69	3.73	3.73	3.70	3.67	3.59	3.58
TC1300098	WBP4	11193	WW domain binding protein 4 (formin	1.10E-06	1	5.37	6.06	5.93	5.88	5.95	5.87	5.83	5.78
TC0X00209	WDR13	64743	WD repeat domain 13 /// WD repeat p	3.46E-07	1	5.10	5.16	5.22	5.23	5.17	5.06	4.99	4.99
TC0900185	WDR32	79269	WD repeat domain 32 /// WD repeat d	5.23E-09	1	4.53	5.37	5.08	5.14	5.25	5.18	5.07	4.94
TC1000007	WDR37	22884	WD repeat domain 37 /// WD repeat p	7.16E-17	1	5.56	6.18	6.35	6.24	6.07	5.90	5.80	5.72
TC0501083	WDR41	55255	WD repeat domain 41	3.97E-12	1	5.22	6.09	6.29	6.01	5.88	5.76	5.79	5.72
TC0X00520	WDR44	54521	WD repeat domain 44 /// WD repeat p	2.99E-11	1	5.49	6.25	6.23	6.11	5.96	6.03	6.04	6.01
TC1201436	WDR51B /// G	282809 //	WD repeat domain 51B /// UDP-N-acet	2.64E-10	1	5.33	5.89	6.13	6.08	5.97	5.92	5.82	5.77
TC0500130	WDR70	55100	WD repeat domain 70	1.49E-05	1	4.16	4.74	4.86	4.64	4.61	4.54	4.53	4.43
TC0701770	WDR86	349136	WD repeat domain 86 /// WD repeat d	0.000721	1	4.88	5.02	5.03	4.95	4.96	4.95	4.83	4.90
TC0202035	WDSUB1	151525	WD repeat, sterile alpha motif and U-b	1.62E-07	1	3.75	3.81	4.12	4.08	4.08	3.96	4.03	3.87
TC1701643	WIPI1	55062	WD repeat domain, phosphoinositide i	2.68E-08	1	6.75	7.13	7.41	7.39	7.30	7.08	7.04	6.91
TC2200560	XBP1	7494	X-box binding protein 1	3.49E-11	1	4.79	5.87	5.93	5.52	5.42	5.33	5.29	4.99
TC0X00547	XIAP	331	X-linked inhibitor of apoptosis	0.000847	1	5.40	5.56	5.77	5.70	5.57	5.56	5.56	5.58
TC0500317	XRCC4	7518	X-ray repair complementing defective r	6.15E-14	1	5.96	6.95	7.25	6.86	6.58	6.63	6.65	6.56
TC2000122	XRN2	22803	5'-3' exoribonuclease 2	2.66E-11	1	7.99	8.11	8.69	8.51	8.25	8.14	8.08	7.93
TC2200481	YDJC	150223	YdjC homolog (bacterial)	9.76E-05	1	5.09	5.32	5.32	5.29	5.29	5.25	5.16	5.18
TC0102272	YIPF1	54432	Yip1 domain family, member 1 /// Prot	3.65E-09	1	6.34	7.11	7.37	7.14	6.86	6.90	6.80	6.80
TC0200158	YIPF4	84272	Yip1 domain family, member 4	4.88E-05	1	5.32	5.81	5.91	5.98	5.87	5.92	5.81	5.82
TC0501374	YIPF5	81555	Yip1 domain family, member 5 /// Prot	1.58E-07	1	5.51	6.48	6.56	6.34	6.32	6.37	6.24	6.26
TC0X00311	YIPF6	286451	Yip1 domain family, member 6 /// Prot	0.000591	1	5.62	5.91	6.02	5.88	5.77	5.91	5.88	5.88
TC1000838	YME1L1	730922 //	YME1-like 1 (S. cerevisiae)	1.66E-06	1	7.36	7.81	7.97	7.89	7.77	7.81	7.87	7.78
TC0103189	YOD1	55432	YOD1 OTU deubiquinating enzyme 1 hc	1.59E-18	1	5.53	6.51	6.17	5.87	5.81	5.56	5.48	5.38
TC0500401	YTHDC2	64848	YTH domain containing 2	6.67E-11	1	4.29	5.07	5.32	4.84	4.67	4.61	4.64	4.43
TC0800335	YTHDF3	253943	YTH domain family, member 3	2.07E-06	1	7.69	8.10	8.06	8.06	7.96	8.04	7.91	7.93

TC2000304	YWHAB	7529	tyrosine 3-monooxygenase/tryptophar	7.23E-14	1	7.44	7.99	8.07	7.93	7.85	7.90	7.87	7.84
TC1700884	YWHAE	7531	tyrosine 3-monooxygenase/tryptophar	8.33E-10	1	7.15	7.74	7.98	7.95	8.04	8.01	7.86	7.75
TC0701358	YWHAG	7532	tyrosine 3-monooxygenase/tryptophar	1.94E-13	1	6.08	6.72	6.90	6.98	6.92	6.76	6.76	6.62
TC0201301	YWHAQ	10971	tyrosine 3-monooxygenase/tryptophar	2.59E-12	1	5.04	5.86	6.01	6.15	6.13	6.06	5.98	5.84
TC0801161	YWHAZ	7534	tyrosine 3-monooxygenase/tryptophar	1.22E-20	1	6.75	7.26	7.29	7.20	7.20	7.19	7.07	7.06
TC1800550	ZADH2	284273	zinc binding alcohol dehydrogenase do	0.00012	1	5.11	5.38	5.53	5.57	5.51	5.46	5.36	5.41
TC0200867	ZAK	51776	sterile alpha motif and leucine zipper c	2.92E-14	1	3.95	5.04	5.77	5.88	5.58	5.46	5.43	4.75
TC1101207	ZBED5	---	Zinc finger BED domain-containing prot	0.000184	1	4.35	4.45	4.72	4.51	4.51	4.50	4.61	4.49
TC0601178	ZBTB22 /// ZBT	9278	zinc finger and BTB domain containing	0.000249	1	4.64	5.51	5.20	5.21	5.20	5.22	5.16	5.20
TC1101974	ZBTB44	29068	zinc finger and BTB domain containing	0.000227	1	6.56	6.87	6.99	7.02	6.81	6.74	6.83	6.73
TC1901049	ZBTB7A	51341	zinc finger and BTB domain containing	1.40E-05	1	5.52	5.85	5.74	5.88	5.92	5.78	5.81	5.76
TC0101108	ZBTB7B	51043	zinc finger and BTB domain containing	0.000104	1	5.65	5.81	5.81	5.74	5.78	5.63	5.52	5.55
TC0501281	ZCCHC10	54819	zinc finger, CCHC domain containing 1C	5.75E-05	1	4.65	5.42	5.38	5.45	5.44	5.40	5.44	5.32
TC0102258	ZCCHC11	23318	zinc finger, CCHC domain containing 11	0.000269	1	5.34	5.75	5.68	5.42	5.40	5.42	5.55	5.50
TC0301891	ZDHHC19	131540	zinc finger, DHHC-type containing 19	1.45E-14	1	4.55	5.21	5.44	5.12	5.05	4.90	4.71	4.70
TC0800104	ZDHHC2	51201	zinc finger, DHHC-type containing 2	1.52E-20	1	5.37	6.85	7.08	6.77	6.70	6.55	6.50	6.38
TC1300332	ZDHHC20	253832	zinc finger, DHHC-type containing 20 //	2.27E-28	1	4.47	6.34	7.07	6.76	6.22	5.58	5.46	5.20
TC0301142	ZDHHC3	51304	zinc finger, DHHC-type containing 3 ///	4.87E-29	1	4.98	6.28	6.21	5.94	5.91	5.68	5.52	5.52
TC0201986	ZEB2	9839	zinc finger E-box binding homeobox 2	7.65E-08	1	6.46	6.67	6.77	6.92	6.48	6.37	6.48	6.30
TC1500875	ZFP106	64397	zinc finger protein 106 homolog (mous	0.000776	1	7.76	8.03	8.02	7.96	7.79	7.67	7.72	7.67
TC0500900	ZFR	730732 //	zinc finger RNA binding protein	1.24E-13	1	6.22	7.00	6.99	7.05	6.87	6.81	6.81	6.74
TC0700531	ZKSCAN1	7586	zinc finger with KRAB and SCAN domair	1.21E-05	1	6.36	6.56	6.47	6.59	6.58	6.46	6.40	6.36
TC0301780	ZMAT3	64393	zinc finger, matrin type 3	1.80E-06	1	4.53	4.78	4.90	4.84	4.85	4.77	4.71	4.71
TC0100384	ZMYM1	79830	zinc finger, MYM-type 1 /// Zinc finger	0.00091	1	3.34	3.52	3.59	3.49	3.46	3.50	3.58	3.49
TC1300316	ZMYM5	9205	zinc finger, MYM-type 5 /// Zinc finger	1.39E-07	1	5.15	5.81	5.61	5.44	5.29	5.43	5.39	5.40
TC1900342	ZNF101	94039	zinc finger protein 101	9.75E-05	1	6.29	6.54	6.25	6.28	6.29	6.32	6.38	6.33
TC0300213	ZNF167	55888	zinc finger protein 167	8.98E-12	1	4.17	4.57	4.90	4.95	4.74	4.80	4.65	4.46
TC0900443	ZNF189	7743	zinc finger protein 189	5.63E-05	1	5.17	5.56	5.57	5.31	5.27	5.29	5.39	5.31
TC0300215	ZNF197	10168	zinc finger protein 197 /// Zinc finger p	0.000943	1	4.06	4.32	4.47	4.41	4.29	4.24	4.25	4.19
TC1600793	ZNF200	7752	zinc finger protein 200	0.000279	1	6.29	6.62	6.39	6.40	6.35	6.47	6.40	6.56
TC1900599	ZNF222	7673	zinc finger protein 222	0.000384	1	3.58	4.07	4.27	4.28	4.03	4.07	3.97	4.03
TC1000896	ZNF25	219749	zinc finger protein 25 /// Zinc finger prc	0.000112	1	3.74	3.91	4.14	4.13	4.01	3.99	4.11	3.98
TC0801350	ZNF250	58500	zinc finger protein 250	1.32E-06	1	3.76	4.16	3.98	4.30	4.09	4.02	3.98	3.95
TC0801352	ZNF252	---	Zinc finger protein 252 (Fragment). [So	3.22E-17	1	4.40	5.83	5.59	4.97	5.04	5.19	5.22	4.99

TC1900378	ZNF254	9534	zinc finger protein 254 /// Zinc finger p	9.59E-18	1	5.11	6.22	6.24	6.00	5.88	5.78	5.56	5.30
TC1800140	ZNF271	10778	zinc finger protein 271	3.01E-06	1	6.27	6.78	6.78	6.82	6.80	6.72	6.70	6.74
TC0700618	ZNF277 /// ZNF	11179	zinc finger protein 277 /// Zinc finger p	3.22E-09	1	4.34	5.36	5.18	5.13	5.04	5.09	5.19	5.05
TC1500985	ZNF280D /// SU	54816	zinc finger protein 280D /// Suppressor	8.19E-11	1	4.22	5.19	5.23	5.11	5.30	5.32	5.25	5.03
TC0103108	ZNF281	23528	zinc finger protein 281 /// Zinc finger p	1.28E-11	1	6.29	6.97	6.99	6.86	6.81	6.73	6.64	6.66
TC0700858	ZNF282	8427	zinc finger protein 282	0.000258	1	4.31	4.46	4.53	4.46	4.47	4.30	4.26	4.18
TC1601131	ZNF319	57567	zinc finger protein 319	1.58E-05	1	4.67	5.36	5.28	5.36	5.30	5.17	5.08	4.96
TC0601037	ZNF322A	79692	zinc finger protein 322A	0.000303	1	3.71	4.20	4.09	3.91	3.88	4.14	4.12	4.16
TC0901175	ZNF322B	387328	zinc finger protein 322B	2.12E-07	1	3.51	4.09	4.13	3.69	3.72	4.01	4.25	4.10
TC0400560	ZNF330	27309	zinc finger protein 330	2.34E-11	1	4.10	4.84	5.05	5.14	4.94	4.75	4.81	4.55
TC1900128	ZNF358	140467	zinc finger protein 358	4.35E-05	1	4.94	5.54	5.42	5.55	5.50	5.47	5.41	5.38
TC0501055	ZNF366	167465	zinc finger protein 366	6.69E-07	1	3.78	3.85	4.27	4.01	3.92	3.89	3.97	3.89
TC1400361	ZNF410	57862	zinc finger protein 410 /// Zinc finger p	2.91E-09	1	5.20	5.79	5.64	5.60	5.54	5.61	5.62	5.59
TC1901128	ZNF414	84330	zinc finger protein 414	0.000569	1	5.41	5.57	5.55	5.45	5.51	5.46	5.45	5.42
TC1901347	ZNF43	7594	zinc finger protein 43	0.000617	1	4.29	4.68	4.43	4.37	4.52	4.50	4.51	4.41
TC1000863	ZNF438	220929	zinc finger protein 438 /// Zinc finger p	5.39E-10	1	5.91	6.76	7.16	6.90	6.58	6.63	6.47	6.36
TC1901201	ZNF443	10224	zinc finger protein 443	0.000135	1	3.92	4.37	4.37	4.27	4.14	4.15	4.03	4.18
TC0301139	ZNF445	353274	zinc finger protein 445 /// Zinc finger p	6.41E-13	1	5.40	5.84	5.75	5.61	5.55	5.41	5.38	5.36
TC0701745	ZNF467	168544	zinc finger protein 467 /// Zinc finger p	3.51E-06	1	5.98	6.53	6.58	6.44	6.35	6.28	6.13	6.22
TC1900771	ZNF613	79898	zinc finger protein 613	0.000349	1	5.71	5.90	5.99	5.83	5.77	5.86	5.85	5.84
TC0500866	ZNF622	90441	zinc finger protein 622	3.60E-11	1	6.39	7.16	7.29	7.40	7.21	7.24	7.32	7.25
TC0102427	ZNF644	84146	zinc finger protein 644	3.24E-05	1	4.61	4.94	4.94	4.98	4.92	4.89	4.93	4.89
TC0300403	ZNF654	55279	zinc finger protein 654	0.000373	1	6.11	6.79	6.68	6.84	6.53	6.64	6.79	6.65
TC0103428	ZNF669	79862	zinc finger protein 669 /// Zinc finger p	2.65E-06	1	4.44	5.02	4.93	4.80	4.87	4.94	5.00	4.99
TC0101728	ZNF672	79894	zinc finger protein 672 /// Zinc finger p	4.57E-08	1	5.67	6.24	6.12	6.01	6.01	6.07	6.01	5.93
TC1600367	ZNF720	---	Zinc finger protein 720. [Source:Unipro	2.32E-07	1	3.53	3.68	3.94	3.76	3.63	3.67	3.76	3.80
TC1500815	ZNF770	54989	zinc finger protein 770	1.32E-12	1	4.77	5.68	5.74	5.95	6.07	5.97	5.71	5.54
TC0700879	ZNF775	285971	zinc finger protein 775 /// Zinc finger p	0.000603	1	4.21	4.39	4.43	4.37	4.37	4.30	4.32	4.28
TC1901502	ZNF780A	284323	zinc finger protein 780A /// Zinc finger	2.01E-09	1	5.28	6.22	6.33	6.17	6.09	5.99	6.10	5.90
TC1901501	ZNF780B	163131	zinc finger protein 780B	3.37E-07	1	4.18	4.78	4.90	4.65	4.67	4.61	4.74	4.59
TC1901836	ZNF787	126208	zinc finger protein 787	1.67E-05	1	5.05	5.53	5.42	5.44	5.44	5.36	5.36	5.32
TC0601556	ZUFSP /// C6or	221302	zinc finger with UFM1-specific peptidas	1.42E-05	1	3.06	3.71	3.71	3.49	3.57	3.46	3.45	3.33
TC1601239		---		0	1	4.23	10.86	10.82	10.62	10.85	10.51	9.93	8.93
TC0900524		---		1.12E-34	1	4.75	8.92	8.93	8.63	8.99	8.31	7.73	6.99

TC0Xr00015	---	1.84E-28	1	9.25	10.22	10.35	10.10	9.98	9.84	9.85	9.74
TC0200179	---	5.32E-28	1	3.73	5.93	5.99	5.56	5.53	5.09	5.03	4.76
TC0Xr00016	---	7.93E-26	1	7.34	8.25	8.32	8.11	7.85	7.80	7.67	7.61
TC0100773	---	2.54E-25	1	2.77	3.42	3.79	3.28	2.95	2.88	2.74	2.74
TC0400499	---	1.78E-24	1	6.03	7.66	8.05	7.69	7.56	7.24	7.09	6.90
TC1901558	---	3.96E-24	1	4.92	8.79	9.07	8.80	8.58	7.08	6.56	5.85
TC0701714	---	9.66E-24	1	6.06	7.44	7.93	7.70	7.67	7.43	7.20	6.93
TC1101307	---	1.30E-23	1	5.71	7.83	7.67	7.44	7.12	6.66	6.41	6.04
TC1201368	---	5.91E-22	1	7.23	8.78	8.65	8.42	8.28	7.98	8.04	7.74
TC0100901	---	7.26E-22	1	3.06	4.46	4.66	4.57	4.59	4.50	4.19	4.00
TC0103351	---	6.49E-21	1	6.37	8.18	8.21	8.20	7.96	7.88	7.71	7.73
TC2200669	---	2.76E-20	1	5.27	6.85	6.46	6.30	6.29	6.09	6.00	5.84
TC1101504	---	1.12E-19	1	5.86	7.54	8.00	7.91	7.70	7.50	7.28	6.92
TC1201134	---	2.31E-19	1	6.57	7.60	7.98	7.33	7.30	7.38	7.35	7.16
TC0600959	---	9.14E-19	1	7.21	9.05	9.11	8.77	8.72	8.68	8.70	8.43
TC0901148	---	1.79E-18	1	8.15	9.65	9.61	9.50	9.54	9.40	9.25	9.17
TC1501129	---	1.36E-17	1	5.07	7.04	6.68	6.46	6.59	6.25	6.06	5.89
TC0103200	---	1.96E-16	1	5.08	7.69	7.29	6.51	6.40	6.06	6.20	5.88
TC0500240	---	2.55E-16	1	6.90	8.60	9.63	9.15	8.70	8.33	8.36	7.57
TC0700190	---	3.17E-16	1	5.17	6.27	6.06	6.04	6.10	5.75	5.42	5.26
TC1300019	---	4.15E-16	1	2.86	3.16	3.38	3.23	3.09	2.84	2.86	2.80
TC0X00364	---	4.59E-16	1	6.57	7.73	7.74	7.45	7.05	7.11	6.98	6.92
TC0100783	---	2.60E-15	1	6.20	7.81	8.26	8.15	8.06	8.05	7.97	7.75
TC1600432	---	3.81E-15	1	5.84	6.58	6.63	6.61	6.55	6.51	6.43	6.39
TC0Xr00005	---	4.32E-15	1	7.23	8.06	8.14	7.98	7.76	7.59	7.42	7.41
TC0500056	---	5.35E-15	1	5.21	6.68	6.73	6.31	6.34	5.95	5.75	5.61
TC0101741	---	8.80E-15	1	7.05	8.88	9.02	9.23	9.42	9.17	9.05	8.81
TC0600334	---	7.84E-14	1	5.74	7.57	7.59	7.14	6.81	6.02	6.36	5.59
TC0501050	---	1.05E-13	1	7.26	8.67	9.43	9.11	8.53	8.16	8.03	7.60
TC1101955	---	1.12E-13	1	5.73	6.86	6.95	6.98	6.80	6.60	6.35	6.19
TC0501049	---	1.55E-13	1	5.84	7.23	8.02	7.61	7.06	6.82	6.74	6.33
TC0300932	---	3.93E-13	1	3.47	6.19	6.32	4.86	4.54	4.30	4.16	3.42
TC1500202	---	4.22E-13	1	4.98	6.09	6.38	6.48	6.74	6.54	6.21	6.02
TC0401452	---	4.93E-13	1	6.24	8.39	8.02	7.28	7.27	7.62	7.54	7.39

TC1400787	---	6.83E-13	1	3.89	4.92	4.84	4.59	4.53	4.35	4.44	4.14
TC0M00026	---	8.14E-13	1	7.54	9.10	9.38	9.52	9.68	9.40	9.33	9.02
TC0800642	---	9.16E-13	1	4.29	5.36	5.07	4.48	4.42	4.59	4.56	4.59
TC1700987	---	4.47E-12	1	6.13	6.99	6.99	6.68	6.55	6.31	6.43	6.16
TC1200649	---	5.79E-12	1	6.79	7.48	7.70	7.72	7.58	7.44	7.38	7.33
TC1300330	---	7.16E-12	1	4.46	5.41	5.69	5.60	5.13	4.76	4.52	4.25
TC2100225	---	8.05E-12	1	4.38	5.50	5.56	5.59	5.72	5.68	5.59	5.25
TC0400113	---	1.06E-11	1	6.07	6.77	7.01	7.10	7.01	7.02	6.95	6.87
TC0500738	---	1.30E-11	1	4.46	5.08	5.42	5.29	5.37	5.10	4.90	4.54
TC0300381	---	1.64E-11	1	8.50	9.23	9.14	8.87	8.90	8.91	8.91	8.78
TC1901779	---	1.84E-11	1	2.49	3.41	3.55	3.49	3.33	3.38	3.31	3.37
TC0701280	---	2.86E-11	1	4.26	5.05	5.09	4.97	5.01	4.92	4.81	4.66
TC1501267	---	2.89E-11	1	3.81	5.07	5.24	4.95	4.32	4.45	4.45	4.06
TC1600405	---	2.90E-11	1	6.51	7.52	7.68	7.52	7.49	7.36	7.32	7.34
TC0201923	---	7.17E-11	1	3.14	3.47	3.46	3.27	3.26	3.26	3.19	3.16
TC0401453	---	8.26E-11	1	3.70	4.80	4.45	3.92	4.15	4.32	4.09	3.98
TC1400001	---	1.02E-10	1	4.46	5.40	5.36	5.06	4.97	4.88	4.88	4.74
TC0701685	---	1.12E-10	1	5.09	7.05	6.65	6.26	6.23	5.97	5.87	5.52
TC0901288	---	1.27E-10	1	5.08	6.32	6.61	6.26	6.40	6.36	6.42	6.13
TC0301802	---	1.31E-10	1	6.40	8.20	7.40	6.87	6.68	7.10	7.13	7.28
TC0600464	---	1.93E-10	1	5.56	7.03	7.00	6.57	6.90	6.37	6.51	5.79
TC0100756	---	2.35E-10	1	3.03	3.32	3.52	3.14	3.05	3.08	2.94	2.99
TC0101744	---	2.51E-10	1	4.83	6.83	6.98	6.80	6.99	7.18	7.04	6.76
TC1400256	---	2.85E-10	1	4.64	5.61	5.80	5.72	5.65	5.73	5.66	5.53
TC0Xr00008	---	3.03E-10	1	4.80	5.84	5.89	5.77	5.68	5.60	5.34	5.27
TC0500066	---	3.11E-10	1	5.09	6.36	6.73	6.32	6.32	6.54	6.38	6.03
TC2200293	---	3.51E-10	1	4.29	5.31	5.53	5.26	5.34	5.01	4.91	4.77
TC0700745	---	4.44E-10	1	4.46	6.10	5.81	5.46	5.12	5.33	4.76	4.56
TC0501349	---	4.78E-10	1	5.95	6.27	6.35	6.76	6.71	6.41	6.21	6.15
TC0100772	---	4.97E-10	1	4.05	4.90	4.91	4.40	4.31	4.20	4.16	4.08
TC0300559	---	5.17E-10	1	6.15	6.58	6.42	6.52	6.41	6.14	5.98	5.73
TC1701420	---	7.30E-10	1	5.68	6.06	6.17	6.09	5.99	5.89	5.88	5.80
TC0400661	---	7.44E-10	1	3.70	4.73	4.38	4.24	3.75	3.70	3.69	3.31
TC0X00306	---	7.50E-10	1	8.61	9.56	9.13	8.81	8.94	8.93	8.74	8.99

TC0900046	---	7.88E-10	1	2.58	3.26	3.67	3.47	3.37	3.27	3.20	3.24
TC0801110	---	8.38E-10	1	3.28	3.27	3.83	4.01	3.81	3.61	3.58	3.44
TC1900181	---	8.77E-10	1	6.57	7.63	7.87	7.75	7.56	7.34	7.12	7.09
TC1100853	---	8.82E-10	1	4.45	5.25	5.59	5.41	5.16	5.00	4.80	4.52
TC0501051	---	9.89E-10	1	4.50	6.18	6.66	6.00	5.46	5.25	5.75	4.77
TC1000112	---	1.01E-09	1	5.21	6.00	6.03	5.89	5.79	5.88	5.76	5.80
TC0102200	---	1.29E-09	1	5.41	6.36	6.47	6.55	6.57	6.53	6.42	6.46
TC1500794	---	1.59E-09	1	5.87	6.95	7.31	7.16	7.10	7.04	6.91	6.67
TC0201924	---	1.60E-09	1	6.32	6.99	7.09	7.00	7.06	7.02	6.84	6.78
TC0600618	---	1.62E-09	1	4.30	6.79	6.45	6.24	6.03	5.81	5.92	5.16
TC0501519	---	1.98E-09	1	4.43	5.80	6.34	6.37	6.12	6.00	5.60	5.30
TC0400891	---	2.30E-09	1	9.47	10.10	10.29	10.28	10.31	10.15	10.19	10.07
TC0501023	---	3.26E-09	1	4.09	5.81	5.23	4.48	4.50	4.88	4.86	4.92
TC0701644	---	3.31E-09	1	4.62	5.37	5.61	5.37	5.41	5.24	5.19	4.98
TC2200527	---	3.75E-09	1	5.00	6.10	6.05	6.21	5.87	5.57	5.50	5.48
TC1000749	---	4.01E-09	1	6.28	7.55	7.15	6.91	6.93	6.49	6.31	5.89
TC1501131	---	4.03E-09	1	5.21	5.94	5.92	5.95	5.90	5.77	5.44	5.56
TC0600617	---	4.43E-09	1	6.32	7.59	7.53	7.16	6.92	6.74	6.77	6.42
TC1400165	---	5.06E-09	1	5.77	6.52	6.62	6.64	6.44	6.50	6.60	6.57
TC0900762	---	9.90E-09	1	6.90	8.09	8.32	8.17	8.35	8.37	8.28	8.08
TC0X00858	---	1.05E-08	1	8.48	9.61	9.55	9.57	9.62	9.64	9.70	9.50
TC1200526	---	1.05E-08	1	6.15	6.87	7.18	7.04	6.96	6.99	7.05	6.87
TC0601208	---	1.05E-08	1	7.39	8.00	7.78	7.69	7.58	7.33	7.22	6.85
TC10r00001	---	1.07E-08	1	5.34	5.92	6.27	6.32	6.10	5.98	6.07	5.87
TC0701718	---	1.49E-08	1	5.17	5.37	5.34	5.30	5.22	5.14	5.15	5.11
TC1401152	---	1.53E-08	1	2.94	3.50	3.97	3.89	3.65	3.45	3.24	3.12
TC0100894	---	1.55E-08	1	4.27	5.15	5.24	5.22	5.17	4.99	4.93	4.94
TC0202265	---	2.63E-08	1	3.31	4.63	3.93	3.61	3.50	3.71	3.83	3.88
TC0100856	---	3.01E-08	1	2.74	4.37	4.13	3.84	3.97	3.90	3.86	3.63
TC0700769	---	3.51E-08	1	4.19	3.88	4.62	4.71	4.53	4.07	4.01	3.79
TC0200407	---	3.57E-08	1	5.53	5.98	6.01	5.86	5.90	5.75	5.66	5.63
TC0400262	---	3.62E-08	1	4.94	5.97	6.06	5.83	5.85	5.84	5.71	5.62
TC1300302	---	3.76E-08	1	5.71	6.48	6.61	6.78	6.77	6.71	6.50	6.52
TC0201818	652842	3.77E-08	1	4.62	5.37	5.23	5.20	5.29	5.24	5.10	5.06

TC0500142	---	3.81E-08	1	5.28	5.61	5.72	5.87	5.82	5.73	5.72	5.59
TC0Xr00006	---	3.81E-08	1	6.46	7.47	7.29	7.06	6.99	6.96	7.10	7.00
TC1900981	---	3.83E-08	1	4.64	5.16	5.17	4.97	5.11	4.96	4.84	4.81
TC0400412	---	4.21E-08	1	7.27	7.92	8.10	7.89	7.90	7.86	7.86	7.81
TC0100385	---	4.33E-08	1	9.15	10.12	10.12	10.16	10.13	10.18	10.18	10.03
TC0201595	---	5.10E-08	1	4.16	4.58	4.65	4.69	4.71	4.56	4.55	4.46
TC2200284	---	5.84E-08	1	3.30	3.91	3.91	3.56	3.83	3.39	3.30	3.18
TC0X00876	---	1.10E-07	1	2.25	3.46	3.43	2.68	2.84	2.86	2.66	2.63
TC0400132	---	1.25E-07	1	9.59	10.00	10.21	10.04	10.04	10.09	9.99	10.04
TC1200364	---	1.35E-07	1	5.12	5.56	6.01	5.75	5.57	5.59	5.55	5.48
TC1000006	---	1.40E-07	1	4.62	5.06	5.06	4.73	4.70	4.73	4.77	4.72
TC0M00029	---	1.51E-07	1	7.22	8.71	8.90	8.63	8.88	8.96	8.80	8.65
TC1600247	---	1.86E-07	1	4.91	6.22	6.36	5.98	5.72	5.67	5.58	5.25
TC0100971	---	1.90E-07	1	5.21	5.62	5.79	5.84	5.69	5.47	5.56	5.55
TC1500147	---	2.11E-07	1	3.97	4.79	5.06	4.94	4.93	4.78	4.69	4.59
TC1500503	---	2.38E-07	1	9.18	10.20	9.99	9.98	10.13	10.11	9.97	9.81
TC1100222	---	2.75E-07	1	3.70	3.72	4.07	3.79	3.71	3.67	3.66	3.54
TC0201906	---	3.16E-07	1	3.60	4.55	4.77	4.75	5.03	4.84	4.67	4.49
TC0401407	---	6.07E-07	1	3.42	4.15	4.05	4.03	3.99	3.86	3.78	3.79
TC1101277	---	6.28E-07	1	2.10	2.80	2.77	2.62	2.67	2.68	2.67	2.56
TC0200851	731061	8.12E-07	1	2.80	3.45	3.58	3.41	3.50	3.51	3.50	3.43
TC0700595	---	9.67E-07	1	3.75	4.61	3.84	3.88	3.99	3.91	3.73	3.68
TC0501045	---	1.18E-06	1	6.59	7.06	7.63	7.34	7.14	6.87	6.86	6.40
TC0301664	---	1.38E-06	1	2.60	2.88	3.25	3.60	3.58	3.23	3.07	2.75
TC1101001	---	1.57E-06	1	4.55	5.01	5.25	5.36	5.35	5.25	4.96	4.80
TC1300309	---	1.65E-06	1	6.01	6.80	6.64	6.47	6.54	6.25	6.30	6.16
TC0200830	---	1.73E-06	1	3.13	3.54	3.58	3.61	3.63	3.60	3.49	3.40
TC1200375	---	1.93E-06	1	6.08	6.66	6.70	6.81	6.67	6.58	6.57	6.42
TC1600246	---	1.99E-06	1	6.96	7.82	7.74	7.56	7.27	7.22	7.21	6.99
TC2200051	---	2.32E-06	1	4.93	5.42	5.45	5.54	5.52	5.08	5.05	5.06
TC0800295	---	2.37E-06	1	4.92	5.47	5.80	5.67	5.46	5.29	5.32	5.29
TC1500203	---	2.64E-06	1	5.16	5.87	5.65	5.70	5.53	5.67	5.53	5.54
TC0X00472	---	2.83E-06	1	2.24	2.47	2.77	2.55	2.43	2.41	2.39	2.20
TC1000737	---	2.96E-06	1	2.72	2.97	3.52	3.50	3.16	3.19	2.94	3.00

TC0200333	---	3.44E-06	1	3.33	4.06	4.38	3.94	4.08	3.96	3.87	3.77
TC1000873	---	3.46E-06	1	5.27	6.15	6.34	6.23	5.98	6.12	6.17	6.07
TC0200553	---	3.56E-06	1	5.39	5.71	5.70	5.65	5.69	5.73	5.59	5.58
TC1300478	---	3.92E-06	1	3.65	4.85	4.57	4.28	4.50	4.45	4.20	4.08
TC0800603	---	4.13E-06	1	4.43	5.36	5.32	4.93	4.72	4.71	4.63	4.61
TC0400466	---	4.13E-06	1	5.70	6.95	7.54	7.52	7.21	6.99	6.99	6.93
TC0X00611	---	5.28E-06	1	5.96	6.56	6.48	6.29	6.31	6.39	6.36	6.28
TC1500355	---	5.67E-06	1	2.68	3.13	3.49	3.70	3.37	3.18	3.16	3.08
TC0600685	---	6.41E-06	1	5.57	6.36	6.46	6.53	6.56	6.38	6.12	6.21
TC0500872	---	6.79E-06	1	4.28	4.71	4.80	4.67	4.60	4.62	4.45	4.32
TC1500539	---	6.88E-06	1	3.53	4.41	4.43	4.04	4.12	4.04	3.84	4.02
TC1201540	---	6.93E-06	1	3.73	4.60	5.19	5.16	4.95	4.45	4.76	4.19
TC0400852	---	7.06E-06	1	8.49	9.03	9.11	8.98	8.97	9.06	8.95	8.92
TC1500252	---	7.72E-06	1	5.71	6.33	6.37	6.43	6.57	6.38	6.36	6.18
TC0500027	---	8.68E-06	1	4.88	5.63	5.78	5.29	5.11	5.22	5.38	5.50
TC0201943	---	9.13E-06	1	5.14	5.57	5.70	5.53	5.52	5.45	5.36	5.50
TC0700768	---	9.74E-06	1	7.61	7.94	8.20	7.95	7.79	7.51	7.38	7.18
TC0700417	---	1.17E-05	1	5.37	5.70	5.68	5.73	5.71	5.78	5.61	5.63
TC0100991	644410	1.19E-05	1	7.27	8.61	8.87	8.89	8.56	8.87	8.84	8.67
TC1701188	---	1.30E-05	1	4.49	4.98	5.10	4.96	4.72	4.80	4.80	4.55
TC15r00011	---	1.32E-05	1	4.41	4.70	4.81	4.69	4.77	4.78	4.71	4.71
TC0500839	---	1.36E-05	1	4.12	4.56	4.57	4.55	4.71	4.48	4.33	4.44
TC0401098	---	1.49E-05	1	3.87	4.95	4.50	4.46	4.18	4.17	4.18	3.98
TC1001044	---	1.55E-05	1	5.51	6.02	6.20	6.14	6.08	5.93	5.86	5.76
TC0401070	---	1.70E-05	1	1.98	2.25	2.66	2.16	2.23	2.03	1.86	1.94
TC1400765	---	1.82E-05	1	2.26	2.19	2.49	2.34	2.35	2.17	2.21	2.26
TC0101748	---	1.99E-05	1	5.49	5.25	5.88	5.92	5.67	5.40	5.18	4.81
TC0200778	727742	2.19E-05	1	3.05	3.18	3.16	3.05	3.06	3.04	3.05	3.09
TC1400591	---	2.27E-05	1	3.94	4.63	4.93	4.77	4.71	4.57	4.43	4.29
TC0600909	---	2.29E-05	1	3.93	4.84	4.25	3.78	3.91	4.25	4.41	4.21
TC0500241	---	2.29E-05	1	4.65	5.43	6.17	5.80	5.54	5.25	5.37	4.94
TC0301120	---	2.34E-05	1	4.06	4.19	4.48	4.45	4.35	4.31	4.16	4.23
TC0Y00013	---	2.37E-05	1	7.09	7.82	7.84	7.85	7.85	7.78	7.65	7.51
TC0300662	---	2.60E-05	1	3.71	3.97	4.17	3.94	3.88	3.91	3.96	3.92

TC0300332	---	2.60E-05	1	4.96	5.71	5.50	5.57	5.51	5.69	5.64	5.52
TC0900618	---	2.83E-05	1	4.57	4.68	5.27	5.20	4.96	5.04	5.03	4.73
TC1100713	---	2.97E-05	1	5.69	6.40	6.24	6.08	6.30	6.22	6.33	6.18
TC0101650	---	3.09E-05	1	6.33	6.84	6.88	6.86	6.82	6.83	6.57	6.60
TC0700205	---	3.26E-05	1	2.42	2.81	2.90	2.81	2.66	2.66	2.67	2.61
TC1500148	---	3.78E-05	1	5.29	6.07	6.41	6.17	6.14	6.09	6.02	5.77
TC1701578	---	4.00E-05	1	2.83	3.83	3.77	3.61	3.68	3.73	3.47	3.51
TC1201455	---	4.27E-05	1	6.54	7.29	7.33	7.63	7.35	7.23	6.97	7.01
TC2100107	---	4.44E-05	1	4.92	5.24	5.38	5.24	5.36	5.20	5.20	5.02
TC0401156	---	4.70E-05	1	4.34	4.54	4.82	4.86	4.72	4.51	4.44	4.44
TC1100216	---	4.82E-05	1	3.97	4.58	4.45	4.40	4.52	4.41	4.44	4.53
TC0201962	---	5.56E-05	1	6.04	6.49	6.62	6.48	6.60	6.54	6.43	6.43
TC0300964	---	5.89E-05	1	3.80	4.17	4.53	4.50	4.27	4.20	4.05	3.96
TC1800304	---	5.90E-05	1	2.98	3.33	3.66	3.54	3.45	3.60	3.35	3.30
TC0401381	---	6.14E-05	1	1.75	2.18	2.15	1.88	1.89	1.87	1.79	1.86
TC0301658	---	6.43E-05	1	5.01	5.51	5.79	5.78	5.69	5.62	5.65	5.59
TC0501200	---	7.05E-05	1	2.94	3.54	4.10	3.56	3.88	3.49	3.61	3.40
TC1500648	---	7.12E-05	1	4.99	6.16	5.81	5.17	5.03	5.07	5.21	5.04
TC1901499	---	7.43E-05	1	6.53	7.42	7.33	7.29	7.26	7.28	6.97	7.17
TC1900405	---	7.43E-05	1	4.38	4.84	4.81	4.86	5.07	4.88	4.80	4.72
TC0300712	---	7.95E-05	1	3.30	3.49	3.67	3.72	3.78	3.60	3.47	3.46
TC0X00810	---	8.27E-05	1	5.77	6.63	6.88	6.95	6.94	6.93	6.71	6.58
TC0100025	---	8.34E-05	1	5.02	5.36	5.29	5.36	5.36	5.29	5.07	5.20
TC1500016	---	8.34E-05	1	4.40	4.98	5.02	4.97	4.89	4.95	4.93	4.87
TC0700837	---	8.47E-05	1	3.46	3.81	3.81	3.76	3.83	3.78	3.76	3.65
TC0800891	---	8.73E-05	1	2.02	2.69	2.56	2.35	2.40	2.03	2.17	2.07
TC0103418	---	9.02E-05	1	4.31	4.54	4.78	4.71	4.65	4.63	4.58	4.50
TC0500246	---	9.46E-05	1	4.76	5.20	5.67	5.45	5.21	4.92	4.96	4.57
TC0X00399	---	0.000113	1	11.35	11.81	11.84	11.89	11.89	11.79	11.73	11.64
TC0X00886	---	0.000114	1	3.92	4.59	4.65	4.75	4.71	4.67	4.72	4.51
TC2000141	---	0.000123	1	2.72	3.51	3.34	3.35	3.27	3.38	2.88	2.82
TC1800283	---	0.000128	1	9.04	9.40	9.47	9.55	9.58	9.40	9.27	9.29
TC0800970	---	0.000141	1	2.46	2.94	2.94	2.80	2.60	2.51	2.43	2.32
TC1300063	---	0.000146	1	5.65	6.26	6.29	6.23	6.25	6.25	6.27	6.26

TC0200577	---	0.000155	1	6.87	7.44	7.53	7.45	7.33	7.44	7.40	7.26
TC1300479	---	0.000155	1	4.92	6.12	5.84	5.47	5.40	5.11	5.45	5.24
TC0701724	730421	0.000163	1	3.11	3.42	3.29	3.23	3.39	3.35	3.35	3.25
TC2000692	---	0.000165	1	5.58	5.93	5.97	6.05	6.00	5.98	5.90	5.93
TC15r00017	---	0.00017	1	6.43	6.91	6.90	6.77	6.68	6.75	6.71	6.72
TC0800324	---	0.000185	1	8.25	8.63	8.65	8.46	8.37	8.41	8.37	8.39
TC0701686	---	0.000185	1	5.44	6.07	5.75	5.68	5.57	5.53	5.63	5.25
TC0800077	---	0.000197	1	2.59	3.32	3.52	3.24	3.13	2.99	3.06	3.07
TC0X00515	---	0.000197	1	3.32	3.82	3.81	3.64	3.49	3.40	3.35	3.59
TC1400234	---	0.000217	1	2.70	2.97	3.28	2.95	2.97	3.00	2.83	2.88
TC0601008	---	0.000227	1	4.44	5.29	5.34	4.99	5.29	5.07	4.79	4.80
TC0301467	---	0.000235	1	7.80	8.38	8.25	8.26	8.20	8.26	8.28	8.35
TC0101798	---	0.000235	1	5.26	5.53	5.55	5.43	5.46	5.46	5.34	5.30
TC0400784	---	0.000271	1	3.39	3.95	4.27	3.82	3.88	3.71	3.75	3.85
TC0600432	---	0.000275	1	3.47	3.90	3.80	3.68	3.76	3.56	3.56	3.39
TC0600662	---	0.000276	1	3.58	3.67	4.01	3.74	3.69	3.57	3.59	3.46
TC0500676	---	0.000284	1	2.49	2.73	2.78	2.50	2.48	2.39	2.63	2.49
TC0200737	---	0.000289	1	2.98	3.46	3.52	3.23	3.10	2.85	2.92	2.80
TC0201746	---	0.000293	1	4.60	4.99	5.22	5.04	5.08	5.01	4.90	4.71
TC0100026	---	0.000296	1	4.51	4.79	4.99	4.83	4.79	4.67	4.60	4.64
TC0301436	---	0.000306	1	4.46	4.78	4.99	4.76	4.76	5.02	4.71	4.84
TC0100461	---	0.000312	1	3.04	4.13	3.54	3.38	3.47	3.75	3.59	3.55
TC0601408	---	0.000322	1	4.73	5.37	5.53	5.42	5.30	5.48	5.48	5.29
TC1101049	---	0.000325	1	4.99	5.48	5.44	5.44	5.49	5.35	5.32	5.19
TC0401262	---	0.000345	1	1.76	2.05	2.25	2.14	2.02	1.98	1.99	2.06
TC0400574	---	0.000374	1	5.85	6.33	6.55	6.44	6.38	6.34	6.16	6.20
TC0800336	---	0.000385	1	2.70	2.87	2.97	2.79	2.69	2.66	2.65	2.83
TC0900401	---	0.000391	1	5.24	5.51	5.56	5.44	5.56	5.47	5.23	5.35
TC0700356	---	0.000392	1	8.08	8.45	8.66	8.54	8.57	8.51	8.37	8.32
TC1501253	---	0.000397	1	2.46	4.63	3.84	4.05	4.04	4.01	4.02	3.82
TC0700165	---	0.000405	1	4.27	4.51	4.50	4.49	4.57	4.47	4.46	4.41
TC0901000	---	0.000405	1	2.38	2.70	2.97	2.94	2.91	2.84	2.89	2.80
TC0103040	---	0.000412	1	4.46	4.54	4.79	4.64	4.57	4.39	4.43	4.36
TC0202101	---	0.000412	1	3.31	3.80	3.93	3.86	3.79	3.96	3.81	3.56

TC0202372	---	0.00043	1	7.45	7.92	8.09	8.19	8.14	7.97	7.72	7.75
TC0X00276	---	0.000438	1	1.87	2.12	2.43	2.17	2.14	2.08	2.13	1.93
TC0901197	---	0.000439	1	2.02	2.16	2.31	2.04	2.09	2.05	2.06	2.08
TC1100841	---	0.00045	1	1.93	2.05	2.25	2.09	2.22	2.10	1.98	2.02
TC1701142	---	0.000451	1	4.15	4.77	4.80	4.80	4.88	4.75	4.70	4.56
TC0200184	---	0.000451	1	2.21	2.08	2.49	2.45	2.28	2.26	2.11	2.13
TC0301177	---	0.000469	1	2.99	3.35	3.74	3.67	3.56	3.39	3.51	3.11
TC1700214	---	0.000503	1	4.96	5.30	5.35	5.28	5.34	5.40	5.22	5.30
TC0300402	---	0.00052	1	3.82	4.46	4.32	4.53	4.29	4.30	4.37	4.36
TC1300601	---	0.000525	1	3.45	3.65	3.84	3.50	3.56	3.54	3.43	3.34
TC0X00874	---	0.000533	1	2.41	3.11	2.84	2.42	2.70	2.54	2.67	2.35
TC0103294	---	0.000572	1	2.19	2.50	2.39	2.49	2.29	2.57	2.25	2.38
TC0102320	---	0.000572	1	4.78	5.54	5.56	5.45	5.44	5.44	5.29	5.29
TC0700058	---	0.000578	1	5.87	6.29	6.38	6.34	6.32	6.35	6.15	6.18
TC1800267	---	0.00064	1	3.42	3.56	3.74	3.69	3.83	3.58	3.59	3.51
TC1600283	---	0.000662	1	4.29	4.70	4.73	4.48	4.51	4.48	4.51	4.36
TC0600352	---	0.00068	1	7.09	7.28	7.43	7.13	7.14	7.19	7.11	7.03
TC0600083	---	0.000684	1	1.67	1.70	1.97	1.82	1.90	1.74	1.76	1.77
TC0100648	---	0.00069	1	3.16	3.41	3.67	3.50	3.44	3.20	3.46	3.24
TC0901139	---	0.000712	1	4.19	4.72	4.38	4.67	5.03	4.65	4.47	4.36
TC0500361	---	0.000724	1	5.91	6.24	6.25	6.28	6.24	6.11	5.95	6.00
TC0500624	---	0.000746	1	4.46	4.80	4.93	4.94	5.11	4.89	4.70	4.83
TC0400069	---	0.000768	1	7.41	7.83	7.90	7.83	7.84	7.83	7.67	7.77
TC0500873	---	0.000769	1	4.19	5.53	5.49	5.52	5.45	5.33	5.02	4.67
TC0X01281	---	0.000771	1	1.83	2.15	2.12	2.01	2.10	2.02	1.99	2.01
TC0102180	---	0.000798	1	4.08	4.22	4.37	4.38	4.34	4.22	4.17	4.14
TC0701005	---	0.000823	1	3.99	4.26	4.76	4.39	4.35	4.29	4.13	4.29
TC1600703	---	0.000835	1	5.01	4.96	5.37	5.39	5.13	4.91	4.88	4.66
TC0701001	---	0.000843	1	4.69	4.95	5.05	4.92	4.95	4.93	4.83	4.78
TC0701272	650136	0.000916	1	4.96	5.29	5.51	5.35	5.37	5.30	5.17	5.18
TC0400150	---	0.000948	1	1.86	1.89	2.11	1.88	1.88	1.83	1.94	1.83
TC1701267	---	0.000982	1	3.31	3.65	3.65	3.53	3.62	3.61	3.58	3.62
TC0801348	---	0.000996	1	3.06	3.76	3.86	3.75	3.79	3.84	3.88	3.68
TC0201438	---	0.000998	1	6.66	7.02	7.35	6.83	6.70	7.13	6.84	7.11

TC0900370		---		0.000999	1	2.62	3.17	3.38	3.09	3.16	3.14	3.04	3.02
TC0900128	A2A2Z9_HUM	---	Ankyrin repeat domain 18B. [Source:Ur	0.000448	2	2.70	2.74	2.77	2.76	2.88	2.83	2.86	2.79
TC0102743	A2A3Q1_HUM	---	Putative novel transcript. [Source:Unip	0.0009	2	4.62	4.84	4.97	5.15	5.11	5.20	5.19	5.35
TC1601218	AARS	16	alanyl-tRNA synthetase	0.00017	2	4.43	4.51	4.47	4.64	4.86	4.77	4.87	4.64
TC1100813	AASDHPPT	60496	aminoadipate-semialdehyde dehydrog	6.37E-05	2	4.72	5.00	5.10	5.12	4.97	5.12	5.21	5.20
TC0700240	ABCA13	154664	ATP-binding cassette, sub-family A (AB	5.98E-12	2	3.13	4.40	3.97	4.86	5.51	5.38	4.95	4.33
TC0103333	ABCB10	23456	ATP-binding cassette, sub-family B (MD	5.15E-06	2	4.45	4.51	4.45	4.85	4.94	5.05	5.04	4.86
TC0100746	ABCD3	5825	ATP-binding cassette, sub-family D (AL	4.86E-07	2	3.68	4.37	4.40	4.57	4.72	4.59	4.52	4.25
TC0400573	ABCE1	6059	ATP-binding cassette, sub-family E (OA	0.000113	2	2.94	3.14	3.02	3.26	3.51	3.36	3.50	3.25
TC0600168	ABT1	29777	activator of basal transcription 1	7.19E-06	2	4.73	4.71	4.94	5.02	4.93	5.09	5.10	5.03
TC1701263	ACACA	31	acetyl-Coenzyme A carboxylase alpha	0.000786	2	3.54	3.53	3.56	3.61	3.73	3.67	3.66	3.58
TC0100659	ACADM	34	acyl-Coenzyme A dehydrogenase, C-4 t	2.85E-10	2	4.24	5.02	5.15	5.19	5.36	5.33	5.30	5.08
TC0600855	ACAT2	39	acetyl-Coenzyme A acetyltransferase 2	9.56E-09	2	4.48	4.82	4.77	4.99	5.08	5.06	5.11	4.92
TC1000840	ACBD5	91452	acyl-Coenzyme A binding domain cont	0.000424	2	6.27	6.36	6.61	6.67	6.49	6.57	6.62	6.63
TC0103041	ACBD6	84320	acyl-Coenzyme A binding domain cont	8.95E-06	2	4.20	4.48	4.59	4.60	4.77	4.76	4.81	4.54
TC0300820	ACTL6A	86	actin-like 6A	1.83E-10	2	4.20	4.17	4.15	4.51	4.83	4.88	4.84	4.65
TC0201769	ACTR1B	10120	ARP1 actin-related protein 1 homolog	0.00011	2	5.07	5.16	5.02	5.17	5.29	5.27	5.25	5.21
TC1200620	ACTR6	64431	ARP6 actin-related protein 6 homolog (	0.00021	2	2.98	3.30	3.47	3.41	3.34	3.40	3.50	3.44
TC1500274	ADAL	161823	adenosine deaminase-like	3.09E-06	2	3.27	3.23	3.23	3.40	3.42	3.39	3.48	3.47
TC0201299	ADAM17	6868	ADAM metallopeptidase domain 17 (tu	5.42E-08	2	7.05	6.90	7.17	7.60	7.49	7.28	7.31	7.18
TC0900799	ADFP	123	adipose differentiation-related protein	5.83E-09	2	4.83	4.69	4.82	5.51	5.28	5.28	5.65	5.58
TC0201277	ADI1	55256	acireductone dioxygenase 1 /// 1,2-dih	1.00E-10	2	4.84	4.88	4.91	5.22	5.28	5.27	5.31	5.34
TC0300530	ADPRH	141	ADP-ribosylarginine hydrolase	0.000494	2	3.79	3.97	3.96	4.09	4.09	4.02	4.11	4.11
TC2200298	ADSL	158	adenylosuccinate lyase /// Adenylosuc	4.86E-06	2	4.39	4.65	4.85	4.94	5.02	5.00	5.04	4.74
TC0103416	ADSS	159	adenylosuccinate synthase	1.11E-09	2	6.10	6.76	6.56	6.91	7.36	7.32	7.11	6.87
TC0X00646	AFF2	2334	AF4/FMR2 family, member 2 /// AF4/F	5.09E-10	2	4.17	5.01	4.32	4.95	5.49	5.56	5.33	4.96
TC1800342	AFG3L2	10939	AFG3 ATPase family gene 3-like 2 (yeas	9.84E-07	2	3.90	3.91	3.81	3.96	4.06	4.02	4.17	4.05
TC0700754	AGK	55750	acylglycerol kinase	5.51E-06	2	3.59	3.76	3.91	4.07	4.01	3.87	3.99	3.88
TC2100165	AGPAT3	56894	1-acylglycerol-3-phosphate O-acyltrans	0.000144	2	4.63	4.83	4.80	4.91	4.83	4.85	4.95	4.96
TC0200894	AGPS	8540	alkylglycerone phosphate synthase	1.61E-10	2	4.48	5.27	5.22	5.75	6.13	6.09	5.90	5.57
TC0100122	AGTRAP	57085	angiotensin II receptor-associated prot	7.59E-16	2	6.37	6.66	6.99	7.28	7.23	6.94	6.92	6.83
TC2000677	AHCY	191	S-adenosylhomocysteine hydrolase	4.54E-05	2	4.47	4.59	4.52	4.66	4.81	4.73	4.66	4.59
TC0103258	AIDA /// C1orf	730996 //	axin interactor, dorsalization associate	6.27E-08	2	5.55	5.66	5.74	5.87	5.79	5.93	6.04	6.01
TC0600773	AIG1	51390	androgen-induced 1 /// Androgen-indu	3.94E-06	2	4.81	5.30	5.55	5.24	5.48	5.54	5.51	5.31

TC0102899	AIM2	9447	absent in melanoma 2 /// Interferon-in	2.80E-15	2	6.23	7.73	8.37	8.78	8.54	8.63	8.55	8.29
TC1100601	AIP	9049	aryl hydrocarbon receptor interacting	0.000115	2	6.11	6.02	6.16	6.49	6.45	6.31	6.34	6.37
TC0102091	AK2	204	adenylate kinase 2	2.47E-07	2	5.93	6.04	5.78	6.07	6.23	6.31	6.30	6.24
TC0900755	AK3	50808	adenylate kinase 3 /// GTP:AMP phosp	2.02E-05	2	3.45	3.70	3.69	3.77	3.81	3.73	3.83	3.68
TC1200702	ALDH2	217	aldehyde dehydrogenase 2 family (mit	3.56E-09	2	4.67	5.57	5.46	5.90	5.98	5.71	5.72	5.37
TC1700224	ALDH3A2	224	aldehyde dehydrogenase 3 family, mer	3.94E-11	2	4.12	4.26	4.25	4.56	4.68	4.72	4.79	4.63
TC1300162	ALG11 /// UTP	440138 //	asparagine-linked glycosylation 11 hor	0.000506	2	5.16	5.30	5.29	5.36	5.27	5.40	5.55	5.50
TC0901191	ALG2	85365	asparagine-linked glycosylation 2 hom	0.000124	2	4.19	4.39	4.42	4.56	4.55	4.51	4.58	4.46
TC1300403	ALG5	29880	asparagine-linked glycosylation 5 hom	2.77E-09	2	3.48	3.71	3.51	3.92	4.16	4.29	4.22	4.02
TC0100613	ALG6	29929	asparagine-linked glycosylation 6 hom	4.15E-06	2	4.65	5.03	5.29	5.27	5.23	5.25	5.30	5.15
TC1101691	ALG8	79053	asparagine-linked glycosylation 8 hom	0.000771	2	4.15	4.39	4.47	4.44	4.57	4.58	4.62	4.47
TC0201019	ALS2CR8	79800	amyotrophic lateral sclerosis 2 (juvenil	3.86E-06	2	3.41	3.65	3.74	3.84	3.80	3.78	3.75	3.67
TC1601116	AMFR	267	autocrine motility factor receptor /// A	2.35E-07	2	5.17	5.55	5.42	5.84	5.73	5.66	5.66	5.65
TC1100769	AMOTL1	154810	angiomotin like 1 /// Angiomotin-like p	4.99E-06	2	4.00	4.07	4.08	4.22	4.37	4.18	4.09	3.99
TC1700712	AMZ2	51321	archaelysin family metallopeptidase 2	7.78E-06	2	5.53	5.52	5.74	5.79	5.75	5.70	5.76	5.73
TC17r00032	ANAPC11	51529	APC11 anaphase promoting complex s	1.66E-09	2	5.79	6.07	6.23	6.32	6.34	6.32	6.16	6.14
TC1700846	ANAPC11	51529	APC11 anaphase promoting complex s	1.17E-06	2	5.61	5.90	6.04	6.19	6.24	6.12	6.07	5.99
TC1201560	ANAPC7	51434	anaphase promoting complex subunit	0.000288	2	5.13	4.94	5.13	5.34	5.25	5.23	5.33	5.22
TC0700472	ANKIB1	54467	ankyrin repeat and IBR domain contain	0.000383	2	5.19	5.38	5.55	5.68	5.49	5.49	5.67	5.52
TC0900923	ANKRD18A	---	Ankyrin repeat domain-containing prot	1.22E-07	2	3.17	3.37	3.45	3.70	3.92	3.85	4.02	3.68
TC0301043	ANKRD28	23243	ankyrin repeat domain 28 /// Ankyrin r	1.40E-05	2	4.36	4.64	5.09	5.19	5.11	5.10	5.16	4.79
TC0500344	ANKRD32	84250	ankyrin repeat domain 32	2.03E-05	2	4.29	4.62	4.80	4.87	4.83	4.89	4.96	4.72
TC1701522	ANKRD40	91369	ankyrin repeat domain 40	0.000423	2	4.26	4.50	4.57	4.69	4.68	4.65	4.71	4.62
TC0700185	ANLN	54443	anillin, actin binding protein	3.54E-11	2	3.00	3.51	3.42	3.99	4.55	4.40	4.19	3.77
TC0900425	ANP32B	10541	acidic (leucine-rich) nuclear phosphopr	6.26E-17	2	7.79	8.06	8.18	8.62	8.91	8.91	8.82	8.63
TC0102716	ANP32E	81611	acidic (leucine-rich) nuclear phosphopr	1.43E-10	2	7.13	8.10	8.16	8.23	8.37	8.29	8.26	8.02
TC0200318	ANXA4	307	annexin A4	1.80E-13	2	4.56	5.47	5.47	5.89	6.10	6.04	5.86	5.47
TC0100245	AOF2	23028	amine oxidase (flavin containing) doma	1.27E-12	2	4.48	4.47	4.42	4.93	5.06	5.19	5.35	5.10
TC1901634	AP2S1	1175	adaptor-related protein complex 2, sig	7.75E-06	2	4.77	4.82	4.92	5.14	5.15	4.99	5.08	5.00
TC1400029	APEX1	328	APEX nuclease (multifunctional DNA re	8.58E-07	2	5.17	5.16	4.93	5.41	5.75	5.69	5.63	5.29
TC1101305	APIP	51074	APAF1 interacting protein	6.26E-06	2	3.98	4.45	4.49	4.52	4.65	4.53	4.56	4.44
TC0100109	APITD1 /// COF	378708 //	apoptosis-inducing, TAF9-like domain 1	1.96E-05	2	3.09	3.22	3.21	3.29	3.36	3.39	3.30	3.21
TC2200281	APOBEC3B	9582	apolipoprotein B mRNA editing enzym	3.42E-08	2	4.93	4.96	4.81	5.13	5.37	5.35	5.27	5.16
TC0X00392	APOOL	139322	apolipoprotein O-like /// Apolipoprotei	5.10E-08	2	4.14	4.76	4.98	4.96	4.89	5.09	5.03	5.00

TC2100249	APP	351	amyloid beta (A4) precursor protein (p	1.31E-20	2	5.20	6.99	6.65	7.23	7.65	7.50	7.18	6.63
TC1701581	APPBP2	10513	amyloid beta precursor protein (cytopl	0.000437	2	5.35	5.50	5.46	5.60	5.45	5.73	5.72	5.75
TC0300325	APPL1	26060	adaptor protein, phosphotyrosine inter	2.70E-13	2	4.26	5.35	5.67	5.70	5.76	5.72	5.74	5.41
TC1601340	APRT	353	adenine phosphoribosyltransferase	9.16E-05	2	6.29	6.31	6.17	6.43	6.44	6.49	6.51	6.45
TC2000352	ARFGEF2	10564	ADP-ribosylation factor guanine nucleo	4.99E-07	2	4.18	4.35	4.28	4.59	4.70	4.63	4.75	4.49
TC1500184	ARHGAP11A	9824	Rho GTPase activating protein 11A	1.04E-05	2	2.53	2.84	2.75	3.00	3.38	3.36	3.26	3.02
TC1500160	ARHGAP11B	89839	Rho GTPase activating protein 11B	0.000129	2	2.95	3.04	3.07	3.16	3.44	3.35	3.36	3.19
TC1000826	ARHGAP21	57584	Rho GTPase activating protein 21 /// Rh	1.83E-08	2	3.73	3.89	3.73	4.17	4.44	4.47	4.43	4.36
TC1201020	ARHGDIB	397	Rho GDP dissociation inhibitor (GDI) be	0.000573	2	10.42	10.29	10.45	10.48	10.46	10.45	10.42	10.42
TC1201493	ARL1	400	ADP-ribosylation factor-like 1	2.17E-06	2	3.97	4.44	4.62	4.81	4.82	4.75	4.82	4.74
TC0500977	ARL15	54622	ADP-ribosylation factor-like 15 /// ADP	8.20E-05	2	5.43	5.33	5.32	5.86	5.57	5.89	5.81	5.82
TC1600471	ARL2BP	23568	ADP-ribosylation factor-like 2 binding p	1.41E-07	2	5.74	6.02	6.19	6.32	6.31	6.37	6.45	6.33
TC0202005	ARL5A	26225	ADP-ribosylation factor-like 5A	2.41E-09	2	4.19	4.49	4.39	4.68	4.69	4.83	4.87	4.83
TC0300361	ARL6IP5	10550	ADP-ribosylation-like factor 6 interactir	2.63E-21	2	6.83	7.62	8.05	8.32	8.03	7.90	7.98	7.90
TC0200788	ARL6IP6	151188	ADP-ribosylation-like factor 6 interactir	1.36E-09	2	4.77	5.40	5.60	5.76	5.67	5.69	5.68	5.69
TC0800981	ARMC1	55156	armadillo repeat containing 1	0.000119	2	3.27	3.39	3.45	3.49	3.72	3.62	3.70	3.66
TC0300292	ARMET	7873	arginine-rich, mutated in early stage tu	0.00081	2	6.49	6.71	6.67	6.74	6.79	6.71	6.84	6.85
TC0101608	ARV1	64801	ARV1 homolog (S. cerevisiae) /// Protei	0.00014	2	4.18	4.11	4.17	4.27	4.29	4.28	4.30	4.22
TC1000743	ASB13	79754	ankyrin repeat and SOCS box-containin	0.000145	2	3.90	4.19	4.13	4.16	4.19	4.25	4.16	4.11
TC0601482	ASCC3	10973	activating signal cointegrator 1 comple	0.000165	2	3.30	3.45	3.43	3.64	3.77	3.71	3.79	3.65
TC0600682	ASF1A	25842	ASF1 anti-silencing function 1 homolog	6.30E-09	2	3.90	4.40	4.50	4.84	4.85	4.90	5.05	4.89
TC0800226	ASH2L	9070	ash2 (absent, small, or homeotic)-like (	0.000145	2	6.25	6.43	6.66	6.70	6.60	6.63	6.67	6.61
TC0103096	ASPM	259266	asp (abnormal spindle) homolog, micro	8.20E-06	2	2.57	2.72	2.69	2.92	3.30	3.20	3.10	2.88
TC0801228	ATAD2	29028	ATPase family, AAA domain containing	9.40E-11	2	3.84	4.23	4.15	4.65	5.07	5.05	4.98	4.60
TC1700334	ATAD5	79915	ATPase family, AAA domain containing	4.25E-05	2	3.62	3.84	3.87	4.12	4.22	4.14	4.18	4.02
TC1600166	ATF7IP2	80063	activating transcription factor 7 interac	1.30E-08	2	3.34	3.53	3.57	3.76	3.89	3.84	3.72	3.58
TC0100609	ATG4C	84938	ATG4 autophagy related 4 homolog C (	2.32E-07	2	3.05	3.09	3.30	3.35	3.32	3.29	3.36	3.37
TC1600614	ATMIN	23300	ATM interactor	1.65E-05	2	4.04	4.16	4.29	4.42	4.47	4.45	4.54	4.42
TC0501428	ATOX1	475	ATX1 antioxidant protein 1 homolog (y	3.90E-05	2	6.14	6.31	6.41	6.54	6.59	6.49	6.52	6.50
TC1800441	ATP5A1	642727 //	ATP synthase, H+ transporting, mitoch	1.34E-06	2	5.87	6.28	6.53	6.61	6.70	6.63	6.66	6.46
TC2000869	ATP5E	514	ATP synthase, H+ transporting, mitoch	9.02E-09	2	10.11	10.37	10.60	10.59	10.56	10.55	10.56	10.54
TC1201255	ATP5G2	517	ATP synthase, H+ transporting, mitoch	8.61E-06	2	4.19	4.29	4.35	4.44	4.51	4.43	4.45	4.36
TC1701684	ATP5H	10476	ATP synthase, H+ transporting, mitoch	2.49E-14	2	7.72	8.19	8.32	8.44	8.45	8.40	8.37	8.29
TC0400747	ATP5I	521	ATP synthase, H+ transporting, mitoch	3.02E-13	2	8.75	8.92	9.00	9.22	9.23	9.22	9.27	9.23

TC2100248	ATP5J	522	ATP synthase, H+ transporting, mitoch	5.51E-09	2	5.48	5.76	5.95	5.93	5.92	5.94	5.89	5.90
TC0701456	ATP5J2	9551	ATP synthase, H+ transporting, mitoch	1.25E-07	2	5.87	6.16	6.35	6.28	6.35	6.29	6.29	6.26
TC1100891	ATP5L	10632	ATP synthase, H+ transporting, mitoch	5.99E-11	2	7.20	7.84	7.96	8.03	8.03	7.98	7.99	7.90
TC1400928	ATP6V1D	51382	ATPase, H+ transporting, lysosomal 34k	3.49E-06	2	5.99	6.40	6.52	6.50	6.42	6.52	6.57	6.48
TC2200417	ATP6V1E1	529	ATPase, H+ transporting, lysosomal 31k	3.75E-07	2	7.51	7.72	7.80	7.83	7.79	7.91	7.92	7.93
TC0700686	ATP6V1F	9296	ATPase, H+ transporting, lysosomal 14k	4.05E-14	2	5.88	6.52	6.62	6.68	6.69	6.63	6.62	6.60
TC0900505	ATP6V1G1	9550	ATPase, H+ transporting, lysosomal 13k	4.26E-09	2	5.55	5.75	5.81	5.81	5.74	5.95	5.99	6.11
TC0400907	ATP8A1	10396	ATPase, aminophospholipid transporte	1.70E-09	2	5.01	4.88	4.88	5.37	5.60	5.58	5.49	5.14
TC1500944	ATP8B4	79895	ATPase, class I, type 8B, member 4 /// I	5.96E-14	2	3.92	5.34	5.65	5.89	6.28	6.10	5.74	5.28
TC0100320	ATPIF1	93974	ATPase inhibitory factor 1	0.000124	2	7.04	7.46	7.40	7.44	7.57	7.53	7.56	7.51
TC2200355	ATXN10	25814	ataxin 10 /// Ataxin-10 (Spinocerebella	1.33E-09	2	4.27	4.44	4.53	4.83	4.98	4.91	5.01	4.81
TC2000849	AURKA	6790	aurora kinase A	1.08E-07	2	4.37	4.74	4.75	4.96	5.13	5.04	4.97	4.82
TC1701007	AURKB	9212	aurora kinase B	5.11E-07	2	4.37	4.45	4.37	4.51	4.70	4.65	4.57	4.49
TC1900019	AZU1	566	azurocidin 1 (cationic antimicrobial pro	5.67E-05	2	5.22	5.33	5.34	5.45	5.60	5.60	5.53	5.41
TC0100031	B3GALT6	126792	UDP-Gal:betaGal beta 1,3-galactosyltra	5.12E-06	2	4.82	4.80	5.02	5.27	5.24	5.32	5.44	5.24
TC0900852	B4GALT1	2683	UDP-Gal:betaGlcNAc beta 1,4- galactos	0.000904	2	7.24	7.21	7.34	7.47	7.45	7.47	7.38	7.44
TC1800401	B4GALT6	9331	UDP-Gal:betaGlcNAc beta 1,4- galactos	5.73E-05	2	3.09	3.31	3.34	3.35	3.51	3.46	3.31	3.44
TC1401147	BAG5	9529	BCL2-associated athanogene 5	2.98E-05	2	5.05	5.18	5.12	5.18	5.22	5.29	5.28	5.33
TC0700609	BCAP29	55973	B-cell receptor-associated protein 29	7.15E-08	2	4.17	4.93	4.95	4.95	5.16	5.03	5.03	4.81
TC1000676	BCCIP	56647	BRCA2 and CDKN1A interacting protein	1.81E-07	2	3.94	4.24	4.08	4.50	4.69	4.74	4.91	4.63
TC0102397	BCL10	8915	B-cell CLL/lymphoma 10	0.000383	2	4.51	4.84	4.81	4.84	4.87	4.96	4.78	4.89
TC0102560	BCL2L15 /// C1	440603	BCL2-like 15 /// Uncharacterized protei	9.78E-15	2	2.90	4.68	3.68	4.94	5.94	5.96	5.42	4.50
TC0301910	BDH1	622	3-hydroxybutyrate dehydrogenase, typ	0.000225	2	3.43	3.47	3.47	3.53	3.70	3.64	3.63	3.53
TC0X01111	BEX1	55859	brain expressed, X-linked 1	2.20E-12	2	4.35	5.10	4.94	5.19	5.58	5.46	5.32	4.99
TC0901136	BICD2	23299	bicaudal D homolog 2 (Drosophila)	0.000568	2	6.32	6.21	6.28	6.55	6.50	6.39	6.41	6.42
TC1700808	BIRC5	332	baculoviral IAP repeat-containing 5 (su	3.52E-09	2	4.44	4.50	4.46	4.58	4.79	4.69	4.59	4.53
TC1300263	BIVM	54841	basic, immunoglobulin-like variable mo	0.000303	2	2.60	2.73	2.75	2.75	2.79	2.81	2.81	2.81
TC1500629	BLM	641	Bloom syndrome	1.51E-05	2	3.24	3.54	3.46	3.65	3.88	3.86	3.89	3.74
TC1001220	BLOC1S2	282991	biogenesis of lysosome-related organel	0.000222	2	6.78	7.01	7.16	7.23	7.10	7.13	7.22	7.18
TC0101270	BLZF1	8548	basic leucine zipper nuclear factor 1 (JE	3.80E-05	2	5.73	5.94	6.00	5.85	5.73	6.05	6.09	6.18
TC1000106	BMI1	648	BMI1 polycomb ring finger oncogene /	2.09E-08	2	3.80	3.84	3.87	4.05	4.12	4.11	4.20	4.16
TC0600055	BMP6	654	bone morphogenetic protein 6	8.28E-05	2	4.41	4.51	4.13	4.62	4.93	4.95	4.80	4.69
TC1000183	BMS1	9790	BMS1 homolog, ribosome assembly pr	1.68E-05	2	3.92	4.16	4.13	4.36	4.59	4.48	4.56	4.36
TC2000250	BPI	671	bactericidal/permeability-increasing pr	5.03E-19	2	4.42	8.38	7.61	8.61	9.22	9.26	8.43	7.67

TC1300074	BRCA2	675	breast cancer 2, early onset	0.000879	2	2.57	2.80	2.65	2.72	3.00	2.99	3.05	2.89
TC1601092	BRD7	29117	bromodomain containing 7	0.000753	2	6.91	6.98	6.98	7.03	7.06	7.22	7.45	7.22
TC0700507	BRI3	25798	brain protein I3	7.74E-11	2	7.19	7.65	7.77	7.79	7.79	7.85	7.74	7.66
TC1200807	BRI3BP	140707	BRI3 binding protein /// BRI3-binding p	5.79E-11	2	5.59	5.53	5.57	5.91	5.83	5.95	5.98	6.02
TC1701589	BRIP1	83990	BRCA1 interacting protein C-terminal h	4.60E-08	2	2.86	3.07	3.12	3.45	3.67	3.63	3.55	3.28
TC0102966	BRP44	25874	brain protein 44	3.17E-13	2	6.03	6.60	6.73	6.69	6.83	6.83	6.77	6.77
TC1901288	BST2	684	bone marrow stromal cell antigen 2	2.97E-05	2	6.16	6.73	6.72	6.74	6.59	7.01	7.32	7.51
TC1501192	BTBD1	53339	BTB (POZ) domain containing 1	1.60E-06	2	4.89	5.18	5.40	5.34	5.30	5.32	5.43	5.35
TC0101433	BTG2	7832	BTG family, member 2	3.68E-05	2	7.68	8.29	7.69	7.86	8.06	8.24	8.08	8.22
TC2100231	BTG3	10950	BTG family, member 3 /// Protein BTG3	0.000287	2	4.12	4.37	4.33	4.41	4.52	4.49	4.39	4.36
TC0201821	BUB1	699	BUB1 budding uninhibited by benzimid	1.38E-08	2	3.37	3.61	3.54	3.85	4.26	4.13	3.99	3.78
TC0500116	BXDC2	55299	brix domain containing 2	6.75E-05	2	2.91	2.94	2.93	2.98	3.11	3.05	3.21	3.03
TC0100691	BXDC5	80135	brix domain containing 5 /// Ribosome	2.28E-06	2	5.68	6.09	6.16	6.09	5.95	6.12	6.28	6.21
TC1000326	C10orf104	119504	chromosome 10 open reading frame 10	2.39E-06	2	5.99	6.46	6.36	6.40	6.43	6.39	6.50	6.49
TC1000358	C10orf11	83938	chromosome 10 open reading frame 11	6.12E-09	2	4.10	4.67	4.67	4.91	5.04	5.00	4.87	4.63
TC1000775	C10orf30	222389	chromosome 10 open reading frame 30	1.53E-06	2	4.02	4.72	4.33	4.58	4.60	4.88	5.05	4.91
TC1101466	C11orf10	746	chromosome 11 open reading frame 10	1.02E-09	2	6.31	6.84	6.94	7.05	7.06	7.03	7.16	7.07
TC1100401	C11orf31	280636	chromosome 11 open reading frame 31	5.79E-05	2	4.49	4.76	4.77	5.00	5.05	5.00	5.09	4.88
TC1100249	C11orf46	120534	chromosome 11 open reading frame 46	0.00014	2	3.48	3.82	3.88	3.96	3.94	3.94	4.28	4.03
TC1101481	C11orf48	79081	chromosome 11 open reading frame 48	3.73E-05	2	4.77	4.92	5.02	5.09	5.04	4.99	5.09	5.06
TC1100847	C11orf57	55216	chromosome 11 open reading frame 57	2.21E-07	2	4.90	4.90	5.01	5.12	5.16	5.20	5.37	5.22
TC1101636	C11orf59	55004	chromosome 11 open reading frame 59	2.46E-06	2	6.25	6.61	6.70	6.82	6.83	6.76	6.68	6.61
TC1100694	C11orf67	28971	chromosome 11 open reading frame 67	1.88E-06	2	4.22	4.34	4.56	4.85	4.77	4.75	4.80	4.66
TC1101557	C11orf68	83638	chromosome 11 open reading frame 68	0.00069	2	7.34	7.39	7.48	7.63	7.59	7.51	7.67	7.70
TC1100283	C11orf74	119710	chromosome 11 open reading frame 74	3.96E-05	2	4.05	4.51	4.54	4.67	4.90	4.89	4.76	4.58
TC1201061	C12orf11	55726	chromosome 12 open reading frame 11	3.48E-08	2	3.64	3.88	4.12	4.30	4.25	3.99	4.06	3.99
TC1200560	C12orf29	91298	chromosome 12 open reading frame 29	4.11E-08	2	3.60	3.78	3.62	3.85	4.32	4.18	4.23	3.96
TC1201366	C12orf31	84298	chromosome 12 open reading frame 31	1.81E-06	2	7.82	8.09	8.24	8.30	8.19	8.25	8.35	8.33
TC1201602	C12orf49	79794	chromosome 12 open reading frame 49	4.31E-06	2	4.89	5.12	5.19	5.24	5.32	5.31	5.38	5.25
TC1200786	C12orf65	91574	chromosome 12 open reading frame 65	2.22E-06	2	4.23	4.24	4.23	4.36	4.43	4.43	4.57	4.52
TC1300489	C13orf1	57213	chromosome 13 open reading frame 1	0.000172	2	3.75	3.82	3.84	3.96	4.04	4.00	4.14	4.02
TC1300103	C13orf15	28984	chromosome 13 open reading frame 15	1.23E-12	2	4.77	5.39	5.01	5.44	6.11	5.91	5.81	5.41
TC1300634	C13orf27	93081	chromosome 13 open reading frame 27	0.000174	2	2.65	2.69	2.80	2.96	2.89	2.99	3.12	3.08
TC1300328	C13orf3	221150	chromosome 13 open reading frame 3	0.000143	2	4.80	5.29	5.44	5.67	5.57	5.73	5.48	5.59

TC1300113	C13orf31	144811	chromosome 13 open reading frame 3	1.99E-05	2	3.56	3.60	3.65	3.83	3.81	3.80	3.97	3.92
TC1401005	C14orf1	11161	chromosome 14 open reading frame 1	1.62E-07	2	5.60	5.43	5.42	5.87	6.00	6.02	5.96	5.81
TC1400830	C14orf104	55172	chromosome 14 open reading frame 1	0.00023	2	3.82	3.85	3.91	4.07	4.08	4.09	4.04	4.14
TC1400456	C14orf109	26175	chromosome 14 open reading frame 1	3.78E-12	2	5.28	5.48	5.67	5.80	5.77	5.91	5.90	5.86
TC1400457	C14orf130	55148	chromosome 14 open reading frame 1	1.14E-05	2	4.54	4.72	4.84	4.97	4.90	4.97	5.14	4.97
TC1401032	C14orf145	145508	chromosome 14 open reading frame 1	4.12E-07	2	3.71	4.10	4.00	4.15	4.34	4.20	4.18	4.11
TC1400611	C14orf153	84334	chromosome 14 open reading frame 1	1.75E-08	2	3.63	3.94	4.08	4.15	4.16	4.09	4.18	4.05
TC1400397	C14orf156	81892	chromosome 14 open reading frame 1	1.01E-08	2	6.63	7.11	7.22	7.41	7.41	7.49	7.54	7.42
TC1400228	C14orf166	51637	chromosome 14 open reading frame 1	1.09E-17	2	4.58	5.66	5.92	6.04	6.14	5.94	5.99	5.75
TC1500803	C15orf24	56851	chromosome 15 open reading frame 2	5.13E-05	2	8.41	8.78	8.93	8.98	8.89	8.95	8.92	8.91
TC1501191	C15orf40	123207	chromosome 15 open reading frame 4	6.62E-09	2	4.62	4.65	4.79	4.82	4.79	4.82	4.99	4.92
TC1501047	C15orf44	81556	chromosome 15 open reading frame 4	7.09E-05	2	3.74	3.88	3.78	4.00	4.10	4.10	4.16	3.98
TC1600003	C16orf33	79622	chromosome 16 open reading frame 3	3.42E-15	2	5.52	5.63	5.30	6.19	6.37	6.49	6.42	6.26
TC1600737	C16orf42	115939	chromosome 16 open reading frame 4	6.25E-06	2	5.77	6.04	6.17	6.17	6.19	6.19	6.23	6.12
TC1601282	C16orf61	56942	chromosome 16 open reading frame 6	4.75E-06	2	4.04	4.16	4.19	4.27	4.43	4.47	4.48	4.49
TC1600894	C16orf63	123811	chromosome 16 open reading frame 6	5.31E-06	2	6.17	6.11	6.16	6.42	6.53	6.56	6.58	6.48
TC1600156	C16orf68	79091	chromosome 16 open reading frame 6	0.000449	2	5.33	5.30	5.34	5.51	5.47	5.42	5.37	5.36
TC1700548	C17orf57	124989	chromosome 17 open reading frame 5	1.52E-05	2	3.15	3.53	3.64	3.79	3.71	3.83	3.83	3.76
TC1700641	C17orf71	55181	chromosome 17 open reading frame 7	4.15E-09	2	4.74	5.11	5.47	5.57	5.44	5.38	5.51	5.34
TC1800110	C18orf17 /// Q	125488	chromosome 18 open reading frame 1	9.01E-08	2	3.79	3.93	3.88	4.18	4.52	4.40	4.32	4.02
TC1800181	C18orf24	220134	chromosome 18 open reading frame 2	1.83E-05	2	2.10	2.27	2.28	2.42	2.69	2.59	2.57	2.35
TC1800466	C18orf32 /// RI	497661 //	chromosome 18 open reading frame 3	1.09E-07	2	5.14	5.17	5.24	5.39	5.47	5.42	5.47	5.31
TC1800191	C18orf54	162681	chromosome 18 open reading frame 5	4.97E-05	2	2.54	2.58	2.78	2.92	2.95	2.73	2.80	2.73
TC1800259	C18orf55	29090	chromosome 18 open reading frame 5	8.16E-07	2	3.67	3.71	3.71	3.81	4.00	3.97	4.12	3.93
TC1800292	C18orf56	494514	chromosome 18 open reading frame 5	0.000576	2	2.31	2.47	2.39	2.47	2.76	2.64	2.69	2.45
TC1901059	C19orf10	56005	chromosome 19 open reading frame 1	0.00014	2	4.22	4.53	4.47	4.67	4.87	4.74	4.80	4.48
TC1900392	C19orf2	8725	chromosome 19 open reading frame 2	3.70E-11	2	3.37	3.57	3.50	4.08	4.33	4.39	4.44	4.07
TC1901278	C19orf42	79086	chromosome 19 open reading frame 4	4.61E-05	2	4.92	5.14	5.21	5.31	5.34	5.28	5.30	5.27
TC1900233	C19orf53	28974	chromosome 19 open reading frame 5	4.00E-08	2	6.73	6.91	7.00	7.35	7.35	7.29	7.32	7.29
TC1901206	C19orf56	51398	chromosome 19 open reading frame 5	3.83E-07	2	5.92	6.17	6.30	6.54	6.57	6.49	6.46	6.37
TC0102535	C1orf103	55791	chromosome 1 open reading frame 10	0.000828	2	5.14	5.22	5.52	5.34	5.20	5.36	5.49	5.50
TC0103346	C1orf131	128061	chromosome 1 open reading frame 13	1.22E-07	2	5.45	5.38	5.50	5.82	5.86	5.86	6.08	5.88
TC0102124	C1orf149	64769	chromosome 1 open reading frame 14	2.07E-09	2	4.81	4.97	4.93	5.10	5.21	5.31	5.38	5.38
TC0100211	C1orf151	440574	chromosome 1 open reading frame 15	2.25E-06	2	5.18	5.27	5.42	5.42	5.42	5.40	5.45	5.42

TC0102984	C1orf156	92342	chromosome 1 open reading frame 15	0.000668	2	5.30	5.42	5.62	5.55	5.56	5.64	5.76	5.68
TC0102273	C1orf41	51668	chromosome 1 open reading frame 41	2.73E-05	2	5.14	5.38	5.47	5.56	5.64	5.66	5.74	5.62
TC0102811	C1orf43	25912	chromosome 1 open reading frame 43	1.28E-08	2	6.83	6.92	7.04	7.22	7.20	7.30	7.27	7.25
TC0100452	C1orf50	79078	chromosome 1 open reading frame 50	3.65E-05	2	5.02	5.11	5.25	5.27	5.31	5.34	5.41	5.39
TC0101553	C1orf67	200095	chromosome 1 open reading frame 67	1.38E-06	2	2.34	2.83	3.06	3.28	3.13	3.13	3.00	2.98
TC0101688	C1orf71	163882	chromosome 1 open reading frame 71	0.000349	2	5.17	5.07	5.10	5.47	5.32	5.45	5.51	5.47
TC0101291	C1orf9	51430	chromosome 1 open reading frame 9	5.46E-05	2	5.98	6.09	6.06	6.13	6.20	6.29	6.32	6.34
TC1700955	C1QBP	708	complement component 1, q subcomp	7.18E-05	2	5.29	5.49	5.45	5.66	5.85	5.75	5.82	5.75
TC2000513	C20orf116	65992	chromosome 20 open reading frame 1	1.43E-16	2	5.27	5.93	6.02	6.29	6.26	6.02	6.14	5.94
TC2000519	C20orf27	54976	chromosome 20 open reading frame 2	1.61E-05	2	5.31	5.47	5.40	5.48	5.59	5.56	5.55	5.42
TC2000531	C20orf30	29058	chromosome 20 open reading frame 3	5.10E-06	2	5.26	5.51	5.57	5.63	5.69	5.63	5.52	5.57
TC2000076	C20orf94	128710	chromosome 20 open reading frame 9	0.000754	2	4.19	4.25	4.42	4.28	4.36	4.55	4.53	4.42
TC2100298	C21orf45	54069	chromosome 21 open reading frame 4	1.37E-10	2	3.84	3.89	3.78	4.32	4.57	4.56	4.59	4.40
TC2100305	C21orf59	56683	chromosome 21 open reading frame 5	4.09E-08	2	4.48	4.44	4.50	4.67	4.74	4.80	4.92	4.75
TC2100307	C21orf66	94104	chromosome 21 open reading frame 6	0.000267	2	3.86	3.81	3.80	3.98	4.11	4.05	4.20	4.02
TC2200332	C22orf32	91689	chromosome 22 open reading frame 3	5.95E-08	2	5.06	5.85	5.82	6.11	6.35	6.17	6.08	5.88
TC2200437	C22orf39	128977	chromosome 22 open reading frame 3	3.11E-05	2	5.06	5.27	5.25	5.23	5.30	5.39	5.34	5.33
TC0200308	C2orf13	200558	chromosome 2 open reading frame 13	2.93E-07	2	4.06	4.44	4.64	4.85	4.77	4.69	4.68	4.75
TC0200519	C2orf15 /// LIP	150590 //	chromosome 2 open reading frame 15	2.23E-06	2	3.99	4.15	4.24	4.25	4.26	4.27	4.29	4.30
TC0202276	C2orf67	151050	chromosome 2 open reading frame 67	1.24E-07	2	4.25	4.24	4.27	4.58	4.63	4.63	4.71	4.56
TC0201621	C2orf7	84279	chromosome 2 open reading frame 7	6.77E-05	2	4.56	4.79	4.82	4.87	4.88	4.85	4.83	4.78
TC0300528	C3orf1	51300	chromosome 3 open reading frame 1	1.66E-05	2	4.79	4.96	5.31	5.36	5.23	5.14	5.31	5.20
TC0301902	C3orf34	84984	chromosome 3 open reading frame 34	3.82E-06	2	7.73	7.65	8.12	8.37	8.29	8.56	8.56	8.60
TC0300687	C3orf58	205428	chromosome 3 open reading frame 58	5.29E-13	2	4.94	5.49	5.80	6.03	5.92	5.85	5.86	5.77
TC0300262	C3orf60	25915	chromosome 3 open reading frame 60	0.000103	2	4.86	5.19	5.16	5.26	5.38	5.33	5.21	5.22
TC0400976	C4orf14	84273	chromosome 4 open reading frame 14	2.29E-06	2	3.92	3.72	3.95	4.16	4.11	4.09	4.22	4.18
TC0400648	C4orf43	55319	chromosome 4 open reading frame 43	2.09E-05	2	4.22	4.34	4.25	4.32	4.57	4.60	4.59	4.40
TC0500732	C5orf25	375484	chromosome 5 open reading frame 25	6.88E-07	2	4.54	4.56	4.55	4.68	4.71	4.74	4.76	4.72
TC0600765	C6orf115	58527	chromosome 6 open reading frame 11	3.03E-12	2	4.56	4.97	5.29	5.50	5.48	5.37	5.39	5.21
TC0601188	C6orf125	84300	chromosome 6 open reading frame 12	1.08E-07	2	3.76	4.05	3.84	4.45	4.85	4.96	4.71	4.39
TC0601222	C6orf129	154467	chromosome 6 open reading frame 12	5.44E-07	2	5.08	5.16	5.30	5.80	5.69	5.58	5.77	5.60
TC0600054	C6orf151	154007	chromosome 6 open reading frame 15	7.17E-07	2	5.19	5.21	5.42	5.63	5.57	5.65	5.70	5.65
TC0601472	C6orf167	253714	chromosome 6 open reading frame 16	0.000958	2	2.74	3.21	3.05	3.05	3.22	3.22	3.16	3.08
TC0600707	C6orf173	387103	chromosome 6 open reading frame 17	5.23E-09	2	3.46	4.14	4.05	4.55	5.14	4.99	4.75	4.15

TC0600605	C6orf203	51250	chromosome 6 open reading frame 20	1.19E-07	2	4.23	4.37	4.46	4.65	4.83	4.74	4.84	4.63
TC0600822	C6orf211	79624	chromosome 6 open reading frame 21	3.30E-05	2	5.36	5.64	5.81	6.00	5.76	5.90	5.96	5.96
TC0600496	C6orf57	135154	chromosome 6 open reading frame 57	0.000603	2	2.99	3.24	3.18	3.28	3.39	3.36	3.30	3.27
TC0701153	C7orf11	136647	chromosome 7 open reading frame 11	1.10E-16	2	4.97	5.81	6.02	6.15	6.10	6.10	6.13	6.05
TC0701106	C7orf24	79017	chromosome 7 open reading frame 24	8.92E-08	2	3.78	3.75	3.72	4.00	4.32	4.31	4.36	4.21
TC0701156	C7orf25	79020	chromosome 7 open reading frame 25	0.000407	2	5.86	5.88	6.14	6.27	6.30	6.31	6.28	6.31
TC0700741	C7orf55	154791	chromosome 7 open reading frame 55	5.21E-09	2	3.98	4.09	4.21	4.39	4.66	4.58	4.40	4.30
TC0800438	C8orf38	137682	chromosome 8 open reading frame 38	0.00033	2	3.92	4.01	4.07	4.14	4.22	4.25	4.22	4.07
TC0800862	C8orf41	80185	chromosome 8 open reading frame 41	5.82E-06	2	5.20	5.12	5.32	5.44	5.28	5.38	5.47	5.45
TC0801076	C8orf59	---	Uncharacterized protein C8orf59. [Sou	5.31E-07	2	3.52	3.81	3.89	4.03	4.11	4.02	4.19	4.02
TC0801225	C8orf76 /// ZH	84933 ///	chromosome 8 open reading frame 76	2.52E-06	2	5.02	5.30	5.41	5.41	5.37	5.38	5.49	5.43
TC0900914	C9orf105	401505	chromosome 9 open reading frame 10	3.73E-09	2	4.00	4.53	4.55	4.90	5.10	4.98	5.05	4.81
TC0901163	C9orf21	195827	chromosome 9 open reading frame 21	6.58E-08	2	3.97	4.17	4.17	4.40	4.41	4.46	4.46	4.50
TC0901049	C9orf40	55071	chromosome 9 open reading frame 40	1.94E-15	2	4.84	4.79	5.14	5.65	5.76	6.14	6.02	6.00
TC0901050	C9orf41	138199	chromosome 9 open reading frame 41	9.23E-05	2	3.90	3.90	3.85	4.02	4.09	4.08	4.21	4.05
TC0901229	C9orf5	23731	chromosome 9 open reading frame 5 /,	1.16E-09	2	4.05	4.01	4.00	4.40	4.45	4.38	4.52	4.29
TC0101302	CACYBP	27101	calcyclin binding protein	1.10E-09	2	5.20	5.18	5.39	5.46	5.56	5.60	5.74	5.65
TC1900657	CALM3	808	calmodulin 3 (phosphorylase kinase, de	0.000904	2	8.71	8.78	8.75	8.99	8.94	8.94	8.95	9.03
TC0700682	CALU	813	calumenin /// Calumenin precursor (Cr	2.87E-09	2	4.34	4.43	4.37	4.83	4.96	5.01	5.05	4.76
TC1201638	CAMKK2	10645	calcium/calmodulin-dependent protein	1.55E-07	2	6.73	6.90	7.04	7.33	7.31	7.09	7.06	6.86
TC0500485	CAMLG	819	calcium modulating ligand	5.02E-10	2	5.60	6.11	6.41	6.46	6.29	6.41	6.49	6.45
TC0300249	CAMP	820	cathelicidin antimicrobial peptide	5.43E-18	2	7.12	9.76	9.06	9.49	10.10	10.35	9.85	9.40
TC1200496	CAND1	55832	cullin-associated and neddylation-disso	1.78E-08	2	3.72	3.81	3.93	4.27	4.42	4.40	4.43	4.20
TC0500775	CANX	821	calnexin /// Calnexin precursor (Major	3.09E-14	2	7.75	8.22	8.16	8.64	8.80	8.81	8.80	8.46
TC0101544	CAPN2	824	calpain 2, (m/II) large subunit /// Calpa	0.000344	2	4.69	5.07	5.08	5.59	5.48	5.31	5.41	5.29
TC1100269	CAPRIN1	4076	cell cycle associated protein 1 /// Capri	7.47E-06	2	7.43	7.51	7.49	7.69	7.64	7.74	7.75	7.77
TC1500289	CASC4	113201	cancer susceptibility candidate 4 /// Pr	1.68E-09	2	8.49	8.67	9.02	9.05	8.90	8.98	8.92	8.87
TC1500238	CASC5	57082	cancer susceptibility candidate 5 /// Pr	3.32E-08	2	3.36	3.72	3.76	4.09	4.44	4.27	4.21	3.89
TC0200993	CASP10	843	caspase 10, apoptosis-related cysteine	2.41E-10	2	4.78	4.95	4.63	5.14	5.48	5.41	5.44	5.20
TC0401186	CASP6	839	caspase 6, apoptosis-related cysteine p	0.000217	2	4.30	4.36	4.39	4.55	4.61	4.47	4.63	4.50
TC1001057	CBARA1	10367	calcium binding atopy-related autoanti	0.000451	2	6.47	6.54	6.61	6.81	6.77	6.69	6.69	6.58
TC0301413	CBLB	868	Cas-Br-M (murine) ecotropic retroviral	2.10E-05	2	4.16	4.12	4.12	4.33	4.30	4.33	4.41	4.38
TC1201260	CBX5	23468	chromobox homolog 5 (HP1 alpha hom	6.80E-07	2	4.32	5.27	4.93	5.32	5.66	5.58	5.47	5.07
TC0200253	CCDC104	112942	coiled-coil domain containing 104 /// C	2.37E-05	2	4.43	4.71	4.67	4.64	4.46	4.67	4.99	4.86

TC1000331	CCDC109A	90550	coiled-coil domain containing 109A ///	7.38E-09	2	5.73	5.55	5.62	5.94	6.16	6.07	6.04	5.81
TC0501220	CCDC112	153733	coiled-coil domain containing 112	6.91E-06	2	4.35	4.35	4.64	4.83	4.61	4.71	4.95	4.88
TC0201395	CCDC121	79635	coiled-coil domain containing 121	4.80E-06	2	4.64	4.53	4.83	4.84	4.78	4.91	4.99	4.95
TC0200566	CCDC138	165055	coiled-coil domain containing 138	0.000661	2	2.36	2.43	2.53	2.56	2.65	2.54	2.60	2.52
TC0301503	CCDC14	64770	coiled-coil domain containing 14	8.95E-05	2	3.80	3.81	3.95	4.13	4.22	4.16	4.25	4.06
TC0100735	CCDC18	343099	coiled-coil domain containing 18 /// Co	1.44E-08	2	4.20	4.82	4.94	5.31	5.28	5.19	5.20	4.89
TC0800828	CCDC25	55246	coiled-coil domain containing 25 /// Co	8.29E-07	2	3.64	3.83	3.88	4.02	4.01	4.10	4.23	4.06
TC1701431	CCDC43	124808	coiled-coil domain containing 43	0.000107	2	4.47	4.82	5.02	5.21	5.24	5.24	5.22	5.01
TC1800165	CCDC5	115106	coiled-coil domain containing 5 (spindl	3.06E-10	2	4.45	4.78	4.75	5.13	5.29	5.28	5.33	5.18
TC1701389	CCDC56	28958	coiled-coil domain containing 56	1.07E-08	2	5.32	6.10	6.07	6.46	6.57	6.53	6.60	6.31
TC1001001	CCDC6	8030	coiled-coil domain containing 6	4.26E-07	2	3.77	4.03	3.88	4.40	4.53	4.47	4.52	4.21
TC0300323	CCDC66	285331	coiled-coil domain containing 66 /// co	0.000272	2	4.13	4.58	4.58	4.57	4.57	4.67	4.75	4.63
TC0501419	CCDC69	26112	coiled-coil domain containing 69 /// co	8.17E-07	2	6.87	6.81	6.73	7.31	7.17	7.05	7.07	7.03
TC1101293	CCDC73	493860	coiled-coil domain containing 73 /// Co	0.000697	2	2.09	2.34	2.54	2.57	2.49	2.55	2.42	2.50
TC0200178	CCDC75	253635	coiled-coil domain containing 75 /// Co	4.40E-10	2	4.51	4.51	4.43	4.61	4.83	4.86	5.10	4.84
TC0100766	CCDC76	54482	coiled-coil domain containing 76 /// Co	1.11E-08	2	3.28	3.11	3.25	3.48	3.57	3.50	3.57	3.40
TC0201524	CCDC88A	55704	coiled-coil domain containing 88A ///	4.06E-06	2	3.38	3.83	3.75	3.99	4.06	4.11	4.28	4.00
TC0600961	CCDC90A	63933	coiled-coil domain containing 90A /// c	2.41E-13	2	3.32	3.98	3.90	4.65	5.22	5.27	5.04	4.82
TC0401092	CCDC98	84142	coiled-coil domain containing 98 /// Co	1.26E-11	2	4.43	4.62	4.66	4.99	4.96	4.98	5.06	4.89
TC0500690	CCDC99	54908	coiled-coil domain containing 99 /// Co	7.16E-05	2	3.14	3.40	3.30	3.56	3.79	3.68	3.73	3.55
TC1701251	CCL23	6368	chemokine (C-C motif) ligand 23	3.69E-13	2	3.58	3.42	3.73	4.70	4.22	4.95	5.29	5.28
TC1701252	CCL3	730422 //	chemokine (C-C motif) ligand 3	0.000459	2	4.87	5.08	4.98	5.16	5.03	5.21	5.28	5.25
TC1700383	CCL4	6351	chemokine (C-C motif) ligand 4	3.50E-05	2	4.55	4.88	4.56	5.39	5.12	5.46	5.90	5.94
TC1701244	CCL5	6352	chemokine (C-C motif) ligand 5	2.80E-05	2	5.61	5.54	4.99	6.30	6.73	7.15	6.63	6.97
TC0401233	CCNA2	890	cyclin A2	3.41E-10	2	3.21	3.41	3.27	3.81	4.29	4.31	4.11	3.74
TC0500232	CCNB1	891	cyclin B1 /// G2/mitotic-specific cyclin-	1.49E-05	2	3.30	3.45	3.34	3.63	3.87	3.81	3.71	3.59
TC1500373	CCNB2	9133	cyclin B2	8.22E-08	2	2.96	3.13	3.14	3.58	3.92	3.88	3.71	3.33
TC1200030	CCND2	894	cyclin D2	1.71E-16	2	4.82	4.70	4.26	5.32	5.52	5.53	5.48	5.28
TC0801128	CCNE2	9134	cyclin E2	5.55E-10	2	3.16	3.09	3.17	3.66	4.02	4.05	3.87	3.46
TC0201050	CCNYL1	151195	cyclin Y-like 1 /// cyclin Y-like 1 [Source	1.42E-05	2	5.72	6.09	6.10	6.24	6.22	6.27	6.16	6.17
TC1200510	CCT2	10576	chaperonin containing TCP1, subunit 2	3.37E-09	2	4.66	4.82	4.74	5.16	5.38	5.38	5.44	5.16
TC0102852	CCT3	7203	chaperonin containing TCP1, subunit 3	0.000249	2	4.77	4.73	4.71	4.96	4.99	4.89	5.07	4.88
TC0201550	CCT4	10575	chaperonin containing TCP1, subunit 4	8.65E-08	2	3.97	4.11	4.24	4.43	4.60	4.60	4.68	4.44
TC0700270	CCT6A	908	chaperonin containing TCP1, subunit 6	1.34E-06	2	4.17	4.27	4.33	4.52	4.70	4.72	4.83	4.62

TC0200342	CCT7	10574	chaperonin containing TCP1, subunit 7	7.38E-05	2	5.30	5.35	5.58	5.68	5.65	5.64	5.77	5.55
TC2100262	CCT8	10694	chaperonin containing TCP1, subunit 8	8.05E-07	2	4.18	4.54	4.65	4.90	4.94	4.91	5.00	4.77
TC0301451	CD200R1	131450	CD200 receptor 1	7.48E-06	2	3.67	3.98	3.84	4.10	4.44	4.54	4.49	4.38
TC1800535	CD226	10666	CD226 molecule	0.000133	2	3.61	4.10	3.86	4.77	5.09	5.11	4.74	4.78
TC0Y00162	CD24	934	CD24 molecule	4.08E-16	2	4.21	6.17	5.78	7.15	7.50	7.61	7.03	6.52
TC0900039	CD274	29126	CD274 molecule /// Programmed cell d	2.30E-05	2	4.95	5.58	5.61	6.56	6.22	6.64	6.58	6.44
TC0600438	CD2AP	23607	CD2-associated protein	4.53E-10	2	4.79	5.06	4.80	5.42	5.17	5.54	6.05	5.97
TC0301426	CD47	961	CD47 molecule /// Leukocyte surface a	1.24E-09	2	6.44	6.50	6.75	6.91	6.96	7.04	7.14	7.00
TC1200960	CD69	969	CD69 molecule	0.000262	2	2.88	3.18	2.93	3.63	3.32	3.55	3.97	3.91
TC0600088	CD83	9308	CD83 molecule	0.000102	2	4.23	4.47	4.39	4.50	4.52	4.56	4.55	4.52
TC0901162	CDC14B /// CD	8555	CDC14 cell division cycle 14 homolog B	5.28E-11	2	3.62	3.74	3.64	3.81	4.05	4.08	3.94	4.00
TC1300298	CDC16	8881	cell division cycle 16 homolog (S. cerevi	3.25E-06	2	4.58	4.44	4.53	4.72	4.77	4.79	4.90	4.79
TC1000271	CDC2	983	cell division cycle 2, G1 to S and G2 to	8.77E-07	2	2.42	2.55	2.50	2.71	3.03	2.98	2.82	2.65
TC0100467	CDC20	991	cell division cycle 20 homolog (S. cerevi	0.000606	2	4.34	4.33	4.25	4.36	4.48	4.47	4.40	4.32
TC0900022	CDC37L1	55664	cell division cycle 37 homolog (S. cerevi	2.98E-07	2	4.84	4.84	4.94	5.10	5.02	5.19	5.28	5.22
TC2200035	CDC45L	8318	CDC45 cell division cycle 45-like (S. cere	3.12E-07	2	3.72	3.87	3.79	3.94	4.27	4.21	4.15	3.95
TC1700433	CDC6	990	cell division cycle 6 homolog (S. cerevis	1.81E-08	2	3.08	3.25	3.11	3.48	4.01	3.94	3.82	3.48
TC0100717	CDC7	8317	cell division cycle 7 homolog (S. cerevis	2.72E-06	2	3.35	3.43	3.34	3.45	3.69	3.65	3.63	3.53
TC0800160	CDCA2	157313	cell division cycle associated 2 /// Cell c	1.55E-05	2	2.70	2.77	2.77	2.89	3.12	3.09	2.99	2.92
TC1401163	CDCA4	55038	cell division cycle associated 4	0.000391	2	4.19	4.51	4.52	4.52	4.62	4.60	4.55	4.51
TC0200868	CDCA7	83879	cell division cycle associated 7	2.08E-05	2	3.96	4.08	4.05	4.13	4.34	4.36	4.23	4.15
TC0701049	CDCA7L	732169 //	cell division cycle associated 7-like	1.49E-08	2	4.41	5.60	5.07	5.57	6.21	6.23	5.98	5.52
TC0100402	CDCA8	55143	cell division cycle associated 8	8.63E-05	2	4.16	4.17	4.05	4.20	4.37	4.40	4.40	4.36
TC1201658	CDK2AP1	8099	CDK2-associated protein 1	6.25E-12	2	4.59	4.83	4.83	5.28	5.41	5.40	5.41	5.31
TC1201327	CDK4	1019	cyclin-dependent kinase 4 /// Cell divisi	4.21E-08	2	4.38	4.55	4.37	4.71	5.03	5.09	4.94	4.79
TC0701414	CDK6	1021	cyclin-dependent kinase 6	1.82E-11	2	3.98	3.99	4.03	4.25	4.48	4.52	4.56	4.44
TC0100539	CDKN2C	1031	cyclin-dependent kinase inhibitor 2C (p	2.89E-09	2	3.62	3.83	4.28	4.39	4.39	4.16	4.15	3.94
TC1400236	CDKN3	1033	cyclin-dependent kinase inhibitor 3 (CD	1.14E-10	2	3.32	3.57	3.73	4.11	4.46	4.24	4.07	3.79
TC1600935	CDR2	1039	cerebellar degeneration-related protei	2.68E-06	2	4.16	4.75	4.70	4.78	5.05	4.80	4.81	4.60
TC1600667	CDT1	81620	chromatin licensing and DNA replicatio	4.50E-05	2	4.60	4.77	4.75	4.78	4.88	4.92	4.84	4.81
TC0300634	CDV3	55573	CDV3 homolog (mouse)	3.59E-05	2	7.87	8.19	8.24	8.21	8.14	8.24	8.24	8.28
TC1900559	CEACAM6 /// C	4680 /// 1	carcinoembryonic antigen-related cell	2.61E-17	2	3.74	4.66	4.23	4.93	5.31	5.36	5.08	4.76
TC1901554	CEACAM8	1088	carcinoembryonic antigen-related cell	1.62E-20	2	4.09	7.62	6.23	8.11	8.99	9.19	8.44	7.64
TC1400715	CEBPE	1053	CCAAT/enhancer binding protein (C/EB	2.59E-18	2	5.60	5.68	5.48	6.35	6.57	6.65	6.42	6.42

TC2200415	CECR1	51816	cat eye syndrome chromosome region,	0.00024	2	4.19	4.20	4.11	4.41	4.26	4.39	4.50	4.38
TC0401163	CENPE	1062	centromere protein E, 312kDa /// Cent	0.000807	2	2.62	3.12	2.90	3.03	3.40	3.29	3.29	3.03
TC0101512	CENPF	1063	centromere protein F, 350/400ka (mitc	4.64E-07	2	3.25	3.48	3.32	3.77	4.29	4.22	4.26	3.72
TC1300347	CENPJ	55835	centromere protein J	4.20E-05	2	3.35	3.34	3.29	3.53	3.77	3.70	3.85	3.61
TC0501026	CENPK	64105	centromere protein K	6.74E-09	2	3.34	3.47	3.46	3.77	4.21	4.21	4.11	3.82
TC2200715	CENPM	79019	centromere protein M	0.000851	2	4.97	4.97	4.99	5.02	5.15	5.11	5.04	4.95
TC1600613	CENPN	55839	centromere protein N	4.60E-10	2	3.63	3.89	3.74	4.07	4.49	4.45	4.43	4.07
TC1201430	CEP290	80184	centrosomal protein 290kDa	0.00024	2	2.78	2.83	2.86	2.92	2.95	2.96	3.06	3.01
TC1000453	CEP55	55165	centrosomal protein 55kDa /// Centros	2.85E-06	2	2.86	3.12	3.04	3.37	3.78	3.63	3.50	3.29
TC1100774	CEP57	9702	centrosomal protein 57kDa /// Centros	4.20E-05	2	4.87	5.18	5.04	5.16	5.18	5.27	5.40	5.31
TC0900313	CEP78	84131	centrosomal protein 78kDa /// Centros	0.000183	2	3.07	3.02	3.00	3.10	3.34	3.21	3.37	3.12
TC0300461	CEP97 /// LRRI	79598	centrosomal protein 97kDa /// Leucine	9.03E-09	2	4.88	5.09	5.25	5.69	5.86	5.76	5.75	5.51
TC0X01361	CETN2	1069	centrin, EF-hand protein, 2	2.01E-06	2	5.93	6.59	6.76	6.69	6.70	6.83	6.81	6.73
TC0501137	CETN3	1070	centrin, EF-hand protein, 3 (CDC31 hon	5.63E-06	2	3.48	3.94	4.10	4.09	4.26	4.36	4.49	4.18
TC1601264	CFDP1	10428	craniofacial development protein 1	8.45E-15	2	7.19	7.20	7.31	7.65	7.73	7.87	8.00	7.85
TC1900091	CHAF1A	10036	chromatin assembly factor 1, subunit A	1.78E-06	2	5.34	5.51	5.43	5.56	5.67	5.64	5.66	5.61
TC1000345	CHCHD1	118487	coiled-coil-helix-coiled-coil-helix domai	6.88E-14	2	4.66	5.35	5.64	5.82	5.77	5.65	5.66	5.50
TC2200512	CHCHD10	646106 //	coiled-coil-helix-coiled-coil-helix domai	0.000597	2	5.70	6.07	5.90	6.03	6.04	6.01	6.12	5.92
TC0701646	CHCHD3	54927	coiled-coil-helix-coiled-coil-helix domai	3.68E-05	2	4.45	5.33	5.10	5.26	5.30	5.27	5.33	5.18
TC0100952	CHD1L	9557	chromodomain helicase DNA binding p	1.05E-09	2	3.69	4.10	4.05	4.48	4.86	4.70	4.64	4.33
TC1100978	CHEK1	1111	CHK1 checkpoint homolog (S. pombe)	5.60E-07	2	3.03	3.16	3.08	3.32	3.67	3.56	3.58	3.29
TC1101052	CHID1	66005	chitinase domain containing 1 /// Chiti	0.000665	2	5.51	5.50	5.46	5.57	5.69	5.63	5.61	5.54
TC0103141	CHIT1	1118	chitinase 1 (chitotriosidase) /// Chitotri	1.03E-07	2	4.33	5.19	4.76	5.31	5.97	5.92	5.43	4.97
TC0900126	CHMP5 /// BA	51510	chromatin modifying protein 5 /// BAG	6.85E-07	2	7.91	7.99	8.12	8.34	8.18	8.39	8.42	8.52
TC0800579	CHRAC1	54108	chromatin accessibility complex 1	1.37E-05	2	4.78	5.01	4.82	5.06	5.12	5.20	5.20	5.14
TC0700021	CHST12	55501	carbohydrate (chondroitin 4) sulfotran	6.43E-08	2	6.08	6.45	6.43	6.55	6.51	6.51	6.52	6.41
TC1400303	CHURC1 /// FN	91612 ///	churchill domain containing 1 /// farne	0.00025	2	4.97	5.03	5.05	5.15	5.11	5.18	5.19	5.21
TC1400744	CIDEB	27141	cell death-inducing DFFA-like effector	1.65E-07	2	5.68	5.64	5.77	6.17	6.12	5.98	6.09	5.89
TC1600550	CIRH1A	84916	cirrhosis, autosomal recessive 1A (cirh	0.000375	2	3.74	3.92	3.93	4.05	4.15	4.09	4.13	4.07
TC1201615	CIT	11113	citron (rho-interacting, serine/threonin	0.000194	2	3.34	3.41	3.39	3.51	3.71	3.64	3.64	3.49
TC0601648	CITED2	10370	Cbp/p300-interacting transactivator, w	3.39E-11	2	5.53	5.95	5.86	6.36	6.77	6.65	6.57	6.31
TC1300164	CKAP2	26586	cytoskeleton associated protein 2 /// C	1.27E-11	2	3.98	4.23	4.04	4.72	5.13	5.12	5.14	4.86
TC0201830	CKAP2L	150468	cytoskeleton associated protein 2-like	3.72E-06	2	2.88	3.11	3.02	3.23	3.58	3.55	3.45	3.23
TC1101339	CKAP5	9793	cytoskeleton associated protein 5 /// C	7.14E-13	2	3.96	3.98	3.85	4.51	4.79	4.72	4.81	4.47

TC0101105	CKS1B	732142 //	CDC28 protein kinase regulatory subun	9.81E-10	2	4.27	4.52	4.38	4.65	4.90	4.87	4.73	4.66
TC0900366	CKS2	1164	CDC28 protein kinase regulatory subun	7.14E-10	2	4.75	5.10	5.09	5.48	5.96	6.06	5.90	5.85
TC1200965	CLEC1B	51266	C-type lectin domain family 1, member	0.000503	2	4.80	5.57	5.46	6.17	6.30	6.11	5.90	5.79
TC0100268	CLIC4	25932	chloride intracellular channel 4	3.92E-08	2	4.38	5.25	5.20	5.70	5.63	5.52	5.53	5.45
TC1101686	CLNS1A	1207	chloride channel, nucleotide-sensitive,	1.04E-12	2	4.51	5.54	5.55	5.95	6.04	6.02	6.09	5.97
TC1101640	CLPB	81570	ClpB caseinolytic peptidase B homolog	0.00094	2	4.31	4.53	4.40	4.55	4.72	4.62	4.59	4.42
TC0102109	CLSPN	63967	claspin homolog (Xenopus laevis) /// Cl	2.79E-09	2	3.91	4.10	4.10	4.47	4.82	4.75	4.73	4.35
TC0900174	CLTA	1211	clathrin, light chain (Lca)	3.15E-06	2	5.90	5.98	5.99	6.07	6.15	6.25	6.28	6.16
TC0501517	CLTB	1212	clathrin, light chain (Lcb)	2.39E-05	2	5.52	5.76	5.91	6.00	5.87	5.91	5.93	5.83
TC2200435	CLTCL1	8218	clathrin, heavy chain-like 1 /// Clathrin	1.42E-05	2	4.07	4.63	4.26	4.50	4.88	4.80	4.59	4.33
TC0800827	CLU	1191	clusterin	3.82E-06	2	5.17	5.61	5.64	6.33	6.53	6.37	6.08	5.99
TC1200191	CMAS	55907	cytidine monophosphate N-acetylneura	1.49E-05	2	4.02	4.68	4.84	5.05	5.06	4.98	5.01	4.83
TC0100523	CMPK1 /// CMI	51727	cytidine monophosphate (UMP-CMP) k	1.72E-06	2	5.07	5.42	5.52	5.71	5.82	5.77	5.79	5.64
TC0300132	CMTM7	112616	CKLF-like MARVEL transmembrane don	0.000102	2	5.44	5.58	5.74	5.92	5.87	5.75	5.86	5.72
TC0500782	CNOT6	57472	CCR4-NOT transcription complex, subu	0.000299	2	5.80	6.09	6.20	6.32	6.29	6.21	6.23	6.13
TC1201292	CNPY2	10330	canopy 2 homolog (zebrafish)	9.97E-10	2	4.95	4.86	4.80	5.19	5.31	5.31	5.43	5.26
TC0101603	COG2	22796	component of oligomeric golgi comple›	1.74E-05	2	3.45	3.57	3.60	3.74	3.76	3.77	3.91	3.76
TC1601204	COG8 /// PDF	84342 ///	component of oligomeric golgi comple›	0.000616	2	3.90	3.85	3.99	4.10	4.06	3.98	4.04	4.02
TC0301654	COMMD2	51122	COMM domain containing 2	0.000264	2	5.83	6.10	6.15	6.06	5.88	6.12	6.27	6.25
TC0801349	COMMD5	28991	COMM domain containing 5	8.67E-07	2	5.27	5.41	5.43	5.57	5.58	5.56	5.52	5.55
TC1300552	COMMD6	170622	COMM domain containing 6	3.91E-19	2	5.55	6.15	6.42	6.41	6.39	6.43	6.41	6.37
TC2000665	COMMD7	149951	COMM domain containing 7	1.43E-05	2	4.87	5.32	5.44	5.48	5.67	5.72	5.71	5.58
TC0400921	COMMD8	54951	COMM domain containing 8 /// COMN	6.18E-11	2	4.73	5.41	5.76	5.82	5.69	5.71	5.83	5.77
TC1500940	COPS2	9318	COP9 constitutive photomorphogenic l	0.000241	2	5.32	5.79	5.78	5.84	5.80	5.89	5.98	5.94
TC0901184	CORO2A	7464	coronin, actin binding protein, 2A	5.06E-05	2	4.41	4.91	4.99	5.05	5.25	5.12	5.11	4.89
TC1601304	COTL1	23406	coactosin-like 1 (Dictyostelium)	0.000159	2	8.69	8.83	9.05	9.43	9.29	9.08	8.94	9.06
TC0700944	COX19	90639	COX19 cytochrome c oxidase assembly	0.000832	2	3.94	3.86	3.97	4.12	4.10	4.06	4.09	4.10
TC1501108	COX5A	9377	cytochrome c oxidase subunit Va	6.32E-12	2	6.94	7.79	7.92	8.19	8.31	8.35	8.35	8.13
TC0200509	COX5B	1329	cytochrome c oxidase subunit Vb	0.000501	2	4.91	5.14	5.22	5.32	5.35	5.32	5.28	5.33
TC1200751	COX6A1	1337	cytochrome c oxidase subunit VIa poly	1.39E-05	2	9.19	9.59	9.64	9.79	9.81	9.79	9.79	9.79
TC1900450	COX6B1	1340	cytochrome c oxidase subunit Vib poly	8.64E-08	2	10.58	10.84	10.98	11.09	11.04	11.04	11.03	11.03
TC0X00375	COX7B	1349	cytochrome c oxidase subunit VIIb	1.89E-14	2	8.13	8.85	9.01	8.98	8.92	8.98	9.02	8.97
TC1001161	CPEB3	22849	cytoplasmic polyadenylation element b	2.10E-05	2	3.96	4.04	4.18	4.39	4.21	4.13	4.26	4.13
TC1600469	CPNE2	221184	copine II /// Copine-2 (Copine II). [Sour	4.08E-05	2	5.60	5.86	5.58	5.89	6.24	6.07	5.91	5.71

TC0800417	CPNE3	8895	copine III	5.82E-17	2	6.92	8.42	8.33	8.65	8.98	8.88	8.51	8.16
TC1400449	CPSF2	53981	cleavage and polyadenylation specific f	6.95E-14	2	5.77	6.28	6.49	6.76	6.65	6.65	6.67	6.48
TC1200505	CPSF6	11052	cleavage and polyadenylation specific f	0.000219	2	5.77	5.74	5.87	6.05	6.05	5.92	6.03	5.93
TC0701665	CREB3L2	64764	cAMP responsive element binding prot	0.000149	2	4.29	4.53	4.49	4.54	4.56	4.65	4.79	4.78
TC0102964	CREG1	8804	cellular repressor of E1A-stimulated ge	4.17E-14	2	5.15	5.52	5.22	5.70	5.84	5.92	6.02	5.90
TC1400638	CRIP1 /// Q8N	1396	cysteine-rich protein 1 (intestinal) /// C	9.74E-07	2	5.91	6.06	6.09	6.33	6.32	6.44	6.61	6.44
TC2200061	CRKL	1399	v-crk sarcoma virus CT10 oncogene ho	4.42E-06	2	6.69	6.95	7.01	7.09	6.98	7.09	7.03	7.09
TC0300137	CRTAP	10491	cartilage associated protein	1.31E-09	2	3.93	4.09	4.03	4.33	4.42	4.43	4.40	4.33
TC2000353	CSE1L	1434	CSE1 chromosome segregation 1-like (	1.45E-08	2	4.78	4.66	4.72	4.99	5.18	5.25	5.18	5.15
TC1501028	CSNK1G1 /// K	53944 ///	casein kinase 1, gamma 1 /// KIAA0101	5.26E-05	2	4.34	4.65	4.60	4.67	4.67	4.76	4.69	4.64
TC0500433	CSNK1G3	1456	casein kinase 1, gamma 3	4.64E-11	2	6.16	6.83	7.03	7.19	6.86	7.06	7.05	6.95
TC0800353	CSPP1	79848	centrosome and spindle pole associate	4.88E-07	2	4.16	4.40	4.55	4.76	4.73	4.63	4.66	4.56
TC0103120	CSRP1	1465	cysteine and glycine-rich protein 1	7.35E-05	2	5.45	5.57	5.58	5.74	5.79	5.69	5.70	5.64
TC0300550	CSTA	1475	cystatin A (stefin A)	0.000505	2	9.36	9.78	9.66	9.88	9.83	10.01	9.95	9.87
TC2100385	CSTB	1476	cystatin B (stefin B)	4.45E-12	2	7.03	7.44	7.59	7.75	7.72	7.71	7.50	7.56
TC1101295	CSTF3	1479	cleavage stimulation factor, 3' pre-RNA	6.56E-07	2	4.01	4.34	4.54	4.68	4.81	4.73	4.77	4.50
TC0300154	CTDSPL	10217	CTD (carboxy-terminal domain, RNA p	9.88E-11	2	4.75	5.05	4.95	5.22	5.61	5.52	5.33	5.17
TC0901227	CTNNAL1	8727	catenin (cadherin-associated protein),	2.65E-06	2	3.26	3.40	3.28	3.51	3.73	3.69	3.66	3.54
TC0X00790	CTPS2	56474	CTP synthase II /// CTP synthase 2 (EC	0.000545	2	3.74	3.76	3.74	3.82	3.90	3.83	3.88	3.81
TC2000328	CTSA	5476	cathepsin A /// Lysosomal protective p	2.77E-09	2	6.47	6.59	6.64	7.27	7.20	7.01	6.94	6.90
TC1400751	CTSG	1511	cathepsin G	1.31E-14	2	3.99	6.12	5.07	6.89	7.77	7.91	7.37	6.62
TC0700851	CUL1	8454	cullin 1	6.86E-05	2	4.78	5.04	5.01	5.19	5.25	5.20	5.31	5.14
TC1300292	CUL4A	8451	cullin 4A /// Cullin-4A (CUL-4A). [Sourc	1.44E-05	2	4.97	4.90	4.96	5.11	5.17	5.18	5.26	5.05
TC1100821	CUL5	8065	cullin 5	4.12E-05	2	3.71	4.26	4.41	4.40	4.40	4.40	4.54	4.29
TC1101751	CWC15	51503	CWC15 homolog (S. cerevisiae)	5.95E-06	2	7.52	7.68	7.79	7.72	7.65	7.83	7.91	7.93
TC0301118	CX3CR1	1524	chemokine (C-X3-C motif) receptor 1	0.000597	2	4.65	4.58	4.81	5.35	4.77	5.11	5.25	5.27
TC0201025	CYP20A1	57404	cytochrome P450, family 20, subfamily	0.000417	2	4.13	4.34	4.21	4.38	4.44	4.54	4.64	4.49
TC0701407	CYP51A1 /// Q	1595	cytochrome P450, family 51, subfamily	5.25E-07	2	3.69	3.85	3.80	4.03	4.21	4.03	3.94	3.83
TC1400271	DAAM1	23002	dishevelled associated activator of mo	1.68E-07	2	3.67	4.17	4.03	4.37	4.54	4.45	4.48	4.28
TC1400699	DAD1	1603	defender against cell death 1	4.97E-06	2	8.40	8.54	8.77	8.86	8.81	8.93	8.91	8.88
TC0700455	DBF4	649412 //	DBF4 homolog (S. cerevisiae)	3.29E-05	2	2.97	3.49	3.36	3.52	3.74	3.70	3.61	3.44
TC0200628	DBI	1622	diazepam binding inhibitor (GABA rece	4.24E-17	2	6.15	6.24	6.55	6.84	6.69	6.76	6.85	6.78
TC1701437	DCAKD	79877	dephospho-CoA kinase domain contain	2.02E-06	2	4.54	4.55	4.65	4.77	4.87	4.77	4.68	4.62
TC0400303	DCK	1633	deoxycytidine kinase	1.97E-10	2	4.44	4.97	5.14	5.34	5.32	5.29	5.28	5.28

TC1001287	DCLRE1A	9937	DNA cross-link repair 1A (PSO2 homolo	4.56E-07	2	3.04	3.20	3.12	3.30	3.52	3.42	3.44	3.36
TC0100858	DCLRE1B	64858	DNA cross-link repair 1B (PSO2 homolo	2.72E-09	2	4.06	4.48	4.48	4.70	4.99	4.98	4.91	4.69
TC1200869	DCP1B	196513	DCP1 decapping enzyme homolog B (S.	0.000677	2	3.90	3.95	3.95	4.21	4.33	4.10	4.30	4.20
TC0401430	DCTD	1635	dCMP deaminase	1.48E-05	2	4.19	4.35	4.32	4.46	4.54	4.43	4.51	4.47
TC0400217	DCUN1D4	23142	DCN1, defective in cullin neddylation 1,	2.65E-05	2	4.89	5.08	5.08	5.22	5.27	5.37	5.32	5.31
TC1101779	DCUN1D5	84259	DCN1, defective in cullin neddylation 1,	9.73E-05	2	4.10	4.63	4.71	4.66	4.66	4.62	4.82	4.70
TC1701796	DCXR	51181	dicarbonyl/L-xylulose reductase	0.000138	2	5.99	6.10	6.01	6.12	6.17	6.16	6.10	6.10
TC1101461	DDB1	652672 //	damage-specific DNA binding protein 1	0.000462	2	4.77	4.77	4.68	4.89	5.01	5.03	5.05	4.97
TC2200128	DDTL	1E+08	D-dopachrome tautomerase-like	0.000923	2	5.25	5.46	5.45	5.58	5.63	5.53	5.49	5.48
TC0200060	DDX1	1653	DEAD (Asp-Glu-Ala-Asp) box polypeptic	3.96E-06	2	4.08	4.58	4.74	4.96	5.05	5.06	5.14	4.95
TC1100825	DDX10	1662	DEAD (Asp-Glu-Ala-Asp) box polypeptic	0.000185	2	3.08	3.25	3.26	3.32	3.38	3.33	3.42	3.39
TC1000297	DDX21	9188	DEAD (Asp-Glu-Ala-Asp) box polypeptic	2.39E-07	2	4.53	5.20	4.67	4.88	4.90	5.17	5.42	5.28
TC1000296	DDX50	79009	DEAD (Asp-Glu-Ala-Asp) box polypeptic	0.000225	2	4.20	4.42	4.36	4.47	4.49	4.53	4.70	4.59
TC1101044	DEAF1	10522	deformed epidermal autoregulatory fa	0.00025	2	5.17	5.33	5.31	5.38	5.37	5.37	5.33	5.28
TC0800421	DECR1	1666	2,4-dienoyl CoA reductase 1, mitochon	0.000381	2	7.46	7.44	7.71	7.69	7.53	7.68	7.69	7.70
TC0800669	DEFA4	1669	defensin, alpha 4, corticostatin	9.78E-22	2	5.30	7.57	6.72	8.67	9.30	9.61	9.10	8.36
TC0600982	DEK	7913	DEK oncogene (DNA binding)	0.000159	2	8.16	8.62	8.70	8.64	8.61	8.68	8.74	8.69
TC0102566	DENND2C	163259	DENN/MADD domain containing 2C ///	2.69E-05	2	3.34	3.58	3.55	3.70	3.90	3.86	3.68	3.56
TC1200781	DENR	8562	density-regulated protein	1.62E-08	2	6.88	7.29	7.46	7.44	7.53	7.58	7.64	7.50
TC0102349	DEPDC1	55635	DEP domain containing 1 /// DEP doma	0.00022	2	2.06	2.13	2.13	2.23	2.41	2.35	2.28	2.26
TC0501006	DEPDC1B	55789	DEP domain containing 1B	5.74E-10	2	3.78	4.09	4.15	4.48	4.64	4.64	4.43	4.30
TC0501110	DHFR	1719	dihydrofolate reductase	4.24E-11	2	4.42	5.22	5.35	5.75	6.00	5.77	5.66	5.26
TC1400112	DHRS4L2 /// DI	731356 //	dehydrogenase/reductase (SDR family)	0.000642	2	5.10	5.16	5.09	5.19	5.21	5.22	5.31	5.22
TC1300521	DIAPH3	81624	diaphanous homolog 3 (Drosophila) ///	0.000265	2	2.62	2.69	2.72	2.81	3.02	2.97	2.86	2.79
TC0501016	DIMT1L	27292	DIM1 dimethyladenosine transferase 1	0.000699	2	3.12	3.28	3.25	3.28	3.39	3.37	3.41	3.40
TC1500418	DIS3L	115752	DIS3 mitotic control homolog (S. cerevi	2.73E-09	2	3.45	3.56	3.49	3.67	4.05	4.04	4.04	3.78
TC0X00710	DKC1	1736	dyskeratosis congenita 1, dyskerin	1.40E-07	2	5.34	5.33	5.22	5.43	5.63	5.62	5.81	5.59
TC1100846	DLAT	1737	dihydrolipoamide S-acetyltransferase	0.000512	2	3.76	3.85	3.84	3.93	4.06	4.04	4.12	4.04
TC1400874	DLGAP5 /// DL	9787	discs, large (Drosophila) homolog-asso	1.22E-06	2	2.85	3.02	2.99	3.24	3.65	3.54	3.50	3.24
TC2200665	DMC1	11144	DMC1 dosage suppressor of mck1 hom	3.80E-06	2	2.47	2.60	2.73	2.92	3.01	2.82	2.70	2.71
TC1000817	DNAJC1	64215	DnaJ (Hsp40) homolog, subfamily C, me	7.80E-06	2	5.12	6.06	5.70	6.07	5.90	5.97	6.07	6.09
TC0200913	DNAJC10	54431	DnaJ (Hsp40) homolog, subfamily C, me	2.18E-08	2	4.18	4.24	4.12	4.62	4.52	4.65	4.80	4.75
TC1300111	DNAJC15	29103	DnaJ (Hsp40) homolog, subfamily C, me	5.37E-05	2	4.21	4.57	4.51	4.73	4.81	4.90	5.03	5.03
TC1500847	DNAJC17	55192	DnaJ (Hsp40) homolog, subfamily C, me	6.65E-05	2	5.59	5.93	5.93	6.09	6.10	6.06	6.26	6.03

TC0500117	DNAJC21 /// D	134218	DnaJ (Hsp40) homolog, subfamily C, m	2.69E-05	2	4.99	5.62	5.58	5.79	5.89	5.95	6.10	5.79
TC1300235	DNAJC3	5611	DnaJ (Hsp40) homolog, subfamily C, m	7.71E-07	2	7.22	7.54	7.68	7.83	7.76	7.77	7.77	7.69
TC1200241	DNM1L	10059	dynamin 1-like /// Dynamin-1-like prot	7.11E-08	2	4.11	4.39	4.37	4.59	4.83	4.76	4.74	4.56
TC1901156	DNMT1	1786	DNA (cytosine-5-)-methyltransferase 1	1.55E-08	2	5.01	5.22	5.12	5.38	5.49	5.51	5.55	5.40
TC2100109	DOPEY2	9980	dopey family member 2	0.000552	2	4.77	4.63	4.68	4.87	5.01	4.91	4.95	4.79
TC1101891	DPAGT1	1798	dolichyl-phosphate (UDP-N-acetylgluc	0.000253	2	4.30	4.35	4.37	4.50	4.62	4.56	4.50	4.36
TC0301044	DPH3	285381	DPH3, KTI11 homolog (S. cerevisiae)	5.26E-07	2	6.93	7.31	7.49	7.55	7.42	7.55	7.44	7.54
TC0102822	DPM3	54344	dolichyl-phosphate mannosyltransfera	0.000126	2	4.62	4.67	4.70	4.89	4.96	4.85	4.91	4.84
TC0701122	DPY19L1	23333	dpy-19-like 1 (C. elegans)	1.31E-08	2	3.95	4.29	4.35	4.46	4.56	4.53	4.57	4.52
TC0800436	DPY19L4	286148	dpy-19-like 4 (C. elegans)	0.000628	2	2.76	2.79	2.76	2.79	3.04	2.98	3.03	2.92
TC0800165	DPYSL2	1808	dihydropyrimidinase-like 2	4.35E-08	2	4.43	5.01	4.92	5.45	5.48	5.48	5.32	5.11
TC1100558	DRAP1	10589	DR1-associated protein 1 (negative cof	1.66E-05	2	5.75	6.05	6.12	6.23	6.12	6.13	6.19	6.27
TC1800397	DSC2	1824	desmocollin 2	1.26E-08	2	7.10	6.81	7.59	7.99	7.32	7.72	8.16	8.06
TC0801215	DSCC1	79075	defective in sister chromatid cohesion	0.000401	2	2.32	2.39	2.32	2.48	2.66	2.60	2.55	2.48
TC2100335	DSCR3	10311	Down syndrome critical region gene 3 /	0.000662	2	6.45	6.68	6.85	6.97	6.83	6.87	6.88	6.79
TC2000096	DSTN	11034	destrin (actin depolymerizing factor)	5.83E-11	2	4.51	5.06	5.35	5.34	5.34	5.37	5.43	5.37
TC2000111	DTD1	92675	D-tyrosyl-tRNA deacylase 1 homolog (S	1.88E-09	2	6.31	6.64	6.58	7.09	7.10	7.29	7.22	7.03
TC0101498	DTL	51514	denticleless homolog (Drosophila) /// D	3.22E-09	2	3.14	3.34	3.19	3.75	4.24	4.20	3.94	3.58
TC0501233	DTWD2	285605	DTW domain containing 2	4.37E-05	2	2.92	3.04	3.16	3.12	3.32	3.35	3.14	3.14
TC0103248	DUSP10	11221	dual specificity phosphatase 10	0.000577	2	3.96	4.26	4.18	4.36	4.29	4.26	4.30	4.30
TC0101181	DUSP23	54935	dual specificity phosphatase 23	5.67E-05	2	5.67	5.76	5.78	5.87	5.91	6.00	5.92	5.90
TC1500319	DUT	1854	deoxyuridine triphosphatase	4.83E-09	2	4.72	4.90	4.87	5.21	5.53	5.57	5.41	5.15
TC1200753	DYNLL1	8655	dynein, light chain, LC8-type 1	3.75E-10	2	5.22	5.70	5.71	5.75	5.81	5.76	5.80	5.71
TC2000210	DYNLRB1	83658	dynein, light chain, roadblock-type 1 //	3.87E-11	2	6.22	6.82	6.81	6.91	6.95	6.90	6.83	6.82
TC1101252	E2F8	79733	E2F transcription factor 8	1.69E-07	2	3.25	3.54	3.48	3.77	4.23	4.07	3.95	3.63
TC0800502	EBAG9	9166	estrogen receptor binding site associat	6.84E-10	2	3.99	4.15	4.13	4.27	4.38	4.39	4.54	4.54
TC0X00206	EBP	10682	emopamil binding protein (sterol isom	2.07E-12	2	5.47	5.44	5.40	5.91	6.20	6.19	6.10	5.91
TC1901476	ECH1	1891	enoyl Coenzyme A hydratase 1, peroxis	1.66E-06	2	5.25	5.29	5.37	5.59	5.60	5.52	5.64	5.45
TC0601394	EEF1A1	1915	eukaryotic translation elongation facto	2.28E-07	2	9.69	10.25	10.16	10.36	10.44	10.42	10.36	10.22
TC0900664	EEF1AL3	---	Eukaryotic translation elongation facto	3.09E-09	2	9.03	9.80	9.76	10.01	10.11	10.08	9.99	9.82
TC0201039	EEF1B2	649440 //	eukaryotic translation elongation facto	1.86E-07	2	4.89	5.04	4.92	5.19	5.30	5.31	5.34	5.20
TC0600939	EEF1E1	9521	eukaryotic translation elongation facto	1.43E-06	2	2.60	2.79	2.76	2.99	3.34	3.11	3.21	2.85
TC1901046	EEF2	1938	eukaryotic translation elongation facto	4.77E-05	2	6.54	6.83	6.53	7.11	7.23	7.03	7.00	6.85
TC0101681	EFCAB2	84288	EF-hand calcium binding domain 2 ///	2.66E-07	2	4.40	4.76	5.14	5.10	4.84	5.08	5.21	5.14

TC0800564	EFR3A /// EFR3	23167	EFR3 homolog A (S. cerevisiae) /// Prot	1.19E-07	2	5.69	6.06	5.99	6.22	6.04	6.31	6.34	6.29
TC1501168	EFTUD1	79631	elongation factor Tu GTP binding doma	1.24E-07	2	4.24	4.21	4.23	4.36	4.47	4.46	4.54	4.44
TC0800796	EGR3	1960	early growth response 3	0.000725	2	3.28	4.24	3.47	3.47	3.61	4.14	3.88	4.20
TC0200280	EHBP1	23301	EH domain binding protein 1 /// EH do	2.85E-06	2	3.79	3.86	3.89	4.00	4.04	4.00	4.06	3.97
TC1100975	EI24	9538	etoposide induced 2.4 mRNA	8.80E-09	2	4.20	4.25	4.15	4.37	4.54	4.61	4.55	4.46
TC1500320	EID1	23741	EP300 interacting inhibitor of differenti	3.07E-07	2	6.94	7.66	7.79	8.04	7.96	7.88	8.04	7.80
TC0X00808	EIF1AX /// EIF1	1964	eukaryotic translation initiation factor	4.19E-05	2	5.63	6.51	6.37	6.47	6.74	6.95	6.78	6.56
TC0300708	EIF2A	83939	eukaryotic translation initiation factor	7.56E-05	2	3.77	4.27	4.08	4.26	4.33	4.30	4.47	4.27
TC0700993	EIF2AK1	27102	eukaryotic translation initiation factor	0.000119	2	6.07	6.16	6.18	6.62	6.69	6.58	6.50	6.26
TC1500221	EIF2AK4	440275	eukaryotic translation initiation factor	9.11E-11	2	3.84	3.92	3.82	4.10	4.25	4.30	4.41	4.19
TC1400313	EIF2S1	1965	eukaryotic translation initiation factor	6.13E-07	2	4.86	5.35	5.34	5.76	5.91	5.83	5.93	5.64
TC0700020	EIF3B	8662	eukaryotic translation initiation factor	1.73E-05	2	4.57	4.56	4.56	4.65	4.78	4.74	4.78	4.70
TC1600296	EIF3C	8663	eukaryotic translation initiation factor	8.03E-08	2	5.73	5.98	5.68	6.16	6.33	6.34	6.44	6.20
TC1600965	EIF3CL /// EIF3	728689 //	eukaryotic translation initiation factor	2.51E-07	2	5.58	5.78	5.53	5.94	6.07	6.09	6.16	5.97
TC0801193	EIF3E	3646	eukaryotic translation initiation factor	3.46E-12	2	4.58	6.36	6.03	6.48	6.70	6.76	6.58	6.13
TC2200265	EIF3EIP	51386	eukaryotic translation initiation factor	2.79E-06	2	6.98	7.02	6.80	7.40	7.52	7.57	7.50	7.28
TC0801206	EIF3H	8667	eukaryotic translation initiation factor	4.21E-07	2	6.51	7.10	6.87	7.05	7.05	7.18	7.31	7.15
TC1500293	EIF3J	8669	eukaryotic translation initiation factor	8.44E-09	2	5.97	6.06	6.04	6.25	6.30	6.39	6.51	6.38
TC1900507	EIF3K	27335	eukaryotic translation initiation factor	0.000153	2	7.78	8.17	8.01	8.17	8.26	8.23	8.29	8.17
TC1100257	EIF3M	10480	eukaryotic translation initiation factor	2.94E-15	2	5.38	5.84	6.18	6.72	6.55	6.41	6.54	6.24
TC1700101	EIF4A1 /// SNO	1973 ///	eukaryotic translation initiation factor	0.000551	2	5.63	5.76	5.63	5.93	5.95	5.91	5.86	5.85
TC1200360	EIF4B	1975	eukaryotic translation initiation factor	5.76E-06	2	7.54	8.11	7.87	8.06	8.13	8.06	8.11	7.95
TC0401136	EIF4E	1977	eukaryotic translation initiation factor	0.00042	2	6.20	6.14	6.24	6.35	6.35	6.31	6.31	6.29
TC0201185	EIF4E2	9470	eukaryotic translation initiation factor	0.000512	2	6.76	6.73	6.89	7.01	6.91	6.95	6.96	6.95
TC1000315	EIF4EBP2	1979	eukaryotic translation initiation factor	0.000199	2	7.56	7.93	7.68	7.91	7.90	8.02	7.94	8.01
TC1900021	ELA2	1991	elastase 2, neutrophil	6.63E-11	2	3.91	4.82	4.48	5.41	6.01	5.91	5.47	4.96
TC1901121	ELAVL1	1994	ELAV (embryonic lethal, abnormal visio	2.32E-06	2	5.94	6.13	6.06	6.30	6.33	6.28	6.26	6.29
TC1300426	ELF1	1997	E74-like factor 1 (ets domain transcript	3.34E-07	2	7.61	7.79	7.79	7.88	7.72	7.99	8.03	8.03
TC0X00889	ELK1	2002	ELK1, member of ETS oncogene family	0.000356	2	4.46	4.64	4.61	4.63	4.70	4.70	4.64	4.68
TC0501157	ELL2	22936	elongation factor, RNA polymerase II, 2	0.000387	2	4.83	5.35	5.24	5.47	5.42	5.48	5.51	5.37
TC0102185	ELOVL1	64834	elongation of very long chain fatty acid	3.78E-05	2	5.59	5.48	5.63	5.68	5.70	5.63	5.61	5.57
TC0501007	ELOVL7	79993	ELOVL family member 7, elongation of	0.000413	2	3.66	4.09	3.99	4.37	4.64	4.68	4.36	4.34
TC1100251	ELP4	26610	elongation protein 4 homolog (S. cerev	0.000163	2	3.52	3.45	3.57	3.59	3.67	3.67	3.81	3.60
TC0400358	ENOPH1	58478	enolase-phosphatase 1 /// Enolase-pho	2.84E-10	2	3.88	4.12	3.98	4.44	4.77	4.67	4.75	4.51

TC0X01236	ENOX2	10495	ecto-NOX disulfide-thiol exchanger 2	0.000468	2	3.85	4.00	3.97	4.16	4.20	4.15	4.38	4.20
TC0200636	EPB41L5	57669	erythrocyte membrane protein band 4.	7.97E-07	2	3.68	3.95	3.72	3.87	3.81	4.10	4.04	4.10
TC0101561	EPHX1	2052	epoxide hydrolase 1, microsomal (xeno	4.67E-07	2	3.86	4.04	3.92	4.05	4.18	4.12	4.06	3.92
TC0103239	EPRS	2058	glutamyl-prolyl-tRNA synthetase	1.70E-06	2	3.77	4.09	4.02	4.34	4.64	4.55	4.69	4.41
TC2100341	ERG	2078	v-ets erythroblastosis virus E26 oncoge	1.20E-11	2	4.00	5.37	4.47	5.12	5.85	5.88	5.52	4.96
TC2000223	ERGIC3	51614	ERGIC and golgi 3 /// Endoplasmic retic	3.81E-08	2	5.04	5.53	5.49	5.75	5.79	5.67	5.76	5.50
TC0900769	ERMP1	79956	endoplasmic reticulum metallopeptida	0.00014	2	3.97	3.96	4.01	4.05	4.10	4.16	4.21	4.18
TC1200704	ERP29	10961	endoplasmic reticulum protein 29	4.67E-10	2	4.36	4.37	4.39	4.75	4.78	4.87	4.91	4.79
TC0800172	ESCO2	157570	establishment of cohesion 1 homolog	0.000129	2	2.68	2.76	2.75	2.95	3.19	3.10	3.10	3.02
TC2000562	ESF1	51575	ESF1, nucleolar pre-rRNA processing pr	4.50E-09	2	3.55	3.85	3.74	4.11	4.33	4.31	4.61	4.25
TC1501123	ETFA	2108	electron-transfer-flavoprotein, alpha p	0.000262	2	5.09	5.58	5.63	5.91	5.91	5.86	5.81	5.76
TC1901738	ETFB	2109	electron-transfer-flavoprotein, beta po	4.19E-11	2	5.89	6.20	6.21	6.55	6.50	6.48	6.48	6.38
TC1901561	ETHE1	23474	ethylmalonic encephalopathy 1	5.44E-08	2	4.32	4.86	4.89	5.06	5.39	5.20	4.95	4.69
TC1101958	ETS1	2113	v-ets erythroblastosis virus E26 oncoge	1.66E-05	2	5.68	6.38	6.15	6.29	6.41	6.43	6.42	6.20
TC1600924	EXOD1	112479	exonuclease domain containing 1 /// e	3.87E-07	2	2.99	3.04	3.00	3.17	3.39	3.42	3.47	3.35
TC0701733	EZH2	2146	enhancer of zeste homolog 2 (Drosoph	8.74E-06	2	3.62	3.77	3.68	3.87	4.13	4.11	4.17	3.91
TC0600930	F13A1	2162	coagulation factor XIII, A1 polypeptide	4.58E-07	2	4.43	4.96	4.73	6.07	6.36	6.50	5.92	5.90
TC1101467	FADS3 /// FAD	3995 ///	fatty acid desaturase 3 /// fatty acid de	9.72E-05	2	4.30	4.37	4.29	4.38	4.52	4.51	4.47	4.40
TC0102244	FAF1	11124	Fas (TNFRSF6) associated factor 1 /// F	6.42E-06	2	3.84	3.98	4.11	4.24	4.34	4.28	4.28	4.17
TC1500541	FAH	2184	fumarylacetoacetate hydrolase (fumar	3.67E-05	2	4.72	4.84	4.81	4.94	5.00	4.97	4.88	4.82
TC1500570	FAM103A1	83640	family with sequence similarity 103, me	3.55E-07	2	6.91	7.21	7.33	7.31	7.20	7.49	7.55	7.60
TC0901036	FAM108B1	51104	family with sequence similarity 108, me	2.17E-09	2	4.30	4.55	4.61	4.80	4.72	4.66	4.72	4.67
TC2000012	FAM110A	83541	family with sequence similarity 110, me	0.000214	2	5.26	5.39	5.42	5.51	5.48	5.50	5.51	5.52
TC0701056	FAM126A	84668	family with sequence similarity 126, me	4.70E-09	2	4.96	5.13	5.37	5.53	5.41	5.51	5.57	5.63
TC0201936	FAM128A	729985 //	family with sequence similarity 128, me	1.97E-06	2	5.79	5.95	5.85	6.04	6.11	6.10	6.07	6.04
TC0200677	FAM128B	80097	family with sequence similarity 128, me	5.77E-11	2	5.25	5.61	5.57	5.68	5.77	5.74	5.76	5.67
TC1400463	FAM14B	122509	family with sequence similarity 14, mer	4.71E-05	2	4.64	4.74	4.65	4.80	4.90	4.94	4.85	4.78
TC0101677	FAM152A /// C	731151 //	family with sequence similarity 152, me	2.34E-08	2	4.94	5.01	5.27	5.35	5.28	5.35	5.38	5.36
TC2200708	FAM152B	27351	family with sequence similarity 152, me	1.91E-06	2	5.49	6.01	6.03	6.23	6.16	6.11	6.03	6.09
TC0300551	FAM162A	26355	family with sequence similarity 162, me	1.24E-13	2	3.78	4.04	3.93	4.35	4.62	4.70	4.68	4.59
TC2100096	FAM165B	54065	family with sequence similarity 165, me	2.51E-05	2	4.34	4.39	4.44	4.60	4.70	4.67	4.78	4.64
TC0101314	FAM20B	9917	family with sequence similarity 20, mer	0.000397	2	4.61	4.88	4.63	4.88	4.97	4.98	5.04	4.96
TC0900232	FAM27A	548321	family with sequence similarity 27, mer	6.91E-05	2	5.35	5.43	5.41	5.63	5.56	5.70	5.49	5.40
TC1900282	FAM32A	26017	family with sequence similarity 32, mer	1.04E-06	2	6.80	6.94	7.00	7.17	7.12	7.15	7.22	7.28

TC1701565	FAM33A /// N	348235	family with sequence similarity 33, mer	8.83E-14	2	4.19	4.73	4.98	5.40	5.67	5.64	5.62	5.28
TC0701589	FAM3C	10447	family with sequence similarity 3, mem	1.84E-06	2	4.04	4.31	4.27	4.32	4.34	4.33	4.42	4.29
TC0601420	FAM46A	55603	family with sequence similarity 46, mer	2.92E-12	2	5.27	5.21	5.37	5.62	5.69	5.79	5.80	5.66
TC0X00704	FAM50A	9130	family with sequence similarity 50, mer	5.41E-06	2	6.35	6.57	6.28	6.57	6.74	6.73	6.75	6.63
TC0X01367	FAM58A	651831 //	family with sequence similarity 58, mer	0.000438	2	4.89	5.00	5.22	5.14	5.17	5.10	5.14	5.14
TC1201080	FAM60A	58516	family with sequence similarity 60, mer	4.07E-13	2	4.38	4.94	4.98	5.28	5.31	5.29	5.28	5.09
TC0701806	FAM62B	57488	family with sequence similarity 62 (C2	3.69E-09	2	5.84	5.84	5.90	6.17	6.27	6.32	6.45	6.29
TC0101458	FAM72A	729533	family with sequence similarity 72, mer	3.25E-05	2	3.79	3.93	3.88	3.93	4.13	4.05	4.08	3.98
TC0100897	FAM72B	653820	family with sequence similarity 72, mer	6.96E-05	2	3.81	3.80	3.81	3.88	4.12	4.10	4.08	3.98
TC1501025	FAM96A	84191	family with sequence similarity 96, mer	1.43E-07	2	6.43	6.89	7.11	7.27	7.16	7.19	7.28	7.20
TC1601167	FAM96B	51647	family with sequence similarity 96, mer	0.000487	2	5.70	5.73	5.68	6.03	6.05	5.93	5.97	5.88
TC0201423	FAM98A	25940	family with sequence similarity 98, mer	2.30E-05	2	3.83	3.82	3.96	4.11	4.15	4.09	4.25	4.09
TC1500215	FAM98B	283742	family with sequence similarity 98, mer	8.34E-05	2	3.35	3.31	3.31	3.37	3.54	3.55	3.58	3.55
TC1500607	FANCI	55215	Fanconi anemia, complementation gro	5.63E-07	2	3.33	3.42	3.33	3.61	4.03	3.97	3.91	3.65
TC0201537	FANCL	55120	Fanconi anemia, complementation gro	0.000244	2	3.25	3.38	3.50	3.56	3.52	3.57	3.69	3.62
TC1200223	FAR2	55711	fatty acyl CoA reductase 2	9.10E-05	2	7.16	7.41	7.68	7.83	7.92	7.75	7.63	7.39
TC1901218	FARSA	2193	phenylalanyl-tRNA synthetase, alpha su	2.54E-06	2	5.10	5.26	5.19	5.38	5.45	5.45	5.45	5.35
TC0202348	FARSB	10056	phenylalanyl-tRNA synthetase, beta su	5.45E-06	2	3.44	3.61	3.57	3.66	3.82	3.79	3.75	3.64
TC1901497	FBL	2091	fibrillarin	5.72E-09	2	5.58	6.12	5.72	6.46	6.74	6.76	6.73	6.30
TC0601473	FBXL4	26235	F-box and leucine-rich repeat protein 4	1.15E-05	2	4.69	4.62	4.86	4.96	4.91	4.84	4.89	4.83
TC0800003	FBXO25	26260	F-box protein 25	0.000248	2	3.79	3.89	3.97	4.00	3.99	3.99	4.18	4.11
TC0300937	FBXO45	200933	F-box protein 45	5.24E-06	2	4.49	4.84	4.81	4.89	5.04	5.09	5.07	4.89
TC0601696	FBXO5	26271	F-box protein 5 /// F-box only protein	3.81E-08	2	3.45	3.70	3.59	4.02	4.41	4.28	4.20	3.91
TC1100464	FEN1	2237	flap structure-specific endonuclease 1	1.83E-09	2	4.11	4.18	4.06	4.35	4.63	4.68	4.58	4.27
TC0800887	FGFR1	2260	fibroblast growth factor receptor 1 (fm	0.000503	2	4.04	3.96	3.98	3.98	4.12	4.07	4.02	3.98
TC0103403	FH	2271	fumarate hydratase	1.68E-06	2	3.67	3.87	3.91	4.15	4.25	4.18	4.33	4.05
TC0701200	FIGNL1	63979	fidgetin-like 1	6.46E-05	2	3.00	3.10	3.04	3.13	3.26	3.28	3.22	3.19
TC1400817	FKBP3	2287	FK506 binding protein 3, 25kDa	3.36E-10	2	6.70	7.59	7.70	7.74	7.71	7.81	7.83	7.69
TC1200018	FKBP4	2288	FK506 binding protein 4, 59kDa	6.73E-05	2	4.39	4.51	4.37	4.84	4.87	4.70	4.81	4.72
TC1501061	FLJ11506	79719	hypothetical protein FLJ11506	0.000113	2	4.69	4.97	5.03	5.10	5.01	5.05	5.10	5.03
TC1201610	FLJ20674	54621	hypothetical protein FLJ20674	1.52E-08	2	4.49	4.32	4.27	4.86	4.79	4.93	4.99	4.79
TC0300334	FLNB	2317	filamin B, beta (actin binding protein 2	0.000415	2	4.13	4.10	4.26	4.58	4.33	4.31	4.53	4.48
TC1300367	FLT3	2322	fms-related tyrosine kinase 3 /// FL cyt	1.51E-07	2	3.17	3.18	3.20	3.43	3.30	3.37	3.73	3.49
TC0800262	FNTA	2339	farnesyltransferase, CAAX box, alpha	3.19E-05	2	5.72	5.83	6.00	6.06	5.98	6.06	6.14	6.09

TC1700864	FOXK2 /// Q6Z	3607	forkhead box K2 /// Forkhead box prot	2.12E-05	2	5.10	5.22	5.30	5.45	5.52	5.36	5.39	5.24
TC1200874	FOXM1	2305	forkhead box M1	0.000309	2	4.05	4.11	4.01	4.14	4.41	4.29	4.30	4.16
TC0901075	FRMD3	257019	FERM domain containing 3 /// FERM d	1.75E-08	2	3.59	3.79	3.71	4.12	4.19	4.27	4.29	4.37
TC1600438	FTO	79068	fat mass and obesity associated	4.94E-05	2	4.12	4.12	4.07	4.25	4.33	4.42	4.46	4.28
TC0601658	FUCA2	2519	fucosidase, alpha-L- 2, plasma /// Plas	3.25E-09	2	3.83	3.99	3.99	4.34	4.42	4.41	4.53	4.31
TC1100766	FUT4	2526	fucosyltransferase 4 (alpha (1,3) fucosy	4.80E-12	2	3.90	5.20	4.96	5.49	5.90	5.89	5.68	5.13
TC1400305	FUT8	2530	fucosyltransferase 8 (alpha (1,6) fucosy	1.56E-05	2	3.64	3.74	3.71	3.95	4.05	4.01	4.04	3.91
TC0300945	FYTTD1	84248	forty-two-three domain containing 1	3.84E-07	2	5.02	5.72	5.62	5.73	5.69	5.81	5.92	5.81
TC0202261	FZD5	7855	frizzled homolog 5 (Drosophila)	0.000184	2	4.53	4.75	4.79	4.73	4.89	4.88	4.83	4.69
TC0500621	G3BP1	10146	GTPase activating protein (SH3 domain	1.46E-11	2	5.36	5.10	5.35	5.75	5.81	5.80	5.81	5.65
TC0401048	G3BP2	9908	GTPase activating protein (SH3 domain	4.49E-06	2	5.24	5.60	5.52	5.67	5.57	5.66	5.70	5.69
TC2100046	GABPA	2551	GA binding protein transcription factor	0.000738	2	5.81	5.90	5.97	6.05	5.93	6.02	6.12	6.12
TC1500947	GABPB2	2553	GA binding protein transcription factor	7.73E-07	2	4.65	5.01	5.18	5.21	5.20	5.23	5.25	5.20
TC0200187	GALM	130589	galactose mutarotase (aldose 1-epimer	4.09E-07	2	4.33	4.57	4.31	4.65	4.83	5.16	5.23	5.09
TC0700155	GARS	2617	glycyl-tRNA synthetase /// Glycyl-tRNA	5.13E-05	2	4.33	4.50	4.57	4.63	4.69	4.71	4.84	4.71
TC2100315	GART	2618	phosphoribosylglycinamide formyltran	0.000646	2	4.13	4.34	4.38	4.43	4.57	4.50	4.50	4.34
TC0900304	GCNT1	2650	glucosaminyl (N-acetyl) transferase 1,	6.25E-08	2	4.80	5.63	5.41	5.54	5.78	5.61	5.61	5.44
TC01r00012	GCUD2	653573	gastric cancer up-regulated-2	0.000509	2	3.68	3.72	3.69	3.81	4.06	4.03	4.02	3.83
TC1700877	GEMIN4	50628	gem (nuclear organelle) associated pro	8.13E-05	2	4.35	4.39	4.35	4.38	4.62	4.57	4.51	4.38
TC0200071	GEN1	348654	Gen homolog 1, endonuclease (Drosop	0.000917	2	3.37	3.31	3.30	3.37	3.63	3.58	3.63	3.48
TC0102438	GFI1	2672	growth factor independent 1 transcript	1.47E-07	2	3.84	4.24	4.17	4.32	4.65	4.53	4.38	4.23
TC0900661	GFI1B	8328	growth factor independent 1B transcri	0.000113	2	4.58	4.55	4.46	4.87	4.92	5.05	5.00	5.02
TC0201589	GFPT1	2673	glutamine-fructose-6-phosphate trans	2.43E-06	2	4.57	4.74	4.71	4.92	5.02	5.08	5.12	4.98
TC0800973	GGH	8836	gamma-glutamyl hydrolase (conjugase,	7.71E-12	2	3.45	4.03	4.12	4.57	5.01	4.84	4.65	4.31
TC0700884	GIMAP1 /// GI	170575 //	GTPase, IMAP family member 1 /// GT	9.46E-07	2	5.79	5.93	6.66	6.73	5.88	6.23	6.72	6.72
TC0501187	GIN1	54826	gypsy retrotransposon integrase 1 ///	2.46E-05	2	3.68	4.13	4.41	4.33	4.34	4.40	4.29	4.36
TC2000147	GINS1	9837	GINS complex subunit 1 (Psf1 homolog	6.33E-05	2	3.77	3.84	3.84	3.93	4.24	4.16	4.06	3.93
TC1601310	GINS2	51659	GINS complex subunit 2 (Psf2 homolog	0.000214	2	3.06	3.05	2.97	3.17	3.40	3.37	3.34	3.16
TC0102139	GJA9 /// MYCB	81025 ///	gap junction protein, alpha 9, 59kDa //	3.89E-11	2	4.87	5.07	5.29	5.40	5.40	5.39	5.37	5.37
TC0601227	GLO1	2739	glyoxalase I	2.71E-07	2	3.54	3.66	3.61	4.02	4.07	3.99	4.10	4.04
TC1000689	GLRX3	10539	glutaredoxin 3	1.31E-05	2	4.23	4.46	4.49	4.56	4.67	4.63	4.71	4.64
TC1201113	GLT8D3	283464	glycosyltransferase 8 domain containin	0.000161	2	4.06	4.03	4.22	4.18	4.18	4.28	4.38	4.42
TC1900675	GLTSCR2 /// S	29997	glioma tumor suppressor candidate re	7.74E-06	2	5.71	5.88	5.68	6.00	6.08	5.98	6.17	6.02
TC0100331	GMEB1	10691	glucocorticoid modulatory element bin	1.37E-07	2	6.22	6.39	6.21	6.45	6.43	6.51	6.61	6.54

TC0600129	GMNN	51053	geminin, DNA replication inhibitor ///	7.86E-07	2	3.47	3.63	3.62	3.90	4.08	4.02	4.12	3.90
TC0300733	GMPS	8833	guanine monphosphate synthetase	2.73E-15	2	4.39	4.96	4.91	5.56	5.83	5.81	5.75	5.39
TC2200115	GNAZ	2781	guanine nucleotide binding protein (G	0.000421	2	5.91	6.26	6.22	6.32	6.47	6.41	6.34	6.29
TC0501574	GNB2L1 /// SN	647756 //	guanine nucleotide binding protein (G	0.0003	2	5.85	6.12	6.19	6.31	6.37	6.21	6.28	6.04
TC0301784	GNB4	59345	guanine nucleotide binding protein (G	2.80E-05	2	6.03	6.07	6.35	6.39	6.20	6.36	6.45	6.55
TC0700481	GNG11	2791	guanine nucleotide binding protein (G	4.62E-07	2	4.01	4.90	4.47	5.55	5.92	6.09	5.60	5.64
TC0102389	GNG5 /// CTBS	2787 /// 1	guanine nucleotide binding protein (G	0.000371	2	7.31	7.55	7.73	7.72	7.63	7.75	7.64	7.71
TC0102126	GNL2	29889	guanine nucleotide binding protein-like	6.30E-05	2	3.78	3.85	3.80	4.08	4.13	4.08	4.30	4.17
TC0300312	GNL3	26354	guanine nucleotide binding protein-like	0.000136	2	4.00	4.11	4.14	4.16	4.28	4.28	4.45	4.21
TC0101610	GNPAT	8443	glyceronephosphate O-acyltransferase	0.000414	2	4.95	5.01	5.30	5.37	5.32	5.21	5.29	5.06
TC0200856	GORASP2	26003	golgi reassembly stacking protein 2, 55	6.84E-10	2	5.86	5.94	5.94	6.42	6.44	6.44	6.55	6.31
TC2200036	GP1BB /// SEPT	5413 /// 2	septin 5 /// glycoprotein Ib (platelet), b	1.58E-08	2	5.42	5.88	5.59	5.72	5.89	5.85	5.75	5.67
TC0300129	GPD1L	23171	glycerol-3-phosphate dehydrogenase 1	1.90E-05	2	3.98	4.02	4.01	4.13	4.22	4.19	4.26	4.17
TC0200802	GPD2	2820	glycerol-3-phosphate dehydrogenase 2	3.98E-08	2	5.30	5.63	5.66	5.95	6.13	6.19	6.21	5.99
TC1900418	GPI	2821	glucose phosphate isomerase	9.01E-08	2	5.59	6.65	6.52	6.90	7.26	7.14	6.88	6.55
TC0200135	GPN1	11321	GPN-loop GTPase 1	8.99E-08	2	3.93	4.12	4.11	4.34	4.51	4.58	4.63	4.40
TC0101639	GPR137B	7107	G protein-coupled receptor 137B /// In	2.83E-08	2	3.90	3.77	4.29	4.90	4.25	4.11	4.50	4.41
TC0301666	GPR171	29909	G protein-coupled receptor 171	0.000188	2	2.77	2.90	2.79	3.14	3.12	3.08	3.40	3.14
TC0100793	GPSM2	29899	G-protein signaling modulator 2 (AGS3-	1.21E-05	2	4.04	3.88	4.02	4.28	4.34	4.37	4.49	4.34
TC1900250	GPSN2	9524	glycoprotein, synaptic 2	2.09E-08	2	5.68	5.94	5.80	5.98	6.21	6.08	6.02	5.94
TC0301205	GPX1	2876	glutathione peroxidase 1	6.70E-05	2	5.58	5.70	5.70	6.04	6.25	6.19	6.07	6.00
TC0401021	GRSF1	2926	G-rich RNA sequence binding factor 1	2.42E-10	2	4.80	5.15	5.21	5.28	5.33	5.25	5.29	5.19
TC1100602	GSTP1	2950	glutathione S-transferase pi	8.06E-11	2	5.65	6.12	5.92	6.40	6.74	6.72	6.63	6.33
TC1401033	GTF2A1	2957	general transcription factor IIA, 1, 19/3	0.000271	2	7.56	7.77	7.83	7.92	7.81	7.94	7.92	7.97
TC0300540	GTF2E1	2960	general transcription factor IIE, polype	3.74E-05	2	5.35	5.57	5.80	5.85	5.67	5.76	5.82	5.78
TC0800846	GTF2E2	2961	general transcription factor IIE, polype	7.22E-05	2	5.72	6.00	6.18	6.18	6.05	6.12	6.18	6.09
TC1901084	GTF2F1	2962	general transcription factor IIF, polype	0.000312	2	6.00	6.26	6.16	6.26	6.24	6.27	6.39	6.39
TC1300049	GTF3A	---	Transcription factor IIIA (Factor A) (TFII	6.08E-12	2	6.04	6.67	6.77	7.00	6.97	6.91	7.02	6.86
TC0900657	GTF3C4	9329	general transcription factor IIIC, polype	9.50E-07	2	4.10	4.18	4.23	4.42	4.27	4.30	4.36	4.31
TC0600641	GTF3C6	112495	general transcription factor IIIC, polype	4.21E-12	2	5.00	6.00	6.23	6.61	6.75	6.70	6.68	6.41
TC1000005	GTPBP4	23560	GTP binding protein 4 /// Nucleolar GT	5.89E-05	2	3.63	3.81	3.60	3.81	3.94	3.90	4.03	3.86
TC1201267	GTSF1	121355	gametocyte specific factor 1	0.000572	2	3.81	4.18	4.19	4.26	4.31	4.44	4.38	4.23
TC0701270	GUSB	2990	glucuronidase, beta /// Beta-glucuroni	5.30E-05	2	5.10	5.27	5.42	5.57	5.59	5.54	5.48	5.33
TC2200262	H1F0	3005	H1 histone family, member 0	1.73E-11	2	4.62	5.74	5.36	5.86	6.22	6.44	6.28	5.79

TC0301548	H1FX	8971	H1 histone family, member X	5.46E-05	2	4.38	4.55	4.39	4.70	4.81	4.79	4.79	4.82
TC0701179	H2AFV	94239	H2A histone family, member V	1.35E-06	2	7.42	7.52	7.57	7.78	7.86	7.93	7.92	7.84
TC1101890	H2AFX	3014	H2A histone family, member X	1.45E-06	2	5.16	5.47	5.36	5.61	5.81	5.77	5.61	5.49
TC2100161	H2BFS	---	Histone H2B type F-S (H2B.s) (H2B/s). [	3.30E-12	2	7.62	7.80	8.10	8.56	8.73	8.84	8.51	8.46
TC0400448	HADH	3033	hydroxyacyl-Coenzyme A dehydrogena	4.38E-06	2	3.62	3.65	3.65	3.69	3.93	3.83	3.85	3.76
TC0101095	HAX1	10456	HCLS1 associated protein X-1	0.0009	2	5.41	5.43	5.44	5.51	5.55	5.62	5.60	5.68
TC1200650	HCFC2	29915	host cell factor C2	8.53E-05	2	4.31	4.49	4.57	4.72	4.88	4.81	4.93	4.75
TC0700222	hCG_18290	644907	hCG18290	9.83E-07	2	7.87	7.83	7.75	8.27	8.42	8.46	8.53	8.28
TC0500711	hCG_1995786	653147 //	hCG1995786 /// ribosomal protein L26	5.15E-05	2	5.31	5.73	5.80	5.80	5.82	5.89	5.82	5.86
TC0201062	hCG_2024410	729020 //	rcRPE /// ribulose-5-phosphate-3-epim	3.93E-06	2	4.75	4.98	5.01	5.26	5.49	5.47	5.40	5.15
TC1201304	hCG_2026038	441050 //	hCG2026038 /// prostaglandin E synth	1.31E-06	2	5.07	5.18	5.39	5.36	5.34	5.40	5.41	5.36
TC0102866	HDGF	3068	hepatoma-derived growth factor (high-	1.17E-06	2	4.63	4.56	4.61	4.69	4.86	4.80	4.76	4.69
TC1501193	HDGFRP3	50810	hepatoma-derived growth factor, relat	0.000115	2	3.80	3.98	3.99	4.19	4.11	4.14	4.06	4.05
TC1000461	HELLS	3070	helicase, lymphoid-specific /// Lympho	6.21E-07	2	2.93	3.10	3.02	3.27	3.65	3.54	3.47	3.24
TC0500271	HEXB	3074	hexosaminidase B (beta polypeptide)	1.73E-10	2	5.41	5.35	5.46	5.78	5.68	5.91	5.91	5.85
TC0700670	HIG2 /// Q96H	29923	hypoxia-inducible protein 2 /// HIG2 pr	0.000923	2	3.95	3.97	4.03	4.06	4.07	4.17	4.15	4.10
TC0500736	HIGD2A	192286	HIG1 domain family, member 2A	4.62E-07	2	4.88	5.35	5.40	5.76	5.74	5.66	5.62	5.61
TC0501263	HINT1	3094	histidine triad nucleotide binding prote	0.000243	2	4.65	4.71	4.81	4.87	4.95	4.94	5.00	4.97
TC0600704	HINT3	135114	histidine triad nucleotide binding prote	9.81E-09	2	4.32	4.63	4.84	4.88	4.79	4.87	4.99	4.95
TC0601052	HIST1H1B	3009	histone cluster 1, H1b	1.99E-08	2	3.89	4.29	4.09	4.49	5.06	4.88	4.61	4.40
TC0601027	HIST1H1D	3007	histone cluster 1, H1d	1.29E-09	2	4.26	4.59	4.48	4.98	5.50	5.48	5.21	4.93
TC0600148	HIST1H1E	3008	histone cluster 1, H1e	2.21E-07	2	5.79	5.74	5.72	6.31	6.71	6.66	6.40	6.26
TC0600153	HIST1H2AB ///	8335 ///	histone cluster 1, H2ab /// histone clus	7.73E-19	2	6.05	7.71	7.71	8.56	9.20	9.44	8.87	8.45
TC0601025	HIST1H2AD	3013	histone cluster 1, H2ad	4.93E-13	2	3.88	3.97	4.19	4.56	4.68	4.92	4.62	4.46
TC0600173	HIST1H2AG	8969	histone cluster 1, H2ag	1.63E-07	2	2.89	3.24	3.43	4.18	4.14	4.22	3.98	4.13
TC0600189	HIST1H2AG ///	8969 ///	histone cluster 1, H2ag /// histone clus	6.16E-10	2	2.91	3.47	3.27	3.76	4.41	4.44	3.93	3.65
TC0601056	HIST1H2AG ///	8969 ///	histone cluster 1, H2ag /// histone clus	6.39E-09	2	3.86	4.39	4.17	4.73	5.35	5.29	4.91	4.54
TC0600185	HIST1H2AG ///	8969 ///	histone cluster 1, H2ag /// histone clus	1.12E-11	2	3.73	4.51	4.72	5.24	5.43	5.91	5.35	5.34
TC0601049	HIST1H2AJ	8331	histone cluster 1, H2aj	1.28E-11	2	5.27	5.87	5.76	6.25	6.74	6.78	6.38	5.98
TC0601022	HIST1H2BC	8347	histone cluster 1, H2bc	2.87E-06	2	7.69	7.52	7.53	7.86	8.06	8.33	7.96	8.10
TC0600151	HIST1H2BC ///	8347 ///	histone cluster 1, H2bc /// histone clus	2.79E-15	2	5.98	5.74	6.10	6.71	7.10	7.36	7.01	6.87
TC0601026	HIST1H2BC ///	8347 ///	histone cluster 1, H2bc /// histone clus	2.42E-16	2	5.07	5.48	5.60	6.36	6.78	6.97	6.53	6.22
TC0600150	HIST1H2BC ///	8347 ///	histone cluster 1, H2bc /// histone clus	1.60E-13	2	7.88	8.18	8.36	8.70	8.96	9.17	8.82	8.74
TC0600149	HIST1H2BD	3017	histone cluster 1, H2bd	3.02E-14	2	6.86	7.43	7.75	8.10	8.11	8.46	8.14	8.03

TC0600156	HIST1H2BH	8345	histone cluster 1, H2bh	6.74E-16	2	4.42	5.10	5.11	5.71	6.06	6.34	5.87	5.78
TC0601041	HIST1H2BJ	8970	histone cluster 1, H2bj	2.11E-12	2	3.47	3.84	4.01	4.41	4.61	4.63	4.29	4.26
TC0601042	HIST1H2BK	85236	histone cluster 1, H2bk	5.30E-10	2	7.68	7.86	8.27	8.77	8.86	8.96	8.61	8.63
TC0601048	HIST1H2BL	8340	histone cluster 1, H2bl	1.06E-11	2	3.89	4.04	4.12	4.45	4.76	4.78	4.44	4.44
TC0600186	HIST1H2BM	8342	histone cluster 1, H2bm	4.90E-13	2	2.78	3.66	3.46	4.65	5.54	5.51	4.88	4.31
TC0600188	HIST1H2BN	8341	histone cluster 1, H2bn	5.46E-08	2	3.27	3.32	3.35	3.43	3.55	3.73	3.55	3.53
TC0600190	HIST1H2BO	8348	histone cluster 1, H2bo	4.13E-11	2	4.25	4.40	4.39	4.79	5.11	5.24	4.88	4.81
TC0600157	HIST1H2BO ///	8348 ///	histone cluster 1, H2bo /// histone clus	1.97E-12	2	5.24	5.48	5.72	6.06	6.37	6.45	6.09	5.92
TC0601029	HIST1H3F	8968	histone cluster 1, H3f	5.15E-08	2	4.08	4.57	4.55	4.88	5.20	5.35	4.91	4.62
TC0601017	HIST1H3F /// H	8968 ///	histone cluster 1, H3f /// histone cluste	1.35E-08	2	3.42	3.70	3.57	4.09	4.45	4.46	4.19	3.90
TC0600144	HIST1H3F /// H	8968 ///	histone cluster 1, H3f /// histone cluste	3.09E-05	2	2.31	2.56	2.49	2.56	2.87	2.75	2.65	2.56
TC0601024	HIST1H3F /// H	8968 ///	histone cluster 1, H3f /// histone cluste	1.06E-08	2	6.76	6.87	7.28	7.42	7.33	7.79	7.57	7.59
TC0601030	HIST1H3F /// H	8968 ///	histone cluster 1, H3f /// histone cluste	7.93E-09	2	3.40	3.96	4.13	4.65	5.30	5.35	4.61	4.34
TC0601053	HIST1H3F /// H	8968 ///	histone cluster 1, H3f /// histone cluste	9.79E-10	2	3.05	4.00	3.72	4.81	5.58	5.48	4.74	4.39
TC0101000	HIST2H2AA3	8337	histone cluster 2, H2aa3	5.47E-11	2	8.54	9.06	9.48	9.80	9.74	9.64	9.36	9.44
TC0102707	HIST2H2AA3	8337	histone cluster 2, H2aa3	1.90E-05	2	8.59	8.75	8.97	9.43	9.36	9.31	9.02	9.10
TC0102711	HIST2H2AB	317772	histone cluster 2, H2ab	1.65E-07	2	4.04	4.79	5.08	5.39	5.98	5.85	5.37	5.28
TC0101003	HIST2H2AC	8338	histone cluster 2, H2ac	9.57E-06	2	7.53	8.15	8.16	8.30	8.49	8.43	8.26	8.29
TC0600146	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	5.20E-08	2	6.31	6.13	6.04	6.66	7.22	7.30	6.95	6.71
TC0601023	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	2.24E-08	2	3.11	3.33	3.31	3.58	4.17	4.04	3.79	3.66
TC0600152	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	5.00E-10	2	7.00	7.63	7.29	8.05	8.61	8.73	8.44	7.97
TC0601032	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	4.64E-09	2	5.53	5.92	5.52	5.96	6.01	6.71	6.52	6.53
TC0600174	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	1.70E-06	2	4.14	4.26	4.27	4.50	4.69	4.78	4.56	4.40
TC0600187	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	3.72E-07	2	5.46	5.31	5.14	5.62	5.89	5.82	5.63	5.48
TC0601050	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	6.88E-08	2	4.20	4.58	4.52	4.70	4.98	4.95	4.83	4.70
TC0601054	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone clust	4.31E-06	2	2.44	2.92	2.84	3.28	3.65	3.42	3.00	3.03
TC0202407	HJURP	55355	Holliday junction recognition protein	2.39E-07	2	4.32	4.51	4.41	4.67	4.97	4.91	4.77	4.58
TC0301646	HLTF	6596	helicase-like transcription factor	0.00018	2	2.84	3.09	3.06	3.17	3.23	3.12	3.23	3.13
TC2000857	HMG1L1	10357	high-mobility group (nonhistone chrom	1.88E-06	2	3.59	4.03	4.26	4.19	4.28	4.29	4.26	4.17
TC2200159	HMG1L10	---	High mobility group protein 1-like 10 (	1.55E-11	2	4.76	5.59	5.94	5.98	5.91	6.05	5.82	5.78
TC0600317	HMGA1	3159	high mobility group AT-hook 1 /// High	0.00072	2	5.28	5.42	5.42	5.45	5.54	5.47	5.43	5.39
TC1300381	HMGB1	3146	high-mobility group box 1 /// High mob	4.56E-10	2	5.59	5.70	5.87	6.00	6.03	6.02	6.04	5.94
TC0X00662	HMGB3	3149	high-mobility group box 3	3.64E-10	2	4.62	4.94	4.73	5.15	5.59	5.48	5.46	5.03
TC0500673	HMMR	3161	hyaluronan-mediated motility receptor	7.98E-06	2	2.43	2.59	2.53	2.90	3.28	3.09	3.09	2.84

TC1600057	HN1L /// HN1L	90861	hematological and neurological expres	9.08E-06	2	4.66	4.95	4.87	4.93	5.05	5.10	5.09	5.00
TC0501312	HNRNPA0	10949	heterogeneous nuclear ribonucleoprot	0.00044	2	5.37	5.43	5.32	5.47	5.58	5.62	5.69	5.63
TC0500764	HNRNPAB /// H	3182	heterogeneous nuclear ribonucleoprot	5.08E-11	2	5.71	6.17	5.75	6.23	6.48	6.49	6.40	6.21
TC0201442	HNRPLL	92906	heterogeneous nuclear ribonucleoprot	1.23E-05	2	4.72	5.13	5.16	5.25	5.37	5.43	5.42	5.21
TC0300699	HPS3	84343	Hermansky-Pudlak syndrome 3	0.0006	2	5.42	5.33	5.42	5.62	5.50	5.54	5.66	5.58
TC0401090	HPSE	10855	heparanase	1.41E-11	2	5.44	6.10	6.28	7.04	6.82	6.82	6.75	6.29
TC1800116	HRH4	59340	histamine receptor H4	3.44E-05	2	3.41	3.07	3.60	4.55	3.93	4.37	4.68	4.54
TC0801143	HRSP12	10247	heat-responsive protein 12	3.37E-06	2	3.98	3.86	4.17	4.30	4.20	4.19	4.30	4.27
TC0100704	HS2ST1 /// NM	9653	heparan sulfate 2-O-sulfotransferase 1	8.48E-06	2	4.07	4.23	4.43	4.58	4.46	4.56	4.43	4.35
TC0500420	HSD17B4	3295	hydroxysteroid (17-beta) dehydrogena	4.98E-13	2	5.56	5.46	5.51	6.01	5.86	6.08	6.30	6.11
TC1200647	HSP90B1	7184	heat shock protein 90kDa beta (Grp94)	0.000951	2	7.57	7.85	7.55	7.81	8.05	8.12	8.30	7.93
TC2100220	HSPA13	6782	heat shock protein 70kDa family, mem	2.09E-05	2	4.30	4.87	4.61	4.79	4.78	4.75	4.79	4.76
TC0500476	HSPA4	3308	heat shock 70kDa protein 4 /// Heat sh	0.00028	2	5.94	6.46	6.43	6.49	6.42	6.50	6.67	6.54
TC0501326	HSPA9	440490 //	heat shock 70kDa protein 9 (mortalin)	6.46E-08	2	4.77	5.10	4.70	5.38	5.52	5.55	5.68	5.38
TC0501516	HSPC111 /// U	51491	hypothetical protein HSPC111 /// UPF	0.000681	2	3.98	4.10	3.94	4.17	4.28	4.22	4.40	4.19
TC1101514	HSPC152	51504	hypothetical protein HSPC152	6.85E-11	2	7.11	7.27	7.30	7.48	7.49	7.56	7.54	7.54
TC0200960	HSPE1	3336	heat shock 10kDa protein 1 (chaperoni	1.89E-11	2	4.43	5.20	4.69	5.30	5.78	5.79	5.70	5.38
TC1300382	HSPH1	10808	heat shock 105kDa/110kDa protein 1 /	0.000158	2	3.54	4.33	3.89	4.35	4.72	4.45	4.65	4.33
TC0X00595	HTATSF1	27336	HIV-1 Tat specific factor 1	5.63E-06	2	4.40	4.52	4.58	4.85	4.93	4.98	5.04	4.85
TC0901128	IARS	3376	isoleucyl-tRNA synthetase /// Isoleucyl-	1.11E-05	2	3.62	3.72	3.65	3.86	4.12	4.06	4.07	3.85
TC0601422	IBTK	25998	inhibitor of Bruton agammaglobulinem	1.55E-08	2	3.40	3.61	3.68	4.01	4.05	4.04	4.19	4.05
TC0701013	ICA1	3382	islet cell autoantigen 1, 69kDa /// Islet	0.000509	2	3.71	4.06	3.85	4.01	4.25	4.15	4.06	3.86
TC0601336	ICK	22858	intestinal cell (MAK-like) kinase	9.52E-05	2	4.30	4.37	4.32	4.49	4.46	4.54	4.64	4.58
TC0101810	ICMT	23463	isoprenylcysteine carboxyl methyltrans	3.88E-05	2	3.41	3.53	3.53	3.64	3.75	3.68	3.79	3.63
TC1700748	ICT1	3396	immature colon carcinoma transcript 1	5.85E-07	2	4.82	4.99	5.02	5.24	5.43	5.40	5.45	5.17
TC0200023	ID2	3398	inhibitor of DNA binding 2, dominant n	4.00E-15	2	5.23	5.17	5.15	5.34	5.49	5.63	5.63	5.58
TC1001164	IDE	3416	insulin-degrading enzyme /// Insulin-de	7.96E-05	2	3.52	3.75	3.83	3.95	4.06	3.94	3.98	3.81
TC0202273	IDH1	3417	isocitrate dehydrogenase 1 (NADP+), s	3.13E-20	2	4.65	4.71	5.02	5.45	5.36	5.16	5.28	5.02
TC1800452	IER3IP1	51124	immediate early response 3 interacting	9.44E-10	2	4.45	5.94	6.00	6.23	6.34	6.33	6.30	5.98
TC0101334	IER5	51278	immediate early response 5	1.77E-10	2	4.86	4.83	4.72	5.34	5.27	5.39	5.52	5.60
TC0101172	IFI16	3428	interferon, gamma-inducible protein 1	4.10E-06	2	9.14	9.65	9.38	9.34	9.27	9.55	9.70	9.67
TC1900316	IFI30	10437	interferon, gamma-inducible protein 3	5.07E-06	2	9.77	10.17	10.41	10.70	10.39	10.38	10.52	10.41
TC1100010	IFITM1	8519	interferon induced transmembrane pr	0.000898	2	10.44	10.75	10.89	10.95	10.76	10.88	10.88	10.92
TC1101031	IFITM3	10410	interferon induced transmembrane pr	0.000404	2	9.55	10.36	10.17	10.31	10.32	10.60	10.51	10.68

TC0900105	IFT74	80173	intraflagellar transport 74 homolog (Ch	1.88E-05	2	3.65	4.06	4.16	4.14	4.04	4.24	4.33	4.22
TC0400977	IGFBP7	3490	insulin-like growth factor binding prote	5.19E-13	2	4.91	5.24	5.60	5.81	5.80	5.68	5.81	5.64
TC0401019	IGJ	3512	immunoglobulin J polypeptide, linker p	3.93E-05	2	3.30	3.42	3.32	3.68	4.62	4.25	4.02	3.87
TC1000747	IL2RA	3559	interleukin 2 receptor, alpha /// Interle	3.70E-06	2	4.20	4.18	4.30	4.91	4.49	4.74	5.02	4.98
TC0X01008	IL2RG	3561	interleukin 2 receptor, gamma (severe	0.000167	2	8.82	8.98	9.03	9.40	9.21	9.10	9.04	9.01
TC1101286	IMMP1L	196294	IMP1 inner mitochondrial membrane p	1.34E-08	2	2.51	2.59	2.54	2.77	3.04	3.02	2.95	2.86
TC1501118	IMP3	55272	IMP3, U3 small nucleolar ribonucleopr	0.000536	2	4.02	4.03	4.05	4.19	4.43	4.31	4.45	4.46
TC1800114	IMPACT	55364	Impact homolog (mouse)	4.02E-08	2	4.46	5.34	5.45	5.66	5.61	5.74	5.80	5.53
TC0400708	ING2	3622	inhibitor of growth family, member 2	8.53E-06	2	5.80	6.32	6.14	6.28	6.24	6.32	6.40	6.30
TC0701154	INHBA	3624	inhibin, beta A	2.70E-12	2	2.40	3.40	2.87	3.56	4.24	4.13	3.84	3.47
TC1000634	INPP5F	22876	inositol polyphosphate-5-phosphatase	6.28E-06	2	3.88	3.79	3.88	3.99	4.02	4.01	4.04	3.97
TC0700914	INSIG1	3638	insulin induced gene 1	8.32E-08	2	5.13	5.44	5.41	5.66	5.75	5.81	5.64	5.58
TC1901105	INSR	3643	insulin receptor	7.55E-05	2	3.90	4.16	4.02	4.09	4.19	4.16	4.09	4.04
TC0103211	INTS7	25896	integrator complex subunit 7 /// Integr	1.88E-08	2	3.41	3.46	3.44	3.68	3.84	3.77	3.90	3.73
TC0500206	IPO11 /// Q7Z2	51194	importin 11 /// Synleurin (CGLQ1891).	3.04E-09	2	2.73	2.79	2.95	3.05	3.08	2.94	2.94	2.88
TC1300243	IPO5 /// RANB	3843	importin 5 /// Importin beta-3 (Karyop	1.00E-08	2	3.36	3.52	3.42	3.64	3.90	3.90	3.98	3.77
TC1100160	IPO7	10527	importin 7	3.06E-06	2	3.45	4.09	4.19	4.30	4.43	4.30	4.36	4.12
TC0101409	IPO9	55705	importin 9	6.26E-06	2	4.04	3.98	3.87	4.13	4.29	4.20	4.31	4.17
TC0301914	IQCG	84223	IQ motif containing G	5.68E-05	2	3.36	3.45	3.40	3.56	3.65	3.60	3.64	3.57
TC0103363	IRF2BP2	359948	interferon regulatory factor 2 binding	3.47E-18	2	6.23	6.36	6.29	7.02	7.26	7.23	7.17	6.98
TC0901093	ISCA1	81689	iron-sulfur cluster assembly 1 homolog	0.000379	2	4.54	4.47	4.61	4.79	4.83	4.86	4.85	4.78
TC1400370	ISCA2	122961	iron-sulfur cluster assembly 2 homolog	5.23E-07	2	5.66	6.03	6.14	6.20	6.22	6.29	6.34	6.36
TC0200863	ITGA6	3655	integrin, alpha 6 /// Integrin alpha-6 pr	3.10E-06	2	5.42	6.29	5.64	6.04	5.96	6.33	6.46	6.29
TC0300153	ITGA9	3680	integrin, alpha 9	6.10E-10	2	3.74	4.03	3.88	4.25	4.66	4.68	4.44	4.11
TC0200926	ITGAV	3685	integrin, alpha V (vitronectin receptor,	4.61E-06	2	4.03	3.96	4.11	4.26	4.30	4.33	4.29	4.24
TC1000874	ITGB1	3688	integrin, beta 1 (fibronectin receptor,	5.02E-07	2	4.64	5.28	5.20	5.71	5.75	5.67	5.51	5.39
TC1700547	ITGB3	3690	integrin, beta 3 (platelet glycoprotein I	4.88E-06	2	4.21	4.67	4.62	5.94	6.28	5.97	5.60	5.46
TC0102318	ITGB3BP	23421	integrin beta 3 binding protein (beta3-	3.09E-07	2	3.08	3.47	3.46	3.71	3.85	3.76	3.65	3.64
TC0201165	ITM2C	81618	integral membrane protein 2C	2.46E-10	2	5.03	4.91	4.96	5.24	5.39	5.42	5.55	5.44
TC2000554	JAG1	182	jagged 1 (Alagille syndrome)	0.000301	2	3.98	3.98	4.05	4.21	4.19	4.19	4.20	4.13
TC0300032	JAGN1	84522	jagunal homolog 1 (Drosophila) /// jag	1.35E-07	2	4.50	4.70	4.87	5.05	4.99	4.97	5.01	4.93
TC1101015	JAM3	83700	junctional adhesion molecule 3	0.000851	2	3.99	4.32	4.08	4.45	4.72	4.82	4.59	4.52
TC0701095	JAZF1	221895	JAZF zinc finger 1	1.88E-05	2	6.33	6.52	6.61	6.86	6.77	6.70	6.72	6.65
TC0102803	JTB	10899	jumping translocation breakpoint /// P	1.70E-07	2	5.85	5.90	6.16	6.19	6.19	6.22	6.23	6.23

TC0800010	KBTBD11	9920	kelch repeat and BTB (POZ) domain cor	9.51E-08	2	5.61	5.76	5.75	5.96	6.06	6.15	6.34	6.27
TC1300555	KCTD12	115207	potassium channel tetramerisation dor	8.40E-07	2	7.05	6.97	7.49	7.66	7.43	7.41	7.44	7.45
TC0101514	KCTD3	51133	potassium channel tetramerisation dor	4.30E-05	2	2.94	3.03	3.08	3.09	3.31	3.24	3.20	3.08
TC1101809	KDELC2	143888	KDEL (Lys-Asp-Glu-Leu) containing 2 //,	0.000416	2	3.84	3.95	3.98	4.00	4.13	4.09	4.05	4.04
TC0900747	KIAA0020	9933	KIAA0020	5.76E-06	2	3.64	3.70	3.67	3.83	3.98	3.96	4.03	3.84
TC1000669	KIAA0157	23172	KIAA0157 /// Uncharacterized protein I	6.33E-07	2	5.22	5.95	6.10	6.22	6.04	6.09	6.14	6.07
TC0801238	KIAA0196	9897	KIAA0196	0.000614	2	5.15	5.16	5.30	5.55	5.47	5.50	5.59	5.37
TC0301141	KIAA1143	57456	KIAA1143	4.86E-05	2	5.64	5.90	5.86	6.12	6.01	6.14	6.30	6.29
TC0501514	KIAA1191	57179	KIAA1191	9.56E-05	2	4.35	4.51	4.42	4.64	4.75	4.61	4.76	4.69
TC1400140	KIAA1333	55632	KIAA1333	0.000444	2	3.45	3.62	3.78	3.78	3.76	3.82	3.88	3.90
TC0301429	KIAA1524	57650	KIAA1524	0.000209	2	2.44	2.58	2.59	2.71	3.00	2.93	2.87	2.75
TC0200272	KIAA1841	84542	KIAA1841 /// CDNA FLJ16202 fis, clone	2.90E-05	2	3.95	3.87	4.05	4.27	4.16	4.20	4.29	4.22
TC0101861	KIAA2013	90231	KIAA2013 /// KIAA2013. [Source:Unipr	0.00016	2	7.25	7.21	7.33	7.45	7.43	7.49	7.42	7.51
TC1000447	KIF11	3832	kinesin family member 11	2.16E-09	2	3.08	3.47	3.26	3.81	4.37	4.34	4.16	3.70
TC0103109	KIF14	9928	kinesin family member 14	5.48E-06	2	2.56	2.79	2.81	3.06	3.32	3.11	3.07	2.88
TC0300219	KIF15	56992	kinesin family member 15 /// kinesin fa	7.49E-07	2	2.92	3.09	3.07	3.43	3.76	3.68	3.60	3.32
TC1101279	KIF18A	81930	kinesin family member 18A	1.26E-06	2	2.44	2.55	2.53	2.67	3.01	2.85	2.81	2.72
TC0500505	KIF20A	10112	kinesin family member 20A	1.41E-05	2	3.11	3.28	3.22	3.42	3.73	3.67	3.51	3.34
TC1600317	KIF22	3835	kinesin family member 22	0.000722	2	5.31	5.28	5.25	5.31	5.41	5.42	5.43	5.34
TC1500437	KIF23	9493	kinesin family member 23	1.96E-07	2	3.13	3.23	3.13	3.46	3.82	3.74	3.70	3.47
TC0500205	KIF2A	3796	kinesin heavy chain member 2A /// Kin	6.20E-10	2	5.96	6.80	6.82	7.15	7.28	7.46	7.32	7.21
TC0X00328	KIF4B /// KIF4A	285643 //	kinesin family member 4B /// kinesin fa	3.33E-05	2	3.24	3.36	3.27	3.48	3.78	3.73	3.65	3.44
TC0600311	KIFC1	3833	kinesin family member C1	6.88E-08	2	3.97	4.12	4.07	4.40	4.70	4.64	4.61	4.31
TC0200031	KLF11	8462	Kruppel-like factor 11	0.000168	2	4.15	4.53	4.51	4.55	4.50	4.59	4.55	4.61
TC1300195	KLF5	688	Kruppel-like factor 5 (intestinal)	1.10E-11	2	4.80	5.82	5.62	5.66	5.93	5.99	5.82	5.62
TC0700111	KLHL7	55975	kelch-like 7 (Drosophila) /// Kelch-like p	9.71E-05	2	4.48	4.80	4.98	5.04	4.85	4.90	5.06	5.02
TC1200780	KNTC1	9735	kinetochore associated 1	2.91E-05	2	3.31	3.15	3.12	3.32	3.61	3.57	3.58	3.38
TC0600668	KPNA5	3841	karyopherin alpha 5 (importin alpha 6)	1.80E-05	2	3.24	3.54	3.64	3.81	3.66	3.68	3.75	3.81
TC1701313	KRT222P /// SN	125113 //	keratin 222 pseudogene /// SWI/SNF re	1.38E-05	2	4.48	4.68	4.73	4.77	4.75	4.73	4.81	4.75
TC0102824	KRTCAP2	200185	keratinocyte associated protein 2	1.46E-08	2	4.60	4.65	4.75	4.85	4.93	4.90	4.93	4.82
TC0300527	KTELC1	56983	KTEL (Lys-Tyr-Glu-Leu) containing 1	0.000309	2	3.28	3.31	3.37	3.46	3.49	3.47	3.58	3.58
TC0801019	LACTB2	51110	lactamase, beta 2	3.60E-11	2	3.69	3.93	4.03	4.22	4.27	4.50	4.60	4.38
TC0X01385	LAGE3	8270	L antigen family, member 3	0.000973	2	4.13	4.43	4.48	4.32	4.59	4.61	4.49	4.33
TC0X01198	LAMP2	3920	lysosomal-associated membrane prote	0.000207	2	8.99	9.05	8.99	9.14	9.10	9.21	9.15	9.29

TC0301799	LAMP3	27074	lysosomal-associated membrane prote	0.000241	2	4.26	4.50	4.38	4.44	4.37	4.55	4.77	4.80
TC0500632	LARP1	23367	La ribonucleoprotein domain family, m	9.42E-09	2	5.69	5.98	6.01	6.56	6.61	6.52	6.57	6.28
TC0400525	LARP2	648136 //	La ribonucleoprotein domain family, m	7.84E-09	2	3.79	4.11	4.33	4.42	4.42	4.36	4.33	4.25
TC1200328	LARP4	113251	La ribonucleoprotein domain family, m	1.44E-09	2	3.82	4.21	4.30	4.53	4.56	4.49	4.54	4.43
TC0501379	LARS	51520	leucyl-tRNA synthetase /// Leucyl-tRNA	6.67E-11	2	4.04	4.11	3.99	4.53	4.76	4.75	4.85	4.53
TC0200835	LASS6	253782	LAG1 homolog, ceramide synthase 6	3.85E-13	2	4.04	4.21	4.15	4.64	4.97	5.03	5.07	4.63
TC1600276	LCMT1	51451	leucine carboxyl methyltransferase 1 //	9.39E-10	2	4.39	4.46	4.55	4.92	4.94	4.81	4.97	4.76
TC1500887	LCMT2	9836	leucine carboxyl methyltransferase 2	1.54E-05	2	3.91	3.96	3.97	4.06	4.16	4.15	4.34	4.19
TC0400845	LCORL	254251	ligand dependent nuclear receptor cor	0.000393	2	4.41	4.61	4.62	4.66	4.61	4.80	4.91	4.75
TC1901793	LENG1	79165	leukocyte receptor cluster (LRC) memb	0.000172	2	6.84	6.81	6.77	6.91	6.97	7.01	6.95	7.01
TC1500960	LEO1	123169	Leo1, Paf1/RNA polymerase II complex	6.72E-07	2	5.01	5.05	5.33	5.84	5.75	5.69	5.96	5.64
TC0100626	LEPROT /// LEP	54741 ///	leptin receptor overlapping transcript /	6.22E-06	2	3.62	3.69	3.81	3.83	3.88	3.96	3.90	3.88
TC1901649	LIG1	3978	ligase I, DNA, ATP-dependent	0.000168	2	4.94	4.91	4.89	4.98	5.11	5.07	5.05	4.99
TC0700384	LIMK1	3984	LIM domain kinase 1	4.50E-05	2	5.35	5.36	5.37	5.62	5.73	5.83	5.70	5.62
TC0103284	LIN9	286826	lin-9 homolog (C. elegans) /// Lin-9 hon	2.21E-05	2	2.98	3.15	3.22	3.30	3.39	3.31	3.23	3.29
TC0100931	LIX1L	128077	Lix1 homolog (mouse)-like	0.000827	2	5.48	5.53	5.79	5.84	5.63	5.72	5.73	5.73
TC1800510	LMAN1	3998	lectin, mannose-binding, 1	1.51E-12	2	3.33	3.62	3.45	4.13	4.63	4.60	4.63	4.20
TC0500916	LMBRD2	92255	LMBR1 domain containing 2	6.37E-05	2	4.17	4.35	4.72	4.73	4.56	4.65	4.64	4.57
TC1901022	LMNB2	84823	lamin B2	3.89E-06	2	5.12	5.41	5.35	5.42	5.58	5.49	5.48	5.41
TC1101300	LMO2	4005	LIM domain only 2 (rhombotin-like 1)	0.000679	2	4.96	5.03	5.14	5.16	5.18	5.09	5.15	5.10
TC0100705	LMO4	8543	LIM domain only 4	5.32E-12	2	4.87	5.16	5.37	5.43	5.23	5.35	5.43	5.44
TC1300362	LNX2	222484	ligand of numb-protein X 2	1.08E-07	2	4.54	4.60	4.53	4.76	4.76	4.79	4.86	4.82
TC1900243	LOC113230	113230	hypothetical protein LOC113230	6.46E-05	2	4.83	5.15	5.14	5.32	5.29	5.23	5.21	5.12
TC0201859	LOC130355	130355	hypothetical protein LOC130355	4.97E-10	2	4.83	5.24	5.73	5.60	5.58	5.59	5.56	5.53
TC0200971	LOC26010	26010	viral DNA polymerase-transactivated pı	3.39E-07	2	3.73	3.97	3.80	4.11	4.12	4.43	4.70	4.59
TC0500145	LOC285636	285636	hypothetical protein LOC285636	4.08E-05	2	4.45	4.91	5.01	4.99	4.94	5.13	5.12	5.02
TC1900679	LOC374920	374920	hypothetical protein LOC374920	0.000727	2	5.23	5.30	5.30	5.37	5.50	5.40	5.66	5.53
TC0400142	LOC389203	389203	hypothetical gene supported by BC032	7.99E-08	2	4.91	5.37	5.67	5.59	5.57	5.59	5.64	5.62
TC2200320	LOC389901 ///	389901 //	hypothetical LOC389901 /// X-ray repa	0.000371	2	6.54	7.02	6.70	6.91	6.99	7.06	7.18	7.00
TC0601271	LOC441150	441150	similar to RIKEN cDNA 2310039H08	0.000165	2	4.56	4.75	4.77	4.96	5.15	4.98	4.95	4.92
TC0700339	LOC441241 ///	441241 //	vitamin K epoxide reductase complex, s	8.60E-06	2	4.49	5.07	5.18	5.28	5.51	5.50	5.43	5.30
TC1300622	LOC441377	441377	similar to ribosomal protein S26	8.30E-09	2	5.79	6.40	6.48	6.70	6.86	6.73	6.67	6.66
TC1300218	LOC441454	441454	hypothetical gene supported by BC013	2.57E-16	2	5.81	5.97	5.69	6.39	6.69	6.82	6.85	6.65
TC0500414	LOC643287	643287	similar to prothymosin alpha	6.81E-15	2	7.68	7.71	7.47	8.10	8.41	8.47	8.49	8.35

TC1600906	LOC644790 ///	644790 //	hypothetical LOC644790 /// ribosomal	2.04E-08	2	7.83	8.24	8.21	8.32	8.41	8.33	8.29	8.23
TC0101809	LOC645231 ///	645231 //	similar to 60S ribosomal protein L22 (H	9.90E-09	2	7.98	8.65	8.31	8.94	9.05	9.21	9.04	8.87
TC1101227	LOC645630 ///	645630 //	hypothetical LOC645630 /// ribosomal	4.81E-05	2	8.20	8.57	8.49	8.71	8.85	8.83	8.83	8.73
TC1200387	LOC645691 ///	645691 //	similar to heterogeneous nuclear ribon	0.000116	2	8.04	8.24	8.09	8.31	8.46	8.53	8.55	8.31
TC1201582	LOC646483 ///	646483 //	similar to DNA-binding protein TAXREB	4.73E-08	2	5.43	5.72	5.62	5.96	6.06	6.04	6.10	5.90
TC1300470	LOC646520 ///	646520 //	hypothetical LOC646520 /// succinate-	0.000314	2	3.88	4.06	4.13	4.13	4.16	4.11	4.17	4.10
TC0400451	LOC646567 ///	646567 //	similar to HSPC307 /// DC2 protein	4.24E-09	2	5.43	5.95	6.10	6.31	6.49	6.40	6.34	6.05
TC2000870	LOC646873 ///	646873 //	similar to orthologue of H. sapiens chr	1.43E-09	2	5.98	6.26	6.28	6.39	6.40	6.53	6.51	6.58
TC0100726	LOC647436 ///	647436 //	similar to ribosomal protein L5 /// ribo	3.80E-09	2	7.75	8.28	7.92	8.57	8.79	8.80	8.74	8.38
TC1700192	LOC650788	650788	similar to 40S ribosomal protein S28	1.84E-10	2	7.74	8.76	8.70	8.87	8.98	9.13	9.08	8.96
TC1100710	LOC650788	650788	similar to 40S ribosomal protein S28	4.26E-07	2	7.24	7.68	7.48	8.01	8.17	8.15	8.11	7.95
TC0500960	LOC651789 ///	651789 //	similar to poly(A) binding protein inter	9.23E-06	2	4.61	5.02	5.19	5.16	5.12	5.14	5.24	5.13
TC0200506	LOC652726 ///	652726 //	similar to ankyrin repeat domain 36 ///	0.000159	2	2.70	2.82	2.60	2.67	2.96	2.95	2.96	2.81
TC0300173	LOC653162 ///	653162 //	similar to 40S ribosomal protein SA (p4	3.14E-06	2	4.55	5.01	4.82	5.27	5.53	5.51	5.47	5.12
TC0301484	LOC653256 ///	653256 //	similar to RAB, member of RAS oncoge	7.59E-05	2	4.73	4.94	5.11	5.35	5.33	5.26	5.26	5.07
TC1700413	LOC653314 ///	653314 //	similar to ribosomal protein L19 /// rib	3.20E-09	2	7.62	7.95	7.79	8.17	8.18	8.25	8.34	8.21
TC2200680	LOC653881 ///	653881 //	similar to 60S ribosomal protein L3 (L4)	0.000273	2	7.20	7.43	7.20	7.60	7.71	7.69	7.70	7.50
TC2100031	LOC654188	654188	similar to peptidylprolyl isomerase A is	1.10E-11	2	7.09	7.90	7.89	8.27	8.42	8.42	8.54	8.20
TC0700225	LOC654188 ///	654188 //	similar to peptidylprolyl isomerase A is	1.81E-12	2	4.87	4.99	4.91	5.36	5.50	5.59	5.56	5.34
TC0201175	LOC728026 ///	728026 //	hypothetical LOC728026 /// prothymos	1.92E-16	2	9.29	9.23	8.99	9.60	9.81	9.87	9.86	9.74
TC0301154	LOC728320 ///	728320 //	hypothetical LOC728320 /// lactotrans	9.12E-16	2	5.01	8.15	6.96	7.75	8.67	8.71	7.90	7.43
TC0800671	LOC728358 ///	728358 //	defensin, alpha 1 /// Retrocyclin. [Sour	3.19E-36	2	9.04	11.55	10.98	11.80	12.01	12.10	11.89	11.76
TC0800673	LOC728358 ///	728358 //	defensin, alpha 1 /// defensin, alpha 3,	1.20E-37	2	9.09	11.92	11.32	12.16	12.36	12.42	12.21	12.12
TC1900100	LOC728688 ///	728688 //	ubiquitin-like, containing PHD and RIN	0.000463	2	4.69	4.77	4.77	4.86	4.98	4.94	4.86	4.81
TC1101678	LOC728748 ///	728748 //	similar to Protein-kinase, interferon-in	1.18E-12	2	5.42	5.61	5.70	5.94	5.88	6.07	6.20	6.04
TC0600677	LOC729148 ///	729148 //	similar to chromosome 6 open reading	9.13E-05	2	3.90	4.63	4.76	4.85	4.86	4.86	4.89	4.59
TC1600848	LOC730038 ///	730038 //	hypothetical LOC730038 /// dexameth	9.65E-06	2	4.95	4.82	4.83	5.05	5.20	5.14	5.19	5.10
TC1400233	LOC730432 ///	730432 //	similar to serine/threonine/tyrosine int	3.02E-05	2	5.29	5.61	5.66	5.66	5.74	5.88	5.87	5.85
TC0201767	LOC730658 ///	731085 //	similar to ankyrin repeat domain 26 ///	1.67E-05	2	3.19	3.62	3.28	3.47	3.77	3.80	3.75	3.45
TC1000561	LOC730792 ///	730792 //	hypothetical LOC730792 /// chromoso	0.000714	2	3.24	3.46	3.40	3.52	3.58	3.56	3.65	3.64
TC1901825	LOC731049 ///	731049 //	similar to Ubiquitin-conjugating enzym	5.15E-06	2	4.13	4.35	4.28	4.32	4.49	4.55	4.49	4.57
TC1500415	LOC732402 ///	732402 //	similar to butyrate-induced transcript 1	1.08E-07	2	3.31	3.40	3.32	3.65	3.93	3.85	3.91	3.69
TC0301494	LOC732448 ///	732448 //	hypothetical LOC732448 /// coiled-coil	1.21E-05	2	3.85	3.87	3.79	4.00	4.10	4.07	4.24	4.04
TC0401196	LOC91431	91431	prematurely terminated mRNA decay f	3.07E-05	2	2.60	2.54	2.62	2.71	2.90	2.76	2.82	2.70

TC0X00524	LONRF3	79836	LON peptidase N-terminal domain and	9.42E-12	2	3.73	3.95	3.89	4.18	4.33	4.69	4.41	4.17
TC0401320	LRBA	987	LPS-responsive vesicle trafficking, beac	0.000582	2	3.95	4.11	3.96	4.21	4.37	4.31	4.34	4.27
TC0301327	LRIG1	26018	leucine-rich repeats and immunoglobu	0.00044	2	4.42	4.40	4.39	4.52	4.61	4.59	4.58	4.53
TC0201473	LRPPRC	10128	leucine-rich PPR-motif containing	4.67E-07	2	3.11	3.14	3.07	3.41	3.63	3.61	3.67	3.48
TC0600469	LRRC1	55227	leucine rich repeat containing 1 /// Leu	0.000688	2	2.54	2.67	2.68	2.69	2.76	2.75	2.69	2.72
TC1500666	LRRC28	123355	leucine rich repeat containing 28 /// Le	9.87E-05	2	4.24	4.53	4.51	4.60	4.61	4.69	4.74	4.56
TC0101803	LRRC47	57470	leucine rich repeat containing 47	5.05E-08	2	4.94	4.89	5.01	5.18	5.19	5.23	5.23	5.24
TC0301480	LRRC58	116064	leucine rich repeat containing 58	1.63E-07	2	4.12	4.27	4.69	4.64	4.63	4.87	4.67	4.70
TC0100713	LRRC8D	55144	leucine rich repeat containing 8 family,	7.58E-06	2	5.98	6.22	6.24	6.24	6.35	6.31	6.23	6.21
TC0102114	LSM10	84967	LSM10, U7 small nuclear RNA associate	1.36E-08	2	5.60	5.61	5.80	5.94	5.97	5.95	5.93	6.04
TC1701416	LSM12	124801	LSM12 homolog (S. cerevisiae)	3.24E-08	2	6.16	6.60	6.63	6.85	6.78	6.78	6.76	6.69
TC1900416	LSM14A	26065	LSM14A, SCD6 homolog A (S. cerevisiae	4.54E-05	2	7.98	8.08	8.10	8.15	8.16	8.21	8.22	8.27
TC0300073	LSM3	648229 //	LSM3 homolog, U6 small nuclear RNA a	0.000336	2	7.38	7.87	7.80	7.68	7.67	7.91	8.03	8.07
TC0701112	LSM5	23658	LSM5 homolog, U6 small nuclear RNA a	2.90E-08	2	4.46	4.79	4.79	5.01	5.25	5.24	5.24	5.06
TC1201471	LTA4H	4048	leukotriene A4 hydrolase	2.88E-14	2	7.14	7.89	7.97	8.32	8.57	8.32	8.03	7.57
TC0601123	LTB	4050	lymphotoxin beta (TNF superfamily, me	0.000124	2	12.56	12.59	12.74	12.83	12.76	12.93	12.94	12.95
TC0200169	LTBP1	4052	latent transforming growth factor beta	0.000141	2	3.77	4.33	4.01	4.52	4.88	4.79	4.50	4.41
TC0600778	LTV1	84946	LTV1 homolog (S. cerevisiae)	5.33E-05	2	3.36	3.47	3.48	3.73	3.85	3.83	3.95	3.72
TC0800382	LY96	23643	lymphocyte antigen 96	3.08E-09	2	7.84	8.43	8.89	8.88	8.68	8.95	8.88	8.93
TC0501139	LYSMD3	116068	LysM, putative peptidoglycan-binding,	7.01E-05	2	6.00	6.43	6.57	6.48	6.25	6.54	6.59	6.61
TC1200506	LYZ	4069	lysozyme (renal amyloidosis)	9.65E-13	2	10.50	11.45	11.16	11.45	11.64	11.71	11.48	11.49
TC0101846	LZIC	84328	leucine zipper and CTNNBIP1 domain c	5.23E-05	2	5.93	6.44	6.51	6.49	6.49	6.54	6.59	6.50
TC1200946	M6PR	4074	mannose-6-phosphate receptor (catio	4.80E-12	2	6.39	6.30	6.22	6.64	6.70	6.87	7.00	6.82
TC0401223	MAD2L1	4085	MAD2 mitotic arrest deficient-like 1 (ye	7.96E-06	2	3.25	3.42	3.39	3.57	3.83	3.81	3.78	3.50
TC1200974	MAGOHB /// M	55110	mago-nashi homolog B (Drosophila) ///	0.000297	2	3.06	3.12	3.18	3.20	3.32	3.29	3.33	3.35
TC0800205	MAK16	84549	MAK16 homolog (S. cerevisiae)	4.21E-06	2	3.81	3.74	3.86	3.92	4.02	3.99	4.11	3.98
TC0601568	MAN1A1	4121	mannosidase, alpha, class 1A, member	2.71E-12	2	6.67	6.59	7.55	7.74	7.29	7.36	7.39	7.28
TC0600574	MANEA	79694	mannosidase, endo-alpha /// Glycopro	9.08E-05	2	2.67	2.88	3.02	3.00	3.22	3.22	3.12	2.98
TC0600863	MAP3K4	4216	mitogen-activated protein kinase kinas	0.000903	2	3.78	3.80	3.77	3.94	4.07	4.00	4.06	3.92
TC0201450	MAP4K3	8491	mitogen-activated protein kinase kinas	0.000172	2	2.97	3.05	3.11	3.15	3.18	3.18	3.23	3.18
TC0X01287	MAP7D3	79649	MAP7 domain containing 3 /// MAP7 d	8.95E-08	2	3.74	4.02	4.03	4.15	4.23	4.17	4.32	4.18
TC0501562	MAPK9	5601	mitogen-activated protein kinase 9	1.08E-12	2	5.02	5.12	4.95	5.50	5.62	5.59	5.66	5.54
TC1800138	MAPRE2	10982	microtubule-associated protein, RP/EB	3.28E-06	2	5.77	5.62	5.70	6.14	6.02	6.16	6.18	6.20
TC0100504	MAST2	23139	microtubule associated serine/threoni	4.08E-05	2	4.23	4.43	4.43	4.41	4.61	4.48	4.48	4.36

TC0500515	MATR3	9782	matrin 3 /// Matrin-3. [Source:Uniprot/	0.000209	2	6.14	6.41	6.27	6.27	6.31	6.42	6.53	6.45
TC1600318	MAZ	4150	MYC-associated zinc finger protein (pu	0.000674	2	5.51	5.49	5.53	5.61	5.68	5.60	5.53	5.52
TC1000064	MCM10	55388	minichromosome maintenance comple	6.13E-05	2	3.23	3.38	3.38	3.55	3.80	3.69	3.63	3.47
TC0601328	MCM3	4172	minichromosome maintenance comple	1.50E-08	2	3.87	3.97	3.86	4.19	4.52	4.53	4.50	4.23
TC0800280	MCM4	4173	minichromosome maintenance comple	1.70E-08	2	3.61	3.85	3.74	4.02	4.35	4.30	4.23	3.95
TC0201958	MCM6	4175	minichromosome maintenance comple	3.12E-14	2	3.91	5.03	4.86	5.45	5.96	5.85	5.62	5.06
TC0800013	MCPH1	79648	microcephalin 1	3.45E-10	2	4.07	3.98	4.08	4.27	4.29	4.31	4.53	4.45
TC0700412	MDH2	4191	malate dehydrogenase 2, NAD (mitoch	3.65E-06	2	6.49	6.80	6.88	7.14	7.16	7.02	7.03	6.93
TC0601274	MEA1	4201	male-enhanced antigen 1	1.57E-12	2	6.00	6.19	6.45	6.68	6.67	6.59	6.67	6.58
TC0300713	MED12L	116931	mediator complex subunit 12-like /// m	6.54E-07	2	3.25	3.53	3.37	3.76	3.92	3.77	3.76	3.52
TC1200210	MED21	9412	mediator complex subunit 21	3.27E-08	2	6.35	6.41	6.28	6.44	6.66	6.80	6.80	6.83
TC0400121	MED28	80306	mediator complex subunit 28	4.05E-07	2	6.65	7.08	7.15	7.17	7.06	7.26	7.23	7.33
TC0800517	MED30	90390	mediator complex subunit 30	5.76E-06	2	5.96	6.33	6.36	6.33	6.21	6.34	6.40	6.51
TC0900176	MELK	9833	maternal embryonic leucine zipper kina	1.07E-05	2	3.25	3.34	3.31	3.49	3.75	3.65	3.57	3.45
TC1200599	METAP2	10988	methionyl aminopeptidase 2 /// Methi	7.71E-11	2	4.24	5.10	4.86	5.56	5.85	5.88	5.89	5.43
TC0202084	METTL5	29081	methyltransferase like 5 /// Methyltra	8.77E-11	2	4.94	6.15	6.36	6.41	6.49	6.51	6.55	6.28
TC1500900	MFAP1	4236	microfibrillar-associated protein 1	0.000373	2	7.63	7.87	7.77	7.84	7.71	7.89	7.94	8.01
TC1400208	MGAT2	4247	mannosyl (alpha-1,6-)-glycoprotein bet	4.97E-06	2	3.98	4.10	4.39	4.37	4.43	4.44	4.43	4.43
TC0301532	MGLL	11343	monoglyceride lipase	1.47E-08	2	4.14	4.27	4.26	4.43	4.56	4.57	4.46	4.38
TC1200171	MGST1	4257	microsomal glutathione S-transferase 1	4.04E-09	2	3.40	3.70	3.88	4.17	4.16	4.07	3.90	3.75
TC1800092	MIB1	57534	mindbomb homolog 1 (Drosophila)	0.000926	2	5.56	5.73	5.70	5.95	5.74	5.84	5.85	5.84
TC1701690	MIF4GD	57409	MIF4G domain containing /// MIF4G d	0.00083	2	4.53	4.62	4.62	4.74	4.81	4.72	4.76	4.69
TC1001350	MKI67	442448 //	antigen identified by monoclonal antib	7.88E-09	2	3.47	4.05	3.70	4.46	5.14	5.07	5.06	4.32
TC0201867	MKI67IP	84365	MKI67 (FHA domain) interacting nucle	6.54E-14	2	4.13	4.27	4.09	4.83	4.98	5.01	5.26	4.99
TC2200775	MLC1	23209	megalencephalic leukoencephalopathy	2.50E-10	2	4.00	4.16	4.11	4.38	4.71	4.66	4.54	4.31
TC0401450	MLF1IP	79682	MLF1 interacting protein	1.20E-10	2	2.94	3.10	2.89	3.45	3.81	3.73	3.75	3.52
TC1000101	MLLT10	8028	myeloid/lymphoid or mixed-lineage leu	0.000162	2	5.36	5.46	5.63	5.74	5.77	5.80	5.85	5.66
TC1701533	MMD	23531	monocyte to macrophage differentiati	7.92E-05	2	3.72	4.09	3.82	4.53	4.71	4.72	4.58	4.53
TC1400277	MNAT1	4331	menage a trois homolog 1, cyclin H ass	2.68E-08	2	3.77	4.21	4.08	4.38	4.57	4.59	4.61	4.35
TC0400611	MND1	84057	meiotic nuclear divisions 1 homolog (S.	1.31E-09	2	3.15	3.41	3.26	3.73	4.20	4.22	3.98	3.66
TC1000433	MPHOSPH1	9585	M-phase phosphoprotein 1 /// M-phas	9.86E-08	2	2.95	3.12	3.16	3.38	3.57	3.51	3.57	3.39
TC0200335	MPHOSPH10	10199	M-phase phosphoprotein 10 (U3 small	3.74E-07	2	4.09	4.08	4.09	4.42	4.55	4.58	4.94	4.66
TC1201656	MPHOSPH9	10198	M-phase phosphoprotein 9 /// M-phas	2.68E-08	2	3.38	3.43	3.40	3.69	3.88	3.87	3.95	3.75
TC1701550	MPO	4353	myeloperoxidase /// Myeloperoxidase	5.80E-12	2	4.65	5.64	5.17	6.49	7.15	6.96	6.63	5.96

TC0400338	MRPL1	65008	mitochondrial ribosomal protein L1 ///	8.90E-07	2	3.89	3.96	4.08	4.26	4.46	4.47	4.58	4.47
TC0801217	MRPL13	28998	mitochondrial ribosomal protein L13	2.80E-05	2	3.52	4.21	4.27	4.32	4.44	4.44	4.50	4.27
TC0800298	MRPL15	29088	mitochondrial ribosomal protein L15	7.97E-05	2	4.15	4.27	4.36	4.46	4.59	4.43	4.59	4.38
TC0600856	MRPL18	29074	mitochondrial ribosomal protein L18	6.40E-05	2	4.73	5.05	5.11	5.26	5.28	5.29	5.33	5.18
TC0200369	MRPL19	9801	mitochondrial ribosomal protein L19 //	0.000224	2	3.80	3.99	4.04	4.11	4.26	4.19	4.21	4.11
TC1101614	MRPL21	219927	mitochondrial ribosomal protein L21	0.000539	2	4.43	4.68	4.81	4.91	4.97	4.91	4.98	4.83
TC0500634	MRPL22	29093	mitochondrial ribosomal protein L22	6.82E-05	2	5.52	5.91	6.07	6.14	6.14	6.16	6.25	6.08
TC1701517	MRPL27	51264	mitochondrial ribosomal protein L27	2.86E-06	2	4.46	4.38	4.45	4.65	4.83	4.75	4.84	4.74
TC0301568	MRPL3	11222	mitochondrial ribosomal protein L3	4.96E-07	2	3.56	3.73	3.74	4.00	4.14	4.17	4.28	4.12
TC0700208	MRPL32	64983	mitochondrial ribosomal protein L32	1.94E-09	2	3.80	3.82	3.73	3.96	4.10	4.13	4.30	4.03
TC0200420	MRPL35	51318	mitochondrial ribosomal protein L35	7.76E-08	2	3.99	4.32	4.55	4.76	4.89	4.82	4.88	4.72
TC0100574	MRPL37	51253	mitochondrial ribosomal protein L37 //	1.16E-06	2	4.29	4.36	4.39	4.57	4.76	4.66	4.80	4.64
TC2100247	MRPL39	54148	mitochondrial ribosomal protein L39	2.70E-06	2	3.96	4.63	4.57	4.83	4.89	5.00	5.01	4.87
TC0900729	MRPL41	64975	mitochondrial ribosomal protein L41	0.000266	2	5.64	5.70	5.79	5.99	6.02	5.90	6.02	5.84
TC1200584	MRPL42	28977	mitochondrial ribosomal protein L42	4.93E-07	2	5.32	5.35	5.60	5.74	5.66	5.73	5.98	5.89
TC0201139	MRPL44	65080	mitochondrial ribosomal protein L44	1.73E-07	2	5.27	5.27	5.37	5.60	5.51	5.60	5.67	5.82
TC1501219	MRPL46	26589	mitochondrial ribosomal protein L46	0.00039	2	3.98	3.91	4.01	4.11	4.19	4.23	4.30	4.22
TC1100657	MRPL48	51642	mitochondrial ribosomal protein L48 //	1.19E-05	2	4.33	4.35	4.37	4.54	4.62	4.55	4.62	4.59
TC0901199	MRPL50	54534	mitochondrial ribosomal protein L50	5.55E-07	2	3.08	3.19	3.10	3.38	3.47	3.63	3.63	3.45
TC1200903	MRPL51	51258	mitochondrial ribosomal protein L51	9.63E-10	2	5.38	5.82	5.97	6.02	6.11	6.03	5.94	5.79
TC1900080	MRPL54	116541	mitochondrial ribosomal protein L54	0.000556	2	5.71	6.29	6.15	6.09	6.34	6.39	6.40	6.35
TC0102753	MRPL9	65005	mitochondrial ribosomal protein L9 ///	1.95E-06	2	3.62	3.79	3.66	3.95	4.14	4.01	4.07	3.96
TC1500599	MRPS11	64963	mitochondrial ribosomal protein S11	4.06E-05	2	4.59	4.72	4.90	4.91	4.99	4.89	4.93	4.94
TC0103020	MRPS14	63931	mitochondrial ribosomal protein S14	1.49E-08	2	4.72	4.76	4.84	4.93	5.05	5.09	5.15	5.06
TC1001065	MRPS16 /// DN	51021 ///	mitochondrial ribosomal protein S16 //	3.14E-11	2	4.58	4.86	4.81	5.12	5.28	5.29	5.30	5.11
TC0601289	MRPS18A	55168	mitochondrial ribosomal protein S18A /	2.11E-05	2	5.81	6.21	6.23	6.37	6.37	6.34	6.38	6.37
TC0600248	MRPS18B	28973	mitochondrial ribosomal protein S18B /	0.00042	2	4.32	4.66	4.57	4.64	4.64	4.72	4.64	4.62
TC0400362	MRPS18C	51023	mitochondrial ribosomal protein S18C	8.63E-15	2	5.62	6.45	6.79	6.87	6.76	6.84	6.90	6.79
TC0101013	MRPS21 /// Q9	54460	mitochondrial ribosomal protein S21	1.87E-06	2	4.47	4.54	4.66	4.88	5.00	4.90	5.03	4.80
TC1701543	MRPS23	51649	mitochondrial ribosomal protein S23	9.50E-14	2	4.28	4.53	4.78	5.32	5.44	5.52	5.61	5.39
TC0501053	MRPS27	23107	mitochondrial ribosomal protein S27	4.98E-06	2	3.67	3.85	3.81	3.85	4.10	4.01	4.05	3.92
TC0801054	MRPS28	28957	mitochondrial ribosomal protein S28	2.90E-10	2	4.28	4.64	4.94	5.02	4.92	4.89	4.89	4.81
TC0500164	MRPS30	10884	mitochondrial ribosomal protein S30	4.43E-08	2	3.35	3.54	3.54	3.74	3.80	3.79	4.01	3.82
TC0701690	MRPS33	51650	mitochondrial ribosomal protein S33	1.64E-06	2	5.22	5.39	5.47	5.64	5.79	5.81	5.80	5.65

TC1200217	MRPS35	60488	mitochondrial ribosomal protein S35 //	5.05E-06	2	3.76	3.85	3.89	4.14	4.21	4.27	4.13	4.08
TC0500234	MRPS36	92259	mitochondrial ribosomal protein S36	3.97E-09	2	5.20	5.70	5.73	5.84	5.93	5.88	5.98	5.92
TC0201737	MRPS5	64969	mitochondrial ribosomal protein S5 ///	0.000203	2	5.25	5.58	5.58	5.79	5.80	5.86	5.88	5.64
TC1700755	MRPS7	51081	mitochondrial ribosomal protein S7	7.12E-07	2	4.64	4.91	4.83	5.09	5.18	5.06	5.11	4.95
TC1100431	MS4A3	932	membrane-spanning 4-domains, subfa	1.50E-20	2	4.03	6.25	5.12	7.20	8.11	8.29	7.69	6.86
TC0200228	MSH2	4436	mutS homolog 2, colon cancer, nonpol	2.20E-11	2	3.45	3.22	3.30	3.59	3.83	3.83	3.95	3.82
TC1200488	MSRB3	253827	methionine sulfoxide reductase B3	1.39E-06	2	4.25	4.95	5.07	4.98	5.23	5.23	5.24	4.99
TC1600460	MT1F	4494	metallothionein 1F	4.11E-07	2	5.08	5.30	5.35	5.73	5.81	5.84	6.07	5.73
TC1600462	MT1X	4501	metallothionein 1X	0.000769	2	5.70	5.76	5.64	5.97	5.88	6.04	6.16	6.10
TC1101360	MTCH2	23788	mitochondrial carrier homolog 2 (C. ele	3.31E-07	2	4.45	5.15	5.08	5.31	5.54	5.45	5.46	5.20
TC1400295	MTHFD1	4522	methylenetetrahydrofolate dehydroge	1.29E-05	2	3.67	3.73	3.66	3.79	3.99	4.01	3.99	3.84
TC0201523	MTIF2	4528	mitochondrial translational initiation fa	2.74E-05	2	4.84	5.07	5.09	5.18	5.27	5.40	5.62	5.39
TC1101612	MTL5	9633	metallothionein-like 5, testis-specific (t	0.000195	2	3.85	4.02	4.09	4.02	4.16	4.14	4.13	4.05
TC0600741	MYB	4602	v-myb myeloblastosis viral oncogene h	3.48E-12	2	4.81	5.20	5.22	5.73	6.03	6.13	6.00	5.86
TC2000288	MYBL2	4605	v-myb myeloblastosis viral oncogene h	0.000111	2	4.23	4.33	4.28	4.40	4.55	4.52	4.44	4.34
TC2000235	MYL9	10398	myosin, light chain 9, regulatory	0.00052	2	5.35	5.71	5.65	6.31	6.71	6.66	6.27	6.26
TC1701187	MYO18A /// TI	399687 //	myosin XVIIIA /// TGFB1-induced anti-a	2.12E-05	2	5.12	5.10	5.26	5.52	5.31	5.20	5.32	5.26
TC1501080	MYO9A	4649	myosin IXA /// myosin IXA [Source:Ref	0.000604	2	3.21	3.25	3.31	3.34	3.33	3.32	3.42	3.35
TC1300322	N6AMT2	221143	N-6 adenine-specific DNA methyltransf	0.000441	2	4.26	4.23	4.34	4.43	4.56	4.51	4.57	4.45
TC1201306	NACA	4666	nascent polypeptide-associated compl	1.16E-07	2	5.68	5.87	5.98	6.04	6.06	5.96	6.02	5.91
TC0400655	NACA3P	389240	NACA family member 3 pseudogene	0.000379	2	2.62	3.05	3.30	3.29	3.18	3.22	3.27	3.22
TC1601162	NAE1	8883	NEDD8 activating enzyme E1 subunit 1	5.14E-06	2	3.69	3.69	3.78	3.95	4.01	3.98	4.11	3.98
TC0201324	NAG	51594	neuroblastoma-amplified protein	7.76E-05	2	3.53	3.73	3.76	3.85	3.98	3.91	3.88	3.77
TC1201404	NAP1L1	4673	nucleosome assembly protein 1-like 1	3.64E-23	2	6.89	6.87	6.50	8.15	8.41	8.55	8.48	8.25
TC0701517	NAPEPLD	222236	N-acyl phosphatidylethanolamine phos	0.000367	2	3.18	3.25	3.37	3.44	3.44	3.39	3.50	3.48
TC0400552	NARG1	80155	NMDA receptor regulated 1	1.87E-08	2	3.54	3.83	3.70	4.02	4.29	4.25	4.31	4.06
TC1501010	NARG2	79664	NMDA receptor regulated 2	8.48E-08	2	3.39	3.48	3.52	3.80	3.96	3.93	4.12	3.97
TC0800112	NAT1	9	N-acetyltransferase 1 (arylamine N-ace	2.36E-05	2	3.54	3.61	3.75	3.72	3.68	3.70	3.91	3.87
TC0301227	NAT6 /// IFRD2	24142 ///	N-acetyltransferase 6 /// hyaluronoglu	2.55E-05	2	4.69	4.68	4.64	4.74	4.81	4.83	4.71	4.71
TC1200053	NCAPD2	9918	non-SMC condensin I complex, subunit	2.30E-06	2	4.90	5.51	5.33	5.43	5.65	5.55	5.52	5.25
TC1101993	NCAPD3	23310	non-SMC condensin II complex, subuni	8.14E-08	2	3.98	3.94	3.90	4.15	4.39	4.42	4.40	4.26
TC0400122	NCAPG	64151	non-SMC condensin I complex, subunit	2.06E-06	2	2.61	2.77	2.70	3.06	3.48	3.42	3.25	3.00
TC0701805	NCAPG2	54892	non-SMC condensin II complex, subuni	0.000211	2	2.94	3.01	2.92	3.09	3.37	3.29	3.32	3.15
TC0200492	NCAPH	23397	non-SMC condensin I complex, subunit	2.29E-05	2	3.50	3.65	3.62	3.82	4.06	3.98	3.92	3.71

TC0900422	NCBP1	4686	nuclear cap binding protein subunit 1,	1.61E-05	2	4.75	4.62	4.70	4.89	4.99	5.01	5.09	4.94
TC0300646	NCK1	4690	NCK adaptor protein 1	1.03E-06	2	5.69	5.99	5.95	6.04	6.05	6.01	6.00	5.95
TC0M00032	ND6	4541	NADH dehydrogenase, subunit 6 (comp	0.000352	2	9.64	9.88	9.93	9.79	9.98	10.17	10.21	10.26
TC2000715	NDRG3 /// HN	57446	NDRG family member 3 /// Protein ND	3.49E-06	2	6.21	6.01	6.30	6.59	6.42	6.33	6.33	6.39
TC1901079	NDUFA11 /// C	126328	NADH dehydrogenase (ubiquinone) 1 a	1.03E-05	2	4.47	4.71	4.77	4.88	4.97	4.88	4.72	4.74
TC1201461	NDUFA12	55967	NADH dehydrogenase (ubiquinone) 1 a	3.56E-09	2	5.21	6.15	6.29	6.42	6.55	6.57	6.75	6.51
TC1900339	NDUFA13	51079	NADH dehydrogenase (ubiquinone) 1 a	5.13E-06	2	5.99	6.47	6.60	6.82	6.82	6.69	6.65	6.52
TC0501351	NDUFA2	4695	NADH dehydrogenase (ubiquinone) 1 a	2.26E-06	2	7.20	7.44	7.56	7.70	7.65	7.69	7.65	7.72
TC2200718	NDUFA6	4700	NADH dehydrogenase (ubiquinone) 1 a	1.60E-08	2	6.46	6.91	7.01	7.24	7.35	7.40	7.39	7.29
TC1901124	NDUFA7	4701	NADH dehydrogenase (ubiquinone) 1 a	2.83E-05	2	4.19	4.45	4.54	4.68	4.58	4.54	4.68	4.49
TC1600942	NDUFAB1	4706	NADH dehydrogenase (ubiquinone) 1,	2.52E-10	2	5.02	5.79	5.92	6.23	6.48	6.44	6.60	6.20
TC1401079	NDUFB1	4707	NADH dehydrogenase (ubiquinone) 1	5.52E-09	2	8.63	8.80	9.00	9.02	9.02	8.96	8.95	8.97
TC1600063	NDUFB10	4716	NADH dehydrogenase (ubiquinone) 1	1.37E-13	2	5.54	5.94	5.98	6.26	6.31	6.18	6.28	6.15
TC0X00883	NDUFB11	54539	NADH dehydrogenase (ubiquinone) 1	3.48E-06	2	5.78	6.17	6.20	6.33	6.36	6.22	6.29	6.15
TC0700750	NDUFB2	4708	NADH dehydrogenase (ubiquinone) 1	1.14E-06	2	4.68	4.73	4.67	4.90	5.11	5.07	5.00	4.88
TC0300821	NDUFB5	4711	NADH dehydrogenase (ubiquinone) 1	2.99E-10	2	4.40	4.92	5.15	5.25	5.18	5.28	5.38	5.29
TC0900846	NDUFB6	4712	NADH dehydrogenase (ubiquinone) 1	4.81E-11	2	6.43	6.34	6.56	6.90	6.86	7.10	7.10	7.10
TC1901244	NDUFB7	4713	NADH dehydrogenase (ubiquinone) 1	2.20E-10	2	6.04	6.47	6.73	6.98	7.04	6.74	6.67	6.45
TC0500017	NDUFS6	4726	NADH dehydrogenase (ubiquinone) Fe-	3.49E-08	2	5.67	5.97	6.11	6.24	6.28	6.29	6.36	6.22
TC2100156	NDUFV3	4731	NADH dehydrogenase (ubiquinone) fla	5.40E-07	2	5.32	5.48	5.53	5.78	5.85	5.88	5.96	5.85
TC0400693	NEIL3	55247	nei endonuclease VIII-like 3 (E. coli)	6.71E-07	2	3.76	4.18	4.27	4.45	4.61	4.54	4.44	4.28
TC0103208	NEK2	4751	NIMA (never in mitosis gene a)-related	7.55E-05	2	3.43	3.43	3.43	3.52	3.84	3.77	3.71	3.57
TC0301261	NEK4	6787	NIMA (never in mitosis gene a)-related	0.000824	2	5.31	5.41	5.38	5.55	5.55	5.52	5.63	5.58
TC0101501	NENF	29937	neuron derived neurotrophic factor	3.49E-07	2	5.37	5.88	5.99	5.88	6.09	6.07	6.00	5.94
TC1000030	NET1	10276	neuroepithelial cell transforming gene	1.19E-06	2	4.21	4.52	4.42	4.55	4.72	4.66	4.70	4.60
TC0100673	NEXN	91624	nexilin (F actin binding protein) /// nex	3.11E-05	2	3.50	4.03	3.87	4.69	4.67	4.78	4.80	4.73
TC1000597	NHLRC2	374354	NHL repeat containing 2	0.0003	2	4.27	4.82	4.71	4.82	4.91	4.98	4.93	4.83
TC2200710	NHP2L1	4809	NHP2 non-histone chromosome protei	2.24E-13	2	5.44	5.59	5.56	5.90	6.10	6.24	6.28	6.07
TC1600554	NIP7	51388	nuclear import 7 homolog (S. cerevisia	7.90E-09	2	5.05	5.29	5.37	5.63	5.53	5.52	5.60	5.52
TC0900454	NIPSNAP3A	25934	nipsnap homolog 3A (C. elegans)	1.36E-06	2	3.53	4.07	4.12	4.20	4.37	4.40	4.34	4.17
TC0300443	NIT2	56954	nitrilase family, member 2	5.09E-08	2	3.76	4.04	3.87	4.31	4.69	4.66	4.50	4.26
TC0301061	NKIRAS1	28512	NFKB inhibitor interacting Ras-like 1	5.66E-05	2	4.65	5.02	5.00	5.08	5.10	5.02	5.05	5.07
TC1200658	NM_207376	---	---	3.25E-06	2	3.60	3.57	3.64	4.41	4.75	4.64	4.41	4.33
TC0300762	NMD3	51068	NMD3 homolog (S. cerevisiae)	1.24E-05	2	3.99	4.70	4.59	4.53	4.87	4.89	4.77	4.59

TC0500160	NNT	23530	nicotinamide nucleotide transhydroger	3.12E-08	2	4.31	4.69	4.82	5.13	5.22	5.15	5.15	4.87
TC0400780	NOL14	8602	nucleolar protein 14	3.94E-05	2	4.28	4.26	4.26	4.33	4.43	4.38	4.53	4.35
TC0400456	NOLA1	54433	nucleolar protein family A, member 1 (	0.00012	2	4.92	4.94	4.93	5.06	5.09	5.11	5.19	5.15
TC0501539	NOLA2	55651	nucleolar protein family A, member 2 (	2.39E-06	2	4.77	5.02	4.99	5.29	5.44	5.46	5.44	5.10
TC1500807	NOLA3	55505	nucleolar protein family A, member 3 (	2.25E-06	2	9.97	10.38	10.42	10.67	10.55	10.58	10.51	10.49
TC1000533	NOLC1	9221	nucleolar and coiled-body phosphopro	5.59E-08	2	4.18	4.28	3.96	4.40	4.52	4.57	4.81	4.62
TC0201009	NOP5/NOP58	51602	nucleolar protein NOP5/NOP58	5.39E-07	2	3.50	3.64	3.48	3.84	4.02	3.99	4.11	3.88
TC1400030	NP	4860	nucleoside phosphorylase	3.44E-05	2	4.42	4.71	4.73	4.86	5.24	5.02	4.92	4.67
TC0801144	NPAL2	79815	NIPA-like domain containing 2	0.00015	2	3.49	3.90	4.12	4.02	4.22	4.25	4.30	4.26
TC0100264	NPAL3	57185	NIPA-like domain containing 3 /// NIPA	3.16E-05	2	3.74	3.72	3.75	3.78	3.94	3.84	3.91	3.82
TC0500702	NPM1	4869	nucleophosmin (nucleolar phosphopro	6.64E-08	2	6.55	7.14	6.89	7.21	7.42	7.51	7.48	7.20
TC1300055	NR_002162.1	---	ATP synthase, H+ transporting, mitocho	2.89E-15	2	7.66	8.31	8.58	8.62	8.57	8.56	8.56	8.49
TC1100965	NRGN	4900	neurogranin (protein kinase C substrat	0.000385	2	5.34	5.84	5.62	6.23	6.51	6.45	6.22	6.18
TC2100224	NRIP1	8204	nuclear receptor interacting protein 1	6.06E-10	2	4.47	5.88	5.75	5.92	6.14	6.07	5.99	5.66
TC0103218	NSL1	25936	NSL1, MIND kinetochore complex com	1.14E-05	2	5.52	5.63	5.65	5.83	5.82	5.80	5.95	5.92
TC1001322	NSMCE4A	54780	non-SMC element 4 homolog A (S. cere	0.000238	2	3.87	4.02	4.03	4.03	4.24	4.13	4.22	4.01
TC0701313	NSUN5	55695	NOL1/NOP2/Sun domain family, mem	3.04E-08	2	5.96	5.85	5.93	6.13	6.25	6.21	6.20	6.02
TC0701118	NT5C3	51251	5'-nucleotidase, cytosolic III	2.75E-07	2	6.69	7.36	7.60	7.47	7.38	7.62	7.72	7.73
TC1600884	NTAN1	123803	N-terminal asparagine amidase	2.33E-08	2	5.85	6.40	6.51	6.66	6.48	6.54	6.67	6.69
TC1600170	NUBP1	4682	nucleotide binding protein 1 (MinD ho	2.05E-10	2	4.99	5.31	5.15	5.57	5.62	5.62	5.75	5.62
TC1100203	NUCB2	4925	nucleobindin 2	4.08E-14	2	5.41	6.24	6.20	6.47	6.73	6.77	6.71	6.43
TC0103168	NUCKS1	64710	nuclear casein kinase and cyclin-depen	1.22E-11	2	5.33	6.54	6.36	6.52	6.78	6.78	6.88	6.48
TC1601117	NUDT21	11051	nudix (nucleoside diphosphate linked	4.34E-06	2	6.55	6.79	7.08	7.17	7.11	7.26	7.32	7.25
TC0601195	NUDT3 /// RPS	732348 //	nudix (nucleoside diphosphate linked	1.17E-07	2	6.85	6.72	6.84	7.10	7.06	7.04	7.13	7.07
TC1200583	NUDT4	11163	nudix (nucleoside diphosphate linked	1.87E-15	2	4.85	5.11	5.25	5.46	5.54	5.54	5.49	5.41
TC0101236	NUF2	83540	NUF2, NDC80 kinetochore complex co	0.000238	2	2.60	2.77	2.77	2.95	3.27	3.19	3.09	2.94
TC1300445	NUFIP1	26747	nuclear fragile X mental retardation pr	0.000542	2	3.56	3.73	3.69	3.86	3.83	3.85	3.90	3.80
TC0900611	NUP188	23511	nucleoporin 188kDa /// nucleoporin 18	9.22E-06	2	4.22	4.24	4.18	4.34	4.53	4.47	4.59	4.38
TC0700726	NUP205	23165	nucleoporin 205kDa	0.000329	2	3.56	3.61	3.54	3.73	3.88	3.84	3.94	3.80
TC0301025	NUP210	23225	nucleoporin 210kDa	7.25E-05	2	4.59	4.54	4.52	4.60	4.76	4.73	4.80	4.66
TC0200917	NUP35	129401	nucleoporin 35kDa /// Nucleoporin NU	6.93E-05	2	2.87	2.88	2.93	2.91	3.06	2.94	3.04	3.03
TC1201504	NUP37	79023	nucleoporin 37kDa	8.65E-06	2	4.30	4.49	4.81	4.86	4.89	4.96	4.97	4.93
TC0601676	NUP43	348995	nucleoporin 43kDa /// Nucleoporin Nu	0.000611	2	3.26	3.42	3.65	3.67	3.71	3.73	3.86	3.73
TC0401058	NUP54	53371	nucleoporin 54kDa /// Nucleoporin p5	9.98E-05	2	4.09	4.10	4.14	4.31	4.30	4.32	4.45	4.36

TC1700954	NUP88	4927	nucleoporin 88kDa	4.08E-08	2	4.35	4.28	4.25	4.46	4.63	4.59	4.73	4.62
TC0700112	NUPL2	11097	nucleoporin like 2 /// Nucleoporin-like	0.000496	2	3.60	3.73	3.74	3.80	3.88	3.82	3.92	3.85
TC1500253	NUSAP1	51203	nucleolar and spindle associated protei	1.37E-13	2	4.34	5.04	5.02	5.70	6.17	6.05	5.84	5.50
TC1600530	NUTF2	731535 //	nuclear transport factor 2	8.52E-11	2	5.89	5.59	5.65	6.25	6.48	6.39	6.36	6.26
TC0103274	NVL	4931	nuclear VCP-like /// Nuclear valosin-co	2.58E-05	2	3.89	3.92	3.88	4.08	4.15	4.17	4.33	4.17
TC1600931	O75704_HUM	---	RRN3 RNA polymerase I transcription f	0.000293	2	2.80	2.72	2.76	2.83	2.95	2.84	2.88	2.89
TC0500290	O95036_HUM	---	---	8.37E-10	2	5.99	6.92	6.85	7.20	7.26	7.39	7.28	7.10
TC1200427	OBFC2B	79035	oligonucleotide/oligosaccharide-bindin	0.000259	2	5.02	5.12	5.14	5.20	5.33	5.32	5.37	5.20
TC1900294	OCEL1	79629	occludin/ELL domain containing 1	0.000453	2	5.27	5.30	5.26	5.54	5.47	5.46	5.47	5.43
TC0900599	ODF2	4957	outer dense fiber of sperm tails 2 /// o	2.80E-07	2	4.88	4.92	4.83	4.95	5.04	5.02	5.14	5.01
TC0202106	OLA1	29789	Obg-like ATPase 1 /// Putative GTP-bin	1.20E-06	2	4.07	4.60	4.58	4.70	4.86	4.82	4.80	4.60
TC1901152	OLFM2	93145	olfactomedin 2	0.000616	2	4.69	4.77	4.80	4.92	4.86	4.88	4.88	4.91
TC1200968	OLR1	4973	oxidized low density lipoprotein (lectin	5.22E-13	2	3.59	5.49	4.03	5.14	6.36	6.58	5.88	5.03
TC0102296	OMA1	115209	OMA1 homolog, zinc metallopeptidase	1.71E-06	2	5.74	5.63	5.88	5.98	5.93	6.05	6.03	6.08
TC1600350	ORAI3 /// FBXL	93129 ///	ORAI calcium release-activated calcium	1.62E-05	2	5.04	5.02	4.98	5.10	5.14	5.13	5.12	5.11
TC0102257	ORC1L	4998	origin recognition complex, subunit 1-li	1.31E-05	2	3.16	3.28	3.24	3.38	3.57	3.50	3.56	3.35
TC0201990	ORC4L	5000	origin recognition complex, subunit 4-li	3.32E-05	2	5.13	5.16	5.46	5.48	5.29	5.41	5.41	5.40
TC0601506	OSTM1	28962	osteopetrosis associated transmembra	2.27E-07	2	6.18	6.23	6.33	6.53	6.45	6.63	6.61	6.67
TC0500948	OXCT1	5019	3-oxoacid CoA transferase 1	1.45E-05	2	3.38	3.41	3.41	3.66	3.84	3.70	3.80	3.67
TC0Y00112	P2RY8	286530	purinergic receptor P2Y, G-protein cou	1.41E-08	2	6.51	6.60	6.61	6.71	6.77	6.84	6.91	6.75
TC17r00049	P4HB	5034	procollagen-proline, 2-oxoglutarate 4-	5.08E-05	2	5.89	6.52	6.30	6.54	6.70	6.53	6.45	6.34
TC1701785	P4HB	5034	procollagen-proline, 2-oxoglutarate 4-	0.000124	2	5.51	6.12	5.92	6.09	6.23	6.11	6.04	5.94
TC0102146	PABPC4	8761	poly(A) binding protein, cytoplasmic 4 (	1.78E-09	2	4.78	5.04	5.01	5.11	5.29	5.25	5.28	5.12
TC0600067	PAK1IP1	55003	PAK1 interacting protein 1	4.88E-05	2	3.56	3.70	3.73	3.83	3.91	3.94	4.04	3.93
TC1500224	PAK6 /// BUB1	56924 ///	p21 protein (Cdc42/Rac)-activated kina	6.36E-06	2	3.44	3.52	3.46	3.63	3.80	3.79	3.70	3.60
TC1600943	PALB2	79728	partner and localizer of BRCA2	0.000502	2	3.18	3.22	3.16	3.26	3.40	3.37	3.44	3.38
TC0600456	PAQR8	85315	progestin and adipoQ receptor family r	3.03E-06	2	3.87	4.17	4.10	4.25	4.38	4.33	4.23	4.13
TC2000371	PARD6B	84612	par-6 partitioning defective 6 homolog	0.000247	2	3.89	3.86	3.78	3.94	4.04	4.00	3.92	3.94
TC0100087	PARK7	11315	Parkinson disease (autosomal recessive	3.86E-15	2	7.42	7.72	8.04	8.12	8.21	8.13	8.09	7.98
TC0103286	PARP1	142	poly (ADP-ribose) polymerase family, m	5.65E-09	2	4.10	4.35	4.31	4.54	4.49	4.58	4.83	4.64
TC0900566	PBX3	5090	pre-B-cell leukemia homeobox 3 /// Pr	6.49E-16	2	5.11	5.54	5.67	5.81	5.75	5.69	5.64	5.59
TC0500490	PCBD2	84105	pterin-4 alpha-carbinolamine dehydrat	6.84E-05	2	3.61	3.90	3.98	3.95	4.09	4.07	4.14	3.99
TC0200324	PCBP1	5093	poly(rC) binding protein 1	1.82E-08	2	9.50	9.88	9.87	9.96	10.03	9.97	9.87	9.92
TC0300643	PCCB	5096	propionyl Coenzyme A carboxylase, be	3.94E-06	2	4.10	4.14	4.10	4.32	4.32	4.27	4.22	4.23

TC0201640	PCGF1	84759	polycomb group ring finger 1 /// Polyc	5.75E-05	2	5.02	4.90	5.04	5.24	5.09	5.18	5.26	5.21
TC1001253	PCGF6	84108	polycomb group ring finger 6	3.78E-06	2	3.38	3.42	3.64	3.71	3.83	3.74	3.72	3.67
TC1300660	PCID2	55795	PCI domain containing 2 /// PCI domai	0.000472	2	3.51	3.47	3.48	3.52	3.61	3.57	3.66	3.59
TC2000533	PCNA	5111	proliferating cell nuclear antigen	3.63E-17	2	4.12	4.37	4.13	5.14	5.66	5.81	5.63	5.15
TC0300455	PCNP	57092	PEST proteolytic signal containing nucl	3.69E-06	2	6.24	6.62	6.76	6.94	6.77	6.85	6.87	6.80
TC0301627	PCOLCE2	26577	procollagen C-endopeptidase enhance	5.58E-13	2	3.66	4.52	5.86	5.89	6.16	6.07	5.51	4.81
TC0200325	PCYOX1	51449	prenylcysteine oxidase 1	5.51E-11	2	4.35	4.31	4.36	4.77	4.92	4.88	5.03	4.76
TC0701453	PDAP1	11333	PDGFA associated protein 1	3.42E-06	2	6.92	7.10	7.02	7.22	7.25	7.17	7.28	7.20
TC0601776	PDCD2	5134	programmed cell death 2	8.18E-11	2	5.08	5.24	5.28	5.45	5.50	5.53	5.56	5.47
TC1900403	PDCD5	9141	programmed cell death 5 /// Program	2.35E-08	2	5.86	6.39	6.52	6.64	6.77	6.70	6.80	6.55
TC1501037	PDCD7	10081	programmed cell death 7 /// Program	3.59E-06	2	5.10	5.21	5.20	5.33	5.48	5.59	5.63	5.46
TC0901312	PDCL	5082	phosducin-like	4.75E-06	2	4.49	4.83	4.74	4.86	4.75	4.76	4.91	4.87
TC0200526	PDCL3	79031	phosducin-like 3	8.06E-10	2	5.10	5.23	5.25	5.86	5.86	5.89	6.06	5.91
TC0X00077	PDHA1	5160	pyruvate dehydrogenase (lipoamide) a	5.56E-05	2	5.23	5.68	5.53	5.61	5.92	5.87	5.79	5.55
TC1500284	PDIA3	2923	protein disulfide isomerase family A, m	4.55E-08	2	6.33	6.43	6.35	6.75	6.63	6.75	6.92	6.84
TC0701735	PDIA4	9601	protein disulfide isomerase family A, m	0.000646	2	4.54	4.67	4.63	4.81	4.91	4.79	4.91	4.78
TC0201310	PDIA6	10130	protein disulfide isomerase family A, m	2.38E-06	2	4.68	4.86	4.86	5.06	5.11	5.15	5.22	5.10
TC0100281	PDIK1L	149420	PDLIM1 interacting kinase 1 like	0.000501	2	3.60	3.69	3.69	3.78	3.94	3.90	3.86	3.80
TC1001179	PDLIM1	9124	PDZ and LIM domain 1 (elfin)	2.19E-10	2	4.99	4.96	4.98	6.00	5.91	6.24	6.20	6.10
TC0400408	PDLIM5	10611	PDZ and LIM domain 5 /// PDZ and LIM	1.32E-05	2	5.20	5.46	5.60	5.70	5.63	5.68	5.59	5.61
TC2000659	PDRG1	81572	p53 and DNA damage regulated 1	0.000349	2	4.13	4.41	4.34	4.46	4.46	4.59	4.79	4.61
TC0400894	PDS5A	23244	PDS5, regulator of cohesion maintenan	0.000686	2	5.06	5.59	5.57	5.70	5.70	5.68	5.77	5.58
TC1600202	PDXDC1	23042	pyridoxal-dependent decarboxylase do	1.09E-08	2	5.01	5.00	4.89	5.14	5.37	5.36	5.32	5.19
TC1200736	PEBP1	5037	phosphatidylethanolamine binding pro	0.000512	2	4.86	5.20	5.30	5.31	5.35	5.37	5.36	5.29
TC0401033	PF4	5196	platelet factor 4 (chemokine (C-X-C mo	2.36E-06	2	5.98	6.82	6.48	7.41	7.77	7.85	7.50	7.59
TC0400314	PF4V1	5197	platelet factor 4 variant 1	1.66E-05	2	3.78	4.58	4.27	5.05	5.39	5.69	5.35	5.45
TC0102932	PFDN2	5202	prefoldin subunit 2	2.60E-12	2	6.60	6.60	6.54	7.00	7.02	7.03	7.13	7.06
TC2000383	PFDN4	5203	prefoldin subunit 4	0.000105	2	4.03	4.22	4.22	4.25	4.41	4.33	4.35	4.20
TC0700466	PFTK1	5218	PFTAIRE protein kinase 1 /// Serine/thr	1.94E-05	2	6.01	6.59	6.49	6.75	6.74	6.86	6.61	6.53
TC0101729	PGBD2	267002	piggyBac transposable element derive	3.33E-06	2	4.43	4.42	4.42	4.47	4.56	4.64	4.67	4.63
TC1900303	PGLS	25796	6-phosphogluconolactonase	1.67E-07	2	5.35	5.72	5.79	5.87	5.88	5.90	5.87	5.87
TC0X00525	PGRMC1	10857	progesterone receptor membrane com	0.000138	2	5.19	5.88	5.68	5.94	6.15	6.10	5.92	5.88
TC0401248	PGRMC2	10424	progesterone receptor membrane com	3.95E-08	2	5.22	5.23	5.19	5.42	5.42	5.42	5.63	5.62
TC0601770	PHF10	55274	PHD finger protein 10 /// PHD finger pr	6.56E-06	2	4.24	4.30	4.34	4.58	4.71	4.70	4.86	4.68

TC0700073	PHF14	9678	PHD finger protein 14	2.95E-07	2	3.72	4.13	4.32	4.53	4.55	4.46	4.62	4.40
TC1000773	PHYH	5264	phytanoyl-CoA 2-hydroxylase /// Phyta	1.92E-07	2	4.17	4.37	4.37	4.47	4.49	4.51	4.54	4.45
TC0400136	PI4K2B	55300	phosphatidylinositol 4-kinase type 2 be	3.23E-08	2	3.87	4.25	4.24	4.45	4.66	4.66	4.74	4.52
TC1800517	PIGN	23556	phosphatidylinositol glycan anchor bio	0.000526	2	3.82	3.89	3.98	4.02	4.03	4.08	4.16	4.05
TC1701168	PIGS	94005	phosphatidylinositol glycan anchor bio	2.20E-05	2	5.43	5.79	5.86	6.01	5.89	5.83	5.90	5.87
TC2000683	PIGU	128869	phosphatidylinositol glycan anchor bio	1.83E-06	2	4.17	4.37	4.36	4.48	4.87	4.81	4.65	4.56
TC0401117	PIGY	84992	phosphatidylinositol glycan anchor bio	8.37E-13	2	4.20	5.41	5.21	5.55	5.53	5.64	5.80	5.50
TC1100767	PIWIL4	143689	piwi-like 4 (Drosophila)	1.86E-10	2	3.08	3.46	3.34	4.00	4.45	4.40	4.30	3.73
TC1201093	PKP2	5318	plakophilin 2	5.60E-09	2	3.90	4.14	4.10	4.37	4.57	4.47	4.60	4.39
TC2000661	PLAGL2	5326	pleiomorphic adenoma gene-like 2	1.45E-05	2	5.33	5.50	5.36	5.60	5.68	5.76	5.72	5.71
TC1000347	PLAU	5328	plasminogen activator, urokinase /// U	3.64E-06	2	3.90	3.97	3.93	3.96	4.09	4.16	4.07	4.00
TC0300093	PLCL2	23228	phospholipase C-like 2	0.000899	2	6.73	6.85	6.79	7.03	6.85	6.98	7.13	7.05
TC0700152	PLEKHA8	84725	pleckstrin homology domain containin	0.000197	2	3.82	3.96	3.91	3.99	4.03	4.03	4.05	4.02
TC1201124	PLEKHA9	51054	pleckstrin homology domain containin	0.000625	2	4.17	4.30	4.24	4.44	4.54	4.58	4.56	4.53
TC1600267	PLK1	5347	polo-like kinase 1 (Drosophila) /// Seri	9.97E-06	2	4.41	4.52	4.50	4.67	4.82	4.82	4.67	4.59
TC0400523	PLK4	10733	polo-like kinase 4 (Drosophila)	1.32E-06	2	2.62	2.77	2.69	2.98	3.37	3.33	3.23	2.96
TC0300679	PLS1	5357	plastin 1 (I isoform)	0.000758	2	2.71	2.85	2.75	2.82	3.04	2.97	2.96	2.87
TC1701048	PMP22	5376	peripheral myelin protein 22	0.000157	2	4.41	4.62	4.62	4.76	4.73	4.78	4.75	4.79
TC0200935	PMS1	5378	PMS1 postmeiotic segregation increase	0.000751	2	3.17	3.25	3.26	3.30	3.38	3.29	3.32	3.30
TC1400980	PNMA1	9240	paraneoplastic antigen MA1	0.000232	2	3.86	4.12	4.39	4.61	4.63	4.47	4.23	4.14
TC0101255	POGK	57645	pogo transposable element with KRAB	4.81E-07	2	4.70	4.89	4.82	4.96	5.09	5.06	5.09	4.97
TC0X00100	POLA1	5422	polymerase (DNA directed), alpha 1 ///	5.69E-07	2	3.33	3.39	3.32	3.58	3.89	3.78	3.81	3.60
TC1201710	POLE	5426	polymerase (DNA directed), epsilon ///	3.25E-06	2	4.25	4.19	4.09	4.25	4.49	4.49	4.44	4.27
TC1300051	POLR1D	51082	polymerase (RNA) I polypeptide D, 16k	2.66E-07	2	5.27	5.46	5.65	5.77	5.79	5.78	5.90	5.78
TC1100486	POLR2G	5436	polymerase (RNA) II (DNA directed) pol	1.88E-09	2	5.77	5.52	5.83	5.99	6.01	5.92	6.07	5.95
TC0300859	POLR2H	5437	polymerase (RNA) II (DNA directed) pol	1.02E-06	2	4.01	4.16	4.03	4.35	4.45	4.46	4.47	4.26
TC1901428	POLR2I	5438	polymerase (RNA) II (DNA directed) pol	2.98E-06	2	5.06	5.27	5.28	5.51	5.58	5.50	5.57	5.62
TC0800464	POLR2K	5440	polymerase (RNA) II (DNA directed) pol	4.74E-08	2	5.83	6.25	6.32	6.74	6.81	6.77	6.88	6.65
TC1101050	POLR2L	5441	polymerase (RNA) II (DNA directed) pol	6.79E-12	2	6.39	7.29	7.46	7.69	7.76	7.69	7.56	7.27
TC0102635	POLR3C	10623	polymerase (RNA) III (DNA directed) po	2.98E-10	2	4.92	4.84	4.95	5.21	5.23	5.28	5.47	5.28
TC0500335	POLR3G	10622	polymerase (RNA) III (DNA directed) po	4.97E-06	2	4.18	4.47	4.45	4.71	4.76	5.08	5.02	4.97
TC0102631	POLR3GL	84265	polymerase (RNA) III (DNA directed) po	5.04E-10	2	5.62	5.85	6.08	6.23	6.03	6.18	6.38	6.27
TC1600706	POLR3K	51728	polymerase (RNA) III (DNA directed) po	1.06E-09	2	4.97	4.81	4.94	5.15	5.22	5.37	5.45	5.36
TC1001041	PPA1	5464	pyrophosphatase (inorganic) 1 /// Inor	4.41E-06	2	3.01	3.45	3.14	3.63	3.82	3.76	3.70	3.45

TC0102290	PPAP2B	8613	phosphatidic acid phosphatase type 2B	0.000284	2	3.33	3.44	3.49	3.47	3.59	3.57	3.44	3.42
TC0401034	PPBP	5473	pro-platelet basic protein (chemokine (	4.08E-11	2	5.68	8.00	7.23	9.25	9.65	9.76	9.22	9.33
TC0X00075	PPEF1	5475	protein phosphatase, EF-hand calcium	8.68E-07	2	2.38	2.43	2.42	2.38	2.71	2.55	2.46	2.42
TC1501027	PPIB	5479	peptidylprolyl isomerase B (cyclophilin	9.28E-07	2	6.50	6.83	6.94	7.21	7.21	7.12	7.11	7.08
TC0100449	PPIH	10465	peptidylprolyl isomerase H (cyclophilin	1.13E-07	2	3.75	3.73	3.68	3.90	4.06	4.01	4.20	4.01
TC0201391	PPM1G	5496	protein phosphatase 1G (formerly 2C),	1.02E-16	2	5.62	5.52	5.55	5.87	5.88	5.95	6.05	5.96
TC0201242	PPP1R7	5510	protein phosphatase 1, regulatory (inhi	2.66E-05	2	7.39	7.34	7.43	7.60	7.51	7.62	7.74	7.71
TC0100314	PPP1R8	5511	protein phosphatase 1, regulatory (inhi	7.83E-05	2	4.87	4.89	4.98	4.99	5.04	5.04	5.15	5.10
TC0800848	PPP2CB	5516	protein phosphatase 2 (formerly 2A), c	0.000605	2	5.59	6.06	5.96	6.24	6.19	6.23	6.22	6.22
TC0101499	PPP2R5A	5525	protein phosphatase 2, regulatory subu	0.000346	2	6.95	7.62	7.60	7.58	7.68	7.72	7.62	7.58
TC1400592	PPP2R5C	5527	protein phosphatase 2, regulatory subu	8.34E-06	2	7.41	7.61	7.68	7.71	7.54	7.67	7.68	7.78
TC0X00216	PQBP1	10084	polyglutamine binding protein 1 /// Po	0.000636	2	6.18	6.42	6.27	6.54	6.51	6.46	6.51	6.43
TC1501243	PRC1	9055	protein regulator of cytokinesis 1	5.71E-09	2	4.04	4.29	4.15	4.48	4.98	4.90	4.71	4.44
TC0100156	PRDM2	7799	PR domain containing 2, with ZNF dom	4.00E-05	2	6.47	6.51	6.55	6.65	6.72	6.71	6.73	6.55
TC1100517	PRDX5	25824	peroxiredoxin 5	8.22E-13	2	9.39	9.91	10.05	10.23	10.19	10.17	10.02	9.92
TC0500748	PRELID1	649930 //	PRELI domain containing 1	0.000691	2	9.34	9.54	9.49	9.63	9.50	9.65	9.71	9.74
TC0601489	PREP	5550	prolyl endopeptidase /// Prolyl endope	1.17E-06	2	3.76	3.96	3.91	4.12	4.26	4.14	4.29	3.97
TC0201476	PREPL	9581	prolyl endopeptidase-like	1.14E-09	2	4.01	4.01	3.96	4.40	4.57	4.60	4.61	4.38
TC1201307	PRIM1	5557	primase, DNA, polypeptide 1 (49kDa)	1.36E-09	2	3.50	3.68	3.63	3.99	4.33	4.26	4.24	4.06
TC0600481	PRIM2	5558	primase, DNA, polypeptide 2 (58kDa)	0.000513	2	2.75	2.89	2.89	2.97	3.04	3.03	3.06	2.98
TC0100686	PRKACB	5567	protein kinase, cAMP-dependent, catal	3.43E-05	2	3.49	3.57	3.54	3.67	3.67	3.79	3.77	3.76
TC0700605	PRKAR2B	5577	protein kinase, cAMP-dependent, regu	3.52E-07	2	3.52	4.39	4.06	5.64	6.13	6.13	5.50	5.48
TC0700574	PRKRIP1	79706	PRKR interacting protein 1 (IL11 induci	1.59E-05	2	5.55	5.53	5.53	5.70	5.67	5.72	5.78	5.70
TC1100227	PRMT3	10196	protein arginine methyltransferase 3 //	2.74E-05	2	3.67	3.64	3.67	3.75	3.80	3.82	3.82	3.83
TC0X00043	PRPS2	5634	phosphoribosyl pyrophosphate synthet	6.95E-08	2	4.10	4.38	4.31	4.49	4.57	4.61	4.67	4.60
TC1701713	PRPSAP1	5635	phosphoribosyl pyrophosphate synthet	1.37E-07	2	4.23	4.40	4.30	4.53	4.70	4.58	4.55	4.36
TC1700640	PRR11	55771	proline rich 11	2.70E-07	2	4.06	4.16	4.21	4.46	4.56	4.56	4.70	4.61
TC0500444	PRRC1	133619	proline-rich coiled-coil 1 /// proline-ric	7.03E-09	2	5.00	5.49	5.72	5.80	5.85	5.77	5.85	5.62
TC1900020	PRTN3	5657	proteinase 3 (serine proteinase, neutr	0.000134	2	5.07	5.31	5.28	5.48	5.62	5.51	5.47	5.26
TC0900314	PSAT1	29968	phosphoserine aminotransferase 1	4.73E-05	2	3.09	3.25	3.24	3.44	3.70	3.50	3.48	3.26
TC0701157	PSMA2	5683	proteasome (prosome, macropain) sub	2.48E-10	2	6.95	7.53	7.78	7.70	7.69	7.74	7.81	7.76
TC1500524	PSMA4	5685	proteasome (prosome, macropain) sub	0.000123	2	6.83	7.32	7.37	7.37	7.22	7.36	7.47	7.46
TC0102518	PSMA5	5686	proteasome (prosome, macropain) sub	2.53E-05	2	5.67	5.95	6.12	6.21	6.15	6.26	6.37	6.37
TC2000879	PSMA7	5688	proteasome (prosome, macropain) sub	1.56E-05	2	6.89	7.00	7.13	7.17	7.20	7.25	7.26	7.16

TC0102107	PSMB2	5690	proteasome (prosome, macropain) sub	3.71E-05	2	4.83	5.16	5.19	5.26	5.35	5.35	5.47	5.38
TC1400712	PSMB5	5693	proteasome (prosome, macropain) sub	1.05E-07	2	4.47	4.52	4.85	4.82	4.80	4.70	4.77	4.68
TC0200817	PSMD14	10213	proteasome (prosome, macropain) 26S	2.47E-06	2	3.80	4.64	4.73	4.77	5.00	4.93	4.88	4.55
TC2100346	PSMG1	8624	proteasome (prosome, macropain) ass	5.03E-10	2	4.44	4.77	4.64	4.95	5.23	5.25	5.23	4.94
TC1800068	PSMG2 /// TN	56984	proteasome (prosome, macropain) ass	8.47E-06	2	4.35	4.64	4.70	4.64	4.72	4.77	4.85	4.79
TC0200418	PTCD3	55037	Pentatricopeptide repeat domain 3	7.50E-08	2	3.66	3.51	3.55	3.85	3.99	4.02	4.14	3.90
TC0800444	PTDSS1	9791	phosphatidylserine synthase 1	1.33E-08	2	4.15	4.56	4.40	4.78	5.08	5.09	5.05	4.67
TC0102074	PTP4A2	8073	protein tyrosine phosphatase type IVA,	1.26E-06	2	8.63	8.84	8.92	8.95	8.93	8.89	8.93	8.96
TC0900807	PTPLAD2	401494	protein tyrosine phosphatase-like A do	0.000259	2	7.41	7.68	7.97	7.84	7.73	7.90	7.83	7.96
TC0301501	PTPLB	201562	protein tyrosine phosphatase-like (prol	1.73E-08	2	4.71	4.61	4.46	5.09	5.20	5.21	5.23	5.09
TC1100323	PTPMT1 /// N	114971 //	protein tyrosine phosphatase, mitocho	2.20E-06	2	5.19	5.27	5.40	5.56	5.58	5.56	5.67	5.48
TC1200709	PTPN11	647552 //	protein tyrosine phosphatase, non-rec	7.07E-05	2	6.82	7.26	7.12	7.32	7.31	7.29	7.38	7.21
TC0500663	PTTG1	9232	pituitary tumor-transforming 1	3.26E-10	2	4.19	4.44	4.21	4.80	5.25	5.12	4.99	4.65
TC0300742	PTX3	5806	pentraxin-related gene, rapidly induce	3.40E-15	2	3.93	4.75	4.45	4.64	4.85	4.86	4.67	4.56
TC0500525	PURA	5813	purine-rich element binding protein A	1.33E-06	2	4.55	4.56	4.63	4.86	4.92	5.00	5.30	5.15
TC1200669	PWP1	11137	PWP1 homolog (S. cerevisiae)	1.69E-05	2	4.56	4.45	4.49	4.76	4.80	4.86	4.96	4.91
TC1200846	PXMP2	5827	peroxisomal membrane protein 2, 22k	1.28E-06	2	4.57	4.76	4.67	4.94	5.13	5.12	4.96	4.81
TC1601037	PYCARD	29108	PYD and CARD domain containing /// A	2.82E-05	2	6.79	6.75	6.92	7.21	7.09	7.07	6.95	7.03
TC0200507	Q08AK5_HUM	---	KIAA1641. [Source:Uniprot/SPTREMBL;	0.000167	2	3.62	4.18	3.83	4.01	4.28	4.31	4.22	3.94
TC1400447	Q15203_HUM	---	Prothymosin alpha. [Source:Uniprot/S	5.13E-07	2	5.37	5.59	5.53	5.78	6.04	5.98	6.02	5.97
TC2000368	Q4G0G3_HUM	---	---	0.000973	2	5.19	5.03	4.93	5.31	5.26	5.31	5.23	4.95
TC0201743	Q53S06_HUM	---	---	0.000361	2	3.91	4.19	4.12	4.27	4.42	4.41	4.39	4.12
TC0300103	Q5T7C6_HUM	---	High-mobility group box 1 (Fragment).	0.000737	2	4.51	4.95	5.05	5.14	5.10	5.19	5.11	5.03
TC0600355	Q5T8I0_HUMA	---	OTTHUMP00000016319. [Source:Unip	5.95E-11	2	7.23	7.79	7.90	7.89	7.91	7.93	7.93	7.88
TC0601272	Q5T8W0_HUM	---	OTTHUMP00000016411 (Fragment). [S	2.66E-09	2	7.66	8.35	8.32	8.73	8.78	8.84	8.80	8.65
TC0102696	Q5TEC7_HUM	---	Family with sequence similarity 72, me	0.000155	2	3.25	3.20	3.10	3.48	3.76	3.66	3.66	3.45
TC0700592	Q6AI40_HUMA	---	---	1.40E-05	2	7.10	7.84	7.69	7.89	7.91	7.83	7.91	7.72
TC0701054	Q75MH1_HUM	---	Ribosomal protein S26 (Fragment). [So	2.81E-08	2	5.92	6.67	6.69	6.82	6.90	6.90	6.86	6.77
TC0800954	Q8N287_HUM	---	CDNA FLJ33669 fis, clone BRAMY20287	0.000828	2	5.13	6.07	6.24	6.28	6.46	6.45	6.53	6.03
TC0300671	Q96NB8_HUM	---	CDNA FLJ31131 fis, clone IMR322009	6.07E-05	2	6.84	7.05	7.17	7.05	7.05	7.43	7.77	7.72
TC1001222	Q9H354_HUM	---	---	2.77E-18	2	4.12	5.92	4.88	6.87	7.60	8.14	7.73	6.87
TC2000488	Q9NQ39_HUM	---	Ribosomal protein S10-like pseudogen	1.99E-05	2	7.38	7.53	7.62	7.73	7.79	7.85	7.76	7.74
TC1200950	Q9NYD3_HUM	---	Prothymosin alpha. [Source:Uniprot/S	1.27E-14	2	8.64	8.85	8.56	9.24	9.58	9.69	9.70	9.46
TC0301006	Q9NZ47_HUM	---	Uncharacterized hematopoietic stem/	2.25E-08	2	9.57	10.07	10.14	10.21	10.20	10.14	10.15	10.14

TC1201241	Q9P192_HUM	---	---	3.45E-06	2	8.41	8.99	8.75	8.99	9.01	8.98	9.12	8.86
TC0102040	Q9UHS2_HUM	---	---	4.53E-05	2	5.34	5.61	5.71	5.83	5.73	5.90	6.19	6.15
TC0400842	QDPR	5860	quinoid dihydropteridine reductase	4.44E-05	2	4.33	4.45	4.37	4.49	4.68	4.60	4.64	4.48
TC1100259	QSER1	---	Glutamine and serine-rich protein 1. [S	6.46E-07	2	3.95	3.96	3.89	4.14	4.25	4.24	4.32	4.21
TC0200738	R3HDM1	23518	R3H domain containing 1 /// R3H doma	1.35E-11	2	5.43	5.97	6.04	6.21	6.14	6.16	6.24	6.18
TC1800039	RAB12	201475	RAB12, member RAS oncogene family	4.30E-06	2	3.83	4.13	4.07	4.39	4.08	4.18	4.39	4.34
TC0102804	RAB13	5872	RAB13, member RAS oncogene family	1.06E-14	2	5.46	6.39	5.86	6.98	7.42	7.43	7.29	6.56
TC0901300	RAB14	51552	RAB14, member RAS oncogene family	4.54E-06	2	6.65	6.74	6.98	7.09	6.93	7.02	6.98	7.01
TC0X01401	RAB39B	116442	RAB39B, member RAS oncogene family	3.56E-09	2	3.70	4.33	4.36	4.76	4.48	4.70	4.71	4.57
TC1201187	RACGAP1	29127	Rac GTPase activating protein 1	4.40E-07	2	4.31	4.40	4.35	4.57	4.97	4.89	4.83	4.58
TC0500910	RAD1	5810	RAD1 homolog (S. pombe) /// Cell cycl	9.15E-07	2	4.66	4.81	4.78	4.86	4.98	5.00	5.00	4.93
TC0300984	RAD18	56852	RAD18 homolog (S. cerevisiae)	2.11E-08	2	3.53	3.52	3.49	3.69	3.82	3.85	4.05	3.95
TC0801207	RAD21	5885	RAD21 homolog (S. pombe)	0.000209	2	8.97	9.18	9.00	9.06	9.02	9.17	9.16	9.22
TC0500466	RAD50	10111	RAD50 homolog (S. cerevisiae)	1.33E-07	2	3.67	3.77	3.68	4.06	4.16	4.19	4.44	4.14
TC1500239	RAD51	5888	RAD51 homolog (RecA homolog, E. coli	5.72E-05	2	3.68	3.79	3.70	3.88	4.15	4.13	4.02	3.89
TC1200032	RAD51AP1	10635	RAD51 associated protein 1 /// RAD51-	3.01E-05	2	2.22	2.37	2.30	2.51	2.87	2.83	2.73	2.56
TC1700634	RAD51C	5889	RAD51 homolog C (S. cerevisiae)	7.35E-09	2	4.21	4.43	4.51	4.75	5.01	5.02	5.03	4.81
TC1701232	RAD51L3	5892	RAD51-like 3 (S. cerevisiae) /// DNA re	0.000618	2	4.61	4.66	4.62	4.66	4.76	4.77	4.76	4.67
TC0101115	RAG1AP1	55974	recombination activating gene 1 activa	9.66E-05	2	5.12	5.30	5.28	5.43	5.51	5.45	5.41	5.38
TC0700199	RALA	5898	v-ral simian leukemia viral oncogene h	2.61E-10	2	4.52	5.12	5.34	5.36	5.29	5.26	5.35	5.24
TC1200827	RAN	5901	RAN, member RAS oncogene family	9.30E-12	2	5.40	5.76	5.84	6.15	6.38	6.32	6.35	6.11
TC2200042	RANBP1	5902	RAN binding protein 1	2.79E-06	2	5.05	5.20	5.12	5.26	5.45	5.48	5.49	5.29
TC0400414	RAP1GDS1	5910	RAP1, GTP-GDP dissociation stimulator	1.44E-06	2	3.90	4.04	4.37	4.46	4.51	4.39	4.48	4.26
TC0500682	RARS	5917	arginyl-tRNA synthetase	4.59E-06	2	5.29	5.66	5.82	5.87	5.86	5.92	5.95	5.79
TC1300048	RASL11A	387496	RAS-like, family 11, member A	2.39E-06	2	3.78	4.07	4.08	4.31	4.34	4.24	4.15	4.05
TC0100365	RBBP4	648695 //	retinoblastoma binding protein 4	2.18E-05	2	6.06	6.19	6.27	6.53	6.63	6.46	6.54	6.38
TC1800101	RBBP8	5932	retinoblastoma binding protein 8 /// R	1.71E-08	2	4.15	4.67	4.57	4.79	4.96	4.86	4.92	4.75
TC2000589	RBBP9	10741	retinoblastoma binding protein 9 /// R	5.63E-06	2	3.38	3.57	3.51	3.68	3.97	3.90	3.72	3.58
TC2000721	RBL1	5933	retinoblastoma-like 1 (p107)	6.65E-08	2	4.12	4.27	4.33	4.60	4.75	4.69	4.69	4.46
TC1101580	RBM4B	83759	RNA binding motif protein 4B	3.36E-06	2	4.46	4.54	4.59	4.71	4.78	4.71	4.67	4.70
TC0100932	RBM8A	9939	RNA binding motif protein 8A /// RNA-	5.21E-05	2	8.23	8.51	8.27	8.28	8.27	8.40	8.54	8.51
TC0X00563	RBMX2	51634	RNA binding motif protein, X-linked 2 /	4.50E-06	2	5.06	5.18	5.26	5.25	5.17	5.32	5.48	5.43
TC0101933	RCC2	55920	regulator of chromosome condensatio	1.11E-08	2	4.84	5.02	4.94	5.13	5.33	5.30	5.31	5.15
TC1500511	RCN2	5955	reticulocalbin 2, EF-hand calcium bindi	1.64E-08	2	3.78	3.81	3.86	3.87	3.94	4.01	4.12	4.03

TC1400936	RDH11	51109	retinol dehydrogenase 11 (all-trans/9-c	0.000513	2	3.78	3.88	3.88	4.12	4.19	4.15	4.20	4.14
TC1101814	RDX	5962	radixin	7.84E-09	2	4.32	5.19	5.24	5.75	5.66	5.65	5.75	5.44
TC1000281	REEP3	221035	receptor accessory protein 3 /// Recep	2.82E-15	2	4.99	5.52	5.62	5.84	5.84	5.84	5.82	5.88
TC0601645	REPS1	85021	RALBP1 associated Eps domain contain	7.11E-12	2	4.35	4.32	4.46	4.70	4.63	4.67	4.78	4.71
TC0400252	REST	5978	RE1-silencing transcription factor /// R	3.51E-08	2	5.93	6.30	6.31	6.45	6.37	6.37	6.39	6.35
TC1100866	REXO2	25996	REX2, RNA exonuclease 2 homolog (S.	2.25E-07	2	4.24	4.19	4.25	4.56	4.64	4.65	4.81	4.66
TC0301834	RFC4	5984	replication factor C (activator 1) 4, 37k	0.000126	2	3.65	3.79	3.75	3.84	4.18	4.15	4.16	3.93
TC0901054	RFK	55312	riboflavin kinase /// Riboflavin kinase (	2.20E-05	2	2.97	3.28	3.42	3.46	3.56	3.42	3.43	3.42
TC0401144	RG9MTD2	93587	RNA (guanine-9-) methyltransferase do	0.000173	2	3.86	4.09	4.24	4.31	4.26	4.25	4.25	4.21
TC1001312	RGS10	6001	regulator of G-protein signaling 10 ///	6.89E-05	2	5.36	5.35	5.21	5.72	6.03	6.10	5.93	5.97
TC0701773	RHEB	6009	Ras homolog enriched in brain	9.30E-12	2	5.07	5.43	5.68	5.74	5.83	5.89	5.91	5.84
TC1201663	RILPL2	196383	Rab interacting lysosomal protein-like	4.18E-08	2	7.88	8.27	8.23	8.47	8.49	8.45	8.53	8.49
TC0600052	RIOK1	83732	RIO kinase 1 (yeast)	3.85E-06	2	4.06	4.67	4.75	4.98	5.09	5.15	5.31	4.93
TC0900338	RMI1	80010	RMI1, RecQ mediated genome instabili	1.72E-05	2	5.86	5.89	6.20	6.08	6.05	6.11	6.09	6.16
TC1400040	RNASE2	6036	ribonuclease, RNase A family, 2 (liver,	2.37E-21	2	5.56	6.90	6.46	8.52	8.98	9.23	9.05	8.50
TC1400038	RNASE3	6037	ribonuclease, RNase A family, 3 (eosin	1.63E-16	2	5.17	6.58	5.77	7.20	7.98	8.22	7.87	7.36
TC1900221	RNASEH2A	10535	ribonuclease H2, subunit A	1.25E-07	2	4.64	4.61	4.63	4.90	5.10	5.07	5.13	4.91
TC1300154	RNASEH2B	79621	ribonuclease H2, subunit B /// Ribonuc	9.27E-11	2	3.81	3.90	4.09	4.40	4.48	4.59	4.59	4.56
TC1101550	RNASEH2C	84153	ribonuclease H2, subunit C	3.04E-05	2	5.04	5.14	5.05	5.15	5.44	5.41	5.24	5.09
TC0X01192	RNF113A	7737	ring finger protein 113A	2.75E-06	2	4.72	4.72	4.78	4.93	4.89	4.87	5.09	4.96
TC0100937	RNF115	27246	ring finger protein 115	2.54E-07	2	4.46	4.73	4.76	4.96	5.02	4.96	5.09	4.93
TC0200414	RNF181	51255	ring finger protein 181	6.20E-08	2	7.68	8.16	8.23	8.31	8.21	8.29	8.29	8.33
TC0600698	RNF217	154214	ring finger protein 217 /// IBR domain-	0.000138	2	2.89	3.32	3.33	3.34	3.58	3.42	3.40	3.22
TC1300563	RNF219	79596	ring finger protein 219	1.50E-08	2	4.66	5.42	5.59	5.54	5.65	5.67	5.69	5.51
TC0100484	RNF220 /// C1	55182	ring finger protein 220 /// RING finger	0.000914	2	4.95	4.91	4.92	5.03	5.06	4.98	5.05	4.98
TC1200764	RNF34	80196	ring finger protein 34	0.000363	2	6.91	6.75	6.93	7.10	7.02	7.10	7.04	7.00
TC1701553	RNF43 /// SUP	54894 ///	ring finger protein 43 /// suppressor of	0.000201	2	5.55	5.60	5.69	5.70	5.68	5.71	5.69	5.72
TC0600359	RNF8	9025	ring finger protein 8	7.80E-06	2	3.58	3.70	3.69	3.84	4.05	3.91	3.98	3.86
TC1600767	RNPS1	731091 //	RNA binding protein S1, serine-rich do	0.000182	2	5.56	5.60	5.61	5.70	5.75	5.72	5.74	5.67
TC0500439	RNUXA	51808	RNA U, small nuclear RNA export adap	7.01E-05	2	5.58	6.00	6.07	6.16	6.12	6.14	6.28	6.14
TC1300541	RP11-11C5.2	440145	similar to RIKEN cDNA 2410129H14	2.35E-09	2	4.21	4.48	4.43	4.76	4.93	4.97	5.07	4.93
TC0101134	RP11-336K24.9	28956	mitogen-activated protein-binding pro	1.30E-13	2	5.30	5.49	5.82	6.05	5.93	5.80	5.89	5.78
TC0102490	RP11-556K13.1	730029	40S ribosomal protein SA pseudogene	0.000197	2	4.36	4.66	4.60	4.96	5.25	5.26	5.10	4.91
TC0101027	RP11-68I18.1 /	126626	hypothetical protein MGC29891 /// GA	9.75E-06	2	4.81	4.91	4.97	5.20	5.14	5.11	5.26	5.07

TC0701116	RP9 /// XIAP //	6100 ///	retinitis pigmentosa 9 (autosomal dom	0.000617	2	4.71	4.84	4.84	4.86	4.91	4.87	4.96	4.86
TC0701012	RPA3	6119	replication protein A3, 14kDa	0.000113	2	4.36	4.38	4.40	4.40	4.52	4.60	4.67	4.59
TC0100724	RPAP2	79871	RNA polymerase II associated protein 2	7.87E-08	2	3.71	3.97	4.00	4.09	4.25	4.18	4.22	4.04
TC0600333	RPL10A	4736	ribosomal protein L10a	6.37E-10	2	4.98	5.50	5.19	5.73	5.81	5.85	5.91	5.59
TC0100255	RPL11	6135	ribosomal protein L11	6.72E-05	2	8.54	8.74	8.74	8.83	8.87	8.98	9.05	8.95
TC0901340	RPL12	652036 //	ribosomal protein L12	1.60E-07	2	7.27	7.29	7.12	7.50	7.63	7.64	7.76	7.49
TC1600684	RPL13 /// SNO	6137	ribosomal protein L13 /// small nucleol	0.000116	2	5.06	5.10	5.03	5.24	5.35	5.27	5.33	5.16
TC0300183	RPL14	9045	ribosomal protein L14	8.65E-08	2	7.98	8.29	8.30	8.62	8.67	8.68	8.79	8.63
TC0300107	RPL15	730925 //	ribosomal protein L15	1.15E-10	2	6.42	7.13	7.03	7.53	7.75	7.71	7.61	7.33
TC1901655	RPL18	6141	ribosomal protein L18	5.95E-07	2	6.99	7.19	7.15	7.49	7.60	7.54	7.58	7.36
TC1900309	RPL18A	6142	ribosomal protein L18a	3.72E-09	2	6.81	7.21	6.87	7.70	7.83	7.80	7.71	7.52
TC0301746	RPL22L1	200916	ribosomal protein L22-like 1	3.29E-06	2	3.22	3.94	3.87	3.84	3.99	4.11	4.14	4.00
TC1701283	RPL23	9349	ribosomal protein L23 /// 60S ribosoma	7.73E-09	2	5.68	6.05	6.01	6.20	6.25	6.28	6.34	6.15
TC1700305	RPL23A	732089 //	ribosomal protein L23a	5.59E-08	2	8.62	8.67	8.36	8.99	9.10	9.20	9.23	9.00
TC0301409	RPL24	6152	ribosomal protein L24	1.93E-07	2	8.85	9.38	9.29	9.69	9.78	9.79	9.78	9.61
TC1701013	RPL26	730343 //	ribosomal protein L26	2.36E-07	2	5.18	5.39	5.35	5.58	5.65	5.64	5.65	5.55
TC1100152	RPL27A	6157	ribosomal protein L27a	1.04E-08	2	8.80	9.08	9.08	9.28	9.41	9.39	9.42	9.32
TC0301247	RPL29	6159	ribosomal protein L29	1.67E-06	2	3.86	3.99	3.93	4.17	4.37	4.27	4.30	4.13
TC0801141	RPL30	6156	ribosomal protein L30	0.000172	2	6.92	7.07	7.09	7.27	7.25	7.39	7.40	7.34
TC0301023	RPL32	652162 //	ribosomal protein L32	1.58E-09	2	5.02	5.03	4.92	5.19	5.29	5.25	5.37	5.22
TC0400450	RPL34	731916 //	ribosomal protein L34	3.74E-18	2	6.67	7.11	7.16	7.43	7.40	7.49	7.57	7.46
TC0901326	RPL35	11224	ribosomal protein L35 /// 60S ribosoma	0.000257	2	3.99	4.09	3.93	4.25	4.42	4.34	4.31	4.11
TC0300948	RPL35A	651825 //	ribosomal protein L35a	0.000498	2	7.69	7.81	7.80	7.94	8.07	8.08	8.06	8.00
TC1900106	RPL36	651453 //	ribosomal protein L36	0.000115	2	5.84	6.00	5.91	6.11	6.21	6.16	6.25	6.07
TC1400829	RPL36AL	6166	ribosomal protein L36a-like	2.35E-06	2	9.50	9.81	9.86	9.92	9.93	9.95	10.01	10.03
TC0500942	RPL37	6167	ribosomal protein L37 /// 60S ribosoma	9.55E-10	2	5.97	6.10	6.14	6.37	6.36	6.33	6.40	6.28
TC0201085	RPL37A	6168	ribosomal protein L37a	4.95E-10	2	3.83	4.13	4.16	4.40	4.40	4.39	4.43	4.29
TC1700735	RPL38	6169	ribosomal protein L38	1.04E-09	2	10.25	10.60	10.55	10.85	10.87	10.92	10.96	10.84
TC0X01189	RPL39	6170	ribosomal protein L39	1.93E-08	2	9.84	10.39	10.40	10.49	10.63	10.57	10.55	10.49
TC1501055	RPL4 /// SNOR	6124	ribosomal protein L4 /// small nucleola	2.01E-05	2	4.15	4.31	4.17	4.43	4.61	4.61	4.62	4.40
TC0500188	RPL41	6171	ribosomal protein L41	5.91E-08	2	9.82	10.11	10.24	10.35	10.47	10.48	10.53	10.57
TC1200579	RPL41	6171	ribosomal protein L41	1.31E-06	2	4.22	4.72	4.87	4.91	4.89	5.05	4.96	5.11
TC0801032	RPL7	6129	ribosomal protein L7	8.30E-07	2	8.66	9.26	9.17	9.46	9.56	9.59	9.60	9.38
TC0801346	RPL8	6132	ribosomal protein L8	3.16E-09	2	6.99	7.57	7.29	7.84	7.94	7.90	7.86	7.72

TC0400888	RPL9	6133	ribosomal protein L9	6.45E-06	2	7.62	8.04	8.03	8.18	8.31	8.32	8.34	8.17
TC1201618	RPLP0	6175	ribosomal protein, large, P0 /// 60S aci	3.43E-07	2	5.08	5.72	5.49	6.10	6.35	6.30	6.18	5.77
TC1500438	RPLP1	731613 //	ribosomal protein, large, P1	7.57E-10	2	8.21	8.80	8.69	9.03	9.23	9.17	9.21	8.99
TC1100025	RPLP2	6181	ribosomal protein, large, P2	3.97E-09	2	9.91	10.46	10.41	10.65	10.70	10.70	10.65	10.55
TC2000241	RPN2	6185	ribophorin II /// Dolichyl-diphosphoolig	1.83E-08	2	4.92	5.24	5.31	5.58	5.76	5.67	5.75	5.50
TC1000437	RPP30	10556	ribonuclease P/MRP 30kDa subunit ///	0.000795	2	3.88	4.09	4.09	4.12	4.21	4.24	4.28	4.19
TC1901492	RPS16	6217	ribosomal protein S16 /// 40S ribosoma	1.86E-10	2	8.73	9.15	9.15	9.53	9.62	9.57	9.57	9.44
TC1501175	RPS17	6218	ribosomal protein S17	5.78E-09	2	7.84	8.19	8.22	8.38	8.49	8.52	8.48	8.37
TC1501183	RPS17	6218	ribosomal protein S17	3.49E-07	2	8.02	8.29	8.28	8.45	8.53	8.55	8.49	8.40
TC1900562	RPS19	731572 //	ribosomal protein S19	7.63E-09	2	7.48	8.06	8.00	8.52	8.64	8.50	8.55	8.31
TC2200683	RPS19BP1	91582	ribosomal protein S19 binding protein	0.000448	2	5.60	5.89	5.91	5.97	6.00	6.01	6.06	5.99
TC0800947	RPS20	6224	ribosomal protein S20	2.52E-07	2	5.05	5.38	5.35	5.46	5.58	5.59	5.56	5.50
TC2000432	RPS21	6227	ribosomal protein S21 /// 40S ribosoma	4.64E-11	2	7.34	7.82	7.80	8.11	8.26	8.24	8.20	8.05
TC0501118	RPS23	6228	ribosomal protein S23	1.71E-06	2	6.71	7.23	7.21	7.41	7.45	7.55	7.51	7.38
TC1101887	RPS25	6230	ribosomal protein S25	0.000166	2	9.81	9.85	9.86	10.00	10.06	10.15	10.23	10.15
TC0200249	RPS27A	732088 //	ribosomal protein S27a	9.38E-07	2	7.77	7.80	7.84	7.96	7.97	8.04	8.12	8.06
TC1501018	RPS27L	51065	ribosomal protein S27-like /// 40S ribo	7.69E-11	2	4.44	4.96	5.06	5.20	5.36	5.37	5.36	5.24
TC1900147	RPS28	6234	ribosomal protein S28	4.88E-07	2	8.27	8.66	8.46	8.81	8.92	8.89	8.88	8.77
TC1400826	RPS29 /// Q0P	647361 //	ribosomal protein S29 /// RPS29 protei	6.90E-07	2	6.36	6.82	6.91	7.16	7.25	7.19	7.23	7.10
TC1100672	RPS3	6188	ribosomal protein S3	1.07E-06	2	9.43	9.70	9.67	9.97	10.00	10.03	10.09	9.90
TC0400597	RPS3A	6189	ribosomal protein S3A	5.54E-08	2	9.80	10.30	10.39	10.48	10.50	10.56	10.57	10.46
TC0X01020	RPS4X	6191	ribosomal protein S4, X-linked /// 40S r	1.86E-07	2	7.79	8.12	8.03	8.42	8.52	8.49	8.46	8.27
TC1900960	RPS5	6193	ribosomal protein S5	5.88E-08	2	6.18	6.50	6.26	6.96	7.08	7.06	7.12	6.88
TC0900801	RPS6	6194	ribosomal protein S6 /// 40S ribosomal	3.15E-09	2	8.66	8.90	8.91	9.16	9.19	9.25	9.30	9.10
TC0200009	RPS7	6201	ribosomal protein S7	0.000168	2	4.33	4.32	4.35	4.41	4.50	4.46	4.55	4.42
TC0100488	RPS8 /// SNOR	642115 //	ribosomal protein S8 /// small nucleola	1.33E-06	2	4.03	4.26	4.30	4.44	4.55	4.49	4.55	4.43
TC0201100	RQCD1	9125	RCD1 required for cell differentiation1	0.000276	2	5.15	5.28	5.31	5.41	5.44	5.48	5.45	5.38
TC0102138	RRAGC	64121	Ras-related GTP binding C	1.23E-06	2	6.74	7.03	7.15	7.18	7.11	7.35	7.32	7.32
TC0601453	RRAGD	58528	Ras-related GTP binding D /// Ras-relat	8.24E-07	2	7.12	7.66	7.65	7.83	7.83	8.01	7.88	7.81
TC1100074	RRM1	6240	ribonucleotide reductase M1	2.56E-11	2	3.34	3.54	3.37	3.93	4.40	4.36	4.24	3.85
TC0200033	RRM2	6241	ribonucleotide reductase M2 polypepti	3.35E-13	2	4.11	4.88	4.50	5.33	6.03	5.93	5.48	5.03
TC1600863	RSL1D1	26156	ribosomal L1 domain containing 1 /// R	8.71E-10	2	4.08	4.62	4.41	5.05	5.23	5.16	5.47	5.10
TC1600470	RSPRY1	89970	ring finger and SPRY domain containing	0.000165	2	5.28	5.63	5.55	5.62	5.47	5.73	5.76	5.74
TC1000794	RSU1	6251	Ras suppressor protein 1 /// Ras suppre	6.64E-09	2	6.79	7.65	7.64	7.78	7.98	7.90	7.63	7.53

TC0601493	RTN4IP1	84816	reticulon 4 interacting protein 1	7.87E-06	2	3.82	3.85	3.79	3.95	4.17	4.08	4.13	3.95
TC0500771	RUFY1	80230	RUN and FYVE domain containing 1 ///	4.22E-06	2	6.22	6.13	6.17	6.53	6.51	6.62	6.64	6.53
TC1900695	RUVBL2	10856	RuvB-like 2 (E. coli)	0.000768	2	4.90	5.00	4.93	5.04	5.18	5.10	5.12	5.01
TC2100261	RWDD2B	10069	RWD domain containing 2B	0.000105	2	3.69	3.67	3.69	3.91	3.92	3.88	4.00	3.81
TC0301583	RYK	6259	RYK receptor-like tyrosine kinase	7.83E-05	2	4.61	4.86	4.79	4.93	4.99	4.92	5.00	4.99
TC0102787	S100A4	6275	S100 calcium binding protein A4	1.78E-11	2	6.42	6.50	6.50	6.99	6.90	6.75	6.65	6.62
TC1101238	SAAL1	113174	serum amyloid A-like 1	1.29E-10	2	3.33	3.63	3.54	3.93	4.18	4.15	4.14	3.99
TC1900666	SAE1	10055	SUMO1 activating enzyme subunit 1	4.95E-07	2	4.90	4.95	4.90	5.07	5.27	5.37	5.32	5.20
TC2200344	SAMM50	25813	sorting and assembly machinery comp	9.93E-06	2	4.13	4.28	4.31	4.43	4.53	4.47	4.65	4.42
TC1300017	SAP18	10284	Sin3A-associated protein, 18kDa	1.61E-06	2	7.76	7.96	8.12	8.12	8.06	8.14	8.18	8.21
TC0100798	SARS	6301	seryl-tRNA synthetase /// Seryl-tRNA s	0.000772	2	5.67	5.90	5.90	6.05	5.98	5.98	6.06	5.98
TC1400847	SAV1	646561 //	salvador homolog 1 (Drosophila)	0.000159	2	3.67	4.01	3.90	4.11	4.30	4.19	4.10	4.12
TC0500294	SCAMP1	9522	secretory carrier membrane protein 1 /	0.000326	2	5.45	5.38	5.53	5.69	5.56	5.66	5.80	5.76
TC0401059	SCARB2	950	scavenger receptor class B, member 2	2.44E-06	2	4.39	4.69	4.73	4.91	4.92	5.03	5.25	5.21
TC1000509	SCD	6319	stearoyl-CoA desaturase (delta-9-desat	5.60E-11	2	3.74	4.20	4.02	4.54	4.98	5.06	4.99	4.47
TC0400949	SCFD2	152579	sec1 family domain containing 2	0.000333	2	3.58	3.85	3.82	3.88	4.09	4.25	4.17	4.06
TC0400557	SCOC	60592	short coiled-coil protein /// short coile	6.52E-07	2	3.59	3.75	3.87	3.86	4.00	3.90	3.90	3.96
TC0400444	SCYE1	9255	small inducible cytokine subfamily E, m	5.18E-05	2	5.20	5.70	5.68	5.82	5.87	5.85	5.94	5.84
TC0401053	SDAD1	55153	SDA1 domain containing 1	2.43E-07	2	3.15	3.33	3.31	3.60	3.68	3.66	3.82	3.63
TC0101670	SDCCAG8	10806	serologically defined colon cancer anti	5.55E-14	2	5.01	5.52	5.91	6.10	6.01	5.90	5.88	5.72
TC0101930	SDHB	6390	succinate dehydrogenase complex, sub	0.000392	2	7.71	7.77	7.97	8.21	7.99	7.99	8.00	8.04
TC0202184	SDPR	8436	serum deprivation response (phosphat	1.92E-05	2	3.61	4.49	4.11	4.97	5.37	5.64	5.27	5.36
TC1501204	SEC11A	23478	SEC11 homolog A (S. cerevisiae)	7.09E-05	2	6.95	7.18	7.42	7.44	7.44	7.40	7.33	7.35
TC1800218	SEC11C	90701	SEC11 homolog C (S. cerevisiae)	3.26E-06	2	4.48	5.07	5.17	5.43	5.63	5.64	5.65	5.36
TC0401214	SEC24D	9871	SEC24 related gene family, member D (	0.000243	2	5.56	5.69	5.76	5.76	5.55	5.72	5.88	5.90
TC0401084	SEC31A	22872	SEC31 homolog A (S. cerevisiae) /// SE	6.79E-05	2	5.36	5.57	5.42	5.71	5.77	5.83	5.85	5.73
TC1800070	SEH1L	81929	SEH1-like (S. cerevisiae)	2.43E-05	2	3.64	3.96	3.81	4.04	4.24	4.26	4.25	3.98
TC0301272	SELK	58515	selenoprotein K	0.000108	2	8.05	8.42	8.19	8.30	8.29	8.51	8.52	8.62
TC1501280	SELS /// SELS_	55829	selenoprotein S /// Selenoprotein S (V	1.57E-08	2	4.41	4.57	4.38	4.66	4.79	4.79	4.83	4.78
TC0501231	SEMA6A	57556	sema domain, transmembrane domain	6.30E-05	2	2.76	2.84	2.77	2.77	3.02	3.01	2.94	2.83
TC1201143	SENP1	29843	SUMO1/sentrin specific peptidase 1 ///	0.000401	2	5.11	5.47	5.48	5.45	5.36	5.53	5.60	5.59
TC1000774	SEPHS1	22929	selenophosphate synthetase 1 /// Sele	1.22E-06	2	4.94	5.13	5.15	5.37	5.58	5.44	5.52	5.22
TC0100276	SEPN1	57190	selenoprotein N, 1 /// Selenoprotein N	5.22E-05	2	5.21	5.21	5.20	5.35	5.42	5.38	5.41	5.39
TC0102339	SERBP1	26135	SERPINE1 mRNA binding protein 1	1.56E-13	2	7.27	7.59	7.84	8.06	8.09	8.05	8.11	7.91

TC0500248	SERF1A	8293	small EDRK-rich factor 1A (telomeric)	7.99E-07	2	5.55	5.79	5.53	5.44	5.72	5.76	5.69	5.64
TC0500243	SERF1B /// SER	728492 //	small EDRK-rich factor 1B (centromeric	1.48E-05	2	5.31	5.71	5.41	5.40	5.61	5.62	5.60	5.52
TC1800240	SERPINB10	5273	serpin peptidase inhibitor, clade B (ova	1.18E-12	2	2.74	5.20	4.24	5.05	5.76	5.76	5.20	4.35
TC0600906	SERPINB6	5269	serpin peptidase inhibitor, clade B (ova	5.32E-06	2	5.25	5.42	5.52	5.54	5.55	5.56	5.53	5.46
TC0401273	SETD7	80854	SET domain containing (lysine methyltr	8.07E-15	2	3.90	4.07	4.24	5.00	4.83	4.63	4.46	4.35
TC1300143	SETDB2	83852	SET domain, bifurcated 2 /// Histone-ly	1.22E-07	2	3.39	3.36	3.57	3.61	3.64	3.75	3.88	3.75
TC1600566	SF3B3	23450	splicing factor 3b, subunit 3, 130kDa //	8.32E-07	2	4.83	4.73	4.71	5.03	5.15	5.20	5.26	5.07
TC0601662	SF3B5	83443	splicing factor 3b, subunit 5, 10kDa	1.11E-09	2	6.13	6.36	6.55	6.77	6.88	6.80	6.87	6.75
TC0301263	SFMBT1	51460	Scm-like with four mbt domains 1 /// S	0.00052	2	4.19	4.17	4.18	4.25	4.32	4.32	4.42	4.37
TC0301054	SGOL1	151648	shugoshin-like 1 (S. pombe) /// Shugosl	3.25E-06	2	3.78	4.22	4.00	4.29	4.64	4.55	4.45	4.32
TC0200973	SGOL2	151246	shugoshin-like 2 (S. pombe) /// Shugosl	8.13E-05	2	2.71	2.89	2.89	3.02	3.17	3.12	3.24	3.02
TC0600522	SH3BGRL2	83699	SH3 domain binding glutamic acid-rich	1.39E-06	2	3.61	4.52	4.17	5.55	5.89	6.06	5.74	5.61
TC0201264	SH3YL1	26751	SH3 domain containing, Ysc84-like 1 (S.	0.000591	2	3.21	3.23	3.21	3.27	3.34	3.26	3.37	3.28
TC1601070	SHCBP1	79801	SHC SH2-domain binding protein 1	0.000364	2	2.88	3.00	2.98	3.09	3.45	3.31	3.23	3.10
TC0301180	SHISA5	51246	shisa homolog 5 (Xenopus laevis)	2.46E-05	2	7.92	7.91	8.04	8.24	8.19	8.22	8.22	8.30
TC1200445	SHMT2	6472	serine hydroxymethyltransferase 2 (mi	0.000762	2	4.62	4.66	4.63	4.72	4.84	4.82	4.85	4.75
TC1101938	SIAE	54414	sialic acid acetylesterase	0.000996	2	4.02	4.06	4.13	4.31	4.42	4.30	4.12	4.10
TC0301662	SIAH2	732092 //	seven in absentia homolog 2 (Drosophi	3.52E-12	2	4.46	4.76	4.82	5.18	5.15	5.08	5.10	5.08
TC1400188	SIP1	8487	survival of motor neuron protein intera	0.000462	2	3.00	3.10	3.12	3.12	3.26	3.23	3.38	3.24
TC0400209	SLAIN2	57606	SLAIN motif family, member 2	0.000387	2	7.24	7.60	7.60	7.74	7.62	7.82	7.78	7.87
TC0401310	SLC10A7	84068	solute carrier family 10 (sodium/bile ac	8.74E-06	2	3.38	3.46	3.70	3.71	3.72	3.65	3.71	3.58
TC0500448	SLC12A2	6558	solute carrier family 12 (sodium/potass	1.47E-08	2	3.26	3.46	3.35	3.76	4.29	4.14	4.06	3.63
TC0200294	SLC1A4	6509	solute carrier family 1 (glutamate/neut	3.38E-07	2	3.81	4.01	3.91	4.13	4.39	4.38	4.38	4.14
TC0601523	SLC22A16	85413	solute carrier family 22 (organic cation,	1.49E-05	2	3.26	3.35	3.37	3.41	3.60	3.61	3.50	3.35
TC1400451	SLC24A4	123041	solute carrier family 24 (sodium/potass	1.02E-10	2	4.37	4.49	4.56	4.84	4.77	4.67	4.58	4.46
TC1300451	SLC25A30	253512	solute carrier family 25, member 30	1.90E-10	2	4.72	4.89	4.99	5.51	5.31	5.62	5.70	5.57
TC0100097	SLC25A33	84275	solute carrier family 25, member 33	1.81E-06	2	2.93	2.99	3.03	3.18	3.22	2.99	3.02	2.98
TC0X00530	SLC25A5	292	solute carrier family 25 (mitochondrial	3.14E-11	2	6.03	6.68	6.54	7.06	7.21	7.08	7.06	6.87
TC0Y00110	SLC25A6	293	solute carrier family 25 (mitochondrial	3.94E-10	2	6.10	6.84	6.73	7.22	7.27	7.14	7.10	6.92
TC0X00730	SLC25A6	293	solute carrier family 25 (mitochondrial	5.43E-07	2	7.04	7.45	7.29	7.64	7.81	7.59	7.56	7.48
TC1500326	SLC27A2	11001	solute carrier family 27 (fatty acid trans	5.19E-09	2	2.83	3.68	3.03	3.38	4.08	3.96	3.73	3.39
TC0901084	SLC28A3	64078	solute carrier family 28 (sodium-couple	1.46E-07	2	3.39	3.61	3.62	3.93	4.33	4.18	4.20	3.85
TC0101834	SLC2A5	6518	solute carrier family 2 (facilitated gluco	1.10E-07	2	4.29	4.47	4.36	4.63	4.83	4.84	4.80	4.55
TC0103207	SLC30A1	7779	solute carrier family 30 (zinc transporte	1.90E-17	2	4.59	4.90	5.42	5.86	5.67	5.47	5.48	5.44

TC0301689	SLC33A1	9197	solute carrier family 33 (acetyl-CoA tra	5.28E-06	2	4.06	4.41	4.61	4.76	4.73	4.73	4.68	4.59
TC0100763	SLC35A3	23443	solute carrier family 35 (UDP-N-acetylg	0.000806	2	3.70	3.81	3.82	3.85	3.93	3.93	3.90	3.87
TC0701649	SLC35B4	84912	solute carrier family 35, member B4	3.14E-05	2	3.73	3.82	3.92	4.01	4.10	4.03	3.98	3.74
TC2000797	SLC35C2	51006	solute carrier family 35, member C2 ///	6.39E-08	2	5.52	5.44	5.39	5.59	5.76	5.68	5.71	5.61
TC0901160	SLC35D2	11046	solute carrier family 35, member D2 //	0.000899	2	3.00	3.36	3.29	3.27	3.42	3.31	3.40	3.30
TC2100153	SLC37A1	54020	solute carrier family 37 (glycerol-3-pho	0.000187	2	4.56	4.61	4.59	4.66	4.63	4.70	4.73	4.77
TC1701660	SLC39A11	201266	solute carrier family 39 (metal ion tran	1.38E-06	2	4.93	4.87	4.76	4.96	5.18	5.20	5.15	5.00
TC1101412	SLC43A3	29015	solute carrier family 43, member 3	3.78E-05	2	4.79	5.17	4.97	5.05	5.26	5.29	5.26	5.10
TC0900458	SLC44A1	23446	solute carrier family 44, member 1 ///	3.74E-16	2	5.02	5.99	5.57	5.98	6.24	6.18	6.01	5.79
TC0401267	SLC7A11	23657	solute carrier family 7, (cationic amino	1.45E-05	2	2.63	2.74	2.85	2.89	2.95	3.03	3.17	2.96
TC0102028	SLC9A1	6548	solute carrier family 9 (sodium/hydrog	4.17E-06	2	5.03	4.90	5.11	5.37	5.26	5.11	5.05	5.07
TC1701235	SLFN11	91607	schlafen family member 11 /// Schlafe	7.66E-05	2	4.22	4.14	4.19	4.35	4.47	4.42	4.51	4.45
TC1701236	SLFN12	55106	schlafen family member 12	7.77E-06	2	4.29	4.40	4.73	4.96	4.87	4.98	5.11	5.09
TC2000770	SLPI	6590	secretory leukocyte peptidase inhibitor	1.87E-17	2	7.77	8.80	8.99	9.88	9.98	10.14	9.98	9.47
TC1800457	SMAD2	4087	SMAD family member 2 /// Mothers ag	1.57E-09	2	6.59	6.88	7.09	7.03	7.04	7.08	7.06	7.02
TC0500498	SMAD5	4090	SMAD family member 5	3.41E-11	2	3.70	3.76	3.82	4.33	4.30	4.29	4.50	4.34
TC0400407	SMARCAD1	56916	SWI/SNF-related, matrix-associated act	0.000163	2	3.05	3.18	3.12	3.28	3.45	3.41	3.46	3.30
TC0201084	SMARCAL1	50485	SWI/SNF related, matrix associated, ac	0.000137	2	4.32	4.32	4.46	4.50	4.46	4.41	4.48	4.46
TC0701767	SMARCD3	6604	SWI/SNF related, matrix associated, ac	5.28E-16	2	5.38	5.47	5.52	6.07	6.12	6.16	6.09	5.92
TC0900449	SMC2	10592	structural maintenance of chromosom	7.31E-10	2	3.42	3.69	3.51	4.10	4.63	4.53	4.53	4.02
TC1000577	SMC3	9126	structural maintenance of chromosom	0.000214	2	6.78	6.73	6.86	7.01	7.04	7.16	7.46	7.23
TC0500244	SMN2	6607	survival of motor neuron 2, centromeri	5.27E-06	2	4.75	5.17	4.99	5.06	5.18	5.14	5.19	5.10
TC0500249	SMN2 /// SMN	6607 ///	survival of motor neuron 2, centromeri	0.000163	2	5.14	5.51	5.34	5.40	5.51	5.48	5.43	5.38
TC1201259	SMUG1	23583	single-strand-selective monofunctional	0.000539	2	5.06	5.08	5.24	5.28	5.20	5.17	5.21	5.24
TC2200060	SNAP29	9342	synaptosomal-associated protein, 29kD	5.75E-05	2	6.83	6.97	7.15	7.23	7.15	7.12	7.28	7.21
TC0900068	SNAPC3	6619	small nuclear RNA activating complex,	2.79E-05	2	4.81	4.89	5.17	5.24	5.16	5.06	5.20	4.95
TC0100324	SNHG3-RCC1 /	751867 //	SNHG3-RCC1 /// regulator of chromos	0.000266	2	4.58	4.58	4.62	4.67	4.78	4.69	4.67	4.63
TC1600178	SNN	8303	stannin	7.84E-05	2	6.92	7.28	6.84	7.09	7.17	7.35	7.20	7.35
TC1900542	SNRPA	6626	small nuclear ribonucleoprotein polyp	0.000479	2	3.97	4.10	4.02	4.24	4.41	4.26	4.41	4.16
TC1501281	SNRPA1	6627	small nuclear ribonucleoprotein polyp	9.54E-07	2	3.93	3.82	3.72	4.09	4.28	4.29	4.36	4.12
TC2000505	SNRPB	6628	small nuclear ribonucleoprotein polyp	0.000458	2	5.02	5.35	5.29	5.38	5.46	5.35	5.41	5.36
TC0600323	SNRPC	6631	small nuclear ribonucleoprotein polyp	7.68E-08	2	4.50	4.46	4.51	4.78	4.90	4.85	5.01	4.85
TC1800090	SNRPD1	6632	small nuclear ribonucleoprotein D1 pol	1.45E-11	2	3.82	4.23	4.20	4.83	5.19	5.24	5.17	4.77
TC1901602	SNRPD2	6633	small nuclear ribonucleoprotein D2 pol	0.000567	2	4.54	4.68	4.63	4.72	4.91	4.81	4.84	4.69

TC2200140	SNRPD3	6634	small nuclear ribonucleoprotein D3 pol	2.53E-06	2	6.26	6.88	7.01	7.04	7.04	7.09	7.13	7.00
TC0101439	SNRPE	6635	small nuclear ribonucleoprotein polype	1.01E-14	2	3.89	3.89	4.03	4.31	4.42	4.50	4.53	4.42
TC1200604	SNRPF	6636	small nuclear ribonucleoprotein polype	1.58E-10	2	5.36	6.35	6.19	6.82	7.13	7.23	7.10	6.81
TC0201604	SNRPG	6637	small nuclear ribonucleoprotein polype	2.98E-07	2	5.88	6.29	6.38	6.49	6.52	6.59	6.59	6.53
TC0801218	SNTB1	6641	syntrophin, beta 1 (dystrophin-associat	1.10E-15	2	5.10	4.91	4.96	5.61	5.44	5.47	5.66	5.64
TC1501117	SNUPN	10073	snurportin 1	4.20E-08	2	4.88	4.92	5.04	5.17	5.27	5.12	5.23	5.03
TC1100525	SNX15 /// ARL	29907 ///	sorting nexin 15 /// ADP-ribosylation fa	1.83E-05	2	4.36	4.62	4.66	4.71	4.78	4.70	4.69	4.61
TC0500429	SNX2	6643	sorting nexin 2	2.58E-09	2	6.63	6.59	7.01	7.05	6.76	6.92	7.10	7.05
TC0500430	SNX24	28966	sorting nexin 24	7.18E-05	2	3.09	3.24	3.24	3.30	3.53	3.45	3.47	3.39
TC2000580	SNX5	27131	sorting nexin 5 /// Sorting nexin-5. [Sou	1.72E-08	2	4.55	4.53	4.49	4.79	4.88	4.91	5.07	4.95
TC1400782	SNX6	58533	sorting nexin 6	1.85E-05	2	7.38	7.41	7.70	7.86	7.65	7.69	7.73	7.64
TC0600843	SNX9	51429	sorting nexin 9	0.000448	2	3.94	4.17	4.04	4.25	4.36	4.21	4.23	4.20
TC2100072	SOD1	6647	superoxide dismutase 1, soluble (amyo	1.39E-14	2	5.39	5.78	6.22	6.37	6.35	6.19	6.29	6.10
TC1701170	SPAG5	10615	sperm associated antigen 5	0.000262	2	3.60	3.67	3.61	3.74	3.99	3.92	3.87	3.73
TC0501424	SPARC	6678	secreted protein, acidic, cysteine-rich (	8.04E-05	2	5.46	5.86	5.74	6.45	6.86	6.79	6.47	6.45
TC0400514	SPATA5	166378	spermatogenesis associated 5	9.47E-05	2	3.25	3.23	3.17	3.26	3.46	3.43	3.44	3.35
TC1200305	SPATS2	65244	spermatogenesis associated, serine-ric	0.000935	2	3.27	3.29	3.31	3.39	3.47	3.41	3.42	3.35
TC0202078	SPC25	57405	SPC25, NDC80 kinetochore complex co	3.41E-07	2	3.35	3.68	3.52	3.89	4.40	4.44	4.19	3.90
TC0300313	SPCS1	28972	signal peptidase complex subunit 1 ho	4.22E-11	2	5.28	5.72	5.84	5.90	5.87	5.92	5.96	5.89
TC0101595	SPHAR /// RAB	10638 ///	S-phase response (cyclin-related) /// R	0.000635	2	4.35	4.91	4.89	5.21	4.97	5.15	5.27	5.23
TC0900361	SPIN1	10927	spindlin 1	6.45E-06	2	5.43	5.77	5.67	5.76	5.87	5.79	5.80	5.71
TC0X00979	SPIN4	139886	spindlin family, member 4 /// spindlin f	1.06E-12	2	3.88	4.13	4.15	4.69	5.07	5.11	5.11	4.86
TC1600313	SPN	6693	sialophorin (leukosialin, CD43)	1.13E-09	2	4.02	4.42	4.20	4.53	4.92	5.00	5.00	4.68
TC0200244	SPTBN1	6711	spectrin, beta, non-erythrocytic 1	6.57E-09	2	5.14	6.06	6.01	6.57	6.74	6.57	6.67	6.30
TC1101246	SPTY2D1	144108	SPT2, Suppressor of Ty, domain contai	0.000278	2	5.93	6.24	6.10	6.15	6.09	6.22	6.28	6.34
TC0800548	SQLE	6713	squalene epoxidase	6.54E-05	2	3.17	3.32	3.27	3.50	3.79	3.66	3.59	3.37
TC0201482	SRBD1	55133	S1 RNA binding domain 1	1.24E-05	2	4.90	5.33	5.11	5.07	4.98	5.25	5.40	5.45
TC2200326	SREBF2	6721	sterol regulatory element binding tran	3.97E-05	2	4.46	4.52	4.45	4.66	4.77	4.62	4.58	4.49
TC0500425	SRFBP1	153443	serum response factor binding protein	2.35E-05	2	3.80	3.96	4.01	4.17	4.31	4.24	4.35	4.25
TC1000299	SRGN	5552	serglycin	5.24E-06	2	10.99	11.29	11.34	11.35	11.36	11.37	11.34	11.38
TC0400248	SRP72	6731	signal recognition particle 72kDa	3.52E-12	2	5.23	5.19	4.96	5.70	5.75	5.92	6.22	5.87
TC0200845	SSB	6741	Sjogren syndrome antigen B (autoantig	8.30E-08	2	5.16	5.88	5.66	6.00	6.08	6.24	6.61	6.29
TC0700757	SSBP1	6742	single-stranded DNA binding protein 1	9.97E-06	2	6.06	6.69	6.67	6.82	6.88	6.92	7.02	6.89
TC0600935	SSR1	6745	signal sequence receptor, alpha (trans	8.67E-05	2	8.10	8.43	8.52	8.52	8.43	8.54	8.53	8.55

TC0301691	SSR3	6747	signal sequence receptor, gamma (tran	3.96E-11	2	4.60	5.20	5.59	5.60	5.57	5.54	5.54	5.44
TC0X00691	SSR4	6748	signal sequence receptor, delta (transl	7.14E-07	2	4.86	5.16	5.12	5.34	5.48	5.37	5.38	5.20
TC1101409	SSRP1	6749	structure specific recognition protein 1	8.81E-07	2	4.05	4.19	4.10	4.27	4.49	4.41	4.54	4.31
TC0102391	SSX2IP	117178	synovial sarcoma, X breakpoint 2 intera	5.22E-07	2	3.90	3.96	3.95	4.13	4.24	4.28	4.20	4.21
TC0300880	ST6GAL1	6480	ST6 beta-galactosamide alpha-2,6-sialy	4.09E-11	2	5.05	4.99	4.82	5.27	5.53	5.50	5.51	5.29
TC0700631	ST7	7982	suppression of tumorigenicity 7 /// sup	0.000406	2	3.04	3.09	3.11	3.12	3.27	3.24	3.22	3.15
TC1000423	STAMBPL1	57559	STAM binding protein-like 1 /// AMSH-	5.24E-05	2	3.30	3.63	3.72	3.73	3.87	3.80	3.87	3.63
TC0501210	STARD4	134429	StAR-related lipid transfer (START) dom	4.77E-06	2	3.72	3.88	3.85	4.08	4.28	4.28	4.22	4.07
TC0201751	STARD7	56910	StAR-related lipid transfer (START) dom	1.06E-11	2	5.83	6.24	6.32	6.76	6.87	6.81	6.78	6.52
TC0400331	STBD1 /// Q6Z	8987	starch binding domain 1 /// CDNA FLJ4	4.80E-05	2	3.71	3.92	3.88	3.89	3.98	3.99	3.91	3.87
TC0102233	STIL	6491	SCL/TAL1 interrupting locus /// SCL-int	0.0003	2	2.97	2.98	3.06	3.22	3.28	3.20	3.13	3.12
TC1100505	STIP1	10963	stress-induced-phosphoprotein 1 (Hsp	1.11E-06	2	5.78	5.81	5.74	6.24	6.25	6.15	6.33	6.09
TC0202073	STK39	27347	serine threonine kinase 39 (STE20/SPS	5.19E-08	2	4.33	4.92	4.98	5.23	5.17	5.01	5.04	4.91
TC0102008	STMN1	3925	stathmin 1/oncoprotein 18 /// Stathmi	8.59E-13	2	4.46	4.73	4.64	5.04	5.48	5.44	5.25	4.95
TC0400712	STOX2	56977	storkhead box 2	8.03E-05	2	3.28	3.38	3.24	3.26	3.62	3.63	3.51	3.37
TC0901318	STRBP	55342	spermatid perinuclear RNA binding pro	3.79E-10	2	3.76	3.78	3.75	4.06	4.10	4.15	4.33	4.13
TC1100977	STT3A	3703	STT3, subunit of the oligosaccharyltran	2.44E-08	2	5.22	5.38	5.40	5.87	5.95	5.89	5.89	5.69
TC0300122	STT3B	201595	STT3, subunit of the oligosaccharyltran	0.000117	2	5.82	5.70	5.88	6.06	6.05	6.05	6.11	6.00
TC0301329	SUCLG2	8801	succinate-CoA ligase, GDP-forming, bet	1.24E-05	2	4.31	4.41	4.62	4.89	4.82	4.77	4.89	4.60
TC0300719	SUCNR1	56670	succinate receptor 1	1.42E-08	2	2.89	3.11	3.01	3.41	3.93	3.84	3.85	3.44
TC1300169	SUGT1	10910	SGT1, suppressor of G2 allele of SKP1 (	1.44E-06	2	3.79	4.40	4.59	4.69	4.80	4.79	4.86	4.72
TC0901251	SUSD1	64420	sushi domain containing 1 /// Sushi do	2.52E-06	2	4.88	5.23	5.60	5.74	5.52	5.53	5.60	5.55
TC0900386	SUSD3	203328	sushi domain containing 3 /// Sushi do	9.81E-08	2	4.38	5.13	4.64	4.88	5.23	5.08	4.93	4.72
TC1000069	SUV39H2	79723	suppressor of variegation 3-9 homolog	1.37E-06	2	3.92	4.12	4.11	4.15	4.33	4.25	4.19	4.13
TC1100167	SWAP70	23075	SWAP-70 protein	8.72E-09	2	5.95	6.09	6.05	6.54	6.28	6.47	6.79	6.69
TC0600844	SYNJ2	8871	synaptojanin 2 /// Synaptojanin-2 (EC	0.000148	2	4.14	4.19	4.14	4.34	4.48	4.32	4.28	4.24
TC0102298	TACSTD2	4070	tumor-associated calcium signal transd	1.61E-05	2	3.30	3.59	3.60	3.94	3.98	3.94	3.93	3.71
TC0102959	TADA1L	117143	transcriptional adaptor 1 (HFI1 homolo	3.43E-06	2	3.73	3.83	3.84	3.91	4.10	4.03	4.10	3.95
TC1700397	TADA2L	6871	transcriptional adaptor 2 (ADA2 homol	1.60E-07	2	3.83	4.08	4.11	4.25	4.29	4.31	4.34	4.27
TC0102051	TAF12	6883	TAF12 RNA polymerase II, TATA box bi	0.000305	2	6.33	6.37	6.60	6.58	6.47	6.56	6.60	6.65
TC0701139	TARP	445347	TCR gamma alternate reading frame pr	1.07E-06	2	3.39	3.69	3.49	3.76	3.92	3.96	3.93	3.75
TC0901185	TBC1D2	55357	TBC1 domain family, member 2 /// TBC	4.73E-06	2	5.13	5.35	5.41	5.63	5.59	5.54	5.40	5.37
TC1600086	TBC1D24	57465	TBC1 domain family, member 24	0.0007	2	3.85	3.79	3.75	3.86	3.97	3.92	3.92	3.79
TC0301831	TBCCD1	55171	TBCC domain containing 1	0.000785	2	3.50	3.63	3.64	3.73	3.76	3.72	3.78	3.69

TC0600735	TBPL1	9519	TBP-like 1 /// TATA box-binding protei	2.37E-06	2	5.15	5.47	5.56	5.66	5.63	5.75	5.64	5.67
TC0600080	tcag7.350	402694	similar to ribosomal protein L15	1.06E-07	2	7.95	8.89	8.61	9.31	9.49	9.42	9.25	8.98
TC0800936	TCEA1	6917	transcription elongation factor A (SII), 1	4.29E-06	2	6.01	6.36	6.54	6.70	6.60	6.68	6.68	6.68
TC0X00459	TCEAL1	9338	transcription elongation factor A (SII)-li	2.60E-05	2	3.82	3.96	3.92	3.97	4.22	4.16	4.09	4.15
TC0X00458	TCEAL3	85012	transcription elongation factor A (SII)-li	1.25E-05	2	4.39	4.64	4.44	4.59	4.83	4.66	4.61	4.56
TC0X01115	TCEAL8	90843	transcription elongation factor A (SII)-li	6.17E-08	2	3.56	4.09	3.92	4.24	4.38	4.33	4.28	4.06
TC1600778	TCEB2	6923	transcription elongation factor B (SIII),	7.68E-05	2	6.42	6.58	6.69	6.78	6.80	6.72	6.71	6.67
TC0100256	TCEB3	6924	transcription elongation factor B (SIII),	1.31E-08	2	4.33	4.29	4.30	4.55	4.54	4.51	4.65	4.55
TC0500574	TCERG1	10915	transcription elongation regulator 1	1.30E-05	2	3.70	3.99	3.88	4.08	4.28	4.28	4.39	4.15
TC0600258	TCF19	6941	transcription factor 19 (SC1)	0.000668	2	3.62	3.61	3.59	3.78	3.90	3.88	3.83	3.70
TC1000590	TCF7L2	6934	transcription factor 7-like 2 (T-cell spec	2.21E-10	2	5.92	6.13	5.87	6.56	6.29	6.03	6.01	6.09
TC1101452	TCN1	6947	transcobalamin I (vitamin B12 binding	8.37E-17	2	5.02	8.36	7.53	8.13	8.94	8.92	8.18	7.41
TC1400435	TDP1	55775	tyrosyl-DNA phosphodiesterase 1 /// T	3.88E-06	2	4.08	4.14	4.07	4.25	4.45	4.57	4.50	4.31
TC1300183	TDRD3	81550	tudor domain containing 3 /// Tudor d	1.02E-10	2	3.87	4.01	4.15	4.29	4.35	4.30	4.24	4.15
TC0800377	TERF1	7013	telomeric repeat binding factor (NIMA-	5.38E-05	2	5.25	5.68	5.70	5.82	5.82	5.86	5.95	5.78
TC1600599	TERF2IP	54386	telomeric repeat binding factor 2, inter	0.000445	2	8.30	8.78	8.74	8.76	8.70	8.82	8.87	8.78
TC0901196	TEX10	54881	testis expressed 10	8.14E-08	2	3.82	3.83	3.84	4.03	4.13	4.10	4.10	3.97
TC1701615	TEX2	55852	testis expressed 2	1.37E-06	2	4.14	4.79	4.45	4.83	5.17	5.04	4.92	4.55
TC0601706	TFB1M	51106	transcription factor B1, mitochondrial	1.58E-06	2	4.19	4.00	4.12	4.30	4.38	4.33	4.36	4.33
TC0103425	TFB2M	64216	transcription factor B2, mitochondrial	0.000838	2	4.13	4.37	4.44	4.48	4.55	4.59	4.57	4.58
TC1901791	TFPT	29844	TCF3 (E2A) fusion partner (in childhoo	3.14E-08	2	5.53	5.99	5.92	6.12	6.12	6.01	6.08	5.93
TC1300584	TGDS	23483	TDP-glucose 4,6-dehydratase	1.75E-06	2	3.01	3.22	3.59	3.48	3.44	3.47	3.53	3.43
TC0201798	TGFBRAP1	9392	transforming growth factor, beta recep	8.67E-10	2	4.47	4.55	4.52	4.86	4.99	4.98	5.03	4.80
TC0701552	THAP5	168451	THAP domain containing 5	0.000908	2	4.88	5.17	5.36	5.35	5.19	5.34	5.31	5.38
TC0600128	THEM2	55856	thioesterase superfamily member 2	1.65E-17	2	4.92	5.01	5.21	5.75	5.73	5.80	5.83	5.62
TC0500756	THOC3	84321	THO complex 3	5.17E-08	2	4.24	4.21	4.08	4.27	4.49	4.58	4.55	4.43
TC0501510	THOC3	84321	THO complex 3	3.49E-06	2	4.59	4.53	4.44	4.63	4.79	4.77	4.77	4.64
TC1701787	THOC4	10189	THO complex 4	0.000338	2	5.01	5.40	5.26	5.30	5.41	5.45	5.42	5.43
TC0301314	THOC7	80145	THO complex 7 homolog (Drosophila)	1.45E-20	2	6.66	7.71	7.76	7.79	7.80	7.86	7.87	7.85
TC0300024	THUMPD3	25917	THUMP domain containing 3	0.000151	2	4.33	4.76	4.73	4.87	4.93	5.02	5.15	4.82
TC0501223	TICAM2 /// TM	353376 //	toll-like receptor adaptor molecule 2 //	7.49E-10	2	4.99	5.43	5.52	5.57	5.50	5.57	5.57	5.63
TC1400890	TIMM9	26520	translocase of inner mitochondrial me	0.000222	2	3.00	3.50	3.27	3.33	3.53	3.52	3.59	3.48
TC0500272	TINP1	10412	TGF beta-inducible nuclear protein 1	1.51E-10	2	6.12	7.22	7.30	7.47	7.48	7.53	7.72	7.33
TC1501052	TIPIN	54962	TIMELESS interacting protein	6.62E-11	2	3.67	4.15	3.96	4.39	4.89	4.84	4.75	4.31

TC0900283	TJP2	9414	tight junction protein 2 (zona occluden	0.000244	2	3.89	3.81	3.84	3.94	4.00	4.05	4.05	3.97
TC1701737	TK1	7083	thymidine kinase 1, soluble	4.20E-05	2	4.30	4.45	4.44	4.55	4.65	4.59	4.52	4.36
TC0202092	TLK1	9874	tousled-like kinase 1 /// Serine/threoni	2.31E-25	2	6.93	7.47	7.74	8.30	8.33	8.25	8.12	7.85
TC1201062	TM7SF3	51768	transmembrane 7 superfamily member	1.39E-11	2	4.76	4.50	4.96	5.19	5.25	5.20	5.25	5.06
TC1001190	TM9SF3	56889	transmembrane 9 superfamily member	0.000585	2	6.47	6.87	6.81	6.81	6.77	6.91	6.92	6.95
TC0102957	TMCO1	54499	transmembrane and coiled-coil domain	1.11E-06	2	5.48	5.82	5.98	5.92	5.94	5.93	5.97	6.00
TC1401002	TMED10	10972	transmembrane emp24-like trafficking	2.45E-06	2	6.41	6.74	6.68	6.88	6.96	6.83	6.86	6.84
TC1200791	TMED2	10959	transmembrane emp24 domain traffick	0.000285	2	8.67	8.92	9.00	9.04	9.07	9.12	9.04	9.06
TC0900440	TMEFF1 /// C9	91283 ///	chromosome 9 open reading frame 30	0.000307	2	3.92	4.14	4.13	4.15	4.25	4.22	4.13	4.15
TC1200281	TMEM106C	79022	transmembrane protein 106C	2.07E-09	2	4.07	4.26	4.30	4.45	4.69	4.66	4.56	4.38
TC1701134	TMEM11	8834	transmembrane protein 11	5.53E-06	2	4.28	4.52	4.65	4.76	4.84	4.75	4.51	4.55
TC1100720	TMEM126A	84233	transmembrane protein 126A	6.86E-06	2	3.90	4.59	4.75	4.81	4.98	4.94	5.01	4.75
TC1900445	TMEM147	10430	transmembrane protein 147	0.000491	2	4.72	4.87	4.87	4.93	5.03	4.95	4.95	4.95
TC0600069	TMEM14B	81853	transmembrane protein 14B /// Trans	8.57E-06	2	5.10	5.24	5.48	5.48	5.45	5.45	5.44	5.45
TC0600068	TMEM14C	51522	transmembrane protein 14C /// Trans	2.98E-08	2	4.76	4.91	5.01	5.27	5.28	5.32	5.41	5.32
TC0301145	TMEM158	25907	transmembrane protein 158 /// transm	7.29E-09	2	4.92	5.50	5.52	5.62	5.66	5.69	5.57	5.45
TC1600239	TMEM159	57146	transmembrane protein 159	2.67E-05	2	3.85	4.06	4.06	4.21	4.29	4.27	4.31	4.24
TC0201650	TMEM159 ///	57146 ///	transmembrane protein 159 /// chrom	0.000572	2	2.86	2.96	2.97	2.98	3.05	3.02	3.09	3.03
TC1200269	TMEM16F	196527	transmembrane protein 16F	4.18E-10	2	3.89	5.08	4.72	5.52	5.92	5.92	5.67	5.41
TC1601265	TMEM170A	124491	transmembrane protein 170A	0.000285	2	5.82	5.86	5.92	6.03	6.01	6.05	6.09	6.08
TC0400584	TMEM184C	55751	transmembrane protein 184C	2.14E-07	2	4.93	4.98	5.27	5.30	5.11	5.27	5.51	5.43
TC1700286	TMEM199	147007	transmembrane protein 199	2.99E-07	2	5.73	5.74	5.62	5.99	5.94	5.94	6.08	6.08
TC0901468	TMEM203 ///	94107	transmembrane protein 203 /// HBeAg	3.27E-13	2	5.69	5.82	5.98	6.24	6.34	6.33	6.43	6.40
TC0701631	TMEM209 ///	84928	transmembrane protein 209 /// CDNA	8.73E-07	2	3.87	3.99	4.04	4.25	4.27	4.28	4.33	4.29
TC1100456	TMEM216 ///	51259	transmembrane protein 216	4.96E-07	2	5.10	5.47	5.63	5.68	5.81	5.81	5.77	5.67
TC1600324	TMEM219	124446	transmembrane protein 219	1.33E-07	2	5.83	6.05	5.98	6.07	6.20	6.26	6.29	6.27
TC0900463	TMEM38B	55151	transmembrane protein 38B /// Trans	3.25E-05	2	3.87	3.91	3.95	4.10	4.17	4.11	4.21	4.12
TC0301474	TMEM39A	55254	transmembrane protein 39A	1.12E-05	2	4.51	4.43	4.61	4.71	4.73	4.71	4.84	4.77
TC0102270	TMEM48	55706	transmembrane protein 48 /// Nucleop	5.20E-07	2	3.55	3.96	3.99	4.13	4.23	4.21	4.24	4.14
TC0801111	TMEM55A	55529	transmembrane protein 55A	0.000768	2	8.12	7.80	8.19	8.24	8.27	8.32	8.14	8.26
TC0100749	TMEM56 /// R	148534 //	transmembrane protein 56 /// RWD d	9.02E-05	2	4.62	4.73	4.53	4.53	4.75	4.84	4.77	4.68
TC0701373	TMEM60	85025	transmembrane protein 60	7.49E-07	2	7.60	8.09	8.47	8.40	8.34	8.60	8.56	8.52
TC1500271	TMEM62	80021	transmembrane protein 62	0.000239	2	3.46	3.49	3.64	3.62	3.63	3.71	3.82	3.77
TC0800940	TMEM68	137695	transmembrane protein 68	1.69E-05	2	4.20	4.22	4.25	4.40	4.40	4.46	4.47	4.47

TC1700586	TMEM92	162461	transmembrane protein 92	0.00071	2	3.57	3.59	3.49	3.58	3.79	3.76	3.58	3.48
TC1700036	TMEM93	83460	transmembrane protein 93	0.000159	2	4.69	4.84	5.03	5.05	5.09	5.05	5.01	5.00
TC1101191	TMEM9B	56674	TMEM9 domain family, member B	7.89E-11	2	5.47	5.90	5.99	6.02	6.01	6.06	6.04	6.08
TC1200615	TMPO	7112	thymopoietin	9.83E-08	2	4.11	4.38	4.30	4.59	4.83	4.80	4.82	4.51
TC0200400	TMSB10	9168	thymosin beta 10	0.000152	2	10.11	10.29	10.38	10.60	10.40	10.46	10.71	10.73
TC0401124	TMSL3	7117	thymosin-like 3	1.07E-09	2	9.98	10.15	10.29	10.39	10.37	10.43	10.35	10.37
TC2000829	TMSL3	7117	thymosin-like 3	1.18E-08	2	8.71	9.05	9.28	9.30	9.32	9.40	9.28	9.24
TC0X00046	TMSL3 /// TMS	7117 ///	thymosin-like 3 /// thymosin beta 4, X-	1.67E-14	2	6.89	6.89	6.94	7.09	7.16	7.15	7.04	7.07
TC0500418	TNFAIP8	25816	tumor necrosis factor, alpha-induced p	5.55E-07	2	5.17	5.50	5.56	5.77	5.82	5.81	5.82	5.64
TC1901812	TNNT1	7138	troponin T type 1 (skeletal, slow) /// Tr	3.43E-05	2	5.45	5.37	5.49	5.77	5.58	5.59	5.72	5.70
TC0500260	TNPO1	3842	transportin 1	1.26E-14	2	5.98	6.26	6.50	6.72	6.67	6.61	6.45	6.29
TC0103366	TOMM20	9804	translocase of outer mitochondrial me	9.51E-10	2	6.08	6.18	6.13	6.54	6.58	6.61	6.72	6.58
TC0301401	TOMM70A	9868	translocase of outer mitochondrial me	1.48E-07	2	3.54	3.60	3.61	3.85	3.94	3.93	4.03	3.93
TC1701308	TOP2A /// P11	7153	topoisomerase (DNA) II alpha 170kDa /	7.03E-12	2	3.33	3.90	3.71	4.39	5.01	4.95	4.77	4.22
TC0701395	TP53AP1	---	P53TG1-A (TP53 activated protein 1) (T	8.95E-07	2	4.60	4.96	5.07	5.16	5.09	5.19	5.39	5.25
TC1500394	TPM1	7168	tropomyosin 1 (alpha) /// Tropomyosi	2.06E-08	2	5.11	5.54	5.44	5.56	5.86	5.78	5.61	5.43
TC1101160	TPP1	1200	tripeptidyl peptidase I /// Tripeptidyl-p	3.97E-05	2	6.43	6.86	6.69	7.09	7.19	7.12	7.01	6.82
TC0500809	TPPP	11076	tubulin polymerization promoting prot	0.00029	2	4.06	4.44	4.36	4.38	4.42	4.52	4.42	4.43
TC0201627	TPRKB	51002	TP53RK binding protein /// TP53RK-bin	0.000527	2	4.57	4.64	4.69	4.65	4.69	4.77	4.87	4.81
TC2000169	TPX2	22974	TPX2, microtubule-associated, homolo	3.35E-09	2	3.67	4.15	4.01	4.49	4.99	4.92	4.68	4.36
TC0801018	TRAM1	23471	translocation associated membrane pr	5.57E-10	2	6.53	7.33	7.46	7.62	7.56	7.56	7.53	7.49
TC0X00777	TRAPPC2	6399	trafficking protein particle complex 2 /	9.03E-05	2	4.26	4.25	4.42	4.46	4.40	4.45	4.49	4.51
TC1900136	TRAPPC5	126003	trafficking protein particle complex 5	0.000111	2	6.62	6.83	6.84	6.99	7.07	7.00	6.92	6.97
TC0601245	TREML1	340205	triggering receptor expressed on myel	0.000691	2	6.22	6.41	6.35	6.83	7.09	7.03	6.77	6.58
TC0800825	TRIM35	23087	tripartite motif-containing 35 /// Tripa	0.000689	2	4.72	4.81	4.91	4.91	5.05	4.98	5.00	4.92
TC1100277	TRIM44	54765	tripartite motif-containing 44	0.000667	2	4.42	4.41	4.40	4.70	4.62	4.64	4.94	4.82
TC1101107	TRIM68	55128	tripartite motif-containing 68	0.000106	2	4.41	4.57	4.61	4.55	4.48	4.63	4.78	4.77
TC1800265	TSHZ1	10194	teashirt zinc finger homeobox 1	0.000452	2	4.39	4.61	4.68	4.77	4.76	4.67	4.76	4.80
TC0200650	TSN	7247	translin	3.03E-09	2	4.67	4.83	5.00	5.16	5.25	5.25	5.27	5.15
TC0102571	TSPAN2	10100	tetraspanin 2 /// Tetraspanin-2 (Tspan-	1.14E-11	2	6.87	7.44	7.65	8.23	8.22	7.78	7.63	7.53
TC0601554	TSPYL1	7259	TSPY-like 1	0.000189	2	5.48	5.85	5.62	5.67	5.68	5.79	5.82	5.80
TC2200640	TST	7263	thiosulfate sulfurtransferase (rhodanes	0.000167	2	5.48	5.78	5.78	5.89	5.93	5.87	5.80	5.88
TC0500660	TTC1	7265	tetratricopeptide repeat domain 1	1.65E-09	2	7.31	7.63	7.86	8.02	7.84	8.00	8.11	8.06
TC0200165	TTC27	55622	tetratricopeptide repeat domain 27	0.000279	2	2.85	2.83	2.82	2.90	3.03	3.01	3.00	2.90

TC2100118	TTC3	7267	tetratricopeptide repeat domain 3	1.55E-11	2	3.61	3.84	3.69	4.23	4.40	4.35	4.48	4.15
TC0501154	TTC37	9652	tetratricopeptide repeat domain 37	0.00014	2	3.35	3.59	3.54	3.76	3.90	3.88	3.93	3.71
TC1400665	TTC5	91875	tetratricopeptide repeat domain 5 /// T	0.000304	2	3.89	3.86	3.90	3.97	4.04	3.90	4.10	4.01
TC1401059	TTC7B	145567	tetratricopeptide repeat domain 7B ///	2.45E-05	2	4.26	4.47	4.39	4.54	4.69	4.77	4.74	4.63
TC1100485	TTC9C	283237	tetratricopeptide repeat domain 9C ///	1.34E-08	2	4.53	4.53	5.06	4.91	4.85	4.83	4.86	4.86
TC0600523	TTK	7272	TTK protein kinase /// Dual specificity p	2.58E-06	2	2.27	2.35	2.36	2.54	2.88	2.80	2.76	2.55
TC0200583	TTL	150465	tubulin tyrosine ligase	4.23E-06	2	3.97	3.97	4.07	4.24	4.23	4.27	4.27	4.32
TC1200301	TUBA1C	84790	tubulin, alpha 1c /// Tubulin alpha-1C c	1.77E-07	2	6.29	6.48	6.54	6.61	6.69	6.66	6.60	6.58
TC2000415	TUBB1	81027	tubulin, beta 1	0.000103	2	4.83	5.04	5.02	6.03	6.15	6.25	5.97	5.90
TC1600971	TUFM	7284	Tu translation elongation factor, mitoch	0.000994	2	5.05	5.20	5.27	5.40	5.34	5.31	5.28	5.24
TC0301230	TUSC2	11334	tumor suppressor candidate 2	1.97E-09	2	6.22	6.34	6.41	6.84	6.74	6.59	6.60	6.68
TC1101475	TUT1 /// EEF1G	731096 //	terminal uridylyl transferase 1, U6 snRN	6.43E-06	2	5.17	5.44	5.50	5.65	5.67	5.64	5.68	5.50
TC1400220	TXNDC1	81542	thioredoxin domain containing 1	1.32E-14	2	6.69	7.62	7.77	7.88	7.87	7.84	7.83	7.66
TC0500489	TXNDC15	79770	thioredoxin domain containing 15	1.49E-09	2	5.34	5.25	5.74	5.70	5.61	5.64	5.82	5.76
TC1700074	TXNDC17	84817	thioredoxin domain containing 17	5.97E-12	2	6.95	7.10	7.62	7.70	7.55	7.60	7.57	7.62
TC0600938	TXNDC5 /// MU	81567 ///	thioredoxin domain containing 5 /// mu	6.16E-06	2	4.71	4.98	5.06	5.08	5.15	5.07	5.12	4.97
TC0201779	TXNDC9	10190	thioredoxin domain containing 9	0.000183	2	5.38	5.63	5.77	5.72	5.68	5.69	5.82	5.79
TC1800561	TXNL4A	10907	thioredoxin-like 4A /// Thioredoxin-like	1.67E-05	2	4.75	4.93	5.06	5.13	5.17	5.07	5.15	5.05
TC1800007	TYMS	7298	thymidylate synthetase /// Thymidylat	1.92E-13	2	4.48	5.30	4.90	5.71	6.43	6.44	6.10	5.61
TC0100655	TYW3	127253	tRNA-yW synthesizing protein 3 homol	1.76E-05	2	3.69	3.91	3.87	4.23	4.40	4.34	4.48	4.18
TC0101229	UAP1	6675	UDP-N-acteylglucosamine pyrophospho	6.77E-09	2	4.24	4.28	4.18	4.43	4.53	4.59	4.64	4.63
TC1900420	UBA2	10054	ubiquitin-like modifier activating enzym	7.64E-08	2	3.53	3.65	3.57	3.86	4.07	4.01	4.02	3.90
TC0300629	UBA5	79876	ubiquitin-like modifier activating enzym	1.54E-07	2	3.36	3.82	3.44	3.88	4.18	4.17	4.23	3.87
TC1100938	UBASH3B	84959	ubiquitin associated and SH3 domain c	2.82E-08	2	5.71	5.49	5.86	6.03	5.88	6.30	6.31	6.22
TC2000324	UBE2C	11065	ubiquitin-conjugating enzyme E2C	3.32E-09	2	5.54	5.46	5.39	5.59	5.78	5.70	5.58	5.54
TC0300106	UBE2E1	7324	ubiquitin-conjugating enzyme E2E 1 (U	6.55E-05	2	6.43	6.92	6.81	7.11	7.13	7.09	7.20	7.13
TC0200906	UBE2E3	10477	ubiquitin-conjugating enzyme E2E 3 (U	8.67E-10	2	5.71	5.72	5.71	5.94	5.92	6.14	6.21	6.18
TC1700931	UBE2G1	7326	ubiquitin-conjugating enzyme E2G 1 (U	9.59E-09	2	7.50	7.84	7.99	8.22	8.13	8.05	7.97	7.98
TC1600049	UBE2I	7329	ubiquitin-conjugating enzyme E2I (UBC	0.000179	2	5.39	5.35	5.36	5.51	5.54	5.49	5.54	5.52
TC1901881	UBE2M	9040	ubiquitin-conjugating enzyme E2M (UB	0.000313	2	5.54	5.83	5.76	5.86	5.86	5.92	5.85	5.88
TC0102813	UBE2Q1	55585	ubiquitin-conjugating enzyme E2Q fam	1.30E-08	2	7.17	7.05	7.20	7.40	7.32	7.37	7.48	7.46
TC1500506	UBE2Q2	92912	ubiquitin-conjugating enzyme E2Q fam	7.07E-11	2	4.98	5.52	5.51	5.96	5.79	5.89	6.00	6.00
TC0103126	UBE2T	29089	ubiquitin-conjugating enzyme E2T (put	2.79E-07	2	3.90	3.95	3.92	4.11	4.55	4.38	4.34	4.14
TC1300202	UCHL3	7347	ubiquitin carboxyl-terminal esterase L3	1.02E-08	2	4.48	4.66	4.61	4.84	4.91	4.89	4.94	4.81

TC0103087	UCHL5	51377	ubiquitin carboxyl-terminal hydrolase L	4.55E-07	2	5.46	5.90	5.88	6.01	6.06	6.00	6.04	5.91
TC0101251	UCK2	7371	uridine-cytidine kinase 2	0.000176	2	3.81	4.11	4.06	4.10	4.20	4.21	4.08	4.01
TC2200183	UCRC /// NP_0	29796	ubiquinol-cytochrome c reductase com	2.45E-08	2	6.02	6.55	6.70	6.75	6.70	6.75	6.76	6.69
TC0101203	UFC1	51506	ubiquitin-fold modifier conjugating enz	3.59E-10	2	5.68	6.07	6.24	6.69	6.61	6.43	6.56	6.30
TC0401458	UFSP2	55325	UFM1-specific peptidase 2	3.26E-05	2	3.74	3.77	3.76	3.87	3.84	3.81	4.02	3.93
TC0400889	UGDH	7358	UDP-glucose dehydrogenase	2.03E-09	2	3.76	3.70	3.63	4.04	4.17	4.26	4.42	4.20
TC1300299	UPF3A	65110	UPF3 regulator of nonsense transcripts	8.81E-08	2	5.01	5.28	5.29	5.35	5.40	5.45	5.50	5.40
TC0X01191	UPF3B	65109	UPF3 regulator of nonsense transcripts	0.000149	2	4.66	4.86	4.74	4.90	5.04	5.07	5.39	5.15
TC1901004	UQCR	10975	ubiquinol-cytochrome c reductase, 6.4	1.69E-06	2	6.98	7.28	7.56	7.76	7.74	7.69	7.61	7.63
TC0100508	UQCRH	7388	ubiquinol-cytochrome c reductase hing	7.63E-15	2	6.17	7.30	7.50	7.62	7.81	7.71	7.59	7.34
TC0500473	UQCRQ	27089	ubiquinol-cytochrome c reductase, con	1.89E-07	2	6.30	6.40	6.47	6.65	6.64	6.63	6.65	6.65
TC1001340	UROS	7390	uroporphyrinogen III synthase (congen	0.000115	2	3.91	3.99	4.03	4.00	4.11	4.12	4.18	4.06
TC0100606	USP1	7398	ubiquitin specific peptidase 1	1.21E-09	2	4.95	5.21	5.35	5.42	5.41	5.53	5.59	5.59
TC1600938	USP31	57478	ubiquitin specific peptidase 31 /// Ubiq	0.000562	2	3.94	3.87	3.95	3.97	4.07	3.95	3.99	3.95
TC1000764	USP6NL	9712	USP6 N-terminal like	2.30E-08	2	3.90	4.17	4.28	4.57	4.51	4.56	4.56	4.37
TC0100408	UTP11L	51118	UTP11-like, U3 small nucleolar ribonucl	6.94E-11	2	4.31	4.59	4.77	5.01	5.10	5.13	5.27	5.00
TC0500267	UTP15	84135	UTP15, U3 small nucleolar ribonucleop	1.99E-06	2	3.22	3.16	3.16	3.19	3.41	3.35	3.41	3.32
TC0400297	UTP3	57050	UTP3, small subunit (SSU) processome	5.65E-05	2	3.75	3.88	3.98	4.34	4.25	4.32	4.70	4.55
TC0201802	UXS1	80146	UDP-glucuronate decarboxylase 1	1.03E-12	2	4.90	5.34	5.23	5.88	6.10	6.00	5.87	5.71
TC0X00890	UXT	8409	ubiquitously-expressed transcript /// P	1.65E-05	2	5.64	6.04	6.10	6.11	6.15	6.19	6.18	6.10
TC0200413	VAMP5	10791	vesicle-associated membrane protein 5	0.000334	2	6.23	6.54	6.54	6.94	6.80	6.85	7.04	7.06
TC0200412	VAMP8	8673	vesicle-associated membrane protein 8	3.22E-17	2	5.82	7.06	7.13	8.00	8.21	8.37	8.32	7.73
TC2000409	VAPB	9217	VAMP (vesicle-associated membrane p	2.40E-05	2	6.02	6.26	6.13	6.25	6.32	6.35	6.26	6.20
TC1701397	VAT1	10493	vesicle amine transport protein 1 homo	0.000247	2	4.54	4.80	4.82	4.97	5.12	5.01	4.87	4.75
TC0501285	VDAC1	7416	voltage-dependent anion channel 1	3.20E-07	2	5.26	5.56	5.52	5.69	5.78	5.70	5.67	5.60
TC1000354	VDAC2	7417	voltage-dependent anion channel 2 ///	1.17E-05	2	5.70	5.69	5.80	5.83	5.89	5.92	5.99	5.94
TC0301697	VEPH1	79674	ventricular zone expressed PH domain	1.05E-07	2	3.09	3.31	3.24	3.32	3.69	3.59	3.50	3.36
TC1200595	VEZT	55591	vezatin, adherens junctions transmemb	0.00063	2	3.93	3.94	3.88	3.97	4.11	4.11	4.10	4.06
TC1601034	VKORC1	79001	vitamin K epoxide reductase complex, s	1.95E-07	2	5.88	6.02	6.16	6.25	6.30	6.25	6.21	6.20
TC0900309	VPS13A	23230	vacuolar protein sorting 13 homolog A	3.61E-10	2	3.82	3.93	3.81	4.18	4.36	4.36	4.42	4.22
TC1500244	VPS18	57617	vacuolar protein sorting 18 homolog (S	9.16E-05	2	5.09	5.12	5.09	5.37	5.38	5.39	5.36	5.46
TC0200258	VRK2	7444	vaccinia related kinase 2	2.11E-07	2	4.86	5.10	5.47	5.48	5.26	5.35	5.51	5.46
TC1901789	VSTM1	284415	V-set and transmembrane domain cont	3.35E-05	2	6.97	7.47	7.82	8.12	8.15	8.09	8.07	7.89
TC0701601	WASL	8976	Wiskott-Aldrich syndrome-like	1.62E-05	2	4.27	4.65	4.61	4.68	4.67	4.78	4.87	4.77

TC1400873	WDHD1	11169	WD repeat and HMG-box DNA binding	6.43E-09	2	3.40	3.56	3.53	3.90	4.34	4.28	4.22	3.91
TC0500390	WDR36	134430	WD repeat domain 36	4.26E-07	2	3.21	3.36	3.25	3.48	3.73	3.71	3.71	3.57
TC0200142	WDR43	---	WD repeat protein 43. [Source:Uniprot	2.34E-09	2	3.49	3.57	3.42	3.78	3.84	3.97	4.07	3.95
TC0900681	WDR5	11091	WD repeat domain 5	9.64E-07	2	4.80	4.75	4.77	4.94	5.08	5.01	5.06	4.97
TC0102066	WDR57	9410	WD repeat domain 57 (U5 snRNP speci	4.32E-08	2	4.27	4.35	4.33	4.55	4.81	4.80	4.77	4.65
TC0700932	WDR60	55112	WD repeat domain 60	0.000198	2	3.95	4.23	4.26	4.28	4.28	4.26	4.29	4.26
TC0800534	WDR67	93594	WD repeat domain 67 /// WD repeat p	3.63E-05	2	3.60	3.53	3.66	3.88	3.87	3.78	3.75	3.69
TC1700677	WDR68	10238	WD repeat domain 68	6.46E-08	2	5.95	6.03	6.10	6.32	6.29	6.36	6.41	6.42
TC0200931	WDR75	84128	WD repeat domain 75	6.58E-06	2	3.53	3.49	3.45	3.61	3.74	3.75	3.92	3.68
TC1500286	WDR76	79968	WD repeat domain 76 /// WD repeat p	1.69E-09	2	3.31	3.58	3.46	3.94	4.46	4.38	4.28	3.90
TC1400908	WDR89	112840	WD repeat domain 89	0.000345	2	3.50	3.72	3.72	3.67	3.83	3.78	3.74	3.75
TC0800491	WDSOF1	25879	WD repeats and SOF1 domain containi	1.36E-06	2	3.76	3.68	3.62	3.91	4.09	4.12	4.13	3.99
TC1100163	WEE1	7465	WEE1 homolog (S. pombe)	9.67E-17	2	3.90	3.65	3.58	4.26	4.58	4.63	4.73	4.58
TC0400023	WHSC1	7468	Wolf-Hirschhorn syndrome candidate 1	3.09E-05	2	4.51	4.49	4.43	4.56	4.77	4.73	4.77	4.61
TC1201285	WIBG	84305	within bgcn homolog (Drosophila) /// P	0.000332	2	4.32	4.45	4.64	4.69	4.74	4.71	4.68	4.59
TC1201609	WSB2	55884	WD repeat and SOCS box-containing 2	5.48E-12	2	5.50	6.06	6.17	6.75	6.58	6.57	6.54	6.38
TC0800416	WWP1	11059	WW domain containing E3 ubiquitin pr	1.28E-06	2	4.12	4.16	4.25	4.55	4.42	4.44	4.75	4.55
TC0X00141	XK	7504	X-linked Kx blood group (McLeod syndr	5.39E-05	2	4.56	4.61	4.60	5.00	5.07	5.13	5.19	5.06
TC0201548	XPO1	7514	exportin 1 (CRM1 homolog, yeast)	5.02E-06	2	5.04	4.90	5.20	5.31	5.30	5.42	5.48	5.41
TC1300323	XPO4	64328	exportin 4 /// Exportin-4 (Exp4). [Sourc	1.42E-05	2	3.42	3.51	3.48	3.59	3.71	3.67	3.73	3.67
TC0601286	XPO5	57510	exportin 5 /// Exportin-5 (Exp5) (Ran-bi	6.78E-09	2	3.86	3.81	3.76	3.96	4.08	4.05	4.20	4.03
TC1200480	XPOT	11260	exportin, tRNA (nuclear export recepto	8.47E-09	2	4.40	4.46	4.86	5.15	5.18	5.03	5.23	4.92
TC1200464	XRCC6BP1	91419	XRCC6 binding protein 1	5.56E-09	2	3.48	3.84	3.85	4.19	4.33	4.45	4.32	4.19
TC1201114	YAF2	10138	YY1 associated factor 2 /// YY1-associat	2.18E-07	2	5.26	5.29	5.31	5.54	5.51	5.59	5.60	5.62
TC1201092	YARS2	51067	tyrosyl-tRNA synthetase 2, mitochondr	0.000215	2	3.42	3.64	3.64	3.74	3.95	3.78	3.81	3.77
TC1200507	YEATS4	8089	YEATS domain containing 4	1.04E-10	2	3.67	4.81	4.98	5.35	5.56	5.66	5.62	5.32
TC0102132	YRDC	79693	yrdC domain containing (E. coli)	0.000667	2	4.55	4.71	4.79	4.93	4.82	4.96	4.72	4.81
TC0100333	YTHDF2	51441	YTH domain family, member 2 /// YTH	3.68E-05	2	5.04	5.44	5.55	5.57	5.55	5.50	5.64	5.55
TC2200217	YWHAH	7533	tyrosine 3-monooxygenase/tryptophar	4.08E-12	2	6.15	6.54	6.54	6.71	6.87	6.77	6.66	6.53
TC0601687	ZBTB2	57621	zinc finger and BTB domain containing	1.23E-12	2	5.29	5.35	5.46	5.61	5.57	5.62	5.69	5.63
TC0X00536	ZBTB33	10009	zinc finger and BTB domain containing	8.76E-05	2	4.65	5.11	5.11	5.03	5.07	5.04	5.17	5.23
TC0901314	ZBTB6	10773	zinc finger and BTB domain containing	8.56E-07	2	3.92	4.30	4.54	4.37	4.26	4.55	4.55	4.70
TC0102082	ZBTB8OS	731379 //	zinc finger and BTB domain containing	8.21E-08	2	5.13	5.42	5.68	5.73	5.70	5.63	5.70	5.66
TC1100829	ZC3H12C	85463	zinc finger CCCH-type containing 12C	6.01E-05	2	2.89	2.80	2.72	2.91	3.21	3.11	3.08	3.03

TC1400424	ZC3H14	79882	zinc finger CCCH-type containing 14 ///	5.17E-05	2	4.22	4.32	4.33	4.53	4.60	4.61	4.73	4.56
TC0200925	ZC3H15	55854	zinc finger CCCH-type containing 15 ///	1.33E-09	2	6.80	7.31	7.48	7.47	7.44	7.50	7.61	7.49
TC0200582	ZC3H6	376940	zinc finger CCCH-type containing 6	1.99E-06	2	5.89	6.33	6.52	6.55	6.43	6.54	6.61	6.49
TC0201826	ZC3H8	84524	zinc finger CCCH-type containing 8	0.000322	2	4.28	4.35	4.39	4.52	4.60	4.59	4.65	4.55
TC0100342	ZCCHC17	51538	zinc finger, CCHC domain containing 17	2.61E-08	2	4.80	5.96	5.81	5.91	6.07	6.12	6.15	5.92
TC0500312	ZCCHC9	84240	zinc finger, CCHC domain containing 9	6.94E-07	2	6.01	6.26	6.08	6.06	6.06	6.21	6.34	6.31
TC1201115	ZCRB1	85437	zinc finger CCHC-type and RNA binding	1.50E-14	2	4.53	5.56	5.75	5.80	5.78	5.79	5.92	5.75
TC0700056	ZDHHC4	55146	zinc finger, DHHC-type containing 4	6.45E-06	2	4.48	4.60	4.68	4.71	4.79	4.75	4.76	4.74
TC0801072	ZFAND1	79752	zinc finger, AN1-type domain 1	4.78E-07	2	4.88	4.87	4.88	5.02	5.08	5.15	5.19	5.20
TC1800312	ZFP161	7541	zinc finger protein 161 homolog (mous	0.000195	2	4.69	4.87	4.94	5.03	5.01	4.95	5.02	4.94
TC0500537	ZMAT2	153527	zinc finger, matrin type 2	3.71E-05	2	7.69	8.07	8.01	8.27	8.14	8.11	8.13	8.10
TC0100427	ZMPSTE24	10269	zinc metallopeptidase (STE24 homolog,	8.93E-05	2	6.96	7.03	7.38	7.41	7.27	7.28	7.24	7.31
TC0100386	ZMYM4	9202	zinc finger, MYM-type 4 /// zinc finger	2.12E-12	2	4.27	5.33	5.28	5.24	5.43	5.40	5.42	5.20
TC1901145	ZNF121	7675	zinc finger protein 121	1.78E-06	2	3.80	3.73	3.67	4.00	4.18	4.08	4.24	4.09
TC0601046	ZNF184	7738	zinc finger protein 184	1.58E-05	2	4.33	4.39	4.46	4.47	4.48	4.53	4.72	4.64
TC1101087	ZNF195	7748	zinc finger protein 195 /// Zinc finger p	0.000289	2	3.75	3.79	3.81	3.84	3.89	3.85	4.01	3.89
TC0X01233	ZNF280C /// S	55609	zinc finger protein 280C /// Suppressor	0.0001	2	3.12	3.44	3.50	3.45	3.51	3.51	3.55	3.49
TC1900422	ZNF302	55900	zinc finger protein 302 /// Zinc finger p	0.000432	2	4.15	4.45	4.40	4.27	4.26	4.35	4.56	4.49
TC0901161	ZNF367	195828	zinc finger protein 367	1.74E-05	2	3.96	4.17	4.08	4.27	4.44	4.42	4.35	4.25
TC0901164	ZNF510	22869	zinc finger protein 510	0.000145	2	3.56	3.62	3.69	3.77	3.79	3.80	3.87	3.79
TC0501249	ZNF608	57507	zinc finger protein 608	0.000394	2	3.88	4.83	4.83	5.08	5.24	5.40	5.24	4.75
TC0300817	ZNF639	51193	zinc finger protein 639	3.45E-07	2	3.93	4.30	4.27	4.42	4.55	4.44	4.52	4.33
TC0100431	ZNF642	339559	zinc finger protein 642	0.000363	2	3.29	3.33	3.30	3.34	3.40	3.44	3.53	3.40
TC1601015	ZNF768	79724	zinc finger protein 768 /// zinc finger p	1.55E-10	2	6.01	6.23	6.25	6.38	6.50	6.45	6.44	6.46
TC1300300	ZNF828	283489	zinc finger protein 828	5.08E-06	2	3.97	4.20	4.23	4.25	4.39	4.33	4.31	4.18
TC0700566	ZNHIT1	10467	zinc finger, HIT type 1	2.18E-10	2	5.70	6.01	6.15	6.32	6.26	6.21	6.25	6.20
TC0701520	ZRF1	27000	zuotin related factor 1 /// DnaJ homol	4.18E-05	2	4.57	4.68	4.73	4.83	4.81	4.85	5.04	4.89
TC1101845	ZW10	9183	ZW10, kinetochore associated, homolo	0.000857	2	3.29	3.29	3.38	3.41	3.53	3.58	3.60	3.49
TC1500421	ZWILCH	55055	Zwilch, kinetochore associated, homol	1.42E-06	2	3.28	3.40	3.43	3.61	3.73	3.75	3.71	3.66
TC1000994	ZWINT	11130	ZW10 interactor /// ZW10 interactor (Z	0.000181	2	4.02	4.05	3.96	4.11	4.29	4.22	4.18	4.09
TC0102374	ZZZ3	26009	zinc finger, ZZ-type containing 3 /// Zin	6.04E-09	2	3.53	3.52	3.54	3.70	3.84	3.78	3.85	3.71
TC03r00009		---		1.36E-25	2	5.53	10.82	9.35	10.33	11.04	11.23	10.44	9.93
TC1201091		---		6.32E-19	2	6.63	6.75	6.49	7.46	7.65	7.76	7.79	7.58
TC0103307		---		9.95E-17	2	6.30	6.90	6.96	7.31	7.46	7.70	7.38	7.27

TC0901303	731515	7.63E-16	2	4.27	5.15	4.93	5.32	5.85	5.70	5.60	5.25
TC1201629	---	2.71E-14	2	5.79	6.83	6.91	7.10	7.31	7.25	7.15	7.05
TC1200140	---	7.44E-14	2	5.75	6.00	5.82	6.57	6.97	7.16	7.06	6.82
TC1901069	---	4.24E-13	2	7.16	7.22	7.27	7.60	7.74	7.79	7.80	7.69
TC0701426	---	2.43E-12	2	6.04	6.79	6.82	6.90	6.99	6.99	7.00	6.96
TC0202124	---	1.11E-11	2	8.59	9.62	9.39	9.92	10.11	10.11	10.02	9.81
TC0301461	---	1.50E-11	2	4.44	4.71	4.93	5.30	5.50	5.60	5.26	5.23
TC0600130	---	1.75E-11	2	5.37	5.30	5.32	5.88	6.06	6.14	6.03	5.68
TC1500380	---	2.17E-11	2	7.52	8.72	8.86	9.05	9.16	9.23	9.08	9.00
TC0102003	---	3.95E-11	2	5.20	5.12	4.87	6.01	5.93	6.11	6.41	6.25
TC1800387	643509	4.76E-11	2	4.34	5.64	5.73	6.40	6.80	6.42	6.34	5.83
TC1800170	---	5.48E-11	2	2.14	4.02	4.22	4.32	4.46	4.53	4.43	4.16
TC1701738	---	5.82E-11	2	3.99	4.80	4.56	5.49	6.14	6.09	5.37	4.82
TC0501199	---	8.81E-11	2	6.07	6.52	6.45	6.62	6.59	6.59	6.49	6.46
TC0102470	653949	1.37E-10	2	5.04	5.97	6.02	6.21	6.35	6.43	6.37	6.06
TC1400039	---	1.89E-10	2	3.25	5.24	4.87	5.94	6.37	6.33	6.19	5.20
TC0200936	---	1.91E-10	2	8.56	8.55	8.69	8.86	8.77	8.89	8.91	8.95
TC0100092	---	2.48E-10	2	7.40	7.50	7.42	7.87	8.19	8.36	8.17	8.05
TC0102623	---	2.61E-10	2	7.12	7.18	7.21	7.48	7.46	7.62	7.66	7.74
TC2000110	---	2.72E-10	2	8.51	9.17	9.46	9.63	9.65	9.76	9.72	9.70
TC1700687	---	3.22E-10	2	4.76	4.81	4.64	5.70	6.00	5.73	5.70	4.92
TC1500883	---	5.78E-10	2	5.50	6.42	6.51	6.56	6.55	6.77	6.68	6.57
TC0801148	---	7.02E-10	2	6.17	5.66	5.98	6.43	6.60	6.52	6.56	6.40
TC0400135	---	7.93E-10	2	5.22	5.25	5.27	5.92	6.07	6.02	5.96	5.85
TC0102628	---	7.95E-10	2	7.20	7.22	7.49	8.01	8.01	8.01	7.92	7.89
TC1701057	---	1.01E-09	2	5.01	5.19	5.34	5.59	5.78	5.77	5.87	5.54
TC1600952	---	1.29E-09	2	8.07	8.11	8.01	8.54	8.84	9.04	8.89	8.66
TC0M00001	---	1.35E-09	2	9.98	10.62	10.63	11.03	11.04	10.93	10.85	10.69
TC1501180	---	1.86E-09	2	7.33	8.31	8.27	8.47	8.68	8.63	8.61	8.31
TC0500761	---	2.29E-09	2	7.07	7.56	7.49	7.82	7.84	7.90	7.99	7.91
TC0102299	---	2.39E-09	2	8.34	8.44	7.92	8.48	8.76	8.84	8.84	8.69
TC1701111	---	3.16E-09	2	7.29	8.28	8.37	8.31	8.38	8.42	8.46	8.28
TC0800672	---	3.81E-09	2	3.82	4.54	4.20	4.57	4.74	4.88	4.55	4.43
TC0X00011	---	4.77E-09	2	3.96	4.88	5.01	5.22	5.40	5.26	5.32	5.03

TC0301101	---	4.91E-09	2	4.09	4.25	4.28	4.40	4.68	4.59	4.55	4.33
TC0100703	---	5.40E-09	2	6.30	6.86	6.89	7.15	7.18	7.14	7.12	6.91
TC0202077	---	1.32E-08	2	4.81	4.76	4.72	5.00	5.18	5.23	5.27	5.15
TC0101745	---	1.46E-08	2	2.80	3.76	3.96	4.02	4.12	4.13	4.00	3.82
TC0301616	---	1.48E-08	2	7.24	7.26	7.11	7.64	7.91	8.11	7.85	7.80
TC1500501	---	1.60E-08	2	5.02	5.48	5.43	5.74	5.93	6.00	6.02	5.76
TC0800990	---	1.67E-08	2	6.74	7.18	7.11	7.62	7.86	7.87	7.98	7.62
TC0501230	---	1.68E-08	2	5.22	5.13	4.98	5.38	5.70	5.88	5.70	5.62
TC0M00030	---	1.97E-08	2	4.81	6.15	6.29	6.34	6.51	6.44	6.42	6.21
TC1600761	---	2.64E-08	2	4.67	4.35	4.16	4.86	5.15	5.12	4.99	4.35
TC2000100	---	2.89E-08	2	3.79	3.83	3.78	4.00	4.38	4.29	4.25	4.32
TC1500136	---	3.02E-08	2	9.27	9.05	9.00	9.49	9.87	10.03	9.75	9.66
TC1700292	---	4.84E-08	2	6.21	6.85	6.79	7.03	7.18	6.99	7.13	6.94
TC0701404	---	5.05E-08	2	4.77	4.57	4.43	5.33	5.68	6.06	6.00	5.92
TC0100303	---	5.15E-08	2	4.90	5.61	5.40	5.95	5.96	5.97	5.95	5.72
TC1201335	---	5.96E-08	2	6.75	6.92	7.14	7.29	7.38	7.71	7.72	7.69
TC0M00007	---	6.26E-08	2	3.51	5.25	5.36	5.79	5.97	5.98	5.77	5.53
TC1400269	---	7.70E-08	2	3.16	3.88	3.83	4.11	4.25	4.29	4.08	4.08
TC0900055	---	7.80E-08	2	6.37	6.91	6.81	7.02	7.11	7.10	7.12	6.92
TC0301308	---	8.33E-08	2	4.79	4.91	4.81	4.90	4.97	5.10	5.17	5.11
TC2000125	---	8.98E-08	2	6.70	7.06	7.27	7.31	7.34	7.48	7.48	7.49
TC1701046	---	9.30E-08	2	5.64	6.36	6.23	6.68	6.84	6.80	6.74	6.53
TC1800317	---	9.93E-08	2	9.34	9.88	9.69	10.14	10.26	10.25	10.33	10.14
TC1601103	---	1.04E-07	2	4.78	4.82	4.67	5.00	5.42	5.54	5.54	5.32
TC1201417	---	1.28E-07	2	2.98	3.60	3.54	3.75	3.85	3.89	4.00	3.78
TC0100012	---	1.40E-07	2	6.36	7.47	7.71	8.49	8.64	8.11	8.07	7.96
TC0501017	---	1.82E-07	2	3.05	3.36	3.16	3.81	4.33	4.32	4.10	3.79
TC0701052	---	1.88E-07	2	7.86	8.89	8.83	9.03	9.15	9.16	8.97	8.83
TC1200490	---	2.06E-07	2	7.72	8.33	8.44	8.48	8.42	8.43	8.63	8.53
TC0200872	---	2.17E-07	2	3.62	3.93	3.95	4.02	4.30	4.38	4.56	4.25
TC0200095	---	2.29E-07	2	4.53	4.67	4.66	4.97	5.17	5.37	5.08	5.15
TC0301594	---	2.35E-07	2	4.12	4.00	4.20	4.54	4.53	4.62	4.56	4.42
TC0501152	---	2.56E-07	2	5.12	6.27	6.60	6.57	6.60	6.80	6.67	6.65
TC1300490	---	2.66E-07	2	6.49	6.03	6.36	6.64	6.70	6.35	6.28	6.15

TC0601508	---	2.83E-07	2	5.94	6.42	6.65	6.60	6.61	6.59	6.66	6.59
TC0201745	730995	3.08E-07	2	3.04	3.07	2.94	3.20	3.55	3.52	3.56	3.22
TC0301405	---	3.13E-07	2	8.97	9.72	9.42	10.04	10.18	10.19	10.06	9.90
TC1500736	---	3.15E-07	2	4.72	5.59	5.34	6.09	6.21	6.34	6.18	5.80
TC0202157	---	3.78E-07	2	3.67	3.97	4.09	4.21	4.29	4.44	4.41	4.52
TC0800531	---	5.02E-07	2	3.84	4.79	4.48	5.78	6.54	6.71	6.10	6.25
TC0100309	---	6.34E-07	2	8.72	9.00	9.13	9.16	9.16	9.28	9.29	9.32
TC0601700	---	6.90E-07	2	8.28	9.14	9.14	9.50	9.52	9.47	9.47	9.23
TC0101116	---	8.92E-07	2	4.20	4.31	4.32	4.56	4.86	4.94	4.77	4.70
TC0701788	---	9.15E-07	2	6.45	6.35	6.44	6.90	6.80	6.94	7.09	7.04
TC0M00021	---	1.01E-06	2	7.51	8.81	8.70	9.36	9.74	9.50	9.59	9.15
TC1501172	---	1.01E-06	2	8.43	9.14	9.18	9.32	9.50	9.47	9.45	9.22
TC1500050	---	1.03E-06	2	3.67	4.72	4.73	4.86	5.19	4.85	5.04	4.79
TC0201797	---	1.16E-06	2	3.69	3.88	3.80	4.23	4.61	4.69	4.79	4.64
TC0601390	---	1.19E-06	2	9.48	10.08	10.05	10.22	10.32	10.30	10.22	10.16
TC0X00821	---	1.26E-06	2	7.28	8.05	7.99	8.17	8.27	8.25	8.23	8.15
TC1400156	---	1.38E-06	2	4.16	5.43	5.56	5.45	5.64	5.74	5.77	5.51
TC1001119	---	1.39E-06	2	4.98	5.62	5.70	5.56	5.75	5.77	5.83	5.74
TC0900843	---	1.43E-06	2	6.36	7.00	6.96	7.11	7.25	7.14	7.25	7.06
TC0301013	---	1.43E-06	2	3.66	3.76	3.55	3.87	4.24	4.19	4.10	3.79
TC1200204	---	1.59E-06	2	5.91	6.53	6.51	6.65	6.62	6.64	6.79	6.70
TC0M00016	---	1.67E-06	2	3.64	5.14	4.78	5.70	5.74	5.94	5.84	5.85
TC0701392	---	1.76E-06	2	4.29	4.36	4.46	4.70	4.79	4.91	4.95	4.74
TC0500678	---	1.78E-06	2	3.71	4.45	4.22	5.00	5.11	5.17	5.09	4.79
TC1401067	---	2.13E-06	2	4.24	4.26	4.06	4.26	4.60	4.47	4.58	4.37
TC0301307	---	2.18E-06	2	4.21	4.96	4.67	5.09	5.41	5.42	5.29	5.10
TC0101375	---	2.40E-06	2	6.13	6.59	6.66	6.78	6.68	6.82	6.79	6.79
TC0300879	---	2.48E-06	2	4.81	5.69	5.58	5.89	5.87	6.05	5.92	5.88
TC0100237	---	2.56E-06	2	4.11	4.15	4.33	4.48	4.49	4.46	4.52	4.43
TC0101624	---	2.71E-06	2	5.28	5.33	5.20	5.61	5.79	5.74	5.78	5.54
TC0500975	---	3.38E-06	2	3.34	3.72	4.43	4.74	4.37	4.34	4.26	4.17
TC0201379	---	3.44E-06	2	8.08	8.82	8.78	8.91	9.13	9.27	8.99	9.12
TC0200186	---	3.77E-06	2	6.55	7.00	6.76	7.14	7.36	7.30	7.22	6.86
TC0700094	---	4.47E-06	2	9.93	10.23	10.11	10.32	10.42	10.46	10.56	10.37

TC1501078	650327	4.49E-06	2	7.95	8.70	8.85	8.99	9.03	9.12	8.98	8.72
TC0201024	---	4.62E-06	2	7.49	7.51	7.26	7.83	7.88	7.98	8.02	7.80
TC0201812	---	4.65E-06	2	5.35	5.64	5.24	5.67	5.86	5.90	5.81	5.78
TC1700524	---	4.88E-06	2	8.69	9.22	9.18	9.35	9.52	9.48	9.50	9.29
TC0X00644	---	5.12E-06	2	8.29	8.67	8.49	8.64	8.66	8.80	8.67	8.72
TC0200557	---	5.39E-06	2	4.01	4.51	4.27	4.66	4.84	4.86	4.71	4.60
TC0201967	---	5.58E-06	2	4.13	4.98	5.00	5.51	5.69	5.51	5.29	5.29
TC0600298	---	5.71E-06	2	5.55	5.79	5.78	5.89	5.99	6.01	6.04	5.96
TC1201711	---	5.87E-06	2	4.55	4.82	4.60	5.11	5.19	5.08	5.14	4.92
TC0801113	---	6.11E-06	2	5.37	6.04	6.01	6.21	6.19	6.29	6.53	6.28
TC1400987	---	6.35E-06	2	8.10	8.09	8.17	8.25	8.25	8.32	8.35	8.34
TC0301096	---	6.52E-06	2	6.72	7.21	6.94	7.41	7.50	7.47	7.58	7.30
TC0M00005	---	7.48E-06	2	9.28	9.46	9.70	9.81	9.89	9.78	9.72	9.70
TC0601452	---	8.39E-06	2	6.70	6.85	7.10	7.29	7.42	7.56	7.34	7.22
TC0600509	---	8.45E-06	2	11.40	11.81	11.78	11.89	11.91	11.93	11.92	11.79
TC1500129	---	8.50E-06	2	5.12	5.65	5.75	5.72	5.76	5.87	5.78	5.70
TC0500606	---	8.55E-06	2	6.92	7.66	7.64	7.93	7.96	8.11	8.20	7.86
TC2200731	---	8.72E-06	2	6.03	6.06	5.79	6.23	6.39	6.43	6.63	6.26
TC0201063	---	9.09E-06	2	3.59	3.76	3.88	4.13	4.42	4.39	4.49	4.09
TC1100245	---	9.17E-06	2	6.84	7.33	7.48	7.50	7.51	7.71	7.70	7.66
TC0900539	731589	1.01E-05	2	1.95	2.00	2.07	2.14	2.29	2.24	2.24	2.15
TC0700836	---	1.07E-05	2	1.94	3.51	2.52	2.57	3.09	3.30	3.31	2.44
TC0200437	---	1.07E-05	2	5.50	6.08	6.10	6.73	6.74	6.62	6.72	6.55
TC0100011	---	1.13E-05	2	5.74	6.59	6.74	7.05	7.25	7.25	7.06	6.90
TC1600429	---	1.40E-05	2	6.43	6.97	6.74	7.02	7.23	7.24	7.26	7.02
TC0700448	---	1.65E-05	2	4.40	4.39	4.38	4.65	4.79	4.83	4.75	4.73
TC2000386	731959	1.65E-05	2	7.73	7.94	7.73	8.25	8.34	8.38	8.48	8.15
TC2000596	---	1.95E-05	2	4.49	4.92	4.94	5.17	5.32	5.35	5.48	5.16
TC03r00001	---	2.21E-05	2	4.44	4.75	4.98	5.28	5.17	5.11	5.10	4.92
TC0401400	---	2.24E-05	2	2.20	2.36	2.48	2.38	2.46	2.43	2.38	2.64
TC0901010	---	2.29E-05	2	5.01	5.29	5.49	5.67	5.66	5.65	5.58	5.50
TC1101800	---	2.36E-05	2	4.46	5.44	5.67	5.65	5.47	5.71	5.87	5.72
TC0101743	---	2.42E-05	2	9.60	9.83	10.01	10.25	10.41	10.33	10.19	9.99
TC1601111	---	2.60E-05	2	2.63	2.70	2.64	2.81	3.15	2.95	2.85	2.84

TC0M00034	---	2.88E-05	2	7.27	7.63	7.73	8.21	8.30	8.34	8.24	8.01
TC0101413	---	3.09E-05	2	5.64	6.01	5.82	6.27	6.44	6.35	6.34	6.11
TC1300592	---	3.34E-05	2	4.73	4.82	5.04	5.29	5.36	5.54	5.52	5.42
TC0601104	---	3.56E-05	2	7.44	7.79	7.50	7.82	8.14	8.15	8.03	7.94
TC0900382	---	3.83E-05	2	4.50	4.89	5.08	5.20	5.38	5.56	5.53	5.33
TC0701536	---	3.83E-05	2	4.59	4.74	4.72	5.09	5.19	5.35	5.36	5.15
TC0601181	731959	3.97E-05	2	5.64	5.93	5.63	6.08	6.19	6.24	6.32	6.09
TC0100666	---	4.08E-05	2	7.64	8.18	8.28	8.41	8.53	8.55	8.48	8.27
TC0501296	---	4.17E-05	2	7.68	8.36	8.73	8.72	8.93	9.11	8.92	8.70
TC0X01384	---	4.22E-05	2	6.25	6.55	6.61	6.69	6.73	6.66	6.63	6.48
TC0700286	---	4.61E-05	2	5.30	5.74	5.92	6.20	6.40	6.35	6.18	6.14
TC1701129	---	5.00E-05	2	4.61	4.94	5.01	5.02	5.20	5.19	5.22	4.99
TC0500381	---	5.04E-05	2	5.48	6.31	6.46	6.52	6.72	6.87	6.89	6.59
TC1100543	649618	5.25E-05	2	4.20	4.25	4.47	4.71	4.65	4.50	4.44	4.28
TC0601543	---	5.29E-05	2	2.55	3.23	3.21	3.35	3.47	3.56	3.50	3.00
TC0200426	---	5.43E-05	2	3.35	3.38	3.35	3.69	3.70	3.76	3.80	3.67
TC0M00013	---	5.90E-05	2	3.28	4.79	4.39	5.00	5.21	4.88	5.39	5.01
TC0100013	---	5.99E-05	2	2.67	3.59	3.79	4.20	4.35	4.18	4.32	4.08
TC0801137	---	6.16E-05	2	4.20	4.39	4.11	4.40	5.07	5.05	4.94	4.76
TC1400755	---	6.27E-05	2	2.09	2.19	2.06	2.34	2.51	2.54	2.32	2.33
TC0M00022	---	7.08E-05	2	5.90	6.01	5.74	6.49	6.69	6.72	6.73	6.56
TC0M00028	---	7.24E-05	2	9.89	10.09	10.38	10.53	10.75	10.64	10.49	10.32
TC1000477	---	7.30E-05	2	9.61	9.77	9.69	10.18	10.22	10.23	10.20	10.04
TC0100753	---	7.73E-05	2	3.34	3.91	3.85	3.96	4.11	4.13	4.09	3.96
TC0M00020	---	7.91E-05	2	10.92	11.20	11.44	11.60	11.76	11.88	11.76	11.52
TC0101432	---	7.96E-05	2	6.37	6.73	6.51	6.28	6.68	6.85	6.63	6.77
TC0301531	---	7.98E-05	2	5.20	5.29	5.36	5.56	5.71	5.69	5.56	5.29
TC1000850	---	8.85E-05	2	4.70	5.00	5.24	5.12	5.21	5.13	5.41	5.13
TC05r00002	---	9.32E-05	2	5.09	5.20	5.23	5.36	5.49	5.50	5.71	5.38
TC0600234	---	9.63E-05	2	4.29	4.42	4.47	4.40	4.40	4.49	4.49	4.57
TC1100177	---	0.000106	2	5.08	5.51	5.82	5.97	5.79	5.89	5.86	5.81
TC1601288	---	0.000113	2	7.24	7.99	7.77	8.05	7.87	7.87	8.07	8.14
TC1001077	---	0.000128	2	5.67	5.92	5.86	6.08	6.22	6.24	6.14	6.23
TC0100951	---	0.000128	2	5.92	6.00	5.89	6.30	6.05	6.23	6.42	6.39

TC0201562	---	0.000129	2	5.08	5.60	5.62	5.61	5.56	5.77	5.71	5.81
TC0301913	---	0.00013	2	8.32	8.66	8.75	8.86	8.95	8.90	8.94	8.74
TC0101250	---	0.000135	2	3.81	4.29	4.32	4.55	4.57	4.59	4.67	4.41
TC0601061	---	0.000135	2	5.20	5.31	5.46	5.50	5.60	5.57	5.54	5.44
TC0900473	---	0.000137	2	4.55	5.05	4.92	5.42	5.35	5.24	5.25	5.12
TC0201596	---	0.000138	2	4.16	4.42	4.24	4.77	5.09	5.13	4.98	4.86
TC0X00277	---	0.000146	2	2.06	2.08	2.43	2.47	2.44	2.32	2.31	2.20
TC0M00008	---	0.000147	2	8.70	8.75	8.85	9.29	9.49	9.25	9.13	9.05
TC1701808	---	0.00015	2	5.12	5.05	5.30	5.68	5.83	5.51	5.58	5.32
TC0700348	---	0.000156	2	4.16	4.65	4.70	4.72	4.73	4.82	4.82	4.76
TC1401058	---	0.000158	2	8.97	9.16	9.11	9.28	9.38	9.41	9.42	9.28
TC0103146	---	0.000159	2	2.53	3.12	2.81	3.22	3.36	3.40	3.15	3.32
TC0100899	---	0.000159	2	7.23	7.44	7.47	7.80	8.00	8.27	7.70	7.90
TC0800868	---	0.000165	2	5.62	6.03	6.20	6.48	6.32	6.39	6.33	6.09
TC0103272	---	0.000169	2	4.74	5.71	5.53	5.24	5.57	5.70	5.94	5.58
TC1601248	---	0.00017	2	3.99	4.60	4.31	4.69	4.88	4.90	4.95	4.62
TC1901870	---	0.000174	2	5.60	5.48	5.57	5.83	5.87	5.94	5.99	5.92
TC1101782	---	0.000185	2	2.24	2.63	2.67	3.15	3.19	3.03	3.04	3.00
TC0400762	---	0.000187	2	5.74	6.01	6.26	6.43	6.32	6.36	6.29	6.27
TC0500952	---	0.000196	2	7.21	8.05	7.65	7.65	7.45	7.81	8.07	7.93
TC1900269	---	0.000199	2	5.67	6.12	5.92	6.31	6.44	6.57	6.59	6.37
TC0M00018	---	0.000202	2	5.44	5.98	5.87	6.42	6.43	6.29	6.33	6.28
TC0103395	---	0.000217	2	3.54	3.89	4.00	4.04	4.31	4.34	4.11	4.06
TC0X00823	---	0.000226	2	5.04	5.60	5.44	5.83	5.93	6.10	6.04	5.81
TC0101921	---	0.000227	2	5.54	6.51	6.24	6.41	6.66	6.80	6.61	6.53
TC0701281	---	0.000253	2	4.37	4.51	4.34	4.69	5.05	5.04	4.81	4.74
TC1500133	---	0.000259	2	4.20	4.50	4.47	4.56	4.60	4.54	4.52	4.45
TC1901471	---	0.000292	2	7.04	7.46	7.28	7.49	7.63	7.58	7.60	7.43
TC0700839	---	0.000313	2	4.29	4.46	4.20	4.17	4.44	4.51	4.39	4.25
TC0100014	---	0.000328	2	3.76	4.50	4.69	5.21	5.43	5.33	5.84	5.31
TC1300333	---	0.000328	2	2.23	2.13	2.21	2.42	2.50	2.46	2.42	2.35
TC0201744	---	0.000335	2	3.16	3.26	3.04	3.20	3.49	3.48	3.50	3.32
TC0501113	---	0.000336	2	2.84	3.36	3.37	3.61	3.64	3.61	3.63	3.31
TC1800429	---	0.000347	2	4.47	5.34	5.14	5.32	5.41	5.53	5.50	5.28

TC0701725	---	0.000352	2	4.30	4.67	4.44	4.45	4.91	4.80	5.00	4.59
TC1901126	---	0.000357	2	4.21	4.26	4.24	4.46	4.56	4.62	4.58	4.41
TC17r00051	---	0.000359	2	5.22	5.56	5.36	5.54	5.63	5.62	5.72	5.64
TC0401341	---	0.000382	2	4.53	5.26	5.16	5.49	5.84	5.73	5.69	5.43
TC1001317	---	0.000389	2	9.48	9.74	9.59	9.87	9.93	10.05	10.08	9.90
TC1200568	---	0.000391	2	6.55	7.04	7.13	7.15	7.35	7.20	7.27	7.01
TC1101200	---	0.000393	2	9.64	9.79	10.21	10.09	10.20	10.18	10.09	10.01
TC1500635	---	0.000398	2	3.42	3.48	3.49	3.57	3.80	3.67	3.64	3.54
TC1700042	---	0.000421	2	6.43	6.57	6.72	6.82	6.54	7.31	7.33	7.22
TC1501093	---	0.00044	2	4.86	4.99	4.96	5.00	5.09	5.06	4.94	4.95
TC1201377	---	0.000441	2	4.01	4.58	4.33	4.81	4.98	5.03	5.02	4.70
TC0100173	---	0.000441	2	3.98	4.01	4.11	4.17	4.24	4.54	4.32	4.12
TC2200219	---	0.000444	2	5.14	5.60	5.57	5.79	6.05	6.10	6.20	5.95
TC0102376	---	0.000445	2	5.76	5.94	6.19	6.37	6.26	6.40	6.57	6.42
TC0100400	---	0.000453	2	7.05	7.87	7.69	7.92	8.01	8.02	8.05	8.05
TC0201132	---	0.000466	2	3.69	3.90	3.92	3.93	3.99	4.03	3.87	3.90
TC0401245	---	0.000484	2	5.65	6.01	6.09	6.10	6.11	6.24	6.33	6.22
TC1900249	---	0.000489	2	4.14	4.77	4.89	4.89	4.85	4.98	5.01	4.86
TC1200150	---	0.000492	2	6.25	6.67	6.70	6.86	6.98	6.99	6.89	6.83
TC0300150	---	0.000494	2	6.66	6.94	6.93	7.21	7.20	7.16	7.25	7.31
TC1600936	---	0.00052	2	4.73	4.90	4.84	4.85	5.01	4.97	5.03	4.92
TC0501150	---	0.000559	2	9.38	9.82	9.91	9.97	10.10	10.14	10.31	10.12
TC0102694	---	0.000567	2	6.80	6.71	6.76	6.99	7.14	7.33	7.06	7.19
TC0501174	---	0.000567	2	2.39	2.96	2.78	3.11	3.40	3.46	3.23	3.14
TC1000798	---	0.000588	2	7.05	6.73	7.22	7.49	7.23	7.49	7.33	7.36
TC0501229	---	0.000609	2	7.16	7.68	7.59	7.63	7.86	7.87	7.89	7.82
TC1400450	---	0.000617	2	2.91	3.32	3.27	3.18	3.21	3.55	3.53	3.36
TC1800408	---	0.000623	2	8.04	8.32	8.15	8.39	8.55	8.61	8.53	8.31
TC1800504	---	0.000639	2	4.91	5.10	4.94	4.90	5.13	5.38	5.43	5.35
TC0400329	---	0.000647	2	3.65	3.47	3.66	3.82	3.99	4.08	4.19	3.94
TC0700843	---	0.000673	2	5.18	5.50	5.60	5.77	5.97	5.95	5.77	5.73
TC0500491	---	0.000677	2	8.66	9.15	9.26	9.30	9.55	9.66	9.65	9.37
TC0100794	---	0.000678	2	8.25	8.41	8.45	8.68	8.71	8.64	8.70	8.49
TC0101645	---	0.000692	2	3.59	3.86	3.69	4.13	4.24	4.31	4.25	4.04

TC17r00038		---		0.000694	2	3.33	3.76	3.55	3.66	3.63	3.60	3.77	3.67
TC0701113		---		0.000704	2	5.87	6.58	6.88	6.67	6.72	6.86	6.84	6.72
TC01r00019		---		0.000709	2	6.50	6.72	6.72	6.71	6.77	6.80	6.81	6.78
TC0700345		---		0.000745	2	4.85	4.77	4.80	5.13	5.14	5.00	5.00	5.01
TC1300515		642209		0.000808	2	7.64	7.83	7.86	8.00	8.03	8.18	8.19	8.07
TC0200796		---		0.000835	2	5.11	5.27	5.51	5.53	5.72	5.85	6.17	5.86
TC0900408		---		0.000846	2	4.47	4.85	5.01	4.96	5.05	4.94	5.05	4.96
TC1500567		---		0.000871	2	4.79	4.74	4.95	5.13	5.24	5.07	5.16	4.86
TC2000868		---		0.000899	2	3.45	4.42	4.31	5.39	5.68	5.61	5.15	5.17
TC1201287		---		0.000916	2	3.22	3.51	3.47	3.87	3.80	3.93	4.00	3.73
TC0102619		---		0.00093	2	2.84	2.60	2.66	2.86	3.14	3.05	3.24	2.85
TC0103360		---		0.000941	2	3.41	3.50	3.34	3.63	3.84	3.83	3.83	3.60
TC0201907		---		0.000963	2	3.46	4.19	4.32	4.30	4.43	4.43	4.55	4.44
TC0701522		---		0.000984	2	5.84	5.79	6.14	6.12	6.04	6.20	6.31	6.16
TC1200808	AACS	65985	acetoacetyl-CoA synthetase /// acetoa	3.77E-05	3	4.29	4.24	4.23	4.35	4.36	4.35	4.42	4.38
TC1600210	ABCC1	4363	ATP-binding cassette, sub-family C (CFT	0.000605	3	5.00	4.75	4.70	4.85	4.85	4.85	4.93	4.96
TC0600247	ABCF1	23	ATP-binding cassette, sub-family F (GC	4.87E-08	3	5.72	5.55	5.56	5.75	5.82	5.89	6.08	5.94
TC0300493	ABHD10	55347	abhydrolase domain containing 10	1.27E-12	3	3.89	3.66	3.73	4.12	4.09	4.21	4.36	4.36
TC1400086	ABHD4	63874	abhydrolase domain containing 4	0.000131	3	6.12	5.72	5.55	5.82	5.73	5.92	5.86	6.00
TC1200681	ACACB	32	acetyl-Coenzyme A carboxylase beta //	0.000335	3	4.20	4.00	3.95	4.09	4.05	4.08	4.17	4.17
TC0900113	ACO1	48	aconitase 1, soluble /// Iron-responsive	6.04E-09	3	5.13	4.66	4.49	4.84	4.80	4.91	5.15	5.03
TC0200001	ACP1	52	acid phosphatase 1, soluble /// Low m	4.91E-06	3	5.26	4.90	4.97	5.17	5.29	5.36	5.34	5.27
TC1200909	ACRBP	84519	acrosin binding protein	0.000159	3	5.13	5.02	4.88	5.15	5.20	5.31	5.26	5.15
TC1600234	ACSM3	6296	acyl-CoA synthetase medium-chain fam	1.47E-12	3	3.07	2.75	2.85	3.05	2.98	3.14	3.45	3.34
TC1500996	ADAM10	102	ADAM metallopeptidase domain 10	0.000225	3	8.59	8.35	8.68	8.70	8.54	8.61	8.55	8.55
TC0700749	ADCK2	90956	aarF domain containing kinase 2	0.000548	3	4.06	4.02	3.90	4.01	4.10	4.10	4.17	4.08
TC1000349	ADK	132	adenosine kinase	8.33E-05	3	5.33	5.03	4.80	5.12	5.35	5.35	5.39	5.35
TC1800286	ADNP2	22850	ADNP homeobox 2	0.000261	3	4.51	4.69	4.49	4.49	4.53	4.69	4.73	4.74
TC0102542	ADORA3	140	adenosine A3 receptor /// Adenosine A	3.74E-06	3	4.85	4.61	4.75	5.18	4.93	4.96	5.22	5.19
TC0500591	ADRB2	154	adrenergic, beta-2-, receptor, surface	3.46E-07	3	6.09	5.28	5.54	5.64	5.53	5.86	5.85	5.86
TC2200153	ADRBK2	157	adrenergic, beta, receptor kinase 2	2.99E-10	3	3.94	3.74	3.73	4.37	4.01	4.09	4.42	4.37
TC0800014	AGPAT5	55326	1-acylglycerol-3-phosphate O-acyltrans	2.37E-11	3	3.32	3.22	3.25	3.44	3.56	3.70	3.79	3.78
TC1500808	AGPAT7	254531	1-acylglycerol-3-phosphate O-acyltrans	2.97E-05	3	4.96	4.71	4.79	5.06	4.94	4.93	4.92	4.89
TC0700089	AHR	196	aryl hydrocarbon receptor	5.36E-06	3	4.65	4.62	4.33	4.95	4.68	4.96	5.42	5.30

TC0600270	AIF1	199	allograft inflammatory factor 1 /// Allo	1.61E-09	3	8.67	8.08	8.46	8.56	8.41	8.59	8.63	8.65
TC1300107	AKAP11	11215	A kinase (PRKA) anchor protein 11 ///	3.79E-09	3	4.32	4.00	3.77	4.00	4.00	4.09	4.31	4.33
TC1400988	ALDH6A1	4329	aldehyde dehydrogenase 6 family, mer	1.64E-10	3	3.86	3.70	3.75	3.95	3.94	4.01	4.14	4.12
TC0102956	ALDH9A1	223	aldehyde dehydrogenase 9 family, mer	3.11E-05	3	6.06	5.82	6.13	6.28	6.16	6.36	6.44	6.37
TC0200345	ALMS1	7840	Alstrom syndrome 1 /// Alstrom syndro	7.32E-09	3	3.45	3.37	3.33	3.52	3.66	3.66	3.84	3.73
TC1700080	ALOX12	239	arachidonate 12-lipoxygenase	0.000331	3	5.27	4.85	4.73	5.01	5.10	5.12	5.03	5.03
TC1700937	ALOX15	246	arachidonate 15-lipoxygenase	4.44E-11	3	5.44	4.01	4.14	4.66	4.44	4.76	5.01	5.15
TC0202231	ALS2	57679	amyotrophic lateral sclerosis 2 (juvenile	6.93E-10	3	4.25	3.70	3.82	4.01	3.84	3.96	4.17	4.16
TC0201018	ALS2CR13	150864	amyotrophic lateral sclerosis 2 (juvenile	9.68E-13	3	5.26	4.38	4.19	4.46	4.49	4.77	4.98	5.16
TC0600638	AMD1	262	adenosylmethionine decarboxylase 1 /,	8.72E-12	3	7.93	6.93	6.82	7.22	7.34	7.58	7.52	7.67
TC0X01153	AMMECR1	9949	Alport syndrome, mental retardation, r	0.000829	3	4.05	3.82	3.87	3.91	3.86	3.88	3.97	4.02
TC0201825	ANAPC1	651763 //	anaphase promoting complex subunit	4.93E-06	3	3.74	3.61	3.57	3.71	3.81	3.85	3.89	3.81
TC0301586	ANAPC13	25847	anaphase promoting complex subunit	2.17E-18	3	6.77	6.03	6.04	6.73	6.65	6.85	6.92	7.08
TC1201639	ANAPC5	51433	anaphase promoting complex subunit	7.36E-15	3	4.83	4.15	4.21	4.51	4.59	4.59	4.70	4.51
TC0103221	ANGEL2	90806	angel homolog 2 (Drosophila) /// Prote	3.96E-06	3	4.95	4.63	4.75	4.85	4.74	4.83	5.01	4.95
TC0800663	ANGPT2	285	angiopoietin 2 /// Angiopoietin-2 precu	0.000293	3	3.40	3.12	3.23	3.29	3.26	3.28	3.32	3.34
TC0200933	ANKAR	150709	ankyrin and armadillo repeat containin	7.58E-05	3	2.74	2.55	2.62	2.65	2.61	2.66	2.73	2.72
TC0701029	ANKMY2	57037	ankyrin repeat and MYND domain cont	0.000147	3	4.27	4.14	4.14	4.21	4.20	4.28	4.33	4.36
TC0X00532	ANKRD58	347454	ankyrin repeat domain 58	1.42E-07	3	5.77	5.25	5.55	5.84	5.82	5.95	6.07	6.04
TC1501068	ANP32A /// Q6	8125	acidic (leucine-rich) nuclear phosphopr	9.28E-07	3	10.77	10.68	10.76	10.88	10.84	10.96	10.93	10.93
TC1000928	ANUBL1	93550	AN1, ubiquitin-like, homolog (Xenopus	5.73E-07	3	4.24	4.07	4.06	4.18	4.17	4.22	4.32	4.29
TC2200282	APOBEC3C ///	140564 //	apolipoprotein B mRNA editing enzyme	7.36E-11	3	5.20	4.78	4.80	5.05	4.90	5.04	5.30	5.35
TC2200242	APOL1	8542	apolipoprotein L, 1	8.31E-07	3	6.32	5.68	5.52	5.81	5.55	6.01	6.33	6.43
TC2200235	APOL6	80830	apolipoprotein L, 6	0.000283	3	6.62	6.94	6.60	6.86	6.48	7.00	7.23	7.54
TC0400607	ARFIP1	27236	ADP-ribosylation factor interacting pro	2.70E-10	3	7.67	7.13	6.88	6.95	6.68	7.29	7.35	7.69
TC0400585	ARHGAP10	79658	Rho GTPase activating protein 10	2.26E-10	3	3.79	3.58	3.65	4.05	3.94	4.20	4.35	4.29
TC0202410	ARL4C	10123	ADP-ribosylation factor-like 4C	1.82E-10	3	5.30	4.72	4.84	5.39	5.04	5.47	5.68	5.61
TC0700588	ARMC10	83787	armadillo repeat containing 10 /// SVH	5.32E-12	3	4.56	4.31	4.56	4.77	4.64	4.71	4.78	4.77
TC1101668	ARRB1	408	arrestin, beta 1	9.66E-24	3	6.56	5.10	4.95	5.59	5.39	5.73	6.00	6.13
TC0501092	ARSB	411	arylsulfatase B	5.03E-09	3	4.55	4.47	4.54	4.75	4.58	4.83	4.97	4.99
TC0201597	ASPRV1	151516	aspartic peptidase, retroviral-like 1	4.60E-06	3	6.12	5.54	5.27	5.49	5.62	6.11	6.21	6.23
TC1100474	ASRGL1	80150	asparaginase like 1	2.32E-11	3	4.95	4.82	4.74	5.10	5.17	5.24	5.35	5.30
TC0301564	ASTE1	28990	asteroid homolog 1 (Drosophila)	0.000315	3	4.30	4.15	4.24	4.30	4.31	4.35	4.32	4.38
TC0400202	ATP10D	57205	ATPase, class V, type 10D	5.37E-06	3	4.51	4.06	4.12	4.25	4.15	4.30	4.44	4.43

TC1700568	ATP5G1	516	ATP synthase, H+ transporting, mitoch	6.48E-07	3	5.39	5.21	5.16	5.35	5.51	5.41	5.49	5.39
TC1200797	ATP6V0A2	23545	ATPase, H+ transporting, lysosomal V0	3.44E-15	3	5.40	4.82	4.80	5.28	5.01	5.39	5.61	5.65
TC0101100	ATP8B2	57198	ATPase, class I, type 8B, member 2 /// I	4.93E-08	3	4.37	4.09	4.12	4.30	4.23	4.35	4.50	4.47
TC1500295	B2M	567	beta-2-microglobulin	1.70E-07	3	10.81	10.69	10.78	10.81	10.76	10.93	10.91	11.04
TC2100138	BACE2	25825	beta-site APP-cleaving enzyme 2	4.08E-11	3	4.60	3.76	3.84	4.35	4.06	4.43	4.67	4.78
TC0900853	BAG1	573	BCL2-associated athanogene /// BAG fa	4.18E-06	3	7.70	7.12	7.00	7.16	7.19	7.28	7.58	7.47
TC0400427	BANK1	55024	B-cell scaffold protein with ankyrin rep	3.37E-06	3	3.28	3.27	3.32	3.52	3.44	3.65	3.74	3.90
TC1101531	BATF2	116071	basic leucine zipper transcription facto	0.000626	3	5.65	5.66	5.54	5.60	5.47	5.75	5.79	6.00
TC0701317	BAZ1B	9031	bromodomain adjacent to zinc finger d	0.000433	3	5.56	5.34	5.26	5.55	5.68	5.66	5.89	5.66
TC1201405	BBS10	79738	Bardet-Biedl syndrome 10 /// Bardet-B	8.33E-12	3	4.27	3.95	4.35	4.62	4.41	4.58	4.66	4.74
TC1601118	BBS2	583	Bardet-Biedl syndrome 2	4.41E-05	3	3.96	3.73	3.83	3.88	3.78	3.82	4.03	3.95
TC0300479	BBX	56987	bobby sox homolog (Drosophila) /// HI	3.14E-06	3	6.07	6.26	5.98	6.15	5.92	6.16	6.37	6.46
TC0102565	BCAS2	10286	breast carcinoma amplified sequence 2	1.37E-09	3	6.45	6.49	6.37	6.63	6.48	6.72	6.94	6.95
TC0201539	BCL11A	53335	B-cell CLL/lymphoma 11A (zinc finger p	1.28E-12	3	4.53	4.33	4.09	4.61	4.80	4.90	4.92	4.76
TC0200576	BCL2L11	10018	BCL2-like 11 (apoptosis facilitator) /// E	1.47E-07	3	6.35	5.87	5.69	6.12	6.04	6.23	6.24	6.25
TC0X00854	BCOR	54880	BCL6 co-repressor /// BCL-6 corepressc	5.44E-12	3	5.47	4.84	4.72	4.98	5.08	5.24	5.44	5.44
TC0300012	BHLHB2	8553	basic helix-loop-helix domain containin	1.26E-11	3	7.10	6.08	5.98	6.89	6.69	7.02	6.94	6.91
TC2200418	BID	637	BH3 interacting domain death agonist ,	4.57E-05	3	7.27	7.10	7.18	7.38	7.34	7.42	7.39	7.52
TC1100793	BIRC3	330	baculoviral IAP repeat-containing 3	0.00034	3	4.64	4.71	4.44	5.05	4.68	4.78	5.19	5.10
TC1500833	BMF	90427	Bcl2 modifying factor	1.14E-08	3	5.10	4.83	4.78	4.89	4.93	4.94	4.98	5.06
TC1201573	BRAP	8315	BRCA1 associated protein	7.07E-07	3	7.02	6.84	6.83	7.00	6.86	7.04	7.10	7.13
TC1701398	BRCA1	672	breast cancer 1, early onset	2.42E-06	3	4.63	4.34	4.23	4.40	4.55	4.62	4.68	4.67
TC0X00716	BRCC3	79184	BRCA1/BRCA2-containing complex, sub	0.00017	3	5.56	5.30	5.61	5.59	5.61	5.74	5.96	5.77
TC0901422	BRD3	8019	bromodomain containing 3 /// Bromod	1.06E-08	3	5.82	5.47	5.39	5.67	5.64	5.68	5.75	5.83
TC2100347	BRWD1	54014	bromodomain and WD repeat domain	3.53E-06	3	5.51	5.06	5.00	5.12	5.13	5.29	5.41	5.34
TC0300085	BTD	686	biotinidase	0.000431	3	4.47	4.38	4.35	4.40	4.50	4.55	4.58	4.59
TC1201444	BTG1	694	B-cell translocation gene 1, anti-prolife	1.33E-07	3	9.28	9.04	8.87	9.20	9.26	9.39	9.31	9.47
TC0600158	BTN3A2	11118	butyrophilin, subfamily 3, member A2	6.64E-18	3	6.84	5.18	5.13	5.64	5.50	6.00	6.35	6.52
TC1000661	BUB3	9184	BUB3 budding uninhibited by benzimid	1.62E-06	3	6.25	6.05	6.10	6.31	6.39	6.45	6.57	6.45
TC1000965	C10orf128	---	Novel protein. [Source:Uniprot/SPTREI	5.47E-19	3	5.75	4.52	4.61	5.31	5.19	5.50	5.65	5.70
TC1000033	C10orf18	54906	chromosome 10 open reading frame 18	3.74E-12	3	4.56	4.31	4.36	4.48	4.48	4.60	4.85	4.80
TC1001208	C10orf33	84795	chromosome 10 open reading frame 3	2.39E-09	3	4.44	4.10	4.19	4.41	4.27	4.44	4.49	4.49
TC1101074	C11orf21	---	Uncharacterized protein C11orf21. [Sou	7.78E-05	3	7.06	6.90	6.61	6.75	6.83	6.98	7.05	7.09
TC1100753	C11orf54	28970	chromosome 11 open reading frame 5	0.000583	3	7.00	6.86	6.93	6.82	6.66	6.99	6.93	7.10

TC1200693	C12orf24	29902	chromosome 12 open reading frame 2	3.59E-05	3	3.42	2.94	3.07	3.15	3.15	3.21	3.26	3.26
TC1200553	C12orf26	84190	chromosome 12 open reading frame 2	0.000107	3	5.33	5.16	5.43	5.53	5.41	5.47	5.61	5.56
TC1201148	C12orf41	54934	chromosome 12 open reading frame 4	6.17E-11	3	5.03	4.59	4.63	4.81	4.93	5.00	5.04	4.98
TC1400819	C14orf106	55320	chromosome 14 open reading frame 1	6.84E-09	3	6.81	6.27	6.41	6.50	6.47	6.72	6.99	6.93
TC1400194	C14orf28	122525	chromosome 14 open reading frame 2	1.64E-05	3	3.59	3.45	3.80	3.70	3.45	3.56	3.72	3.78
TC1400981	C14orf43	91748	chromosome 14 open reading frame 4	2.71E-19	3	5.44	4.84	4.94	5.40	5.32	5.42	5.54	5.63
TC1400711	C14orf93	60686	chromosome 14 open reading frame 9	8.73E-07	3	4.15	3.85	3.99	3.99	3.92	4.02	4.15	4.12
TC1500231	C15orf23	90417	chromosome 15 open reading frame 2	8.55E-06	3	4.29	4.17	4.18	4.37	4.48	4.53	4.66	4.51
TC1500805	C15orf29	79768	chromosome 15 open reading frame 2	2.57E-13	3	7.37	6.46	6.29	6.74	6.86	7.42	7.35	7.28
TC1601133	C16orf80	29105	chromosome 16 open reading frame 8	2.51E-08	3	4.66	4.46	4.32	4.63	4.67	4.83	4.88	4.91
TC1700176	C17orf39	79018	chromosome 17 open reading frame 3	9.27E-09	3	4.59	4.40	4.60	4.79	4.71	4.78	4.88	4.82
TC1700132	C17orf48	56985	chromosome 17 open reading frame 4	0.000875	3	4.40	4.15	4.25	4.31	4.06	4.28	4.48	4.59
TC1900407	C19orf40	91442	chromosome 19 open reading frame 4	1.39E-05	3	4.04	3.89	3.82	3.87	3.85	3.97	3.93	4.18
TC1900168	C19orf66 /// N	55337	chromosome 19 open reading frame 6	4.23E-05	3	5.09	4.99	4.90	4.90	4.88	5.00	5.07	5.08
TC0101611	C1orf124	83932	chromosome 1 open reading frame 12	0.000937	3	5.18	4.99	4.85	4.95	4.97	5.05	5.08	5.12
TC0101805	C1orf174	339448	chromosome 1 open reading frame 17	1.51E-05	3	4.34	4.07	4.16	4.23	4.21	4.24	4.32	4.34
TC0102400	C1orf181	54680	chromosome 1 open reading frame 18	4.19E-06	3	3.34	3.30	3.20	3.39	3.58	3.64	3.74	3.66
TC0103282	C1orf55	163859	chromosome 1 open reading frame 55	1.94E-20	3	7.28	6.37	5.96	6.37	6.48	7.12	7.01	7.34
TC0100572	C1orf83	127428	chromosome 1 open reading frame 83	8.73E-07	3	5.08	4.66	4.77	4.89	4.88	4.94	5.10	5.04
TC0103329	C1orf96	126731	chromosome 1 open reading frame 96	3.18E-08	3	6.04	5.90	5.93	5.93	5.95	6.21	6.26	6.35
TC2000754	C20orf111	51526	chromosome 20 open reading frame 1	1.51E-06	3	6.64	6.24	6.17	6.39	6.32	6.55	6.50	6.57
TC2000099	C20orf72	92667	chromosome 20 open reading frame 7	2.45E-08	3	5.10	4.55	4.84	4.90	4.91	4.98	5.19	5.18
TC2200017	C22orf37	---	Putative uncharacterized protein C22o	3.11E-06	3	6.83	6.19	6.43	6.45	6.40	6.75	6.66	6.73
TC0301452	C3orf17	25871	chromosome 3 open reading frame 17	0.000415	3	4.79	4.68	4.86	4.86	4.69	4.81	4.95	4.95
TC0400773	C4orf15	79441	chromosome 4 open reading frame 15	1.00E-08	3	4.12	3.84	3.99	3.97	3.95	4.12	4.24	4.25
TC0400844	C4orf30	54876	chromosome 4 open reading frame 30	1.14E-10	3	5.13	4.80	4.72	4.77	4.96	5.08	5.27	5.23
TC0500196	C5orf29	202309	chromosome 5 open reading frame 29	7.85E-07	3	7.33	7.32	7.40	7.30	7.07	7.39	7.78	7.96
TC0500917	C5orf33	133686	chromosome 5 open reading frame 33	1.94E-12	3	3.77	3.65	3.63	3.88	4.04	4.17	4.17	4.13
TC0500714	C5orf41	153222	chromosome 5 open reading frame 41	2.19E-10	3	8.45	7.91	7.66	8.02	7.93	8.25	8.29	8.42
TC0601197	C6orf106	64771	chromosome 6 open reading frame 10	5.60E-11	3	6.94	6.97	6.64	6.91	6.87	7.10	7.22	7.26
TC0600958	C6orf114 /// G	85411 ///	chromosome 6 open reading frame 11	1.15E-08	3	4.81	4.56	4.53	4.85	4.93	5.00	5.15	5.04
TC0601564	C6orf204	387119	chromosome 6 open reading frame 20	2.00E-09	3	4.84	4.30	4.29	4.73	4.52	4.72	4.82	4.86
TC0600802	C6orf72	116254	chromosome 6 open reading frame 72	6.72E-05	3	6.19	6.28	6.25	6.23	6.23	6.45	6.51	6.51
TC0600823	C6orf97	80129	chromosome 6 open reading frame 97	6.22E-09	3	4.15	3.72	3.62	3.94	3.71	3.91	4.43	4.47

TC0701393	C7orf23	79161	chromosome 7 open reading frame 23	0.000434	3	5.69	5.48	5.49	5.48	5.48	5.63	5.64	5.73
TC0700197	C7orf36	57002	chromosome 7 open reading frame 36	2.79E-07	3	3.64	3.55	3.66	3.69	3.78	3.91	4.02	3.98
TC0700153	C7orf41	222166	chromosome 7 open reading frame 41	9.43E-08	3	6.13	5.55	5.11	5.64	5.91	6.16	6.10	6.15
TC0701653	C7orf49	78996	chromosome 7 open reading frame 49	1.06E-09	3	7.29	6.84	6.56	6.83	6.76	7.01	7.07	7.23
TC0700537	C7orf59	389541	chromosome 7 open reading frame 59	5.80E-13	3	8.88	7.81	7.72	8.29	8.43	8.68	8.63	8.77
TC0901013	C9orf71	169693	chromosome 9 open reading frame 71	0.00069	3	5.17	4.56	4.85	4.84	4.96	5.15	5.10	5.06
TC0901384	C9orf78	51759	chromosome 9 open reading frame 78	4.13E-06	3	7.88	7.69	7.49	7.87	8.02	8.05	8.26	8.11
TC0900506	C9orf91	203197	chromosome 9 open reading frame 91	2.10E-07	3	4.99	4.77	4.73	4.74	4.73	4.83	4.89	5.01
TC2000883	CABLES2	81928	Cdk5 and Abl enzyme substrate 2 /// C	0.0008	3	5.03	5.13	4.87	4.91	4.99	5.02	5.02	5.07
TC1900853	CACNG6	59285	calcium channel, voltage-dependent, g	0.000165	3	3.60	3.44	3.50	3.60	3.66	3.67	3.71	3.83
TC1700566	CALCOCO2	10241	calcium binding and coiled-coil domain	5.57E-08	3	7.76	7.73	7.48	7.47	7.43	7.61	7.71	7.86
TC0201493	CALM3 /// CAL	808 /// 8	calmodulin 3 (phosphorylase kinase, d	3.07E-05	3	9.28	9.23	9.33	9.37	9.33	9.41	9.44	9.49
TC0300992	CAMK1	8536	calcium/calmodulin-dependent protei	1.09E-09	3	5.69	5.20	5.22	5.66	5.47	5.72	5.88	5.88
TC1000061	CAMK1D	57118	calcium/calmodulin-dependent protei	9.47E-07	3	7.26	6.47	6.12	6.51	6.32	6.87	6.97	7.05
TC1001079	CAMK2G	818	calcium/calmodulin-dependent protei	1.11E-11	3	6.97	6.24	6.21	6.63	6.60	6.64	6.69	6.69
TC0901431	CAMSAP1	157922	calmodulin regulated spectrin-associat	0.00044	3	4.39	4.25	4.29	4.33	4.44	4.40	4.49	4.43
TC0401449	CASP3	836	caspase 3, apoptosis-related cysteine p	6.73E-05	3	6.84	6.99	6.72	7.05	6.87	7.05	7.13	7.18
TC0600562	CASP8AP2	9994	CASP8 associated protein 2	2.61E-05	3	5.14	4.94	4.83	5.03	5.02	5.13	5.45	5.26
TC1100272	CAT	847	catalase	3.02E-05	3	9.17	8.49	8.83	9.07	8.81	8.84	9.14	9.25
TC1601343	CBFA2T3	863	core-binding factor, runt domain, alph	4.81E-09	3	5.41	5.00	5.04	5.13	5.12	5.30	5.35	5.39
TC0700611	CBLL1	79872	Cas-Br-M (murine) ecotropic retroviral	5.32E-07	3	6.72	6.66	6.64	6.73	6.60	6.85	6.95	7.03
TC0900742	CBWD1 /// Q5J	55871	COBW domain containing 1 /// COBW	8.80E-10	3	5.20	4.68	4.67	4.77	4.85	4.95	5.04	5.06
TC0200600	CBWD2	150472	COBW domain containing 2 /// COBW	1.17E-16	3	4.62	3.77	3.85	3.99	4.06	4.23	4.42	4.35
TC0400714	CCDC111	201973	coiled-coil domain containing 111	1.11E-08	3	3.93	3.48	3.41	3.53	3.54	3.63	3.85	3.85
TC0501041	CCDC125	202243	coiled-coil domain containing 125 /// C	2.10E-09	3	8.55	8.09	7.79	7.84	8.09	8.31	8.36	8.34
TC0700428	CCDC146	57639	coiled-coil domain containing 146	1.11E-19	3	6.07	4.74	4.55	4.74	4.53	5.40	5.85	6.05
TC0102909	CCDC19 /// TA	25790 ///	coiled-coil domain containing 19 /// tra	3.25E-11	3	6.56	5.50	5.52	6.05	6.00	6.19	6.09	6.16
TC0100287	CCDC21	64793	coiled-coil domain containing 21	3.98E-10	3	4.66	4.47	4.49	4.70	4.73	4.88	4.89	4.87
TC1700691	CCDC45	90799	coiled-coil domain containing 45	1.88E-05	3	4.37	4.07	3.94	4.01	4.08	4.22	4.40	4.24
TC1201421	CCDC59	29080	coiled-coil domain containing 59	1.04E-07	3	7.37	7.17	7.22	7.28	7.31	7.45	7.59	7.61
TC0300254	CCDC72	51372	coiled-coil domain containing 72	8.05E-07	3	8.59	8.55	8.63	8.69	8.69	8.76	8.79	8.86
TC1200002	CCDC77	84318	coiled-coil domain containing 77	9.60E-07	3	4.61	4.16	4.25	4.53	4.36	4.49	4.68	4.48
TC1401064	CCDC88C	---	Protein Daple (Dvl-associating protein	1.98E-08	3	5.02	4.86	4.62	4.79	4.94	4.97	5.01	4.89
TC1900553	CCDC97	90324	coiled-coil domain containing 97	0.000361	3	5.92	5.98	5.90	6.12	5.96	6.11	6.14	6.26

TC1701254	CCL3L3 /// CCL	730422 //	chemokine (C-C motif) ligand 3-like 3 //	3.04E-07	3	6.06	6.04	5.79	6.22	6.10	6.39	6.53	6.71
TC17r00041	CCL3L3 /// CCL	414062 //	chemokine (C-C motif) ligand 3-like 3 //	1.25E-06	3	6.05	6.19	5.90	6.39	6.25	6.68	6.90	6.96
TC17r00024	CCL4L2 /// CCL	388372 //	chemokine (C-C motif) ligand 4-like 2 //	5.98E-07	3	5.88	6.01	5.52	6.73	6.30	6.90	7.40	7.43
TC1700385	CCL4L2 /// CCL	730424 //	chemokine (C-C motif) ligand 4-like 2 //	3.23E-06	3	4.88	4.85	4.56	5.51	5.18	5.72	6.20	6.23
TC0700226	CCM2	83605	cerebral cavernous malformation 2	0.00026	3	6.16	5.78	5.91	6.15	6.01	6.05	5.98	6.07
TC0400336	CCNG2	901	cyclin G2 /// Cyclin-G2. [Source:Unipro	1.06E-05	3	9.07	8.64	8.80	8.83	8.71	8.96	8.93	9.08
TC1201152	CCNT1	904	cyclin T1	0.000367	3	6.12	5.93	5.77	5.92	5.84	5.99	6.09	6.17
TC0300231	CCR3	1232	chemokine (C-C motif) receptor 3	5.32E-21	3	5.76	3.36	3.43	4.12	3.85	4.53	4.80	5.20
TC0102925	CD244	51744	CD244 molecule, natural killer cell rece	1.94E-10	3	4.73	4.41	4.48	4.83	4.67	4.92	5.09	5.10
TC1700740	CD300A	11314	CD300a molecule /// CMRF35-H antige	0.000191	3	7.84	7.22	7.29	7.61	7.47	7.79	7.69	7.83
TC1701672	CD300LB	124599	CD300 molecule-like family member b	4.12E-16	3	7.13	5.45	5.28	6.10	5.97	6.47	6.54	6.77
TC0202038	CD302	9936	CD302 molecule	2.01E-08	3	8.39	7.95	8.02	8.18	8.13	8.28	8.40	8.41
TC1900757	CD33	945	CD33 molecule	8.89E-05	3	5.22	5.03	5.00	5.07	5.08	5.22	5.25	5.27
TC0400115	CD38	952	CD38 molecule	1.16E-05	3	4.30	3.89	3.86	4.03	4.16	4.19	4.15	4.08
TC0101477	CD46	4179	CD46 molecule, complement regulator	1.50E-14	3	8.95	8.24	8.09	8.39	8.38	8.66	8.67	8.81
TC0100290	CD52	1043	CD52 molecule	1.38E-16	3	6.13	4.89	5.04	6.82	6.17	6.64	7.24	7.17
TC0501408	CD74	972	CD74 molecule, major histocompatibili	1.89E-14	3	7.83	7.16	6.49	7.52	7.10	7.48	7.92	8.24
TC0102922	CD84	8832	CD84 molecule /// SLAM family membe	2.92E-07	3	4.99	4.25	4.32	4.74	4.49	4.61	4.90	4.87
TC1200048	CD9	928	CD9 molecule /// CD9 antigen (p24) (L	2.47E-14	3	5.91	5.16	5.43	6.05	5.85	6.13	6.39	6.35
TC0300491	CD96	10225	CD96 molecule	6.88E-12	3	4.41	4.12	4.07	4.52	4.56	4.74	5.19	4.86
TC0500457	CDC42SE2	56990	CDC42 small effector 2	4.71E-06	3	8.85	8.69	8.71	8.91	8.84	8.95	8.99	9.07
TC0400706	CDKN2AIP	55602	CDKN2A interacting protein	8.79E-09	3	5.26	4.87	5.11	5.23	5.34	5.34	5.47	5.44
TC0501286	CDKN2AIPNL	91368	CDKN2A interacting protein N-terminal	2.29E-06	3	4.81	4.60	4.52	4.71	4.71	4.77	4.95	4.85
TC2000054	CDS2	8760	CDP-diacylglycerol synthase (phosphati	7.71E-09	3	7.19	6.57	6.71	7.11	6.94	6.91	6.97	6.96
TC2200413	CECR6	27439	cat eye syndrome chromosome region,	0.000736	3	5.47	5.43	5.24	5.39	5.53	5.60	5.56	5.58
TC0103011	CENPL /// SNO	91687	centromere protein L /// small nucleol	1.59E-05	3	3.62	3.56	3.49	3.46	3.69	3.67	3.71	3.61
TC1500935	CEP152	22995	centrosomal protein 152kDa /// Centr	0.000147	3	4.14	3.86	3.80	4.04	4.22	4.14	4.39	4.17
TC0300640	CEP63	80254	centrosomal protein 63kDa	3.06E-22	3	9.01	7.52	7.61	8.27	8.21	8.48	8.62	8.70
TC1900022	CFD	1675	complement factor D (adipsin)	0.000438	3	6.53	6.02	5.84	6.20	6.17	6.64	6.49	6.62
TC1600434	CHD9	80205	chromodomain helicase DNA binding p	3.19E-05	3	4.81	4.76	4.66	4.82	4.91	5.01	5.13	4.99
TC1500234	CHST14	113189	carbohydrate (N-acetylgalactosamine 4	0.000247	3	4.44	4.45	4.47	4.68	4.57	4.62	4.94	4.90
TC0X00176	CHST7	56548	carbohydrate (N-acetylglucosamine 6-	4.50E-10	3	5.84	5.17	5.05	5.40	5.49	5.89	5.76	5.90
TC0200490	CIAO1	9391	cytosolic iron-sulfur protein assembly 1	4.59E-05	3	5.20	4.96	4.99	5.19	5.18	5.22	5.25	5.22
TC1600172	CIITA	4261	class II, major histocompatibility compl	1.19E-07	3	4.84	4.54	4.49	4.66	4.54	4.64	4.70	4.79

TC0202110	CIR /// CIR_HU	9541	CBF1 interacting corepressor /// CBF1-i	1.34E-10	3	9.75	9.18	9.01	9.20	9.06	9.45	9.75	9.82
TC0400432	CISD2	493856	CDGSH iron sulfur domain 2	1.27E-14	3	5.97	5.54	5.77	6.45	6.35	6.35	6.47	6.46
TC1901495	CLC	1178	Charcot-Leyden crystal protein	4.08E-11	3	10.46	9.45	9.16	10.63	10.34	10.85	10.97	11.05
TC0102508	CLCC1	23155	chloride channel CLIC-like 1 /// Mid-1-r	5.48E-07	3	4.61	4.40	4.42	4.64	4.71	4.69	4.78	4.70
TC1200961	CLEC2B	9976	C-type lectin domain family 2, member	9.57E-09	3	8.20	8.09	8.15	8.37	8.21	8.56	8.57	8.67
TC0201287	CMPK2	129607	cytidine monophosphate (UMP-CMP) k	6.32E-07	3	4.86	4.69	4.56	4.68	4.60	5.09	5.46	5.67
TC0X00081	CNKSR2	22866	connector enhancer of kinase suppress	5.03E-07	3	3.04	2.91	2.91	2.96	2.89	2.99	3.12	3.14
TC0300133	CNOT10	25904	CCR4-NOT transcription complex, subu	3.65E-08	3	4.50	4.07	4.15	4.20	4.13	4.27	4.42	4.38
TC0800771	CNOT7	29883	CCR4-NOT transcription complex, subu	3.58E-12	3	5.72	5.45	5.54	5.73	5.76	5.87	5.97	5.98
TC0101988	CNR2	1269	cannabinoid receptor 2 (macrophage)	2.19E-10	3	4.18	3.44	3.55	3.87	3.65	3.86	4.09	4.20
TC1000105	COMMD3	23412	COMM domain containing 3 /// COMN	1.52E-05	3	4.16	3.96	4.04	4.16	4.26	4.24	4.33	4.21
TC1101313	COMMD9	29099	COMM domain containing 9	0.000101	3	5.10	4.97	5.07	5.19	5.21	5.26	5.29	5.26
TC0700533	COPS6	10980	COP9 constitutive photomorphogenic h	1.28E-05	3	6.40	6.07	6.06	6.32	6.37	6.33	6.40	6.35
TC0201177	COPS7B	64708	COP9 constitutive photomorphogenic h	5.04E-05	3	4.60	4.26	4.32	4.37	4.40	4.43	4.54	4.45
TC1600475	COQ9	57017	coenzyme Q9 homolog (S. cerevisiae)	1.45E-05	3	5.62	5.45	5.49	5.50	5.53	5.63	5.61	5.64
TC1201539	CORO1C	23603	coronin, actin binding protein, 1C	3.59E-05	3	8.41	7.87	7.93	8.23	8.22	8.26	8.27	8.32
TC0400110	CPEB2	132864	cytoplasmic polyadenylation element b	9.65E-07	3	6.67	6.14	5.97	6.19	6.21	6.52	6.45	6.54
TC0700138	CREB5	9586	cAMP responsive element binding prot	6.23E-05	3	6.94	6.61	6.69	6.91	6.78	6.91	6.82	6.83
TC1201291	CS	1431	citrate synthase	1.23E-09	3	5.98	5.58	5.59	5.96	6.07	6.04	6.20	6.04
TC0100813	CSF1	1435	colony stimulating factor 1 (macrophag	6.05E-12	3	4.79	4.50	4.59	4.77	4.67	4.89	4.87	4.95
TC0700892	CSGlcA-T /// CH	54480	chondroitin sulfate glucuronyltransfera	3.07E-05	3	5.67	5.63	5.65	5.75	5.70	5.85	5.83	5.86
TC1600524	CTCF	10664	CCCTC-binding factor (zinc finger prote	2.17E-10	3	7.94	7.31	7.46	7.80	7.69	7.81	7.96	7.96
TC1500292	CTDSPL2	51496	CTD (carboxy-terminal domain, RNA pc	1.77E-11	3	5.68	5.17	5.08	5.33	5.29	5.53	5.71	5.72
TC1700035	CTNS	1497	cystinosis, nephropathic	0.000298	3	4.40	4.26	4.30	4.44	4.47	4.45	4.48	4.45
TC1101728	CTSC	1075	cathepsin C /// Dipeptidyl-peptidase 1	1.21E-10	3	7.53	6.58	7.50	7.87	7.46	7.56	7.83	7.71
TC0102730	CTSS	1520	cathepsin S	5.83E-14	3	9.85	9.63	9.45	9.40	9.39	9.75	9.79	9.92
TC1101802	CWF19L2	143884	CWF19-like 2, cell cycle control (S. pom	1.90E-07	3	5.69	5.76	5.55	5.34	5.23	5.53	5.86	5.86
TC0400315	CXCL1	2919	chemokine (C-X-C motif) ligand 1 (mela	3.85E-05	3	7.09	7.50	7.07	6.74	7.17	7.53	7.24	7.49
TC0400313	CXCL6	6372	chemokine (C-X-C motif) ligand 6 (granı	0.00032	3	3.65	3.70	3.59	3.48	3.69	3.82	3.71	3.72
TC0201960	CXCR4	7852	chemokine (C-X-C motif) receptor 4	2.10E-18	3	9.30	8.29	8.12	8.62	8.72	9.03	9.00	9.18
TC0X00069	CXorf15	55787	chromosome X open reading frame 15	4.84E-12	3	4.32	4.00	3.83	4.41	4.71	4.77	4.83	4.66
TC0X00834	CXorf21	80231	chromosome X open reading frame 21	1.84E-09	3	6.41	5.85	5.86	6.17	5.90	6.23	6.48	6.61
TC1600426	CYLD	1540	cylindromatosis (turban tumor syndror	4.24E-05	3	7.94	7.87	7.63	7.77	7.61	7.86	7.91	7.98
TC0201106	CYP27A1	1593	cytochrome P450, family 27, subfamily	3.41E-11	3	5.04	4.54	4.23	4.69	5.00	5.24	5.05	5.11

TC0800979	CYP7B1	9420	cytochrome P450, family 7, subfamily E	0.000567	3	3.14	2.97	3.07	3.05	2.97	3.13	3.22	3.25
TC0X01058	CYSLTR1	10800	cysteinyl leukotriene receptor 1	5.26E-13	3	6.61	5.69	5.76	5.97	5.33	6.08	6.48	6.88
TC1300136	CYSLTR2	57105	cysteinyl leukotriene receptor 2	8.72E-15	3	4.27	2.86	2.89	3.71	3.20	3.65	4.16	4.44
TC0700999	DAGLB /// KDE	221955 //	diacylglycerol lipase, beta /// KDEL (Lys	7.36E-13	3	5.85	5.32	5.45	5.71	5.75	5.73	5.72	5.72
TC0500853	DAP	1611	death-associated protein /// Death-ass	0.000291	3	6.04	6.03	5.74	6.04	6.12	6.26	6.14	6.22
TC0400424	DAPP1	27071	dual adaptor of phosphotyrosine and 3	4.35E-09	3	8.41	7.79	7.64	8.20	8.00	8.49	8.57	8.66
TC0301600	DBR1	51163	debranching enzyme homolog 1 (S. cer	2.35E-13	3	4.59	4.34	4.43	4.83	4.81	4.97	5.18	5.03
TC0102483	DBT	1629	dihydrolipoamide branched chain trans	5.70E-07	3	3.56	3.40	3.45	3.61	3.48	3.55	3.73	3.69
TC1400866	DDHD1	80821	DDHD domain containing 1 /// Probabl	9.60E-09	3	4.58	4.12	4.12	4.47	4.20	4.37	4.47	4.46
TC0800229	DDHD2	23259	DDHD domain containing 2 /// DDHD d	1.51E-05	3	3.51	3.49	3.47	3.46	3.62	3.59	3.67	3.64
TC1201323	DDIT3	1649	DNA-damage-inducible transcript 3	1.58E-09	3	6.46	6.06	5.66	5.77	5.82	6.25	6.30	6.31
TC0200621	DDX18	8886	DEAD (Asp-Glu-Ala-Asp) box polypeptic	1.10E-07	3	5.21	5.00	4.77	5.08	5.14	5.25	5.54	5.39
TC0100839	DDX20	11218	DEAD (Asp-Glu-Ala-Asp) box polypeptic	1.06E-07	3	3.90	3.70	3.80	3.84	3.86	3.92	4.00	3.99
TC1401090	DDX24	57062	DEAD (Asp-Glu-Ala-Asp) box polypeptic	2.09E-10	3	5.36	5.21	4.92	5.25	5.27	5.48	5.64	5.61
TC2000355	DDX27	55661	DEAD (Asp-Glu-Ala-Asp) box polypeptic	0.000242	3	4.94	4.76	4.52	4.60	4.75	4.76	4.91	4.80
TC1601191	DDX28	55794	DEAD (Asp-Glu-Ala-Asp) box polypeptic	5.97E-07	3	4.74	4.24	4.37	4.60	4.70	4.69	4.87	4.85
TC1901240	DDX39	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptic	5.52E-06	3	5.07	4.77	4.72	4.82	5.00	5.04	4.95	4.85
TC1200146	DDX47 /// APO	81575 ///	apolipoprotein L domain containing 1 /	1.14E-08	3	4.10	3.77	3.78	3.89	3.98	4.02	4.10	3.95
TC1200792	DDX55	57696	DEAD (Asp-Glu-Ala-Asp) box polypeptic	2.08E-06	3	4.23	3.95	3.96	4.04	4.26	4.18	4.32	4.18
TC0900844	DDX58 /// TOP	23586 ///	DEAD (Asp-Glu-Ala-Asp) box polypeptic	1.05E-12	3	8.07	7.18	7.01	7.44	7.25	7.84	8.19	8.35
TC0401390	DDX60	55601	DEAD (Asp-Glu-Ala-Asp) box polypeptic	2.42E-06	3	4.42	4.30	4.19	4.32	4.02	4.78	5.51	5.72
TC1501048	DENND4A	10260	DENN/MADD domain containing 4A	2.19E-07	3	5.05	4.86	4.80	5.21	5.13	5.21	5.46	5.34
TC0900084	DENND4C	55667	DENN/MADD domain containing 4C ///	2.32E-12	3	4.60	4.37	4.29	4.74	4.72	4.87	5.05	4.93
TC2200213	DEPDC5	9681	DEP domain containing 5 /// DEP doma	3.31E-14	3	5.17	4.58	4.58	4.81	4.75	4.81	5.00	4.97
TC2200041	DGCR8	54487	DiGeorge syndrome critical region gene	0.00084	3	4.34	4.17	4.11	4.21	4.30	4.28	4.38	4.32
TC0301828	DGKG	1608	diacylglycerol kinase, gamma 90kDa	7.48E-12	3	5.08	4.50	4.02	4.38	4.68	4.83	4.84	4.81
TC0400855	DHX15	1665	DEAH (Asp-Glu-Ala-His) box polypeptid	0.000603	3	6.61	6.40	6.48	6.60	6.66	6.73	6.80	6.65
TC1201645	DIABLO	56616	diablo homolog (Drosophila)	0.000927	3	4.72	4.83	4.75	4.72	4.74	4.84	4.85	4.90
TC1600134	DNAJA3	9093	DnaJ (Hsp40) homolog, subfamily A, m	0.000183	3	4.38	4.15	4.18	4.33	4.42	4.36	4.36	4.31
TC2200690	DNAJB7	150353	DnaJ (Hsp40) homolog, subfamily B, m	1.07E-05	3	3.65	3.13	3.19	3.37	3.36	3.28	3.50	3.60
TC1901215	DNASE2	1777	deoxyribonuclease II, lysosomal	4.99E-06	3	4.84	4.42	4.43	4.67	4.60	4.90	4.78	4.80
TC0701556	DOCK4	9732	dedicator of cytokinesis 4 /// Dedicato	0.000119	3	5.52	6.16	5.28	5.47	5.39	5.93	5.98	5.93
TC2000717	DSN1	79980	DSN1, MIND kinetochore complex com	3.77E-09	3	4.13	3.79	3.84	3.88	4.00	4.11	4.21	4.16
TC0300554	DTX3L	151636	deltex 3-like (Drosophila) /// Protein de	2.20E-06	3	8.00	7.97	7.86	7.96	7.78	8.13	8.27	8.43

TC1600534	DUS2L	54920	dihydrouridine synthase 2-like, SMM1	1.13E-07	3	5.45	5.06	5.19	5.59	5.55	5.37	5.30	5.32
TC1201435	DUSP6	1848	dual specificity phosphatase 6	5.56E-15	3	7.61	6.78	6.27	6.65	6.65	7.38	7.38	7.67
TC0301082	DYNC1LI1	51143	dynein, cytoplasmic 1, light intermedia	1.14E-10	3	8.48	7.74	7.96	8.14	7.97	8.21	8.23	8.38
TC1300613	EBI2	1880	Epstein-Barr virus induced gene 2 (lym	3.41E-16	3	5.82	4.47	4.26	5.12	4.98	5.42	6.05	6.03
TC1600255	EEF2K	29904	eukaryotic elongation factor-2 kinase	1.81E-10	3	4.45	4.29	4.28	4.48	4.45	4.55	4.63	4.65
TC1701433	EFTUD2	9343	elongation factor Tu GTP binding doma	1.82E-05	3	4.90	4.59	4.68	4.93	4.93	4.89	5.01	4.93
TC0103348	EGLN1	54583	egl nine homolog 1 (C. elegans)	1.45E-05	3	9.19	8.93	9.16	9.36	9.25	9.43	9.33	9.39
TC1700450	EIF1	731937 //	eukaryotic translation initiation factor	0.000254	3	10.18	10.16	9.99	9.95	10.01	10.14	10.17	10.24
TC0201705	EIF2AK3	9451	eukaryotic translation initiation factor	1.13E-05	3	3.62	3.56	3.48	3.69	3.78	3.76	3.88	3.79
TC0300849	EIF2B5	8893	eukaryotic translation initiation factor	6.24E-05	3	4.73	4.59	4.57	4.63	4.73	4.78	4.82	4.75
TC1001307	EIF3A	8661	eukaryotic translation initiation factor	1.28E-07	3	6.95	6.86	6.39	6.84	6.95	7.11	7.33	7.07
TC2200633	EIF3D	8664	eukaryotic translation initiation factor	0.000665	3	6.86	6.62	6.66	6.89	6.81	6.82	6.95	6.90
TC2200600	EIF4ENIF1	56478	eukaryotic translation initiation factor	0.000404	3	5.89	5.62	5.61	5.75	5.80	5.88	5.80	5.79
TC0200521	EIF5B	9669	eukaryotic translation initiation factor	1.27E-09	3	4.93	4.53	4.40	4.94	5.15	5.26	5.77	5.40
TC1800143	ELP2	55250	elongation protein 2 homolog (S. cerev	9.43E-14	3	3.95	3.51	3.45	3.66	3.73	3.83	3.96	3.90
TC1400986	ENTPD5	957	ectonucleoside triphosphate diphosph	1.48E-08	3	4.35	4.07	4.11	4.35	4.33	4.42	4.53	4.41
TC0300641	EPHB1	2047	EPH receptor B1 /// Ephrin type-B rece	9.08E-15	3	5.50	4.41	4.30	4.77	4.73	5.03	5.04	5.10
TC1300438	EPSTI1	94240	epithelial stromal interaction 1 (breast)	3.29E-08	3	5.88	5.36	4.90	5.17	4.74	6.00	6.78	7.34
TC0501160	ERAP1	51752	endoplasmic reticulum aminopeptidas	3.89E-08	3	6.14	5.66	5.50	5.86	5.83	5.89	6.05	6.04
TC0500355	ERAP2 /// NP_	64167	endoplasmic reticulum aminopeptidas	0.000132	3	5.09	4.79	4.62	4.87	4.70	4.96	5.53	5.61
TC0500223	ERBB2IP	55914	erbb2 interacting protein /// Protein L	0.000128	3	8.53	8.20	8.33	8.30	8.14	8.44	8.44	8.46
TC1800365	ESCO1	114799	establishment of cohesion 1 homolog 1	6.67E-09	3	5.60	5.18	5.20	5.32	5.21	5.47	5.74	5.64
TC0601211	ETV7	51513	ets variant gene 7 (TEL2 oncogene) ///	1.03E-05	3	4.14	4.10	3.85	4.00	3.92	4.30	4.47	4.70
TC1701212	EVI2A	2123	ecotropic viral integration site 2A	8.01E-11	3	6.38	6.21	6.20	6.57	6.54	6.92	6.83	7.00
TC0101856	EXOSC10	5394	exosome component 10	0.000348	3	5.11	4.96	4.86	5.01	5.13	5.12	5.32	5.19
TC0900642	EXOSC2	23404	exosome component 2 /// Exosome co	6.76E-05	3	4.05	3.86	3.90	3.98	4.14	4.05	4.22	4.08
TC0400507	EXOSC9	5393	exosome component 9	6.12E-10	3	4.62	4.49	4.42	4.75	4.97	5.05	5.28	5.04
TC0500284	F2RL1	2150	coagulation factor II (thrombin) recept	6.73E-06	3	6.56	5.77	5.67	6.24	6.06	6.54	6.58	6.73
TC0901355	FAM102A	399665	family with sequence similarity 102, m	5.03E-12	3	5.49	5.15	5.07	5.45	5.29	5.50	5.84	5.76
TC1701663	FAM104A	84923	family with sequence similarity 104, m	7.11E-06	3	6.09	6.10	6.05	6.11	6.11	6.19	6.24	6.34
TC0202257	FAM119A	151194	family with sequence similarity 119, m	4.50E-08	3	4.96	4.73	4.69	4.89	5.01	5.01	5.08	5.03
TC0501315	FAM13B1	51306	family with sequence similarity 13, me	0.000828	3	6.54	6.66	6.42	6.46	6.40	6.56	6.73	6.72
TC0500369	FAM174A	345757	family with sequence similarity 174, m	9.40E-05	3	5.80	5.61	5.42	5.48	5.49	5.79	5.66	5.91
TC1201345	FAM19A2	338811	family with sequence similarity 19 (che	1.30E-09	3	4.47	3.95	3.84	4.12	4.00	4.23	4.34	4.34

TC1000245	FAM21A	652446 //	family with sequence similarity 21, mer	3.57E-07	3	7.31	6.61	6.47	6.81	6.81	6.91	7.14	7.03
TC1000220	FAM21B	652446	Protein FAM21B (Fragment). [Source:U	5.76E-07	3	7.08	6.43	6.32	6.63	6.61	6.75	7.03	6.88
TC1000235	FAM21D	---	Protein FAM21D (Fragment). [Source:U	4.48E-05	3	7.67	6.84	6.80	7.12	7.03	7.21	7.58	7.43
TC1000202	FAM21D /// FA	653450 //	family with sequence similarity 21, mer	5.37E-07	3	7.28	6.70	6.53	6.81	6.83	6.93	7.15	7.01
TC0300916	FAM43A	131583	family with sequence similarity 43, mer	1.46E-06	3	4.14	3.76	3.80	4.06	4.05	4.12	4.08	4.23
TC0501502	FAM44B	91272	family with sequence similarity 44, mer	5.66E-11	3	3.59	3.28	3.28	3.64	3.78	3.85	4.10	3.94
TC0601628	FAM54A	113115	family with sequence similarity 54, mer	0.000219	3	2.85	2.73	2.65	2.71	2.95	2.99	2.87	2.77
TC0100277	FAM54B	56181	family with sequence similarity 54, mer	0.00032	3	5.09	4.78	4.79	4.93	4.89	4.97	4.96	5.02
TC1200425	FAM62A	23344	family with sequence similarity 62 (C2	1.50E-15	3	5.93	4.91	4.82	5.86	5.56	5.90	6.24	6.22
TC0100311	FAM76A	654163 //	family with sequence similarity 76, mer	2.71E-08	3	4.48	4.37	4.40	4.47	4.56	4.54	4.61	4.56
TC0901392	FAM78A	286336	family with sequence similarity 78, mer	2.26E-09	3	4.51	4.18	4.24	4.38	4.41	4.40	4.52	4.49
TC0600102	FAM8A1	51439	family with sequence similarity 8, mem	6.52E-06	3	8.35	8.14	8.08	8.13	8.02	8.39	8.31	8.51
TC1601353	FANCA	2175	Fanconi anemia, complementation gro	6.47E-07	3	4.30	4.15	4.05	4.07	4.15	4.21	4.25	4.23
TC0900888	FANCG	2189	Fanconi anemia, complementation gro	6.32E-05	3	4.59	4.44	4.42	4.45	4.62	4.59	4.58	4.52
TC1400200	FANCM	57697	Fanconi anemia, complementation gro	0.000201	3	2.57	2.47	2.46	2.50	2.60	2.55	2.69	2.69
TC1000425	FAS	355	Fas (TNF receptor superfamily, membe	3.68E-07	3	6.95	6.48	6.61	6.72	6.48	6.88	6.96	7.12
TC0901150	FBP1	2203	fructose-1,6-bisphosphatase 1	5.34E-05	3	4.87	4.86	4.75	5.05	4.78	4.97	5.26	5.24
TC0701516	FBXL13	222235	F-box and leucine-rich repeat protein 1	4.40E-07	3	4.62	3.86	3.81	4.38	4.32	4.46	4.47	4.37
TC0800833	FBXO16 /// ZN	157574 //	F-box protein 16 /// zinc finger protein	2.58E-05	3	4.24	4.20	4.18	4.21	4.27	4.29	4.32	4.31
TC0101175	FCER1A	2205	Fc fragment of IgE, high affinity I, recep	2.45E-06	3	4.42	4.01	4.02	4.12	4.00	4.14	4.26	4.53
TC0101220	FCGR2C /// FC	9103 ///	Fc fragment of IgG, low affinity IIc, rece	6.92E-09	3	6.28	5.36	5.36	5.73	5.59	5.90	5.93	6.04
TC0701369	FGL2	10875	fibrinogen-like 2	1.23E-16	3	10.90	9.78	9.14	9.61	9.62	10.45	10.63	10.86
TC0400226	FIP1L1	81608	FIP1 like 1 (S. cerevisiae) /// Pre-mRNA	1.30E-08	3	6.93	6.91	6.87	6.96	6.94	7.03	7.16	7.20
TC1701076	FLCN	201163	folliculin	1.21E-11	3	5.33	4.97	4.87	5.00	5.10	5.27	5.13	5.18
TC1100997	FLI1	2313	Friend leukemia virus integration 1 ///	0.000731	3	8.20	7.89	7.77	8.15	8.08	8.14	8.07	8.18
TC1100279	FLJ14213 /// N	79899	protor-2 /// CDNA FLJ14213 fis, clone	6.70E-11	3	4.16	3.67	3.55	3.70	3.62	3.83	3.95	4.09
TC0800264	FLJ23356	84197	hypothetical protein FLJ23356	0.000558	3	5.25	4.94	4.98	5.15	5.17	5.07	5.18	5.15
TC0301085	FLJ45032 /// G	643853 //	similar to F40B5.2b /// galactosidase, b	0.000496	3	5.96	5.66	5.88	6.13	5.96	5.95	5.99	5.94
TC0600240	FLJ45422	441140	FLJ45422 protein	0.000989	3	6.45	6.20	6.08	6.23	6.17	6.34	6.34	6.50
TC1300369	FLT1	2321	fms-related tyrosine kinase 1 (vascular	7.99E-06	3	3.30	3.01	2.96	3.05	3.06	3.16	3.23	3.18
TC0101507	FLVCR1	28982	feline leukemia virus subgroup C cellula	3.04E-12	3	5.94	5.33	5.10	5.48	5.65	5.75	6.01	6.20
TC1201178	FMNL3	91010	formin-like 3 /// Formin-like protein 3 (	0.000402	3	4.46	4.49	4.43	4.49	4.50	4.57	4.66	4.63
TC0X00642	FMR1	2332	fragile X mental retardation 1 /// Fragil	7.95E-10	3	7.50	7.15	6.94	7.02	6.91	7.25	7.37	7.44
TC1700866	FN3KRP	79672	fructosamine-3-kinase-related protein	0.000691	3	4.64	4.52	4.49	4.52	4.66	4.68	4.74	4.62

TC1101362	FNBP4	23360	formin binding protein 4	2.17E-11	3	5.26	4.46	4.44	4.71	4.77	4.82	5.11	4.95
TC0102174	FOXJ3	22887	forkhead box J3 /// Forkhead box prot	9.57E-06	3	6.09	6.16	6.10	6.15	5.99	6.21	6.20	6.29
TC0102476	FRRS1	391059	ferric-chelate reductase 1 /// stromal c	1.50E-11	3	3.84	3.13	3.44	4.06	3.66	4.13	4.53	4.53
TC1900700	FTL	2512	ferritin, light polypeptide /// Ferritin lig	0.000338	3	11.89	11.70	11.72	11.94	11.87	11.99	11.93	11.99
TC0101987	FUCA1	2517	fucosidase, alpha-L- 1, tissue /// Tissue	0.000846	3	4.66	4.44	4.58	4.78	4.63	4.74	4.92	4.87
TC0X00870	FUNDC1	139341	FUN14 domain containing 1	9.02E-09	3	4.71	4.62	4.40	4.53	4.50	4.80	4.99	5.08
TC01r00024	FUSIP1	10772	FUS interacting protein (serine/argini	3.27E-05	3	5.16	4.98	5.03	5.16	5.26	5.31	5.42	5.31
TC1500322	GALK2	2585	galactokinase 2	1.45E-05	3	4.67	4.46	4.57	4.60	4.59	4.66	4.71	4.71
TC0400680	GALNT7	51809	UDP-N-acetyl-alpha-D-galactosamine:p	0.000978	3	6.93	6.82	6.81	7.09	6.98	7.07	7.16	7.04
TC0X00213	GATA1	2623	GATA binding protein 1 (globin transcri	1.50E-06	3	5.11	4.78	4.74	4.93	4.81	4.98	5.04	5.06
TC0700473	GATAD1	57798	GATA zinc finger domain containing 1	0.000679	3	5.22	5.01	5.04	5.09	5.13	5.15	5.31	5.19
TC0102415	GBP1	2633	guanylate binding protein 1, interferon	2.80E-09	3	7.88	7.04	6.55	7.00	6.54	7.85	8.09	8.65
TC0102413	GBP3	2635	guanylate binding protein 3 /// Guanyl	5.48E-06	3	5.85	5.49	5.51	5.77	5.37	6.05	6.32	6.58
TC0102418	GBP4	115361	guanylate binding protein 4	1.14E-12	3	6.32	4.76	3.97	4.76	4.36	5.59	6.17	6.81
TC0102419	GBP5	115362	guanylate binding protein 5	8.25E-12	3	8.81	7.28	6.65	7.17	6.76	8.16	8.51	9.09
TC0100709	GBP6	163351	guanylate binding protein family, mem	2.23E-06	3	3.56	3.36	3.25	3.45	3.37	3.72	3.88	4.04
TC0102417	GBP7 /// GBP2	388646 //	guanylate binding protein 7 /// guanyl	1.35E-07	3	6.43	5.81	5.94	6.15	5.85	6.20	6.33	6.49
TC0701610	GCC1	79571	GRIP and coiled-coil domain containing	0.000142	3	6.10	6.20	6.00	6.04	5.90	6.08	6.27	6.29
TC0601343	GCLC	2729	glutamate-cysteine ligase, catalytic sub	2.60E-08	3	4.25	3.77	3.74	4.04	4.10	4.12	4.22	4.20
TC0300746	GFM1	85476	G elongation factor, mitochondrial 1 //	3.65E-05	3	3.66	3.54	3.56	3.64	3.71	3.73	3.83	3.78
TC1600940	GGA2	23062	golgi associated, gamma adaptin ear c	1.05E-08	3	4.37	4.26	4.20	4.52	4.54	4.64	4.77	4.67
TC0301009	GHRL	51738	ghrelin/obestatin preprohormone ///	9.22E-09	3	6.43	5.89	6.03	6.23	6.16	6.24	6.50	6.44
TC0901079	GKAP1	80318	G kinase anchoring protein 1 /// G kina	0.000934	3	5.11	4.96	4.94	5.16	5.10	5.22	5.32	5.29
TC0900600	GLE1	2733	GLE1 RNA export mediator homolog (	0.000117	3	5.50	5.21	5.22	5.35	5.27	5.33	5.42	5.36
TC1400470	GLRX5	51218	glutaredoxin 5	1.76E-11	3	6.94	6.43	6.55	7.22	7.37	7.37	7.48	7.30
TC0200941	GLS	2744	glutaminase /// Glutaminase kidney is	2.24E-05	3	5.03	4.55	4.85	4.98	4.86	4.93	5.13	5.03
TC0301260	GLT8D1	55830	glycosyltransferase 8 domain containin	2.51E-07	3	4.85	4.52	4.73	4.89	4.80	4.85	4.95	4.90
TC0200319	GMCL1	64395	germ cell-less homolog 1 (Drosophila)	7.70E-10	3	6.79	6.33	6.52	6.76	6.68	6.92	6.98	7.04
TC1201714	GOLGA3	2802	golgi autoantigen, golgin subfamily a, 3	6.43E-06	3	4.61	4.51	4.40	4.55	4.60	4.62	4.69	4.59
TC0301734	GOLIM4	27333	golgi integral membrane protein 4	1.41E-15	3	4.77	4.63	4.62	5.16	5.12	5.34	5.69	5.52
TC0102728	GOLPH3L	55204	golgi phosphoprotein 3-like /// GPP34-	3.22E-17	3	5.72	4.60	4.58	5.06	5.37	5.54	5.68	5.45
TC0601562	GOPC	57120	golgi associated PDZ and coiled-coil m	7.67E-09	3	5.17	4.88	5.21	5.37	5.28	5.35	5.54	5.42
TC1900409	GPATCH1	55094	G patch domain containing 1	8.25E-13	3	4.63	4.23	4.21	4.34	4.39	4.52	4.72	4.75
TC0500193	GPBP1	65056	GC-rich promoter binding protein 1 ///	1.22E-07	3	8.80	8.69	8.54	8.61	8.55	8.75	8.81	8.89

TC1201650	GPR109A /// G	338442 //	G protein-coupled receptor 109A /// G	9.31E-05	3	7.30	7.34	6.44	6.82	6.74	7.33	7.20	7.38
TC1201651	GPR109B	8843	G protein-coupled receptor 109B	5.04E-05	3	7.69	7.76	7.02	7.59	7.52	8.11	7.96	8.10
TC1600477	GPR114	654091 //	G protein-coupled receptor 114	6.27E-07	3	4.50	4.14	4.17	4.32	4.26	4.39	4.44	4.47
TC0102346	GPR177	79971	G protein-coupled receptor 177 /// Int	2.95E-09	3	8.18	7.04	6.56	7.64	7.85	8.08	7.91	7.83
TC0X00161	GPR34	2857	G protein-coupled receptor 34 /// Prob	5.98E-13	3	3.23	2.70	2.85	3.49	3.18	3.64	4.09	4.12
TC1101455	GPR44	11251	G protein-coupled receptor 44	3.10E-11	3	5.20	4.24	4.47	4.91	4.78	4.98	5.22	5.27
TC0X00162	GPR82	27197	G protein-coupled receptor 82	4.04E-14	3	3.51	2.90	2.97	3.22	2.94	3.31	4.00	4.22
TC0100940	GPR89C	728932	G protein-coupled receptor 89C	3.00E-08	3	4.16	3.57	3.50	3.90	3.95	4.14	4.31	4.08
TC0102638	GPR89C	728932	G protein-coupled receptor 89C	8.09E-08	3	3.69	3.34	3.36	3.50	3.63	3.64	3.71	3.63
TC0100957	GPR89C /// GP	728932 //	G protein-coupled receptor 89C /// G p	1.61E-07	3	3.91	3.45	3.45	3.65	3.79	3.76	3.90	3.74
TC1900032	GPX4	2879	glutathione peroxidase 4 (phospholipid	1.45E-09	3	6.08	5.88	5.52	6.15	6.25	6.35	6.30	6.36
TC1100945	GRAMD1B	57476	GRAM domain containing 1B	2.39E-09	3	4.16	4.08	3.95	4.23	4.26	4.51	4.60	4.63
TC0200030	GRHL1	29841	grainyhead-like 1 (Drosophila)	0.000651	3	3.07	3.01	3.06	3.11	3.05	3.11	3.10	3.20
TC1600865	GSPT1	2935	G1 to S phase transition 1	3.76E-06	3	6.02	4.97	4.74	5.41	5.50	5.42	5.63	5.42
TC1100218	GTF2H1	2965	general transcription factor IIH, polype	2.18E-06	3	4.50	4.42	4.22	4.39	4.41	4.53	4.69	4.60
TC0700464	GTPBP10	85865	GTP-binding protein 10 (putative) /// G	0.000181	3	4.86	4.79	5.01	5.00	4.94	5.13	5.26	5.21
TC0300501	GTPBP8	29083	GTP-binding protein 8 (putative) /// GT	4.46E-06	3	3.84	3.69	3.80	4.01	3.94	3.98	4.12	4.13
TC0301042	hCG_1644884 ,	728070 //	similar to chromosome 16 open readin	0.00012	3	4.14	4.01	4.03	4.07	4.13	4.22	4.33	4.25
TC0600262	HCP5 /// HLA-F	10866 ///	HLA complex P5 /// major histocompat	5.89E-15	3	6.39	5.45	5.51	5.72	5.54	6.15	6.15	6.40
TC0100360	HDAC1	3065	histone deacetylase 1 /// Histone deac	2.48E-06	3	7.14	6.60	6.80	6.99	6.88	6.99	7.14	7.00
TC1701417	HDAC5	10014	histone deacetylase 5 /// Histone deac	2.56E-06	3	6.13	5.74	5.67	5.84	5.84	5.93	5.97	6.05
TC0202446	HDLBP	3069	high density lipoprotein binding protei	5.02E-09	3	6.87	6.38	6.23	6.61	6.68	6.65	6.71	6.66
TC1701576	HEATR6	63897	HEAT repeat containing 6	1.94E-11	3	3.73	3.54	3.52	3.81	3.90	4.00	4.19	3.98
TC1201004	HEBP1	50865	heme binding protein 1	6.35E-08	3	4.95	4.87	5.01	5.21	5.10	5.22	5.35	5.54
TC0400390	HERC5	51191	hect domain and RLD 5	7.74E-14	3	6.43	5.44	4.80	5.08	4.99	6.49	7.19	7.63
TC0400389	HERC6	55008	hect domain and RLD 6 /// Probable E3	1.66E-08	3	4.42	4.14	4.04	4.15	4.16	4.48	4.83	4.77
TC2200436	HIRA	7290	HIR histone cell cycle regulation defect	3.30E-08	3	5.44	5.10	4.87	5.09	5.23	5.29	5.35	5.28
TC0601020	HIST1H1C	3006	histone cluster 1, H1c	1.07E-18	3	7.91	7.54	7.39	8.39	8.47	8.98	8.72	8.87
TC0600147	HIST1H2AC	8334	histone cluster 1, H2ac	0.000117	3	10.40	10.20	10.37	10.33	10.19	10.61	10.50	10.61
TC0600154	HIST1H3F /// H	8968 ///	histone cluster 1, H3f /// histone cluste	0.000485	3	3.62	3.80	3.39	3.24	3.37	3.88	3.69	3.78
TC0601016	HIST1H4B	8366	histone cluster 1, H4b	3.94E-06	3	4.61	4.07	4.09	4.49	5.06	5.12	4.76	4.68
TC0102704	HIST2H2BF	440689	histone cluster 2, H2bf	3.74E-07	3	8.01	6.84	6.84	7.01	7.23	7.68	7.40	7.61
TC0102709	HIST2H4A	8370	histone cluster 2, H4a	3.55E-14	3	8.59	7.61	7.28	7.62	7.71	8.17	8.08	8.27
TC0600143	HIST2H4A ///	8370 ///	histone cluster 2, H4a /// histone cluste	8.51E-05	3	3.63	3.51	3.52	3.60	3.77	3.91	3.58	3.71

TC0100998	HIST2H4B /// H	554313 //	histone cluster 2, H4b /// histone clust	1.26E-14	3	7.88	6.83	6.52	6.81	6.92	7.46	7.33	7.55
TC0601117	HLA-C /// HLA-	3107 ///	major histocompatibility complex, clas	1.75E-06	3	10.03	9.91	9.86	9.94	9.94	10.01	10.02	10.15
TC0601167	HLA-DMB /// N	3109	major histocompatibility complex, clas	1.12E-09	3	4.35	4.01	3.91	4.02	3.89	4.06	4.24	4.45
TC0600300	HLA-DPB1	3115	major histocompatibility complex, clas	0.000334	3	4.23	4.16	4.14	4.30	4.13	4.27	4.52	4.63
TC0600293	HLA-DRA	3122	major histocompatibility complex, clas	1.88E-10	3	6.99	6.43	5.69	6.88	6.28	6.71	7.29	7.69
TC0600233	HLA-G /// HLA-	3135 ///	major histocompatibility complex, clas	1.68E-07	3	6.24	6.15	6.14	6.18	6.17	6.29	6.28	6.35
TC2100349	HMGN1	731028 //	high-mobility group nucleosome bindi	3.58E-07	3	5.06	5.00	4.92	4.94	5.19	5.25	5.24	5.11
TC0100293	HMGN2	732081 //	high-mobility group nucleosomal bindi	3.88E-11	3	6.25	5.81	5.85	6.17	6.48	6.60	6.59	6.39
TC0600165	HMGN4	10473	high mobility group nucleosomal bindi	2.65E-13	3	5.03	4.79	4.88	4.93	4.87	5.25	5.29	5.35
TC1600135	HMOX2	3163	heme oxygenase (decycling) 2	1.76E-08	3	7.44	7.15	7.19	7.27	7.23	7.41	7.45	7.49
TC1400684	HNRNPC /// HN	3183	heterogeneous nuclear ribonucleoprot	9.34E-12	3	9.32	9.16	9.21	9.44	9.36	9.50	9.50	9.56
TC0101973	HNRNPR	10236	heterogeneous nuclear ribonucleoprot	1.25E-07	3	4.89	4.82	4.66	4.88	5.04	5.15	5.39	5.28
TC0102729	HORMAD1	84072	HORMA domain containing 1 /// HORM	4.58E-05	3	4.50	3.88	4.00	4.44	4.49	4.83	4.67	4.60
TC0101959	HP1BP3	50809	heterochromatin protein 1, binding pro	3.24E-11	3	7.08	6.53	6.17	6.50	6.65	6.74	6.89	6.77
TC2200546	HPS4	89781	Hermansky-Pudlak syndrome 4 /// Her	3.81E-08	3	4.21	4.05	3.97	4.10	4.21	4.21	4.29	4.18
TC1101501	HRASLS5	117245	HRAS-like suppressor family, member 5	1.72E-08	3	3.97	3.59	3.61	3.86	3.72	3.82	3.81	4.03
TC1201603	HRK	8739	harakiri, BCL2 interacting protein (cont	3.14E-05	3	4.83	4.52	4.46	4.66	4.65	4.91	5.12	4.98
TC1601298	HSDL1	83693	hydroxysteroid dehydrogenase like 1	7.60E-05	3	4.70	4.42	4.54	4.67	4.58	4.69	4.74	4.80
TC1900281	HSH2D /// RAB	84941 ///	hematopoietic SH2 domain containing	2.09E-18	3	7.68	7.13	6.78	7.05	7.03	7.43	7.50	7.67
TC0101217	HSPA6	3310	heat shock 70kDa protein 6 (HSP70B')	1.13E-09	3	6.52	6.05	5.82	6.05	6.05	6.30	6.37	6.43
TC0200288	HSPC159	29094	galectin-related protein	3.91E-12	3	7.03	6.69	6.28	7.12	7.43	7.40	7.39	7.15
TC0202201	HSPD1	3329	heat shock 60kDa protein 1 (chaperoni	2.87E-13	3	6.09	5.87	5.77	6.19	6.46	6.59	6.65	6.44
TC0800234	HTRA4	203100	HtrA serine peptidase 4	5.46E-05	3	3.49	3.27	3.19	3.23	3.33	3.46	3.56	3.44
TC0102187	HYI	81888	hydroxypyruvate isomerase homolog (	0.000333	3	5.58	5.50	5.44	5.50	5.63	5.55	5.58	5.52
TC1501237	IDH2	3418	isocitrate dehydrogenase 2 (NADP+),	1.12E-08	3	4.95	4.77	4.74	5.01	5.17	5.12	5.14	5.08
TC0100679	IFI44	10561	interferon-induced protein 44	4.07E-07	3	5.45	5.04	4.46	4.49	4.46	5.46	6.23	6.50
TC0100678	IFI44L	10964	interferon-induced protein 44-like	5.49E-07	3	4.31	4.22	3.74	3.79	3.73	4.76	5.54	5.90
TC0102037	IFI6	2537	interferon, alpha-inducible protein 6	9.89E-09	3	5.34	5.23	4.99	5.11	5.07	5.77	6.07	6.39
TC0202052	IFIH1	64135	interferon induced with helicase C do	1.56E-13	3	7.49	6.19	5.53	6.73	6.54	7.33	7.88	8.18
TC1000429	IFIT1	3434	interferon-induced protein with tetratr	1.50E-15	3	6.90	5.54	4.78	5.16	5.11	6.74	7.20	7.75
TC1000426	IFIT2	3433	interferon-induced protein with tetratr	6.58E-16	3	9.09	7.62	7.15	7.70	7.66	8.86	9.10	9.47
TC1000427	IFIT3	3437	interferon-induced protein with tetratr	1.42E-13	3	7.74	6.98	6.47	6.58	6.62	7.63	8.18	8.50
TC1000430	IFIT5	24138	interferon-induced protein with tetratr	1.95E-11	3	5.77	5.56	5.41	5.72	5.44	6.35	6.72	6.99
TC1300013	IFT88	8100	intraflagellar transport 88 homolog (Ch	0.000781	3	3.61	3.73	3.54	3.49	3.49	3.63	3.71	3.69

TC0301824	IGF2BP2	10644	insulin-like growth factor 2 mRNA bind	0.000808	3	4.48	4.10	3.93	4.25	4.44	4.38	4.38	4.39
TC0100876	IGSF2	9398	immunoglobulin superfamily, member	9.45E-11	3	5.11	4.70	4.60	5.23	5.24	5.47	5.71	5.68
TC0500533	IK	3550	IK cytokine, down-regulator of HLA II	4.83E-07	3	9.32	9.26	9.15	9.11	9.02	9.27	9.41	9.42
TC1201482	IKIP	121457	IKK interacting protein	2.93E-10	3	8.16	7.21	7.29	7.43	7.51	8.03	8.04	8.28
TC0202289	IKZF2	22807	IKAROS family zinc finger 2 (Helios) ///	1.31E-12	3	4.16	3.60	3.55	3.93	3.78	4.05	4.36	4.47
TC1701299	IKZF3	22806	IKAROS family zinc finger 3 (Aiolos) ///	8.03E-07	3	4.24	3.93	3.90	4.03	3.92	4.03	4.28	4.27
TC0X00522	IL13RA1	3597	interleukin 13 receptor, alpha 1 /// Inte	1.79E-11	3	8.72	8.03	8.27	8.19	7.97	8.38	8.50	8.76
TC0200537	IL1RL1	9173	interleukin 1 receptor-like 1	5.47E-08	3	4.61	3.63	3.87	4.43	3.93	4.24	4.55	4.55
TC0300961	IL5RA	3568	interleukin 5 receptor, alpha /// Interle	1.60E-20	3	5.75	3.61	4.06	5.69	5.14	5.77	6.32	6.43
TC1900179	ILF3	3609	interleukin enhancer binding factor 3,	6.91E-05	3	5.12	5.05	4.88	5.15	5.31	5.28	5.40	5.17
TC0202425	ILKAP	80895	integrin-linked kinase-associated serin	1.62E-08	3	5.56	5.34	5.34	5.53	5.63	5.70	5.74	5.60
TC0301197	IMPDH2	3615	IMP (inosine monophosphate) dehydr	1.95E-07	3	5.16	4.87	4.79	4.95	5.05	5.06	5.16	5.09
TC0100601	INADL	10207	InaD-like (Drosophila) /// InaD-like prot	1.68E-10	3	3.79	3.33	3.30	3.49	3.33	3.53	3.78	3.84
TC0800241	INDO	3620	indoleamine-pyrrole 2,3 dioxygenase	5.77E-11	3	4.14	3.26	3.27	3.68	3.40	3.88	4.47	4.62
TC0700643	ING3	54556	inhibitor of growth family, member 3 /,	0.000298	3	6.32	6.28	6.22	6.14	6.13	6.38	6.44	6.46
TC0800437	INTS8	55656	integrator complex subunit 8	0.000322	3	5.45	5.06	5.43	5.40	5.26	5.35	5.42	5.31
TC0800834	INTS9	55756	integrator complex subunit 9	0.000673	3	4.19	3.99	4.03	4.09	4.03	4.06	4.08	4.20
TC0500281	IQGAP2	10788	IQ motif containing GTPase activating	0.000272	3	8.04	7.42	7.74	8.21	7.93	8.00	8.21	7.98
TC0X00946	IQSEC2	23096	IQ motif and Sec7 domain 2 /// IQ moti	0.000553	3	4.26	4.12	4.09	4.18	4.08	4.11	4.23	4.24
TC0501272	IRF1	3659	interferon regulatory factor 1	3.29E-06	3	8.48	7.85	7.65	8.01	7.78	8.27	8.08	8.45
TC1200674	ISCU	23479	iron-sulfur cluster scaffold homolog (E.	5.63E-05	3	5.81	5.64	5.64	5.62	5.61	5.75	5.81	5.86
TC0100022	ISG15	9636	ISG15 ubiquitin-like modifier	5.25E-08	3	6.02	5.87	5.97	5.98	5.84	6.34	6.64	6.81
TC1500602	ISG20	3669	interferon stimulated exonuclease gen	1.18E-11	3	8.44	7.88	7.40	7.67	7.64	8.27	8.43	8.65
TC0102863	ISG20L2	81875	interferon stimulated exonuclease gen	2.54E-07	3	6.05	5.87	5.89	6.13	6.05	6.19	6.27	6.31
TC0500450	ISOC1	51015	isochorismatase domain containing 1	0.000333	3	4.26	4.01	3.99	4.38	4.39	4.38	4.39	4.46
TC0200908	ITGA4	3676	integrin, alpha 4 (antigen CD49D, alpha	4.32E-23	3	6.20	4.14	4.19	5.17	4.87	5.40	6.02	6.09
TC1201245	ITGB7	3695	integrin, beta 7 /// Integrin beta-7 prec	1.33E-05	3	4.90	4.69	4.64	4.80	4.69	4.80	4.94	4.91
TC0X01060	ITM2A	9452	integral membrane protein 2A	2.88E-12	3	4.34	3.75	3.86	4.36	4.40	4.59	4.85	4.83
TC1300132	ITM2B	9445	integral membrane protein 2B /// Integ	2.93E-07	3	10.81	10.55	10.69	10.71	10.69	10.85	10.79	10.96
TC1401081	ITPK1	3705	inositol 1,3,4-triphosphate 5/6 kinase /	6.10E-13	3	7.51	6.52	6.52	6.94	6.89	7.32	7.25	7.50
TC0103291	ITPKB	3707	inositol 1,4,5-trisphosphate 3-kinase B	1.60E-06	3	5.59	5.28	5.36	5.58	5.47	5.51	5.58	5.61
TC0500299	JMY /// NP_68	133746	junction-mediating and regulatory prot	7.76E-07	3	3.91	3.73	3.53	3.67	3.80	3.81	4.05	3.96
TC0102301	JUN	3725	jun oncogene	5.61E-07	3	4.22	4.18	3.91	3.97	4.10	4.40	4.17	4.43
TC1601270	KARS	3735	lysyl-tRNA synthetase /// Lysyl-tRNA sy	6.82E-10	3	6.07	5.92	5.71	6.28	6.22	6.52	6.82	6.77

TC1600992	KCTD13	253980	potassium channel tetramerisation dor	5.86E-07	3	5.17	4.77	4.87	5.02	5.03	5.02	5.12	4.99
TC0600361	KIAA0082	23070	KIAA0082 /// KIAA0082 (Fragment). [Sc	3.83E-06	3	5.35	5.15	4.99	5.16	5.03	5.33	5.65	5.72
TC0101938	KIAA0090	23065	KIAA0090 /// Uncharacterized protein	3.17E-07	3	4.17	4.08	4.09	4.14	4.26	4.26	4.30	4.24
TC1701174	KIAA0100	9703	KIAA0100	2.98E-07	3	5.86	5.35	5.38	5.73	5.70	5.65	5.85	5.73
TC1200756	KIAA0152	9761	KIAA0152	2.24E-13	3	5.34	4.93	4.74	5.43	5.66	5.79	5.76	5.61
TC1600642	KIAA0182	23199	KIAA0182	1.01E-15	3	5.22	4.67	4.60	4.80	4.80	4.91	5.03	5.03
TC0102106	KIAA0319L	79932	KIAA0319-like /// polycystic kidney dise	3.47E-07	3	6.84	6.24	6.50	6.63	6.54	6.62	6.70	6.65
TC1400195	KIAA0423	23116	KIAA0423 /// Uncharacterized protein	0.000183	3	3.26	3.15	3.17	3.23	3.18	3.19	3.31	3.31
TC0101286	KIAA0859	51603	KIAA0859 /// Uncharacterized protein	0.00095	3	4.66	4.54	4.52	4.69	4.65	4.66	4.71	4.68
TC0601428	KIAA1009	22832	KIAA1009 /// KIAA1009. [Source:Unipr	1.51E-05	3	4.63	4.42	4.56	4.78	4.59	4.75	5.09	4.95
TC1500537	KIAA1024	23251	KIAA1024	6.52E-05	3	4.28	4.21	4.00	4.28	4.27	4.52	4.56	4.67
TC1700825	KIAA1618	57714	KIAA1618	2.45E-05	3	7.72	7.03	6.87	7.17	6.99	7.23	7.48	7.50
TC1100749	KIAA1731	---	CDNA FLJ37899 fis, clone CD34C30003	2.69E-15	3	5.31	4.31	4.19	4.35	4.42	4.71	5.03	4.90
TC0600645	KIAA1919	91749	KIAA1919	4.30E-08	3	4.31	3.95	4.03	4.21	4.22	4.36	4.42	4.37
TC16r00003	KIF22	3835	kinesin family member 22	1.75E-05	3	5.26	5.15	5.12	5.17	5.35	5.31	5.27	5.23
TC0501275	KIF3A	11127	kinesin family member 3A /// Kinesin-li	0.000612	3	3.18	3.17	3.21	3.29	3.22	3.29	3.37	3.36
TC0400164	KLF3	51274	Kruppel-like factor 3 (basic)	5.06E-09	3	8.37	7.80	7.85	8.16	8.10	8.32	8.24	8.34
TC0300266	KLHDC8B	200942	kelch domain containing 8B /// Kelch d	4.65E-08	3	5.12	4.86	4.83	4.88	4.94	5.19	5.08	5.15
TC0300843	KLHL24	54800	kelch-like 24 (Drosophila) /// Kelch-like	8.20E-05	3	6.66	6.44	6.29	6.59	6.43	6.61	6.57	6.71
TC1700709	KPNA2	3838	karyopherin alpha 2 (RAG cohort 1, im	5.97E-08	3	5.52	4.98	4.81	5.16	5.60	5.56	5.51	5.25
TC17r00043	KPNA2	3838	karyopherin alpha 2 (RAG cohort 1, im	6.36E-07	3	5.15	4.82	4.66	4.97	5.29	5.30	5.19	5.01
TC1700551	KPNB1	3837	karyopherin (importin) beta 1	1.08E-07	3	8.43	8.00	8.02	7.98	7.93	8.22	8.30	8.39
TC1201400	KRR1	11103	KRR1, small subunit (SSU) processome	3.05E-13	3	6.53	5.77	6.01	6.06	6.06	6.16	6.35	6.33
TC0400120	LAP3	51056	leucine aminopeptidase 3	1.38E-07	3	5.37	5.37	5.01	5.34	5.19	5.69	6.31	6.52
TC0X00986	LAS1L	81887	LAS1-like (S. cerevisiae) /// LAS1-like pr	0.000319	3	4.62	4.47	4.35	4.48	4.58	4.61	4.64	4.54
TC0102735	LASS2	29956	LAG1 homolog, ceramide synthase 2 //	0.000126	3	7.10	6.70	6.85	7.09	7.08	7.08	6.98	7.07
TC0301092	LBA1	9881	lupus brain antigen 1	4.87E-18	3	9.25	7.46	6.95	7.64	7.63	8.31	8.50	8.84
TC1201036	LDHB	3945	lactate dehydrogenase B	2.18E-06	3	5.24	4.98	4.80	5.28	5.54	5.42	5.60	5.39
TC0700668	LEP	3952	leptin	5.34E-06	3	4.00	3.65	3.61	3.88	3.90	4.08	3.89	4.05
TC0800184	LEPROTL1	23484	leptin receptor overlapping transcript-l	7.75E-07	3	7.12	6.93	6.92	7.07	7.01	7.24	7.27	7.45
TC0800230	LETM2	137994	leucine zipper-EF-hand containing tran	8.62E-18	3	5.65	4.29	4.26	5.00	5.30	5.51	5.34	5.56
TC1100493	LGALS12	85329	lectin, galactoside-binding, soluble, 12	3.37E-06	3	5.16	5.13	4.90	5.27	5.34	5.36	5.40	5.34
TC0103179	LGTN	1939	ligatin /// Ligatin (Hepatocellular carcin	2.91E-06	3	5.29	5.08	5.02	5.16	5.21	5.27	5.28	5.19
TC0400171	LIAS	11019	lipoic acid synthetase /// Lipoic acid sy	1.41E-05	3	4.00	3.70	3.78	3.82	3.81	3.88	4.05	3.98

TC1700367	LIG3	3980	ligase III, DNA, ATP-dependent	9.56E-13	3	4.59	4.20	4.01	4.34	4.66	4.63	4.68	4.52
TC1400365	LIN52	91750	lin-52 homolog (C. elegans)	1.68E-07	3	4.38	4.01	4.08	4.27	4.29	4.37	4.49	4.35
TC1001143	LIPA	3988	lipase A, lysosomal acid, cholesterol est	5.76E-08	3	4.72	4.57	4.52	4.60	4.58	4.77	4.92	4.89
TC1300203	LMO7	4008	LIM domain 7 /// LIM domain only prot	0.000946	3	2.85	2.78	2.79	2.78	2.77	2.77	2.85	2.87
TC0201568	LOC130773	130773	similar to ribosomal protein L23a	8.26E-07	3	6.32	5.61	5.56	5.86	6.02	5.95	6.06	6.01
TC1701125	LOC284194 ///	284194	galectin-9 like /// galectin-9 like [Sourc	4.34E-05	3	6.58	6.23	6.23	6.49	6.31	6.50	6.73	6.77
TC1600913	LOC400506	400506	similar to TSG118.1	0.000451	3	4.71	4.53	4.42	4.53	4.76	4.72	4.80	4.70
TC0500464	LOC441108 ///	441108	hypothetical gene supported by AK128	2.57E-14	3	6.89	5.94	5.85	6.02	5.90	6.37	6.52	6.80
TC0400736	LOC642236 ///	642236 //	similar to FRG1 protein (FSHD region ge	0.000224	3	6.96	6.92	7.11	7.08	6.98	7.17	7.30	7.26
TC1900464	LOC644096	644096	hypothetical protein LOC644096	2.22E-06	3	3.07	2.91	2.87	2.99	3.12	3.20	3.49	3.37
TC1500909	LOC645212	645212	hypothetical LOC645212	0.000348	3	5.15	4.89	4.96	4.94	4.97	5.05	5.15	5.12
TC1701450	LOC652203	652203	hypothetical protein LOC652203	0.000106	3	5.26	4.59	4.65	4.97	5.12	5.01	5.05	4.87
TC0102942	LOC652578 ///	652578 //	similar to Fc fragment of IgG, low affini	0.00025	3	9.33	8.86	8.87	8.98	8.93	9.20	9.14	9.25
TC1500569	LOC652637	652637	similar to junction-mediating and regul	7.08E-06	3	4.96	4.81	4.86	5.03	4.90	5.16	5.32	5.15
TC1500471	LOC652671 ///	652671 //	similar to promyelocytic leukemia prot	2.51E-05	3	5.50	5.69	5.47	5.58	5.49	5.74	5.89	6.05
TC1200536	LOC652725 ///	652725 //	similar to neuron navigator 3 /// neuro	1.88E-09	3	2.92	2.62	2.58	2.58	2.68	2.94	2.89	2.81
TC0400232	LOC653882 ///	653882 //	similar to Mast/stem cell growth factor	3.94E-09	3	3.64	3.23	3.16	3.39	3.23	3.40	3.65	3.81
TC0101989	LOC653884 ///	727922 //	similar to FUS interacting protein (serin	4.66E-07	3	4.82	4.69	4.76	4.89	4.98	5.02	5.13	5.03
TC2000472	LOC653889 ///	653889 //	similar to U5 snRNP-associated 102 kDa	1.97E-05	3	5.82	5.72	5.53	5.68	5.62	5.74	5.91	5.87
TC1700191	LOC654346	654346	similar to galectin 9 short isoform	0.000395	3	5.81	5.61	5.59	5.87	5.74	5.78	5.94	6.06
TC0600841	LOC729446 ///	729446 //	hypothetical LOC729446 /// AT rich int	1.20E-10	3	5.38	5.16	5.12	5.28	5.20	5.28	5.32	5.35
TC0800920	LOC731751 ///	731751 //	similar to protein kinase, DNA-activate	5.29E-11	3	5.39	5.48	4.75	5.05	5.49	5.67	5.73	5.58
TC0800763	LONRF1	91694	LON peptidase N-terminal domain and	3.87E-05	3	5.03	4.99	4.77	4.80	4.84	5.14	5.12	5.17
TC0200051	LPIN1	23175	lipin 1	2.35E-09	3	4.06	3.92	3.94	4.04	3.96	4.07	4.18	4.20
TC1200201	LRMP	4033	lymphoid-restricted membrane protein	3.32E-15	3	9.11	7.74	8.12	8.35	8.21	8.60	8.65	8.83
TC0700585	LRRC17	10234	leucine rich repeat containing 17	6.56E-06	3	3.62	3.16	2.97	3.34	3.27	3.46	3.40	3.44
TC0300938	LRRC33	375387	leucine rich repeat containing 33	3.83E-06	3	4.88	4.74	4.78	4.95	4.94	5.03	5.06	5.08
TC0100711	LRRC8B	23507	leucine rich repeat containing 8 family,	8.63E-05	3	4.44	4.00	4.12	4.31	4.28	4.45	4.43	4.46
TC0301871	LSG1	55341	large subunit GTPase 1 homolog (S. cer	6.63E-06	3	3.92	3.80	3.70	3.89	3.98	4.04	4.17	4.03
TC0600269	LST1	7940	leukocyte specific transcript 1 /// Leuk	0.000212	3	8.99	8.71	8.76	8.90	8.86	8.93	8.93	8.97
TC0301701	LXN	56925	latexin	7.32E-13	3	5.68	4.87	5.21	5.28	5.33	5.72	5.90	5.85
TC0800594	LY6E	4061	lymphocyte antigen 6 complex, locus E	2.29E-05	3	5.64	5.58	5.47	5.53	5.45	5.88	6.12	6.33
TC0202039	LY75	4065	lymphocyte antigen 75	1.24E-10	3	7.42	6.48	5.82	6.45	6.35	6.95	7.18	7.09
TC0400789	LYAR	55646	Ly1 antibody reactive homolog (mouse	1.82E-12	3	4.82	4.37	4.43	4.89	4.68	4.91	5.26	5.15

TC0101522	LYPLAL1	127018	lysophospholipase-like 1 /// Lysophosp	3.62E-06	3	4.63	4.32	4.64	4.75	4.61	4.81	4.87	4.80
TC0601454	LYRM2	57226	LYR motif containing 2	0.000526	3	4.42	4.37	4.39	4.38	4.50	4.47	4.61	4.50
TC0500456	LYRM7	90624	Lyrm7 homolog (mouse) /// LYR motif-	0.00019	3	4.80	4.76	4.75	4.86	4.76	4.81	5.02	4.96
TC0102740	LYSMD1	388695	LysM, putative peptidoglycan-binding,	1.38E-05	3	4.99	4.45	4.60	4.81	4.79	4.90	4.84	4.86
TC1500959	LYSMD2	256586	LysM, putative peptidoglycan-binding,	1.12E-15	3	5.77	4.91	5.04	5.49	5.38	5.94	6.16	6.37
TC0301149	LZTFL1	54585	leucine zipper transcription factor-like	1.02E-13	3	3.59	3.06	3.05	3.21	3.12	3.33	3.52	3.54
TC1101759	MAML2	84441	mastermind-like 2 (Drosophila)	1.50E-23	3	6.74	5.32	4.47	5.12	5.18	6.01	6.25	6.51
TC0500386	MAN2A1	4124	mannosidase, alpha, class 2A, member	1.67E-11	3	5.51	4.73	4.75	5.32	5.35	5.36	5.38	5.31
TC0401157	MANBA	4126	mannosidase, beta A, lysosomal	1.74E-09	3	7.78	6.91	7.30	7.52	7.36	7.49	7.54	7.53
TC0601631	MAP3K5	4217	mitogen-activated protein kinase kinas	0.000186	3	7.59	7.30	7.69	7.60	7.33	7.50	7.54	7.58
TC1400845	MAP4K5	11183	mitogen-activated protein kinase kinas	2.78E-14	3	4.61	4.09	4.12	4.82	4.70	4.87	5.21	5.14
TC0300289	MAPKAPK3	7867	mitogen-activated protein kinase-activ	1.07E-07	3	7.08	6.76	6.50	6.68	6.73	6.90	6.95	7.02
TC0401374	MAR1	55016	membrane-associated ring finger (C3H	9.41E-05	3	4.29	4.31	4.33	4.40	4.33	4.33	4.48	4.46
TC1000132	MASTL	84930	microtubule associated serine/threoni	3.69E-08	3	4.67	4.52	4.46	4.77	4.92	4.93	5.01	4.87
TC0500674	MAT2B	27430	methionine adenosyltransferase II, bet	2.33E-05	3	6.40	6.48	6.47	6.46	6.36	6.66	6.62	6.79
TC1400921	MAX	4149	MYC associated factor X	0.000171	3	7.34	7.31	7.23	7.27	7.29	7.48	7.46	7.49
TC1300240	MBNL2	10150	muscleblind-like 2 (Drosophila) /// Mu	3.22E-09	3	4.41	4.40	4.32	4.63	4.47	4.70	4.83	4.90
TC1800554	MBP	4155	myelin basic protein /// Myelin basic p	0.000152	3	6.63	6.24	6.18	6.46	6.33	6.51	6.45	6.55
TC0301798	MCCC1	56922	methylcrotonoyl-Coenzyme A carboxyl	3.48E-11	3	4.08	3.62	3.61	3.91	4.00	4.03	4.25	4.15
TC2200233	MCM5	4174	minichromosome maintenance comple	0.000181	3	5.03	4.83	4.79	4.96	5.14	5.19	5.14	5.06
TC0701469	MCM7	4176	minichromosome maintenance comple	3.81E-11	3	5.32	4.65	4.52	4.82	5.12	5.14	5.11	4.88
TC1701293	MED1	5469	mediator complex subunit 1	3.98E-05	3	5.42	5.27	5.38	5.54	5.43	5.55	5.70	5.61
TC1101417	MED19	219541	mediator complex subunit 19	0.000719	3	4.76	4.75	4.69	4.89	4.86	4.88	4.96	4.95
TC1700964	MED31	51003	mediator complex subunit 31	0.000557	3	6.77	6.38	6.75	6.81	6.68	6.91	6.91	6.96
TC0400417	METAP1	23173	methionyl aminopeptidase 1	2.79E-15	3	4.70	4.15	4.11	4.62	4.70	4.72	4.83	4.67
TC1001332	METTL10 /// N	399818 //	methyltransferase like 10 /// family wit	1.26E-06	3	4.60	4.43	4.49	4.62	4.65	4.70	4.71	4.65
TC1800299	METTL4	64863	methyltransferase like 4	7.92E-11	3	5.86	5.35	5.22	5.38	5.40	5.83	5.94	5.98
TC1200336	METTL7A	25840	methyltransferase like 7A	1.83E-14	3	4.26	4.11	4.12	4.63	4.61	4.66	4.97	4.91
TC2200649	MFNG	4242	MFNG O-fucosylpeptide 3-beta-N-acet	2.72E-05	3	5.46	5.34	5.28	5.35	5.41	5.46	5.48	5.55
TC1200366	MFSD5	84975	major facilitator superfamily domain c	5.05E-07	3	5.59	5.43	5.65	5.76	5.60	5.76	5.78	5.83
TC1500258	MGA	---	CDNA: FLJ22098 fis, clone HEP17040. (	3.08E-09	3	4.94	4.61	4.50	4.86	4.92	5.06	5.32	5.06
TC0200733	MGAT5	4249	mannosyl (alpha-1,6-)-glycoprotein bet	1.49E-08	3	5.39	4.94	4.91	5.24	5.33	5.42	5.42	5.33
TC0101536	MIA3	375056	melanoma inhibitory activity family, m	2.31E-09	3	6.45	6.09	5.98	6.23	6.06	6.37	6.64	6.65
TC0600263	MICB /// A2AC	4277	MHC class I polypeptide-related seque	0.000604	3	5.15	5.01	5.02	5.20	5.15	5.28	5.29	5.34

TC0X00149	MID1IP1	58526	MID1 interacting protein 1 (gastrulatio	2.08E-05	3	5.05	4.61	4.69	4.91	4.95	5.06	4.94	5.05
TC0201776	MITD1	129531	MIT, microtubule interacting and trans	3.50E-05	3	5.32	4.98	5.18	5.34	5.20	5.40	5.65	5.53
TC1100892	MLL	4297	myeloid/lymphoid or mixed-lineage leu	7.43E-07	3	5.63	5.35	5.05	5.43	5.46	5.61	5.99	5.77
TC0300731	MME	4311	membrane metallo-endopeptidase ///	5.67E-16	3	9.64	8.94	7.48	8.78	9.08	9.53	9.38	9.55
TC0101170	MNDA	4332	myeloid cell nuclear differentiation ant	0.000508	3	11.17	11.07	11.13	11.12	11.11	11.20	11.19	11.24
TC2200589	MORC2	22880	MORC family CW-type zinc finger 2	1.91E-05	3	4.02	3.97	3.87	4.04	4.07	4.02	4.13	4.07
TC2100110	MORC3	23515	MORC family CW-type zinc finger 3 ///	0.000208	3	7.50	7.23	7.20	7.23	7.10	7.30	7.42	7.46
TC0X01121	MORF4L2	9643	mortality factor 4 like 2 /// Mortality fa	6.01E-06	3	5.26	5.47	5.18	5.05	5.11	5.41	5.30	5.48
TC0100848	MOV10	4343	Mov10, Moloney leukemia virus 10, ho	0.000222	3	4.94	4.61	4.57	4.77	4.69	4.81	4.96	5.00
TC0400805	MRFAP1L1	114932	Morf4 family associated protein 1-like	2.77E-09	3	5.86	5.46	5.76	5.67	5.54	5.83	5.94	6.05
TC0102118	MRPS15	64960	mitochondrial ribosomal protein S15	0.000104	3	4.86	4.63	4.43	4.68	4.96	4.75	4.79	4.59
TC2100092	MRPS6 /// SLC	64968 ///	mitochondrial ribosomal protein S6 ///	8.47E-12	3	4.65	4.24	4.17	4.38	4.58	4.65	4.73	4.76
TC0200547	MRPS9	64965	mitochondrial ribosomal protein S9	0.000657	3	3.78	3.69	3.69	3.76	3.85	3.87	3.88	3.86
TC1700621	MSI2	124540	musashi homolog 2 (Drosophila)	4.07E-06	3	4.69	4.71	4.54	4.78	4.61	4.74	4.87	4.97
TC0301591	MSL2L1	55167	male-specific lethal 2-like 1 (Drosophila	0.000445	3	7.61	7.44	7.62	7.72	7.64	7.80	7.70	7.80
TC1600458	MT1CP	441771	metallothionein 1C (pseudogene)	0.000446	3	3.71	3.55	3.45	3.40	3.38	3.60	3.70	3.73
TC0103382	MT1P2	645745	metallothionein 1 pseudogene 2	0.000254	3	5.76	5.65	5.41	5.67	5.59	5.80	5.99	5.98
TC1600452	MT2A	4502	metallothionein 2A	4.07E-15	3	7.39	6.94	6.69	7.48	7.39	8.00	8.33	8.59
TC1600450	MT4	84560	metallothionein 4	0.000102	3	4.10	3.92	3.69	3.91	4.03	4.03	4.22	4.26
TC0701406	MTERF	7978	mitochondrial transcription terminatio	0.000505	3	4.32	4.12	4.34	4.18	4.01	4.24	4.40	4.43
TC1501034	MTFMT	123263	mitochondrial methionyl-tRNA formylt	8.05E-08	3	6.51	5.84	6.15	6.28	6.25	6.48	6.46	6.48
TC0X00658	MTM1	4534	myotubularin 1 /// Myotubularin (EC 3	7.57E-05	3	5.91	5.97	6.02	6.06	5.96	6.09	6.20	6.23
TC0500898	MTMR12	54545	myotubularin related protein 12 /// my	0.000378	3	5.42	4.98	5.23	5.51	5.29	5.39	5.41	5.51
TC0101644	MTR /// Q96B	4548	5-methyltetrahydrofolate-homocystein	3.11E-08	3	3.82	3.74	3.67	3.89	4.03	4.07	4.16	4.05
TC0501098	MTX3	345778	metaxin 3	0.000253	3	3.37	3.25	3.28	3.39	3.42	3.39	3.58	3.50
TC2100142	MX1	4599	myxovirus (influenza virus) resistance 1	1.34E-10	3	6.97	6.37	5.89	6.05	5.97	6.81	7.32	7.58
TC0600829	MYCT1	80177	myc target 1	1.48E-06	3	2.52	2.47	2.52	2.70	2.69	2.80	3.08	3.08
TC0600095	MYLIP	29116	myosin regulatory light chain interacti	6.25E-07	3	7.99	7.60	7.63	8.07	7.92	8.26	8.29	8.28
TC0200940	NAB1	4664	NGFI-A binding protein 1 (EGR1 binding	2.37E-10	3	6.89	6.18	6.28	6.77	6.61	6.86	6.93	7.00
TC0200334	NAGK	55577	N-acetylglucosamine kinase	0.000996	3	8.27	7.71	7.94	8.10	8.06	8.32	8.26	8.23
TC1101080	NAP1L4	4676	nucleosome assembly protein 1-like 4	8.54E-06	3	5.47	5.00	5.08	5.29	5.31	5.26	5.37	5.20
TC1901642	NAPA	8775	N-ethylmaleimide-sensitive factor atta	8.64E-05	3	5.78	5.54	5.28	5.48	5.45	5.66	5.75	5.90
TC1800052	NAPG	8774	N-ethylmaleimide-sensitive factor atta	2.08E-08	3	6.72	6.14	6.50	6.78	6.60	6.69	6.72	6.63
TC1800501	NARS	4677	asparaginyl-tRNA synthetase	4.40E-14	3	6.65	5.66	5.56	6.20	6.07	6.27	6.43	6.40

TC1100499	NAT11	79829	N-acetyltransferase 11	0.000526	3	4.63	4.45	4.40	4.41	4.46	4.51	4.62	4.51
TC0301459	NAT13	80218	N-acetyltransferase 13 /// N-acetyltran	4.78E-06	3	8.26	7.66	7.79	7.98	8.02	8.06	7.96	8.15
TC1700485	NBR2	---	Protein NBR2 (Next to BRCA1 gene 2 p	5.52E-05	3	5.39	5.14	5.18	5.32	5.29	5.36	5.36	5.31
TC0700392	NCF1	653361	neutrophil cytosolic factor 1, (chronic g	2.93E-05	3	9.90	9.26	9.07	9.49	9.46	9.55	9.50	9.71
TC0701337	NCF1 /// LOC6	653361 //	neutrophil cytosolic factor 1, (chronic g	3.48E-06	3	10.06	9.40	9.21	9.63	9.61	9.66	9.66	9.86
TC0202386	NCL	4691	nucleolin /// Nucleolin (Protein C23). [S	5.57E-18	3	7.78	7.37	7.02	7.93	8.08	8.19	8.48	8.23
TC1000240	NCOA4 /// MSI	8031 ///	nuclear receptor coactivator 4 /// micr	7.75E-21	3	7.86	6.61	6.55	6.98	7.01	7.25	7.27	7.47
TC1800009	NDC80	10403	NDC80 homolog, kinetochore complex	2.69E-18	3	3.97	3.39	3.19	3.77	4.21	4.50	4.70	4.63
TC1300215	NDFIP2	54602	Nedd4 family interacting protein 2 ///	1.13E-06	3	2.88	2.84	2.91	2.99	2.87	3.01	3.12	3.15
TC1900854	NDUFA3	4696	NADH dehydrogenase (ubiquinone) 1 a	7.96E-05	3	6.97	6.82	6.83	7.00	7.05	7.01	7.02	6.98
TC0601138	NEU1	4758	sialidase 1 (lysosomal sialidase)	0.000406	3	5.67	5.49	5.58	5.74	5.69	5.74	5.72	5.75
TC2200180	NF2	4771	neurofibromin 2 (merlin) /// Merlin (M	0.000641	3	3.95	3.83	3.84	3.80	3.92	3.87	3.94	3.92
TC2000833	NFATC2	4773	nuclear factor of activated T-cells, cyto	3.05E-13	3	4.34	3.64	3.55	4.09	3.80	4.17	4.59	4.58
TC1600302	NFATC2IP	84901	nuclear factor of activated T-cells, cyto	0.00019	3	4.38	4.37	4.15	4.26	4.40	4.47	4.47	4.37
TC1600535	NFATC3	4775	nuclear factor of activated T-cells, cyto	3.59E-13	3	6.87	6.21	6.31	6.54	6.53	6.63	6.69	6.75
TC0202131	NFE2L2	4780	nuclear factor (erythroid-derived 2)-lik	0.000247	3	4.36	4.33	4.28	4.36	4.41	4.43	4.42	4.35
TC0900127	NFX1	4799	nuclear transcription factor, X-box bin	3.63E-11	3	4.75	4.49	4.36	4.69	4.87	4.90	5.02	4.88
TC1201520	NFYB	4801	nuclear transcription factor Y, beta	8.56E-17	3	4.66	4.72	4.70	4.97	4.81	5.16	5.30	5.32
TC1400103	NGDN	---	Neuroguidin (EIF4E-binding protein). [S	8.29E-08	3	4.44	4.34	4.33	4.51	4.53	4.62	4.77	4.68
TC0102976	NME7	29922	non-metastatic cells 7, protein express	0.000112	3	3.60	3.48	3.52	3.58	3.49	3.60	3.78	3.74
TC0202002	NMI	9111	N-myc (and STAT) interactor	0.000234	3	8.37	8.45	8.61	8.55	8.34	8.65	8.67	8.77
TC1000787	NMT2	9397	N-myristoyltransferase 2 /// Glycylpept	1.37E-11	3	3.99	3.62	3.66	3.77	3.72	3.85	4.07	4.06
TC0701105	NOD1	10392	nucleotide-binding oligomerization do	3.40E-08	3	3.92	3.62	3.67	3.72	3.70	3.75	3.99	3.96
TC1700706	NOL11	25926	nucleolar protein 11	5.35E-07	3	3.41	3.34	3.32	3.41	3.58	3.58	3.68	3.59
TC0901129	NOL8	55035	nucleolar protein 8 /// Nucleolar prote	2.06E-06	3	4.91	4.34	4.29	4.57	4.63	4.68	4.91	4.71
TC1600198	NOMO1	652388 //	NODAL modulator 1	1.61E-09	3	6.85	6.49	6.30	6.75	6.88	6.92	6.90	6.85
TC1600905	NOMO2	652388 //	NODAL modulator 2	5.74E-10	3	6.84	6.51	6.32	6.76	6.88	6.94	6.92	6.84
TC1600211	NOMO3	652388 //	NODAL modulator 3	6.72E-09	3	7.02	6.63	6.46	6.91	7.06	7.10	7.06	7.01
TC0800523	NOV	4856	nephroblastoma overexpressed gene	8.51E-25	3	6.60	5.21	4.69	5.07	5.10	6.24	6.41	6.74
TC1700386	NP_996890.1	730424	chemokine (C-C motif) ligand 4-like 2 p	2.49E-06	3	4.62	4.60	4.38	5.20	4.99	5.58	5.89	5.97
TC1101806	NPAT	4863	nuclear protein, ataxia-telangiectasia l	4.29E-05	3	5.80	6.08	5.69	5.71	5.76	5.96	5.97	6.07
TC1400993	NPC2	10577	Niemann-Pick disease, type C2	1.61E-17	3	7.62	7.50	7.28	7.51	7.52	7.95	8.08	8.20
TC0300108	NR1D2	9975	nuclear receptor subfamily 1, group D,	0.000169	3	3.71	3.66	3.67	3.74	3.67	3.72	3.86	3.89
TC0501372	NR3C1	2908	nuclear receptor subfamily 3, group C,	6.12E-07	3	6.88	6.64	6.91	7.01	6.81	6.83	6.75	6.85

TC0500838	NSUN2	54888	NOL1/NOP2/Sun domain family, memb	3.27E-06	3	5.14	4.71	4.77	4.97	4.91	4.98	5.18	5.05
TC0600659	NT5DC1	221294	5'-nucleotidase domain containing 1 //	4.58E-07	3	4.37	4.16	4.09	4.21	4.21	4.33	4.42	4.48
TC0700893	NUB1	51667	negative regulator of ubiquitin-like pro	1.99E-15	3	7.58	7.06	6.64	6.97	6.90	7.40	7.65	7.81
TC0100301	NUDC	10726	nuclear distribution gene C homolog (A	1.25E-12	3	7.27	7.02	7.02	7.30	7.24	7.39	7.60	7.52
TC0701173	NUDCD3	23386	NudC domain containing 3 /// NudC dc	0.000347	3	4.55	4.34	4.30	4.46	4.44	4.47	4.47	4.45
TC1300131	NUDT15	55270	nudix (nucleoside diphosphate linked n	0.000521	3	3.59	3.53	3.47	3.58	3.73	3.70	3.81	3.69
TC1000768	NUDT5	11164	nudix (nucleoside diphosphate linked n	5.19E-10	3	6.17	5.30	5.33	5.66	5.47	5.79	5.88	5.84
TC0103332	NUP133	55746	nucleoporin 133kDa /// Nuclear pore c	0.000564	3	3.82	3.69	3.78	3.84	3.83	3.83	3.96	3.92
TC1101363	NUP160	23279	nucleoporin 160kDa /// Nuclear pore c	5.10E-10	3	4.46	4.04	3.93	4.11	4.14	4.32	4.52	4.42
TC2200350	NUP50	10762	nucleoporin 50kDa	5.35E-06	3	8.15	7.74	7.73	7.86	7.83	7.99	7.97	8.05
TC1600463	NUP93	9688	nucleoporin 93kDa	6.80E-15	3	5.43	5.04	4.83	5.19	5.19	5.40	5.72	5.71
TC1901282	NY-SAR-48 ///	93323	sarcoma antigen NY-SAR-48 /// sarcom	4.00E-13	3	5.00	4.76	4.62	4.94	5.08	5.10	5.21	5.11
TC1200712	OAS1	4938	2',5'-oligoadenylate synthetase 1, 40/4	4.47E-07	3	5.08	4.68	4.48	4.86	4.46	5.23	6.10	6.59
TC1200714	OAS2	4939	2'-5'-oligoadenylate synthetase 2, 69/7	7.60E-07	3	4.61	4.28	4.04	4.34	4.04	4.81	5.74	6.12
TC1200713	OAS3	4940	2'-5'-oligoadenylate synthetase 3, 100k	2.13E-06	3	5.08	4.92	4.62	4.80	4.75	5.19	5.66	5.88
TC1201637	OASL	8638	2'-5'-oligoadenylate synthetase-like	9.74E-11	3	6.40	5.49	5.08	6.25	6.16	6.70	6.91	7.20
TC0400935	OCIAD2	132299	OCIA domain containing 2	2.90E-11	3	4.80	4.72	4.60	4.99	4.89	5.23	5.42	5.42
TC0201307	ODC1	4953	ornithine decarboxylase 1	6.03E-07	3	5.94	5.72	5.53	6.00	6.30	6.53	6.37	6.37
TC1600448	OGFOD1	55239	2-oxoglutarate and iron-dependent ox	6.84E-13	3	4.33	3.92	4.07	4.37	4.46	4.51	4.65	4.52
TC2100083	OLIG1	116448	oligodendrocyte transcription factor 1	5.17E-12	3	5.12	4.08	4.40	5.06	4.91	4.94	5.18	5.21
TC2100082	OLIG2	10215	oligodendrocyte lineage transcription f	7.93E-10	3	4.07	3.77	3.77	4.06	4.06	4.10	4.13	4.21
TC1101444	OSBP	5007	oxysterol binding protein /// Oxysterol	2.26E-06	3	5.46	5.41	5.33	5.53	5.43	5.59	5.69	5.66
TC1400670	OSGEP	55644	O-sialoglycoprotein endopeptidase	1.23E-10	3	4.84	4.24	4.38	4.48	4.51	4.64	4.72	4.74
TC0800420	OSGIN2	734	oxidative stress induced growth inhibit	1.36E-08	3	6.27	6.17	6.10	6.41	6.46	6.82	6.80	6.81
TC0100214	OTUD3	23252	OTU domain containing 3	0.000165	3	3.75	3.55	3.58	3.60	3.74	3.72	3.74	3.69
TC0401302	OTUD4	54726	OTU domain containing 4	7.29E-09	3	5.31	5.28	5.33	5.36	5.31	5.60	5.80	5.74
TC1800421	P15RS /// NP_	55197	cyclin-dependent kinase 2B-inhibitor-re	7.33E-05	3	5.11	4.79	4.90	5.13	5.08	5.14	5.05	5.02
TC0301667	P2RY14	9934	purinergic receptor P2Y, G-protein cou	6.07E-08	3	6.13	5.44	4.96	6.09	5.64	6.39	7.04	7.24
TC1100652	P2RY2	5029	purinergic receptor P2Y, G-protein cou	8.73E-06	3	5.46	5.20	5.13	5.32	5.28	5.40	5.36	5.39
TC0X00732	P2RY8	286530	purinergic receptor P2Y, G-protein cou	6.45E-06	3	5.49	5.43	5.35	5.47	5.67	5.62	5.65	5.61
TC1200422	PA2G4	5036	proliferation-associated 2G4, 38kDa	1.26E-10	3	7.12	6.57	6.40	6.97	7.20	7.23	7.36	7.07
TC0102009	PAFAH2	5051	platelet-activating factor acetylhydrola	1.84E-13	3	4.75	4.27	4.34	4.64	4.47	4.63	4.79	4.83
TC2000046	PANK2	80025	pantothenate kinase 2 (Hallervorden-S	9.93E-05	3	6.55	6.42	6.46	6.51	6.37	6.52	6.57	6.65
TC2200378	PANX2	56666	pannexin 2	5.24E-05	3	6.38	6.31	6.22	6.28	6.41	6.44	6.40	6.41

TC1000858	PAPD1 /// Q6Z	55149	PAP associated domain containing 1 //,	1.14E-06	3	4.13	4.09	4.10	4.10	4.15	4.20	4.24	4.24
TC1600420	PAPD5	64282	PAP associated domain containing 5	2.58E-07	3	6.30	6.05	6.27	6.46	6.32	6.45	6.57	6.56
TC0401071	PAQR3	152559	progestin and adipoQ receptor family r	7.36E-05	3	3.50	3.33	3.35	3.40	3.31	3.48	3.55	3.51
TC0102006	PAQR7	164091	progestin and adipoQ receptor family r	2.03E-14	3	4.08	3.82	3.70	4.01	4.13	4.28	4.45	4.52
TC1600877	PARN	5073	poly(A)-specific ribonuclease (deadenyl	7.64E-06	3	5.94	5.62	5.58	5.68	5.61	5.72	5.92	5.84
TC0701680	PARP12	64761	poly (ADP-ribose) polymerase family, m	4.55E-10	3	5.97	5.14	4.94	5.20	5.23	5.51	5.87	5.98
TC0300556	PARP14	54625	poly (ADP-ribose) polymerase family, m	2.43E-12	3	7.92	6.72	6.16	6.76	6.46	7.41	7.78	8.10
TC1400027	PARP2	10038	poly (ADP-ribose) polymerase family, m	1.14E-09	3	4.38	4.14	4.08	4.46	4.70	4.78	4.85	4.52
TC0301497	PARP9	83666	poly (ADP-ribose) polymerase family, m	1.52E-05	3	7.35	7.05	7.08	7.16	6.90	7.28	7.43	7.59
TC0701785	PAXIP1	22976	PAX interacting (with transcription-acti	1.46E-05	3	4.70	4.39	4.52	4.43	4.54	4.55	4.66	4.60
TC0102817	PBXIP1	57326	pre-B-cell leukemia homeobox interact	1.82E-11	3	5.91	5.52	5.52	5.62	5.60	5.75	5.77	5.82
TC1000439	PCGF5	84333	polycomb group ring finger 5 /// Polycc	2.16E-16	3	5.71	5.15	5.02	5.64	5.43	6.11	6.38	6.60
TC1201473	PCTK2	5128	PCTAIRE protein kinase 2	1.12E-07	3	5.86	5.72	5.57	5.63	5.58	5.89	6.01	6.01
TC1000556	PDCD11	22984	programmed cell death 11	0.000416	3	4.21	4.08	4.12	4.12	4.19	4.18	4.26	4.18
TC1000583	PDCD4	27250	programmed cell death 4 (neoplastic tr	1.18E-17	3	8.03	7.77	7.17	7.37	7.40	7.83	8.00	8.16
TC0701433	PDK4	5166	pyruvate dehydrogenase kinase, isozyn	1.03E-08	3	4.26	4.03	4.25	4.98	4.59	4.87	5.31	5.37
TC0701412	PEX1	5189	peroxisome biogenesis factor 1	3.32E-07	3	4.02	3.64	3.75	3.85	3.78	3.83	3.98	3.88
TC1000968	PGBD3 /// ERC	267004 //	piggyBac transposable element derivec	9.37E-23	3	5.47	4.64	4.54	4.82	4.87	4.96	5.14	5.18
TC0601425	PGM3	5238	phosphoglucomutase 3 /// Phosphoace	0.00062	3	3.91	3.78	3.74	3.76	3.86	3.84	3.96	3.84
TC2200705	PHF5A	84844	PHD finger protein 5A	3.52E-11	3	5.04	4.78	4.60	5.00	4.98	5.18	5.23	5.32
TC2000307	PI3	5266	peptidase inhibitor 3, skin-derived (SKA	1.51E-06	3	9.64	9.28	8.77	10.05	10.28	10.37	10.48	10.18
TC1800446	PIAS2	9063	protein inhibitor of activated STAT, 2 //,	3.27E-08	3	3.90	3.60	3.85	4.24	3.88	3.91	4.15	4.04
TC0201488	PIGF	5281	phosphatidylinositol glycan anchor bios	2.17E-05	3	4.64	4.27	4.58	4.64	4.52	4.58	4.61	4.56
TC0300939	PIGX	54965	phosphatidylinositol glycan anchor bios	8.95E-13	3	5.73	4.89	5.05	5.27	5.17	5.40	5.57	5.72
TC1101230	PIK3C2A	5286	phosphoinositide-3-kinase, class 2, alpl	5.52E-11	3	5.18	4.82	4.65	4.79	4.69	4.92	5.07	5.14
TC0102219	PIK3R3	8503	phosphoinositide-3-kinase, regulatory s	9.25E-11	3	4.17	3.96	3.99	4.23	4.09	4.31	4.52	4.69
TC0700541	PILRA	29992	paired immunoglobin-like type 2 recep	5.22E-10	3	10.76	10.09	9.63	10.32	10.22	10.43	10.45	10.73
TC0800736	PINX1 /// PINX	54984	PIN2-interacting protein 1 /// Pin2-inte	0.000617	3	3.53	3.46	3.38	3.45	3.64	3.57	3.74	3.55
TC1000819	PIP4K2A	5305	phosphatidylinositol-5-phosphate 4-kir	0.000421	3	8.22	7.83	7.77	8.25	8.09	8.01	8.09	8.04
TC1701280	PIP4K2B	8396	phosphatidylinositol-5-phosphate 4-kir	1.59E-06	3	5.34	5.12	5.17	5.43	5.39	5.45	5.53	5.39
TC1200454	PIP4K2C	79837	phosphatidylinositol-5-phosphate 4-kir	2.60E-05	3	5.50	5.23	5.20	5.43	5.42	5.48	5.51	5.51
TC0900280	PIP5K1B	8395	phosphatidylinositol-4-phosphate 5-kir	1.97E-08	3	4.55	4.12	4.39	4.54	4.44	4.59	4.78	4.79
TC2200554	PITPNB	23760	phosphatidylinositol transfer protein, b	3.47E-09	3	7.37	7.18	7.16	7.49	7.40	7.53	7.67	7.54
TC0400383	PKD2	5311	polycystic kidney disease 2 (autosomal	1.96E-08	3	3.92	3.88	3.63	3.81	3.95	4.01	4.10	4.06

TC0200807	PKP4	8502	plakophilin 4	1.16E-05	3	5.23	4.83	4.55	4.85	5.26	5.21	5.13	4.98
TC1901567	PLAUR	5329	plasminogen activator, urokinase recep	1.49E-05	3	7.76	7.42	6.92	7.33	7.39	7.62	7.53	7.74
TC1800221	PMAIP1	5366	phorbol-12-myristate-13-acetate-induc	1.68E-23	3	6.10	4.85	4.89	5.43	5.33	6.35	6.49	6.93
TC1600159	PMM2	5373	phosphomannomutase 2	0.000753	3	4.37	4.23	4.14	4.24	4.39	4.45	4.46	4.41
TC0700991	PMS2	5395	PMS2 postmeiotic segregation increase	0.00066	3	4.22	3.89	4.02	4.15	4.07	4.11	4.24	4.11
TC0X00679	PNMA6A	84968	paraneoplastic antigen like 6A	3.10E-10	3	5.60	4.70	4.20	4.48	4.44	5.54	5.69	5.90
TC0201529	PNPT1	87178	polyribonucleotide nucleotidyltransfera	1.21E-06	3	3.26	3.14	3.03	3.09	3.20	3.41	3.79	3.61
TC0800255	POLB	5423	polymerase (DNA directed), beta	7.60E-18	3	6.53	5.87	5.30	5.49	5.35	6.25	6.46	6.90
TC0600413	POLH	5429	polymerase (DNA directed), eta /// DN	8.00E-07	3	4.42	4.30	4.26	4.45	4.57	4.57	4.74	4.57
TC2200269	POLR2F /// Q5	5435	polymerase (RNA) II (DNA directed) pol	1.64E-05	3	5.19	5.11	5.12	5.23	5.21	5.25	5.30	5.30
TC1200661	POLR3B	55703	polymerase (RNA) III (DNA directed) po	3.82E-06	3	3.87	3.78	3.77	3.94	4.03	4.01	4.11	4.01
TC0101261	POU2F1	5451	POU class 2 homeobox 1 /// POU doma	2.56E-10	3	5.67	5.49	5.27	5.42	5.34	5.53	5.59	5.59
TC0800884	PPAPDC1B	84513	phosphatidic acid phosphatase type 2	4.15E-05	3	4.72	4.51	4.46	4.54	4.65	4.65	4.71	4.65
TC0900021	PPAPDC2	403313	phosphatidic acid phosphatase type 2	7.44E-06	3	4.94	4.62	4.80	4.81	4.77	5.03	5.07	5.11
TC1000370	PPIF	10105	peptidylprolyl isomerase F (cyclophilin	2.56E-11	3	6.28	5.62	5.17	5.53	5.66	6.06	5.98	6.16
TC0401114	PPM1K	152926	protein phosphatase 1K (PP2C domain	0.000246	3	3.66	3.52	3.53	3.60	3.52	3.67	3.93	3.83
TC1201566	PPP1CC	5501	protein phosphatase 1, catalytic subun	6.09E-24	3	7.74	6.42	6.88	7.38	7.23	7.47	7.71	7.78
TC1900696	PPP1R15A	23645	protein phosphatase 1, regulatory (inhi	0.000857	3	7.51	7.59	7.19	7.29	7.38	7.55	7.52	7.67
TC1400719	PPP1R3E /// H	90673 ///	protein phosphatase 1, regulatory (inhi	7.68E-10	3	4.81	4.44	4.45	4.62	4.66	4.71	4.76	4.67
TC1701514	PPP1R9B	84687	protein phosphatase 1, regulatory (inhi	9.71E-14	3	8.32	6.58	6.75	7.26	7.21	7.44	7.61	7.79
TC0800141	PPP3CC	5533	protein phosphatase 3 (formerly 2B),	2.06E-05	3	4.35	4.21	4.33	4.48	4.41	4.47	4.72	4.59
TC1201564	PPTC7	160760	PTC7 protein phosphatase homolog (S.	1.78E-17	3	7.59	6.52	6.68	7.16	7.07	7.36	7.33	7.51
TC0200041	PQLC3	130814	PQ loop repeat containing 3	0.000156	3	4.15	4.12	4.08	4.31	4.21	4.29	4.39	4.33
TC0600596	PRDM1	639	PR domain containing 1, with ZNF dom	7.89E-14	3	7.80	6.93	6.42	6.65	6.44	7.16	7.46	7.68
TC0701774	PRKAG2	51422	protein kinase, AMP-activated, gamma	7.90E-19	3	4.91	4.29	4.32	4.69	4.49	4.79	5.02	5.16
TC0200215	PRKCE	5581	protein kinase C, epsilon	3.58E-08	3	4.03	3.94	3.83	3.91	3.85	3.97	4.03	4.10
TC0202137	PRKRA	8575	protein kinase, interferon-inducible do	1.69E-05	3	3.81	3.80	3.72	3.80	3.85	3.79	3.92	3.96
TC0X00742	PRKX	729116 //	protein kinase, X-linked	1.80E-11	3	4.68	4.38	4.34	4.75	4.60	4.73	5.03	4.98
TC1400196	PRPF39	55015	PRP39 pre-mRNA processing factor 39	2.39E-06	3	3.68	3.30	3.39	3.52	3.61	3.57	3.72	3.63
TC1100258	PRRG4	79056	proline rich Gla (G-carboxyglutamic aci	1.79E-12	3	7.43	6.00	6.23	7.11	6.97	7.31	7.60	7.72
TC0900789	PSIP1	11168	PC4 and SFRS1 interacting protein 1 //	5.03E-11	3	7.97	7.33	7.42	7.74	7.57	7.75	7.99	7.99
TC0601164	PSMB8	5696	proteasome (prosome, macropain) sub	1.11E-06	3	6.02	5.30	5.31	5.54	5.36	5.68	5.66	5.86
TC0600297	PSMB9	5698	proteasome (prosome, macropain) sub	7.60E-07	3	7.63	7.20	7.17	7.33	7.22	7.68	7.70	7.79
TC1400118	PSME1	5720	proteasome (prosome, macropain) acti	7.35E-12	3	8.78	8.54	8.39	8.60	8.48	8.84	8.96	9.07

TC1400736	PSME2	5721	proteasome (prosome, macropain) acti	1.98E-11	3	5.90	5.25	4.87	5.23	5.21	5.68	5.99	6.18
TC1900018	PTBP1	5725	polypyrimidine tract binding protein 1	7.54E-05	3	5.72	5.51	5.47	5.70	5.80	5.73	5.76	5.73
TC0500141	PTGER4	730882 //	prostaglandin E receptor 4 (subtype EP	3.80E-22	3	6.19	4.89	4.82	5.49	5.30	5.76	5.75	6.03
TC0103081	PTGS2	5743	prostaglandin-endoperoxide synthase	8.80E-11	3	8.76	8.88	7.78	7.77	8.00	8.98	8.68	9.22
TC0800583	PTP4A3	11156	protein tyrosine phosphatase type IVA,	5.30E-14	3	6.39	5.80	5.69	5.99	6.01	6.37	6.25	6.36
TC0200633	PTPN4	5775	protein tyrosine phosphatase, non-rec	8.82E-07	3	4.35	3.91	4.07	4.16	4.00	4.13	4.31	4.30
TC1701570	PTRH2 /// Q96	51651	peptidyl-tRNA hydrolase 2 /// CDNA FL	3.32E-12	3	4.97	4.27	4.10	4.51	4.51	4.61	4.72	4.71
TC0201343	PUM2	23369	pumilio homolog 2 (Drosophila) /// Pur	9.43E-05	3	7.77	7.60	7.52	7.59	7.51	7.72	7.72	7.78
TC0701180	PURB	5814	purine-rich element binding protein B	3.77E-05	3	5.54	5.36	5.32	5.25	5.21	5.43	5.57	5.56
TC0501460	PWWP2A	114825	PWWP domain containing 2A	5.60E-05	3	4.79	4.42	4.60	4.71	4.71	4.72	4.83	4.78
TC0901006	Q5JTY1_HUMA	---	COBW domain containing 3 (DC36 prot	5.21E-06	3	7.27	6.37	6.38	6.90	6.63	6.99	7.15	7.07
TC0600261	Q5SS58_HUM	---	MHC class I polypeptide-related seque	2.23E-05	3	4.91	4.60	4.72	4.72	4.67	4.80	4.88	4.87
TC1701627	Q6GMT2_HU	---	---	8.16E-07	3	4.08	3.77	3.79	3.84	3.73	3.88	4.04	4.11
TC1600670	Q6ZP14_HUM	---	CDNA FLJ26728 fis, clone PNC06635. [S	0.000999	3	4.53	4.32	4.46	4.38	4.33	4.56	4.65	4.66
TC0600348	Q6ZV19_HUM	---	CDNA FLJ43093 fis, clone CORDB10001	2.93E-05	3	4.88	4.56	4.50	4.65	4.71	4.81	4.86	4.80
TC1700779	Q6ZVW4_HU	---	CDNA FLJ41999 fis, clone SPLEN20296	5.09E-07	3	4.72	4.13	4.16	4.37	4.44	4.48	4.48	4.52
TC1901169	Q71MM4_HU	---	---	2.66E-09	3	6.17	5.52	5.45	6.07	6.30	6.69	6.93	6.59
TC2000228	Q8N2C8_HUM	51230	PHD finger protein 20 /// PHD finger pr	2.54E-17	3	7.61	6.91	6.60	6.99	6.92	7.22	7.46	7.51
TC0900116	Q8N7I0_HUM	---	CDNA FLJ25547 fis, clone JTH01487 (Ti	2.18E-08	3	4.86	4.49	4.53	4.68	4.78	4.83	4.74	4.81
TC0401279	Q8N984_HUM	---	CDNA FLJ38235 fis, clone FCBBF200542	0.000184	3	2.86	2.83	2.90	2.83	2.97	2.97	3.03	3.04
TC0103220	Q8TAF5_HUM	---	---	7.43E-09	3	4.38	3.84	3.75	3.99	4.12	4.29	4.45	4.54
TC1900911	Q96HF5_HUM	---	MGC9913 protein. [Source:Uniprot/SP	8.68E-05	3	4.62	4.31	4.37	4.75	4.56	4.66	4.66	4.71
TC2000775	Q96JR8_HUMA	---	---	1.81E-05	3	4.40	3.63	3.69	3.86	3.87	4.10	4.55	4.17
TC1000241	Q9P1K1_HUM	---	---	1.07E-05	3	5.62	5.06	5.11	5.50	5.63	5.76	5.92	5.76
TC0600867	QKI	9444	quaking homolog, KH domain RNA bin	0.000101	3	7.39	7.15	7.10	7.27	7.15	7.37	7.37	7.47
TC0800878	RAB11FIP1	80223	RAB11 family interacting protein 1 (cla	2.27E-12	3	8.10	7.19	7.27	7.58	7.50	7.77	7.73	7.89
TC2000408	RAB22A	57403	RAB22A, member RAS oncogene family	6.14E-05	3	6.89	6.84	6.86	7.01	6.92	7.15	7.17	7.16
TC1700742	RAB37	326624	RAB37, member RAS oncogene family	1.30E-15	3	6.42	5.73	5.59	5.92	5.79	6.08	6.15	6.27
TC1700066	RABEP1	9135	rabaptin, RAB GTPase binding effector	4.39E-06	3	5.90	5.65	5.55	5.74	5.70	5.87	6.11	5.96
TC0101299	RABGAP1L	9910	RAB GTPase activating protein 1-like //	6.56E-06	3	6.41	5.94	5.94	6.14	6.06	6.23	6.26	6.27
TC1200694	RAD9B	144715	RAD9 homolog B (S. cerevisiae)	3.51E-05	3	3.36	3.07	3.15	3.24	3.24	3.24	3.23	3.27
TC0100837	RAP1A	5906	RAP1A, member of RAS oncogene fami	0.000259	3	8.87	8.65	8.85	8.90	8.81	8.85	8.83	8.88
TC1100494	RARRES3	5920	retinoic acid receptor responder (tazar	7.03E-11	3	5.44	5.34	4.56	5.21	4.91	5.69	6.18	6.72
TC1500827	RASGRP1	10125	RAS guanyl releasing protein 1 (calciu	0.000477	3	3.88	3.84	3.58	3.80	3.81	3.84	3.96	3.89

TC0103159	RBBP5	5929	retinoblastoma binding protein 5 /// R	1.43E-05	3	6.31	6.10	6.25	6.35	6.22	6.40	6.45	6.50
TC1600272	RBBP6	5930	retinoblastoma binding protein 6 /// R	5.93E-08	3	6.43	6.14	5.70	5.87	5.92	6.13	6.38	6.31
TC0X00791	RBBP7	5931	retinoblastoma binding protein 7 /// Hi	2.87E-12	3	5.21	4.97	4.94	5.34	5.58	5.53	5.64	5.46
TC2000010	RBCK1	10616	RanBP-type and C3HC4-type zinc finge	0.000891	3	5.98	5.86	5.85	5.85	5.85	5.97	5.97	6.03
TC0901307	RBM18	92400	RNA binding motif protein 18	0.000133	3	5.64	5.63	5.62	5.80	5.70	5.80	5.89	5.94
TC1300564	RBM26	64062	RNA binding motif protein 26 /// RNA-	3.60E-10	3	6.03	5.42	5.47	5.56	5.55	5.75	5.95	5.84
TC0500572	RBM27	---	RNA-binding protein 27 (RNA-binding	6.29E-07	3	6.54	6.51	6.47	6.59	6.50	6.72	6.88	6.86
TC0701614	RBM28	55131	RNA binding motif protein 28	3.82E-12	3	4.98	4.61	4.70	4.97	5.04	5.09	5.18	5.08
TC0103368	RBM34	23029	RNA binding motif protein 34 /// RNA-	5.15E-08	3	6.07	5.87	5.81	5.99	5.99	6.18	6.45	6.42
TC0202001	RBM43	375287	RNA binding motif protein 43	0.000105	3	5.10	5.03	5.00	5.10	4.98	5.09	5.31	5.21
TC1300476	RCBTB2	1102	regulator of chromosome condensatio	6.10E-13	3	6.42	5.58	5.99	6.64	6.52	6.51	6.45	6.45
TC1101549	RELA	5970	v-rel reticuloendotheliosis viral oncoge	1.44E-05	3	6.18	6.44	6.03	6.18	6.17	6.24	6.20	6.32
TC0601529	REV3L	5980	REV3-like, catalytic subunit of DNA pol	3.77E-11	3	4.72	4.12	4.18	4.37	4.30	4.47	4.61	4.55
TC1200734	RFC5	5985	replication factor C (activator 1) 5, 36.5	5.73E-11	3	4.53	4.05	4.09	4.40	4.41	4.46	4.53	4.50
TC0101373	RGS1	5996	regulator of G-protein signaling 1 /// R	8.22E-08	3	3.11	2.88	2.90	3.11	2.92	3.26	3.46	3.70
TC0200080	RHOB	388	ras homolog gene family, member B	6.88E-09	3	7.74	7.74	7.56	7.59	7.77	8.12	7.88	8.14
TC0500352	RHOBTB3	22836	Rho-related BTB domain containing 3	1.07E-12	3	4.02	3.62	3.80	4.11	4.00	4.26	4.42	4.52
TC0200219	RHOQ	23433	ras homolog gene family, member Q	9.08E-14	3	6.59	5.77	5.94	6.59	6.25	6.63	6.73	6.79
TC1700893	RILP	83547	Rab interacting lysosomal protein	6.01E-06	3	5.15	5.08	4.98	5.16	5.17	5.26	5.17	5.23
TC0700600	RINT1	60561	RAD50 interactor 1	5.76E-05	3	3.73	3.44	3.53	3.55	3.59	3.58	3.72	3.62
TC0600024	RIPK1	8737	receptor (TNFRSF)-interacting serine-th	0.00097	3	6.72	6.75	6.57	6.73	6.58	6.75	6.88	6.89
TC0800419	RIPK2	8767	receptor-interacting serine-threonine	5.77E-11	3	6.03	5.53	5.56	5.73	5.44	5.89	6.21	6.59
TC0601689	RMND1	55005	required for meiotic nuclear division 1	3.57E-07	3	4.07	3.96	4.01	4.21	4.22	4.14	4.37	4.23
TC0200423	RMND5A	64795	required for meiotic nuclear division 5	1.09E-13	3	7.38	6.45	6.56	6.92	6.88	7.14	7.05	7.21
TC0201691	RNF103	7844	ring finger protein 103	1.18E-07	3	5.76	5.49	5.42	5.54	5.62	5.79	5.70	5.77
TC2000361	RNF114	55905	ring finger protein 114	4.20E-07	3	7.23	6.81	6.88	7.02	7.05	7.22	7.24	7.47
TC1100640	RNF121	55298	ring finger protein 121	8.73E-07	3	5.37	4.95	4.92	5.13	5.18	5.21	5.28	5.24
TC0800863	RNF122	79845	ring finger protein 122	4.52E-11	3	6.23	5.58	5.27	5.78	5.56	5.88	5.99	6.20
TC1800131	RNF125	54941	ring finger protein 125	7.15E-08	3	4.02	3.48	3.75	4.13	3.86	3.91	4.10	4.19
TC0501558	RNF130	55819	ring finger protein 130	4.75E-06	3	9.20	8.79	8.95	9.17	9.07	9.23	9.23	9.35
TC0200020	RNF144A	9781	ring finger protein 144A	2.96E-13	3	4.77	4.67	4.47	4.76	4.81	5.01	5.19	5.12
TC0900445	RNF20	56254	ring finger protein 20 /// E3 ubiquitin-	3.21E-05	3	7.32	6.96	7.11	7.33	7.07	7.19	7.39	7.40
TC0400029	RNF4	650020 //	ring finger protein 4	7.83E-06	3	8.04	7.65	7.60	7.80	7.76	7.88	7.91	7.90
TC1800073	RNMT	8731	RNA (guanine-7-) methyltransferase	2.12E-05	3	3.94	3.79	3.78	3.97	4.00	4.11	4.20	4.16

TC0X00569	RP6-213H19.1 /	51765	serine/threonine protein kinase MST4 /	0.000526	3	6.08	6.01	5.93	6.15	6.26	6.28	6.16	6.26
TC1700018	RPA1 /// Q7Z4	6117	replication protein A1, 70kDa /// MSTP	2.57E-08	3	4.51	4.33	4.22	4.41	4.65	4.62	4.67	4.59
TC1201136	RPAP3	79657	RNA polymerase II associated protein 3	2.44E-18	3	7.02	5.78	5.83	6.41	6.27	6.61	6.94	7.04
TC0200444	RPIA	22934	ribose 5-phosphate isomerase A (ribos	3.65E-06	3	4.40	4.27	4.12	4.36	4.56	4.64	4.64	4.42
TC1300045	RPL21	731567 //	ribosomal protein L21	9.57E-05	3	5.20	5.12	5.10	5.23	5.32	5.29	5.39	5.27
TC1900882	RPL28	6158	ribosomal protein L28	7.48E-06	3	5.76	5.64	5.50	5.73	5.75	5.79	5.89	5.81
TC1200423	RPL41	6171	ribosomal protein L41	8.85E-08	3	8.01	7.73	7.82	7.98	8.02	8.18	8.19	8.16
TC0301539	RPN1	6184	ribophorin I	7.96E-05	3	8.30	7.86	8.11	8.30	8.21	8.24	8.22	8.26
TC1900717	RPS11 /// SNO	6205	ribosomal protein S11 /// small nucleol	4.55E-10	3	9.75	9.55	9.52	9.88	9.82	9.90	9.97	9.87
TC1000365	RPS24	6229	ribosomal protein S24	0.000358	3	4.19	4.03	4.09	4.12	4.19	4.22	4.28	4.19
TC0600051	RREB1	6239	ras responsive element binding protein	1.74E-07	3	5.31	5.05	5.01	5.32	5.26	5.23	5.32	5.22
TC0801168	RRM2B	50484	ribonucleotide reductase M2 B (TP53 i	1.91E-08	3	6.49	5.96	5.98	6.07	5.93	6.32	6.25	6.55
TC1001196	RRP12	23223	ribosomal RNA processing 12 homolog	0.00055	3	5.79	5.45	5.60	5.73	5.78	5.78	5.61	5.61
TC0200019	RSAD2	91543	radical S-adenosyl methionine domain	4.13E-11	3	6.33	5.40	4.64	5.08	4.85	6.43	7.15	7.99
TC0700431	RSBN1L	222194	round spermatid basic protein 1-like	1.05E-15	3	7.34	6.38	6.52	6.91	6.78	7.03	7.17	7.25
TC0300884	RTP4	64108	receptor (chemosensory) transporter p	0.000502	3	4.73	4.47	4.43	4.54	4.25	4.81	5.20	5.36
TC1001023	RUFY2	55680	RUN and FYVE domain containing 2 ///	0.000278	3	4.19	4.16	4.17	4.30	4.15	4.28	4.42	4.32
TC1700481	RUNDC1	146923	RUN domain containing 1	0.000164	3	5.74	5.38	5.42	5.60	5.50	5.66	5.70	5.79
TC0600428	RUNX2	860	runt-related transcription factor 2 /// R	1.86E-14	3	5.41	4.83	4.70	5.05	5.04	5.21	5.24	5.36
TC0500285	S100Z	170591	S100 calcium binding protein Z	4.99E-06	3	4.48	3.96	4.10	4.37	4.12	4.26	4.43	4.39
TC0701417	SAMD9	54809	sterile alpha motif domain containing 9	2.89E-09	3	8.01	7.38	7.36	7.37	7.08	7.63	8.01	8.13
TC0701418	SAMD9L	219285	sterile alpha motif domain containing 9	1.28E-05	3	7.67	7.29	7.21	7.12	6.84	7.48	7.90	8.06
TC2000720	SAMHD1	25939	SAM domain and HD domain 1 /// SAM	8.75E-06	3	7.00	7.01	6.67	6.96	6.57	7.25	7.66	7.79
TC1201536	SART3	9733	squamous cell carcinoma antigen recog	2.41E-05	3	5.84	5.69	5.50	5.67	5.68	5.79	5.92	5.88
TC0102481	SASS6	163786	spindle assembly 6 homolog (C. elegans	2.79E-09	3	3.97	3.86	3.84	4.10	4.24	4.35	4.55	4.41
TC0701284	SBDS	51119	Shwachman-Bodian-Diamond syndrom	4.25E-05	3	5.46	5.50	5.41	5.64	5.64	5.74	5.91	5.86
TC0401250	SCLT1	132320	sodium channel and clathrin linker 1	2.01E-06	3	7.85	7.35	7.65	7.79	7.56	7.85	7.94	7.93
TC0601503	SCML4	256380	sex comb on midleg-like 4 (Drosophila)	1.09E-08	3	4.43	3.97	4.05	4.11	4.02	4.38	4.51	4.53
TC0101029	SCNM1	79005	sodium channel modifier 1 /// Sodium	4.41E-05	3	7.36	7.06	7.19	7.28	7.28	7.37	7.31	7.40
TC1701032	SCO1	6341	SCO cytochrome oxidase deficient hom	3.68E-07	3	4.52	4.35	4.36	4.62	4.60	4.65	4.71	4.69
TC0701103	SCRN1	9805	secernin 1	2.97E-12	3	4.42	4.34	4.32	4.54	4.51	4.61	4.80	4.85
TC0200870	SCRN3	79634	secernin 3	1.40E-11	3	5.44	4.84	4.96	5.14	5.07	5.23	5.33	5.30
TC2000308	SEMG1	6406	semenogelin I	6.89E-07	3	2.85	2.44	2.46	2.67	2.47	2.74	3.07	3.02
TC0300941	SENP5	205564	SUMO1/sentrin specific peptidase 5	0.000328	3	4.84	4.64	4.56	4.70	4.61	4.74	4.86	4.85

TC0400859	SEPSECS	51091	Sep (O-phosphoserine) tRNA:Sec (selen	7.99E-05	3	3.93	3.64	3.66	3.82	3.79	3.81	3.81	3.88
TC0400335	SEPT11	55752	septin 11	1.52E-12	3	4.40	4.13	4.10	4.73	4.70	5.00	5.09	5.05
TC1100393	SERPING1	710	serpin peptidase inhibitor, clade G (C1	9.90E-09	3	6.68	6.40	5.73	6.14	5.95	6.99	7.37	7.78
TC1101752	SESN3	143686	sestrin 3	3.97E-08	3	5.40	4.69	4.71	4.96	4.96	5.21	5.26	5.23
TC0900603	SET	6418	SET nuclear oncogene /// Protein SET (	4.35E-23	3	6.99	6.55	6.45	6.86	7.08	7.25	7.35	7.36
TC0102135	SF3A3	10946	splicing factor 3a, subunit 3, 60kDa	3.13E-12	3	6.20	4.94	4.93	5.41	5.63	5.59	5.90	5.48
TC1000751	SFMBT2	57713	Scm-like with four mbt domains 2 /// S	2.33E-08	3	4.15	3.74	3.73	3.97	3.85	4.01	4.22	4.24
TC2100296	SFRS15	57466	splicing factor, arginine/serine-rich 15	3.39E-07	3	5.66	5.62	5.54	5.68	5.66	5.75	5.89	5.82
TC1201127	SFRS2IP	9169	splicing factor, arginine/serine-rich 2, i	4.73E-05	3	7.00	6.69	6.65	6.73	6.58	6.78	7.02	6.98
TC2000283	SFRS6	6431	splicing factor, arginine/serine-rich 6 //	4.24E-05	3	6.29	5.96	5.89	5.99	6.25	6.25	6.23	6.11
TC0201443	SFRS7	6432	splicing factor, arginine/serine-rich 7, 3	0.000181	3	6.03	5.63	5.43	5.71	5.97	6.12	6.19	5.90
TC0200670	SFT2D3	84826	SFT2 domain containing 3	3.39E-06	3	5.53	5.31	5.47	5.51	5.61	5.80	5.96	5.70
TC0601619	SGK1 /// SGK	6446	serum/glucocorticoid regulated kinase	2.91E-18	3	7.35	5.57	5.37	6.13	5.98	6.69	6.67	7.10
TC1000980	SGMS1	259230	sphingomyelin synthase 1	1.72E-05	3	5.79	5.88	5.50	5.70	5.71	5.95	5.91	6.11
TC1901743	SIGLEC10	89790	sialic acid binding Ig-like lectin 10 /// Si	1.69E-15	3	7.83	6.00	6.22	7.42	7.07	7.05	7.31	7.44
TC1901744	SIGLEC8	27181	sialic acid binding Ig-like lectin 8 /// Sia	5.17E-11	3	4.65	3.91	4.01	4.42	4.24	4.43	4.61	4.77
TC1000286	SIRT1	23411	sirtuin (silent mating type information	8.64E-06	3	6.76	6.38	6.49	6.64	6.60	6.77	6.81	6.92
TC0500122	SKP2	6502	S-phase kinase-associated protein 2 (p	2.30E-10	3	4.56	4.12	4.31	4.69	4.84	4.82	5.02	4.77
TC0102921	SLAMF6	114836	SLAM family member 6 /// SLAM famil	8.89E-15	3	4.94	3.62	3.66	4.54	4.03	4.49	5.12	5.10
TC0400765	SLBP	7884	stem-loop binding protein	2.00E-13	3	6.77	6.27	6.25	6.56	6.76	6.81	6.80	6.85
TC1201684	SLC15A4	121260	solute carrier family 15, member 4 ///	1.66E-05	3	8.24	7.63	7.78	8.03	7.90	8.09	8.12	8.10
TC0300667	SLC25A36	55186	solute carrier family 25, member 36	2.54E-07	3	3.92	3.84	3.84	4.00	4.09	4.22	4.41	4.24
TC0300172	SLC25A38	54977	solute carrier family 25, member 38	5.68E-07	3	3.58	3.35	3.27	3.47	3.59	3.59	3.80	3.69
TC0101088	SLC27A3	11000	solute carrier family 27 (fatty acid tran	8.12E-10	3	5.08	4.63	4.72	4.83	4.86	4.87	4.99	4.96
TC0600423	SLC29A1	2030	solute carrier family 29 (nucleoside tra	2.07E-12	3	5.36	4.95	5.05	5.37	5.25	5.45	5.47	5.50
TC0500231	SLC30A5	64924	solute carrier family 30 (zinc transporte	3.28E-07	3	4.59	4.53	4.50	4.58	4.57	4.68	4.82	4.75
TC1200501	SLC35E3	55508	solute carrier family 35, member E3 ///	3.32E-11	3	5.85	5.23	5.26	5.54	5.52	5.52	5.68	5.70
TC1201128	SLC38A1	81539	solute carrier family 38, member 1 ///	1.85E-18	3	5.04	4.63	4.50	5.14	5.30	5.42	5.69	5.47
TC1800422	SLC39A6	25800	solute carrier family 39 (zinc transporte	5.75E-16	3	5.59	5.10	5.12	5.57	5.50	5.65	5.80	5.80
TC1601195	SLC7A6OS	84138	solute carrier family 7, member 6 oppo	3.00E-12	3	5.92	5.20	5.50	5.73	5.53	5.66	5.93	5.90
TC1400716	SLC7A8	23428	solute carrier family 7 (cationic amino	2.85E-08	3	4.32	4.10	4.10	4.33	4.22	4.37	4.52	4.60
TC1701237	SLFN13	146857	schlafen family member 13 /// Schlafe	2.25E-10	3	4.15	3.66	3.67	4.21	4.44	4.47	4.60	4.32
TC0501465	SLU7	10569	SLU7 splicing factor homolog (S. cerevi	8.54E-05	3	8.50	8.42	8.26	8.35	8.26	8.42	8.56	8.59
TC1500424	SMAD3	4088	SMAD family member 3	2.13E-08	3	5.41	5.17	5.08	5.44	5.31	5.46	5.61	5.61

TC0400567	SMARCA5	8467	SWI/SNF related, matrix associated, act	1.96E-07	3	6.77	6.76	6.63	6.81	6.68	6.94	7.12	7.11
TC0301170	SMARCC1	6599	SWI/SNF related, matrix associated, act	1.53E-06	3	7.59	7.29	7.27	7.31	7.24	7.40	7.55	7.52
TC0300755	SMC4	10051	structural maintenance of chromosome	1.62E-07	3	5.77	5.52	5.37	5.50	5.74	5.88	6.09	5.93
TC0201331	SMC6	79677	structural maintenance of chromosome	2.49E-05	3	4.95	4.63	4.80	5.14	5.05	5.10	5.44	5.12
TC1401068	SMEK1	55671	SMEK homolog 1, suppressor of mek1 (	0.000683	3	6.70	6.41	6.46	6.45	6.36	6.59	6.75	6.69
TC1001275	SMNDC1	10285	survival motor neuron domain containi	1.15E-05	3	6.67	6.67	6.71	6.75	6.74	6.90	6.89	6.93
TC1601198	SMPD3	55512	sphingomyelin phosphodiesterase 3, ne	1.55E-08	3	4.94	4.55	4.58	4.84	4.74	4.92	5.03	5.03
TC0201902	SMPD4	55627	sphingomyelin phosphodiesterase 4, ne	4.27E-05	3	4.47	4.38	4.39	4.47	4.52	4.53	4.58	4.51
TC0X00084	SMS	6611	spermine synthase /// Spermine syntha	7.65E-23	3	7.18	6.10	5.72	6.77	6.88	7.34	7.43	7.54
TC0101511	SMYD2	56950	SET and MYND domain containing 2	3.31E-05	3	3.60	3.51	3.54	3.61	3.75	3.84	3.81	3.81
TC1501054	SNAPC5	10302	small nuclear RNA activating complex,	5.18E-07	3	5.16	5.10	5.07	5.21	5.19	5.30	5.54	5.49
TC0900671	SNORD36B ///	650992 //	ribosomal protein L7a /// small nucleol	5.02E-07	3	4.16	4.00	3.98	4.07	4.15	4.13	4.30	4.14
TC1101746	SNORD6	---	small nucleolar RNA, C/D box 6 (SNORD	2.26E-09	3	6.10	5.09	5.06	5.26	5.52	5.80	5.79	5.78
TC0300203	SNRK	54861	SNF related kinase	1.74E-07	3	7.71	7.34	7.26	7.31	7.29	7.55	7.47	7.69
TC0900491	SNX30	401548	sorting nexin family member 30 /// Sor	1.18E-09	3	5.32	4.87	4.84	5.04	4.98	5.09	5.17	5.20
TC1500302	SORD	6652	sorbitol dehydrogenase	4.94E-11	3	5.93	5.63	5.63	5.96	5.78	6.09	6.24	6.30
TC0202379	SP110	3431	SP110 nuclear body protein /// Sp110 r	1.03E-09	3	9.44	9.06	9.01	8.93	8.72	9.16	9.36	9.44
TC0201158	SP140	11262	SP140 nuclear body protein /// Nuclear	1.68E-11	3	7.22	7.16	6.22	6.37	6.22	6.99	7.36	7.65
TC0800465	SPAG1	6674	sperm associated antigen 1	2.63E-05	3	3.76	3.63	3.43	3.76	3.95	3.87	3.99	3.93
TC0200155	SPAST	6683	spastin	0.000472	3	7.60	7.57	7.78	7.75	7.62	7.80	7.84	7.92
TC0102239	SPATA6	54558	spermatogenesis associated 6 /// Sperr	2.37E-05	3	4.69	4.15	4.37	4.48	4.13	4.30	4.55	4.71
TC1700229	SPECC1	92521	sperm antigen with calponin homology	3.04E-17	3	5.94	5.17	5.00	5.33	5.15	5.36	5.60	5.78
TC1701507	SPOP	8405	speckle-type POZ protein	2.77E-08	3	7.29	6.88	6.98	7.16	7.00	7.22	7.25	7.39
TC0500777	SQSTM1	8878	sequestosome 1	9.30E-11	3	6.20	5.73	5.61	5.98	5.97	6.11	6.13	6.23
TC0300986	SRGAP3	9901	SLIT-ROBO Rho GTPase activating prote	1.20E-07	3	3.81	3.61	3.66	3.77	3.66	3.81	3.87	3.92
TC0100267	SRRM1	10250	serine/arginine repetitive matrix 1 /// S	9.89E-07	3	7.39	7.07	6.98	7.08	7.03	7.16	7.39	7.35
TC2000486	SRXN1 /// SCRT	140809 //	sulfiredoxin 1 homolog (S. cerevisiae) /	4.23E-06	3	5.27	4.97	5.15	5.30	5.29	5.39	5.33	5.32
TC0300194	SS18L2	51188	synovial sarcoma translocation gene or	1.53E-11	3	6.36	6.02	6.30	6.55	6.50	6.65	6.77	6.83
TC0501116	SSBP2	23635	single-stranded DNA binding protein 2	1.91E-22	3	5.75	4.70	4.40	4.98	4.92	5.24	5.33	5.58
TC0102279	SSBP3	23648	single stranded DNA binding protein 3 ,	1.60E-09	3	5.28	5.19	5.15	5.30	5.32	5.38	5.46	5.49
TC1200206	SSPN	8082	sarcospan (Kras oncogene-associated g	6.39E-13	3	4.10	3.80	3.79	3.71	3.65	4.12	4.17	4.37
TC2200689	ST13	731047 //	suppression of tumorigenicity 13 (color	9.01E-08	3	8.14	7.98	7.81	8.22	8.32	8.44	8.65	8.41
TC0801265	ST3GAL1	6482	ST3 beta-galactoside alpha-2,3-sialyltra	2.83E-10	3	5.85	5.80	5.34	5.72	5.65	5.89	5.90	5.88
TC0300436	ST3GAL6	10402	ST3 beta-galactoside alpha-2,3-sialyltra	6.83E-18	3	6.59	5.47	6.26	6.33	6.22	6.61	6.65	6.80

TC0501182	ST8SIA4	7903	ST8 alpha-N-acetyl-neuraminide alpha-	7.78E-09	3	9.21	8.69	8.87	8.82	8.60	9.07	9.01	9.20
TC0202007	STAM2	10254	signal transducing adaptor molecule (S	0.000959	3	7.50	7.46	7.52	7.47	7.28	7.57	7.61	7.67
TC0200348	STAMBP	10617	STAM binding protein	4.84E-05	3	5.64	5.40	5.41	5.53	5.52	5.65	5.72	5.71
TC0400267	STAP1	26228	signal transducing adaptor family mem	4.78E-09	3	3.24	3.13	3.34	3.55	3.28	3.66	4.11	4.12
TC1501165	STARD5	80765	StAR-related lipid transfer (START) dom	8.83E-14	3	5.67	5.00	5.08	5.29	5.37	5.38	5.47	5.41
TC0202181	STAT1	6772	signal transducer and activator of trans	2.07E-09	3	8.54	8.17	7.74	8.07	7.83	8.54	8.67	9.02
TC0400146	STIM2	57620	stromal interaction molecule 2 /// Stro	3.71E-05	3	5.70	5.72	5.60	5.51	5.22	5.48	5.82	5.80
TC0900890	STOML2	30968	stomatin (EPB72)-like 2	0.000798	3	4.74	4.70	4.60	4.69	4.83	4.79	4.86	4.72
TC1901222	STX10	8677	syntaxin 10 /// Syntaxin-10 (Syn10). [Sc	2.66E-06	3	6.90	6.40	6.56	6.91	6.85	6.77	6.73	6.72
TC0900436	STX17	55014	syntaxin 17	0.000159	3	4.52	4.90	4.57	4.68	4.55	4.79	4.93	5.03
TC1200738	SUDS3	64426	suppressor of defective silencing 3 hom	0.000246	3	5.86	5.71	5.50	5.73	5.72	5.88	5.92	5.83
TC1400685	SUPT16H	11198	suppressor of Ty 16 homolog (S. cerevis	2.86E-13	3	5.86	5.42	5.42	5.86	5.85	5.99	6.20	6.06
TC1900522	SUPT5H	6829	suppressor of Ty 5 homolog (S. cerevisi	0.000182	3	6.10	5.96	5.85	6.01	5.98	6.02	6.10	6.14
TC1000302	SUPV3L1	6832	suppressor of var1, 3-like 1 (S. cerevisia	0.000174	3	3.89	3.74	3.74	3.83	3.92	3.85	3.99	3.93
TC1700349	SUZ12	23512	suppressor of zeste 12 homolog (Droso	1.26E-11	3	7.10	7.07	6.97	7.18	7.28	7.46	7.53	7.46
TC0101999	SYF2	25949	SYF2 homolog, RNA splicing factor (S. c	0.000106	3	9.80	9.81	9.76	9.85	9.77	9.93	9.94	10.02
TC1700377	TAF15	8148	TAF15 RNA polymerase II, TATA box bir	1.49E-07	3	7.80	7.55	7.25	7.62	7.62	7.71	7.97	7.84
TC1000045	TAF3	83860	TAF3 RNA polymerase II, TATA box binc	4.97E-09	3	5.47	5.23	5.15	5.29	5.35	5.43	5.63	5.47
TC1000555	TAF5	6877	TAF5 RNA polymerase II, TATA box binc	1.13E-09	3	4.11	3.90	3.90	4.17	4.21	4.28	4.39	4.37
TC0601721	TAGAP	117289	T-cell activation RhoGTPase activating	1.02E-16	3	8.47	7.52	7.31	7.74	7.75	8.33	8.27	8.65
TC0601165	TAP1	6890	transporter 1, ATP-binding cassette, su	1.68E-09	3	7.64	6.79	6.63	6.95	6.94	7.41	7.39	7.45
TC0601163	TAP2	6891	transporter 2, ATP-binding cassette, su	1.86E-10	3	6.62	5.76	5.68	5.94	5.75	6.18	6.27	6.42
TC1200052	TAPBPL /// CD2	55080 ///	TAP binding protein-like /// CD27 mole	1.15E-15	3	5.88	5.32	5.31	5.46	5.42	5.59	5.66	5.77
TC0103361	TARBP1	6894	TAR (HIV-1) RNA binding protein 1	0.000528	3	3.00	3.01	2.99	3.03	3.04	3.05	3.20	3.13
TC0101506	TATDN3	128387	TatD DNase domain containing 3	1.28E-11	3	6.49	5.65	5.81	6.24	6.07	6.39	6.66	6.69
TC0400162	TBC1D1	23216	TBC1 (tre-2/USP6, BUB2, cdc16) domai	4.14E-10	3	7.72	7.01	6.98	7.30	7.13	7.35	7.44	7.53
TC0600890	TBP	6908	TATA box binding protein	4.36E-06	3	6.03	5.53	5.52	5.72	5.73	5.82	5.93	5.87
TC2000892	TCFL5	10732	transcription factor-like 5 (basic helix-lo	0.00039	3	4.57	4.30	4.35	4.62	4.57	4.60	4.58	4.61
TC0400929	TEC	7006	tec protein tyrosine kinase	2.72E-11	3	4.91	4.53	4.54	5.03	5.02	5.15	5.39	5.28
TC1601206	TERF2	7014	telomeric repeat binding factor 2	3.87E-06	3	5.57	5.44	5.37	5.57	5.48	5.63	5.75	5.72
TC1000264	TFAM	7019	transcription factor A, mitochondrial //	5.08E-10	3	5.34	5.03	5.07	5.53	5.59	5.71	5.84	5.66
TC0800310	TGS1	96764	trimethylguanosine synthase homolog	3.97E-05	3	5.63	5.60	5.58	5.75	5.66	5.88	6.12	6.01
TC2000414	TH1L	51497	TH1-like (Drosophila)	7.88E-14	3	5.73	5.04	5.06	5.36	5.37	5.45	5.57	5.46
TC0201469	THADA	63892	thyroid adenoma associated /// thyroic	9.46E-12	3	4.38	4.08	3.97	4.10	4.13	4.20	4.31	4.27

TC1600529	THAP11	57215	THAP domain containing 11	8.76E-09	3	4.71	4.27	4.62	4.96	4.90	4.86	5.00	4.93
TC0400324	THAP6	152815	THAP domain containing 6 /// THAP do	8.12E-08	3	4.74	4.39	4.46	4.43	4.40	4.55	4.64	4.70
TC0500305	THBS4	7060	thrombospondin 4	1.00E-06	3	4.07	3.93	3.93	4.09	4.01	4.14	4.16	4.19
TC1700427	THRA	7067	thyroid hormone receptor, alpha (eryth	2.01E-06	3	5.49	5.17	5.07	5.34	5.42	5.45	5.47	5.46
TC1600923	THUMPD1	55623	THUMP domain containing 1	3.79E-07	3	4.67	4.51	4.61	4.84	4.76	4.83	5.07	4.96
TC1100540	TIGD3	220359	tigger transposable element derived 3	4.76E-11	3	7.19	6.21	5.98	6.36	6.40	6.75	6.66	6.87
TC1600795	TIGD7	91151	tigger transposable element derived 7	1.48E-05	3	4.53	4.25	4.20	4.20	4.11	4.41	4.50	4.48
TC1101414	TIMM10	26519	translocase of inner mitochondrial mer	2.50E-09	3	6.09	5.42	5.29	5.96	6.32	6.46	6.45	6.10
TC1000972	TIMM23	10431	translocase of inner mitochondrial mer	9.88E-10	3	5.56	5.10	5.25	5.47	5.51	5.50	5.60	5.48
TC0X00698	TKTL1	8277	transketolase-like 1 /// Transketolase-li	0.000257	3	4.01	3.89	3.85	4.11	3.95	4.09	4.16	4.22
TC0400882	TLR10	81793	toll-like receptor 10	8.26E-07	3	5.12	3.96	4.39	4.88	4.65	4.73	4.75	4.60
TC17r00016	TMEM106A	113277	transmembrane protein 106A	4.74E-05	3	5.50	5.24	5.21	5.27	5.29	5.41	5.40	5.39
TC1101769	TMEM123	114908	transmembrane protein 123 /// Porimi	6.16E-10	3	7.53	7.62	7.25	7.40	7.57	7.97	8.10	8.19
TC1100455	TMEM138	51524	transmembrane protein 138	2.48E-05	3	4.21	4.05	4.05	4.31	4.37	4.26	4.27	4.28
TC0700724	TMEM140	55281	transmembrane protein 140	2.68E-09	3	8.91	8.18	7.82	8.31	8.15	8.59	8.63	8.85
TC0600460	TMEM14A	28978	transmembrane protein 14A	3.02E-07	3	3.91	3.85	3.82	4.03	4.05	4.12	4.24	4.23
TC0401327	TMEM154	201799	transmembrane protein 154 /// Transn	1.90E-13	3	10.02	9.48	9.40	9.61	9.56	9.87	9.85	10.05
TC0400885	TMEM156	80008	transmembrane protein 156	6.91E-08	3	2.75	2.52	2.67	2.78	2.65	2.87	3.18	3.25
TC0X00494	TMEM164	84187	transmembrane protein 164 /// Transn	2.54E-07	3	6.53	6.13	6.16	6.48	6.42	6.61	6.69	6.84
TC0600849	TMEM181	57583	transmembrane protein 181 /// Transn	7.59E-05	3	4.41	4.17	4.28	4.45	4.35	4.39	4.46	4.40
TC2200661	TMEM184B	25829	transmembrane protein 184B	6.18E-05	3	6.37	6.47	5.86	6.24	6.33	6.54	6.31	6.49
TC1201314	TMEM194A ///	23306	transmembrane protein 194A /// Unch	9.24E-08	3	4.19	3.65	3.56	3.76	3.93	4.01	3.97	4.01
TC0102054	TMEM200B	399474	transmembrane protein 200B	3.28E-05	3	5.70	5.42	5.35	5.47	5.51	5.54	5.50	5.66
TC2100312	TMEM50B	757	transmembrane protein 50B	6.63E-11	3	6.58	6.18	6.23	6.46	6.59	6.61	6.60	6.53
TC0800841	TMEM66	51669	transmembrane protein 66	1.58E-06	3	8.82	8.59	8.43	8.55	8.48	8.70	8.70	8.86
TC0100500	TMEM69	51249	transmembrane protein 69 /// Transme	1.52E-06	3	5.12	5.00	5.16	5.30	5.25	5.29	5.51	5.41
TC0103158	TMEM81	388730	transmembrane protein 81	0.000472	3	4.10	3.68	3.83	4.09	4.00	4.07	4.07	4.13
TC1500338	TMOD2	29767	tropomodulin 2 (neuronal)	1.25E-16	3	6.65	5.26	5.28	5.73	5.39	5.86	6.16	6.39
TC0Y00053	TMSB4Y	9087	thymosin beta 4, Y-linked	0.00084	3	3.96	3.70	3.59	3.82	3.82	4.13	4.00	3.96
TC0301755	TNFSF10	8743	tumor necrosis factor (ligand) superfan	3.80E-05	3	10.02	9.75	9.86	9.95	9.73	10.06	10.17	10.23
TC0301750	TNIK	23043	TRAF2 and NCK interacting kinase /// T	2.16E-18	3	5.22	4.51	4.38	5.33	5.07	5.38	5.83	5.74
TC2000765	TOMM34	10953	translocase of outer mitochondrial mer	2.46E-08	3	4.57	4.23	4.27	4.53	4.64	4.61	4.72	4.57
TC2000269	TOP1	7150	topoisomerase (DNA) I	4.78E-06	3	7.83	7.92	7.65	7.65	7.49	7.79	7.96	7.98
TC2000290	TOX2	84969	TOX high mobility group box family me	0.000387	3	4.51	4.38	4.37	4.51	4.47	4.53	4.50	4.58

TC1300261	TPP2	7174	tripeptidyl peptidase II /// Tripeptidyl-p	3.73E-08	3	4.53	4.15	4.03	4.46	4.46	4.55	4.66	4.57
TC1400600	TRAF3	7187	TNF receptor-associated factor 3	5.27E-13	3	5.49	5.10	4.96	5.80	5.72	5.71	5.80	5.65
TC0601532	TRAF3IP2	10758	TRAF3 interacting protein 2 /// Adapte	3.46E-15	3	3.90	3.79	3.72	3.73	3.76	3.93	4.02	3.99
TC0202226	TRAK2	66008	trafficking protein, kinesin binding 2	6.51E-05	3	5.82	5.17	5.32	5.62	5.54	5.56	5.69	5.61
TC0601329	TRAM2	9697	translocation associated membrane pr	3.16E-07	3	4.38	4.18	4.10	4.20	4.32	4.43	4.46	4.41
TC1600668	TRAPPC2L	51693	trafficking protein particle complex 2-li	0.000273	3	4.71	4.69	4.53	4.63	4.80	4.79	4.82	4.74
TC0601250	TREM1	54210	triggering receptor expressed on myelc	6.60E-05	3	10.25	10.47	9.89	10.13	10.06	10.38	10.31	10.50
TC0601266	TRERF1	55809	transcriptional regulating factor 1 /// T	2.45E-24	3	6.46	5.02	5.10	5.79	5.59	5.79	6.10	6.06
TC1101104	TRIM21	6737	tripartite motif-containing 21	1.23E-05	3	7.81	7.51	7.62	7.96	7.83	8.16	8.13	8.29
TC0700737	TRIM24	8805	tripartite motif-containing 24 /// Trans	4.07E-25	3	6.43	5.58	5.45	5.93	6.02	6.70	6.70	6.67
TC0601094	TRIM26	7726	tripartite motif-containing 26 /// Tripar	0.000407	3	5.29	5.21	5.18	5.29	5.30	5.34	5.42	5.46
TC0102564	TRIM33	51592	tripartite motif-containing 33	2.49E-09	3	7.90	7.41	7.38	7.52	7.40	7.64	7.76	7.77
TC0600140	TRIM38	10475	tripartite motif-containing 38	7.87E-11	3	7.68	7.50	7.12	7.20	7.02	7.55	7.64	7.78
TC1101138	TRIM5	85363	tripartite motif-containing 5 /// Tripart	6.14E-05	3	5.12	5.20	5.01	5.22	5.06	5.30	5.52	5.61
TC1500403	TRIP4	9325	thyroid hormone receptor interactor 4	0.000181	3	5.92	5.66	5.96	6.02	5.80	5.84	5.94	5.94
TC1101766	TRPC6	731423 //	transient receptor potential cation cha	9.86E-05	3	2.80	2.68	2.73	2.82	2.78	2.82	2.90	3.02
TC1500953	TRPM7	54822	transient receptor potential cation cha	1.05E-10	3	4.40	3.94	3.98	4.43	4.48	4.49	4.67	4.47
TC1200463	TSFM	10102	Ts translation elongation factor, mitoch	1.69E-06	3	5.44	5.20	5.20	5.23	5.29	5.36	5.36	5.33
TC1700152	TTC19	54902	tetratricopeptide repeat domain 19	9.38E-06	3	4.61	4.36	4.29	4.47	4.52	4.54	4.55	4.44
TC0202066	TTC21B	79809	tetratricopeptide repeat domain 21B	8.53E-14	3	3.32	2.91	2.90	2.99	2.99	3.05	3.19	3.21
TC1400383	TTLL5	23093	tubulin tyrosine ligase-like family, mem	3.51E-16	3	4.92	4.16	4.20	4.40	4.39	4.49	4.69	4.61
TC0601002	TTRAP	51567	TRAF and TNF receptor associated prot	2.13E-08	3	8.28	7.84	8.03	8.44	8.41	8.57	8.37	8.40
TC1500275	TUBGCP4	27229	tubulin, gamma complex associated pr	1.00E-12	3	4.31	3.78	3.72	3.87	3.98	4.04	4.26	4.23
TC0400926	TXK	7294	TXK tyrosine kinase	1.09E-07	3	3.82	3.37	3.36	3.61	3.60	3.67	3.81	3.69
TC0601647	TXLNB	167838	taxilin beta /// Beta-taxilin (Muscle-der	1.60E-13	3	3.74	3.31	3.39	3.34	3.28	3.58	3.76	3.85
TC0901194	TXNDC4	727931 //	thioredoxin domain containing 4 (endo	3.45E-06	3	7.04	7.33	7.31	7.18	7.00	7.27	7.40	7.49
TC0700351	TYW1	55253	tRNA-yW synthesizing protein 1 homol	1.91E-05	3	3.97	3.89	3.83	4.07	4.09	4.10	4.23	4.14
TC1900323	UBA52	7311	ubiquitin A-52 residue ribosomal prote	9.02E-12	3	7.98	7.74	7.67	7.92	7.92	8.00	8.04	8.01
TC1101415	UBE2L6	9246	ubiquitin-conjugating enzyme E2L 6	8.07E-08	3	6.55	6.36	6.07	6.48	6.34	6.76	6.81	7.13
TC0301087	UBP1	7342	upstream binding protein 1 (LBP-1a) //,	0.000128	3	5.33	5.11	5.26	5.46	5.40	5.34	5.40	5.29
TC1701421	UBTF	7343	upstream binding transcription factor,	4.76E-06	3	6.68	6.36	6.39	6.67	6.71	6.66	6.74	6.71
TC0900048	UHRF2	115426	ubiquitin-like, containing PHD and RIN(	3.37E-13	3	4.82	4.03	4.04	4.42	4.50	4.53	4.75	4.68
TC1200757	UNC119B	84747	unc-119 homolog B (C. elegans)	2.79E-07	3	4.66	4.39	4.25	4.48	4.58	4.64	4.78	4.66
TC2200020	USP18	11274	ubiquitin specific peptidase 18	0.000257	3	3.22	3.01	2.97	2.97	3.01	3.19	3.32	3.25

TC0102285	USP24	---	Ubiquitin carboxyl-terminal hydrolase	8.37E-09	3	5.75	5.02	5.10	5.32	5.20	5.35	5.57	5.47
TC2100019	USP25	29761	ubiquitin specific peptidase 25 /// Ubiq	1.30E-05	3	7.15	6.92	7.00	7.05	6.86	7.14	7.31	7.33
TC1101846	USP28	57646	ubiquitin specific peptidase 28 /// Ubiq	9.15E-10	3	3.66	3.48	3.43	3.62	3.69	3.69	3.80	3.74
TC0200415	USP39	10713	ubiquitin specific peptidase 39	0.000536	3	5.94	5.49	5.68	5.86	5.82	5.79	5.90	5.87
TC0700053	USP42	84132	ubiquitin specific peptidase 42	6.43E-06	3	4.96	4.97	4.96	5.08	4.95	5.09	5.24	5.27
TC1300064	USPL1	10208	ubiquitin specific peptidase like 1	2.70E-17	3	5.47	4.44	4.35	4.53	4.62	4.86	5.17	5.32
TC0800511	UTP23 /// C8or	84294	UTP23, small subunit (SSU) processome	8.47E-06	3	3.91	3.75	3.80	3.82	3.77	3.89	3.91	3.98
TC1100679	UVRAG	7405	UV radiation resistance associated gen	1.03E-05	3	6.43	6.22	6.10	6.22	6.17	6.34	6.53	6.49
TC0600418	VEGFA	7422	vascular endothelial growth factor A //	1.48E-08	3	4.80	4.67	4.50	4.76	4.95	4.95	4.90	4.86
TC1701545	VEZF1	7716	vascular endothelial zinc finger 1	7.18E-06	3	8.15	8.08	8.06	8.23	8.10	8.30	8.32	8.41
TC0900013	VLDLR	7436	very low density lipoprotein receptor /	7.91E-05	3	3.58	3.46	3.46	3.89	3.80	3.80	4.02	3.91
TC1501012	VPS13C	54832	vacuolar protein sorting 13 homolog C	8.43E-05	3	4.94	4.66	4.64	4.99	4.90	5.01	5.24	5.10
TC1401124	WARS	7453	tryptophanyl-tRNA synthetase	4.40E-05	3	6.49	6.42	6.00	6.24	6.11	6.48	6.71	6.92
TC0202355	WDFY1	57590	WD repeat and FYVE domain containin	3.27E-10	3	5.75	5.33	5.21	5.37	5.41	5.66	5.77	6.01
TC0300167	WDR48	57599	WD repeat domain 48	1.57E-05	3	6.41	6.18	6.03	6.14	6.01	6.23	6.30	6.39
TC0301900	WDR53	348793	WD repeat domain 53	3.11E-06	3	5.60	5.18	5.28	5.37	5.51	5.45	5.55	5.47
TC0301495	WDR5B	54554	WD repeat domain 5B	0.0005	3	4.58	4.15	4.26	4.41	4.37	4.46	4.43	4.36
TC0800885	WHSC1L1 /// N	54904	Wolf-Hirschhorn syndrome candidate 1	6.77E-17	3	8.18	7.34	7.19	7.59	7.67	7.76	7.78	7.85
TC1700076	XAF1 /// NP_9	54739	XIAP associated factor 1 /// XIAP associ	4.19E-11	3	6.13	5.01	4.78	4.86	4.64	5.57	6.22	6.57
TC2200305	XPNPEP3	63929	X-prolyl aminopeptidase (aminopeptid	1.12E-07	3	4.78	4.52	4.56	4.63	4.65	4.64	4.80	4.72
TC0800128	XPO7	23039	exportin 7	1.89E-13	3	5.88	5.04	5.01	5.50	5.52	5.53	5.60	5.60
TC0100451	YBX1	4904	Y box binding protein 1 /// Nuclease se	6.95E-08	3	9.18	8.97	8.88	9.27	9.41	9.44	9.53	9.35
TC0300844	YEATS2	55689	YEATS domain containing 2 /// YEATS d	1.01E-07	3	4.71	4.51	4.52	4.84	4.75	4.70	4.73	4.77
TC1400372	YLPM1	---	YLP motif-containing protein 1 (Nuclea	0.000669	3	6.13	5.84	5.77	6.07	6.04	6.07	6.30	6.16
TC1400498	YY1	7528	YY1 transcription factor	3.22E-17	3	8.14	7.90	7.87	8.41	8.41	8.41	8.49	8.45
TC2000859	ZBP1	81030	Z-DNA binding protein 1 /// Z-DNA-bin	7.81E-11	3	5.94	5.30	5.02	5.23	5.08	5.62	5.87	5.99
TC0301407	ZBTB11	27107	zinc finger and BTB domain containing	7.64E-10	3	5.28	4.97	5.17	5.52	5.42	5.43	5.52	5.47
TC0601515	ZBTB24	9841	zinc finger and BTB domain containing	4.39E-09	3	4.92	4.66	4.53	4.83	4.88	4.91	5.08	4.99
TC0100080	ZBTB48	3104	zinc finger and BTB domain containing	0.0003	3	5.47	5.26	5.23	5.35	5.34	5.42	5.38	5.41
TC1800231	ZCCHC2	54877	zinc finger, CCHC domain containing 2	5.44E-18	3	7.00	5.58	5.36	5.70	5.68	6.48	6.89	7.08
TC0900178	ZCCHC7	84186	zinc finger, CCHC domain containing 7	4.57E-06	3	5.55	5.43	5.50	5.45	5.40	5.56	5.69	5.69
TC1000149	ZEB1	6935	zinc finger E-box binding homeobox 1 /	0.000218	3	6.05	5.94	5.81	5.88	5.79	6.03	6.08	6.11
TC0901041	ZFAND5	7763	zinc finger, AN1-type domain 5	5.15E-13	3	7.55	7.17	7.33	7.64	7.56	7.56	7.64	7.61
TC0201468	ZFP36L2	678	zinc finger protein 36, C3H type-like 2	2.27E-23	3	6.35	5.04	4.96	5.32	5.45	5.84	5.97	6.09

TC0601063	ZKSCAN4	387032	zinc finger with KRAB and SCAN domai	4.58E-14	3	4.17	3.86	3.93	4.13	4.14	4.36	4.39	4.46
TC1000002	ZMYND11	10771	zinc finger, MYND domain containing 1	1.92E-09	3	4.96	4.58	4.69	5.18	5.01	5.19	5.45	5.34
TC2000806	ZMYND8	23613	zinc finger, MYND-type containing 8 //	8.47E-09	3	5.45	4.89	5.03	5.26	5.23	5.22	5.40	5.25
TC1900212	ZNF136	7695	zinc finger protein 136	2.58E-13	3	5.68	5.39	5.27	5.29	5.06	5.43	5.73	5.78
TC1200853	ZNF140	7699	zinc finger protein 140	8.64E-05	3	4.18	4.27	4.24	4.10	4.16	4.22	4.36	4.33
TC0600199	ZNF192	7745	zinc finger protein 192	7.44E-09	3	3.83	3.77	3.73	3.82	3.83	3.93	4.14	4.06
TC0600202	ZNF193	7746	zinc finger protein 193	0.000145	3	3.77	3.71	3.61	3.60	3.66	3.77	3.96	3.89
TC0200477	ZNF2	7549	zinc finger protein 2 /// Zinc finger prot	1.19E-05	3	4.26	3.97	4.31	4.26	4.23	4.15	4.25	4.26
TC1900207	ZNF20	7568	zinc finger protein 20	8.47E-16	3	6.46	5.72	5.36	5.68	5.45	6.00	6.21	6.55
TC0700859	ZNF212	7988	zinc finger protein 212	1.01E-07	3	6.07	5.74	5.80	5.76	5.77	5.90	6.01	5.95
TC1900603	ZNF224	7767	zinc finger protein 224 /// Zinc finger p	3.75E-05	3	4.35	4.31	4.22	4.20	4.16	4.34	4.48	4.46
TC1800270	ZNF236	7776	zinc finger protein 236 /// Zinc finger p	0.000646	3	4.62	4.51	4.56	4.66	4.63	4.60	4.66	4.59
TC1800415	ZNF24	7572	zinc finger protein 24	5.99E-05	3	6.62	6.50	6.52	6.66	6.45	6.68	6.71	6.82
TC1900369	ZNF253	---	zinc finger protein 253 [Source:RefSeq_	0.000325	3	6.04	5.83	5.84	5.85	5.86	5.94	6.02	6.02
TC1101856	ZNF259	8882	zinc finger protein 259	1.22E-05	3	4.56	4.41	4.29	4.67	4.74	4.75	4.85	4.79
TC2100364	ZNF295	49854	zinc finger protein 295	7.30E-06	3	4.49	4.52	4.35	4.51	4.44	4.57	4.64	4.63
TC1901772	ZNF320	---	zinc finger protein 320 [Source:RefSeq_	7.44E-06	3	8.87	8.30	8.43	8.61	8.48	8.74	8.83	8.85
TC1901404	ZNF324B /// ZN	388569 //	zinc finger protein 324B /// zinc finger	0.000272	3	4.51	4.35	4.31	4.52	4.38	4.41	4.54	4.57
TC1901357	ZNF429	353088	zinc finger protein 429	0.000259	3	3.87	3.71	3.60	3.67	3.74	3.82	3.88	3.88
TC1900353	ZNF430	80264	zinc finger protein 430	0.000124	3	5.92	5.80	5.76	5.71	5.60	5.85	5.95	5.97
TC1901441	ZNF461	92283	zinc finger protein 461	0.000874	3	3.65	3.54	3.56	3.46	3.59	3.61	3.71	3.73
TC1901770	ZNF468 /// ZN	90333 ///	zinc finger protein 468 /// zinc finger p	4.85E-05	3	4.57	4.33	4.46	4.58	4.51	4.49	4.63	4.63
TC1900776	ZNF480	147657	zinc finger protein 480	7.38E-07	3	3.96	3.77	3.71	4.09	4.02	4.16	4.45	4.24
TC1900348	ZNF486	---	Zinc finger protein 486. [Source:Unipro	0.000872	3	5.26	5.22	5.44	5.23	4.99	5.49	5.56	5.68
TC0700525	ZNF498	221785	zinc finger protein 498 /// zinc finger a	0.000412	3	4.92	4.72	4.74	4.81	4.77	4.79	4.88	4.89
TC1900400	ZNF507	22847	zinc finger protein 507 /// Zinc finger p	7.97E-11	3	5.07	4.64	4.82	5.01	5.07	5.15	5.33	5.17
TC0400046	ZNF509	166793	zinc finger protein 509 /// Zinc finger p	7.14E-07	3	4.26	3.95	3.98	4.08	3.92	4.15	4.31	4.28
TC0400819	ZNF518B	85460	zinc finger protein 518B	2.12E-06	3	5.26	5.19	5.08	5.08	4.89	5.10	5.22	5.38
TC1900778	ZNF528 /// Q6I	---	Zinc finger protein 528. [Source:Unipro	0.000336	3	4.37	4.17	4.21	4.35	4.30	4.26	4.50	4.44
TC1900063	ZNF555	148254	zinc finger protein 555 /// Zinc finger p	1.83E-05	3	3.09	3.04	2.99	3.12	3.12	3.20	3.23	3.25
TC1900124	ZNF557	79230	zinc finger protein 557	3.90E-06	3	5.47	5.05	5.04	5.19	5.05	5.25	5.37	5.27
TC1901446	ZNF585A	199704	zinc finger protein 585A /// Zinc finger	1.30E-05	3	5.13	5.06	5.24	5.04	4.82	5.08	5.31	5.32
TC1701501	ZNF652	22834	zinc finger protein 652	3.27E-08	3	7.98	7.30	7.28	7.57	7.35	7.69	7.75	7.93
TC1900785	ZNF701	55762	zinc finger protein 701	3.62E-07	3	5.77	5.44	5.48	5.58	5.42	5.66	5.68	5.75

TC0400746	ZNF721	170960	zinc finger protein 721	4.40E-05	3	4.26	4.14	4.16	4.19	4.10	4.24	4.36	4.36
TC1200365	ZNF740	283337	zinc finger protein 740	8.46E-06	3	5.53	5.18	5.45	5.41	5.21	5.37	5.58	5.51
TC1900775	ZNF766	90321	zinc finger protein 766	6.15E-11	3	5.60	5.29	5.28	5.39	5.32	5.40	5.52	5.56
TC1901188	ZNF823	55552	zinc finger protein 823	3.90E-05	3	3.98	3.79	3.93	4.13	4.00	4.13	4.33	4.26
TC1700366	ZNF830	91603	zinc finger protein 830	9.97E-05	3	5.68	5.39	5.39	5.54	5.65	5.71	5.92	5.74
TC1900347	ZNF90	731498	Zinc finger protein 90 (Zinc finger prote	0.000793	3	3.32	3.25	3.32	3.21	3.25	3.35	3.35	3.41
TC0700328	ZNF92	168374	zinc finger protein 92 /// Zinc finger pr	2.87E-05	3	4.48	4.58	4.54	4.46	4.53	4.63	4.80	4.86
TC1900346	ZNF93 /// ZNF	81931	zinc finger protein 93 /// Zinc finger pr	3.81E-06	3	5.48	5.63	5.65	5.43	5.39	5.63	5.75	5.79
TC2000817	ZNFX1	57169	zinc finger, NFX1-type containing 1 ///	1.32E-06	3	6.98	7.15	6.72	6.99	6.95	7.14	7.20	7.25
TC1700387	ZNHIT3	9326	zinc finger, HIT type 3	1.91E-07	3	5.07	4.78	4.83	4.90	4.98	5.03	5.18	5.17
TC0600198	ZSCAN16	80345	zinc finger and SCAN domain containin	3.29E-08	3	5.04	4.67	4.66	4.67	4.56	4.75	4.96	5.01
TC1500888	ZSCAN29	146050	zinc finger and SCAN domain containin	2.19E-12	3	4.00	3.40	3.33	3.69	3.51	3.65	4.05	3.96
TC0301093		---		1.24E-17	3	8.34	6.27	5.86	6.37	6.41	7.19	7.36	7.80
TC1400358		---		2.99E-17	3	7.59	6.16	6.41	7.21	7.03	7.29	7.48	7.54
TC1400697		---		2.74E-15	3	3.33	2.69	2.62	2.81	2.66	2.92	3.15	3.27
TC1300135		---		4.05E-15	3	4.67	3.04	3.01	3.93	3.51	4.06	4.59	4.75
TC0900977		---		9.56E-15	3	8.02	6.43	6.57	6.73	6.74	7.34	7.45	7.51
TC0600852		---		1.32E-14	3	5.66	4.91	4.86	5.16	5.19	5.66	5.78	5.89
TC0X00357		---		2.19E-14	3	5.95	4.93	4.91	5.15	5.11	5.44	5.69	5.59
TC0601034		---		6.51E-14	3	6.20	4.72	4.92	5.42	5.27	5.56	5.77	5.76
TC1100079		---		7.12E-14	3	6.89	4.87	4.56	5.20	5.32	6.03	6.14	6.50
TC0901016		---		8.69E-14	3	5.61	4.13	4.31	4.88	4.37	4.85	5.12	5.15
TC1100650		---		1.32E-13	3	7.93	5.89	5.65	6.40	6.29	6.87	7.25	7.34
TC1700372		---		2.46E-13	3	6.18	5.45	5.41	5.88	5.99	6.21	6.33	6.38
TC0400274		---		3.37E-13	3	6.79	6.36	6.16	7.00	6.69	7.49	8.11	8.45
TC0600321		---		4.14E-13	3	7.05	6.75	6.75	7.20	7.18	7.39	7.40	7.44
TC1001207		---		6.25E-13	3	4.93	3.96	4.32	5.29	4.81	5.34	5.64	5.63
TC1500913		---		7.60E-13	3	5.19	4.79	4.81	5.12	4.94	5.27	5.37	5.41
TC0301556		---		1.04E-12	3	8.48	7.55	7.00	7.31	7.43	8.15	8.14	8.40
TC0900585		---		1.28E-12	3	4.55	4.13	3.92	4.35	4.41	4.61	4.86	4.87
TC0401326		---		1.52E-12	3	5.49	3.77	3.12	3.91	3.94	4.60	4.87	4.64
TC1401104		---		2.89E-12	3	4.73	3.94	4.16	4.41	4.76	4.85	4.89	4.57
TC1900631		---		3.45E-12	3	6.58	6.18	6.22	6.47	6.43	6.69	6.83	6.79
TC0301342		---		4.83E-12	3	5.61	5.06	4.88	5.00	4.93	5.32	5.39	5.68

TC1200567	---	1.01E-11	3	5.66	5.45	5.43	5.63	5.49	6.10	6.13	6.22
TC1200276	---	2.95E-11	3	6.36	5.73	5.58	6.13	5.97	6.34	6.44	6.44
TC0102617	---	1.24E-10	3	5.60	5.01	4.96	5.12	5.08	5.35	5.38	5.51
TC0400279	---	5.56E-10	3	4.10	2.02	2.32	3.10	2.50	3.01	3.56	3.45
TC1400645	---	6.16E-10	3	5.45	5.39	5.37	5.43	5.41	5.67	6.06	5.87
TC0200660	---	8.66E-10	3	5.84	5.25	5.25	5.00	5.38	6.08	6.22	5.96
TC0400272	---	1.10E-09	3	7.49	7.58	7.26	7.41	7.41	7.99	8.17	8.31
TC1600307	---	1.16E-09	3	5.78	4.52	4.55	5.05	4.97	5.29	5.36	5.42
TC0200811	---	1.41E-09	3	8.48	7.55	7.46	7.97	8.07	8.15	8.12	8.21
TC0301713	---	1.44E-09	3	9.44	9.25	8.91	9.50	9.65	9.77	9.87	9.65
TC1701257	730422	1.64E-09	3	5.55	5.51	5.22	5.84	5.76	6.01	6.36	6.54
TC1700967	---	1.68E-09	3	4.98	4.62	4.56	4.78	4.71	4.82	4.92	4.81
TC1701577	---	1.81E-09	3	3.41	3.11	3.17	3.44	3.27	3.65	3.80	3.70
TC0600296	---	2.21E-09	3	7.69	7.42	7.40	7.66	7.57	7.91	7.97	8.04
TC01r00009	---	2.41E-09	3	4.52	3.96	3.96	4.26	4.14	4.42	4.67	4.53
TC1901871	---	2.42E-09	3	6.80	6.30	6.50	6.99	6.90	6.89	6.99	7.03
TC0700322	---	3.09E-09	3	4.91	4.31	4.36	4.47	4.49	4.71	4.95	4.80
TC0200422	---	3.26E-09	3	6.60	6.01	5.74	6.14	6.14	6.31	6.50	6.53
TC1001266	---	3.80E-09	3	5.57	5.19	5.29	5.80	5.61	6.32	6.34	6.51
TC0700586	---	4.41E-09	3	5.01	4.35	4.38	5.23	5.39	5.44	5.55	5.36
TC0100994	---	5.06E-09	3	7.34	6.61	6.79	6.81	6.74	7.01	7.13	7.15
TC0100989	---	6.75E-09	3	4.76	4.21	4.14	4.39	4.37	4.60	4.72	4.59
TC0700587	---	6.98E-09	3	8.16	7.38	7.42	8.35	8.44	8.57	8.60	8.48
TC0900278	---	7.31E-09	3	5.49	4.46	4.35	4.54	4.61	5.19	5.11	5.03
TC0700332	---	8.47E-09	3	4.09	3.71	3.69	3.80	3.87	4.05	4.17	4.09
TC0500360	---	1.04E-08	3	4.83	4.47	4.16	4.46	4.44	4.81	5.18	5.37
TC0102620	---	1.36E-08	3	6.82	6.48	6.60	7.03	6.89	7.03	7.06	7.05
TC0100987	---	1.65E-08	3	6.81	6.39	6.52	6.81	6.78	6.92	6.89	6.97
TC0900279	---	2.23E-08	3	4.08	3.43	3.25	3.59	3.81	3.93	3.81	3.93
TC2100094	---	2.36E-08	3	3.08	2.82	2.51	2.48	2.67	2.83	2.99	3.06
TC0101917	---	2.95E-08	3	4.01	3.63	3.62	3.85	3.89	3.97	4.18	4.02
TC1500227	---	3.47E-08	3	6.85	6.86	6.55	6.84	6.74	7.28	7.36	7.35
TC0601057	---	4.23E-08	3	6.72	6.02	5.76	5.73	5.90	6.57	6.26	6.59
TC0900605	---	7.18E-08	3	5.02	4.61	4.35	5.12	5.16	5.01	5.04	5.21

TC1101960	---	9.14E-08	3	5.70	5.25	5.05	5.37	5.41	5.47	5.51	5.52
TC1701123	---	1.01E-07	3	4.18	2.77	2.64	3.36	2.89	3.50	3.96	3.89
TC0101927	---	1.06E-07	3	4.91	4.76	4.89	5.09	5.03	5.17	5.48	5.37
TC0200714	---	1.94E-07	3	2.84	2.39	2.50	2.95	2.71	2.98	3.14	3.06
TC0901367	---	3.40E-07	3	5.54	5.43	5.31	5.31	5.20	5.51	5.61	5.72
TC0300686	---	8.83E-07	3	6.80	6.38	6.24	6.39	6.33	6.64	6.65	6.81
TC0300269	---	8.95E-07	3	7.15	5.72	5.83	6.36	6.62	6.74	6.86	6.87
TC1700933	---	9.94E-07	3	4.81	4.42	4.44	4.76	4.86	4.94	5.07	5.05
TC0301425	---	1.27E-06	3	4.90	4.16	4.06	4.24	4.26	4.32	4.84	4.49
TC0900344	---	2.51E-06	3	4.81	4.51	4.36	4.47	4.49	4.56	4.78	4.64
TC1400917	---	3.09E-06	3	4.11	3.39	3.58	3.80	3.77	3.82	4.03	3.97
TC0600049	---	3.34E-06	3	4.25	3.68	3.65	3.87	4.02	4.17	4.23	4.11
TC1701256	---	3.38E-06	3	6.67	6.50	6.24	6.79	6.48	6.78	7.09	7.39
TC0900290	---	4.14E-06	3	4.09	3.74	3.79	4.00	3.94	4.01	4.18	4.18
TC0801104	---	4.79E-06	3	6.35	5.55	5.62	5.89	5.91	6.18	6.23	6.08
TC2200144	---	5.99E-06	3	3.76	3.37	3.54	3.92	4.02	4.16	4.40	4.08
TC0400757	---	6.31E-06	3	2.78	2.17	2.19	2.33	2.33	2.57	2.61	2.79
TC0600967	---	6.31E-06	3	2.86	2.61	2.52	2.93	2.95	3.27	3.76	3.49
TC1100447	---	6.73E-06	3	4.50	4.01	4.10	4.54	4.48	4.73	4.95	4.96
TC1700156	---	7.02E-06	3	3.64	3.15	3.32	3.66	3.47	3.60	3.84	3.85
TC0100710	---	8.64E-06	3	4.09	3.80	3.74	3.89	3.67	4.30	4.62	4.88
TC0900991	---	8.81E-06	3	4.84	4.63	4.80	4.80	4.74	4.82	4.96	5.00
TC1400925	---	1.07E-05	3	5.46	5.14	5.13	5.34	5.44	5.41	5.58	5.48
TC0102607	---	1.16E-05	3	6.60	5.92	5.76	5.95	6.05	6.12	6.34	6.39
TC0201742	---	2.02E-05	3	4.26	4.17	3.97	4.15	4.51	4.54	4.63	4.30
TC1100943	---	2.18E-05	3	6.43	5.88	5.79	6.21	6.14	6.42	6.50	6.61
TC0103143	---	2.20E-05	3	4.47	4.68	4.24	4.25	4.69	4.89	4.42	4.78
TC0600828	---	2.26E-05	3	2.80	2.50	2.60	2.81	2.70	2.92	3.09	3.05
TC0100923	---	2.66E-05	3	6.98	7.03	6.83	6.99	6.98	7.53	7.66	8.08
TC0100708	---	3.64E-05	3	3.25	2.60	2.61	2.68	2.51	3.03	3.21	3.28
TC0600320	---	3.65E-05	3	4.94	4.25	4.04	4.07	4.32	4.69	4.71	4.85
TC0301238	---	3.75E-05	3	5.47	4.89	4.82	5.07	4.92	5.27	5.20	5.49
TC0X00880	---	4.37E-05	3	3.82	3.19	3.15	3.16	3.12	3.50	3.57	3.68
TC0100950	---	5.34E-05	3	3.33	3.07	3.07	3.25	3.19	3.38	3.42	3.43

TC0201467	---	5.44E-05	3	4.36	4.21	3.97	3.89	4.10	4.25	4.36	4.29
TC1000929	---	5.44E-05	3	4.81	4.27	4.18	4.39	4.39	4.50	4.79	4.56
TC1700013	---	6.26E-05	3	6.51	6.29	6.33	6.49	6.61	6.62	6.73	6.66
TC0101730	---	6.66E-05	3	7.74	7.06	7.18	7.40	7.37	7.67	7.66	7.67
TC1300614	---	7.92E-05	3	3.93	3.69	3.68	3.88	3.73	3.85	3.85	4.32
TC1101707	---	8.56E-05	3	3.65	3.66	3.31	3.42	3.49	3.62	3.67	3.67
TC1400628	---	9.87E-05	3	5.06	4.81	4.83	4.83	4.79	5.01	5.10	5.16
TC1800023	---	9.88E-05	3	4.46	4.03	3.90	4.43	4.15	4.41	4.41	4.31
TC0500404	---	0.000101	3	3.63	3.57	3.61	3.66	3.57	3.62	3.81	3.98
TC0X00600	---	0.00011	3	3.67	2.88	2.97	3.08	3.01	3.27	3.40	3.54
TC0800528	---	0.000112	3	3.91	3.53	3.48	3.90	3.78	3.86	4.00	3.79
TC0102690	---	0.000114	3	5.29	4.51	4.24	4.72	4.76	4.92	5.03	4.98
TC0500475	---	0.000116	3	6.43	6.68	5.75	5.92	6.18	6.28	6.53	6.56
TC0400278	---	0.000116	3	2.34	2.06	2.09	2.42	2.36	2.53	2.58	2.54
TC0100100	---	0.000118	3	5.33	5.23	5.09	4.88	5.10	5.17	5.61	5.44
TC0500517	---	0.000131	3	6.68	6.13	5.82	5.92	6.07	6.25	6.56	6.47
TC2000891	---	0.000137	3	6.33	6.39	6.35	6.50	6.42	6.51	6.47	6.74
TC0901014	---	0.000139	3	10.29	10.15	10.37	10.26	10.39	10.63	10.50	10.66
TC1100164	---	0.000183	3	5.09	4.60	4.44	4.62	4.85	4.98	5.22	4.99
TC0100205	---	0.000201	3	4.86	4.40	4.42	4.63	4.68	4.65	4.81	4.59
TC0401040	---	0.000221	3	3.60	3.10	3.11	3.35	3.46	3.72	3.63	3.57
TC0103398	---	0.000226	3	3.46	3.20	3.22	3.42	3.26	3.42	3.64	3.52
TC0401405	---	0.000244	3	5.14	4.74	4.91	5.16	5.08	5.07	5.17	5.01
TC2000678	---	0.000246	3	3.58	3.36	3.14	3.13	2.84	3.19	3.81	3.51
TC0601432	---	0.000249	3	5.87	5.26	5.34	5.59	5.70	5.85	6.01	5.72
TC1100946	---	0.00031	3	3.30	3.07	3.14	3.28	3.44	3.42	3.44	3.52
TC0900606	---	0.000324	3	6.35	5.86	5.24	5.40	5.59	5.99	6.54	6.15
TC1200571	---	0.000338	3	4.80	4.52	4.56	4.59	4.57	4.68	4.77	4.83
TC1701566	---	0.000348	3	3.74	3.77	3.73	3.40	3.58	3.95	4.10	3.85
TC0800921	---	0.00035	3	4.49	4.12	3.82	3.81	4.05	4.51	4.66	4.59
TC0701302	---	0.000354	3	4.05	3.89	3.88	4.02	4.09	4.02	4.15	4.02
TC1500916	---	0.000372	3	3.20	2.30	2.56	2.47	2.66	2.72	3.30	3.09
TC0201766	---	0.000432	3	3.76	3.63	3.53	3.54	3.88	3.86	3.89	3.77
TC1300491	---	0.000443	3	5.39	5.05	5.19	5.38	5.41	5.52	5.45	5.46

TC01r00021		---		0.000487	3	4.39	4.03	4.06	4.24	4.19	4.21	4.35	4.32
TC0700033		641911		0.000488	3	4.80	4.64	4.83	4.81	4.78	4.84	4.90	4.92
TC1000143		---		0.000496	3	3.24	2.83	2.79	2.88	3.49	3.36	3.27	3.14
TC0900245		---		0.000525	3	7.70	7.49	7.90	7.79	7.62	8.13	8.09	8.06
TC0800537		---		0.000526	3	3.34	3.04	2.87	3.14	3.46	3.70	3.67	3.46
TC1500915		---		0.000529	3	3.26	2.61	2.82	2.76	2.84	3.21	3.29	3.04
TC0900002		---		0.000536	3	8.48	8.28	8.19	8.31	8.24	8.45	8.50	8.49
TC1500478		---		0.000539	3	3.55	3.36	3.43	3.42	3.47	3.48	3.58	3.53
TC1100166		---		0.00057	3	6.81	6.33	6.38	6.52	6.56	6.62	6.72	6.56
TC1400067		---		0.000613	3	4.85	4.93	4.90	4.95	4.96	4.99	5.09	5.27
TC0101048		---		0.000628	3	4.42	4.16	4.33	4.31	4.28	4.35	4.47	4.48
TC0102675		---		0.000752	3	5.41	5.38	4.96	5.29	5.49	5.40	5.58	5.37
TC1300110		---		0.000831	3	2.76	2.45	2.41	2.41	2.30	2.64	2.98	3.24
TC0100418		---		0.00084	3	3.78	3.46	3.32	3.56	3.69	3.70	3.84	3.69
TC2100151		---		0.000894	3	5.46	4.28	4.10	4.77	4.88	4.82	5.13	4.94
TC1100077		---		0.000993	3	4.92	4.74	4.59	4.68	4.71	4.98	5.10	4.95
TC0901212	ABCA1	19	ATP-binding cassette, sub-family A (AB	7.19E-07	4	7.07	5.98	5.75	6.26	6.10	6.37	6.62	6.57
TC1900030	ABCA7	10347	ATP-binding cassette, sub-family A (AB	2.88E-26	4	5.69	5.14	5.01	5.06	5.13	5.11	5.13	5.13
TC1000504	ABCC2	1244	ATP-binding cassette, sub-family C (CFT	6.62E-09	4	3.14	2.77	2.81	2.92	2.88	2.81	2.83	2.81
TC0301810	ABCC5	10057	ATP-binding cassette, sub-family C (CFT	1.71E-11	4	5.48	4.72	4.43	4.58	4.66	4.55	4.55	4.54
TC2100150	ABCG1	9619	ATP-binding cassette, sub-family G (WH	4.33E-06	4	4.81	4.38	4.27	4.40	4.33	4.41	4.43	4.49
TC1500606	ABHD2	11057	abhydrolase domain containing 2	0.000661	4	8.48	8.09	8.08	7.94	7.75	7.99	8.09	8.28
TC1800366	ABHD3	171586	abhydrolase domain containing 3	1.87E-16	4	6.65	5.45	5.57	5.64	5.53	5.91	6.02	6.05
TC1700574	ABI3	51225	ABI gene family, member 3	1.78E-09	4	5.52	4.90	4.96	4.95	5.00	5.06	4.96	5.01
TC1200701	ACAD10	80724	acyl-Coenzyme A dehydrogenase famil	2.66E-14	4	4.56	4.12	4.13	4.11	4.10	4.13	4.18	4.20
TC1700084	ACADVL	37	acyl-Coenzyme A dehydrogenase, very	6.75E-05	4	5.95	5.67	5.70	5.77	5.74	5.64	5.69	5.58
TC1100297	ACCS	84680	1-aminocyclopropane-1-carboxylate sy	1.97E-05	4	4.86	4.56	4.54	4.52	4.52	4.55	4.66	4.60
TC1601181	ACD	65057	adrenocortical dysplasia homolog (mou	8.12E-07	4	5.15	4.89	4.83	4.88	4.97	4.90	4.98	4.96
TC1400714	ACIN1	22985	apoptotic chromatin condensation indu	5.25E-05	4	6.48	5.89	5.93	6.08	6.08	6.03	6.19	6.07
TC0X00342	ACRC	93953	acidic repeat containing	1.40E-05	4	3.60	3.24	3.42	3.51	3.46	3.33	3.31	3.35
TC1700589	ACSF2	80221	acyl-CoA synthetase family member 2	0.000289	4	4.34	4.06	4.05	4.12	4.04	4.07	4.13	4.22
TC2000261	ACTR5	79913	ARP5 actin-related protein 5 homolog (	0.000104	4	3.91	3.61	3.62	3.64	3.60	3.58	3.62	3.62
TC0800155	ADAM28	10863	ADAM metallopeptidase domain 28	4.25E-27	4	5.49	3.64	3.15	3.25	3.10	3.48	3.77	4.17
TC0101018	ADAMTSL4	54507	ADAMTS-like 4 /// ADAMTS-like protei	3.46E-08	4	5.52	5.19	5.05	5.13	5.16	5.19	5.14	5.19

TC1601269	ADAT1	23536	adenosine deaminase, tRNA-specific 1	2.70E-06	4	4.63	4.04	4.01	4.09	4.12	4.27	4.33	4.34
TC0102965	ADCY10 /// NP	55811	adenylate cyclase 10 (soluble) /// solub	0.000188	4	2.91	2.74	2.77	2.74	2.76	2.71	2.72	2.74
TC1400745	ADCY4	196883	adenylate cyclase 4	6.17E-19	4	5.15	4.74	4.66	4.59	4.64	4.65	4.61	4.62
TC1501088	ADPGK	83440	ADP-dependent glucokinase /// ADP-de	4.50E-06	4	6.65	6.12	6.08	6.17	6.09	6.15	6.25	6.16
TC0601149	AGER	177	advanced glycosylation end product-sp	4.54E-18	4	6.36	5.59	5.53	5.57	5.59	5.63	5.67	5.60
TC0103426	AHCTF1	25909	AT hook containing transcription factor	3.52E-08	4	8.15	7.43	7.21	7.23	7.17	7.44	7.44	7.56
TC0200274	AHSA2	130872	AHA1, activator of heat shock 90kDa pr	9.32E-18	4	5.61	4.23	4.30	4.39	4.29	4.32	4.44	4.29
TC1901260	AKAP8L	26993	A kinase (PRKA) anchor protein 8-like	0.000141	4	6.97	6.61	6.59	6.79	6.82	6.79	6.82	6.74
TC0901271	AKNA	80709	AT-hook transcription factor /// AT-hoc	6.85E-06	4	7.14	6.56	6.44	6.58	6.55	6.57	6.61	6.73
TC1401158	AKT1	207	v-akt murine thymoma viral oncogene	1.49E-12	4	5.87	5.28	5.19	5.33	5.27	5.43	5.45	5.60
TC2200772	ALG12	79087	asparagine-linked glycosylation 12 hom	5.22E-05	4	4.79	4.65	4.67	4.62	4.60	4.61	4.64	4.75
TC0701511	ALKBH4	54784	alkB, alkylation repair homolog 4 (E. co	1.23E-08	4	5.38	4.81	4.72	4.84	4.80	4.84	4.78	4.82
TC1901425	ALKBH6	84964	alkB, alkylation repair homolog 6 (E. co	6.52E-06	4	4.78	4.47	4.48	4.46	4.47	4.40	4.43	4.42
TC0400467	ALPK1	80216	alpha-kinase 1 /// Alpha-protein kinase	4.45E-06	4	7.33	6.77	7.04	6.72	6.51	6.81	6.93	6.86
TC0202225	ALS2CR12	130540	amyotrophic lateral sclerosis 2 (juvenil	2.00E-10	4	5.70	4.16	4.04	4.32	4.30	4.35	4.48	4.60
TC0200996	ALS2CR2	650168 //	amyotrophic lateral sclerosis 2 (juvenil	0.000204	4	6.22	4.65	4.51	5.00	5.05	4.95	5.14	5.16
TC1101873	AMICA1	120425	adhesion molecule, interacts with CXAI	6.27E-09	4	9.94	9.08	9.29	9.37	9.19	9.40	9.41	9.50
TC0100806	AMPD2	271	adenosine monophosphate deaminase	8.00E-19	4	6.99	5.80	5.65	5.83	5.82	6.02	5.96	6.12
TC0301207	AMT	275	aminomethyltransferase	1.07E-10	4	4.57	4.22	4.23	4.24	4.23	4.29	4.25	4.28
TC0801191	ANGPT1	284	angiopoietin 1	2.43E-15	4	4.46	3.14	2.92	3.17	3.20	3.48	3.59	3.94
TC1500408	ANKDD1A	348094	ankyrin repeat and death domain cont	6.74E-10	4	5.30	4.96	4.97	4.91	5.00	4.98	5.01	4.96
TC1700930	ANKFY1	51479	ankyrin repeat and FYVE domain conta	4.56E-10	4	5.74	5.15	5.02	5.23	5.18	5.37	5.52	5.48
TC0500530	ANKHD1 /// EI	404734 //	ANKHD1-EIF4EBP3 /// ankyrin repeat a	1.38E-06	4	7.47	7.05	6.82	6.89	6.81	6.96	7.12	7.06
TC1601346	ANKRD11	653103 //	ankyrin repeat domain 11 /// Ankyrin r	0.000243	4	6.42	6.17	5.94	5.97	6.00	5.94	6.13	6.04
TC1200689	ANKRD13A	88455	ankyrin repeat domain 13A /// Ankyrin	7.11E-09	4	8.81	8.16	8.10	8.29	8.19	8.32	8.37	8.47
TC1100593	ANKRD13D	338692	ankyrin repeat domain 13 family, mem	8.66E-08	4	6.01	5.59	5.53	5.55	5.56	5.61	5.60	5.60
TC0202198	ANKRD44	91526	ankyrin repeat domain 44 /// Ankyrin r	1.51E-12	4	7.54	6.51	6.48	6.78	6.52	6.80	6.83	6.99
TC0201114	ANKZF1	55139	ankyrin repeat and zinc finger domain	5.71E-19	4	5.78	5.11	5.06	5.11	5.12	5.04	5.06	4.99
TC1501234	ANPEP	290	alanyl (membrane) aminopeptidase (ar	1.59E-05	4	9.97	9.12	9.14	9.86	9.76	9.46	9.46	9.49
TC0101022	ANXA9	8416	annexin A9 /// Annexin A9 (Annexin-9)	0.000505	4	4.36	4.16	4.20	4.12	4.18	4.18	4.06	4.18
TC0701133	AOAH	313	acyloxyacyl hydrolase (neutrophil)	0.000124	4	8.30	7.60	7.58	8.08	7.83	7.77	7.87	7.90
TC1700476	AOC2	314	amine oxidase, copper containing 2 (re	1.23E-19	4	6.19	4.22	4.02	4.28	4.47	4.52	4.57	4.69
TC1700477	AOC3	8639	amine oxidase, copper containing 3 (va	6.49E-19	4	4.35	3.46	3.40	3.43	3.59	3.46	3.49	3.55
TC1400731	AP1G2 /// JPH	84502 ///	junctophilin 4 /// adaptor-related prot	4.28E-15	4	5.44	4.95	4.93	4.89	4.93	4.92	4.94	4.87

TC1701264	AP1GBP1	11276	AP1 gamma subunit binding protein 1 /	4.05E-06	4	6.88	6.48	6.32	6.43	6.26	6.45	6.55	6.60
TC2200280	APOBEC3A	200315	apolipoprotein B mRNA editing enzyme	3.37E-15	4	9.22	7.77	7.37	7.46	7.45	7.53	7.63	7.65
TC2200628	APOL2	23780	apolipoprotein L, 2	2.11E-08	4	6.54	5.66	5.43	5.70	5.50	5.82	5.95	6.20
TC1201525	APPL2	55198	adaptor protein, phosphotyrosine inter	1.38E-10	4	6.79	6.03	6.11	5.95	5.96	6.06	6.06	6.07
TC0X01374	ARD1A	8260	ARD1 homolog A, N-acetyltransferase (	2.99E-05	4	5.29	4.97	5.03	5.09	5.20	5.18	5.12	5.14
TC1300641	ARGLU1 /// U4	55082	arginine and glutamate rich 1 /// UPF0	2.26E-08	4	7.57	6.68	6.52	6.53	6.61	6.61	6.82	6.63
TC0200311	ARHGAP25	9938	Rho GTPase activating protein 25	6.09E-12	4	9.53	8.46	8.58	8.85	8.75	9.01	8.95	9.15
TC0500567	ARHGAP26	23092	Rho GTPase activating protein 26 /// Rh	2.10E-06	4	9.62	9.21	9.18	9.11	8.94	9.10	9.08	9.14
TC1701444	ARHGAP27	201176	Rho GTPase activating protein 27 /// Rh	0.0003	4	6.06	5.60	5.62	5.65	5.65	5.66	5.63	5.62
TC1201320	ARHGAP9	64333	Rho GTPase activating protein 9 /// Rho	2.68E-20	4	8.03	6.99	6.97	7.13	7.16	7.18	7.16	7.14
TC1900564	ARHGEF1	9138	Rho guanine nucleotide exchange facto	9.79E-14	4	6.38	5.81	5.71	5.78	5.83	5.74	5.74	5.71
TC1900126	ARHGEF18	23370	rho/rac guanine nucleotide exchange fa	2.22E-07	4	6.38	5.89	5.79	5.93	5.95	6.06	6.11	6.20
TC1400264	ARID4A	5926	AT rich interactive domain 4A (RBP1-lik	0.000642	4	8.57	8.48	8.27	8.22	8.13	8.36	8.49	8.49
TC0103369	ARID4B	51742	AT rich interactive domain 4B (RBP1-lik	0.000959	4	8.77	8.69	8.48	8.43	8.35	8.55	8.71	8.64
TC1701783	ARL16	339231	ADP-ribosylation factor-like 16	7.07E-05	4	4.48	4.20	4.21	4.20	4.23	4.21	4.22	4.17
TC0600624	ARMC2	84071	armadillo repeat containing 2 /// Arma	3.31E-07	4	3.61	3.13	3.36	3.33	3.33	3.19	3.26	3.26
TC1100187	ARNTL	406	aryl hydrocarbon receptor nuclear tran	2.51E-08	4	6.47	5.86	5.87	5.91	5.76	6.04	6.05	6.14
TC0501142	ARRDC3	57561	arrestin domain containing 3	1.32E-12	4	9.60	8.17	8.33	8.43	8.18	8.99	8.78	9.28
TC0700556	ARS2 /// ARS2_	51593	arsenate resistance protein 2 /// Arsen	0.0002	4	5.45	5.20	4.96	5.05	5.21	5.18	5.24	5.13
TC1700713	ARSG	22901	arylsulfatase G	1.58E-10	4	6.30	5.48	5.47	5.61	5.59	5.65	5.67	5.67
TC2200571	ASCC2	84164	activating signal cointegrator 1 comple	1.95E-07	4	5.61	5.07	4.93	5.18	5.19	5.19	5.31	5.27
TC1901237	ASF1B	55723	ASF1 anti-silencing function 1 homolog	5.82E-10	4	5.14	4.20	4.17	4.37	4.61	4.68	4.66	4.71
TC0102833	ASH1L	55870	ash1 (absent, small, or homeotic)-like (	0.000667	4	6.81	6.42	6.26	6.28	6.24	6.34	6.49	6.45
TC1600323	ASPHD1	253982	aspartate beta-hydroxylase domain cor	1.96E-05	4	4.63	4.32	4.35	4.29	4.34	4.31	4.28	4.38
TC2000181	ASXL1	171023	additional sex combs like 1 (Drosophila	0.000173	4	5.36	5.16	5.02	5.02	5.09	5.05	5.21	5.16
TC2200290	ATF4	730136 //	activating transcription factor 4 (tax-re	5.18E-05	4	7.62	7.03	6.73	6.83	7.08	7.14	7.13	7.04
TC1200163	ATF7IP	55729	activating transcription factor 7 interac	1.01E-06	4	7.65	7.07	7.18	7.29	7.25	7.29	7.31	7.41
TC0201196	ATG16L1	55054	ATG16 autophagy related 16-like 1 (S. c	5.45E-08	4	4.90	4.39	4.60	4.68	4.58	4.63	4.67	4.57
TC1100651	ATG16L2	89849	ATG16 autophagy related 16-like 2 (S. c	5.20E-40	4	8.01	5.99	5.85	6.03	5.99	6.10	6.17	6.21
TC1101528	ATG2A	23130	ATG2 autophagy related 2 homolog A (	1.26E-11	4	5.43	5.22	4.90	4.88	4.98	5.07	4.98	5.14
TC1401109	ATG2B	55102	ATG2 autophagy related 2 homolog B (	2.19E-05	4	5.41	4.99	4.91	4.99	4.86	4.90	5.06	4.94
TC1401108	ATG2B	55102	ATG2 autophagy related 2 homolog B (	2.23E-05	4	5.51	4.92	4.91	4.92	4.88	4.90	5.02	4.90
TC1100008	ATHL1	80162	ATH1, acid trehalase-like 1 (yeast) /// A	2.58E-42	4	6.93	5.51	5.54	5.57	5.55	5.58	5.56	5.59
TC1201437	ATP2B1	490	ATPase, Ca++ transporting, plasma mer	3.28E-15	4	8.00	6.87	6.43	6.51	6.39	7.10	7.24	7.43

TC1700460	ATP6V0A1	535	ATPase, H+ transporting, lysosomal V0	1.60E-06	4	7.14	6.80	6.57	6.56	6.53	6.62	6.62	6.66
TC0100477	ATP6V0B	533	ATPase, H+ transporting, lysosomal 21k	4.62E-05	4	7.21	6.54	6.41	6.59	6.60	6.75	6.53	6.73
TC0300507	ATP6V1A	523	ATPase, H+ transporting, lysosomal 70k	2.83E-06	4	8.09	7.43	7.71	7.85	7.68	7.79	7.77	7.87
TC0800121	ATP6V1B2	526	ATPase, H+ transporting, lysosomal 56/	1.44E-08	4	9.13	8.15	8.40	8.67	8.45	8.58	8.50	8.68
TC0300349	ATXN7	6314	ataxin 7	1.40E-08	4	8.14	7.92	7.60	7.71	7.60	7.82	7.85	8.06
TC0201642	AUP1	550	ancient ubiquitous protein 1 /// Ancien	4.95E-10	4	5.83	5.23	5.25	5.15	5.19	5.31	5.41	5.28
TC1201330	AVIL	10677	advillin	1.21E-26	4	5.82	4.21	4.10	4.39	4.36	4.51	4.56	4.56
TC1701812	B3GNTL1	146712	UDP-GlcNAc:betaGal beta-1,3-N-acetyl	9.93E-06	4	5.20	4.88	4.89	4.77	4.83	4.87	4.77	4.80
TC2100059	BACH1 /// C21	571	BTB and CNC homology 1, basic leucine	1.58E-06	4	6.81	6.25	6.33	6.47	6.34	6.51	6.44	6.55
TC2100209	BAGE2 /// BAG	85319 ///	B melanoma antigen family, member 2	3.09E-09	4	4.87	4.65	4.59	4.50	4.47	4.56	4.60	4.58
TC1600657	BANP	648196 //	BTG3 associated nuclear protein /// BT	1.46E-15	4	5.98	5.18	5.21	5.35	5.29	5.36	5.41	5.52
TC0601121	BAT1 /// ATP6	7919 ///	HLA-B associated transcript 1 /// ATPas	3.78E-09	4	6.01	5.53	5.51	5.52	5.59	5.53	5.53	5.43
TC0600271	BAT2	7916	HLA-B associated transcript 2 /// HLA-B	0.000105	4	6.16	5.97	5.78	5.86	5.86	5.78	5.80	5.80
TC0101283	BAT2D1	23215	BAT2 domain containing 1 /// HBxAg tr	3.35E-05	4	8.70	8.24	7.93	7.98	7.93	8.04	8.33	8.20
TC0601125	BAT3	7917	HLA-B associated transcript 3 /// Large	4.57E-07	4	5.64	5.36	5.39	5.33	5.36	5.35	5.33	5.34
TC1201300	BAZ2A	11176	bromodomain adjacent to zinc finger d	1.75E-06	4	7.33	6.92	6.52	6.64	6.61	6.73	6.78	6.89
TC0202036	BAZ2B	29994	bromodomain adjacent to zinc finger d	3.47E-11	4	9.00	8.11	7.69	7.92	7.95	8.12	8.27	8.29
TC1500463	BBS4	585	Bardet-Biedl syndrome 4	6.22E-06	4	3.40	3.03	3.09	3.10	2.97	3.05	3.15	3.13
TC2000843	BCAS1	8537	breast carcinoma amplified sequence 1	2.50E-05	4	3.59	3.38	3.34	3.30	3.35	3.35	3.35	3.37
TC0601629	BCLAF1	9774	BCL2-associated transcription factor 1	3.79E-08	4	7.91	7.50	7.24	7.28	7.24	7.42	7.60	7.58
TC0201103	BCS1L	617	BCS1-like (yeast)	2.98E-06	4	3.89	3.60	3.59	3.59	3.64	3.59	3.69	3.59
TC1100467	BEST1	7439	bestrophin 1 /// Bestrophin-1 (Vitellifo	6.25E-07	4	6.06	5.66	5.38	5.35	5.28	5.63	5.42	5.62
TC0200160	BIRC6	57448	baculoviral IAP repeat-containing 6 (ap	2.46E-05	4	6.24	5.88	5.63	5.70	5.69	5.77	5.87	5.81
TC0400343	BMP2K	55589	BMP2 inducible kinase /// BMP-2-induc	7.79E-06	4	7.18	6.79	6.79	6.86	6.56	7.00	6.98	7.06
TC0800164	BNIP3L	665	BCL2/adenovirus E1B 19kDa interacting	2.68E-07	4	9.30	8.61	8.26	8.53	8.52	8.58	8.60	8.65
TC0101024	BNIPL	651044 //	BCL2/adenovirus E1B 19kD interacting	8.08E-15	4	4.29	3.67	3.71	3.76	3.77	3.78	3.74	3.75
TC1600981	BOLA2B /// BO	654483 //	bolA homolog 2B (E. coli) /// bolA hom	9.36E-06	4	7.30	6.97	6.91	6.87	6.94	7.00	7.04	6.94
TC1901258	BRD4	23476	bromodomain containing 4 /// Bromod	6.39E-05	4	6.61	6.37	6.16	6.29	6.29	6.28	6.41	6.43
TC0501319	BRD8	10902	bromodomain containing 8	6.74E-10	4	6.42	5.87	5.84	5.72	5.63	5.84	5.98	5.97
TC0X01062	BRWD3	254065	bromodomain and WD repeat domain	2.14E-06	4	7.18	6.96	6.80	6.68	6.51	6.75	6.79	6.84
TC1000442	BTAF1	9044	BTAF1 RNA polymerase II, B-TFIID trans	0.000602	4	5.41	5.12	4.94	5.05	4.95	5.02	5.12	5.01
TC1200666	BTBD11	121551	BTB (POZ) domain containing 11	6.81E-13	4	4.20	3.90	3.92	3.86	3.91	3.97	3.96	4.08
TC0600163	BTN2A1	11120	butyrophilin, subfamily 2, member A1 /	1.32E-15	4	7.71	6.61	6.71	6.84	6.81	7.05	7.19	7.25
TC0600159	BTN2A2	10385	butyrophilin, subfamily 2, member A2	7.44E-19	4	4.86	4.03	4.00	4.05	4.02	4.23	4.51	4.58

TC0600161	BTN2A3	54718	butyrophilin, subfamily 2, member A3 /	6.78E-08	4	3.88	3.54	3.64	3.55	3.56	3.67	3.63	3.70
TC0600160	BTN3A1	11119	butyrophilin, subfamily 3, member A1 /	2.34E-20	4	7.44	5.41	5.21	5.63	5.38	6.24	6.50	6.85
TC0600162	BTN3A3	10384	butyrophilin, subfamily 3, member A3	4.91E-21	4	6.78	4.66	4.53	5.03	4.83	5.49	5.88	6.04
TC1000674	C10orf137	26098	chromosome 10 open reading frame 1	1.81E-07	4	4.85	4.30	4.49	4.56	4.56	4.59	4.67	4.62
TC1000763	C10orf31	---	Putative uncharacterized protein C10o	1.68E-16	4	7.83	6.31	6.11	6.25	6.13	6.43	6.39	6.50
TC1100682	C11orf30	56946	chromosome 11 open reading frame 3	8.97E-05	4	6.38	6.21	6.12	6.17	6.05	6.20	6.29	6.38
TC1101836	C11orf34	349633	chromosome 11 open reading frame 3	1.63E-05	4	4.30	3.77	3.54	3.53	3.48	3.55	3.65	3.82
TC1201438	C12orf12	196477	chromosome 12 open reading frame 1	0.000676	4	4.04	3.67	3.79	3.70	3.75	3.72	3.58	3.70
TC1200238	C12orf35	55196	chromosome 12 open reading frame 3	9.16E-13	4	9.80	9.16	8.97	8.98	9.02	9.32	9.45	9.54
TC1201579	C12orf51	283450	chromosome 12 open reading frame 5	1.77E-06	4	5.97	5.31	5.09	5.32	5.32	5.31	5.47	5.33
TC1200607	C12orf55	144535	chromosome 12 open reading frame 5	0.00097	4	2.49	2.25	2.27	2.26	2.29	2.32	2.34	2.39
TC1400841	C14orf138	79609	chromosome 14 open reading frame 1	3.26E-05	4	5.54	4.91	4.74	4.81	4.72	4.71	4.75	4.64
TC1400443	C14orf159	80017	chromosome 14 open reading frame 1	8.20E-29	4	7.49	5.49	5.32	5.62	5.69	6.15	6.32	6.44
TC1500487	C15orf39	56905	chromosome 15 open reading frame 3	7.19E-06	4	6.58	6.26	6.10	6.25	6.17	6.35	6.28	6.47
TC1500299	C15orf43	145645	chromosome 15 open reading frame 4	0.000216	4	2.80	2.45	2.50	2.56	2.51	2.50	2.55	2.66
TC1600934	C16orf65	255762	chromosome 16 open reading frame 6	1.28E-06	4	3.32	2.98	3.05	2.96	3.01	2.99	3.00	3.05
TC1701773	C17orf56	146705	chromosome 17 open reading frame 5	1.09E-07	4	4.98	4.66	4.70	4.68	4.72	4.71	4.64	4.66
TC1701009	C17orf68	80169	chromosome 17 open reading frame 6	8.60E-21	4	6.32	5.65	5.51	5.53	5.52	5.59	5.62	5.63
TC1800418	C18orf37	125476	chromosome 18 open reading frame 3	3.05E-06	4	5.18	5.04	4.92	4.93	4.92	5.02	5.12	5.12
TC1901010	C19orf34	255193	chromosome 19 open reading frame 3	0.000682	4	4.95	4.62	4.60	4.49	4.60	4.59	4.56	4.57
TC1900322	C19orf50	79036	chromosome 19 open reading frame 5	2.64E-06	4	6.02	5.57	5.60	5.66	5.74	5.68	5.69	5.75
TC1900457	C19orf55	148137	chromosome 19 open reading frame 5	0.000679	4	5.17	5.06	5.02	5.01	4.98	5.06	5.04	5.03
TC1900990	C19orf6	91304	chromosome 19 open reading frame 6	0.000288	4	5.99	5.75	5.72	5.82	5.82	5.82	5.74	5.76
TC0100397	C1orf113 /// Q	79729	chromosome 1 open reading frame 11	2.59E-13	4	4.96	4.64	4.55	4.54	4.58	4.61	4.55	4.63
TC0100257	C1orf128	57095	chromosome 1 open reading frame 12	2.16E-06	4	5.61	4.88	4.88	4.95	5.04	5.12	5.16	5.16
TC0103194	C1orf132	---	Uncharacterized protein C1orf132 (Fra	2.23E-13	4	5.67	4.95	4.75	4.88	4.82	5.05	5.05	5.15
TC0102720	C1orf138	---	Uncharacterized protein C1orf138. [So	1.51E-07	4	5.64	4.88	4.66	4.96	4.92	5.03	4.98	5.10
TC0100305	C1orf160	84065	chromosome 1 open reading frame 16	5.97E-07	4	4.58	4.32	4.35	4.29	4.33	4.37	4.37	4.41
TC0100869	C1orf161	126868	chromosome 1 open reading frame 16	0.000144	4	4.02	3.57	3.56	3.69	3.60	3.61	3.60	3.61
TC0102546	C1orf183	55924	chromosome 1 open reading frame 18	8.28E-06	4	6.96	6.38	6.47	6.50	6.47	6.54	6.53	6.64
TC0102810	C1orf189	388701	chromosome 1 open reading frame 18	0.000311	4	3.04	2.56	2.71	2.61	2.63	2.62	2.69	2.72
TC0101841	C1orf200	644997	chromosome 1 open reading frame 20	7.37E-05	4	5.68	4.93	4.81	4.88	4.87	4.70	4.71	4.80
TC0101025	C1orf56	54964	chromosome 1 open reading frame 56	3.63E-07	4	6.83	6.33	6.37	6.43	6.42	6.49	6.46	6.47
TC0102000	C1orf63	57035	chromosome 1 open reading frame 63	3.91E-08	4	6.67	5.66	6.13	6.23	6.12	6.15	6.02	6.11

TC0101083	C1orf77	26097	chromosome 1 open reading frame 77	6.23E-11	4	6.64	6.03	6.18	6.19	6.08	6.20	6.36	6.33
TC0100468	C1orf84 /// KIA	149469 //	chromosome 1 open reading frame 84	1.26E-14	4	4.75	4.49	4.42	4.42	4.44	4.46	4.42	4.44
TC0103106	C1orf98	---	---	3.82E-06	4	4.83	3.92	4.10	4.40	4.26	4.20	4.20	4.04
TC0400111	C1QTNF7	114905	C1q and tumor necrosis factor related	7.81E-05	4	3.12	2.67	2.66	2.63	2.69	2.79	2.77	2.67
TC1200919	C1R	727728 //	complement component 1, r subcomp	9.25E-05	4	3.75	3.53	3.48	3.47	3.50	3.50	3.49	3.51
TC2000396	C20orf107 ///	388799 //	chromosome 20 open reading frame 1	6.11E-05	4	5.05	4.71	4.67	4.60	4.65	4.73	4.72	4.63
TC2000121	C20orf19	55857	chromosome 20 open reading frame 1	3.01E-18	4	6.26	5.17	5.09	5.24	5.12	5.40	5.61	5.69
TC2000421	C20orf197	284756	chromosome 20 open reading frame 1	2.55E-09	4	4.92	4.59	4.42	4.28	4.36	4.52	4.54	4.53
TC2200603	C22orf30	253143	chromosome 22 open reading frame 3	6.06E-05	4	6.34	5.80	5.70	5.84	5.76	5.82	5.98	5.98
TC2200770	C22orf34	---	Novel protein (LOC348645). [Source:Ur	5.57E-05	4	4.89	4.66	4.69	4.63	4.63	4.65	4.58	4.68
TC1100913	C2CD2L	9854	C2CD2-like	6.81E-13	4	5.24	4.71	4.63	4.78	4.85	4.88	4.85	4.83
TC1101653	C2CD3 /// Q9Y	26005	C2 calcium-dependent domain contain	5.11E-18	4	5.45	4.72	4.62	4.75	4.64	4.80	4.97	4.96
TC0200530	C2orf29	55571	chromosome 2 open reading frame 29	0.000185	4	7.70	7.38	7.15	7.34	7.31	7.40	7.37	7.39
TC0201293	C2orf46	---	Putative uncharacterized protein C2orf	8.97E-13	4	3.88	3.16	3.17	3.38	3.25	3.35	3.58	3.61
TC0301655	C3orf16	389161	chromosome 3 open reading frame 16	5.65E-23	4	4.26	3.07	3.02	2.99	3.03	3.22	3.36	3.63
TC0300051	C3orf42	---	Putative uncharacterized protein C3orf	7.65E-06	4	6.07	5.19	4.99	5.28	5.31	5.46	5.41	5.40
TC0301204	C3orf62 /// US	375341 //	chromosome 3 open reading frame 62	1.97E-14	4	8.90	7.86	7.84	7.98	7.91	8.09	8.15	8.23
TC0400030	C4orf8	8603	chromosome 4 open reading frame 8 /	8.95E-08	4	6.16	5.77	5.68	5.76	5.68	5.71	5.80	5.83
TC0600594	C6orf112	---	OTTHUMP00000016912. [Source:Unipr	0.00057	4	2.57	2.34	2.41	2.44	2.28	2.26	2.33	2.38
TC0600545	C6orf163	---	Uncharacterized protein C6orf163. [Sou	1.12E-05	4	3.76	3.19	3.27	3.20	3.49	3.54	3.62	3.40
TC0600546	C6orf164	---	Uncharacterized protein C6orf164. [Sou	1.22E-05	4	4.09	3.72	3.55	3.58	3.63	3.63	3.73	3.70
TC0600623	C6orf181	---	OTTHUMP00000016945. [Source:Unipr	0.000816	4	3.98	3.77	3.71	3.66	3.68	3.76	3.74	3.79
TC0600281	C6orf48 /// SN	50854	chromosome 6 open reading frame 48	3.80E-05	4	4.72	4.38	4.42	4.46	4.60	4.49	4.50	4.41
TC0601003	C6orf62	81688	chromosome 6 open reading frame 62	4.41E-05	4	8.98	8.66	8.52	8.67	8.61	8.69	8.80	8.70
TC0701473	C7orf43	55262	chromosome 7 open reading frame 43	8.18E-15	4	7.07	6.02	5.92	6.14	6.23	6.43	6.28	6.40
TC0701160	C7orf44	55744	chromosome 7 open reading frame 44	2.16E-10	4	6.66	6.39	6.08	5.98	6.15	6.38	6.49	6.49
TC0700620	C7orf53	286006	chromosome 7 open reading frame 53	0.000764	4	5.02	4.11	4.23	4.70	4.79	4.71	4.70	4.37
TC0700666	C7orf54	27099	chromosome 7 open reading frame 54	2.34E-05	4	5.82	4.40	4.71	4.83	4.78	4.91	5.18	4.93
TC0100914	C9orf131	138724	chromosome 9 open reading frame 13	5.39E-12	4	10.35	9.00	8.96	9.10	9.10	9.07	9.33	9.08
TC0900154	C9orf131	138724	chromosome 9 open reading frame 13	3.57E-05	4	5.82	5.54	5.49	5.36	5.34	5.47	5.44	5.53
TC0901181	C9orf156	51531	chromosome 9 open reading frame 15	3.90E-05	4	5.38	5.17	5.06	5.04	5.08	5.19	5.26	5.31
TC0901112	C9orf164	349236	chromosome 9 open reading frame 16	3.57E-08	4	5.62	4.95	4.94	5.11	5.07	5.14	5.19	5.25
TC0900773	C9orf38	---	Uncharacterized protein C9orf38. [Sou	1.31E-05	4	3.25	2.72	2.71	2.73	2.81	2.76	3.01	3.05
TC0101009	CA14	23632	carbonic anhydrase XIV	8.33E-12	4	3.82	3.34	3.34	3.37	3.29	3.36	3.37	3.37

TC0101570	CABC1	56997	chaperone, ABC1 activity of bc1 compl	2.68E-06	4	5.28	5.01	5.05	5.12	5.05	5.08	5.07	5.11
TC0202006	CACNB4	785	calcium channel, voltage-dependent, b	3.12E-25	4	4.61	3.33	3.21	3.27	3.26	3.40	3.37	3.66
TC0801106	CALB1	793	calbindin 1, 28kDa	0.000235	4	3.05	2.76	2.80	2.90	2.84	2.85	2.86	2.81
TC1201256	CALCOCO1	57658	calcium binding and coiled-coil domain	1.15E-13	4	7.13	6.32	6.08	6.21	6.07	6.24	6.28	6.45
TC1700926	CAMKK1	84254	calcium/calmodulin-dependent protei	0.000449	4	4.20	3.88	3.97	3.90	3.89	3.92	3.88	3.90
TC0300080	CAPN7	23473	calpain 7	6.29E-07	4	5.87	5.50	5.28	5.34	5.34	5.40	5.60	5.50
TC1201076	CAPRIN2	65981	caprin family member 2	6.26E-07	4	4.41	3.75	3.80	3.88	3.79	3.81	3.97	3.91
TC1901651	CARD8	22900	caspase recruitment domain family, m	9.77E-09	4	7.69	6.96	7.17	7.09	7.00	7.21	7.21	7.21
TC0200994	CASP8	841	caspase 8, apoptosis-related cysteine p	4.74E-13	4	7.47	6.76	6.77	6.77	6.67	6.96	7.00	7.12
TC2000392	CASS4 /// C20c	57091	Cas scaffolding protein family member	1.45E-13	4	7.48	6.28	5.95	5.89	5.86	6.64	6.62	7.08
TC2000200	CBFA2T2	9139	core-binding factor, runt domain, alph	0.000875	4	4.89	4.74	4.72	4.78	4.83	4.79	4.77	4.75
TC0900996	CBWD6	644019	COBW domain containing 6 /// COBW	1.04E-14	4	5.89	5.03	5.12	5.13	5.18	5.34	5.51	5.45
TC2200676	CBX7	23492	chromobox homolog 7	1.80E-12	4	5.56	4.99	4.95	5.00	4.95	5.08	5.05	5.19
TC0901371	CCBL1	883	cysteine conjugate-beta lyase, cytoplas	2.40E-06	4	4.91	4.61	4.66	4.65	4.66	4.68	4.65	4.68
TC1900231	CCDC130	81576	coiled-coil domain containing 130 /// C	6.93E-11	4	5.33	4.92	4.88	4.83	4.89	4.92	4.93	4.90
TC1201391	CCDC131	196441	coiled-coil domain containing 131 /// C	3.18E-08	4	6.97	6.41	6.36	6.21	6.18	6.31	6.39	6.30
TC1000565	CCDC147 /// C	159686	coiled-coil domain containing 147 /// L	1.13E-06	4	4.72	4.42	4.44	4.28	4.10	4.50	4.72	4.64
TC1701281	CCDC49	54883	coiled-coil domain containing 49	2.48E-07	4	7.91	7.54	7.34	7.47	7.49	7.63	7.70	7.72
TC0301457	CCDC52	152185	coiled-coil domain containing 52	2.72E-09	4	3.64	3.25	3.31	3.43	3.42	3.38	3.51	3.46
TC1200297	CCDC65	85478	coiled-coil domain containing 65 /// Co	1.72E-09	4	3.58	3.22	3.12	3.16	3.12	3.10	3.19	3.15
TC1100909	CCDC84	338657	coiled-coil domain containing 84	1.08E-16	4	5.60	4.69	4.66	4.70	4.69	4.77	4.93	4.88
TC1400489	CCNK	8812	cyclin K /// Cyclin-K. [Source:Uniprot/S	1.25E-05	4	6.95	6.94	6.78	6.77	6.66	6.83	6.89	6.95
TC0301695	CCNL1	57018	cyclin L1 /// Cyclin-L1 (Cyclin-L). [Sourc	0.000559	4	8.11	7.65	7.37	7.28	7.33	7.50	7.39	7.38
TC0101773	CCNL2	81669	cyclin L2 /// Cyclin-L2 (Paneth cell-enh	7.58E-32	4	6.27	5.39	5.46	5.48	5.50	5.56	5.59	5.56
TC0200735	CCNT2	905	cyclin T2	3.96E-07	4	6.63	6.03	6.08	6.04	5.94	6.12	6.22	6.23
TC0400545	CCRN4L	25819	CCR4 carbon catabolite repression 4-lik	3.69E-07	4	4.96	4.59	4.24	4.47	4.80	4.68	4.88	4.56
TC1100580	CCS	9973	copper chaperone for superoxide dism	0.000434	4	5.03	4.78	4.82	4.82	4.81	4.85	4.88	4.84
TC0100874	CD2	914	CD2 molecule /// T-cell surface antigen	7.04E-05	4	3.85	3.28	3.19	3.21	3.21	3.21	3.30	3.27
TC1100889	CD3G	917	CD3g molecule, gamma (CD3-TCR com	0.000302	4	4.84	3.94	3.83	4.00	3.88	3.84	4.01	4.20
TC1200061	CD4	920	CD4 molecule	0.000191	4	4.86	4.68	4.58	4.57	4.60	4.57	4.59	4.64
TC1701611	CD79B	974	CD79b molecule, immunoglobulin-asso	9.61E-05	4	4.92	4.79	4.76	4.74	4.63	4.69	4.69	4.81
TC0601525	CDC2L6	23097	cell division cycle 2-like 6 (CDK8-like) //	6.31E-10	4	8.51	7.64	7.57	7.73	7.67	7.88	7.91	8.04
TC1800395	CDH2	1000	cadherin 2, type 1, N-cadherin (neuron	3.13E-06	4	3.35	3.02	2.82	2.85	2.80	2.92	2.90	3.05
TC1000323	CDH23	64072	cadherin-like 23 /// Cadherin-23 precu	3.51E-12	4	4.60	4.22	4.22	4.26	4.27	4.28	4.24	4.30

TC1700559	CDK5RAP3	80279	CDK5 regulatory subunit associated pr	0	4	6.97	5.38	5.30	5.30	5.31	5.38	5.48	5.41
TC1900613	CEACAM19	56971	carcinoembryonic antigen-related cell	0.000219	4	4.22	4.00	4.02	3.94	3.97	4.00	3.93	3.97
TC1900560	CEACAM3	1084	carcinoembryonic antigen-related cell	9.37E-06	4	7.82	7.47	7.23	7.45	7.57	7.74	7.57	7.60
TC1101643	CENTD2 /// ST	116985 //	centaurin, delta 2 /// StAR-related lipid	4.78E-09	4	6.39	5.80	5.67	5.83	5.78	5.78	5.72	5.83
TC0501363	CENTD3	64411	centaurin, delta 3	1.14E-13	4	6.31	5.29	5.27	5.46	5.44	5.54	5.53	5.61
TC1100882	CEP164	22897	centrosomal protein 164kDa /// centro	1.14E-10	4	4.90	4.63	4.66	4.61	4.59	4.61	4.68	4.70
TC0200296	CEP68	23177	centrosomal protein 68kDa /// Centros	4.61E-08	4	6.01	5.83	5.58	5.68	5.61	5.62	5.62	5.64
TC0600283	CFB	629	complement factor B	1.36E-05	4	3.50	3.22	3.21	3.18	3.22	3.28	3.15	3.23
TC1500645	CHD2	1106	chromodomain helicase DNA binding p	1.65E-11	4	8.39	7.82	7.53	7.63	7.64	7.84	7.97	7.93
TC0103140	CHI3L1	1116	chitinase 3-like 1 (cartilage glycoprotei	4.66E-18	4	7.76	5.76	4.89	5.34	5.98	6.47	6.24	6.34
TC1200654	CHST11	50515	carbohydrate (chondroitin 4) sulfotran	1.07E-16	4	8.06	7.08	6.65	7.26	7.12	7.45	7.52	7.69
TC1901269	CIB3	117286	calcium and integrin binding family me	4.24E-12	4	5.18	4.53	4.52	4.51	4.48	4.61	4.77	4.83
TC1900036	CIRBP	1153	cold inducible RNA binding protein	6.38E-11	4	7.57	6.92	6.68	6.50	6.58	6.69	6.81	6.84
TC0X00034	CLCN4	1183	chloride channel 4 /// Chloride channe	4.24E-12	4	5.13	4.61	4.42	4.47	4.45	4.56	4.63	4.80
TC1200962	CLEC2A	---	C-type lectin domain family 2 member	0.000801	4	2.68	2.29	2.39	2.31	2.39	2.28	2.35	2.45
TC1200116	CLEC2D /// Q5	29121	C-type lectin domain family 2, member	0.000299	4	5.45	5.08	5.05	4.84	4.91	4.94	5.10	5.01
TC1200967	CLEC7A	64581	C-type lectin domain family 7, member	1.53E-15	4	9.51	8.06	7.92	8.06	8.10	8.55	8.58	8.75
TC1200120	CLEC9A	283420	C-type lectin domain family 9, member	4.35E-13	4	4.84	3.75	3.63	3.70	3.75	3.99	4.02	4.27
TC0202212	CLK1	1195	CDC-like kinase 1 /// Dual specificity pr	4.01E-09	4	8.65	7.77	7.65	7.53	7.57	7.84	7.85	7.90
TC0102829	CLK2	1196	CDC-like kinase 2 /// Dual specificity pr	9.83E-07	4	5.90	5.33	5.31	5.38	5.40	5.41	5.50	5.39
TC1500480	CLK3 /// Q6ZV	649407 //	CDC-like kinase 3 /// CDNA FLJ42022 fi	5.34E-05	4	6.28	5.92	5.85	6.00	5.93	5.96	5.94	5.93
TC1501065	CLN6	54982	ceroid-lipofuscinosis, neuronal 6, late i	5.45E-05	4	4.39	4.10	4.06	4.16	4.18	4.27	4.19	4.27
TC0101843	CLSTN1	22883	calsyntenin 1 /// Calsyntenin-1 precurs	9.89E-07	4	5.26	4.85	4.88	5.08	5.01	4.99	5.09	5.04
TC1200079	CLSTN3	9746	calsyntenin 3 /// Calsyntenin-3 precurs	9.60E-07	4	4.86	4.53	4.53	4.47	4.50	4.50	4.51	4.48
TC0200502	CNNM3	26505	cyclin M3 /// cyclin M3 isoform 2 [Sour	4.06E-09	4	4.71	4.32	4.26	4.34	4.31	4.39	4.38	4.51
TC0200501	CNNM4	26504	cyclin M4	0.000863	4	4.32	4.04	4.00	4.10	4.00	4.08	4.12	4.20
TC1900856	CNOT3	4849	CCR4-NOT transcription complex, subu	2.91E-07	4	6.62	6.16	6.06	6.24	6.26	6.23	6.24	6.32
TC0600395	CNPY3 /// TNR	10695	canopy 3 homolog (zebrafish) /// trinu	5.27E-06	4	7.74	7.15	7.23	7.46	7.40	7.43	7.42	7.52
TC0700535	CNPY4	245812	canopy 4 homolog (zebrafish)	0.000108	4	4.74	4.31	4.41	4.61	4.60	4.46	4.59	4.50
TC1700473	CNTD1	124817	cyclin N-terminal domain containing 1	8.50E-10	4	4.62	3.92	3.82	3.90	3.83	3.93	4.09	4.08
TC1700733	COG1 /// SSTR	9382 ///	component of oligomeric golgi comple	5.93E-14	4	4.94	4.61	4.61	4.70	4.68	4.74	4.82	4.81
TC1601222	COG4	25839	component of oligomeric golgi comple	1.24E-08	4	5.44	4.77	4.90	5.09	5.10	5.08	5.18	5.10
TC0201047	CREB1	1385	cAMP responsive element binding prot	8.41E-11	4	8.95	8.14	8.21	8.44	8.24	8.48	8.49	8.62
TC0900164	CREB3	10488	cAMP responsive element binding prot	3.31E-05	4	5.46	5.39	5.01	5.06	5.05	5.06	5.08	5.26

TC0101090	CREB3L4	148327	cAMP responsive element binding prot	0.00095	4	4.09	3.92	3.91	3.91	3.93	3.92	3.88	3.89
TC1600808	CREBBP	1387	CREB binding protein (Rubinstein-Taybi	2.60E-05	4	9.08	8.55	8.19	8.41	8.34	8.46	8.55	8.64
TC0400020	CRIPAK	285464	cysteine-rich PAK1 inhibitor /// cystein	4.33E-06	4	6.53	5.99	5.89	5.82	5.88	5.97	6.03	5.94
TC1700414	CRKRS	51755	Cdc2-related kinase, arginine/serine-ric	4.19E-05	4	7.08	7.18	6.76	6.76	6.72	6.76	7.00	6.99
TC1700597	CROP /// CROP	51747	cisplatin resistance-associated overexp	1.52E-07	4	7.27	6.26	6.43	6.47	6.52	6.52	6.80	6.60
TC1100306	CRY2	1408	cryptochrome 2 (photolyase-like)	0.000189	4	4.69	4.51	4.50	4.51	4.50	4.59	4.53	4.60
TC1201244	CSAD	51380	cysteine sulfinic acid decarboxylase ///	7.80E-40	4	6.74	5.40	5.45	5.38	5.43	5.38	5.36	5.43
TC1200976	CSDA	8531	cold shock domain protein A /// DNA-b	0.000314	4	5.64	4.69	4.18	4.74	4.91	5.01	5.04	5.08
TC0501404	CSF1R	1436	colony stimulating factor 1 receptor, fo	7.54E-22	4	5.81	4.70	4.42	4.52	4.41	4.63	4.82	5.09
TC0102119	CSF3R	1441	colony stimulating factor 3 receptor (gr	5.99E-07	4	9.64	8.74	8.84	8.96	8.81	8.72	8.64	8.74
TC1900050	CSNK1G2	1455	casein kinase 1, gamma 2 /// Casein ki	0.000502	4	6.05	5.72	5.64	5.76	5.68	5.75	5.73	5.80
TC1001075	CTGLF2	729092	centaurin, gamma-like family, member	6.61E-11	4	6.08	5.20	5.26	5.25	5.28	5.38	5.62	5.58
TC1000975	CTGLF2 /// CT	729092 //	centaurin, gamma-like family, member	9.34E-27	4	6.17	3.60	3.58	3.82	3.89	4.21	4.43	4.65
TC1000244	CTGLF3	414189	centaurin, gamma-like family, member	5.64E-27	4	6.59	4.35	4.40	4.59	4.74	5.09	5.32	5.40
TC1000222	CTGLF9P	728005	centaurin, gamma-like family, member	9.91E-15	4	5.99	5.28	5.25	5.46	5.48	5.63	5.60	5.62
TC1000930	CTGLF9P /// CT	728005 //	centaurin, gamma-like family, member	5.68E-17	4	5.79	4.90	4.89	4.94	4.97	5.07	5.13	5.24
TC1000954	CTGLF9P /// Q	728005	centaurin, gamma-like family, member	1.15E-10	4	4.11	3.70	3.69	3.71	3.78	3.87	3.86	3.89
TC1000796	CUBN	8029	cubilin (intrinsic factor-cobalamin rece	0.000932	4	2.94	2.83	2.86	2.94	2.91	2.82	2.84	2.83
TC1701544	CUEDC1	731636 //	CUE domain containing 1	6.10E-07	4	4.98	4.64	4.60	4.51	4.52	4.61	4.60	4.64
TC1101354	CUGBP1	10658	CUG triplet repeat, RNA binding protei	6.09E-10	4	6.14	5.52	5.54	5.69	5.62	5.63	5.66	5.66
TC1000052	CUGBP2	10659	CUG triplet repeat, RNA binding protei	1.56E-13	4	8.63	7.82	7.73	7.83	7.75	7.91	7.93	8.02
TC0601277	CUL7	9820	cullin 7	0.000178	4	4.90	4.69	4.69	4.73	4.75	4.76	4.73	4.71
TC0X00620	CXorf18	---	CDNA FLJ36186 fis, clone TESTI202701	0.000394	4	3.80	3.51	3.43	3.39	3.47	3.45	3.42	3.43
TC0X01089	CXorf34	79979	chromosome X open reading frame 34	1.91E-05	4	4.52	4.26	4.24	4.25	4.30	4.29	4.40	4.37
TC0X00855	CXorf38	159013	chromosome X open reading frame 38	7.22E-05	4	5.99	5.69	5.67	5.74	5.63	5.80	5.89	5.88
TC0X00707	CXorf52	---	Uncharacterized protein CXorf52 (SPC	0.000123	4	6.22	5.15	5.07	5.46	5.48	5.58	5.82	5.70
TC1700657	CXorf6 /// BCA	54828	breast carcinoma amplified sequence 3	7.95E-09	4	6.19	5.67	5.67	5.73	5.65	5.69	5.69	5.70
TC1800475	CXXC1	30827	CXXC finger 1 (PHD domain)	7.01E-06	4	5.00	4.68	4.73	4.89	4.87	4.82	4.88	4.82
TC0900738	CXYorf1	---	FAM39B protein (Fragment). [Source:U	3.14E-09	4	6.10	5.70	5.77	5.72	5.77	5.74	5.74	5.70
TC1700111	CYB5D1	124637	cytochrome b5 domain containing 1 //,	1.42E-08	4	5.02	4.51	4.51	4.41	4.56	4.45	4.37	4.44
TC1101222	CYP2R1	120227	cytochrome P450, family 2, subfamily F	1.52E-05	4	4.35	4.14	3.94	3.98	3.99	4.03	4.08	4.10
TC1900272	CYP4F12 /// CY	66002 ///	cytochrome P450, family 4, subfamily F	1.27E-16	4	4.76	3.69	3.61	3.78	3.80	3.95	4.03	4.08
TC1901267	CYP4F2	8529	cytochrome P450, family 4, subfamily F	0.000202	4	5.81	5.68	5.50	5.50	5.69	5.73	5.60	5.62
TC1900271	CYP4F3	4051	cytochrome P450, family 4, subfamily F	7.57E-07	4	9.10	8.71	7.94	8.35	8.82	8.84	8.47	8.60

TC0900350	DAPK1	1612	death-associated protein kinase 1 /// D	3.61E-14	4	6.41	4.98	4.81	5.24	5.19	5.39	5.35	5.52
TC1501024	DAPK2	23604	death-associated protein kinase 2	0.000117	4	7.75	6.84	6.62	6.94	6.91	7.01	7.04	7.05
TC0501530	DBN1	1627	drebrin 1	2.25E-05	4	5.18	4.84	4.76	4.86	4.93	4.92	4.88	4.89
TC0301396	DCBLD2 /// Q9	131566	discoidin, CUB and LCCL domain contai	1.22E-05	4	3.11	2.85	2.91	2.87	2.88	2.88	2.84	2.89
TC2200664	DDX17	10521	DEAD (Asp-Glu-Ala-Asp) box polypeptic	2.87E-19	4	10.48	9.46	9.44	9.48	9.47	9.53	9.55	9.47
TC0X00585	DDX26B	203522	DEAD/H (Asp-Glu-Ala-Asp/His) box poly	6.21E-05	4	4.48	4.04	4.17	4.22	4.31	4.22	4.30	4.19
TC0X00159	DDX3X	1654	DEAD (Asp-Glu-Ala-Asp) box polypeptic	6.95E-10	4	9.58	9.09	8.70	8.88	8.89	9.03	8.98	9.05
TC1701620	DDX5	1655	DEAD (Asp-Glu-Ala-Asp) box polypeptic	1.05E-13	4	8.08	7.59	7.23	7.01	7.09	7.21	7.26	7.24
TC0701176	DDX56	54606	DEAD (Asp-Glu-Ala-Asp) box polypeptic	6.87E-07	4	4.68	4.44	4.41	4.40	4.55	4.55	4.51	4.49
TC1101883	DDX6	1656	DEAD (Asp-Glu-Ala-Asp) box polypeptic	2.67E-08	4	8.59	8.53	8.17	8.16	8.00	8.18	8.24	8.33
TC0800581	DENND3	22898	DENN/MADD domain containing 3	1.19E-22	4	8.18	6.98	6.79	6.73	6.67	6.82	6.80	6.88
TC1100311	DGKZ	8525	diacylglycerol kinase, zeta 104kDa /// D	0.000169	4	5.38	5.11	5.04	5.18	5.26	5.23	5.19	5.20
TC0100292	DHDDS	79947	dehydrodolichyl diphosphate synthase	0.000145	4	4.59	4.30	4.37	4.45	4.46	4.47	4.46	4.37
TC1900670	DHX34	9704	DEAH (Asp-Glu-Ala-His) box polypeptid	1.26E-06	4	5.44	5.09	5.07	5.06	5.10	5.11	5.09	5.12
TC1700495	DHX8	1659	DEAH (Asp-Glu-Ala-His) box polypeptid	0.000153	4	6.56	6.37	6.17	6.25	6.17	6.32	6.47	6.47
TC1401100	DICER1	647691 //	dicer 1, ribonuclease type III	1.53E-13	4	8.87	7.94	8.34	8.18	7.98	8.05	8.09	8.12
TC2000893	DIDO1	11083	death inducer-obliterator 1 /// Death-i	5.28E-08	4	5.71	5.38	5.30	5.46	5.43	5.46	5.54	5.54
TC2100201	DIP2A	23181	DIP2 disco-interacting protein 2 homol	4.30E-08	4	5.27	4.90	4.83	4.86	4.98	4.95	4.93	4.88
TC1300151	DLEU1	---	Leukemia-associated protein 1 (Delete	0.000375	4	3.05	2.87	2.87	2.78	2.82	2.82	2.80	2.85
TC1400373	DLST /// DLSTP	1743	dihydrolipoamide S-succinyltransferase	9.47E-07	4	5.77	5.11	4.99	5.15	5.17	5.13	5.21	5.27
TC0700451	DMTF1	9988	cyclin D binding myb-like transcription	6.63E-06	4	6.30	5.76	5.79	5.70	5.66	5.75	5.90	5.78
TC1500958	DMXL2	23312	Dmx-like 2	6.16E-10	4	7.39	5.96	5.97	6.42	6.26	6.43	6.65	6.54
TC0300307	DNAH1	25981	dynein, axonemal, heavy chain 1	6.82E-31	4	5.00	4.44	4.33	4.32	4.39	4.40	4.35	4.39
TC1001056	DNAJB12	54788	DnaJ (Hsp40) homolog, subfamily B, me	1.38E-05	4	6.28	5.93	5.79	5.96	5.90	6.02	6.09	6.17
TC0900153	DNAJB5	25822	DnaJ (Hsp40) homolog, subfamily B, me	8.95E-05	4	4.69	4.55	4.38	4.28	4.35	4.53	4.49	4.63
TC1100131	DNHD1L /// C1	387750 //	dynein heavy chain domain 1-like /// cl	2.32E-08	4	3.77	3.52	3.52	3.48	3.49	3.50	3.53	3.54
TC0500691	DOCK2	1794	dedicator of cytokinesis 2 /// Dedicator	0.000129	4	8.67	8.21	8.12	8.15	8.06	8.11	8.14	8.13
TC0800159	DOCK5 /// PPP	80005 ///	dedicator of cytokinesis 5 /// protein p	2.57E-20	4	9.01	7.68	7.47	7.52	7.51	7.78	7.81	7.92
TC0900004	DOCK8	81704	dedicator of cytokinesis 8 /// Dedicator	1.98E-11	4	9.04	8.08	8.03	8.11	7.98	8.13	8.24	8.32
TC0601143	DOM3Z	1797	dom-3 homolog Z (C. elegans)	2.81E-10	4	5.24	4.84	4.86	4.79	4.87	4.90	4.82	4.95
TC1601189	DPEP2	64174	dipeptidase 2 /// Dipeptidase 2 precurs	9.39E-24	4	8.34	6.17	6.19	6.72	6.69	7.06	7.12	7.24
TC1601188	DPEP3	64180	dipeptidase 3	6.93E-33	4	6.36	4.65	4.61	4.77	4.72	4.96	4.94	5.11
TC1100539	DPF2	5977	D4, zinc and double PHD fingers family	3.80E-05	4	7.36	6.69	6.64	6.81	6.72	6.95	6.91	7.15
TC0201641	DQX1	165545	DEAQ box polypeptide 1 (RNA-depende	0.00042	4	4.01	3.84	3.80	3.74	3.81	3.80	3.77	3.79

TC1100417	DTX4	23220	deltex 4 homolog (Drosophila)	5.45E-21	4	5.33	4.34	3.99	4.12	4.13	4.19	4.24	4.61
TC0700184	EEPD1	80820	endonuclease/exonuclease/phosphata	1.18E-15	4	6.41	5.21	5.15	5.55	5.44	5.78	5.76	5.86
TC1101554	EFEMP2	30008	EGF-containing fibulin-like extracellular	1.32E-05	4	4.77	4.56	4.59	4.63	4.64	4.54	4.51	4.55
TC0600457	EFHC1	114327	EF-hand domain (C-terminal) containin	7.72E-27	4	3.13	2.49	2.46	2.44	2.45	2.51	2.52	2.59
TC0100391	EIF2C1	26523	eukaryotic translation initiation factor	4.88E-06	4	5.89	5.37	5.35	5.63	5.56	5.47	5.56	5.49
TC0801282	EIF2C2	27161	eukaryotic translation initiation factor	0.000222	4	6.58	6.43	6.07	6.47	6.40	6.40	6.21	6.27
TC0100392	EIF2C3	192669	eukaryotic translation initiation factor	2.03E-12	4	5.89	5.11	5.09	5.25	5.21	5.30	5.39	5.40
TC0701135	ELMO1	9844	engulfment and cell motility 1	1.35E-05	4	6.95	6.49	6.22	6.43	6.40	6.59	6.58	6.63
TC0601341	ELOVL5	60481	ELOVL family member 5, elongation of	5.53E-05	4	7.74	7.33	7.29	7.29	7.32	7.53	7.51	7.60
TC1101477	EML3	256364	echinoderm microtubule associated pr	2.24E-07	4	5.51	5.20	5.27	5.23	5.18	5.18	5.23	5.10
TC1901245	EMR3	84658	egf-like module containing, mucin-like,	1.72E-07	4	9.19	8.13	7.63	7.86	7.90	8.49	8.39	8.72
TC1901099	EMR4P	326342	egf-like module containing, mucin-like,	4.67E-16	4	5.37	3.62	3.67	4.15	3.92	4.18	4.44	4.47
TC0800803	ENTPD4	9583	ectonucleoside triphosphate diphosph	2.53E-06	4	6.90	6.80	6.52	6.59	6.49	6.56	6.67	6.66
TC1200838	EP400	57634	E1A binding protein p400 /// E1A-bindi	8.77E-07	4	5.00	4.68	4.59	4.70	4.80	4.79	4.88	4.78
TC0100335	EPB41	2035	erythrocyte membrane protein band 4.	1.48E-19	4	8.21	6.84	6.55	7.09	7.09	7.40	7.56	7.65
TC0400318	EPGN	255324	epithelial mitogen homolog (mouse)	5.17E-05	4	2.88	2.53	2.66	2.51	2.56	2.53	2.53	2.57
TC1700206	EPN2	22905	epsin 2	4.07E-06	4	5.52	5.21	5.10	5.11	5.07	5.16	5.18	5.23
TC1901271	EPS15L1	58513	epidermal growth factor receptor path	5.03E-17	4	7.58	6.30	6.27	6.60	6.53	6.69	6.74	6.86
TC0202023	ERMN	57471	ermin, ERM-like protein	6.89E-07	4	3.31	3.03	2.93	2.85	2.83	2.84	2.88	2.93
TC1701614	ERN1 /// Q96D	2081	endoplasmic reticulum to nucleus signa	6.90E-08	4	6.96	6.41	5.88	6.09	6.10	6.13	6.13	6.24
TC0103379	ERO1LB	56605	ERO1-like beta (S. cerevisiae) /// ERO1-	3.95E-07	4	4.94	4.54	4.31	4.49	4.33	4.55	4.70	4.69
TC1201019	ERP27	121506	endoplasmic reticulum protein 27 kDa	4.42E-08	4	6.08	5.32	5.74	5.88	5.83	5.64	5.66	5.52
TC1400496	EVL	51466	Enah/Vasp-like	1.35E-06	4	5.58	5.18	5.11	5.25	5.18	5.27	5.44	5.41
TC2200176	EWSR1	2130	Ewing sarcoma breakpoint region 1 ///	0.000418	4	7.08	6.88	6.91	6.78	6.74	6.79	6.91	6.82
TC0400241	EXOC1	55763	exocyst complex component 1	0.000246	4	6.01	5.83	5.86	5.85	5.63	5.83	5.92	5.98
TC0500006	EXOC3	11336	exocyst complex component 3 /// Exoc	1.44E-06	4	6.08	5.69	5.65	5.71	5.64	5.73	5.72	5.73
TC1701387	EZH1	2145	enhancer of zeste homolog 1 (Drosoph	7.35E-16	4	7.50	6.42	6.29	6.39	6.37	6.47	6.46	6.59
TC0501080	F2RL2	2151	coagulation factor II (thrombin) recept	7.10E-05	4	5.70	4.85	5.02	5.15	5.09	5.14	5.01	5.19
TC0100016	FA87B_HUMAN	---	Protein FAM87B. [Source:Uniprot/SWIS	0.000112	4	3.92	3.59	3.39	3.36	3.40	3.44	3.33	3.49
TC0103183	FAIM3	9214	Fas apoptotic inhibitory molecule 3	1.07E-15	4	6.56	4.99	4.87	4.99	4.87	5.00	5.23	5.67
TC1100416	FAM111A	63901	family with sequence similarity 111, me	1.98E-23	4	5.39	3.97	3.79	4.16	4.27	4.54	4.67	4.70
TC0400165	FAM114A1	92689	family with sequence similarity 114, me	4.99E-06	4	3.73	3.52	3.65	3.83	3.67	3.58	3.59	3.68
TC0900391	FAM120A	23196	family with sequence similarity 120A //	0.000205	4	7.09	6.64	6.64	6.83	6.77	6.78	6.78	6.85
TC0600889	FAM120B	84498	family with sequence similarity 120B	7.24E-06	4	6.37	6.00	5.98	6.11	6.00	6.09	6.18	6.19

TC0X00577	FAM122C	159091	family with sequence similarity 122C //	7.11E-08	4	3.57	3.40	3.32	3.28	3.28	3.37	3.45	3.44
TC1101646	FAM168A /// K	23201	family with sequence similarity 168, me	1.66E-17	4	6.57	5.64	5.67	5.88	5.80	5.86	5.85	5.78
TC0200604	FAM39B	---	Protein FAM39B (CXYorf1-like protein	1.04E-06	4	5.72	5.40	5.34	5.37	5.40	5.39	5.37	5.41
TC0100815	FAM40A	85369	family with sequence similarity 40, me	7.05E-13	4	5.54	4.97	4.89	5.01	4.97	5.08	5.14	5.16
TC0400826	FAM44A	259282	family with sequence similarity 44, me	3.96E-06	4	9.90	9.06	8.78	8.90	8.85	9.03	9.31	9.28
TC0100881	FAM46C	54855	family with sequence similarity 46, me	1.27E-07	4	7.19	6.18	6.02	6.52	6.55	6.59	6.76	6.75
TC0201328	FAM49A	81553	family with sequence similarity 49, me	3.28E-08	4	8.68	7.64	7.63	8.03	7.73	7.95	7.90	8.20
TC1600523	FAM65A	79567	family with sequence similarity 65, me	6.79E-15	4	5.81	5.26	5.19	5.32	5.30	5.37	5.42	5.48
TC0700678	FAM71F2	346653	family with sequence similarity 71, me	1.23E-14	4	4.79	4.11	4.09	4.13	4.12	4.14	4.15	4.14
TC1101755	FAM76B	143684	family with sequence similarity 76, me	8.73E-06	4	5.25	4.92	4.86	4.87	4.85	4.99	5.13	5.12
TC0800540	FAM91A1	157769	family with sequence similarity 91, me	2.30E-10	4	7.09	6.44	6.43	6.47	6.31	6.58	6.55	6.68
TC0300039	FANCD2	2177	Fanconi anemia, complementation gro	2.15E-05	4	4.24	4.07	3.67	3.64	3.95	3.99	4.04	3.89
TC1701292	FBXL20	84961	F-box and leucine-rich repeat protein 2	2.45E-08	4	8.28	7.20	7.25	7.52	7.41	7.51	7.48	7.55
TC1000034	FBXO18	84893	F-box protein, helicase, 18 /// F-box on	0.000364	4	5.71	5.40	5.51	5.59	5.44	5.49	5.59	5.52
TC0300544	FBXO40	51725	F-box protein 40	6.75E-06	4	3.87	3.45	3.42	3.43	3.30	3.45	3.44	3.51
TC2200225	FBXO7	25793	F-box protein 7	5.86E-09	4	7.01	5.70	5.72	5.78	5.78	5.62	5.66	5.65
TC0401325	FBXW7	55294	F-box and WD repeat domain containi	3.83E-07	4	5.70	5.45	5.18	5.26	5.20	5.43	5.47	5.52
TC0101218	FCGR2C	9103	Fc fragment of IgG, low affinity IIc, rece	1.50E-06	4	7.48	7.02	7.08	7.24	7.08	7.33	7.25	7.31
TC1900719	FCGRT	2217	Fc fragment of IgG, receptor, transport	9.91E-12	4	6.36	5.83	5.79	5.80	5.82	5.89	5.89	5.94
TC1900307	FCHO1	23149	FCH domain only 1	1.20E-10	4	5.78	5.25	5.21	5.33	5.31	5.37	5.33	5.40
TC0500261	FCHO2	115548	FCH domain only 2 /// FCH domain onl	9.24E-09	4	7.17	6.16	6.12	6.04	5.88	6.35	6.39	6.56
TC0501362	FCHSD1	89848	FCH and double SH3 domains 1	1.90E-21	4	5.81	5.08	5.04	5.11	5.08	5.18	5.15	5.17
TC1101644	FCHSD2	9873	FCH and double SH3 domains 2	7.80E-08	4	7.80	7.19	7.26	7.45	7.21	7.34	7.44	7.40
TC1800500	FECH	2235	ferrochelatase (protoporphyria)	2.91E-06	4	5.25	4.06	4.03	4.32	4.38	4.38	4.47	4.45
TC0900385	FGD3	89846	FYVE, RhoGEF and PH domain containi	2.75E-08	4	7.26	6.52	6.43	6.56	6.54	6.52	6.50	6.59
TC0800886	FGFR1	2260	fibroblast growth factor receptor 1 (fm	4.97E-06	4	5.16	3.94	4.04	4.29	4.42	4.75	4.64	4.53
TC0600878	FGFR1OP /// C	11116 ///	FGFR1 oncogene partner /// chemokin	5.75E-16	4	4.71	3.97	4.20	4.37	4.26	4.37	4.45	4.43
TC0400609	FHDC1	85462	FH2 domain containing 1	3.37E-06	4	3.28	2.91	2.83	2.89	2.89	2.93	3.01	3.00
TC1201157	FKBP11	51303	FK506 binding protein 11, 19 kDa	5.30E-15	4	5.80	5.19	5.03	4.96	5.02	5.09	5.17	5.01
TC0501534	FLJ10404	54540	hypothetical protein FLJ10404	7.20E-21	4	5.62	5.06	4.98	5.06	5.07	5.05	5.05	5.04
TC1600871	FLJ11151	55313	hypothetical protein FLJ11151	1.19E-07	4	8.42	7.13	7.30	7.64	7.42	7.63	7.55	7.86
TC1200277	FLJ20489	55652	hypothetical protein FLJ20489	3.52E-07	4	4.75	4.34	4.42	4.48	4.50	4.56	4.56	4.61
TC1701173	FLJ25006 /// S	124923	hypothetical protein FLJ25006 /// Unc	9.29E-19	4	4.69	3.94	3.93	3.92	3.94	3.97	4.05	3.99
TC1600119	FLJ39639	283876	hypothetical protein FLJ39639	1.04E-05	4	7.46	6.62	6.74	6.86	6.82	6.94	7.17	7.08

TC1200728	FLJ42957	400077	FLJ42957 protein	2.28E-05	4	6.30	5.70	5.77	5.83	5.92	5.98	5.91	5.84
TC1900251	FLJ45910 /// N	388512	FLJ45910 protein /// CDNA FLJ45910 fis	2.76E-20	4	6.09	4.91	4.78	4.92	5.05	5.19	5.22	5.25
TC1700521	FMNL1	752	formin-like 1 /// Formin-like protein 1 (	0.000177	4	8.05	7.51	7.28	7.46	7.37	7.39	7.36	7.43
TC0200787	FMNL2	114793	formin-like 2 /// Formin-like protein 2 (	0.000202	4	3.00	2.91	2.92	2.91	2.81	2.88	2.94	2.95
TC0102652	FMO5	2330	flavin containing monooxygenase 5 ///	0.000851	4	3.34	3.08	3.03	3.14	3.18	3.19	3.14	3.28
TC1401051	FOXN3	1112	forkhead box N3	2.58E-11	4	7.09	6.26	6.18	6.59	6.52	6.60	6.69	6.78
TC0101857	FRAP1	2475	FK506 binding protein 12-rapamycin as	6.95E-05	4	5.37	4.91	4.89	4.94	4.95	4.96	5.05	5.00
TC1300073	FRY	10129	furry homolog (Drosophila) /// Protein	1.76E-20	4	7.56	5.84	5.50	5.91	5.82	6.18	6.41	6.53
TC0400934	FRYL	---	Protein furry homolog-like (ALL1-fused	1.50E-05	4	5.77	5.48	5.42	5.32	5.29	5.44	5.50	5.45
TC0700663	FSCN3	29999	fascin homolog 3, actin-bundling prote	0.000184	4	3.56	3.38	3.36	3.36	3.36	3.39	3.22	3.44
TC1600357	FUS	2521	fusion (involved in t(12;16) in malignan	7.16E-12	4	8.62	8.25	7.84	7.67	7.79	8.10	8.21	8.18
TC0800861	FUT10	84750	fucosyltransferase 10 (alpha (1,3) fucos	4.95E-10	4	3.95	3.32	3.39	3.40	3.44	3.50	3.49	3.57
TC1901696	FUZ	80199	fuzzy homolog (Drosophila) /// fuzzy ho	3.43E-13	4	5.46	5.03	4.96	4.98	4.99	5.04	4.99	5.09
TC1700992	FXR2	9513	fragile X mental retardation, autosoma	2.40E-05	4	4.94	4.65	4.61	4.70	4.67	4.78	4.75	4.75
TC1700480	G6PC	2538	glucose-6-phosphatase, catalytic subur	0.000459	4	2.90	2.69	2.65	2.53	2.67	2.67	2.56	2.63
TC0400565	GAB1	2549	GRB2-associated binding protein 1	2.16E-16	4	7.52	6.41	6.30	6.48	6.17	6.60	6.61	6.93
TC1101693	GAB2	9846	GRB2-associated binding protein 2	1.59E-06	4	8.90	8.78	8.29	8.37	8.34	8.70	8.61	8.75
TC1200123	GABARAPL1	23710	GABA(A) receptor-associated protein lil	3.07E-13	4	6.68	5.95	5.61	5.64	5.78	5.86	5.81	5.98
TC0601449	GABRR2	2570	gamma-aminobutyric acid (GABA) rece	0.000125	4	4.67	4.40	4.49	4.50	4.44	4.44	4.40	4.41
TC0400753	GAK	2580	cyclin G associated kinase /// Cyclin G-a	5.46E-05	4	5.59	5.30	5.26	5.26	5.30	5.29	5.30	5.30
TC0700900	GALNT11	63917	UDP-N-acetyl-alpha-D-galactosamine:p	1.47E-05	4	4.87	4.61	4.65	4.68	4.68	4.69	4.81	4.73
TC1700027	GARNL4	23108	GTPase activating Rap/RanGAP domain	0.000285	4	6.22	5.70	5.73	5.87	5.79	5.81	5.78	5.76
TC0900900	GBA2	57704	glucosidase, beta (bile acid) 2 /// Non-l	1.53E-13	4	5.81	5.17	5.07	5.09	5.08	5.15	5.12	5.16
TC0200563	GCC2	9648	GRIP and coiled-coil domain containing	1.40E-05	4	6.50	6.27	5.82	5.85	5.80	5.94	6.37	6.33
TC0601338	GCM1	8521	glial cells missing homolog 1 (Drosophil	1.05E-12	4	4.45	3.41	3.38	3.68	3.64	3.85	3.88	3.89
TC2000850	GCNT7	---	Uncharacterized protein C20orf105. [Sc	3.71E-05	4	6.36	6.03	5.68	5.69	5.69	6.05	6.04	5.91
TC1600999	GDPD3	79153	glycerophosphodiester phosphodiester	1.85E-16	4	5.99	4.67	4.59	4.63	4.67	4.76	4.86	4.84
TC1900628	GEMIN7	79760	gem (nuclear organelle) associated pro	2.38E-06	4	4.33	3.70	3.78	3.81	3.90	3.82	3.89	3.88
TC1700935	GGT6	124975	gamma-glutamyltransferase 6 /// gamr	0.000845	4	5.55	5.38	5.36	5.30	5.31	5.36	5.30	5.35
TC1101451	GIF	2694	gastric intrinsic factor (vitamin B synthe	0.000195	4	3.52	3.02	3.08	3.18	3.15	3.18	3.15	3.08
TC0701486	GIGYF1	64599	GRB10 interacting GYF protein 1	0.000907	4	4.95	4.83	4.78	4.76	4.81	4.78	4.77	4.79
TC0700883	GIMAP4	55303	GTPase, IMAP family member 4	1.41E-10	4	7.76	7.00	6.71	6.75	6.28	6.94	7.15	7.59
TC1201557	GIT2	9815	G protein-coupled receptor kinase inte	0.000456	4	9.10	8.62	8.80	8.91	8.81	8.84	8.84	8.86
TC1600312	GIYD1 /// SULT	548593 //	GIY-YIG domain containing 1 /// sulfotr	2.08E-06	4	6.28	6.02	5.94	5.97	6.03	6.03	6.02	6.01

TC1600332	GIYD2 /// SULT	79008 ///	GIY-YIG domain containing 2 /// sulfotr	2.33E-05	4	6.59	6.43	6.33	6.40	6.40	6.43	6.40	6.36
TC1200450	GLI1	2735	glioma-associated oncogene homolog	1.87E-12	4	5.73	5.13	5.12	5.24	5.31	5.34	5.22	5.27
TC1200530	GLIPR1	11010	GLI pathogenesis-related 1 (glioma)	0.000108	4	9.57	8.65	8.77	8.89	8.57	8.92	8.94	9.15
TC0103049	GLUL	2752	glutamate-ammonia ligase (glutamine	6.12E-09	4	7.69	7.25	6.80	7.26	7.14	7.46	7.32	7.46
TC1901323	GMIP	51291	GEM interacting protein	0.000409	4	6.96	6.53	6.45	6.56	6.50	6.41	6.37	6.45
TC1800056	GNAL	2774	guanine nucleotide binding protein (G	0.000466	4	3.01	2.75	2.78	2.81	2.79	2.76	2.86	2.82
TC0102523	GNAT2	2780	guanine nucleotide binding protein (G	9.55E-10	4	5.23	4.51	4.50	4.76	4.56	4.67	4.70	4.57
TC0200416	GNLY	10578	granulysin	0.000115	4	5.05	4.84	4.66	4.68	4.68	4.76	4.82	4.88
TC0600396	GNMT	27232	glycine N-methyltransferase	8.36E-17	4	4.46	3.58	3.50	3.64	3.72	3.66	3.69	3.60
TC0800815	GNRH1	2796	gonadotropin-releasing hormone 1 (lut	3.28E-06	4	5.05	4.00	4.09	4.21	4.32	4.39	4.43	4.47
TC1201486	GOLGA2L1	55592	golgi autoantigen, golgin subfamily a, 2	4.25E-07	4	4.05	3.82	3.80	3.75	3.80	3.76	3.77	3.83
TC1500809	GOLGA8B /// G	440270 //	golgi autoantigen, golgin subfamily a, 8	9.84E-07	4	5.46	5.17	5.17	5.17	5.20	5.19	5.24	5.17
TC0301490	GOLGB1	2804	golgin B1, golgi integral membrane pro	5.39E-06	4	6.67	5.95	5.68	5.70	5.67	5.80	6.12	6.01
TC0102838	GON4L	54856	gon-4-like (C. elegans) /// GON-4-like p	6.58E-13	4	6.56	6.01	5.77	5.83	5.83	5.96	6.14	6.08
TC0102961	GPA33	10223	glycoprotein A33 (transmembrane)	0.000412	4	4.11	3.73	3.82	3.78	3.78	3.76	3.65	3.80
TC0300446	GPR128	84873	G protein-coupled receptor 128	6.46E-05	4	2.54	2.24	2.30	2.23	2.17	2.14	2.19	2.21
TC0202111	GPR155	151556	G protein-coupled receptor 155	2.33E-08	4	6.40	6.21	5.71	5.60	5.40	5.91	5.95	5.98
TC1200062	GPR162 /// LE	27239 ///	G protein-coupled receptor 162 /// lep	0.000703	4	4.85	4.71	4.71	4.65	4.70	4.69	4.66	4.67
TC1300612	GPR18	2841	G protein-coupled receptor 18	5.39E-06	4	4.79	4.08	4.01	4.11	4.05	4.31	4.34	4.37
TC1200999	GPR19	2842	G protein-coupled receptor 19	5.01E-09	4	3.48	2.98	2.93	2.95	3.04	3.00	2.94	3.11
TC0100803	GPR61	83873	G protein-coupled receptor 61	0.000243	4	3.64	3.38	3.38	3.31	3.38	3.41	3.33	3.43
TC1401063	GPR68	8111	G protein-coupled receptor 68	2.55E-11	4	6.12	5.75	5.65	5.56	5.62	5.75	5.76	5.79
TC1900669	GPR77	27202	G protein-coupled receptor 77	0.000142	4	4.95	4.31	4.33	4.39	4.32	4.41	4.26	4.40
TC0300508	GRAMD1C	54762	GRAM domain containing 1C	2.05E-28	4	5.10	2.93	2.74	2.83	2.95	3.38	3.53	3.68
TC0901202	GRIN3A	116443	glutamate receptor, ionotropic, N-met	2.36E-06	4	3.57	3.29	3.35	3.32	3.25	3.29	3.37	3.45
TC1701300	GSDML	55876	gasdermin-like /// gasdermin-like isofo	8.60E-18	4	4.94	3.85	3.74	3.96	3.83	3.99	4.19	4.18
TC0100807	GSTM4 /// GST	642160 //	glutathione S-transferase M4 /// glutat	9.87E-08	4	5.04	4.44	4.41	4.56	4.56	4.66	4.80	4.76
TC0201388	GTF3C2	2976	general transcription factor IIIC, polype	0.000302	4	4.95	4.63	4.67	4.67	4.72	4.76	4.82	4.80
TC2000427	GTPBP5	26164	GTP binding protein 5 (putative) /// GT	1.77E-05	4	5.12	5.14	4.83	4.84	4.89	4.96	4.90	5.00
TC0601264	GUCA1B	2979	guanylate cyclase activator 1B (retina)	2.33E-06	4	4.47	3.98	4.06	4.04	4.00	4.01	4.03	4.03
TC1101163	GVIN1	---	CDNA FLJ13373 fis, clone PLACE100074	2.13E-08	4	6.48	5.37	5.17	5.11	4.69	5.26	6.11	6.14
TC0401299	GYPA	2993	glycophorin A (MNS blood group) /// G	5.06E-05	4	4.70	3.24	3.17	3.49	3.46	3.48	3.44	3.49
TC1201470	HAL	3034	histidine ammonia-lyase	3.37E-09	4	7.87	6.48	6.04	6.50	6.46	6.64	6.72	6.88
TC1100313	HARBI1 /// KIA	9776	harbinger transposase derived 1 /// Un	0.000136	4	6.45	6.23	6.08	6.15	6.09	6.21	6.21	6.26

TC0501353	HARS	3035	histidyl-tRNA synthetase	0.000895	4	4.96	4.59	4.65	4.77	4.70	4.75	4.85	4.79
TC0500536	HARS2	23438	histidyl-tRNA synthetase 2, mitochondı	6.84E-06	4	5.85	5.21	5.28	5.31	5.24	5.36	5.40	5.32
TC1600007	HBA2 /// HBA1	3040 /// 3	hemoglobin, alpha 2 /// hemoglobin, a	3.22E-05	4	11.97	9.28	8.60	9.63	9.40	9.62	9.59	9.68
TC1201140	HDAC7	51564	histone deacetylase 7	2.20E-05	4	6.13	5.82	5.86	5.87	5.87	5.88	5.80	5.84
TC0700091	HDAC9	9734	histone deacetylase 9 /// Histone deac	3.98E-08	4	4.00	3.76	3.74	3.73	3.69	3.71	3.70	3.81
TC0901182	HEMGN	55363	hemogen	1.44E-13	4	5.43	3.50	3.26	3.48	3.50	3.59	3.51	3.65
TC1501022	HERC1	8925	hect (homologous to the E6-AP (UBE3A	2.73E-05	4	6.58	6.05	5.95	6.06	5.95	5.98	6.13	6.05
TC0400391	HERC3	8916	hect domain and RLD 3	3.61E-12	4	8.61	7.75	7.75	7.62	7.54	7.73	7.71	7.72
TC1600466	HERPUD1	9709	homocysteine-inducible, endoplasmic r	6.74E-10	4	7.01	6.30	6.35	6.38	6.35	6.47	6.50	6.69
TC1700519	HEXIM1	10614	hexamethylene bis-acetamide inducibl	8.02E-10	4	7.49	6.62	6.60	7.07	6.94	6.93	6.99	6.95
TC0801051	HEY1	23462	hairy/enhancer-of-split related with YR	0.000355	4	4.36	4.20	3.96	3.90	3.69	4.11	4.04	4.23
TC1700843	HGS	9146	hepatocyte growth factor-regulated tyı	1.40E-05	4	5.50	5.14	5.08	5.17	5.13	5.15	5.11	5.15
TC1201014	HIST4H4 /// HI	121504 //	histone cluster 4, H4 /// histone cluster	1.40E-07	4	4.48	3.97	3.83	3.77	3.74	4.05	3.82	4.13
TC0601655	HIVEP2	3097	human immunodeficiency virus type I	2.19E-09	4	6.99	7.20	6.52	6.50	6.21	6.81	7.00	7.03
TC1900485	HKR1	284459	GLI-Kruppel family member HKR1 /// K	3.32E-06	4	4.65	4.41	4.41	4.34	4.35	4.34	4.38	4.39
TC0601168	HLA-DMA	3108	major histocompatibility complex, class	7.83E-06	4	4.81	4.29	4.31	4.39	4.33	4.38	4.61	4.69
TC0601162	HLA-DOB	3112	major histocompatibility complex, class	0.000961	4	3.87	3.50	3.47	3.39	3.39	3.50	3.48	3.60
TC0600230	HLA-F	3134	major histocompatibility complex, class	1.03E-12	4	7.06	6.47	6.41	6.46	6.39	6.66	6.79	6.84
TC2000164	HM13	81502	histocompatibility (minor) 13 /// Minor	0.000263	4	6.07	5.65	5.61	5.70	5.74	5.87	5.87	5.91
TC1900031	HMHA1	23526	histocompatibility (minor) HA-1	0.000204	4	6.02	5.74	5.60	5.66	5.70	5.67	5.64	5.72
TC0501551	HNRNPH1 /// H	3187	heterogeneous nuclear ribonucleoprot	4.59E-06	4	5.52	5.00	4.84	4.92	5.16	5.23	5.33	5.10
TC1000289	HNRNPH3	3189	heterogeneous nuclear ribonucleoprot	4.22E-15	4	8.60	7.98	7.83	7.77	7.85	8.19	8.28	8.32
TC0701082	HOXA2	3199	homeobox A2	1.27E-06	4	5.98	4.82	4.63	4.79	4.74	4.91	4.86	5.00
TC1101155	HPX	3263	hemopexin	0.000197	4	3.91	3.72	3.69	3.67	3.68	3.67	3.65	3.70
TC0301253	hsa-let-7g	---	hsa-let-7g [Source:miRBase;Acc:MI000	4.48E-13	4	7.63	5.51	5.40	5.57	5.36	5.94	6.13	6.31
TC0102328	hsa-mir-101-1	---	hsa-mir-101-1 [Source:miRBase;Acc:MI	0.000224	4	4.06	3.39	3.35	3.28	3.13	3.51	3.76	3.64
TC2000047	hsa-mir-103-2	---	hsa-mir-103-2 [Source:miRBase;Acc:MI	2.38E-21	4	9.76	8.11	7.85	7.98	7.92	8.33	8.45	8.79
TC0100436	hsa-mir-30e	---	hsa-mir-30e [Source:miRBase;Acc:MI0	0.000655	4	4.97	3.73	3.81	4.02	3.86	3.98	4.18	4.19
TC1700977	hsa-mir-324	---	hsa-mir-324 [Source:miRBase;Acc:MI0	0.00046	4	4.34	3.82	3.74	3.79	3.80	3.65	3.66	3.68
TC0101233	HSD17B7	730412 //	hydroxysteroid (17-beta) dehydrogena	1.75E-11	4	4.56	4.06	4.11	4.13	4.13	4.29	4.41	4.35
TC1000171	HSD17B7P2	---	hydroxysteroid (17-beta) dehydrogena	6.90E-11	4	4.72	4.30	4.34	4.32	4.27	4.41	4.56	4.46
TC1200007	HSN2	378465	hereditary sensory neuropathy, type II	1.21E-13	4	7.40	6.30	6.09	6.08	6.09	6.31	6.29	6.19
TC0301498	HSPBAP1	79663	HSPB (heat shock 27kDa) associated pr	6.45E-06	4	6.59	5.86	5.82	5.98	5.95	5.99	5.90	5.86
TC0200361	HTRA2	27429	HtrA serine peptidase 2 /// Serine prot	3.59E-05	4	5.77	5.39	5.44	5.38	5.45	5.50	5.52	5.46

TC0X00949	HUWE1	10075	HECT, UBA and WWE domain containi	0.000128	4	6.20	5.94	5.67	5.75	5.71	5.77	5.95	5.84
TC1201565	HVCN1	84329	hydrogen voltage-gated channel 1 ///	1.18E-19	4	6.21	5.23	5.05	5.27	5.30	5.48	5.62	5.88
TC1901160	ICAM3	3385	intercellular adhesion molecule 3	3.04E-05	4	6.47	5.96	6.01	6.15	6.11	6.09	6.05	6.13
TC1200904	IFFO /// NP_54	25900	intermediate filament family orphan //	1.36E-10	4	4.89	4.32	4.43	4.46	4.45	4.43	4.49	4.42
TC1101030	IFITM5	387733	interferon induced transmembrane pr	0.000759	4	5.56	5.06	5.15	5.03	5.12	5.10	5.02	5.12
TC0900108	IFNK	56832	interferon, kappa	1.03E-07	4	4.49	3.53	3.53	3.99	3.47	3.82	3.56	3.55
TC0201392	IFT172	26160	intraflagellar transport 172 homolog (C	0.000506	4	3.45	3.32	3.36	3.31	3.30	3.28	3.30	3.31
TC0600859	IGF2R	3482	insulin-like growth factor 2 receptor	3.57E-07	4	10.09	9.42	8.99	9.12	9.14	9.33	9.22	9.36
TC0301188	IHPK2	51447	inositol hexaphosphate kinase 2	5.16E-06	4	5.35	5.12	5.06	5.10	5.04	5.15	5.18	5.21
TC0800254	IKBKB	3551	inhibitor of kappa light polypeptide ge	2.63E-12	4	6.11	5.40	5.33	5.39	5.42	5.37	5.49	5.41
TC1001326	IKZF5	64376	IKAROS family zinc finger 5 (Pegasus) //	0.000197	4	5.65	5.57	5.52	5.51	5.40	5.54	5.65	5.64
TC0900149	IL11RA /// GAL	3590 ///	interleukin 11 receptor, alpha /// galac	0.000496	4	4.40	4.22	4.26	4.24	4.24	4.25	4.28	4.25
TC1901295	IL12RB1	3594	interleukin 12 receptor, beta 1	1.46E-08	4	5.18	4.80	4.68	4.76	4.77	4.88	4.96	5.06
TC1500548	IL16	3603	interleukin 16 (lymphocyte chemoattra	2.00E-09	4	5.59	5.00	5.17	5.28	5.21	5.27	5.30	5.36
TC1100641	IL18BP	10068	interleukin 18 binding protein /// interl	2.02E-08	4	4.58	4.22	4.19	4.20	4.18	4.26	4.26	4.33
TC1200431	IL23A	51561	interleukin 23, alpha subunit p19	1.21E-05	4	3.80	3.37	3.30	3.31	3.33	3.40	3.31	3.45
TC0101468	IL24	11009	interleukin 24	3.04E-15	4	3.94	3.30	3.28	3.23	3.22	3.28	3.29	3.40
TC1600110	IL32	9235	interleukin 32	1.38E-12	4	5.35	4.62	4.53	4.66	4.67	4.68	4.71	4.77
TC0500120	IL7R	3575	interleukin 7 receptor /// Interleukin-7	2.18E-05	4	4.85	3.73	3.60	3.82	3.66	3.70	3.90	3.91
TC0400312	IL8	3576	interleukin 8	1.69E-15	4	9.55	8.59	7.07	6.91	7.43	8.36	8.06	9.12
TC0Y00105	IL9R	3581	interleukin 9 receptor	5.58E-05	4	5.65	5.43	5.37	5.37	5.42	5.46	5.35	5.42
TC0X00184	INE1	---	Putative inactivation escape 1 protein.	5.98E-10	4	5.19	4.13	4.09	3.99	4.14	4.16	4.18	4.24
TC1200910	ING4	51147	inhibitor of growth family, member 4	1.85E-17	4	6.00	5.22	5.23	5.40	5.39	5.42	5.46	5.52
TC0102134	INPP5B	3633	inositol polyphosphate-5-phosphatase,	1.67E-09	4	5.12	4.33	4.41	4.56	4.48	4.58	4.82	4.76
TC0201195	INPP5D /// Q6	3635	inositol polyphosphate-5-phosphatase,	2.07E-07	4	8.09	7.40	7.35	7.51	7.46	7.44	7.53	7.60
TC0101087	INTS3	65123	integrator complex subunit 3 /// Integr	8.46E-05	4	6.55	6.07	6.04	5.97	5.94	6.00	6.01	5.99
TC1101688	INTS4	92105	integrator complex subunit 4	0.000245	4	5.46	5.12	5.03	5.20	5.17	5.20	5.28	5.25
TC0700025	IQCE	23288	IQ motif containing E /// IQ domain-co	4.70E-07	4	5.49	5.12	5.21	5.18	5.02	5.18	5.33	5.32
TC0300298	IQCF2	389123	IQ motif containing F2	9.41E-05	4	2.78	2.40	2.40	2.36	2.40	2.33	2.26	2.42
TC1901693	IRF3	3661	interferon regulatory factor 3 /// Interf	1.46E-05	4	5.57	5.29	5.27	5.33	5.34	5.35	5.36	5.33
TC1500509	ISL2	64843	ISL LIM homeobox 2	0.000961	4	4.58	4.51	4.40	4.36	4.40	4.39	4.35	4.55
TC2200228	ISX	91464	intestine-specific homeobox	0.000312	4	3.88	3.69	3.72	3.58	3.68	3.69	3.63	3.68
TC1200019	ITFG2	55846	integrin alpha FG-GAP repeat containin	7.03E-08	4	5.07	4.75	4.76	4.80	4.81	4.81	4.88	4.91
TC1201266	ITGA5	3678	integrin, alpha 5 (fibronectin receptor,	1.55E-11	4	7.15	6.19	6.09	6.33	6.34	6.58	6.47	6.67

TC1600361	ITGAD	3681	integrin, alpha D /// Integrin alpha-D p	2.79E-05	4	4.51	4.31	4.32	4.28	4.28	4.27	4.24	4.26
TC1600339	ITGAL	3683	integrin, alpha L (antigen CD11A (p180	1.39E-05	4	7.49	6.80	7.11	7.41	7.15	7.12	7.16	7.15
TC1600360	ITGAX	3687	integrin, alpha X (complement compon	3.98E-12	4	9.25	7.65	7.84	8.06	7.88	7.77	7.63	7.63
TC1000043	ITIH2	3698	inter-alpha (globulin) inhibitor H2 /// I	0.00031	4	2.87	2.68	2.70	2.63	2.66	2.66	2.69	2.69
TC0300011	ITPR1	3708	inositol 1,4,5-triphosphate receptor, ty	6.26E-08	4	5.03	4.59	4.44	4.65	4.48	4.54	4.76	4.81
TC1201058	ITPR2	3709	inositol 1,4,5-triphosphate receptor, ty	3.02E-06	4	6.58	5.90	6.17	6.29	6.08	6.17	6.35	6.24
TC0201356	ITSN2	50618	intersectin 2	9.24E-08	4	7.44	7.13	7.07	6.97	6.93	6.97	7.04	6.97
TC0102325	JAK1	3716	Janus kinase 1 (a protein tyrosine kinas	2.07E-05	4	9.07	8.55	8.36	8.50	8.39	8.55	8.58	8.66
TC1200861	JARID1A	5927	jumonji, AT rich interactive domain 1A	4.26E-05	4	7.89	7.81	7.53	7.60	7.48	7.67	7.66	7.69
TC0X00945	JARID1C	8242	jumonji, AT rich interactive domain 1C	0.00036	4	5.95	5.51	5.39	5.54	5.51	5.44	5.40	5.42
TC0600093	JARID2	3720	jumonji, AT rich interactive domain 2	1.36E-23	4	7.53	6.23	6.00	6.60	6.60	6.77	6.88	7.04
TC0200421	JMJD1A	55818	jumonji domain containing 1A /// JmjC	3.05E-13	4	7.51	6.71	6.63	6.94	6.85	7.07	7.13	7.19
TC1001011	JMJD1C	221037	jumonji domain containing 1C /// Prob	3.14E-11	4	8.98	8.15	8.00	8.04	7.89	8.30	8.36	8.48
TC1101745	JOSD3	79101	Josephin domain containing 3	7.27E-14	4	5.30	4.44	4.40	4.54	4.58	4.82	5.02	4.91
TC1700998	KCNAB3	9196	potassium voltage-gated channel, shak	1.51E-06	4	3.85	3.59	3.55	3.47	3.51	3.50	3.55	3.48
TC0202400	KCNJ13	3769	potassium inwardly-rectifying channel,	9.18E-05	4	4.98	4.50	4.36	4.41	4.30	4.36	4.38	4.33
TC0101185	KCNJ9	3765	potassium inwardly-rectifying channel,	0.000788	4	4.51	4.17	4.18	4.15	4.12	4.22	4.01	4.21
TC1101546	KCNK7	10089	potassium channel, subfamily K, memb	3.49E-07	4	5.51	5.35	5.25	5.17	5.21	5.26	5.30	5.27
TC1300150	KCNRG /// TRI	283518 //	potassium channel regulator /// tripart	1.10E-09	4	6.91	6.31	6.43	6.46	6.44	6.45	6.52	6.43
TC1300447	KCTD4	386618	potassium channel tetramerisation do	0.000119	4	2.90	2.65	2.64	2.55	2.44	2.53	2.57	2.58
TC2200274	KDELR3	11015	KDEL (Lys-Asp-Glu-Leu) endoplasmic re	7.23E-05	4	4.43	4.10	4.16	4.10	4.12	4.18	4.10	4.22
TC0500563	KIAA0141	9812	KIAA0141	6.53E-09	4	4.91	4.72	4.54	4.60	4.71	4.76	4.78	4.71
TC1600580	KIAA0174	9798	KIAA0174 /// Uncharacterized protein	0.000416	4	8.22	7.90	7.82	7.89	7.80	7.92	7.84	7.93
TC0301912	KIAA0226	9711	KIAA0226 /// Uncharacterized protein	9.04E-05	4	5.63	5.32	5.23	5.37	5.22	5.29	5.40	5.53
TC0601001	KIAA0319	9856	KIAA0319	1.21E-10	4	4.32	3.65	3.59	3.83	3.86	4.02	4.08	3.96
TC1900417	KIAA0355	9710	KIAA0355	3.79E-12	4	5.40	5.01	4.77	4.77	4.71	4.96	5.05	5.17
TC1600892	KIAA0430	9665	KIAA0430 /// Limkain-b1. [Source:Unip	1.15E-10	4	8.57	7.59	7.50	7.74	7.60	7.72	7.77	7.83
TC1600640	KIAA0513	9764	KIAA0513	0.000124	4	7.05	6.63	6.41	6.61	6.54	6.60	6.54	6.69
TC1600286	KIAA0556	23247	KIAA0556 /// CDNA FLJ40166 fis, clone	1.03E-08	4	5.28	4.85	4.73	4.77	4.76	4.83	4.81	4.86
TC1700962	KIAA0753	9851	KIAA0753	1.03E-16	4	4.96	4.09	4.06	4.10	4.06	4.26	4.40	4.36
TC0701131	KIAA0895 /// N	23366	KIAA0895 protein	2.68E-05	4	3.29	2.96	2.99	3.03	3.06	3.00	2.94	2.99
TC0102840	KIAA0907	22889	KIAA0907 /// BLOM7 beta (Novel prote	1.46E-08	4	5.63	5.09	5.18	5.25	5.20	5.34	5.42	5.48
TC1000346	KIAA0913	23053	KIAA0913	1.34E-08	4	6.10	5.64	5.42	5.50	5.50	5.51	5.51	5.45
TC1101860	KIAA0999 /// C	23387	KIAA0999 protein /// Serine/threonine	1.14E-10	4	7.38	6.88	6.50	6.75	6.64	6.75	6.83	6.93

TC0400509	KIAA1109	84162	KIAA1109 /// KIAA1109 (KIAA1109), m	1.75E-05	4	7.23	6.92	6.61	6.48	6.45	6.60	6.72	6.67
TC2000257	KIAA1219	57148	KIAA1219 /// K1219_HUMAN Isoform	0.000513	4	7.07	6.79	6.74	6.68	6.52	6.65	6.75	6.74
TC0301545	KIAA1257 /// C	57501	KIAA1257 /// CDNA FLJ43738 fis, clone	5.63E-14	4	5.01	4.18	4.09	4.25	4.28	4.48	4.45	4.60
TC1701453	KIAA1267	284058	KIAA1267	0.000379	4	6.79	6.20	6.17	6.33	6.25	6.32	6.31	6.38
TC0400843	KIAA1276	27146	KIAA1276 protein	8.26E-07	4	4.60	4.37	4.32	4.36	4.33	4.36	4.42	4.45
TC0100797	KIAA1324	57535	KIAA1324 /// K1324_HUMAN Isoform	0.000831	4	7.32	6.07	5.58	6.37	6.38	6.80	6.52	6.77
TC1500966	KIAA1370	56204	KIAA1370	7.89E-21	4	6.13	4.95	4.75	4.81	4.77	5.03	5.25	5.37
TC1800228	KIAA1468	57614	KIAA1468	8.87E-11	4	6.29	5.56	5.55	5.51	5.41	5.63	5.73	5.65
TC0400019	KIAA1530 ///	57654	KIAA1530	5.39E-12	4	5.19	4.92	4.88	4.81	4.78	4.83	4.81	4.85
TC1601303	KIAA1609	57707	KIAA1609	0.000734	4	4.65	4.54	4.50	4.46	4.46	4.45	4.49	4.51
TC1901298	KIAA1683	80726	KIAA1683 /// Uncharacterized protein	1.49E-13	4	5.22	4.55	4.49	4.66	4.52	4.66	4.73	4.83
TC1400390	KIAA1737	85457	KIAA1737	0.000289	4	5.25	5.08	4.94	5.00	5.10	5.06	5.08	5.16
TC1700986	KIAA1787 /// G	84461 ///	KIAA1787 protein /// G protein pathwa	2.12E-07	4	5.31	5.12	5.03	5.08	5.09	5.12	5.09	5.16
TC1901056	KIAA1881	729359	KIAA1881	3.87E-05	4	4.57	4.36	4.33	4.26	4.27	4.25	4.31	4.24
TC0901080	KIF27 /// C17o	55582	kinesin family member 27 /// Uncharac	7.70E-11	4	7.05	5.54	5.44	5.60	5.60	6.07	6.32	6.35
TC0301164	KIF9	64147	kinesin family member 9	4.47E-06	4	3.62	3.47	3.48	3.54	3.62	3.51	3.49	3.54
TC0600401	KLC4	89953	kinesin light chain 4	2.19E-10	4	5.07	4.80	4.75	4.76	4.75	4.77	4.75	4.85
TC1400211	KLHDC2	23588	kelch domain containing 2	0.000179	4	5.70	5.25	5.33	5.35	5.24	5.33	5.51	5.54
TC0101816	KLHL21	9903	kelch-like 21 (Drosophila) /// Kelch-like	2.18E-05	4	5.52	4.97	5.06	5.17	5.15	5.19	5.18	5.30
TC1200956	KLRB1	3820	killer cell lectin-like receptor subfamily	3.18E-05	4	3.88	3.20	3.03	3.06	3.06	3.03	3.21	3.45
TC1200107	KLRG1	10219	killer cell lectin-like receptor subfamily	2.38E-05	4	3.52	2.96	3.02	2.96	2.96	2.93	3.09	3.00
TC0101063	KPRP	448834	keratinocyte proline-rich protein	0.000117	4	4.56	4.19	4.13	4.04	4.12	4.19	4.21	4.31
TC1200359	KRT18	3875	keratin 18	5.87E-05	4	4.96	4.75	4.71	4.70	4.71	4.81	4.77	4.77
TC17r00013	KRT40	125115	keratin 40	0.00017	4	3.56	3.35	3.37	3.30	3.37	3.34	3.27	3.36
TC1201234	KRT77	374454	keratin 77	0.000172	4	4.41	4.14	4.14	4.15	4.01	4.04	4.04	4.13
TC2100289	KRTAP21-1	337977	keratin associated protein 21-1	0.000931	4	4.36	4.09	4.03	3.93	3.97	4.05	4.28	4.19
TC0301587	KY	339855	kyphoscoliosis peptidase /// Kyphoscol	1.16E-26	4	6.36	4.65	4.49	4.88	4.95	5.24	5.16	5.29
TC1201189	LASS5	91012	LAG1 homolog, ceramide synthase 5 //	7.16E-08	4	5.14	4.85	4.78	4.75	4.66	4.77	4.85	4.85
TC0501484	LCP2	3937	lymphocyte cytosolic protein 2 (SH2 do	1.02E-05	4	9.64	9.28	9.13	9.32	9.23	9.38	9.38	9.56
TC1001241	LDB1	8861	LIM domain binding 1	4.25E-07	4	7.73	6.96	6.87	7.07	7.14	7.15	7.19	7.25
TC0500474	LEAP2	116842	liver expressed antimicrobial peptide 2	2.84E-05	4	4.43	3.99	3.85	3.91	3.86	3.94	3.93	3.89
TC1900860	LENG8	114823	leukocyte receptor cluster (LRC) memb	3.13E-16	4	6.31	5.64	5.53	5.63	5.66	5.62	5.63	5.60
TC1200338	LETMD1	25875	LETM1 domain containing 1 /// LETM1	5.65E-05	4	4.39	4.05	3.99	4.09	4.18	4.19	4.19	4.14
TC1700275	LGALS9 /// KSR	8844 ///	kinase suppressor of ras 1 /// lectin, ga	1.21E-09	4	6.16	5.51	5.63	5.75	5.53	5.70	5.84	5.89

TC1900864	LILRA1	11024	leukocyte immunoglobulin-like receptc	1.13E-08	4	8.05	6.97	7.06	7.27	7.17	7.43	7.47	7.62
TC1201167	LMBR1L	55716	limb region 1 homolog (mouse)-like ///	2.36E-13	4	5.48	5.06	4.92	4.89	4.84	4.92	4.91	5.00
TC1500261	LOC100137047	8681	hypothetical protein LOC8681 /// Cytos	7.45E-06	4	4.55	4.38	4.37	4.30	4.34	4.35	4.34	4.34
TC0X01007	LOC158830	158830	similar to Ab2-183	1.79E-15	4	6.77	5.27	4.92	5.51	5.46	5.67	5.68	5.56
TC0301514	LOC200810	200810	similar to beta-1,4-mannosyltransferas	2.68E-06	4	5.56	5.31	5.29	5.26	5.24	5.32	5.24	5.27
TC1600929	LOC23117 /// N	23117	KIAA0220-like protein /// solute carrier	1.04E-14	4	6.92	5.93	5.79	5.72	5.83	5.81	5.97	5.87
TC1600258	LOC23117 /// C	23117	KIAA0220-like protein /// Uncharacteri	9.95E-14	4	7.04	6.14	5.99	5.92	6.03	6.03	6.20	6.04
TC1101892	LOC283152	283152	hypothetical protein LOC283152	1.08E-05	4	4.70	4.38	4.35	4.33	4.34	4.39	4.48	4.47
TC0200489	LOC285033	285033	hypothetical protein LOC285033	8.59E-10	4	4.44	3.92	3.91	4.08	4.17	4.11	4.12	4.11
TC0701273	LOC285908	285908	hypothetical protein LOC285908	1.22E-07	4	4.52	4.18	4.14	4.10	4.12	4.17	4.12	4.14
TC1600562	LOC348174 ///	348174 //	secretory protein LOC348174 /// hypot	2.75E-06	4	5.50	5.27	5.24	5.25	5.27	5.29	5.25	5.26
TC0500068	LOC391767	391767	similar to hCG1989915	0.000311	4	3.84	3.30	3.37	3.23	3.12	3.12	3.11	3.35
TC1400005	LOC400879	400879	hypothetical LOC400879	0.000711	4	3.36	3.22	3.16	3.15	3.16	3.14	3.13	3.15
TC0701480	LOC402573	402573	hypothetical LOC402573	0.000258	4	4.51	3.87	3.83	4.05	4.03	4.16	4.13	3.97
TC1600591	LOC440348	440348	similar to nuclear pore complex interac	6.31E-12	4	3.88	3.27	3.27	3.24	3.29	3.33	3.45	3.24
TC1701624	LOC440456	440456	similar to pleckstrin homology domain	1.16E-10	4	6.47	5.75	5.53	5.63	5.69	5.61	5.62	5.62
TC0700408	LOC442590	442590	similar to Williams Beuren syndrome ch	2.12E-10	4	6.07	5.20	5.06	5.23	5.31	5.35	5.53	5.48
TC0501555	LOC51149 /// N	51149	hypothetical LOC51149 /// Truncated c	0.000526	4	4.25	4.04	4.03	4.01	4.00	4.08	4.07	4.11
TC0600393	LOC642451 ///	642451 //	similar to ribosomal protein L7-like 1 //	7.01E-06	4	4.82	4.50	4.48	4.55	4.63	4.60	4.73	4.59
TC1701625	LOC644397 ///	644397 //	similar to hCG2036502 /// leucine rich	0.000126	4	5.75	5.45	5.53	5.61	5.64	5.63	5.58	5.59
TC0X00376	LOC644732 ///	644732 //	similar to ATPase, Cu++ transporting, a	2.41E-08	4	6.34	5.79	6.03	5.84	5.60	5.95	6.06	6.09
TC0701777	LOC645159 ///	645159 //	similar to ALR-like protein /// myeloid/	1.33E-13	4	8.61	7.71	7.43	7.52	7.49	7.62	7.74	7.76
TC1600563	LOC650883 ///	650883 //	similar to pyruvate dehydrogenase phc	6.72E-09	4	5.42	4.81	4.81	4.94	4.87	4.92	5.03	5.06
TC0100779	LOC652899 ///	652899 //	similar to Salivary alpha-amylase precu	1.36E-06	4	3.92	3.64	3.72	3.62	3.61	3.59	3.63	3.60
TC1200106	LOC653441 ///	653441 //	similar to polyhomeotic 1-like /// polyh	6.33E-05	4	4.58	4.48	4.41	4.49	4.43	4.42	4.50	4.52
TC0102673	LOC653598	653598	similar to cyclophilin-LC (COAS2)	0.000489	4	3.10	2.82	2.89	2.76	2.85	2.89	2.98	2.93
TC0102622	LOC653598 ///	653598 //	similar to cyclophilin-LC (COAS2) /// pe	0.000933	4	2.78	2.53	2.47	2.41	2.53	2.58	2.65	2.54
TC0201251	LOC727737 ///	727737 //	similar to APG4 autophagy 4 homolog I	1.13E-05	4	5.90	5.65	5.61	5.59	5.66	5.66	5.66	5.66
TC0X01336	LOC727913 ///	727913 //	similar to iduronate 2-sulfatase (Hunte	2.84E-05	4	6.35	5.80	5.83	5.92	5.84	5.94	5.90	6.03
TC0601359	LOC727945	727945	similar to hCG1651100	5.25E-06	4	6.09	4.93	5.24	5.19	5.28	5.27	5.33	5.28
TC0201835	LOC728601	728601	similar to HDCMB45P	8.85E-08	4	6.62	5.48	5.47	5.54	5.60	5.82	5.79	5.85
TC0901011	LOC728601	728601	similar to HDCMB45P	7.30E-05	4	3.79	2.75	2.81	2.93	2.90	2.94	2.91	2.99
TC0900265	LOC728601	728601	similar to HDCMB45P	0.000278	4	2.96	2.48	2.47	2.46	2.40	2.40	2.56	2.64
TC1600964	LOC728741	728741	hypothetical LOC728741	5.94E-05	4	5.76	5.10	5.15	5.07	5.12	5.16	5.27	5.17

TC1600963	LOC728741 ///	728741 //	hypothetical LOC728741 /// similar to	6.58E-06	4	5.39	5.19	5.12	5.15	5.20	5.20	5.20	5.17
TC1600295	LOC728741 ///	728741 //	hypothetical LOC728741 /// similar to	7.24E-11	4	6.26	5.79	5.78	5.73	5.81	5.81	5.83	5.78
TC0900274	LOC728877 ///	728877	similar to COBW domain containing 3 /	1.12E-20	4	5.01	4.01	4.03	4.04	4.07	4.34	4.44	4.45
TC0901005	LOC728877 ///	728877 //	similar to COBW domain containing 3 /	3.38E-18	4	5.14	4.24	4.29	4.29	4.28	4.57	4.68	4.63
TC0700352	LOC729597	729597	similar to Williams-Beuren syndrome c	2.08E-07	4	5.58	5.07	5.04	5.12	5.11	5.12	5.10	5.17
TC0700216	LOC729597 ///	729597 //	similar to Williams-Beuren syndrome c	1.86E-10	4	4.68	4.09	3.93	4.07	4.07	4.15	4.26	4.25
TC1800337	LOC729602	729602	similar to nuclear pore complex interac	9.15E-13	4	5.82	5.02	4.72	4.80	4.83	4.83	4.96	4.86
TC1600891	LOC729978	729978	similar to LOC339047 protein	8.20E-09	4	6.90	5.89	5.67	5.68	5.85	5.67	5.98	5.88
TC0701340	LOC730323 ///	730323 //	similar to postmeiotic segregation incr	1.17E-16	4	6.45	5.73	5.66	5.88	5.83	5.89	6.01	5.93
TC0700373	LOC730324 ///	730324 //	similar to postmeiotic segregation incr	4.13E-06	4	4.66	4.25	4.24	4.31	4.39	4.39	4.46	4.40
TC0100778	LOC730924 ///	730924 //	similar to Pancreatic alpha-amylase pr	7.99E-25	4	4.71	3.71	3.79	3.73	3.68	3.76	3.86	3.82
TC1601024	LOC90835	90835	hypothetical protein LOC90835	1.82E-26	4	5.21	4.47	4.45	4.47	4.51	4.56	4.55	4.66
TC0201159	LOC93349 ///	93349	hypothetical protein BC004921 /// CD	6.46E-06	4	6.10	5.92	5.69	5.65	5.54	5.82	6.08	6.01
TC1901322	LPAR2	9170	lysophosphatidic acid receptor 2	4.27E-12	4	5.30	4.67	4.63	4.62	4.74	4.77	4.75	4.74
TC1800301	LPIN2	9663	lipin 2	1.30E-17	4	7.80	6.74	6.54	6.92	6.88	7.06	7.14	7.34
TC0300889	LPP	4026	LIM domain containing preferred trans	4.58E-10	4	6.54	6.13	5.94	5.87	5.81	5.96	5.91	6.04
TC1101432	LPXN	9404	leupaxin	2.90E-07	4	4.65	4.08	4.24	4.32	4.10	4.17	4.32	4.25
TC0701483	LRCH4 /// Q8T	4034	leucine-rich repeats and calponin hom	3.36E-10	4	5.84	5.48	5.45	5.47	5.48	5.49	5.47	5.48
TC1700532	LRRC37A	9884	leucine rich repeat containing 37A ///	0.000345	4	6.96	6.38	6.34	6.55	6.57	6.60	6.72	6.65
TC1200250	LRRK2	120892	leucine-rich repeat kinase 2 /// Leucin	3.84E-07	4	9.66	8.80	8.76	9.07	8.89	9.11	9.08	9.25
TC0700576	LRWD1	222229	leucine-rich repeats and WD repeat do	7.45E-13	4	5.65	5.26	5.20	5.23	5.28	5.28	5.27	5.24
TC1600709	LUC7L	55692	LUC7-like (S. cerevisiae)	0.000151	4	5.12	4.76	4.57	4.56	4.59	4.64	4.75	4.56
TC0600275	LY6G5B /// CS	58496 ///	lymphocyte antigen 6 complex, locus G	1.61E-19	4	5.70	5.12	5.02	5.02	5.11	5.11	5.09	5.15
TC1901540	LYPD4	147719	LY6/PLAUR domain containing 4 /// Ly	8.31E-06	4	4.14	3.78	3.88	3.84	3.80	3.80	3.77	3.78
TC0103376	LYST	1130	lysosomal trafficking regulator	4.01E-16	4	9.29	8.20	8.15	8.17	8.11	8.42	8.46	8.54
TC1101204	LYVE1	10894	lymphatic vessel endothelial hyalurona	9.64E-10	4	5.04	4.14	4.07	4.02	4.01	4.32	4.26	4.24
TC2200271	MAFF	23764	v-maf musculoaponeurotic fibrosarco	2.57E-06	4	4.98	4.84	4.43	4.36	4.53	4.79	4.79	4.99
TC1101542	MALAT_HUMA	---	Metastasis-associated lung adenocarci	2.81E-05	4	12.29	12.05	12.09	11.99	11.99	12.12	12.15	12.24
TC2000242	MANBAL	731453 //	mannosidase, beta A, lysosomal-like	0.000115	4	4.94	4.64	4.70	4.76	4.72	4.79	4.77	4.81
TC1201251	MAP3K12	7786	mitogen-activated protein kinase kinas	3.64E-07	4	4.80	4.53	4.46	4.46	4.49	4.53	4.48	4.51
TC1701442	MAP3K14	9020	mitogen-activated protein kinase kinas	7.37E-15	4	4.93	4.45	4.40	4.43	4.44	4.49	4.46	4.55
TC0X00803	MAP3K15	389840	mitogen-activated protein kinase kinas	0.000379	4	3.25	3.09	3.11	3.06	3.20	3.16	3.16	3.14
TC0600799	MAP3K7IP2	23118	mitogen-activated protein kinase kinas	0.000351	4	8.83	8.55	8.49	8.61	8.52	8.69	8.67	8.76
TC0X00835	MAP3K7IP3	257397	mitogen-activated protein kinase kinas	0.000257	4	5.60	5.41	5.32	5.33	5.19	5.29	5.27	5.33

TC1400962	MAP3K9	4293	mitogen-activated protein kinase kinas	0.000664	4	4.09	3.91	3.95	3.90	3.88	3.90	3.89	3.89
TC1101521	MAP4K2	5871	mitogen-activated protein kinase kinas	0.000516	4	5.09	5.03	4.86	4.96	5.01	5.03	4.90	4.99
TC0601630	MAP7	9053	microtubule-associated protein 7 /// Er	6.52E-08	4	4.80	4.51	4.42	4.46	4.43	4.56	4.56	4.66
TC0600340	MAPK13	5603	mitogen-activated protein kinase 13 //,	6.99E-12	4	5.93	5.56	5.53	5.48	5.44	5.53	5.38	5.40
TC1000228	MAPK8	5599	mitogen-activated protein kinase 8 ///	9.72E-10	4	4.49	4.08	3.91	3.97	3.95	4.03	4.18	4.22
TC1600058	MAPK8IP3	23162	mitogen-activated protein kinase 8 inte	2.71E-08	4	5.21	4.90	4.91	4.91	4.89	4.86	4.81	4.85
TC1000927	MAR8	220972	membrane-associated ring finger (C3H(	9.82E-08	4	7.24	6.75	6.55	6.75	6.66	6.95	6.97	7.06
TC1200451	MARS	4141	methionyl-tRNA synthetase /// Methio	6.28E-24	4	7.21	5.86	5.76	5.91	5.96	5.98	6.15	5.96
TC0101854	MASP2	10747	mannan-binding lectin serine peptidase	3.66E-07	4	4.22	3.99	3.90	3.92	3.89	3.95	3.91	3.95
TC1900314	MAST3	23031	microtubule associated serine/threonir	0.000831	4	7.55	7.13	6.80	6.90	6.90	6.92	6.87	7.06
TC1800474	MBD1	4152	methyl-CpG binding domain protein 1 /	0.000199	4	5.99	5.79	5.74	5.79	5.77	5.79	5.88	5.89
TC1200452	MBD6	114785	methyl-CpG binding domain protein 6 /	1.60E-14	4	7.24	6.48	6.30	6.33	6.36	6.39	6.33	6.36
TC1400794	MBIP	51562	MAP3K12 binding inhibitory protein 1 /	0.000803	4	4.22	4.12	3.87	3.86	3.92	4.02	4.16	4.21
TC0X01246	MBNL3	55796	muscleblind-like 3 (Drosophila) /// Mus	4.93E-10	4	6.64	4.68	4.48	5.03	5.14	5.12	5.16	5.13
TC2100198	MC3AP_HUMA	---	Uncharacterized protein C21orf85 prec	0.000159	4	3.87	3.61	3.60	3.68	3.63	3.63	3.69	3.69
TC1200503	MDM2	4193	Mdm2 p53 binding protein homolog (m	9.86E-10	4	7.94	7.03	7.09	7.33	7.22	7.33	7.51	7.69
TC0101442	MDM4	4194	Mdm4 p53 binding protein homolog (m	8.47E-18	4	8.03	7.13	7.00	6.76	6.75	7.03	7.15	7.18
TC1201601	MED13L	23389	mediator complex subunit 13-like	4.45E-11	4	8.95	8.31	8.08	8.18	8.09	8.30	8.39	8.44
TC1900731	MED25	81857	mediator complex subunit 25 /// ARC/r	3.23E-21	4	6.73	5.86	5.73	5.84	5.88	5.97	5.95	6.11
TC1901315	MEF2B	731041 //	myocyte enhancer factor 2B	0.000443	4	5.32	5.14	5.22	5.28	5.29	5.21	5.17	5.19
TC0501135	MEF2C	4208	myocyte enhancer factor 2C	8.09E-14	4	5.94	5.50	4.75	4.80	4.67	5.22	5.20	5.64
TC1800134	MEP1B	4225	meprin A, beta	0.000569	4	2.82	2.62	2.62	2.62	2.57	2.59	2.59	2.59
TC0700542	MEPCE	56257	methylphosphate capping enzyme	5.80E-08	4	5.50	5.05	4.84	5.02	5.15	5.18	5.06	5.14
TC1400691	METTL3	56339	methyltransferase like 3	4.30E-06	4	5.46	5.07	4.99	5.01	5.02	5.10	5.17	5.15
TC0401246	MFSD8	256471	major facilitator superfamily domain cc	3.34E-11	4	4.29	3.79	3.83	3.79	3.77	3.89	4.02	3.98
TC0700578	MGC119295	441273	similar to Williams-Beuren syndrome cı	0.000329	4	5.05	4.24	4.44	4.38	4.39	4.40	4.37	4.31
TC1001238	MGEA5	10724	meningioma expressed antigen 5 (hyalı	8.32E-21	4	8.86	7.66	7.47	7.45	7.37	7.76	7.84	7.86
TC1600140	MGRN1	23295	mahogunin, ring finger 1	0.000478	4	6.14	5.89	5.71	5.87	5.86	5.70	5.67	5.74
TC1100181	MICAL2	9645	microtubule associated monoxygenase	8.79E-05	4	7.25	6.27	6.17	6.25	6.27	6.50	6.41	6.53
TC1100182	MICALCL	84953	MICAL C-terminal like	3.98E-06	4	5.72	4.55	4.76	4.87	4.78	5.07	5.08	5.05
TC0700712	MKLN1	4289	muskelin 1, intracellular mediator cont	2.77E-09	4	7.65	6.98	7.01	7.18	7.06	7.31	7.26	7.40
TC0300064	MKRN2	23609	makorin, ring finger protein, 2	1.31E-06	4	5.71	5.19	5.37	5.48	5.36	5.47	5.48	5.48
TC1201164	MLL2	8085	myeloid/lymphoid or mixed-lineage leu	2.10E-09	4	7.05	6.42	6.11	6.23	6.26	6.21	6.27	6.26
TC0700597	MLL5	55904	myeloid/lymphoid or mixed-lineage leu	4.48E-11	4	9.13	8.78	8.59	8.60	8.51	8.69	8.79	8.85

TC2000220	MMP24	10893	matrix metallopeptidase 24 (membran	4.93E-05	4	5.05	4.73	4.73	4.75	4.75	4.72	4.73	4.70
TC1200470	MON2	23041	MON2 homolog (S. cerevisiae) /// MON	2.35E-08	4	5.79	5.42	5.29	5.18	5.08	5.14	5.26	5.19
TC1201641	MORN3	283385	MORN repeat containing 3	0.000383	4	4.87	4.54	4.52	4.52	4.53	4.51	4.55	4.61
TC1300009	MPHOSPH8	54737	M-phase phosphoprotein 8 /// M-phas	4.01E-08	4	7.40	6.65	6.58	6.67	6.60	6.71	7.06	6.99
TC1800338	MPPE1	65258	metallophosphoesterase 1 /// metallop	2.53E-17	4	7.13	5.61	5.87	6.18	6.07	6.22	6.34	6.35
TC1700166	MPRIP /// MRI	23164	myosin phosphatase Rho interacting pr	6.05E-09	4	4.82	4.50	4.40	4.49	4.50	4.45	4.56	4.56
TC0101263	MPZL1	9019	myelin protein zero-like 1 /// Myelin pr	7.88E-09	4	7.71	5.63	5.97	6.49	6.12	6.49	6.67	6.94
TC1101750	MRE11A	4361	MRE11 meiotic recombination 11 hom	8.30E-09	4	4.44	3.79	3.76	3.95	3.96	4.03	4.22	4.10
TC1101450	MRPL16	54948	mitochondrial ribosomal protein L16	1.96E-08	4	5.69	5.17	5.20	5.39	5.45	5.39	5.50	5.38
TC1700428	MSL-1	339287	male-specific lethal-1 homolog	8.49E-05	4	9.96	9.48	9.49	9.58	9.57	9.65	9.59	9.60
TC1600454	MT1E /// MT1	4493	metallothionein 1E /// Metallothionein	7.78E-05	4	5.43	5.32	5.11	5.18	5.21	5.32	5.37	5.36
TC1500774	MTMR10	54893	myotubularin related protein 10 /// My	5.40E-06	4	7.50	6.79	6.90	6.95	6.82	6.96	6.87	6.96
TC1300430	MTRF1	9617	mitochondrial translational release fac	2.86E-06	4	4.85	4.46	4.58	4.65	4.66	4.65	4.67	4.63
TC2100141	MX2 /// Q6ZTY	4600	myxovirus (influenza virus) resistance 2	7.75E-09	4	8.32	7.41	7.32	7.44	7.31	7.70	7.80	7.90
TC1000575	MXI1	4601	MAX interactor 1 /// MAX-interacting p	1.07E-08	4	5.97	5.20	5.26	5.53	5.57	5.56	5.69	5.64
TC0103139	MYBPH	4608	myosin binding protein H	2.94E-15	4	5.02	4.49	4.43	4.40	4.46	4.47	4.42	4.50
TC1300557	MYCBP2	23077	MYC binding protein 2 /// Probable E3	3.25E-06	4	6.54	5.85	5.75	5.83	5.77	5.97	6.25	6.16
TC1701015	MYH10	4628	myosin, heavy chain 10, non-muscle //	2.30E-08	4	3.99	3.81	3.71	3.69	3.67	3.70	3.65	3.71
TC1600893	MYH11	4629	myosin, heavy chain 11, smooth muscl	9.91E-20	4	5.34	4.67	4.60	4.76	4.77	4.81	4.76	4.85
TC1701031	MYH3	4621	myosin, heavy chain 3, skeletal muscle,	1.28E-07	4	3.56	3.35	3.34	3.29	3.32	3.33	3.35	3.39
TC1901129	MYO1F	4542	myosin IF /// Myosin-If (Myosin-Ie). [Sc	1.49E-07	4	9.19	8.15	8.07	8.26	8.18	8.24	8.20	8.30
TC1500963	MYO5C	55930	myosin VC	0.000243	4	2.80	2.71	2.63	2.60	2.61	2.62	2.67	2.73
TC1900291	MYO9B	4650	myosin IXB	3.43E-09	4	7.61	6.82	6.54	6.68	6.66	6.74	6.88	6.94
TC0102300	MYSM1	114803	myb-like, SWIRM and MPN domains 1	3.24E-05	4	6.62	6.08	5.97	6.05	5.92	6.09	6.14	6.06
TC1600356	MYST1	84148	MYST histone acetyltransferase 1	0.0001	4	6.04	5.64	5.64	5.80	5.71	5.73	5.75	5.82
TC1700579	MYST2	11143	MYST histone acetyltransferase 2	1.39E-07	4	5.80	5.43	5.25	5.37	5.29	5.50	5.58	5.66
TC1300384	N4BP2L1 /// N	90634	NEDD4 binding protein 2-like 1 /// Nov	3.72E-06	4	3.57	3.26	3.25	3.25	3.27	3.31	3.36	3.38
TC1300386	N4BP2L2 /// N	10443	NEDD4 binding protein 2-like 2 /// pho	1.59E-06	4	6.51	5.99	5.99	5.86	5.80	6.02	6.16	6.09
TC0401052	NAAA	27163	N-acylethanolamine acid amidase	1.35E-05	4	6.03	4.82	4.84	5.26	4.94	5.00	5.06	5.18
TC1200441	NAB2	4665	NGFI-A binding protein 2 (EGR1 bindin	2.71E-12	4	4.87	4.29	4.17	4.22	4.38	4.37	4.27	4.33
TC0101779	NADK	65220	NAD kinase /// NAD kinase (EC 2.7.1.2	8.22E-05	4	7.04	6.61	6.49	6.58	6.62	6.73	6.64	6.69
TC1100629	NADSYN1	55191	NAD synthetase 1	1.50E-13	4	6.12	5.64	5.45	5.40	5.51	5.43	5.41	5.38
TC0401120	NAP1L5	266812	nucleosome assembly protein 1-like 5	8.79E-08	4	5.27	4.65	4.60	4.56	4.70	4.66	4.75	4.58
TC1701677	NAT9	26151	N-acetyltransferase 9	1.45E-18	4	5.09	4.37	4.35	4.42	4.39	4.45	4.41	4.44

TC0101916	NBPF10 /// Q8	440673	neuroblastoma breakpoint family, men	2.05E-06	4	6.55	5.83	5.83	6.02	6.03	6.07	6.32	6.09
TC0100920	NBPF20 /// Q5	400818	neuroblastoma breakpoint family, men	5.93E-05	4	5.91	5.17	5.18	5.34	5.28	5.35	5.48	5.30
TC0102676	NBPF9 /// NBP	728980 //	neuroblastoma breakpoint family, men	9.76E-05	4	6.99	6.20	6.15	6.37	6.28	6.33	6.54	6.33
TC0200097	NCOA1	8648	nuclear receptor coactivator 1	0.000508	4	8.98	8.47	8.48	8.59	8.36	8.54	8.62	8.69
TC0801016	NCOA2	10499	nuclear receptor coactivator 2	7.36E-05	4	8.78	8.58	8.31	8.41	8.32	8.47	8.46	8.55
TC1600209	NDE1	54820	nudE nuclear distribution gene E homo	7.17E-25	4	8.11	6.73	6.54	6.87	6.87	7.04	7.09	7.26
TC0202003	NEB	4703	nebulin	1.41E-05	4	2.96	2.82	2.82	2.78	2.79	2.80	2.79	2.83
TC0600952	NEDD9	4739	neural precursor cell expressed, develo	9.68E-09	4	8.01	7.24	6.81	7.04	7.02	7.30	7.30	7.59
TC1201121	NELL2	4753	NEL-like 2 (chicken)	7.27E-05	4	3.23	3.05	3.09	3.00	2.99	2.96	3.02	3.05
TC1600558	NFAT5	10725	nuclear factor of activated T-cells 5, to	3.15E-05	4	6.82	6.34	6.15	6.32	6.20	6.21	6.29	6.27
TC0700126	NFE2L3	9603	nuclear factor (erythroid-derived 2)-lik	0.000283	4	4.05	3.56	3.61	3.71	3.68	3.65	3.75	3.68
TC1901422	NFKBID /// NP_	84807	nuclear factor of kappa light polypepti	0.000917	4	5.05	4.91	4.87	4.78	4.89	4.93	4.81	4.87
TC1101969	NFRKB	4798	nuclear factor related to kappaB bindi	0.000606	4	5.11	4.90	4.81	4.78	4.84	4.93	4.93	4.85
TC0400924	NFXL1	152518	nuclear transcription factor, X-box bin	0.000206	4	6.16	4.44	4.41	5.05	4.94	5.11	5.08	5.30
TC0600376	NFYA	4800	nuclear transcription factor Y, alpha	9.45E-05	4	6.72	6.63	6.41	6.36	6.35	6.47	6.46	6.50
TC0301068	NGLY1	55768	N-glycanase 1 /// Peptide-N(4)-(N-acet	4.67E-07	4	6.30	5.92	6.32	6.10	5.99	6.07	6.19	6.03
TC0X00072	NHS	4810	Nance-Horan syndrome (congenital cat	5.22E-23	4	5.78	4.48	4.17	4.30	4.38	4.83	4.86	5.06
TC0X00346	NHSL2	340527	NHS-like 2	3.26E-09	4	7.22	6.04	5.97	6.31	6.11	6.37	6.33	6.57
TC1601123	NIP30	80011	NEFA-interacting nuclear protein NIP3	3.13E-10	4	7.52	7.10	7.13	7.19	7.10	7.21	7.31	7.34
TC0500126	NIPBL	25836	Nipped-B homolog (Drosophila)	2.87E-06	4	8.33	7.85	7.52	7.51	7.38	7.62	7.93	7.90
TC0300309	NISCH	11188	nischarin	3.95E-09	4	4.92	4.68	4.61	4.65	4.61	4.64	4.66	4.65
TC0600203	NKAPL	222698	NFKB activating protein-like	7.92E-05	4	4.60	4.08	3.89	4.13	4.05	4.25	4.21	4.08
TC0300195	NKTR	4820	natural killer-tumor recognition seque	2.12E-16	4	7.12	5.62	5.65	5.67	5.71	5.85	6.10	5.89
TC0800806	NKX3-1	4824	NK3 homeobox 1 /// Homeobox protei	1.40E-05	4	4.77	4.26	4.07	4.17	4.14	4.29	4.41	4.55
TC0X00335	NLGN3	54413	neuroligin 3 /// Neuroligin-3 precursor	4.59E-14	4	4.96	4.35	4.26	4.29	4.43	4.46	4.41	4.41
TC1600804	NLRC3	197358	NLR family, CARD domain containing 3	0.000238	4	4.84	4.70	4.65	4.68	4.69	4.67	4.60	4.67
TC1700958	NLRP1	730994 //	NLR family, pyrin domain containing 1	2.73E-31	4	7.94	6.14	5.70	5.76	5.62	6.02	6.13	6.27
TC0701304	NM_00103484	---	Similar to Williams Beuren syndrome c	1.69E-08	4	5.59	4.92	4.86	4.96	4.89	4.99	5.08	5.07
TC1900952	NM_138781	---	---	8.68E-17	4	6.65	5.97	5.73	5.92	5.98	6.14	6.30	6.37
TC1600704	NM_182905.2	---	family with sequence similarity 39, me	0.000577	4	6.55	6.33	6.32	6.27	6.38	6.41	6.35	6.33
TC0102670	NM_207400	---	CDNA FLJ39739 fis, clone SMINT2016	4.20E-11	4	6.20	5.82	5.84	5.83	5.90	6.02	6.02	6.10
TC1600816	NMRAL1	57407	NmrA-like family domain containing 1	0.000201	4	5.27	5.02	5.04	5.08	5.12	5.10	5.11	5.18
TC2000027	NOL5A	10528	nucleolar protein 5A (56kDa with KKE/	0.000184	4	5.04	4.81	4.83	4.81	4.85	4.86	4.95	4.88
TC0901443	NOTCH1	4851	Notch homolog 1, translocation-associ	0.000528	4	6.50	6.13	5.92	6.04	6.01	6.12	6.06	6.19

TC0100925	NOTCH2NL ///	388677 //	Notch homolog 2 (Drosophila) N-termi	3.32E-09	4	8.48	7.49	7.52	7.67	7.58	7.64	7.75	7.62
TC0202263	NP_001073944	---	CDNA FLJ41210 fis, clone BRALZ201448	3.41E-05	4	5.23	4.81	4.84	5.22	5.11	4.94	4.99	4.96
TC0501442	NP10_HUMAN	---	HERV-K_5q33.3 provirus Np9 protein (	2.74E-05	4	6.87	6.40	6.44	6.35	6.13	6.28	6.36	6.28
TC0102836	NP12_HUMAN	---	HERV-K_1q22 provirus Np9 protein (HE	2.69E-14	4	6.25	5.04	4.93	5.12	5.02	5.45	5.65	5.86
TC2000412	NPEPL1 /// STX	79716 ///	aminopeptidase-like 1 /// syntaxin 16 /	1.86E-18	4	6.47	5.98	5.98	5.98	5.96	5.93	5.84	5.82
TC1600201	NPIP /// Q6ZM	9284	nuclear pore complex interacting prote	0.000386	4	5.30	5.11	5.11	5.05	5.10	5.05	5.10	5.03
TC0101346	NPL	80896	N-acetylneuraminate pyruvate lyase (d	5.37E-06	4	7.76	7.02	7.14	7.23	7.14	7.46	7.38	7.42
TC0700062	NR_002217.1	---	PMS2-C terminal-like (PMS2CL) on chr	0.000969	4	4.56	4.33	4.37	4.28	4.34	4.30	4.41	4.36
TC2200199	NR_002323.1	---	taurine upregulated gene 1 (TUG1) on	2.58E-10	4	9.27	8.65	8.50	8.59	8.64	8.87	8.94	8.83
TC1601005	NR_002453.4	---	PI-3-kinase-related kinase SMG-1 pseu	1.17E-06	4	7.64	7.04	6.94	6.92	6.96	7.03	7.14	7.04
TC2200720	NR_002570.2	---	cytochrome P450, family 2, subfamily	0.000674	4	5.04	4.82	4.82	4.80	4.81	4.81	4.78	4.82
TC1600983	NR_002603.1	---	nuclear pore complex interacting prote	6.88E-10	4	7.71	6.62	6.33	6.30	6.50	6.41	6.73	6.57
TC1101492	NR_002761.1	---	RNA, U2B small nuclear (RNU2B) on ch	0.000468	4	4.68	4.25	4.39	4.21	4.76	4.69	4.77	4.05
TC1100544	NR_002819.1	---	metastasis associated lung adenocarci	4.59E-06	4	10.98	10.40	10.44	10.35	10.38	10.50	10.50	10.54
TC1400537	NR_003204.1	---	small nucleolar RNA, C/D box 114-11 (S	0.000641	4	2.78	2.31	2.39	2.11	2.25	2.22	2.32	2.21
TC1500080	NR_003307.1	---	small nucleolar RNA, C/D box 115-15 (S	3.43E-05	4	2.29	1.71	1.85	1.78	1.77	1.63	1.68	1.70
TC0500076	NR_003656.1	---	glucuronidase, beta pseudogene 1 (GU	0.000102	4	8.97	8.66	8.68	8.65	8.72	8.73	8.64	8.69
TC2000495	NSFL1C	55968	NSFL1 (p97) cofactor (p47) /// NSFL1 c	9.01E-06	4	7.83	7.13	7.25	7.38	7.23	7.30	7.38	7.43
TC0700407	NSUN5B	155400	NOL1/NOP2/Sun domain family, memb	3.95E-07	4	5.57	5.32	5.32	5.35	5.44	5.43	5.44	5.37
TC0701306	NSUN5C	260294	NOL1/NOP2/Sun domain family, memb	5.89E-05	4	5.41	5.22	5.24	5.24	5.33	5.31	5.35	5.30
TC0200587	NT5DC4	---	5'-nucleotidase domain-containing pro	5.18E-07	4	4.35	4.16	4.17	4.07	4.05	4.11	4.11	4.12
TC0103161	NUAK2 /// C11	81788 ///	NUAK family, SNF1-like kinase, 2 /// ch	1.03E-05	4	7.91	7.16	7.00	7.12	6.95	7.34	7.25	7.48
TC1000334	NUDT13	25961	nudix (nucleoside diphosphate linked	8.57E-05	4	4.20	3.92	3.83	3.81	3.83	3.88	4.02	3.92
TC0900646	NUP214	8021	nucleoporin 214kDa /// Nuclear pore c	6.50E-09	4	6.78	6.10	6.10	6.23	6.16	6.29	6.35	6.40
TC1101095	NUP98	4928	nucleoporin 98kDa /// Nuclear pore co	1.03E-07	4	7.49	7.43	6.93	6.94	6.87	7.10	7.06	7.13
TC1101488	NXF1	10482	nuclear RNA export factor 1	8.83E-09	4	8.02	7.05	6.93	6.93	6.98	7.03	7.12	7.04
TC1600196	O15103_HUM	---	---	3.22E-09	4	6.05	4.75	4.66	4.57	4.78	4.72	5.16	4.85
TC1501030	OAZ2	4947	ornithine decarboxylase antizyme 2	0.000137	4	7.39	6.66	6.85	6.97	6.76	6.98	7.00	7.11
TC0901408	OBP2B	29989	odorant binding protein 2B /// Odoran	0.00043	4	5.50	5.30	5.31	5.27	5.30	5.28	5.21	5.33
TC0600499	OGFRL1	79627	opioid growth factor receptor-like 1	1.75E-19	4	8.92	7.72	7.49	7.65	7.67	8.23	8.21	8.55
TC0X00341	OGT	8473	O-linked N-acetylglucosamine (GlcNAc)	1.32E-14	4	8.20	7.06	7.11	6.95	6.90	6.85	6.97	6.78
TC1100341	OR4C46	119749	olfactory receptor, family 4, subfamily	0.000622	4	2.40	2.04	1.98	1.89	1.95	1.96	1.92	2.14
TC1100080	OR52K1	390036	olfactory receptor, family 52, subfamily	5.14E-12	4	4.73	3.35	3.06	3.30	3.25	3.81	3.49	3.76
TC1100078	OR52K2	119774	olfactory receptor, family 52, subfamily	5.82E-11	4	3.90	2.73	2.63	2.56	2.81	2.91	2.91	3.03

TC0202174	ORMDL1	94101	ORM1-like 1 (S. cerevisiae)	1.32E-10	4	5.48	4.57	4.76	4.71	4.78	4.75	4.89	4.80
TC0X00907	OTUD5	55593	OTU domain containing 5 /// OTU dom	6.77E-14	4	7.72	7.05	6.77	7.02	7.01	7.11	7.17	7.24
TC1400430	P1768_HUMAN	---	Protein PRO1768. [Source:Uniprot/SWI	4.20E-11	4	4.28	2.90	2.96	2.96	3.05	3.02	3.09	3.35
TC1700927	P2RX1	5023	purinergic receptor P2X, ligand-gated i	2.68E-05	4	6.34	5.56	5.52	5.52	5.58	5.45	5.47	5.39
TC0X00380	P2RY10	27334	purinergic receptor P2Y, G-protein cou	2.69E-21	4	6.13	3.33	3.16	4.16	3.67	4.31	4.83	5.17
TC0301669	P2RY13	53829	purinergic receptor P2Y, G-protein cou	8.51E-05	4	10.73	10.40	10.60	10.42	10.31	10.49	10.40	10.53
TC1100653	P2RY6	5031	pyrimidinergic receptor P2Y, G-protein	0.000275	4	4.46	4.22	4.22	4.17	4.12	4.20	4.17	4.19
TC1600775	P461_HUMAN	---	Protein PRO0461. [Source:Uniprot/SWI	8.26E-06	4	9.82	9.31	9.11	9.17	9.13	9.21	9.23	9.34
TC1600771	P461_HUMAN	---	Protein PRO0461. [Source:Uniprot/SWI	4.26E-05	4	8.29	7.95	7.76	7.81	7.69	7.78	7.86	7.92
TC2000741	P628_HUMAN	---	Protein PRO0628. [Source:Uniprot/SWI	9.02E-05	4	3.40	2.72	2.45	2.60	2.65	2.73	2.97	3.14
TC2000305	PABPC1L /// C2	80336	poly(A) binding protein, cytoplasmic 1-	2.18E-25	4	5.30	4.45	4.47	4.49	4.59	4.53	4.54	4.47
TC1100565	PACS1	55690	phosphofurin acidic cluster sorting pro	1.16E-05	4	8.01	7.11	6.93	7.12	7.05	7.29	7.27	7.40
TC1101684	PAK1	5058	p21 protein (Cdc42/Rac)-activated kina	4.05E-07	4	9.50	8.74	8.83	8.89	8.78	9.07	9.09	9.31
TC1300057	PAN3	255967	PAN3 polyA specific ribonuclease subu	3.29E-12	4	7.66	6.88	6.80	6.86	6.75	6.94	6.98	7.01
TC0101792	PANK4	55229	pantothenate kinase 4	1.50E-10	4	5.69	5.23	5.16	5.32	5.28	5.32	5.32	5.36
TC0500166	PARP8 /// A2RU	79668	poly (ADP-ribose) polymerase family, m	1.87E-09	4	9.11	8.40	8.49	8.47	8.42	8.70	8.70	8.84
TC2200347	PARVG	64098	parvin, gamma	7.56E-10	4	7.94	7.09	7.10	7.16	7.16	7.20	7.26	7.22
TC1001022	PBLD	64081	phenazine biosynthesis-like protein do	0.000122	4	3.68	3.42	3.47	3.49	3.47	3.54	3.56	3.55
TC0601150	PBX2	5089	pre-B-cell leukemia homeobox 2	1.24E-11	4	7.25	6.37	6.25	6.29	6.37	6.43	6.34	6.44
TC1100714	PCF11	51585	PCF11, cleavage and polyadenylation fa	0.000293	4	7.08	6.69	6.57	6.61	6.54	6.76	6.85	6.85
TC2000478	PCMTD2	55251	protein-L-isoaspartate (D-aspartate) O-	1.68E-15	4	6.09	5.12	5.11	5.41	5.32	5.50	5.66	5.68
TC1100550	PCNXL3	399909	pecanex-like 3 (Drosophila)	0.000228	4	5.25	5.06	5.05	5.04	5.04	5.09	5.01	5.06
TC1101863	PCSK7	9159	proprotein convertase subtilisin/kexin	5.76E-11	4	5.18	4.77	4.74	4.81	4.77	4.81	4.80	4.75
TC1100194	PDE3B	5140	phosphodiesterase 3B, cGMP-inhibited	3.58E-09	4	6.92	6.86	6.16	6.15	6.02	6.27	6.30	6.54
TC0100628	PDE4B	5142	phosphodiesterase 4B, cAMP-specific (	2.32E-16	4	5.68	5.16	4.55	4.77	4.75	5.24	5.22	5.53
TC1601211	PDXDC2	---	pyridoxal-dependent decarboxylase do	1.10E-09	4	4.94	4.39	4.28	4.32	4.45	4.44	4.56	4.42
TC0500097	PDZD2	23037	PDZ domain containing 2 /// PDZ doma	1.33E-05	4	3.86	3.68	3.66	3.69	3.69	3.66	3.65	3.67
TC1100917	PDZD3	79849	PDZ domain containing 3 /// PDZ doma	0.000288	4	4.21	4.03	4.01	3.96	4.00	4.02	3.98	4.04
TC1701617	PECAM1	5175	platelet/endothelial cell adhesion mole	9.66E-11	4	10.07	8.71	8.97	9.25	8.95	9.36	9.42	9.56
TC0201566	PELI1	57162	pellino homolog 1 (Drosophila)	1.93E-12	4	8.72	8.62	8.05	7.92	7.88	8.19	8.19	8.40
TC0601273	PEX6	5190	peroxisomal biogenesis factor 6 /// Per	1.51E-05	4	5.13	4.84	4.87	4.88	4.92	4.88	4.81	4.84
TC0600309	PFDN6	10471	prefoldin subunit 6	7.78E-08	4	5.14	4.53	4.62	4.76	4.84	4.80	4.86	4.79
TC0701167	PGAM2	5224	phosphoglycerate mutase 2 (muscle)	1.11E-10	4	5.98	5.27	5.22	5.11	5.17	5.10	5.15	5.06
TC1500194	PGBD4	161779	piggyBac transposable element derive	2.69E-06	4	4.38	3.74	3.79	3.95	3.99	4.14	4.18	4.01

TC0800446	PGCP /// NP_0	10404	plasma glutamate carboxypeptidase //	0.000115	4	7.87	7.09	7.21	7.36	7.21	7.26	7.30	7.42
TC0600312	PHF1	5252	PHD finger protein 1	1.81E-12	4	6.55	6.47	6.07	6.01	6.05	6.27	6.25	6.34
TC0500482	PHF15	23338	PHD finger protein 15 /// Protein Jade-	2.12E-09	4	5.31	5.01	4.96	5.01	4.95	5.02	5.11	5.24
TC0400530	PHF17	79960	PHD finger protein 17	0.000965	4	6.35	6.10	6.09	5.89	5.78	6.00	6.06	6.10
TC0601413	PHIP	55023	pleckstrin homology domain interactin	3.48E-07	4	7.27	6.96	6.78	6.66	6.59	6.70	6.88	6.79
TC1601234	PHLPPL	23035	PH domain and leucine rich repeat pro	0.000547	4	3.62	3.43	3.40	3.40	3.43	3.43	3.44	3.52
TC1701500	PHOSPHO1	162466	phosphatase, orphan 1	2.44E-13	4	6.35	4.87	4.74	5.01	5.22	5.42	5.44	5.53
TC2200462	PI4KA	5297	phosphatidylinositol 4-kinase, catalytic	4.06E-06	4	5.84	5.43	5.23	5.33	5.36	5.35	5.47	5.43
TC2200478	PI4KAP2	375133	phosphatidylinositol 4-kinase, catalytic	1.02E-05	4	6.01	5.80	5.74	5.78	5.80	5.81	5.77	5.79
TC0102744	PI4KB	5298	phosphatidylinositol 4-kinase, catalytic	6.02E-13	4	6.01	5.33	5.25	5.44	5.42	5.47	5.50	5.58
TC2200270	PICK1	9463	protein interacting with PRKCA 1	0.000815	4	4.77	4.55	4.63	4.51	4.59	4.61	4.56	4.61
TC1500353	PIGB	9488	phosphatidylinositol glycan anchor bio	1.56E-17	4	6.92	5.37	5.56	5.95	5.94	6.17	6.31	6.31
TC0400006	PIGG	54872	phosphatidylinositol glycan anchor bio	2.26E-08	4	4.97	4.53	4.56	4.62	4.60	4.52	4.60	4.56
TC2200596	PIK3IP1	113791	phosphoinositide-3-kinase interacting	2.92E-07	4	5.47	4.96	4.70	4.94	4.92	4.95	4.96	4.97
TC0301560	PIK3R4	30849	phosphoinositide-3-kinase, regulatory	4.06E-08	4	4.57	4.21	4.11	4.27	4.10	4.28	4.39	4.50
TC1701021	PIK3R5	23533	phosphoinositide-3-kinase, regulatory	0.000748	4	7.03	6.52	6.37	6.58	6.59	6.62	6.58	6.69
TC1701020	PIK3R6	146850	phosphoinositide-3-kinase, regulatory	4.08E-15	4	5.75	4.84	4.85	5.17	5.08	5.22	5.35	5.35
TC0X00906	PIM2	11040	pim-2 oncogene	4.29E-09	4	5.53	5.52	4.78	4.91	4.97	5.36	5.33	5.57
TC2200602	PISD	23761	phosphatidylserine decarboxylase ///	1.53E-05	4	5.94	5.35	5.35	5.50	5.55	5.60	5.44	5.56
TC1700888	PITPNA	5306	phosphatidylinositol transfer protein, a	1.61E-09	4	8.54	8.11	7.59	7.84	7.62	8.04	8.16	8.29
TC0100706	PKN2	5586	protein kinase N2 /// Serine/threonine-	1.82E-19	4	8.32	6.95	6.85	7.02	7.03	7.47	7.56	7.70
TC2200660	PLA2G6	8398	phospholipase A2, group VI (cytosolic,	8.19E-06	4	4.41	4.21	4.19	4.20	4.23	4.20	4.15	4.22
TC2100357	PLAC4	191585	placenta-specific 4	0.000336	4	3.61	2.93	2.94	3.08	3.02	3.12	3.07	3.26
TC0601661	PLAGL1	5325	pleiomorphic adenoma gene-like 1	9.85E-16	4	4.66	3.87	3.88	3.89	3.70	3.88	4.06	4.00
TC2000068	PLCB1	23236	phospholipase C, beta 1 (phosphoinosi	9.49E-08	4	3.77	3.51	3.47	3.50	3.47	3.53	3.66	3.63
TC1500839	PLCB2	5330	phospholipase C, beta 2	2.74E-16	4	7.87	6.57	6.58	6.75	6.70	6.79	6.79	6.80
TC1400301	PLEKHG3	26030	pleckstrin homology domain containin	2.36E-22	4	6.73	5.60	5.35	5.63	5.71	5.98	5.95	6.14
TC1701446	PLEKHM1	9842	pleckstrin homology domain containin	0.000182	4	6.69	6.40	6.14	6.25	6.25	6.24	6.20	6.21
TC0101005	PLEKHO1	51177	pleckstrin homology domain containin	6.56E-21	4	6.63	5.38	5.23	5.44	5.42	5.75	5.92	6.20
TC0600862	PLG	5340	plasminogen /// Plasminogen precurso	3.25E-09	4	3.38	3.16	3.13	3.05	3.11	3.07	3.05	3.08
TC0200552	PLGLA1	---	Plasminogen-like A1. [Source:Uniprot/	2.42E-06	4	2.87	2.45	2.44	2.37	2.46	2.50	2.48	2.52
TC0200436	PLGLB1	5343	plasminogen-like B1	2.41E-08	4	3.93	3.02	3.10	3.13	3.16	3.29	3.29	3.25
TC0201694	PLGLB1 /// PLG	5343 ///	plasminogen-like B1 /// plasminogen-li	7.69E-10	4	4.15	3.19	3.23	3.28	3.26	3.42	3.44	3.39
TC0600681	PLN	5350	phospholamban	3.81E-08	4	3.47	2.74	2.87	3.08	3.05	3.06	3.20	3.04

TC1000098	PLXDC2	84898	plexin domain containing 2 /// Plexin d	6.32E-06	4	8.05	7.62	7.43	7.91	7.28	7.75	7.68	7.96
TC0103196	PLXNA2	5362	plexin A2	1.44E-09	4	4.64	4.27	4.17	4.18	4.15	4.23	4.26	4.37
TC0900698	PMPCA	23203	peptidase (mitochondrial processing) a	0.00013	4	4.19	4.01	3.96	4.00	4.04	4.06	4.04	4.01
TC0701285	PMS2L4	---	PMS6 protein (HPMS6 protein) (Fragm	5.87E-05	4	5.06	4.65	4.66	4.77	4.71	4.78	4.82	4.73
TC2100412	POFUT2	23275	protein O-fucosyltransferase 2	2.37E-07	4	4.42	4.21	4.07	4.04	4.07	4.10	4.05	4.09
TC1100537	POLA2	23649	polymerase (DNA directed), alpha 2 (7(	3.25E-05	4	4.81	4.37	4.17	4.32	4.47	4.49	4.51	4.52
TC1700098	POLR2A	5430	polymerase (RNA) II (DNA directed) pol	0.000184	4	7.81	7.21	7.10	7.57	7.45	7.35	7.43	7.41
TC1900991	POLR2E	5434	polymerase (RNA) II (DNA directed) pol	5.16E-05	4	5.03	4.49	4.56	4.65	4.65	4.60	4.68	4.71
TC0701512	POLR2J3 /// PC	652668 //	RPB11b2 protein /// DNA directed RNA	1.66E-09	4	6.02	5.73	5.74	5.77	5.78	5.80	5.77	5.77
TC1500486	PPCDC	60490	phosphopantothenoylcysteine decarbo	4.32E-15	4	6.17	5.33	5.24	5.18	5.17	5.58	5.55	5.79
TC1100624	PPFIA1	8500	protein tyrosine phosphatase, receptor	9.04E-07	4	6.87	6.48	6.21	6.46	6.54	6.65	6.64	6.64
TC1100145	PPFIBP2	8495	PTPRF interacting protein, binding prot	0.000627	4	4.75	4.61	4.40	4.48	4.51	4.58	4.44	4.61
TC1200261	PPHLN1	51535	periphilin 1 /// Periphilin-1 (Gastric can	0.000741	4	5.83	5.82	5.66	5.58	5.59	5.69	5.78	5.81
TC1600825	PPL	5493	periplakin	2.93E-07	4	5.21	4.86	4.83	4.86	4.88	4.90	4.82	4.94
TC2200486	PPM1F	9647	protein phosphatase 1F (PP2C domain	2.39E-14	4	6.59	5.77	5.79	5.95	5.85	5.96	5.96	6.08
TC0101205	PPOX	5498	protoporphyrinogen oxidase	0.000134	4	4.46	4.27	4.27	4.26	4.31	4.30	4.23	4.29
TC0600237	PPP1R11	6992	protein phosphatase 1, regulatory (inhi	1.49E-05	4	4.87	4.50	4.53	4.49	4.42	4.58	4.58	4.69
TC0101424	PPP1R12B	4660	protein phosphatase 1, regulatory (inhi	5.14E-12	4	6.15	5.41	5.05	5.15	5.36	5.56	5.56	5.57
TC2000863	PPP4R1L /// PP	---	Serine/threonine-protein phosphatase	3.75E-05	4	5.52	5.06	4.82	4.87	4.91	5.02	4.94	4.83
TC2000815	PREX1	57580	phosphatidylinositol 3,4,5-trisphosphat	0.000367	4	8.51	8.11	7.77	7.98	7.88	7.89	7.88	8.02
TC0101362	PRG4	10216	proteoglycan 4 /// Proteoglycan-4 prec	0.000219	4	2.90	2.67	2.65	2.64	2.63	2.73	2.72	2.69
TC0100049	PRKCZ	5590	protein kinase C, zeta /// Protein kinas	4.09E-05	4	5.60	5.24	5.25	5.33	5.31	5.42	5.44	5.47
TC1901629	PRKD2	25865	protein kinase D2	2.17E-08	4	7.27	6.95	6.51	6.68	6.75	6.98	6.93	7.11
TC2000217	PROCR	10544	protein C receptor, endothelial (EPCR)	2.05E-05	4	4.32	4.13	4.03	4.04	4.08	4.10	4.05	4.10
TC0100823	PROK1	84432	prokineticin 1	0.000904	4	5.11	5.09	4.99	4.92	4.94	5.07	4.94	5.14
TC0101014	PRPF3	9129	PRP3 pre-mRNA processing factor 3 ho	1.09E-14	4	6.56	5.59	5.50	5.39	5.37	5.47	5.61	5.53
TC0600035	PRPF4B	8899	PRP4 pre-mRNA processing factor 4 ho	3.71E-07	4	5.50	4.72	4.82	4.97	5.00	4.98	5.21	5.05
TC1700894	PRPF8	10594	PRP8 pre-mRNA processing factor 8 ho	5.32E-05	4	7.42	6.98	6.68	6.84	6.87	6.93	7.02	6.96
TC0500422	PRR16	51334	proline rich 16	0.000473	4	4.67	4.52	4.51	4.46	4.54	4.52	4.44	4.52
TC0600246	PRR3	80742	proline rich 3 /// Proline-rich protein 3	3.96E-06	4	4.44	4.00	4.00	4.08	4.10	4.18	4.17	4.21
TC1701750	PSCD1	9267	pleckstrin homology, Sec7 and coiled-c	1.09E-10	4	8.32	7.74	7.55	7.68	7.66	7.80	7.88	7.88
TC0200596	PSD4	23550	pleckstrin and Sec7 domain containing	5.10E-07	4	6.26	5.71	5.64	5.86	5.84	5.90	5.89	6.02
TC1601186	PSMB10 /// CT	5699 /// 1	proteasome (prosome, macropain) sub	3.77E-16	4	6.02	5.37	5.28	5.43	5.42	5.61	5.61	5.75
TC1701383	PSMC3IP	29893	PSMC3 interacting protein	2.23E-09	4	5.85	5.46	5.37	5.44	5.48	5.43	5.58	5.52

TC1700475	PSME3	10197	proteasome (prosome, macropain) acti	0.000584	4	7.83	7.18	7.28	7.31	7.34	7.22	7.14	7.33
TC0201517	PSME4	23198	proteasome (prosome, macropain) acti	4.26E-10	4	5.95	5.38	5.25	5.36	5.22	5.46	5.62	5.58
TC0102046	PTAFR	5724	platelet-activating factor receptor	1.00E-08	4	8.11	7.66	7.69	7.86	7.69	7.82	7.81	7.96
TC1900732	PTOV1	53635	prostate tumor overexpressed gene 1 /	3.13E-08	4	6.33	5.90	5.88	6.09	6.08	6.05	6.01	6.07
TC0400163	PTTG2 /// NM_	10744	pituitary tumor-transforming 2 /// pitu	9.16E-15	4	6.39	4.65	4.36	4.95	5.09	5.23	5.36	5.46
TC0700538	PVRIG /// STAG	79037 ///	poliovirus receptor related immunoglo	4.98E-10	4	4.59	4.42	4.29	4.31	4.34	4.31	4.32	4.35
TC1101519	PYGM	5837	phosphorylase, glycogen; muscle (McA	1.86E-05	4	4.45	4.08	4.07	4.17	4.14	4.12	4.13	4.11
TC1300348	Q5T6R2_HUM	651239	OTTHUMP00000018135. [Source:Unipr	0.000984	4	4.08	3.95	3.99	3.87	3.88	3.98	3.96	3.98
TC1701277	Q6JHZ5_HUM	---	NS5ATP13TP1. [Source:Uniprot/SPTRE	0.000373	4	5.92	5.90	5.43	5.49	5.37	5.27	5.58	5.81
TC0701141	Q6PIW0_HUM	---	TRGV7 protein. [Source:Uniprot/SPTRE	7.81E-05	4	5.83	5.46	5.44	5.41	5.59	5.54	5.57	5.51
TC0800713	Q6SA06_HUM	---	Liver-related low express protein 1. [So	0.000132	4	6.11	4.81	4.73	4.68	4.79	5.01	4.90	4.91
TC1101760	Q6UXQ5_HUM	---	MRSS6228. [Source:Uniprot/SPTREMBL	1.79E-09	4	5.74	4.28	4.14	4.29	4.37	4.45	4.54	4.64
TC0300888	Q6UXS4_HUM	---	AVPC1948. [Source:Uniprot/SPTREMBL	5.93E-06	4	3.99	3.70	3.34	3.37	3.37	3.31	3.41	3.50
TC1701735	Q6YL35_HUM	---	---	5.64E-06	4	5.63	5.14	4.95	4.98	4.98	5.35	5.41	5.28
TC0600646	Q6ZMM1_HU	---	CDNA FLJ16829 fis, clone UTERU30205	9.22E-10	4	4.22	3.45	3.55	3.66	3.55	3.83	3.87	3.81
TC1901759	Q6ZN19_HUM	---	CDNA FLJ16515 fis, clone MESAN20155	3.42E-11	4	5.09	4.49	4.49	4.52	4.45	4.64	4.74	4.73
TC1900292	Q6ZN60_HUM	---	CDNA FLJ16405 fis, clone UTERU20112	0.00086	4	4.74	4.44	4.32	4.24	4.32	4.38	4.43	4.45
TC1600886	Q6ZNL0_HUM	---	---	0.000437	4	5.48	5.33	5.28	5.23	5.31	5.34	5.29	5.32
TC1700857	Q6ZNS0_HUM	---	CDNA FLJ27256 fis, clone SYN09689. [	0.000128	4	7.21	6.76	6.10	6.21	6.16	6.26	6.29	6.02
TC0800089	Q6ZP57_HUM	---	CDNA FLJ26472 fis, clone KDN04506. [S	5.87E-11	4	4.96	4.43	4.37	4.41	4.39	4.49	4.59	4.54
TC0500644	Q6ZP60_HUM	---	CDNA FLJ26465 fis, clone KDN04238. [S	0.000151	4	4.72	4.40	4.15	4.10	4.10	4.23	4.73	4.31
TC1700858	Q6ZPC0_HUM	---	CDNA FLJ26091 fis, clone RCT06468. (F	0.000539	4	6.22	5.05	4.88	4.98	5.24	4.94	5.14	4.71
TC1900970	Q6ZQS4_HUM	---	CDNA FLJ45445 fis, clone BRSSN20136	7.84E-05	4	6.53	6.08	6.03	5.95	5.99	5.93	6.01	5.90
TC1900536	Q6ZQS5_HUM	---	CDNA FLJ45443 fis, clone BRSSN20121	6.93E-07	4	5.04	4.19	4.26	4.35	4.22	4.30	4.69	4.35
TC1401114	Q6ZR94_HUM	---	CDNA FLJ46540 fis, clone THYMU30037	0.000184	4	3.72	3.38	3.44	3.35	3.30	3.32	3.30	3.43
TC0300923	Q6ZRC0_HUM	---	CDNA FLJ46488 fis, clone THYMU30026	1.41E-06	4	4.54	4.08	3.97	3.95	3.97	4.04	4.04	4.03
TC0600377	Q6ZRD8_HUM	---	CDNA FLJ46432 fis, clone THYMU30014	5.05E-18	4	4.23	3.25	3.33	3.34	3.27	3.31	3.27	3.27
TC1900442	Q6ZRN6_HUM	---	CDNA FLJ46220 fis, clone TESTI401377	0.000393	4	4.26	4.04	4.01	3.94	3.96	3.98	3.97	4.01
TC1100971	Q6ZRR8_HUM	---	CDNA FLJ46155 fis, clone TESTI400151	0.000238	4	4.38	3.99	4.01	3.85	3.89	3.83	3.85	3.92
TC0300996	Q6ZS22_HUM	---	CDNA FLJ45887 fis, clone OCBBF30215	6.80E-09	4	6.46	5.74	5.73	5.78	5.77	5.78	5.69	5.60
TC1000239	Q6ZS34_HUM	---	CDNA FLJ45867 fis, clone OCBBF30037	2.33E-08	4	4.66	3.31	3.47	3.51	3.63	3.82	3.96	3.96
TC0201599	Q6ZS71_HUM	---	CDNA FLJ45779 fis, clone NETRP20052	0.000112	4	6.32	4.98	4.79	4.67	4.83	5.18	5.01	5.13
TC0200287	Q6ZSS0_HUM	---	CDNA FLJ45251 fis, clone BRHIP200917	3.53E-08	4	4.74	3.32	3.01	3.52	3.43	3.43	3.58	3.70
TC1600184	Q6ZT39_HUM	---	CDNA FLJ44991 fis, clone BRAWH3008	4.00E-05	4	5.35	4.83	4.85	4.79	4.85	4.85	4.75	4.89

TC2200374	Q6ZTH8_HUM	---	CDNA FLJ44641 fis, clone BRACE20300	3.60E-05	4	5.49	4.85	5.08	4.99	4.94	4.96	5.08	5.17
TC1900092	Q6ZTI5_HUMA	---	CDNA FLJ44616 fis, clone BRACE20129	1.86E-08	4	4.44	3.60	3.28	3.38	3.34	3.71	3.67	3.50
TC1600856	Q6ZTK2_HUM	---	CDNA FLJ44575 fis, clone UTERU30181	9.63E-16	4	5.49	4.94	4.90	4.94	4.96	4.97	4.92	4.95
TC1701546	Q6ZTQ9_HUM	---	CDNA FLJ44342 fis, clone TRACH30052	1.47E-20	4	6.49	4.27	4.55	4.75	4.77	4.91	5.26	4.96
TC0101478	Q6ZU99_HUM	---	CDNA FLJ43880 fis, clone TESTI400902	1.23E-10	4	4.78	3.82	3.70	3.75	3.88	4.08	3.94	4.18
TC0801181	Q6ZUG1_HUM	---	CDNA FLJ43745 fis, clone TESTI201964	3.31E-07	4	4.12	3.82	3.83	3.77	3.81	3.80	3.67	3.79
TC0501495	Q6ZUG4_HUM	---	CDNA FLJ43741 fis, clone TESTI201772	8.63E-08	4	4.67	4.25	4.20	4.24	4.24	4.34	4.25	4.31
TC0501485	Q6ZUH0_HUM	---	CDNA FLJ43720 fis, clone TESOP20060	0.000514	4	4.16	3.79	3.67	3.74	3.60	3.82	3.73	3.90
TC1600727	Q6ZUK6_HUM	---	CDNA FLJ43617 fis, clone SPLEN20168	0.000229	4	6.82	6.54	6.59	6.48	6.53	6.43	6.56	6.57
TC1600636	Q6ZUP2_HUM	---	CDNA FLJ43495 fis, clone PEBLM20003	4.82E-07	4	7.84	6.89	6.75	6.87	6.90	7.08	6.98	7.14
TC1201686	Q6ZUW1_HU	---	CDNA FLJ43282 fis, clone LIVER200741	3.83E-05	4	7.73	6.98	7.12	7.25	7.15	7.08	7.13	6.84
TC1600786	Q6ZV49_HUM	---	CDNA FLJ42988 fis, clone BRTHA20089	4.05E-12	4	6.76	5.76	5.80	5.76	5.65	5.71	5.78	5.65
TC0202290	Q6ZV57_HUM	---	CDNA FLJ42970 fis, clone BRSTN20171	0.000302	4	3.72	3.36	3.33	3.28	3.32	3.39	3.33	3.38
TC0201758	Q6ZVB7_HUM	---	CDNA FLJ42791 fis, clone BRAWH3007	8.90E-05	4	5.65	5.02	5.02	4.96	4.82	4.76	4.91	5.01
TC0202149	Q6ZVF4_HUM	---	CDNA FLJ42639 fis, clone BRACE30246	0.00037	4	2.72	2.18	2.16	2.24	2.26	2.23	2.41	2.65
TC0201286	Q6ZVL4_HUM	---	CDNA FLJ42418 fis, clone BLADE20019	9.47E-05	4	3.31	3.09	3.10	3.01	3.02	3.06	3.11	3.04
TC0200221	Q6ZVP5_HUM	---	CDNA FLJ42255 fis, clone TKIDN200988	1.52E-07	4	4.77	3.87	4.02	3.97	3.84	3.98	4.00	4.06
TC1101626	Q6ZVU0_HUM	---	CDNA FLJ42102 fis, clone TESOP20067	3.26E-05	4	3.87	3.60	3.55	3.44	3.58	3.57	3.54	3.49
TC1701403	Q6ZW54_HUM	---	CDNA FLJ45519 fis, clone BRTHA20241	1.17E-13	4	4.94	4.55	4.53	4.50	4.50	4.54	4.51	4.61
TC0700901	Q86U85_HUM	---	Phosphoserine phosphatase-like. [Sour	3.65E-11	4	6.62	5.20	5.04	5.11	5.28	5.27	5.28	5.23
TC0701514	Q86UW5_HU	---	---	1.81E-06	4	6.47	5.62	5.52	5.47	5.51	5.70	5.66	5.68
TC0701513	Q8IV37_HUM	---	---	5.12E-06	4	4.28	3.85	3.74	3.80	3.78	3.78	3.86	3.88
TC1701622	Q8N0T0_HUM	---	---	1.10E-15	4	6.06	5.33	5.25	5.25	5.31	5.32	5.37	5.31
TC1401060	Q8N1R0_HUM	---	CDNA FLJ37957 fis, clone CTONG20095	6.58E-23	4	6.61	4.06	3.84	4.16	4.28	4.74	4.82	5.19
TC1501220	Q8N2D2_HUM	---	CDNA FLJ33447 fis, clone BRAMY10000	0.000178	4	5.91	5.56	5.56	5.45	5.60	5.64	5.50	5.52
TC0901097	Q8N646_HUM	---	---	1.15E-06	4	4.31	3.90	3.88	3.85	3.83	3.92	3.87	3.82
TC0900211	Q8N7U8_HUM	---	COBW domain containing 3. [Source:U	2.21E-14	4	4.37	3.55	3.55	3.54	3.59	3.73	3.88	3.76
TC1701699	Q8N811_HUM	---	CDNA FLJ40144 fis, clone TESTI201301	8.04E-06	4	4.21	3.61	3.64	3.60	3.53	3.62	3.62	3.78
TC0701107	Q8N867_HUM	---	CDNA FLJ39921 fis, clone SPLEN202041	3.59E-13	4	6.14	5.46	5.47	5.45	5.39	5.47	5.54	5.45
TC1600696	Q8N8B4_HUM	---	CDNA FLJ39725 fis, clone SMINT20152	8.35E-07	4	4.73	4.40	4.37	4.37	4.47	4.43	4.55	4.44
TC0701183	Q8N8T1_HUM	---	CDNA FLJ38910 fis, clone NT2NE20068	0.000118	4	5.49	4.09	4.47	4.39	4.63	4.51	4.71	4.78
TC0800091	Q8NAJ9_HUM	---	CDNA FLJ35225 fis, clone PROST20011	0.000102	4	3.64	3.09	3.03	3.03	2.96	2.96	3.21	2.98
TC1500951	Q8NE92_HUM	---	---	0.000254	4	10.27	10.02	10.06	10.00	10.08	10.08	9.99	10.07
TC0401444	Q8NEQ2_HUM	---	MGC24125 protein. [Source:Uniprot/S	2.41E-06	4	5.12	4.51	4.52	4.72	4.74	4.70	4.65	4.54

TC0600191	Q8NHA6_HUM	---	Seven transmembrane helix receptor. [	5.10E-05	4	7.84	7.45	7.49	7.38	7.49	7.54	7.35	7.47
TC0102898	Q8NHC2_HUM	---	Seven transmembrane helix receptor. [	2.87E-19	4	6.34	4.34	4.08	4.54	4.52	5.03	5.06	5.45
TC1201331	Q8WYW9_HU	---	---	1.35E-06	4	4.84	3.86	3.60	3.89	3.83	3.91	3.93	4.06
TC1600933	Q92617-5 /// C	---	K0220_HUMAN Isoform 5 of Q92617 -	9.30E-13	4	6.58	5.66	5.49	5.46	5.55	5.55	5.72	5.57
TC1100065	Q96FU4_HUM	---	---	7.41E-05	4	6.55	6.71	5.77	6.05	5.89	6.31	6.29	6.59
TC0700978	Q96JH1_HUM	---	CDNA FLJ14435 fis, clone HEMBA1007	0.000428	4	6.06	5.83	5.74	5.83	5.86	5.84	5.81	5.86
TC0600461	Q96MJ2_HUM	---	CDNA FLJ32293 fis, clone PROST20017	9.03E-10	4	5.40	4.74	4.66	4.73	4.70	4.91	4.87	4.87
TC0400876	Q96PS2_HUM	---	FGF-2 activity-associated protein 3. [So	2.85E-06	4	9.54	8.66	9.18	9.31	9.23	9.18	9.22	9.11
TC1601287	Q96PS3_HUM	---	FGF-2 activity-associated protein 2. [So	3.23E-09	4	5.74	4.65	4.48	4.55	4.48	4.49	4.41	4.74
TC1900895	Q9BZ77_HUM	---	---	2.36E-05	4	4.43	3.71	3.71	3.61	3.71	3.69	3.45	3.80
TC0500177	Q9H385_HUM	---	---	6.62E-08	4	4.25	3.00	2.96	3.04	3.23	3.14	3.17	3.19
TC1701124	Q9H3A7_HUM	---	---	0.000273	4	4.06	3.41	3.29	3.51	3.32	3.33	3.36	3.75
TC1700761	Q9H614_HUM	---	Myosin-XVB (Unconventional myosin-1	9.93E-08	4	5.20	5.03	5.01	4.97	4.98	4.97	4.94	4.99
TC0100922	Q9H762_HUM	---	CDNA: FLJ21272 fis, clone COL01753. [	9.78E-06	4	5.05	4.34	4.37	4.31	4.28	4.47	4.66	4.62
TC2000382	Q9H800_HUM	---	CDNA FLJ14031 fis, clone HEMBA1004	6.46E-05	4	6.84	6.16	6.14	6.18	6.11	6.18	6.26	6.22
TC1600902	Q9NRE7_HUM	---	KIAA0220-like protein (LOC339047 pro	6.34E-06	4	6.19	5.87	5.85	5.69	5.83	5.78	5.86	5.74
TC1701447	Q9NWC8_HU	---	leucine rich repeat containing 37, mem	1.83E-10	4	6.75	5.11	5.01	5.34	5.64	5.66	5.94	5.79
TC1000246	Q9P136_HUM	---	---	5.94E-07	4	5.86	5.91	5.24	5.29	5.28	5.50	5.62	5.69
TC1200502	Q9P175_HUM	---	---	6.67E-09	4	5.20	4.05	4.09	4.24	4.22	4.21	4.21	4.35
TC1000247	Q9P194_HUM	---	---	0.000754	4	4.23	3.76	3.51	3.60	3.54	3.51	3.69	3.81
TC1100101	Q9P1B9_HUM	---	---	0.000114	4	9.10	6.40	5.88	7.30	7.72	7.86	7.37	7.77
TC1200864	Q9P1F0_HUM	---	---	9.36E-08	4	6.51	5.09	5.16	5.29	5.14	5.30	5.41	5.56
TC1100060	Q9P1L5_HUM	---	---	2.36E-05	4	5.96	4.77	4.83	5.03	5.02	4.97	5.31	5.08
TC0X00795	Q9P1M3_HUM	---	---	0.000508	4	6.93	5.87	5.53	5.75	5.52	5.94	5.79	5.87
TC1201577	Q9UFT6_HUM	196515	GR AF-1 specific protein phosphatase (	6.01E-06	4	5.06	4.68	4.56	4.68	4.69	4.68	4.78	4.71
TC1600836	Q9UI82_HUM	---	---	0.000185	4	8.05	7.14	7.07	7.06	6.90	7.38	7.01	7.14
TC0301198	QRICH1	54870	glutamine-rich 1	0.000838	4	5.90	5.60	5.43	5.47	5.48	5.59	5.60	5.63
TC1201319	R3HDM2	22864	R3H domain containing 2	8.90E-05	4	7.03	6.66	6.56	6.61	6.52	6.63	6.79	6.76
TC0900543	RABGAP1	23637	RAB GTPase activating protein 1 /// RA	1.34E-07	4	5.84	5.51	5.38	5.51	5.51	5.63	5.73	5.66
TC0700054	RAC1	5879	ras-related C3 botulinum toxin substra	8.18E-09	4	7.95	7.48	7.60	7.74	7.71	7.78	7.72	7.79
TC0301021	RAF1	5894	v-raf-1 murine leukemia viral oncogene	1.20E-14	4	8.73	7.46	7.46	7.76	7.77	7.94	7.86	8.03
TC1401136	RAGE	5891	renal tumor antigen /// MAPK/MAK/M	1.68E-10	4	3.57	3.28	3.28	3.25	3.25	3.27	3.30	3.35
TC1800046	RALBP1	10928	ralA binding protein 1	5.05E-08	4	8.16	7.64	7.44	7.65	7.63	7.79	7.91	7.91
TC0900572	RALGPS1	9649	Ral GEF with PH domain and SH3 bindi	3.09E-07	4	3.78	3.50	3.57	3.54	3.56	3.54	3.51	3.50

TC0700227	RAMP3	10268	receptor (G protein-coupled) activity m	0.000444	4	5.05	4.67	4.89	4.62	4.77	4.81	4.74	4.74
TC1901080	RANBP3	8498	RAN binding protein 3 /// Ran-binding	6.53E-05	4	5.62	5.31	5.27	5.45	5.43	5.41	5.44	5.52
TC0901396	RAPGEF1	2889	Rap guanine nucleotide exchange facto	5.21E-07	4	5.95	5.59	5.31	5.38	5.34	5.33	5.35	5.37
TC0400644	RAPGEF2	9693	Rap guanine nucleotide exchange facto	4.68E-10	4	7.36	6.64	6.26	6.39	6.27	6.68	6.70	6.81
TC1700430	RAPGEFL1	51195	Rap guanine nucleotide exchange facto	1.49E-08	4	3.81	3.51	3.45	3.45	3.47	3.44	3.39	3.46
TC1300672	RASA3	22821	RAS p21 protein activator 3	1.44E-06	4	5.29	4.75	4.58	4.93	4.93	4.97	5.01	5.02
TC0301231	RASSF1	11186	Ras association (RalGDS/AF-6) domain	4.48E-09	4	4.93	4.48	4.50	4.61	4.61	4.65	4.54	4.59
TC0700987	RBAK /// RNF2	57786 ///	RB-associated KRAB zinc finger /// ring	0.000286	4	5.99	5.55	5.74	5.82	5.64	5.72	5.86	5.84
TC1100581	RBM14 /// RBM	10432 ///	RNA binding motif protein 14 /// RNA b	0.000681	4	5.59	5.35	5.29	5.40	5.35	5.39	5.48	5.53
TC0100821	RBM15	64783	RNA binding motif protein 15 /// Putat	1.78E-05	4	5.17	5.31	5.02	4.96	4.98	5.18	5.18	5.15
TC1400348	RBM25	58517	RNA binding motif protein 25	4.49E-13	4	7.51	6.43	6.36	6.31	6.39	6.46	6.71	6.57
TC0700918	RBM33	732019 //	RNA binding motif protein 33 /// Prolin	9.67E-12	4	7.18	6.71	6.58	6.70	6.67	6.80	6.81	6.86
TC2000706	RBM39	9584	RNA binding motif protein 39 /// RNA-b	1.71E-07	4	9.40	8.85	8.91	8.88	8.79	8.87	8.90	8.87
TC0201219	RBM44 /// LRR	375316 //	RNA binding motif protein 44 /// leucin	2.08E-08	4	6.41	5.97	6.03	6.13	6.01	6.14	6.26	6.21
TC0300278	RBM5	10181	RNA binding motif protein 5	2.26E-12	4	8.70	7.91	7.71	7.75	7.62	7.85	7.91	7.91
TC0300276	RBM6	10180	RNA binding motif protein 6	1.55E-05	4	7.10	6.28	6.28	6.28	6.29	6.12	6.41	6.23
TC0103014	RC3H1	149041	ring finger and CCCH-type zinc finger d	1.49E-05	4	8.81	8.26	8.23	8.44	8.23	8.33	8.38	8.41
TC1900720	RCN3	57333	reticulocalbin 3, EF-hand calcium bindi	7.75E-21	4	5.76	5.06	5.02	5.00	4.92	4.97	4.96	5.04
TC0101492	RCOR3	55758	REST corepressor 3 /// REST corepresso	2.32E-09	4	6.61	6.34	6.21	6.23	6.22	6.39	6.51	6.50
TC0101262	RCSD1	92241	RCSD domain containing 1 /// RCSD do	1.00E-09	4	6.94	6.17	6.25	6.40	6.42	6.50	6.58	6.63
TC1400122	REC8	9985	REC8 homolog (yeast)	1.58E-19	4	5.73	4.98	4.77	4.82	4.88	4.94	5.00	5.06
TC1701695	RECQL5	9400	RecQ protein-like 5	0.000182	4	4.48	4.25	4.26	4.32	4.27	4.26	4.21	4.23
TC0400874	RELL1	768211	RELT-like 1	6.74E-06	4	8.24	7.38	7.16	7.49	7.50	7.58	7.64	7.91
TC1400092	REM2	161253	RAS (RAD and GEM)-like GTP binding 2	4.70E-22	4	6.49	4.87	4.68	4.93	5.00	5.15	5.28	5.09
TC0101828	RERE	473	arginine-glutamic acid dipeptide (RE) re	2.84E-08	4	6.11	5.81	5.70	5.83	5.75	5.93	5.95	5.98
TC0201780	REV1	51455	REV1 homolog (S. cerevisiae)	4.88E-08	4	4.81	4.11	4.23	4.29	4.42	4.39	4.45	4.34
TC1701230	RFFL	117584	ring finger and FYVE-like domain contai	0.000639	4	6.90	6.44	6.30	6.56	6.58	6.56	6.49	6.58
TC0103025	RFWD2	731621 //	ring finger and WD repeat domain 2 //,	4.78E-05	4	8.71	8.31	8.36	8.31	8.23	8.44	8.35	8.44
TC0X01018	RGAG4	340526	retrotransposon gag domain containing	1.01E-08	4	6.08	5.14	5.32	5.26	5.32	5.29	5.18	5.42
TC0601176	RGL2	5863	ral guanine nucleotide dissociation stim	1.33E-23	4	6.07	5.34	5.28	5.25	5.31	5.38	5.30	5.35
TC0200427	RGPD1	400966	RANBP2-like and GRIP domain containi	3.60E-05	4	4.67	4.22	3.94	3.91	3.97	4.16	4.31	4.12
TC0201698	RGPD2	729857	RANBP2-like and GRIP domain containi	0.000653	4	4.91	4.29	4.03	3.90	4.00	4.28	4.41	4.26
TC0201819	RGPD5	84220	RANBP2-like and GRIP domain containi	4.03E-05	4	5.30	5.27	5.07	5.03	5.09	5.12	5.22	5.17
TC1201642	RHOF	54509	ras homolog gene family, member F (in	7.77E-05	4	5.33	5.01	5.01	5.11	5.13	5.12	5.16	5.06

TC1600026	RHOT2	89941	ras homolog gene family, member T2	3.12E-06	4	5.39	5.13	5.12	5.12	5.14	5.14	5.11	5.10
TC0500933	RICTOR /// NP_	253260	rapamycin-insensitive companion of m	6.51E-23	4	8.58	7.24	6.89	7.10	7.03	7.61	7.67	7.91
TC1400037	RNASE6	6039	ribonuclease, RNase A family, k6	2.68E-08	4	7.78	6.79	5.53	5.87	5.69	6.00	6.24	6.72
TC0601755	RNASET2	8635	ribonuclease T2 /// Ribonuclease T2 pr	4.82E-16	4	7.98	6.71	6.85	7.08	6.90	7.17	7.25	7.25
TC1601335	RNF166	115992	ring finger protein 166	2.83E-07	4	6.57	6.01	6.02	6.14	6.21	6.22	6.21	6.28
TC1100666	RNF169	254225	ring finger protein 169	1.02E-05	4	7.53	7.00	7.02	7.18	7.06	7.23	7.23	7.32
TC2200204	RNF185	91445	ring finger protein 185 /// RING finger	2.59E-05	4	5.57	5.29	5.18	5.20	5.27	5.41	5.34	5.44
TC0102090	RNF19B	127544	ring finger protein 19B /// IBR domain-	8.11E-08	4	8.79	8.23	8.09	8.23	8.21	8.52	8.43	8.70
TC1700827	RNF213	57674	ring finger protein 213	4.57E-06	4	7.73	6.66	6.47	6.86	6.67	6.91	7.23	7.21
TC1400120	RNF31 /// IRF9	55072 ///	ring finger protein 31 /// interferon reg	2.23E-05	4	6.53	6.17	6.03	6.11	6.01	6.25	6.27	6.41
TC0101778	RP11-345P4.4 /	728661 //	similar to solute carrier family 35, mem	7.12E-07	4	6.67	6.33	6.25	6.36	6.38	6.39	6.49	6.45
TC0X00587	RP13-36C9.1 //	728911 //	cancer/testis antigen CT45 /// cancer/t	2.49E-05	4	3.81	3.45	3.50	3.44	3.42	3.47	3.45	3.49
TC0100912	RP3-365I19.1	647135	SLIT-ROBO Rho GTPase-activating prote	2.01E-24	4	7.05	5.70	5.30	5.65	5.84	6.08	6.38	6.37
TC0102041	RPA2	6118	replication protein A2, 32kDa /// Replic	6.57E-13	4	7.01	6.27	6.13	6.02	5.93	6.17	6.26	6.30
TC0X00847	RPGR	6103	retinitis pigmentosa GTPase regulator /	5.13E-10	4	7.02	5.94	5.98	5.88	5.80	6.10	6.31	6.35
TC1400050	RPGRIP1	57096	retinitis pigmentosa GTPase regulator i	3.50E-30	4	4.25	3.04	2.82	2.92	2.84	3.07	3.16	3.35
TC0301550	RPL32P3	---	ribosomal protein L32 pseudogene 3 (R	9.13E-08	4	6.17	5.71	5.64	5.77	5.81	5.90	6.04	5.88
TC1401062	RPS6KA5	9252	ribosomal protein S6 kinase, 90kDa, po	5.82E-21	4	8.23	6.19	5.51	5.97	6.20	6.95	7.08	7.38
TC0601720	RSPH3	83861	radial spoke 3 homolog (Chlamydomon	6.83E-17	4	4.94	4.08	4.08	4.22	4.19	4.34	4.52	4.61
TC1600309	RUNDC2B /// C	400509	RUN domain containing 2B /// CDNA FL	2.20E-06	4	4.84	4.61	4.54	4.55	4.60	4.57	4.53	4.62
TC0601173	RXRB	6257	retinoid X receptor, beta /// Retinoic ac	1.12E-11	4	6.82	5.78	5.77	5.80	5.77	5.86	5.82	5.79
TC1900103	SAFB	6294	scaffold attachment factor B	3.35E-06	4	7.20	6.79	6.78	6.95	6.87	6.95	7.06	7.02
TC1901070	SAFB2	9667	scaffold attachment factor B2	6.35E-13	4	7.54	6.79	6.79	7.03	7.03	7.05	7.23	7.18
TC1900517	SAMD4B	55095	sterile alpha motif domain containing 4	2.57E-06	4	5.83	5.63	5.42	5.49	5.51	5.57	5.55	5.58
TC0201888	SAP130	79595	Sin3A-associated protein, 130kDa /// H	9.42E-08	4	6.80	6.35	6.19	6.41	6.34	6.50	6.56	6.61
TC2200382	SAPS2	9701	SAPS domain family, member 2 /// SAP	2.23E-16	4	5.42	5.08	4.97	5.03	5.04	5.02	5.01	5.02
TC1500586	SCAND2	---	SCAN domain-containing protein 2. [So	3.50E-09	4	3.95	3.44	3.55	3.58	3.50	3.55	3.67	3.59
TC0301166	SCAP	22937	SREBF chaperone /// Sterol regulatory	3.00E-17	4	6.04	5.27	5.32	5.40	5.40	5.46	5.46	5.56
TC0800445	SDC2	6383	syndecan 2	7.36E-08	4	4.11	3.52	3.19	3.29	3.29	3.32	3.47	3.88
TC1200722	SDSL	113675	serine dehydratase-like	4.76E-07	4	5.19	4.97	4.97	4.91	4.92	4.94	4.85	4.95
TC1700794	SEC14L1	6397	SEC14-like 1 (S. cerevisiae)	2.23E-13	4	8.85	7.93	7.75	7.88	7.83	8.15	8.05	8.32
TC1000343	SEC24C	9632	SEC24 related gene family, member C (	1.63E-12	4	5.41	4.81	4.75	4.73	4.66	4.75	4.76	4.76
TC1000058	SEC61A2	55176	Sec61 alpha 2 subunit (S. cerevisiae) //,	1.15E-22	4	5.68	4.30	4.09	4.25	4.25	4.38	4.50	4.41
TC0900367	SECISBP2	79048	SECIS binding protein 2 /// SECIS-bindir	6.86E-23	4	6.60	5.49	5.36	5.55	5.49	5.78	5.94	6.01

TC0701378	SEMA3C	10512	sema domain, immunoglobulin domain	9.38E-08	4	3.46	3.21	3.03	3.04	2.98	3.12	3.15	3.29
TC0901113	SEMA4D	10507	sema domain, immunoglobulin domain	4.84E-08	4	8.99	8.42	8.09	8.35	8.28	8.52	8.51	8.69
TC1500899	SERINC4	619189	serine incorporator 4 /// serine incorpo	5.17E-09	4	4.86	4.49	4.48	4.42	4.53	4.61	4.57	4.58
TC0501100	SERINC5	256987	serine incorporator 5	3.30E-08	4	5.46	4.96	4.87	4.96	4.84	5.05	5.13	5.07
TC1200770	SETD1B	23067	SET domain containing 1B	2.62E-10	4	6.68	5.91	5.74	6.04	5.98	6.10	6.20	6.20
TC0301163	SETD2	29072	SET domain containing 2	2.23E-08	4	7.97	7.38	7.26	7.36	7.35	7.46	7.64	7.60
TC2100328	SETD4	54093	SET domain containing 4 /// SET domai	0.000197	4	4.11	3.95	3.96	3.97	3.91	3.93	4.00	4.00
TC0901400	SETX	23064	senataxin /// Probable helicase senata	2.26E-16	4	8.48	7.69	7.17	7.52	7.44	7.78	7.92	8.07
TC0202200	SF3B1	23451	splicing factor 3b, subunit 1, 155kDa	5.92E-17	4	9.32	8.42	8.20	8.31	8.29	8.38	8.45	8.38
TC2200212	SFI1	9814	Sfi1 homolog, spindle assembly associa	5.97E-29	4	5.36	4.69	4.66	4.68	4.68	4.72	4.73	4.76
TC0100299	SFN	2810	stratifin	0.00049	4	5.42	5.22	5.07	5.19	5.21	5.26	5.30	5.25
TC1901313	SFRS14	10147	splicing factor, arginine/serine-rich 14 /	6.46E-08	4	4.99	4.53	4.52	4.53	4.62	4.60	4.67	4.55
TC1900626	SFRS16	11129	splicing factor, arginine/serine-rich 16 /	2.95E-15	4	6.38	5.80	5.67	5.64	5.67	5.66	5.71	5.72
TC0X00006	SFRS17A /// AS	8227 /// 4	splicing factor, arginine/serine-rich 17A	0.00066	4	5.11	4.95	4.93	4.92	4.90	4.87	4.90	4.91
TC0601476	SFRS18	25957	splicing factor, arginine/serine-rich 18	2.08E-16	4	7.82	6.72	6.62	6.72	6.70	6.85	7.07	6.98
TC0100916	SFRS2IP /// NB	9169	splicing factor, arginine/serine-rich 2, ir	4.18E-17	4	9.91	8.13	8.25	8.39	8.32	8.35	8.36	8.23
TC1400326	SFRS5	6430	splicing factor, arginine/serine-rich 5 //	2.20E-10	4	9.34	8.85	8.63	8.54	8.60	8.82	8.92	8.95
TC1200699	SH2B3	10019	SH2B adaptor protein 3	1.09E-11	4	5.53	4.66	4.66	4.98	4.96	5.11	5.06	5.17
TC0400031	SH3BP2	6452	SH3-domain binding protein 2	3.31E-07	4	5.85	5.45	5.37	5.45	5.46	5.47	5.46	5.47
TC1100877	SIDT2	51092	SID1 transmembrane family, member 2	1.99E-05	4	5.40	5.18	5.11	5.27	5.19	5.14	5.14	5.18
TC1900756	SIGLECP3	---	SIGLECP3 protein (Fragment). [Source:U	1.46E-05	4	4.60	4.12	4.16	4.13	4.09	4.11	4.13	4.20
TC1900289	SIN3B	23309	SIN3 homolog B, transcription regulato	3.97E-07	4	4.64	4.25	4.28	4.22	4.23	4.21	4.24	4.22
TC1400339	SIPA1L1	26037	signal-induced proliferation-associated	1.50E-12	4	7.50	7.07	6.23	6.58	6.53	6.97	7.04	7.23
TC2000496	SIRPB2	284759	signal-regulatory protein beta 2 /// Sigı	1.24E-08	4	7.30	6.34	6.37	6.38	6.12	6.26	6.38	6.47
TC1701474	SKAP1	8631	src kinase associated phosphoprotein 1	0.000568	4	4.25	3.89	3.87	3.96	3.91	3.88	4.01	4.04
TC1700887	SKIP	51763	skeletal muscle and kidney enriched in	0.000935	4	5.59	5.30	5.20	5.26	5.34	5.42	5.34	5.46
TC0600284	SKIV2L	6499	superkiller viralicidic activity 2-like (S. c	9.90E-13	4	5.20	4.77	4.69	4.71	4.68	4.71	4.69	4.69
TC1601187	SLC12A4 /// LC	6560 /// 3	solute carrier family 12 (potassium/chl	4.84E-13	4	4.74	4.38	4.35	4.41	4.39	4.42	4.44	4.50
TC1500806	SLC12A6	9990	solute carrier family 12 (potassium/chl	3.86E-06	4	9.27	8.84	8.77	8.75	8.60	8.69	8.70	8.69
TC1700751	SLC16A5	9121	solute carrier family 16, member 5 (mo	2.35E-06	4	5.09	4.74	4.85	4.87	4.87	4.79	4.78	4.84
TC0200586	SLC20A1	6574	solute carrier family 20 (phosphate trai	3.32E-07	4	6.43	6.04	5.57	5.73	5.69	5.95	6.10	6.04
TC0600860	SLC22A1	6580	solute carrier family 22 (organic cation	2.54E-10	4	5.54	4.61	4.54	4.80	4.92	5.00	4.97	4.88
TC0500463	SLC22A5	6584	solute carrier family 22 (organic cation,	1.18E-08	4	4.56	4.11	4.10	4.08	4.07	4.12	4.17	4.22
TC2000529	SLC23A2	9962	solute carrier family 23 (nucleobase tra	1.84E-14	4	4.90	4.39	4.18	4.28	4.22	4.35	4.38	4.46

TC0X00562	SLC25A14	9016	solute carrier family 25 (mitochondrial	7.27E-09	4	4.57	4.27	4.34	4.18	4.09	4.19	4.32	4.35
TC1101541	SLC25A45	283130	solute carrier family 25, member 45 ///	6.17E-06	4	4.77	4.58	4.64	4.51	4.63	4.60	4.58	4.63
TC0600303	SLC39A7	7922	solute carrier family 39 (zinc transporte	0.000238	4	4.90	4.60	4.62	4.60	4.65	4.64	4.57	4.57
TC1700889	SLC43A2	124935	solute carrier family 43, member 2 ///	2.04E-05	4	7.00	6.51	6.13	6.57	6.45	6.66	6.52	6.80
TC1900177	SLC44A2	57153	solute carrier family 44, member 2 ///	9.57E-07	4	8.18	7.19	7.06	7.26	7.25	7.28	7.24	7.43
TC0801287	SLC45A4 /// Q	57210	solute carrier family 45, member 4 ///	1.38E-09	4	6.70	5.84	5.62	5.87	5.85	5.97	5.90	6.08
TC1200341	SLC4A8	9498	solute carrier family 4, sodium bicarbo	0.00052	4	3.17	2.96	3.02	2.98	2.95	3.00	3.02	3.05
TC0300075	SLC6A6	6533	solute carrier family 6 (neurotransmitt	0.000656	4	8.78	8.48	8.27	8.45	8.31	8.28	8.26	8.30
TC1600538	SLC7A6	9057	solute carrier family 7 (cationic amino	2.50E-16	4	4.95	4.17	4.36	4.58	4.48	4.47	4.58	4.52
TC1400705	SLC7A7	9056	solute carrier family 7 (cationic amino	2.30E-06	4	5.71	4.65	4.77	4.93	4.76	4.77	5.02	5.09
TC0X00881	SLC9A7	84679	solute carrier family 9 (sodium/hydrog	6.10E-11	4	4.40	4.02	4.03	3.99	4.06	4.16	4.20	4.17
TC0100428	SMAP2 /// SM	64744	stromal membrane-associated GTPase-	9.81E-05	4	10.34	9.82	9.73	9.79	9.66	9.70	9.78	9.94
TC1201288	SMARCC2	6601	SWI/SNF related, matrix associated, ac	1.22E-13	4	7.51	6.88	6.74	7.02	7.00	7.08	7.26	7.25
TC1800012	SMCHD1	23347	structural maintenance of chromosom	3.41E-17	4	10.24	9.31	9.11	9.34	9.33	9.69	9.78	9.92
TC1600908	SMG1 /// NR_	23049	PI-3-kinase-related kinase SMG-1 /// sc	3.39E-06	4	6.98	6.43	6.16	6.14	6.15	6.22	6.36	6.21
TC0102849	SMG5	23381	Smg-5 homolog, nonsense mediated m	2.44E-05	4	5.32	4.65	4.59	4.67	4.78	4.70	4.75	4.75
TC0100317	SMPDL3B	27293	sphingomyelin phosphodiesterase, acid	4.69E-05	4	4.56	4.29	4.25	4.19	4.21	4.25	4.21	4.32
TC1701621	SMURF2	64750	SMAD specific E3 ubiquitin protein liga	5.34E-07	4	6.05	5.80	5.62	5.58	5.57	5.83	5.89	5.91
TC0401123	SNCA	6622	synuclein, alpha (non A4 component o	3.25E-06	4	6.72	4.75	4.54	5.08	5.25	5.25	5.13	5.22
TC0102125	SNIP1	79753	Smad nuclear interacting protein 1	0.000424	4	6.51	6.38	6.11	6.24	6.19	6.28	6.41	6.40
TC1701284	SNORA21	---	small nucleolar RNA, H/ACA box 21 (SN	2.48E-06	4	4.65	3.35	3.54	3.51	3.45	3.68	3.72	3.82
TC1101493	SNORD31 /// S	---	small nucleolar RNA, C/D box 31 (SNO	5.72E-09	4	3.46	2.89	2.91	2.96	3.18	3.16	3.20	3.11
TC2200682	SNORD43	---	small nucleolar RNA, C/D box 43 (SNO	0.000536	4	4.85	3.90	3.99	3.99	4.38	4.04	3.90	3.98
TC1201302	SNORD59B	---	small nucleolar RNA, C/D box 59B (SN	0.000846	4	4.79	3.49	3.72	3.93	3.84	3.98	4.12	4.01
TC1900706	SNRP70	6625	small nuclear ribonucleoprotein 70kDa	1.89E-33	4	6.39	5.17	5.15	5.16	5.29	5.22	5.21	5.10
TC2100088	SON	6651	SON DNA binding protein /// SON prot	6.80E-06	4	7.74	7.43	7.15	7.18	7.16	7.24	7.42	7.35
TC1100934	SORL1	6653	sortilin-related receptor, L(DLR class) A	0.000369	4	10.63	10.11	10.27	10.30	10.09	10.12	10.03	10.09
TC1701526	SPAG9	9043	sperm associated antigen 9 /// C-jun-a	3.38E-16	4	8.04	6.99	6.75	6.90	6.89	7.20	7.31	7.40
TC0100174	SPEN	23013	spen homolog, transcriptional regulato	7.35E-09	4	7.46	6.52	6.39	6.47	6.42	6.57	6.81	6.79
TC1600683	SPG7	6687	spastic paraplegia 7 (pure and complic	3.13E-10	4	5.25	4.99	4.99	4.94	4.96	4.97	4.97	5.01
TC1500243	SPINT1	6692	serine peptidase inhibitor, Kunitz type	1.33E-08	4	5.59	5.20	5.11	5.18	5.24	5.30	5.26	5.42
TC1201242	SPRYD3	84926	SPRY domain containing 3	2.66E-05	4	5.39	5.05	5.19	5.18	5.06	5.10	5.13	5.22
TC1600748	SPSB3	90864	splA/ryanodine receptor domain and S	0.000891	4	5.84	5.61	5.64	5.67	5.65	5.67	5.65	5.61
TC1600344	SRCAP /// NP_	10847	Snf2-related CREBBP activator protein ,	2.60E-09	4	6.36	5.65	5.53	5.78	5.79	5.71	5.78	5.83

TC0101461	SRGAP2	23380	SLIT-ROBO Rho GTPase activating prote	6.44E-22	4	6.08	5.06	4.60	5.00	5.06	5.35	5.51	5.57
TC0100900	SRGAP2P1	653464	SLIT-ROBO Rho GTPase activating prote	9.23E-20	4	6.42	5.50	5.21	5.46	5.53	5.79	5.92	6.01
TC0701532	SRPK2	6733	SFRS protein kinase 2	4.38E-12	4	7.88	6.90	6.90	7.18	7.03	7.23	7.29	7.42
TC1600093	SRRM2	23524	serine/arginine repetitive matrix 2 /// S	7.40E-31	4	7.74	6.43	6.07	6.21	6.32	6.37	6.54	6.51
TC1701195	SSH2	85464	slingshot homolog 2 (Drosophila) /// Pr	7.83E-05	4	9.22	8.77	8.73	8.82	8.66	8.70	8.76	8.82
TC1100594	SSH3	54961	slingshot homolog 3 (Drosophila) /// Pr	3.16E-05	4	5.62	5.47	5.42	5.40	5.39	5.40	5.38	5.40
TC0X00940	SSX2B /// SSX2	727837 //	synovial sarcoma, X breakpoint 2B /// s	0.000292	4	3.72	3.42	3.56	3.41	3.44	3.43	3.49	3.45
TC1701718	ST6GALNAC2	10610	ST6 (alpha-N-acetyl-neuraminyl-2,3-be	7.83E-07	4	6.40	5.51	5.55	5.89	5.87	5.98	5.84	6.10
TC0701328	STAG3L1 /// NI	54441	stromal antigen 3-like 1 /// STAG3-like.	5.22E-08	4	6.77	6.36	6.31	6.37	6.55	6.49	6.56	6.50
TC0700404	STAG3L2 /// ST	442582 //	stromal antigen 3-like 2 /// stromal ant	4.00E-06	4	6.53	6.12	6.06	6.11	6.28	6.20	6.34	6.18
TC0701309	STAG3L2 /// ST	442582 //	stromal antigen 3-like 2 /// stromal ant	7.40E-06	4	6.46	5.98	5.93	6.01	6.14	6.16	6.26	6.12
TC0700353	STAG3L4	64940	stromal antigen 3-like 4	7.06E-12	4	4.29	3.60	3.58	3.64	3.77	3.91	3.95	4.01
TC1201294	STAT2	6773	signal transducer and activator of trans	5.10E-09	4	6.69	5.63	5.37	5.51	5.28	5.89	6.22	6.43
TC1201315	STAT6	6778	signal transducer and activator of trans	3.65E-11	4	7.68	6.48	6.42	6.75	6.68	6.71	6.57	6.72
TC2000306	STK4	6789	serine/threonine kinase 4 /// Serine/th	1.72E-05	4	9.36	9.10	8.99	9.08	9.00	9.19	9.17	9.25
TC0102113	STK40	83931	serine/threonine kinase 40 /// Serine/t	3.52E-05	4	6.88	6.29	6.05	6.43	6.37	6.44	6.35	6.51
TC1901632	STRN4	29888	striatin, calmodulin binding protein 4	2.04E-07	4	5.76	5.26	5.30	5.43	5.41	5.35	5.28	5.33
TC2000809	SULF2	55959	sulfatase 2 /// Extracellular sulfatase Su	2.89E-20	4	8.19	6.57	5.43	6.39	6.34	7.12	7.17	7.49
TC1600968	SULT1A2	6799	sulfotransferase family, cytosolic, 1A, p	2.77E-05	4	5.73	5.63	5.43	5.40	5.44	5.56	5.44	5.48
TC0600800	SUMO4	387082	SMT3 suppressor of mif two 3 homolog	0.000288	4	4.40	3.90	3.94	3.88	3.85	3.90	3.89	4.03
TC1200418	SUOX	6821	sulfite oxidase	0.00036	4	5.29	4.94	4.96	4.97	4.99	5.02	5.07	5.10
TC1700333	SUZ12P	---	SUZ12P protein. [Source:Uniprot/SPTRI	5.67E-14	4	6.96	6.22	6.28	6.42	6.51	6.55	6.66	6.64
TC1901609	SYMPK	8189	symplekin /// Symplekin. [Source:Unipr	0.000306	4	5.42	5.18	5.18	5.28	5.28	5.27	5.31	5.26
TC1400294	SYNE2	23224	spectrin repeat containing, nuclear env	1.21E-05	4	7.24	6.50	5.88	6.11	6.02	5.91	6.27	6.23
TC1001074	SYNPO2L	79933	synaptopodin 2-like /// Synaptopodin 2	8.38E-07	4	3.82	3.64	3.55	3.51	3.49	3.50	3.53	3.59
TC0103129	SYT2	127833	synaptotagmin II	2.39E-14	4	4.91	4.37	4.24	4.22	4.35	4.42	4.39	4.42
TC0800231	TACC1	6867	transforming, acidic coiled-coil contain	1.90E-13	4	7.89	7.21	7.29	7.41	7.30	7.47	7.56	7.64
TC0X00340	TAF1 /// Q70T(	6872	TAF1 RNA polymerase II, TATA box bin	0.000145	4	5.89	5.59	5.45	5.39	5.37	5.45	5.56	5.51
TC2000878	TAF4	6874	TAF4 RNA polymerase II, TATA box bin	2.82E-11	4	5.83	5.24	5.19	5.37	5.40	5.50	5.55	5.58
TC1100597	TBC1D10C	374403	TBC1 domain family, member 10C	3.87E-09	4	5.78	5.46	5.44	5.40	5.42	5.46	5.45	5.42
TC1900733	TBC1D17	79735	TBC1 domain family, member 17	7.64E-13	4	5.72	5.36	5.32	5.33	5.34	5.37	5.35	5.38
TC2200366	TBC1D22A	25771	TBC1 domain family, member 22A /// T	3.54E-15	4	7.21	6.36	6.27	6.42	6.39	6.54	6.55	6.63
TC1701268	TBC1D3E /// TE	729877 //	TBC1 domain family, member 3E /// TB	1.21E-08	4	5.30	4.77	4.73	4.77	4.85	4.77	4.79	4.71
TC1701269	TBC1D3H /// TI	727735	TBC1 domain family, member 3H /// TE	1.50E-07	4	6.57	6.00	6.02	6.02	6.01	6.00	5.96	6.06

TC0700743	TBXAS1	6916	thromboxane A synthase 1 (platelet, cy	0.000269	4	7.47	6.93	7.08	7.03	6.86	6.94	7.02	7.04
TC0701361	tcag7.1017	441272	similar to Williams Beuren syndrome ch	3.69E-19	4	6.76	5.91	5.81	5.94	5.92	5.97	6.06	6.00
TC2200721	TCF20	6942	transcription factor 20 (AR1)	4.53E-12	4	7.17	6.26	5.86	6.22	6.25	6.41	6.66	6.73
TC1600692	TCF25	22980	transcription factor 25 (basic helix-loop	5.04E-12	4	6.83	6.27	6.01	6.13	6.11	6.17	6.20	6.25
TC1100608	TCIRG1	10312	T-cell, immune regulator 1, ATPase, H+	1.90E-09	4	6.71	6.35	6.32	6.31	6.32	6.32	6.25	6.29
TC1200695	TCTN1	79600	tectonic family member 1 /// Tectonic-	1.38E-33	4	4.03	3.10	3.13	3.09	3.11	3.27	3.34	3.51
TC0900106	TEK	7010	TEK tyrosine kinase, endothelial (venou	4.30E-08	4	3.19	2.73	2.73	2.70	2.72	2.86	2.80	2.87
TC1400668	TEP1	7011	telomerase-associated protein 1 /// Tel	2.07E-11	4	5.63	4.88	5.06	5.06	4.93	4.99	5.06	5.10
TC0400436	TET2 /// KIAA1	54790	tet oncogene family member 2 /// CDN	7.06E-10	4	8.84	8.30	8.12	8.06	7.80	7.95	8.13	8.11
TC0300121	TGFBR2	7048	transforming growth factor, beta recep	2.74E-08	4	8.80	7.98	8.08	8.22	7.98	8.24	8.14	8.38
TC2000024	TGM3	7053	transglutaminase 3 (E polypeptide, pro	1.05E-06	4	4.71	4.68	4.48	4.43	4.50	4.72	4.60	4.67
TC0102825	THBS3	7059	thrombospondin 3	7.48E-11	4	5.54	5.04	5.03	5.11	5.11	5.05	5.08	5.05
TC0100396	THRAP3	9967	thyroid hormone receptor associated p	3.97E-05	4	8.26	8.02	7.69	7.84	7.75	7.90	8.04	8.01
TC1400104	THTPA	79178	thiamine triphosphatase	6.69E-08	4	4.71	4.48	4.42	4.37	4.38	4.35	4.35	4.40
TC0600838	TIAM2 /// RBM	26230 ///	T-cell lymphoma invasion and metastas	2.69E-06	4	4.75	4.51	4.48	4.54	4.55	4.64	4.63	4.63
TC0202399	TIGD1	200765	tigger transposable element derived 1	0.000616	4	2.96	2.53	2.63	2.61	2.65	2.64	2.80	2.70
TC1700669	TLK2	11011	tousled-like kinase 2 /// Serine/threoni	0.000107	4	7.47	7.54	7.33	7.34	7.27	7.40	7.48	7.45
TC0400884	TLR6	10333	toll-like receptor 6	7.22E-05	4	7.90	7.30	7.54	7.51	7.27	7.64	7.61	7.74
TC2000178	TM9SF4	9777	transmembrane 9 superfamily protein	0.000461	4	5.49	5.21	4.89	5.13	5.09	5.16	5.14	5.18
TC0301555	TMCC1	23023	transmembrane and coiled-coil domai	4.43E-19	4	8.14	6.76	6.46	6.59	6.62	7.21	7.21	7.45
TC0500534	TMCO6	55374	transmembrane and coiled-coil domai	0.000374	4	5.78	5.41	5.62	5.59	5.44	5.52	5.50	5.53
TC1601205	TMED6	146456	transmembrane emp24 protein transp	8.39E-05	4	3.21	2.75	2.85	2.76	2.92	2.78	2.76	2.82
TC0202185	TMEFF2	23671	transmembrane protein with EGF-like a	0.000126	4	2.99	2.84	2.83	2.74	2.85	2.85	2.74	2.81
TC2100166	TMEM1	7109	transmembrane protein 1	0.000116	4	6.40	6.12	5.97	6.04	5.98	6.05	6.14	6.14
TC0400010	TMEM175	84286	transmembrane protein 175	9.47E-06	4	5.08	4.84	4.79	4.83	4.81	4.75	4.75	4.77
TC1901177	TMEM205 /// F	374882 //	transmembrane protein 205 /// RAB3D	0.000165	4	5.54	5.38	5.29	5.38	5.50	5.40	5.32	5.36
TC1700647	TMEM49	81671	transmembrane protein 49	7.26E-07	4	10.17	9.49	9.41	9.59	9.57	9.82	9.78	9.97
TC1400671	TMEM55B	90809	transmembrane protein 55B	1.86E-14	4	5.77	5.15	5.17	5.26	5.28	5.41	5.43	5.36
TC0103278	TMEM63A	9725	transmembrane protein 63A	1.56E-06	4	5.79	5.86	5.32	5.62	5.91	5.77	5.70	5.55
TC0102741	TMOD4	29765	tropomodulin 4 (muscle)	2.94E-09	4	4.58	4.17	4.19	4.08	4.11	4.16	4.27	4.21
TC1400604	TNFAIP2	7127	tumor necrosis factor, alpha-induced p	1.61E-17	4	7.52	5.86	5.86	6.15	6.18	6.44	6.37	6.60
TC0800799	TNFRSF10B	8795	tumor necrosis factor receptor superfa	3.53E-16	4	5.64	4.89	4.76	4.85	4.83	5.01	4.99	5.15
TC0800149	TNFRSF10C	8794	tumor necrosis factor receptor superfa	0.000266	4	8.82	8.63	8.48	8.38	8.28	8.54	8.48	8.57
TC0101796	TNFRSF14	8764	tumor necrosis factor receptor superfa	3.22E-10	4	5.64	5.19	5.24	5.30	5.28	5.34	5.32	5.38

TC0101822	TNFRSF9	3604	tumor necrosis factor receptor superfa	4.65E-05	4	5.06	4.46	4.51	4.50	4.48	4.85	4.77	4.77
TC1901094	TNFSF14	8740	tumor necrosis factor (ligand) superfan	0.000186	4	7.05	6.25	6.30	6.43	6.51	6.49	6.44	6.57
TC1100046	TNNT3	7140	troponin T type 3 (skeletal, fast) /// Trc	1.75E-10	4	5.77	5.36	5.37	5.36	5.37	5.33	5.31	5.36
TC2200297	TNRC6B	23112	trinucleotide repeat containing 6B	5.02E-08	4	8.00	7.40	7.25	7.42	7.35	7.48	7.55	7.63
TC0100496	TOE1	114034	target of EGR1, member 1 (nuclear)	4.96E-06	4	4.52	4.20	4.24	4.29	4.25	4.34	4.31	4.34
TC1701085	TOM1L2	146691	target of myb1-like 2 (chicken) /// TOM	2.84E-08	4	5.45	4.85	4.81	4.81	4.84	4.92	4.93	4.96
TC1701089	TOP3A	7156	topoisomerase (DNA) III alpha	1.32E-08	4	5.90	5.36	5.16	5.42	5.48	5.52	5.54	5.53
TC2200487	TOP3B	8940	topoisomerase (DNA) III beta	0.000632	4	4.77	4.61	4.67	4.59	4.60	4.59	4.61	4.61
TC1500890	TP53BP1	7158	tumor protein p53 binding protein 1 //,	3.55E-14	4	5.33	5.09	4.70	4.72	4.75	4.98	5.10	5.09
TC0801130	TP53INP1	94241	tumor protein p53 inducible nuclear pr	2.44E-07	4	8.46	7.63	7.78	7.88	7.75	7.93	7.79	7.98
TC2000212	TP53INP2	58476	tumor protein p53 inducible nuclear pr	1.58E-11	4	5.62	5.41	5.04	5.17	5.32	5.37	5.28	5.48
TC0103079	TPR	7175	translocated promoter region (to activa	0.000257	4	8.34	7.62	7.41	7.42	7.29	7.47	7.89	7.74
TC0701062	TRA2A	29896	transformer-2 alpha	1.06E-09	4	7.94	7.33	7.19	7.22	7.20	7.42	7.54	7.49
TC1900957	TRIM28	10155	tripartite motif-containing 28 /// Trans	3.33E-08	4	5.57	5.29	5.28	5.33	5.32	5.38	5.36	5.37
TC0600238	TRIM40	135644	tripartite motif-containing 40 /// Tripar	9.27E-07	4	5.22	4.91	4.93	4.77	4.86	4.95	4.93	4.94
TC0700562	TRIM56	81844	tripartite motif-containing 56	8.73E-07	4	5.83	5.53	5.46	5.50	5.53	5.62	5.71	5.68
TC0301707	TRIM59 /// IFT	286827 //	tripartite motif-containing 59 /// intraf	0.000487	4	3.00	2.82	2.82	2.83	2.89	2.89	2.94	2.92
TC1101185	TRIM66	---	Tripartite motif-containing protein 66.	9.53E-05	4	4.22	3.97	3.96	3.97	3.98	3.94	3.96	3.95
TC2200260	TRIOBP	11078	TRIO and F-actin binding protein	0.000455	4	5.66	5.51	5.39	5.46	5.53	5.51	5.47	5.50
TC2200364	TRMU	55687	tRNA 5-methylaminomethyl-2-thiourid	2.15E-07	4	4.30	3.87	3.89	4.00	3.89	3.89	3.97	3.96
TC2000688	TRPC4AP	26133	transient receptor potential cation cha	1.43E-10	4	7.01	6.56	6.41	6.45	6.46	6.55	6.54	6.52
TC0901404	TSC1	7248	tuberous sclerosis 1	2.57E-16	4	5.81	5.00	4.82	5.00	5.06	5.06	5.15	5.11
TC1600072	TSC2	7249	tuberous sclerosis 2 /// Tuberin (Tuber	2.40E-05	4	5.42	5.15	5.13	5.17	5.16	5.15	5.12	5.14
TC0700087	TSPAN13	27075	tetraspanin 13	0.00013	4	4.66	4.28	4.22	4.29	4.40	4.52	4.35	4.58
TC1900188	TSPAN16	26526	tetraspanin 16 /// Tetraspanin-16 (Tspa	1.36E-06	4	6.91	5.51	5.40	5.50	5.56	5.90	5.95	5.87
TC0X00257	TSPYL2	64061	TSPY-like 2	3.87E-13	4	4.61	3.76	3.64	3.63	3.69	3.75	4.01	3.97
TC0100361	TSSK3	81629	testis-specific serine kinase 3	2.36E-11	4	5.22	4.45	4.39	4.52	4.46	4.46	4.55	4.53
TC1400123	TSSK4	283629	testis-specific serine kinase 4 /// Testis-	4.21E-05	4	4.93	4.50	4.63	4.49	4.48	4.57	4.54	4.59
TC1100857	TTC12	54970	tetratricopeptide repeat domain 12 ///	6.52E-06	4	3.73	3.57	3.55	3.56	3.53	3.57	3.56	3.62
TC1100289	TTC17	55761	tetratricopeptide repeat domain 17 ///	9.53E-07	4	5.73	5.21	5.14	5.28	5.29	5.29	5.48	5.36
TC1001066	TTC18	118491	tetratricopeptide repeat domain 18 ///	9.24E-12	4	2.96	2.55	2.64	2.59	2.60	2.57	2.60	2.63
TC0901401	TTF1	7270	transcription termination factor, RNA p	1.68E-11	4	5.31	4.50	4.33	4.48	4.50	4.67	4.96	4.96
TC0300029	TTLL3 /// ARPC	26140 ///	tubulin tyrosine ligase-like family, mem	7.79E-10	4	5.80	5.47	5.44	5.48	5.51	5.49	5.44	5.42
TC0201105	TTLL4	9654	tubulin tyrosine ligase-like family, mem	2.93E-11	4	5.65	4.79	4.68	4.90	5.07	5.29	5.19	5.23

TC0Y00166	TTY10_HUMAN	---	Transcript Y 10 protein. [Source:Unipro	0.000234	4	4.78	4.33	4.30	4.25	4.27	4.36	4.43	4.44
TC0Y00120	TTY8_HUMAN	---	Transcript Y 8 protein. [Source:Uniprot,	0.000798	4	3.19	2.92	2.94	2.88	2.77	2.78	2.82	2.95
TC1300659	TUBGCP3	10426	tubulin, gamma complex associated pr	1.46E-11	4	5.82	5.06	5.63	5.87	5.65	5.43	5.49	5.43
TC2200777	TUBGCP6	85378	tubulin, gamma complex associated pr	2.68E-06	4	4.62	4.42	4.44	4.39	4.42	4.41	4.40	4.42
TC0101037	TUFT1	7286	tuftelin 1 /// Tuftelin. [Source:Uniprot/	2.76E-07	4	4.78	4.33	4.31	4.40	4.42	4.57	4.51	4.62
TC0301233	TUSC4	10641	tumor suppressor candidate 4	1.63E-11	4	5.36	4.80	4.90	5.05	4.97	4.95	4.99	5.01
TC1400861	TXNDC16	57544	thioredoxin domain containing 16	3.01E-18	4	3.58	2.87	2.96	2.99	2.99	3.05	3.19	3.20
TC0100929	TXNIP	10628	thioredoxin interacting protein	3.76E-08	4	11.08	10.53	10.32	10.62	10.46	10.69	10.74	10.90
TC1901161	TYK2	7297	tyrosine kinase 2	4.71E-14	4	5.86	5.20	5.25	5.32	5.24	5.25	5.22	5.28
TC1901417	U2AF1L4 /// T	199746 //	U2 small nuclear RNA auxiliary factor 1	6.58E-12	4	5.98	5.61	5.54	5.52	5.54	5.57	5.49	5.57
TC1900892	U2AF2	11338	U2 small nuclear RNA auxiliary factor 2	0.000185	4	5.29	4.95	4.88	4.99	5.03	5.02	5.03	5.01
TC0301218	UBA7 /// SIRP	7318	ubiquitin-like modifier activating enzym	8.52E-12	4	6.27	5.35	5.33	5.52	5.41	5.46	5.60	5.63
TC0101093	UBAP2L	9898	ubiquitin associated protein 2-like /// U	1.26E-09	4	7.24	6.81	6.70	6.83	6.82	6.93	6.96	7.01
TC1201671	UBC	7316	ubiquitin C /// Ubiquitin. [Source:Unipr	0.000819	4	11.03	10.73	10.78	10.81	10.76	10.83	10.83	10.90
TC0100104	UBE4B	10277	ubiquitination factor E4B (UFD2 homol	7.18E-08	4	7.57	6.82	6.81	6.88	6.84	6.90	6.95	6.97
TC1600145	UBN1	29855	ubinuclein 1	1.45E-08	4	8.12	7.53	7.21	7.55	7.60	7.76	7.70	7.81
TC0600389	UBR2	23304	ubiquitin protein ligase E3 component	5.97E-14	4	9.00	7.97	7.98	8.24	8.09	8.34	8.39	8.54
TC0101937	UBR4	23352	ubiquitin protein ligase E3 component	2.77E-06	4	6.55	6.16	5.93	6.04	6.02	5.96	6.02	5.93
TC1101652	UCP3	7352	uncoupling protein 3 (mitochondrial, p	5.23E-05	4	4.45	4.11	4.12	4.15	4.18	4.20	4.14	4.08
TC0400276	UGT2B10	7365	UDP glucuronosyltransferase 2 family,	7.65E-07	4	2.62	2.19	2.30	2.39	2.33	2.30	2.49	2.49
TC0401011	UGT2B11	10720	UDP glucuronosyltransferase 2 family,	3.38E-14	4	4.29	2.76	2.91	3.27	3.03	3.39	3.66	3.59
TC0400280	UGT2B28 /// U	54490	UDP glucuronosyltransferase 2 family,	5.89E-09	4	2.90	2.28	2.35	2.50	2.35	2.50	2.57	2.71
TC1701167	UNC119	9094	unc-119 homolog (C. elegans)	2.81E-06	4	6.52	5.60	5.62	5.95	5.88	5.93	5.93	6.02
TC1700766	UNK	85451	unkempt homolog (Drosophila)	2.15E-05	4	4.93	4.72	4.59	4.66	4.66	4.71	4.78	4.81
TC1900328	UPF1	5976	UPF1 regulator of nonsense transcripts	1.52E-07	4	5.44	4.86	4.77	4.88	4.87	4.91	4.95	5.05
TC1000766	UPF2	26019	UPF2 regulator of nonsense transcripts	6.09E-09	4	7.73	7.11	7.03	7.09	7.07	7.24	7.44	7.43
TC0102929	USF1	7391	upstream transcription factor 1 /// Ups	2.90E-11	4	6.63	5.63	5.58	5.88	5.70	5.89	5.94	6.10
TC1900436	USF2	7392	upstream transcription factor 2, c-fos i	0.000442	4	6.71	6.53	6.44	6.76	6.72	6.56	6.57	6.54
TC1200469	USP15	9958	ubiquitin specific peptidase 15 /// Ubiq	7.17E-06	4	9.33	8.79	8.82	8.84	8.67	8.83	8.86	8.93
TC0301200	USP19	10869	ubiquitin specific peptidase 19 /// Ubiq	3.25E-09	4	5.65	5.22	5.14	5.26	5.19	5.26	5.29	5.37
TC0101204	USP21	27005	ubiquitin specific peptidase 21 /// Ubiq	0.000564	4	4.79	4.49	4.52	4.63	4.66	4.60	4.66	4.62
TC0101964	USP48	84196	ubiquitin specific peptidase 48 /// Ubiq	3.19E-05	4	6.68	6.01	6.06	6.22	6.20	6.14	6.30	6.23
TC1701215	UTP6	55813	UTP6, small subunit (SSU) processome	9.49E-23	4	6.58	5.16	5.19	5.45	5.44	5.76	6.04	6.13
TC0600781	UTRN	7402	utrophin /// Utrophin (Dystrophin-rela	7.93E-16	4	7.60	6.68	6.39	6.60	6.35	6.70	7.00	7.01

TC1200902	VAMP1	6843	vesicle-associated membrane protein 1	1.95E-22	4	6.70	5.63	5.71	5.79	5.84	5.93	6.08	6.03
TC1701004	VAMP2	6844	vesicle-associated membrane protein 2	2.34E-12	4	8.05	7.44	7.24	7.30	7.25	7.41	7.50	7.66
TC0601611	VNN3	55350	vanin 3 /// Vascular non-inflammatory	1.19E-13	4	8.08	6.87	6.13	6.26	6.42	6.89	6.81	7.17
TC0800460	VPS13B	157680	vacuolar protein sorting 13 homolog B	2.31E-09	4	6.97	6.39	6.46	6.38	6.21	6.39	6.36	6.40
TC1500872	VPS39	23339	vacuolar protein sorting 39 homolog (S	2.56E-06	4	6.78	6.12	5.98	6.14	6.04	6.14	6.24	6.22
TC0701148	VPS41	27072	vacuolar protein sorting 41 homolog (S	9.80E-15	4	6.65	5.69	5.61	5.54	5.36	5.77	5.99	6.14
TC0601174	VPS52	6293	vacuolar protein sorting 52 homolog (S	0.000104	4	4.61	4.36	4.36	4.32	4.28	4.36	4.34	4.35
TC0300863	VPS8	23355	vacuolar protein sorting 8 homolog (S.	2.04E-14	4	7.48	6.17	6.44	6.66	6.52	6.68	6.68	6.68
TC0102907	VSIG8	391123	V-set and immunoglobulin domain con	0.0002	4	4.33	4.06	4.10	4.12	4.13	4.08	4.10	4.16
TC1200894	VWF	7450	von Willebrand factor /// von Willebra	0.000979	4	4.56	4.33	4.32	4.31	4.37	4.37	4.35	4.33
TC0101731	WASH1 /// Q7Z	375690	WAS protein family homolog 1 /// FAM	6.22E-12	4	6.06	5.67	5.58	5.62	5.68	5.72	5.72	5.67
TC1500692	WASH1 /// Q9	375690	WAS protein family homolog 1 /// Prot	7.62E-10	4	5.69	5.34	5.34	5.31	5.37	5.39	5.38	5.34
TC1201015	WBP11	730693 //	WW domain binding protein 11	7.47E-14	4	8.21	7.99	7.45	7.24	7.35	7.71	7.94	8.05
TC0400167	WDR19	57728	WD repeat domain 19	5.69E-18	4	3.65	3.12	3.09	3.06	3.04	3.21	3.29	3.30
TC0102916	WDR42A	50717	WD repeat domain 42A	3.37E-09	4	5.80	5.26	5.23	5.43	5.34	5.32	5.46	5.38
TC0X00912	WDR45	11152	WD repeat domain 45 /// WD repeat d	3.28E-07	4	6.21	5.93	5.91	5.97	5.90	5.87	5.86	5.89
TC0601175	WDR46 /// NM	9277	WD repeat domain 46 /// WD repeat d	0.000193	4	4.46	4.13	4.09	3.94	4.07	4.08	4.04	4.03
TC0301456	WDR52	55779	WD repeat domain 52 /// WD repeat d	1.13E-05	4	2.89	2.66	2.67	2.69	2.69	2.70	2.72	2.70
TC1601260	WDR59	79726	WD repeat domain 59	0.000333	4	4.96	4.68	4.71	4.75	4.78	4.79	4.84	4.81
TC1500968	WDR72	256764	WD repeat domain 72	2.68E-06	4	2.97	2.78	2.79	2.74	2.76	2.78	2.73	2.73
TC1501202	WDR73	84942	WD repeat domain 73 /// WD repeat d	7.02E-10	4	5.11	4.72	4.71	4.75	4.77	4.91	4.96	4.97
TC0301252	WDR82 /// NM	80335	WD repeat domain 82 /// MSTP107. [S	7.28E-07	4	6.86	6.23	6.34	6.51	6.30	6.47	6.52	6.59
TC0901477	WDR85	92715	WD repeat domain 85	0.000142	4	4.32	4.09	4.11	4.09	4.08	4.13	4.08	4.09
TC0701654	WDR91	29062	WD repeat domain 91 /// WD repeat d	1.11E-15	4	5.55	5.04	4.95	5.07	5.05	5.17	5.17	5.18
TC0202113	WIPF1	7456	WAS/WASL interacting protein family,	1.81E-09	4	9.34	8.76	8.64	8.82	8.76	8.94	9.01	9.13
TC0700038	WIPI2	26100	WD repeat domain, phosphoinositide i	1.45E-05	4	6.41	6.11	5.99	6.14	6.04	6.21	6.19	6.25
TC1200005	WNK1	65125	WNK lysine deficient protein kinase 1 /	0.000128	4	8.30	7.71	7.61	7.76	7.67	7.73	7.83	7.82
TC0X00032	WWC3	55841	WWC family member 3	4.12E-07	4	6.68	5.92	5.85	6.07	5.96	6.09	6.04	6.11
TC1600559	WWP2	11060	WW domain containing E3 ubiquitin pr	0.000773	4	7.95	7.38	7.24	7.39	7.30	7.35	7.31	7.42
TC0800372	XKR9	389668	XK, Kell blood group complex subunit-r	5.13E-05	4	2.64	2.35	2.40	2.29	2.34	2.32	2.40	2.36
TC0301029	XPC	7508	xeroderma pigmentosum, complement	1.11E-15	4	7.31	6.07	6.16	6.65	6.47	6.65	6.76	6.82
TC1101665	XRRA1	---	X-ray radiation resistance-associated p	2.66E-10	4	4.91	4.35	4.34	4.47	4.42	4.44	4.49	4.56
TC0102627	XXyac-YX155B	728920 //	phosphodiesterase 4D interacting prot	1.12E-08	4	4.44	4.26	4.25	4.28	4.29	4.29	4.34	4.36
TC1600899	XYLT1	64131	xylosyltransferase I	1.02E-07	4	5.33	4.84	4.65	4.90	4.84	5.03	5.08	5.16

TC1600998	YPEL3	83719	yippee-like 3 (Drosophila)	1.05E-18	4	7.02	6.29	6.18	6.32	6.31	6.42	6.38	6.45
TC0401003	YTHDC1	91746	YTH domain containing 1	6.66E-15	4	7.86	7.37	7.11	7.10	7.02	7.35	7.48	7.62
TC2200208	YV007_HUMA	---	Putative uncharacterized protein MGC	0.000274	4	4.55	4.00	3.96	3.92	4.03	4.12	4.45	4.23
TC0102837	YY1AP1	55249	YY1 associated protein 1 /// YY1-associ	7.88E-06	4	7.62	7.32	7.20	7.37	7.34	7.38	7.36	7.38
TC0101438	ZC3H11A	9877	zinc finger CCCH-type containing 11A	0.000449	4	8.55	8.24	7.97	8.18	8.08	8.15	8.17	8.14
TC0X00302	ZC3H12B	340554	zinc finger CCCH-type containing 12B /	0.000158	4	2.84	2.63	2.64	2.61	2.62	2.61	2.55	2.62
TC0901094	ZCCHC6	79670	zinc finger, CCHC domain containing 6	1.17E-18	4	9.39	8.53	8.35	8.42	8.35	8.74	8.87	9.01
TC0701478	ZCWPW1	55063	zinc finger, CW type with PWWP doma	1.40E-30	4	6.24	4.64	4.43	4.69	4.70	4.82	4.97	5.13
TC0100298	ZDHHC18	84243	zinc finger, DHHC-type containing 18 //	3.69E-05	4	9.15	8.48	8.15	8.51	8.52	8.69	8.47	8.74
TC0201113	ZFAND2B	130617	zinc finger, AN1-type domain 2B	0.000148	4	5.94	5.76	5.63	5.64	5.76	5.77	5.72	5.68
TC1000493	ZFYVE27	118813	zinc finger, FYVE domain containing 27	2.48E-19	4	5.42	4.81	4.74	4.77	4.79	4.89	4.89	4.92
TC0800532	ZHX2	22882	zinc fingers and homeoboxes 2	0.000395	4	6.45	6.54	5.91	6.08	5.95	6.19	6.17	6.31
TC1000369	ZMIZ1	57178	zinc finger, MIZ-type containing 1 /// Zi	2.46E-07	4	6.74	5.90	5.87	6.21	6.02	6.12	6.22	6.33
TC1001069	ZMYND17	118490	zinc finger, MYND-type containing 17	5.04E-05	4	3.83	3.55	3.60	3.52	3.51	3.47	3.52	3.48
TC0701264	ZNF117	51351	zinc finger protein 117 /// Zinc finger p	5.83E-23	4	7.69	5.88	5.79	6.08	5.94	6.35	6.52	6.74
TC1900786	ZNF137	---	Zinc finger protein 137. [Source:Unipro	4.36E-10	4	3.25	2.59	2.57	2.69	2.58	2.73	2.82	2.74
TC1901326	ZNF14	7561	zinc finger protein 14 /// Zinc finger pr	1.58E-05	4	4.44	4.20	4.19	4.18	4.09	4.26	4.34	4.43
TC1901775	ZNF160	90338	zinc finger protein 160 /// Zinc finger p	2.03E-07	4	5.00	4.74	4.62	4.64	4.53	4.57	4.74	4.79
TC0600196	ZNF165	7718	zinc finger protein 165	0.000163	4	3.67	3.53	3.59	3.46	3.43	3.46	3.52	3.61
TC0900400	ZNF169	169841	zinc finger protein 169 /// Zinc finger p	0.000165	4	4.30	4.12	4.13	4.05	4.05	4.03	4.13	4.10
TC1701038	ZNF18	7566	zinc finger protein 18	0.000142	4	5.64	5.27	5.25	5.35	5.32	5.41	5.40	5.46
TC1901582	ZNF180	7733	zinc finger protein 180	6.90E-05	4	5.16	4.94	4.89	4.94	4.90	4.99	4.99	5.03
TC0X00892	ZNF182 /// ZN	7569	zinc finger protein 182 /// Zinc finger p	8.39E-05	4	5.71	5.36	5.35	5.29	5.19	5.40	5.46	5.48
TC0600204	ZNF187	7741	zinc finger protein 187	3.07E-09	4	4.08	3.58	3.64	3.68	3.70	3.73	3.77	3.88
TC1900936	ZNF211 /// ZN	10520 ///	zinc finger protein 211 /// zinc finger p	6.30E-08	4	5.09	4.68	4.67	4.61	4.49	4.66	4.78	4.90
TC1900606	ZNF226	7769	zinc finger protein 226	3.76E-11	4	4.43	4.24	4.15	3.94	3.96	4.18	4.33	4.33
TC1901578	ZNF235	9310	zinc finger protein 235 /// Zinc finger p	0.00021	4	3.64	3.52	3.60	3.44	3.50	3.50	3.63	3.60
TC0101672	ZNF238	10472	zinc finger protein 238	1.06E-12	4	7.75	6.78	6.86	6.98	6.81	7.16	7.14	7.19
TC1900362	ZNF257	113835	zinc finger protein 257	0.00051	4	4.01	3.85	3.83	3.78	3.89	3.88	3.83	3.93
TC1600120	ZNF263	10127	zinc finger protein 263	1.13E-08	4	4.78	4.51	4.36	4.44	4.42	4.63	4.59	4.62
TC1901142	ZNF266	10781	zinc finger protein 266	6.90E-22	4	4.97	4.21	4.09	4.07	4.04	4.09	4.22	4.30
TC1900949	ZNF274	10782	zinc finger protein 274	4.44E-08	4	4.82	4.61	4.50	4.52	4.52	4.57	4.63	4.73
TC1900155	ZNF317	57693	zinc finger protein 317 /// Zinc finger p	7.48E-12	4	5.05	4.60	4.65	4.66	4.58	4.65	4.84	4.81
TC1901869	ZNF329	79673	zinc finger protein 329	0.000115	4	5.24	5.01	5.06	5.02	4.99	5.06	5.10	5.12

TC1900254	ZNF333	84449	zinc finger protein 333	1.35E-18	4	5.76	5.09	5.03	5.04	4.98	5.06	5.07	5.11
TC2000792	ZNF335	63925	zinc finger protein 335 /// Zinc finger p	0.000649	4	5.14	4.93	4.91	4.92	4.91	4.94	4.88	4.87
TC1000167	ZNF33A	7581	zinc finger protein 33A /// Zinc finger p	1.41E-08	4	8.07	7.36	7.39	7.34	7.28	7.56	7.72	7.80
TC0500745	ZNF346	23567	zinc finger protein 346 /// Zinc finger p	2.02E-06	4	4.41	3.92	3.91	4.13	4.08	4.08	4.18	4.17
TC1901777	ZNF347	84671	zinc finger protein 347 /// Zinc finger p	0.000249	4	3.49	3.13	3.16	3.25	3.12	3.24	3.34	3.36
TC1901755	ZNF350	59348	zinc finger protein 350	0.000684	4	7.00	6.71	6.61	6.68	6.54	6.79	6.90	6.91
TC1900483	ZNF383	163087	zinc finger protein 383	0.000194	4	4.65	4.45	4.47	4.37	4.36	4.42	4.43	4.48
TC1200911	ZNF384	171017	zinc finger protein 384	3.18E-05	4	6.27	5.93	5.90	5.96	5.97	5.99	6.09	6.07
TC1800139	ZNF397	84307	zinc finger protein 397 /// Zinc finger p	0.000355	4	5.81	5.45	5.56	5.53	5.28	5.48	5.58	5.57
TC1901862	ZNF417	147687	zinc finger protein 417	1.01E-09	4	5.83	5.41	5.28	5.28	5.21	5.37	5.45	5.49
TC1900355	ZNF431	170959	zinc finger protein 431	0.000173	4	4.13	3.87	3.75	3.75	3.81	3.83	3.88	3.97
TC1600801	ZNF434	54925	zinc finger protein 434	4.01E-05	4	4.96	4.78	4.70	4.73	4.69	4.78	4.83	4.82
TC1900201	ZNF439	90594	zinc finger protein 439	1.68E-07	4	4.79	4.25	4.24	4.31	4.25	4.27	4.50	4.56
TC1900200	ZNF440	126070	zinc finger protein 440	9.69E-08	4	4.87	4.31	4.32	4.48	4.34	4.53	4.70	4.63
TC1000189	ZNF487	642819	zinc finger protein 487	2.86E-06	4	5.65	4.94	4.92	4.94	4.80	5.13	5.27	5.33
TC1901329	ZNF506	440515	zinc finger protein 506	1.72E-12	4	5.00	4.76	4.71	4.57	4.54	4.76	4.85	4.93
TC1900935	ZNF530	348327	zinc finger protein 530	0.000197	4	3.56	3.46	3.41	3.33	3.37	3.47	3.51	3.57
TC1900929	ZNF547 /// TRA	284306 //	zinc finger protein 547 /// trafficking pr	0.000746	4	3.95	3.89	3.80	3.86	3.79	3.85	3.79	4.04
TC1901859	ZNF552	79818	zinc finger protein 552	0.0002	4	7.18	6.53	6.50	6.60	6.48	6.58	6.75	6.69
TC1900159	ZNF559 /// ZNF	84527 ///	zinc finger protein 559 /// zinc finger pr	1.45E-11	4	4.22	3.94	4.04	3.96	3.95	4.03	4.08	4.14
TC1900480	ZNF568	374900	zinc finger protein 568	0.000431	4	4.16	3.97	4.03	3.99	3.96	3.96	4.04	4.05
TC1900890	ZNF581 /// ZNF	51545 ///	zinc finger protein 581 /// zinc finger pr	8.22E-06	4	5.54	5.55	5.26	5.33	5.37	5.45	5.47	5.49
TC1900939	ZNF586	---	Zinc finger protein 586. [Source:Unipro	2.41E-08	4	7.23	6.02	6.12	6.13	6.02	6.18	6.33	6.27
TC1900940	ZNF587 /// Q92	84914	zinc finger protein 587 /// Zinc finger p	5.17E-16	4	6.70	5.91	5.71	5.75	5.75	5.85	6.00	5.93
TC1901866	ZNF606	80095	zinc finger protein 606	0.00022	4	4.82	4.61	4.63	4.60	4.58	4.64	4.69	4.71
TC1500404	ZNF609	23060	zinc finger protein 609	1.19E-12	4	6.40	5.51	5.60	6.01	5.63	5.55	5.86	5.94
TC1901767	ZNF611 /// Q9	81856	zinc finger protein 611 /// ZNF611 prot	9.79E-06	4	5.44	5.24	5.17	5.15	5.12	5.20	5.19	5.26
TC1901336	ZNF626 /// O75	199777	zinc finger protein 626 /// Zinc finger p	1.94E-12	4	4.33	3.59	3.63	3.62	3.45	3.73	3.97	4.17
TC0X00173	ZNF673	55634	zinc finger family member 673 /// Prote	2.76E-18	4	5.02	4.56	4.48	4.49	4.52	4.68	4.82	4.85
TC0X00879	ZNF674	641339	zinc finger family member 674	2.76E-20	4	5.36	4.47	4.53	4.51	4.49	4.78	4.71	4.84
TC1900202	ZNF69 /// Q6ZV	7620	zinc finger protein 69 /// CDNA FLJ4154	2.38E-08	4	4.85	4.52	4.61	4.48	4.50	4.55	4.64	4.64
TC0103461	ZNF692	55657	zinc finger protein 692 /// Zinc finger p	6.61E-11	4	5.57	5.19	5.20	5.16	5.17	5.22	5.21	5.19
TC1900203	ZNF700	90592	zinc finger protein 700	0.000494	4	7.28	6.75	6.73	6.67	6.57	6.69	6.90	6.79
TC1500615	ZNF710	374655	zinc finger protein 710	6.11E-06	4	6.20	5.61	5.71	5.81	5.76	5.83	5.85	5.89

TC1900932	ZNF749 /// ZNF	388567 //	zinc finger protein 749 /// zinc finger pr	6.11E-06	4	4.01	3.86	3.83	3.82	3.75	3.81	3.86	3.91
TC1900204	ZNF763	729745 //	zinc finger protein 763	2.13E-07	4	5.61	4.92	5.03	4.86	4.87	4.99	5.24	5.38
TC0701743	ZNF767	79970	zinc finger family member 767 /// Prot	5.20E-22	4	6.29	5.12	5.13	5.25	5.30	5.32	5.39	5.40
TC1900938	ZNF776 /// ZNF	284309 //	zinc finger protein 776 /// zinc finger pr	8.54E-05	4	6.17	5.94	5.83	5.76	5.68	5.87	5.92	5.94
TC1900951	ZNF8	7554	zinc finger protein 8	0.000351	4	5.17	4.85	4.83	4.93	4.86	4.91	5.02	4.98
TC1900784	ZNF808 /// Q6	388558	zinc finger protein 808	6.37E-09	4	5.37	4.80	4.79	4.82	4.73	4.92	5.11	5.10
TC1901766	ZNF83	55769	zinc finger protein 83 /// Zinc finger pr	5.05E-14	4	4.75	4.19	4.20	4.21	4.20	4.19	4.28	4.27
TC1900352	ZNF85	7639	zinc finger protein 85 /// Zinc finger pr	2.23E-09	4	4.60	4.26	4.24	4.28	4.22	4.35	4.45	4.57
TC0200358	ZNHIT4 /// WB	83444 ///	zinc finger, HIT type 4 /// WW domain	2.53E-05	4	5.63	5.34	5.33	5.39	5.43	5.36	5.44	5.40
TC1000671	ZRANB1	54764	zinc finger, RAN-binding domain contai	0.000847	4	7.60	7.55	7.19	7.26	7.24	7.44	7.45	7.43
TC0X00063	ZRSR2	8233	zinc finger (CCCH type), RNA-binding m	2.05E-07	4	7.97	7.50	7.60	7.59	7.46	7.65	7.84	7.84
TC1901867	ZSCAN18	65982	zinc finger and SCAN domain containin	9.87E-05	4	5.05	4.87	4.86	4.82	4.82	4.84	4.81	4.86
TC0301521	ZXDC	79364	ZXD family zinc finger C	1.05E-07	4	5.92	5.45	5.45	5.50	5.53	5.57	5.56	5.61
TC1700929	ZZEF1	23140	zinc finger, ZZ-type with EF-hand doma	1.23E-07	4	6.77	6.19	5.95	6.05	5.98	6.06	6.15	6.09
TC2200786		---		8.40E-34	4	6.25	5.24	5.18	5.15	5.16	5.23	5.29	5.26
TC1001251		---		2.05E-11	4	8.16	7.70	7.49	7.38	7.46	7.63	7.63	7.61
TC0700540		---		9.62E-09	4	5.43	5.13	5.11	5.15	5.23	5.26	5.24	5.25
TC1400737		---		4.09E-06	4	5.12	4.96	4.89	4.92	4.93	5.00	4.97	4.99
TC0101128		---		1.83E-05	4	4.77	4.58	4.56	4.52	4.56	4.61	4.61	4.60
TC0400393		---		8.71E-32	4	7.21	5.11	4.87	4.96	4.93	5.04	5.31	5.18
TC1701440		---		1.26E-31	4	6.29	4.29	4.17	4.26	4.31	4.40	4.34	4.38
TC0200286		---		3.09E-30	4	9.25	7.01	6.50	6.52	6.52	6.75	7.01	7.30
TC0201695		---		8.58E-30	4	6.55	5.13	5.20	5.39	5.33	5.56	5.64	5.75
TC0103192		---		1.01E-28	4	9.10	5.72	5.56	5.96	5.83	6.44	6.67	6.81
TC01r00007		---		1.72E-28	4	5.90	5.02	5.05	5.09	5.11	5.18	5.17	5.11
TC2100418		---		2.80E-25	4	7.44	5.09	5.07	5.28	5.23	5.35	5.32	5.45
TC0700672		---		2.45E-23	4	8.96	7.97	7.75	7.87	7.85	7.92	7.95	7.96
TC2200749		---		2.55E-23	4	6.90	5.77	5.55	5.68	5.77	5.96	6.11	6.15
TC0301453		---		3.01E-23	4	6.94	4.88	4.65	4.84	4.91	5.27	5.52	5.59
TC0600094		---		6.19E-23	4	6.69	3.40	3.33	3.81	3.65	4.17	4.40	4.44
TC1500911		---		2.99E-22	4	5.57	4.45	4.39	4.60	4.55	4.73	4.80	4.77
TC1000201		---		9.94E-22	4	6.19	5.04	4.94	5.16	5.16	5.34	5.54	5.57
TC0103068		---		3.62E-21	4	9.35	8.01	7.69	7.72	7.54	7.92	8.00	8.10
TC0101006		---		5.31E-21	4	5.77	4.22	3.79	3.96	3.88	4.41	4.71	5.14

TC0102327	---	1.14E-20	4	4.55	3.13	3.15	3.28	3.34	3.61	3.57	3.67
TC0500338	---	1.16E-20	4	9.14	5.78	5.52	6.16	6.26	6.85	6.87	7.00
TC1001278	---	2.67E-20	4	6.48	4.80	3.99	4.13	4.35	4.76	5.14	5.22
TC0501141	---	7.01E-20	4	7.80	5.41	5.11	5.94	5.94	6.56	6.40	6.67
TC0Y00086	---	8.50E-20	4	7.85	5.83	5.20	5.24	5.58	6.06	6.07	6.44
TC0501371	---	9.95E-20	4	6.47	5.33	4.96	4.92	4.77	5.03	4.85	4.96
TC1600330	---	1.11E-19	4	6.17	4.58	4.20	4.40	4.52	4.89	4.93	5.14
TC1901272	---	1.32E-19	4	7.51	5.25	5.20	5.56	5.31	5.65	5.51	5.65
TC0201487	---	2.59E-19	4	7.10	5.32	5.24	5.77	5.60	5.85	6.01	6.04
TC1700891	---	2.60E-19	4	8.01	5.50	5.21	5.49	5.38	5.88	5.80	6.23
TC1100545	---	4.72E-19	4	11.05	10.16	10.10	9.99	10.01	10.16	10.17	10.24
TC0700967	---	9.25E-19	4	6.35	4.87	4.81	4.93	4.76	5.00	5.27	5.24
TC0301588	---	4.01E-18	4	4.10	1.99	1.82	2.22	2.25	2.19	2.24	2.28
TC0103128	---	4.15E-18	4	8.03	5.60	4.75	4.63	5.19	5.79	5.85	5.97
TC0Y00100	---	9.27E-18	4	7.40	5.12	4.22	4.33	4.49	5.16	5.54	5.30
TC0200873	---	1.21E-17	4	5.12	4.04	4.08	4.40	4.41	4.50	4.58	4.54
TC1901698	---	1.61E-17	4	6.37	5.54	5.56	5.67	5.69	5.67	5.76	5.73
TC0300607	---	2.19E-17	4	7.84	5.22	4.57	4.45	4.75	5.36	5.28	5.51
TC1800011	---	2.49E-17	4	9.92	8.97	8.73	8.97	8.94	9.35	9.41	9.56
TC0701640	---	2.81E-17	4	7.35	6.24	5.94	6.07	6.10	6.34	6.34	6.46
TC1000936	---	3.26E-17	4	7.12	5.11	5.10	5.30	5.41	5.93	5.98	6.19
TC1400428	---	3.61E-17	4	6.69	5.02	4.96	5.07	5.08	5.22	5.43	5.56
TC0700598	---	5.23E-17	4	7.23	5.15	5.12	5.23	5.17	5.23	5.28	5.34
TC0400392	---	1.15E-16	4	6.75	4.71	4.46	4.36	4.32	4.64	5.06	4.84
TC1601004	---	1.26E-16	4	7.61	6.42	6.36	6.21	6.36	6.38	6.49	6.38
TC1900351	---	1.31E-16	4	6.18	5.12	4.87	4.96	4.90	5.19	5.43	5.61
TC1800014	---	1.70E-16	4	5.88	3.47	3.57	3.56	3.58	4.05	4.38	4.41
TC0102545	---	1.96E-16	4	9.96	8.29	8.11	8.26	8.16	8.33	8.48	8.38
TC0201598	---	2.79E-16	4	5.74	5.28	5.12	5.18	5.27	5.37	5.35	5.39
TC1600333	---	4.15E-16	4	10.59	9.10	8.96	8.93	9.08	9.00	9.22	9.11
TC2000605	---	4.89E-16	4	3.94	3.39	3.40	3.36	3.35	3.35	3.31	3.44
TC0500337	---	5.23E-16	4	4.84	2.30	2.37	2.56	2.74	2.79	3.44	3.08
TC0800694	---	8.90E-16	4	5.40	3.89	3.92	3.95	3.86	4.14	4.25	4.35
TC1500441	---	1.50E-15	4	4.36	2.91	2.92	2.89	2.80	2.85	3.02	3.13

TC0701367	---	1.65E-15	4	6.86	5.38	5.58	5.57	5.63	5.87	6.02	5.95
TC1400445	---	2.83E-15	4	4.43	3.29	3.01	3.24	3.32	3.47	3.57	3.62
TC1400431	---	3.87E-15	4	7.77	5.37	5.57	5.44	5.59	5.92	6.45	6.47
TC0801040	---	4.22E-15	4	10.00	9.02	8.78	8.88	8.89	8.95	9.00	8.86
TC0700711	---	5.18E-15	4	7.33	6.39	6.07	6.07	6.09	6.33	6.27	6.33
TC1600112	---	5.35E-15	4	5.46	3.59	3.45	3.37	3.50	3.86	4.42	4.35
TC0Y00178	---	5.74E-15	4	6.96	5.02	4.29	4.09	4.29	4.91	5.10	5.18
TC0202114	---	6.60E-15	4	8.94	7.65	7.46	7.65	7.55	7.85	7.95	7.95
TC0300350	---	6.71E-15	4	7.55	6.25	5.91	6.08	5.95	6.17	6.37	6.35
TC0500198	---	6.94E-15	4	9.65	8.95	9.05	8.98	9.10	9.14	9.07	9.08
TC0102719	---	9.77E-15	4	6.79	6.02	5.89	5.94	6.05	6.08	5.93	6.03
TC0300245	---	1.30E-14	4	5.68	4.61	4.56	4.69	4.63	4.73	4.76	4.87
TC1701729	---	1.33E-14	4	9.20	7.09	6.40	6.83	6.51	7.12	7.23	7.20
TC0301774	---	1.47E-14	4	6.40	5.78	5.77	5.73	5.76	5.79	5.78	5.81
TC0601520	---	2.64E-14	4	10.87	9.98	9.82	9.94	9.96	10.18	10.03	10.22
TC1700890	---	3.54E-14	4	6.33	4.34	4.11	4.24	4.29	4.46	4.56	4.64
TC1800013	---	6.02E-14	4	7.11	5.16	4.96	4.99	4.98	5.70	5.68	5.96
TC0601412	---	6.75E-14	4	5.64	4.34	4.32	4.35	4.34	4.50	4.66	4.70
TC0Y00195	---	8.69E-14	4	6.06	4.47	4.02	4.19	4.33	4.63	4.69	4.65
TC0200435	---	1.40E-13	4	5.66	4.46	4.56	4.67	4.66	4.84	5.01	4.98
TC1100566	---	1.64E-13	4	6.48	4.81	4.59	4.42	4.49	4.49	5.00	4.81
TC0601620	---	1.68E-13	4	8.75	6.04	5.19	4.98	4.80	6.17	6.67	7.31
TC1201346	---	1.78E-13	4	8.14	6.66	6.25	6.26	6.09	6.48	6.42	6.54
TC1001050	---	1.89E-13	4	4.72	4.11	4.05	4.33	4.17	4.45	4.39	4.47
TC0600390	---	2.56E-13	4	6.80	4.55	4.29	4.67	4.66	4.98	5.13	4.86
TC0701310	730307	2.65E-13	4	6.82	5.48	5.47	5.53	5.75	5.72	5.97	6.10
TC0100977	---	3.10E-13	4	8.40	7.72	7.54	7.53	7.55	7.67	7.80	7.76
TC0901397	---	3.43E-13	4	7.09	5.68	5.15	5.38	5.17	5.27	5.13	5.45
TC0501482	---	3.68E-13	4	5.41	4.48	4.20	4.32	4.23	4.39	4.19	4.26
TC0400566	---	3.69E-13	4	4.54	3.47	3.33	3.35	3.23	3.52	3.28	3.62
TC0700582	---	4.20E-13	4	5.87	4.84	4.86	5.09	5.18	5.24	5.39	5.23
TC1000957	---	5.44E-13	4	5.65	4.98	5.02	5.00	4.98	5.04	5.16	5.21
TC2000548	---	6.41E-13	4	3.25	2.58	2.43	2.47	2.51	2.49	2.57	2.55
TC1600984	---	6.88E-13	4	7.40	6.36	6.26	6.13	6.27	6.31	6.46	6.36

TC0700131	---	7.28E-13	4	6.56	5.06	5.08	5.40	5.35	5.74	5.88	6.00
TC1601003	---	9.31E-13	4	7.24	6.10	5.87	5.82	5.92	5.91	6.10	5.89
TC0700673	---	9.53E-13	4	8.43	7.54	7.55	7.42	7.48	7.58	7.51	7.49
TC1601250	---	1.18E-12	4	5.71	4.92	4.88	5.00	4.97	5.07	5.02	5.12
TC1701571	---	1.23E-12	4	7.44	5.84	5.59	5.94	6.15	6.07	6.33	6.17
TC0101444	---	1.25E-12	4	5.92	4.55	4.56	4.84	4.79	4.84	5.01	4.93
TC0701165	---	1.55E-12	4	6.83	5.84	5.65	5.95	5.93	5.88	6.01	5.89
TC0100968	---	1.83E-12	4	6.75	5.57	5.59	5.76	5.79	6.05	6.33	6.19
TC0700862	---	2.64E-12	4	6.56	4.69	4.51	5.05	4.99	5.01	5.33	5.27
TC1100667	---	3.01E-12	4	8.04	6.24	6.41	6.70	6.69	6.97	6.70	6.90
TC1600217	---	3.17E-12	4	9.05	7.65	7.38	7.37	7.53	7.52	7.94	7.73
TC1000190	---	4.54E-12	4	7.71	6.79	6.75	6.54	6.53	6.78	6.92	7.01
TC0100707	---	5.37E-12	4	6.11	4.94	4.79	4.93	4.95	5.32	5.63	5.58
TC0500797	---	5.38E-12	4	10.30	9.32	9.19	9.01	8.96	9.01	9.09	8.89
TC1900252	---	5.82E-12	4	7.10	5.65	5.54	5.72	5.79	6.08	5.97	6.02
TC0601380	---	9.34E-12	4	7.66	6.20	6.17	6.33	6.28	6.87	6.78	7.06
TC0300608	---	1.44E-11	4	3.87	2.43	2.23	2.16	2.03	2.40	2.38	2.54
TC1600310	---	1.47E-11	4	9.60	8.36	8.14	8.11	8.29	8.14	8.39	8.30
TC0X01392	---	1.48E-11	4	7.74	6.45	6.41	6.53	6.50	6.85	6.94	6.83
TC0801221	---	1.84E-11	4	5.89	4.73	3.93	4.12	3.92	4.31	4.44	4.60
TC0X00174	---	1.93E-11	4	4.84	3.26	3.29	3.38	3.19	3.55	3.68	3.63
TC1701400	---	2.22E-11	4	6.10	5.43	5.49	5.51	5.51	5.54	5.65	5.67
TC1201521	---	2.23E-11	4	10.09	9.23	9.16	9.19	9.28	9.33	9.25	9.39
TC0700675	---	2.65E-11	4	9.42	8.63	8.60	8.47	8.50	8.57	8.62	8.50
TC1500336	---	2.89E-11	4	5.29	3.92	3.94	4.29	4.03	4.28	4.19	4.24
TC1701751	---	2.91E-11	4	7.84	6.74	6.47	6.61	6.60	6.87	7.07	7.04
TC1000905	---	2.98E-11	4	5.42	4.93	4.93	4.91	4.91	4.94	5.00	4.97
TC1100542	---	3.10E-11	4	8.42	6.80	6.44	6.34	6.62	6.68	6.57	6.59
TC0701365	---	3.68E-11	4	6.07	5.17	5.17	5.19	5.31	5.26	5.44	5.30
TC1600243	---	3.69E-11	4	9.51	8.24	8.04	7.96	8.11	8.01	8.34	8.22
TC1600204	---	4.92E-11	4	8.10	6.97	6.80	6.70	6.88	6.77	7.08	6.90
TC1700580	731443	5.53E-11	4	3.95	3.06	3.08	3.14	3.09	3.23	3.21	3.29
TC0202037	---	5.60E-11	4	8.84	7.30	6.92	7.15	7.34	7.55	7.51	7.56
TC1101437	730916	9.19E-11	4	9.05	7.45	6.54	6.98	6.39	6.78	6.86	7.54

TC0900337	---	9.66E-11	4	6.07	4.46	4.61	4.46	4.59	5.09	5.40	5.40
TC0700219	---	1.09E-10	4	5.95	5.32	5.26	5.18	5.17	5.17	5.19	5.18
TC0301781	---	1.15E-10	4	6.44	5.72	5.67	5.69	5.65	5.72	5.76	5.80
TC1800091	---	1.27E-10	4	6.96	5.59	5.59	5.66	5.76	6.15	6.48	6.43
TC1101164	---	1.46E-10	4	6.52	5.57	5.39	5.28	4.83	5.41	5.95	6.20
TC1600177	---	1.54E-10	4	5.24	4.23	4.14	4.23	4.16	4.41	4.09	4.23
TC1500744	---	1.64E-10	4	11.14	10.40	10.50	10.44	10.46	10.53	10.43	10.49
TC0301643	---	1.80E-10	4	3.52	2.19	2.23	2.35	2.13	2.47	2.54	2.57
TC0201725	---	2.04E-10	4	8.49	7.86	7.67	7.68	7.65	7.81	7.92	7.93
TC1000062	---	2.21E-10	4	5.15	3.37	2.70	3.04	2.93	3.59	3.35	3.62
TC0400645	---	2.30E-10	4	3.68	2.50	2.52	2.57	2.49	2.63	2.89	2.91
TC1701502	---	2.43E-10	4	4.82	3.45	3.46	3.40	3.35	3.53	3.86	3.81
TC0X00566	---	2.73E-10	4	10.53	9.95	9.88	9.78	9.86	9.93	9.99	9.90
TC1100786	---	3.07E-10	4	3.66	2.35	2.38	2.39	2.45	2.58	2.66	2.76
TC0400606	---	3.40E-10	4	7.86	6.24	6.17	6.34	6.17	6.79	6.74	6.82
TC1900253	---	4.31E-10	4	5.39	4.40	4.12	4.30	4.37	4.33	4.64	4.54
TC17r00035	---	4.55E-10	4	6.67	5.96	5.98	6.00	6.05	6.12	6.27	6.18
TC1601013	---	5.75E-10	4	7.92	6.18	6.70	6.53	6.63	6.79	6.89	6.92
TC0601086	---	5.89E-10	4	5.68	5.11	5.06	5.01	5.07	5.32	5.36	5.45
TC1700963	---	6.09E-10	4	5.13	4.29	4.17	4.18	4.21	4.47	4.32	4.47
TC0600965	---	6.57E-10	4	3.84	2.13	2.15	2.18	2.11	2.12	2.30	2.26
TC1201338	---	6.82E-10	4	3.55	2.83	2.76	2.85	2.74	2.95	3.08	3.06
TC1701730	---	7.45E-10	4	6.07	5.00	4.57	4.89	4.86	4.94	4.87	5.00
TC1401012	---	7.57E-10	4	6.76	5.66	5.15	4.67	4.94	5.49	5.36	5.96
TC1600937	---	8.06E-10	4	9.13	7.86	7.58	7.54	7.75	7.55	7.95	7.78
TC0601580	---	9.06E-10	4	3.62	3.24	3.12	3.23	3.20	3.39	3.39	3.51
TC0202404	---	9.23E-10	4	10.61	10.01	10.15	9.97	10.07	10.11	10.04	10.02
TC0401446	---	9.65E-10	4	4.86	3.98	3.98	4.20	4.18	4.28	4.30	4.18
TC0600637	---	1.00E-09	4	5.43	3.38	3.53	3.32	3.12	3.66	3.59	3.68
TC1900660	---	1.09E-09	4	6.24	4.13	4.21	4.56	4.11	4.69	4.94	4.55
TC1600880	---	1.29E-09	4	8.42	7.08	6.86	6.81	6.99	6.88	7.34	7.17
TC0600331	---	1.33E-09	4	5.27	4.88	4.24	4.09	4.15	4.32	4.35	4.27
TC21r00001	---	1.50E-09	4	5.92	5.55	5.48	5.40	5.33	5.56	5.45	5.49
TC0601225	---	1.71E-09	4	8.90	7.76	7.41	7.52	7.45	7.68	7.57	7.56

TC1600979	---	2.04E-09	4	4.29	3.61	3.53	3.40	3.47	3.49	3.58	3.48
TC1600858	---	2.05E-09	4	8.59	8.32	7.71	7.48	7.35	7.90	7.89	7.89
TC1901860	---	2.11E-09	4	5.32	4.66	4.69	4.68	4.67	4.70	4.84	4.83
TC1501111	---	2.29E-09	4	5.83	4.64	4.55	5.09	4.86	5.09	4.98	5.10
TC1200863	---	2.33E-09	4	4.86	3.18	3.37	3.28	3.18	3.57	3.21	3.32
TC1001185	---	2.45E-09	4	4.21	3.83	3.72	3.65	3.67	3.72	3.69	3.71
TC1600978	---	2.52E-09	4	8.82	8.08	7.89	7.84	8.02	7.91	8.09	7.95
TC1600411	---	3.37E-09	4	6.05	5.23	5.07	5.09	5.10	5.29	5.48	5.53
TC0101445	---	3.39E-09	4	4.51	3.76	3.77	3.86	3.82	3.73	3.89	3.74
TC1201295	---	3.41E-09	4	7.46	5.93	5.66	5.80	5.79	6.35	6.87	6.84
TC1900953	---	3.46E-09	4	3.62	2.43	2.32	2.48	2.43	2.68	2.67	2.91
TC0601526	---	3.49E-09	4	6.39	4.61	4.50	4.62	4.37	4.59	4.79	4.78
TC0100090	---	4.27E-09	4	5.10	4.28	4.09	4.03	4.13	4.35	4.59	4.49
TC0301573	---	4.43E-09	4	4.39	3.67	3.15	3.29	3.29	3.26	3.41	3.70
TC0601411	---	4.75E-09	4	5.09	3.91	3.88	3.93	3.74	3.96	4.27	4.18
TC2000760	---	5.32E-09	4	11.99	11.75	11.73	11.68	11.69	11.69	11.62	11.70
TC1400107	---	5.72E-09	4	5.91	5.51	5.51	5.48	5.55	5.50	5.51	5.40
TC2000229	---	6.58E-09	4	5.06	3.93	3.29	3.79	3.63	4.09	4.40	4.43
TC1600289	---	6.75E-09	4	8.45	7.53	7.14	7.01	6.94	7.33	7.03	7.18
TC1600304	---	6.97E-09	4	5.37	4.52	4.40	4.35	4.52	4.37	4.61	4.50
TC0102698	---	7.29E-09	4	7.29	5.63	5.70	5.69	5.95	6.06	6.29	6.20
TC0103269	---	7.44E-09	4	8.45	7.92	7.92	7.74	7.78	7.80	7.77	7.69
TC1701039	---	8.72E-09	4	9.55	7.89	7.81	7.78	8.21	8.45	8.33	8.61
TC0102045	---	9.90E-09	4	5.35	3.28	3.65	4.22	4.11	4.02	4.16	4.29
TC0101443	---	9.93E-09	4	6.37	5.14	5.07	5.44	5.36	5.50	5.45	5.62
TC1001098	---	1.01E-08	4	12.06	11.62	11.67	11.61	11.62	11.66	11.69	11.65
TC0401445	---	1.04E-08	4	5.42	4.20	4.04	4.40	4.31	4.34	4.58	4.20
TC0300204	---	1.06E-08	4	6.45	5.41	5.26	5.19	5.14	5.28	5.27	5.33
TC0800657	---	1.10E-08	4	4.39	3.92	3.81	3.84	3.92	3.93	4.05	4.10
TC0102972	---	1.15E-08	4	3.76	3.35	3.21	3.26	3.22	3.27	3.28	3.31
TC0901253	---	1.42E-08	4	7.57	6.36	6.20	6.09	6.18	6.42	6.25	6.21
TC1201209	---	1.55E-08	4	6.09	4.74	4.62	4.63	4.68	5.15	5.40	5.10
TC1701190	---	1.62E-08	4	3.93	3.19	3.04	2.74	2.93	3.00	3.02	3.01
TC1000667	---	1.66E-08	4	4.12	3.38	3.36	3.39	3.33	3.47	3.39	3.51

TC0800387	---	1.77E-08	4	3.20	2.69	2.63	2.65	2.62	2.60	2.60	2.62
TC1400341	---	1.78E-08	4	3.97	2.98	2.66	2.68	2.62	2.68	2.87	2.86
TC0103377	---	1.83E-08	4	7.66	6.66	6.64	6.69	6.65	6.89	6.80	6.89
TC0300575	---	1.94E-08	4	6.72	5.99	5.86	6.04	5.91	6.19	6.24	6.30
TC0701372	---	1.95E-08	4	6.35	5.66	5.70	5.50	5.58	5.93	6.09	6.08
TC1901176	---	1.97E-08	4	9.77	7.71	7.62	7.86	7.74	8.27	8.35	8.20
TC1400054	---	2.26E-08	4	3.81	3.44	3.45	3.42	3.39	3.36	3.44	3.47
TC2100239	---	2.27E-08	4	6.77	6.19	6.12	6.10	6.14	6.22	6.23	6.22
TC2100193	---	2.43E-08	4	6.94	6.53	6.47	6.34	6.41	6.47	6.40	6.47
TC0200196	---	3.08E-08	4	5.16	3.71	4.00	4.20	3.93	4.06	4.13	3.87
TC0601756	---	3.11E-08	4	5.36	3.96	3.99	4.17	3.96	4.18	4.27	4.18
TC0202312	---	3.20E-08	4	5.73	3.22	3.08	3.75	3.55	4.06	3.98	3.55
TC1100701	---	3.23E-08	4	6.35	5.27	4.99	4.85	4.88	5.11	4.88	4.90
TC1800016	---	3.44E-08	4	6.32	5.42	5.28	5.13	5.13	5.38	5.49	5.46
TC0103193	---	3.64E-08	4	3.74	2.56	2.62	2.76	2.63	2.79	2.94	2.82
TC0700599	---	3.66E-08	4	4.59	3.45	3.25	3.31	3.35	3.45	3.69	3.49
TC0400064	---	3.66E-08	4	5.88	5.08	4.85	4.79	4.83	5.00	5.08	4.95
TC1600249	---	3.69E-08	4	9.07	8.23	8.02	7.91	7.95	7.95	8.21	8.02
TC0301889	---	3.69E-08	4	5.65	5.22	5.15	5.23	5.18	5.17	5.25	5.26
TC0700961	---	4.06E-08	4	5.99	4.07	3.96	4.11	3.95	4.23	4.20	4.57
TC1700522	---	4.72E-08	4	5.27	4.94	4.89	4.88	4.90	4.94	4.90	5.00
TC0701366	---	5.20E-08	4	5.07	3.75	3.75	3.80	3.84	4.05	4.19	4.12
TC1701260	---	5.51E-08	4	3.97	2.90	2.93	2.99	2.79	3.36	3.70	3.58
TC1901715	---	5.65E-08	4	8.84	8.06	8.03	7.97	7.99	8.14	8.23	8.17
TC1600495	---	6.17E-08	4	8.20	7.42	7.47	7.45	7.54	7.70	7.66	7.62
TC0102691	---	6.34E-08	4	7.32	5.87	5.91	6.00	6.10	6.27	6.43	6.24
TC0201786	---	6.63E-08	4	9.08	8.54	8.21	8.16	8.05	8.21	8.39	8.28
TC0300065	---	7.05E-08	4	7.31	5.64	5.56	5.60	5.83	6.25	6.30	6.24
TC2000460	---	7.62E-08	4	6.20	5.37	5.36	5.63	5.56	5.61	5.67	5.46
TC0201510	---	7.68E-08	4	4.39	3.86	3.80	3.84	3.94	4.01	3.92	3.96
TC0100969	---	8.20E-08	4	6.01	4.69	4.79	4.95	4.81	4.96	5.46	5.34
TC1400769	---	8.53E-08	4	5.41	4.62	4.78	4.51	4.51	4.58	4.70	4.73
TC1901310	---	9.39E-08	4	4.42	3.71	3.71	3.70	3.66	3.57	3.67	3.68
TC0400475	---	9.51E-08	4	9.90	9.25	9.29	9.12	9.17	9.32	9.32	9.28

TC1601212	---	1.02E-07	4	10.96	10.45	10.47	10.43	10.50	10.52	10.48	10.49
TC1700793	---	1.06E-07	4	6.87	6.56	6.58	6.54	6.58	6.61	6.55	6.62
TC0500151	---	1.07E-07	4	5.44	4.38	4.46	4.59	4.87	4.77	5.04	4.89
TC0800944	---	1.07E-07	4	8.76	8.28	7.79	7.75	7.45	7.92	7.94	7.96
TC0700188	---	1.08E-07	4	5.18	3.73	3.58	3.84	3.54	3.94	4.28	4.06
TC0700377	---	1.09E-07	4	10.46	9.75	9.59	9.99	9.97	10.06	10.05	10.24
TC0600680	---	1.15E-07	4	3.95	3.18	3.09	3.54	3.32	3.46	3.60	3.55
TC1201069	---	1.23E-07	4	5.45	4.60	4.53	4.62	4.64	4.76	4.80	4.62
TC1001214	---	1.23E-07	4	4.68	3.98	3.98	4.04	4.02	4.19	4.25	4.19
TC0100911	---	1.27E-07	4	5.65	4.67	4.55	4.66	4.72	4.94	5.14	5.05
TC1700449	---	1.28E-07	4	12.44	12.25	12.24	12.21	12.23	12.27	12.24	12.25
TC1501053	---	1.39E-07	4	4.92	3.63	3.50	3.42	3.54	3.56	3.66	3.76
TC0200222	---	1.40E-07	4	4.28	3.37	3.38	3.38	3.40	3.35	3.50	3.51
TC1500826	---	1.41E-07	4	4.15	3.62	3.55	3.58	3.56	3.60	3.59	3.59
TC0101101	---	1.43E-07	4	5.22	4.33	4.18	4.14	4.13	4.34	4.65	4.75
TC0700024	---	1.47E-07	4	9.37	8.57	8.79	8.75	8.67	8.78	8.82	8.93
TC2200029	---	1.59E-07	4	8.73	7.58	7.42	7.43	7.43	7.73	7.55	7.78
TC0801041	---	1.64E-07	4	4.30	3.86	3.89	3.74	3.81	3.83	3.86	3.71
TC1400964	---	1.78E-07	4	5.07	4.80	4.62	4.54	4.56	4.91	4.87	5.08
TC1900971	---	1.82E-07	4	10.78	10.27	10.27	10.10	10.09	10.09	10.15	10.04
TC1201685	---	1.96E-07	4	11.07	9.19	9.03	9.30	9.11	9.49	9.68	9.39
TC1000341	---	2.15E-07	4	4.83	3.26	3.08	3.21	3.48	3.36	3.18	3.23
TC1600219	---	2.32E-07	4	4.44	4.14	4.10	4.16	4.19	4.24	4.19	4.26
TC1000174	---	2.34E-07	4	9.43	8.84	8.78	8.57	8.57	8.61	8.69	8.52
TC1601192	---	2.36E-07	4	4.47	3.20	3.29	3.35	3.41	3.36	3.82	3.64
TC0800047	---	2.43E-07	4	4.12	2.98	2.70	2.87	2.81	2.91	2.87	3.03
TC0500693	---	2.45E-07	4	5.16	4.60	4.49	4.55	4.54	4.75	4.85	4.73
TC1601214	652516	2.58E-07	4	4.26	3.79	3.76	3.67	3.71	3.72	3.83	3.73
TC0500067	---	2.66E-07	4	4.95	4.50	4.23	4.04	4.02	4.26	4.37	4.88
TC1300385	---	2.66E-07	4	5.33	4.51	4.24	4.50	4.26	4.56	4.79	4.58
TC1600921	---	2.74E-07	4	3.74	2.30	2.05	2.45	2.29	2.40	2.85	2.85
TC0400599	---	2.80E-07	4	6.69	5.09	5.11	5.46	5.32	5.36	5.97	5.64
TC0901391	---	2.90E-07	4	4.24	3.57	3.58	3.65	3.62	3.75	3.81	3.87
TC2200162	---	3.08E-07	4	5.66	5.04	5.08	5.15	5.06	5.14	5.14	5.12

TC17r00023	---	3.27E-07	4	6.19	5.57	5.59	5.65	5.70	5.62	5.64	5.53
TC1700781	---	3.46E-07	4	6.01	4.11	4.05	4.04	4.32	4.29	4.49	4.55
TC0300921	---	3.52E-07	4	6.04	5.61	5.53	5.59	5.53	5.51	5.66	5.63
TC2000292	---	3.52E-07	4	5.24	4.80	4.78	4.81	4.83	5.07	4.93	5.08
TC0103268	---	3.68E-07	4	10.06	9.19	9.19	9.00	9.06	8.95	9.13	8.84
TC1200006	---	3.86E-07	4	6.21	4.49	4.30	4.53	4.33	4.44	4.55	4.78
TC1701382	---	4.28E-07	4	3.38	2.86	2.76	2.73	2.84	2.90	2.87	2.97
TC1700479	---	4.32E-07	4	4.07	3.33	3.12	3.09	3.32	3.48	3.19	3.47
TC0500983	---	4.61E-07	4	8.02	7.29	7.21	6.99	7.14	7.32	7.38	7.34
TC01r00010	---	4.86E-07	4	7.76	7.05	7.13	7.22	7.19	7.22	7.28	7.17
TC0102721	---	4.95E-07	4	9.09	8.04	7.82	8.24	8.08	8.44	8.33	8.37
TC2000351	---	5.00E-07	4	6.59	5.68	5.31	5.46	5.40	5.38	5.33	5.49
TC0800942	---	5.03E-07	4	6.64	5.30	4.95	4.91	4.64	4.90	5.03	4.98
TC1100723	---	5.21E-07	4	7.75	6.83	6.68	6.83	6.75	6.93	7.04	6.97
TC1601140	---	5.33E-07	4	4.44	3.61	3.57	3.34	3.48	3.45	3.49	3.59
TC1600980	---	5.48E-07	4	6.22	4.92	5.11	4.93	4.94	4.84	5.12	5.12
TC1701196	---	6.26E-07	4	8.10	6.94	6.69	6.85	6.68	6.81	6.97	6.94
TC1900658	---	6.30E-07	4	3.78	3.22	3.13	3.03	3.07	3.16	3.13	3.32
TC1201321	---	6.41E-07	4	10.98	10.53	10.57	10.50	10.58	10.57	10.57	10.58
TC2000841	---	6.46E-07	4	5.28	4.46	4.52	4.43	4.46	4.74	4.81	4.67
TC0101749	---	6.83E-07	4	10.73	10.28	10.30	10.15	10.15	10.17	10.26	10.06
TC0100259	---	7.17E-07	4	11.29	10.90	10.98	10.90	10.92	10.97	10.91	10.89
TC0201464	---	7.61E-07	4	4.96	4.53	4.48	4.35	4.38	4.50	4.43	4.44
TC0100638	---	7.72E-07	4	4.04	3.36	3.37	3.61	3.66	3.75	3.75	3.65
TC2000219	---	7.83E-07	4	7.30	6.39	6.33	6.60	6.60	6.76	6.82	6.65
TC0103349	---	8.03E-07	4	5.28	3.72	3.62	3.89	3.68	3.86	3.87	4.11
TC1101278	---	8.04E-07	4	3.06	2.66	2.61	2.65	2.63	2.57	2.58	2.61
TC0701190	---	8.07E-07	4	6.47	5.77	5.87	5.61	5.46	5.73	5.77	5.71
TC1101202	---	8.55E-07	4	8.00	6.78	6.73	6.96	6.85	6.92	6.99	6.72
TC1200667	---	8.57E-07	4	4.94	3.81	3.81	3.70	3.89	3.60	3.71	3.86
TC0102027	---	9.67E-07	4	10.90	10.20	10.28	10.26	10.32	10.36	10.39	10.33
TC0800085	---	1.03E-06	4	4.65	4.01	4.00	4.08	3.98	4.07	4.03	4.09
TC0100910	---	1.03E-06	4	6.50	5.99	6.07	6.15	6.13	6.19	6.22	6.23
TC1901333	---	1.04E-06	4	12.51	12.06	11.97	12.01	12.00	12.05	12.14	12.04

TC1100523	---	1.14E-06	4	8.12	7.71	7.62	7.60	7.70	7.71	7.62	7.68
TC0300264	---	1.16E-06	4	3.02	2.37	2.37	2.34	2.25	2.39	2.25	2.39
TC0600268	---	1.24E-06	4	6.47	5.54	5.53	5.59	5.69	5.82	6.01	5.76
TC0100988	---	1.28E-06	4	7.36	6.64	6.74	6.77	6.58	6.84	7.03	6.98
TC0600392	---	1.44E-06	4	6.45	5.68	5.64	5.51	5.42	5.78	5.86	5.88
TC2200247	---	1.45E-06	4	7.34	6.01	5.85	5.38	5.71	6.49	6.58	6.55
TC0100356	---	1.46E-06	4	5.41	5.09	4.89	4.90	4.90	5.00	4.96	4.97
TC0501203	---	1.51E-06	4	4.10	3.54	3.26	3.46	3.10	3.21	3.19	3.30
TC1201158	---	1.52E-06	4	5.42	3.84	3.18	3.61	3.37	3.58	3.71	4.08
TC1701527	---	1.55E-06	4	7.00	6.53	6.18	6.22	6.14	6.41	6.38	6.41
TC1901529	---	1.58E-06	4	7.06	6.10	6.08	6.18	6.17	6.36	6.40	6.40
TC0800716	---	1.63E-06	4	4.98	5.02	4.25	4.37	4.36	4.64	4.49	4.79
TC1901568	---	1.64E-06	4	6.60	5.79	4.99	5.38	5.42	6.09	6.08	6.11
TC1900265	---	1.68E-06	4	7.20	6.41	6.08	6.31	6.34	6.28	6.15	6.09
TC1900264	---	1.69E-06	4	6.92	6.01	5.56	5.84	5.88	5.90	5.78	5.78
TC0200445	---	1.75E-06	4	3.10	2.70	2.65	2.70	2.77	2.73	2.75	2.73
TC1700039	---	1.78E-06	4	5.13	3.75	3.88	3.74	3.98	3.73	3.87	3.95
TC0101125	---	1.81E-06	4	5.31	4.25	3.86	3.92	4.21	4.16	4.30	4.30
TC0300448	---	1.83E-06	4	3.45	2.57	2.72	2.49	2.66	2.76	2.88	2.88
TC0400461	---	1.83E-06	4	4.43	3.71	3.58	3.64	3.65	3.66	3.73	3.64
TC0102621	---	1.84E-06	4	4.24	2.93	3.33	3.18	3.18	3.52	3.35	3.37
TC1000359	---	1.89E-06	4	8.45	7.84	7.90	7.80	7.79	7.91	7.88	7.86
TC0501095	---	2.06E-06	4	10.83	9.92	9.90	9.99	10.09	10.17	10.37	10.23
TC0800692	---	2.10E-06	4	7.20	6.48	6.31	6.48	6.27	6.61	6.77	6.97
TC1000897	---	2.14E-06	4	8.17	6.75	6.66	6.75	6.79	6.99	7.32	7.24
TC1600413	---	2.17E-06	4	6.13	5.51	5.16	5.21	4.95	5.16	5.27	5.29
TC0301677	---	2.22E-06	4	3.71	3.47	3.46	3.40	3.54	3.46	3.36	3.46
TC1600436	---	2.28E-06	4	6.60	5.09	4.90	4.95	4.95	5.56	5.33	5.51
TC1400824	---	2.45E-06	4	4.63	4.33	4.35	4.33	4.34	4.32	4.26	4.35
TC1100391	---	2.50E-06	4	5.21	4.65	4.62	4.68	4.78	4.81	4.92	4.97
TC1600867	---	2.61E-06	4	7.30	6.14	5.79	6.00	6.06	6.03	6.36	6.15
TC0200597	---	2.70E-06	4	4.63	3.78	4.02	4.32	4.30	4.25	4.13	4.30
TC0800052	---	2.73E-06	4	4.77	3.86	3.78	3.71	3.74	3.93	3.90	3.90
TC22r00001	---	2.81E-06	4	7.69	7.21	6.93	7.04	6.97	7.05	7.21	7.34

TC0600801	---	2.82E-06	4	5.93	5.25	4.65	4.78	4.79	5.15	5.18	5.10
TC0901045	---	3.08E-06	4	3.66	2.93	3.39	2.80	3.13	3.05	3.20	3.09
TC1200727	---	3.11E-06	4	8.46	7.22	7.04	7.16	7.07	7.52	7.50	7.43
TC1500727	---	3.11E-06	4	3.63	3.17	2.84	3.02	2.96	3.01	3.12	3.18
TC0700969	---	3.27E-06	4	3.15	2.34	2.29	2.34	2.27	2.40	2.64	2.60
TC2100035	---	3.28E-06	4	4.07	3.60	3.57	3.35	3.34	3.57	3.50	3.45
TC1800061	---	3.30E-06	4	3.31	2.64	2.70	2.58	2.60	2.69	2.76	2.90
TC1700826	---	3.33E-06	4	9.11	8.10	7.94	8.27	8.09	8.45	8.74	8.67
TC0601198	---	3.37E-06	4	7.03	6.29	6.21	6.34	6.41	6.51	6.64	6.54
TC0300268	---	3.60E-06	4	8.31	6.85	6.89	7.39	7.37	7.53	7.59	7.82
TC0900140	---	3.67E-06	4	7.74	7.02	6.63	6.56	6.27	6.54	6.58	6.48
TC1200729	---	3.72E-06	4	4.65	3.95	3.89	4.00	4.04	3.98	3.98	4.00
TC0500493	---	3.73E-06	4	5.03	4.67	4.59	4.65	4.70	4.64	4.72	4.69
TC0202199	---	3.83E-06	4	7.03	6.25	6.21	6.25	6.29	6.35	6.35	6.31
TC1900125	---	3.98E-06	4	4.81	4.27	4.31	4.26	4.29	4.34	4.44	4.31
TC2000132	---	4.08E-06	4	9.13	8.38	8.43	8.41	8.47	8.55	8.54	8.49
TC1600216	---	4.23E-06	4	5.91	4.75	4.62	4.19	4.68	4.67	5.18	4.73
TC0401085	---	4.26E-06	4	4.40	3.47	3.43	3.36	3.63	3.80	3.85	4.04
TC0601691	---	4.33E-06	4	5.25	4.55	4.72	4.59	4.53	4.75	4.62	4.77
TC1901795	---	4.71E-06	4	4.08	3.05	2.99	2.95	2.97	2.97	3.09	3.07
TC0600745	---	5.12E-06	4	6.85	5.90	5.98	6.05	5.80	6.02	6.06	6.12
TC1601001	---	5.28E-06	4	6.44	6.07	6.08	6.02	6.02	6.28	6.11	6.29
TC0202224	---	5.30E-06	4	9.23	8.05	7.94	8.04	8.14	8.37	8.66	8.49
TC0X01238	---	5.48E-06	4	3.80	3.39	3.35	3.14	3.08	3.19	3.24	3.34
TC0200205	---	5.69E-06	4	5.54	4.83	4.82	4.88	4.90	4.95	5.05	5.00
TC0202194	---	5.74E-06	4	5.84	5.40	5.31	5.30	5.30	5.41	5.34	5.34
TC1900735	---	5.89E-06	4	5.58	5.18	5.21	5.24	5.22	5.28	5.31	5.31
TC0300721	---	6.29E-06	4	5.42	4.39	4.43	4.25	4.26	4.42	4.67	4.68
TC1901697	---	6.29E-06	4	4.69	4.19	4.07	4.13	4.14	4.56	4.32	4.57
TC1700410	---	6.35E-06	4	6.61	5.74	5.93	6.26	6.18	6.22	6.21	5.89
TC0700398	730307	6.73E-06	4	5.66	4.74	4.69	4.64	4.78	4.72	5.15	4.99
TC0600119	---	6.85E-06	4	12.10	11.83	11.81	11.79	11.85	11.84	11.76	11.83
TC0800048	---	6.88E-06	4	5.47	5.44	5.14	5.10	5.15	5.25	5.20	5.32
TC0401303	---	7.02E-06	4	5.87	4.93	5.32	4.89	5.06	5.20	5.56	5.31

TC1500422	---	7.09E-06	4	8.32	7.91	7.95	7.87	7.94	7.91	7.82	7.95
TC0900481	---	7.10E-06	4	5.70	4.83	4.82	5.01	4.66	4.85	4.99	4.97
TC0202065	---	7.12E-06	4	2.93	2.55	2.55	2.50	2.47	2.50	2.49	2.65
TC1701399	---	8.11E-06	4	6.91	6.48	6.52	6.47	6.53	6.56	6.54	6.54
TC1200901	---	8.61E-06	4	5.04	4.80	4.75	4.85	4.90	4.95	4.87	4.89
TC0200323	---	9.19E-06	4	6.02	5.18	5.21	5.11	5.18	5.16	5.27	5.12
TC2200211	---	9.22E-06	4	3.71	3.22	3.15	3.10	3.29	3.14	3.40	3.16
TC1701231	---	9.54E-06	4	4.75	3.34	2.98	3.31	3.00	3.37	3.46	3.31
TC1100099	---	1.02E-05	4	4.86	4.29	4.24	4.33	4.30	4.57	4.57	4.46
TC1100390	---	1.02E-05	4	6.48	6.01	5.93	5.91	5.93	6.00	6.13	6.35
TC1400340	---	1.04E-05	4	5.81	4.91	4.31	4.31	4.27	5.00	4.89	5.01
TC0800715	---	1.07E-05	4	6.58	6.46	5.85	6.11	6.08	6.09	6.16	6.24
TC0601633	---	1.09E-05	4	4.30	4.02	4.02	3.95	3.94	3.99	3.95	4.02
TC0100668	---	1.09E-05	4	6.25	5.69	5.58	5.49	5.30	5.73	5.72	5.68
TC0201547	---	1.12E-05	4	5.45	4.70	4.75	4.59	4.49	4.79	4.72	4.72
TC1000770	---	1.16E-05	4	6.20	5.64	5.68	5.57	5.57	5.68	5.78	5.76
TC0500333	---	1.18E-05	4	3.54	3.17	3.15	3.22	3.26	3.30	3.21	3.40
TC0500893	---	1.19E-05	4	3.83	3.01	3.17	3.11	3.09	3.48	3.36	3.34
TC1701726	---	1.20E-05	4	11.65	11.37	11.37	11.30	11.40	11.40	11.32	11.38
TC0700403	730307	1.24E-05	4	6.46	5.58	5.67	5.60	5.82	5.67	5.73	5.81
TC0301100	---	1.25E-05	4	3.69	2.99	2.96	2.86	2.82	3.11	3.03	3.17
TC0501444	---	1.25E-05	4	4.15	3.32	3.33	3.36	3.20	3.55	3.56	3.71
TC0700376	---	1.26E-05	4	9.29	8.72	8.77	8.84	8.77	8.75	8.76	8.85
TC0401067	---	1.31E-05	4	5.33	4.46	4.45	4.53	4.55	4.60	4.66	4.72
TC1000510	---	1.38E-05	4	5.07	4.72	4.64	4.71	4.75	4.79	4.73	4.75
TC0200290	---	1.38E-05	4	6.68	5.77	5.69	5.58	5.40	5.48	5.71	5.66
TC0100862	---	1.42E-05	4	6.02	5.11	5.06	4.97	5.06	5.05	5.04	5.33
TC1800121	---	1.45E-05	4	12.59	12.33	12.29	12.24	12.25	12.29	12.30	12.26
TC1200298	---	1.46E-05	4	5.32	4.61	4.44	4.61	4.52	4.72	4.74	4.64
TC1201151	---	1.49E-05	4	4.29	3.20	3.30	3.08	3.23	3.34	3.50	3.42
TC0600796	---	1.52E-05	4	11.14	10.83	10.79	10.79	10.79	10.85	10.83	10.85
TC1700856	---	1.53E-05	4	6.01	5.19	5.02	5.21	5.40	5.21	5.22	5.17
TC1200821	---	1.57E-05	4	2.77	2.43	2.46	2.45	2.46	2.45	2.46	2.48
TC0Xr00011	---	1.63E-05	4	5.97	5.58	5.81	5.47	5.16	5.60	5.65	5.79

TC1000322	---	1.64E-05	4	4.45	4.17	3.84	3.71	3.82	3.94	3.83	3.93
TC2200359	---	1.76E-05	4	5.06	4.64	4.48	4.51	4.50	4.50	4.19	4.67
TC0300967	---	1.80E-05	4	3.98	3.22	3.37	3.23	3.10	3.14	3.27	3.41
TC1400304	---	1.83E-05	4	6.94	6.41	6.36	6.38	6.37	6.49	6.42	6.55
TC0200988	---	1.83E-05	4	7.74	7.08	6.89	6.91	6.97	6.87	7.18	7.09
TC0701063	---	1.83E-05	4	6.44	5.69	5.47	5.26	5.40	5.89	5.71	5.92
TC2000077	---	1.89E-05	4	3.59	3.18	3.19	3.05	3.08	3.07	3.10	3.21
TC0100409	---	1.93E-05	4	5.89	5.27	5.15	5.16	5.26	5.38	5.37	5.37
TC0Y00106	---	1.93E-05	4	7.39	6.87	6.82	6.87	6.91	7.01	7.00	6.91
TC0601402	---	1.94E-05	4	5.87	4.61	4.87	4.74	4.84	5.12	5.04	5.08
TC0900663	---	1.96E-05	4	6.41	5.73	5.54	5.63	5.73	5.83	5.95	5.91
TC1900592	---	1.96E-05	4	9.69	9.40	9.43	9.35	9.43	9.42	9.35	9.41
TC1201247	---	1.97E-05	4	5.63	4.90	4.98	5.11	5.02	5.22	5.19	5.18
TC0102326	---	1.97E-05	4	5.46	4.88	4.88	4.91	4.90	4.93	4.81	4.86
TC1901630	---	2.10E-05	4	5.92	5.35	5.16	5.17	5.34	5.53	5.46	5.43
TC0101980	---	2.11E-05	4	11.31	10.88	10.91	10.85	10.96	10.96	10.83	10.91
TC1400935	---	2.13E-05	4	5.49	5.11	4.82	4.76	4.83	5.14	4.91	4.94
TC0600465	---	2.19E-05	4	5.63	4.95	4.75	4.82	5.09	5.14	5.20	5.18
TC1901386	---	2.21E-05	4	3.64	3.01	3.13	2.86	3.06	3.04	3.17	3.16
TC0501108	---	2.21E-05	4	5.43	5.20	5.25	5.27	5.48	5.43	5.28	5.26
TC0700677	---	2.28E-05	4	6.90	5.86	6.09	6.09	6.04	6.05	6.21	5.95
TC0300174	---	2.35E-05	4	4.21	2.97	3.12	3.39	3.28	3.04	3.42	3.41
TC0100966	---	2.40E-05	4	6.30	5.82	5.89	5.90	5.93	6.04	6.02	6.04
TC1401139	---	2.43E-05	4	7.67	7.14	6.69	6.38	6.66	6.81	7.00	6.76
TC2200084	---	2.75E-05	4	7.81	6.47	6.59	6.53	6.49	6.60	6.63	6.33
TC1900767	730718	2.77E-05	4	5.25	5.06	4.78	4.92	4.95	5.01	4.98	4.99
TC2200457	---	2.88E-05	4	5.17	3.97	3.93	4.02	3.85	4.42	4.81	4.44
TC2100428	---	3.03E-05	4	7.01	6.25	6.02	6.09	6.21	6.19	6.37	6.38
TC1501247	---	3.04E-05	4	7.30	6.78	6.85	6.80	6.72	6.90	6.75	6.84
TC0500465	---	3.08E-05	4	3.10	2.14	2.41	2.16	2.37	2.23	2.10	2.20
TC0900417	---	3.11E-05	4	6.01	5.83	5.82	5.79	5.76	5.79	5.76	5.80
TC0701364	730307	3.13E-05	4	3.81	3.30	3.22	3.16	3.22	3.28	3.28	3.31
TC1200446	---	3.40E-05	4	5.68	5.02	4.78	4.85	4.91	5.23	5.41	5.07
TC0800122	---	3.43E-05	4	7.52	6.38	6.47	6.68	6.59	6.72	6.87	6.91

TC2200272	---	3.45E-05	4	5.39	4.91	4.41	4.70	4.48	4.72	4.68	4.65
TC1601141	---	3.48E-05	4	7.13	5.91	5.88	5.75	6.01	6.05	6.08	5.94
TC1100102	---	3.55E-05	4	9.34	6.51	5.83	7.48	7.84	7.94	7.42	7.88
TC1000931	---	3.62E-05	4	5.48	4.52	4.59	4.66	4.65	4.62	4.91	4.59
TC1701618	---	3.73E-05	4	4.33	3.21	3.28	2.94	3.13	3.10	3.26	3.26
TC0700325	653841	3.75E-05	4	4.48	4.21	4.13	4.20	4.21	4.24	4.31	4.25
TC0102544	---	3.83E-05	4	3.87	3.54	3.46	3.56	3.57	3.47	3.51	3.55
TC1701396	---	3.89E-05	4	2.75	2.09	2.04	1.99	2.03	2.00	2.05	1.97
TC1201443	---	3.97E-05	4	3.60	3.30	3.19	3.23	3.35	3.26	3.32	3.38
TC0101842	---	4.05E-05	4	5.26	4.75	4.77	4.76	4.79	4.73	4.70	4.76
TC0600302	---	4.09E-05	4	5.66	5.16	4.93	4.77	4.98	4.82	5.32	4.89
TC0301488	---	4.11E-05	4	9.52	9.11	8.69	8.81	8.67	9.04	8.97	8.93
TC0500016	---	4.11E-05	4	5.90	5.08	5.14	5.27	5.22	5.20	5.23	5.28
TC0400643	---	4.26E-05	4	6.96	6.28	5.81	6.12	5.89	6.31	6.31	6.36
TC1101490	---	4.30E-05	4	7.49	6.75	6.30	6.35	6.42	6.54	6.80	6.76
TC0900255	---	4.46E-05	4	5.87	5.33	5.18	5.19	5.30	5.12	5.37	5.25
TC1100844	---	4.49E-05	4	5.97	5.75	5.70	5.69	5.64	5.75	5.75	5.75
TC1700373	---	4.51E-05	4	4.34	3.52	3.54	3.37	3.56	3.61	3.70	3.80
TC1500999	---	4.60E-05	4	4.52	4.03	3.90	3.97	4.00	4.16	4.00	3.88
TC1700652	---	4.65E-05	4	5.97	5.40	4.91	5.12	4.87	5.32	5.42	5.29
TC0201465	---	4.65E-05	4	3.45	3.10	3.07	3.04	3.10	3.10	3.03	3.08
TC0601550	---	4.76E-05	4	5.60	4.39	4.08	4.35	4.48	4.54	4.77	4.69
TC0102908	---	4.79E-05	4	3.44	2.28	2.53	2.68	2.61	2.80	2.93	2.68
TC0401278	---	5.23E-05	4	3.78	3.08	3.02	3.13	3.07	2.88	3.00	2.97
TC0800194	---	5.27E-05	4	5.70	5.21	5.26	5.07	5.19	5.16	5.18	5.12
TC0400177	---	5.27E-05	4	5.35	4.48	4.20	4.61	4.05	4.23	4.23	4.25
TC1101886	---	5.33E-05	4	3.14	2.54	2.46	2.42	2.52	2.58	2.69	2.62
TC0501081	---	5.46E-05	4	6.24	5.00	4.67	5.24	4.87	5.27	5.43	5.20
TC2000838	---	5.62E-05	4	5.14	4.65	4.66	4.68	4.66	4.63	4.62	4.65
TC1201337	---	5.64E-05	4	4.08	3.58	3.54	3.51	3.56	3.58	3.61	3.60
TC0300016	---	5.66E-05	4	4.17	3.87	3.81	3.74	3.82	3.89	3.77	3.85
TC0500387	---	5.76E-05	4	3.75	2.87	3.03	3.10	3.19	3.30	3.22	3.15
TC1200769	---	5.88E-05	4	7.73	6.79	6.72	6.98	6.91	7.08	7.02	7.12
TC1000507	---	5.88E-05	4	10.86	10.55	10.55	10.50	10.58	10.57	10.50	10.56

TC0200353	---	6.12E-05	4	4.06	3.59	3.65	3.82	3.70	3.83	3.83	3.83
TC0701617	---	6.22E-05	4	4.09	3.32	3.41	3.10	3.21	3.33	3.38	3.40
TC0600746	---	6.24E-05	4	8.82	7.70	7.92	8.07	7.75	7.95	7.94	7.89
TC1100154	---	6.47E-05	4	6.12	5.20	5.09	5.31	5.31	5.67	5.68	5.68
TC1600819	---	6.48E-05	4	4.70	4.22	4.27	4.45	4.28	4.16	4.09	4.14
TC1900975	650495	6.51E-05	4	6.34	5.63	5.70	5.56	5.65	5.72	5.64	5.93
TC1201188	---	6.53E-05	4	10.61	10.20	10.19	10.16	10.18	10.24	10.26	10.23
TC0Y00118	---	6.56E-05	4	3.08	2.76	2.74	2.69	2.73	2.80	2.63	2.73
TC1800257	---	6.66E-05	4	4.94	4.56	4.42	4.48	4.48	4.49	4.38	4.42
TC0700788	---	6.66E-05	4	3.54	3.05	2.98	3.06	2.88	2.87	2.94	2.90
TC0201976	---	6.77E-05	4	4.54	3.93	3.74	3.54	3.59	3.71	3.71	3.71
TC0701289	---	6.86E-05	4	4.33	3.55	3.53	3.64	3.53	3.72	3.90	3.64
TC2000842	---	6.86E-05	4	6.01	5.24	4.72	5.00	5.45	5.61	5.50	5.65
TC0801252	---	7.00E-05	4	8.18	7.30	7.12	6.95	6.79	7.17	7.15	7.22
TC0301684	---	7.07E-05	4	3.43	3.09	3.20	3.05	3.13	3.07	3.05	3.21
TC1201433	---	7.13E-05	4	3.94	3.50	3.43	3.37	3.40	3.45	3.56	3.58
TC0103175	---	7.25E-05	4	5.23	4.78	4.67	4.78	4.86	4.87	5.08	5.04
TC1800503	---	7.36E-05	4	6.53	6.28	6.32	6.24	6.30	6.30	6.26	6.30
TC0102276	---	7.38E-05	4	4.78	4.15	4.03	4.06	3.82	4.31	4.43	4.46
TC0100191	---	7.51E-05	4	3.53	3.09	3.06	3.02	3.01	3.20	3.11	3.17
TC1701560	---	7.51E-05	4	6.71	5.06	5.05	4.60	5.26	5.45	5.30	5.05
TC0401108	---	7.79E-05	4	5.79	4.64	4.63	4.76	4.71	5.05	5.04	4.94
TC1400487	---	8.01E-05	4	7.66	6.56	6.78	6.81	6.89	6.88	6.94	6.66
TC1600345	---	8.07E-05	4	5.07	4.32	3.97	3.94	4.16	4.05	4.35	4.11
TC0202411	---	8.12E-05	4	3.67	3.28	3.25	3.27	3.31	3.32	3.29	3.17
TC2000536	---	8.21E-05	4	3.67	3.27	3.31	3.24	3.29	3.25	3.24	3.27
TC0101925	---	8.22E-05	4	4.32	3.72	3.69	3.50	3.56	3.48	3.65	3.66
TC0700596	---	8.33E-05	4	6.61	5.50	5.18	5.55	5.40	5.56	5.77	5.61
TC0701776	---	8.51E-05	4	4.40	3.39	3.55	3.51	3.58	3.41	3.69	3.76
TC0201878	---	8.60E-05	4	6.78	5.54	5.91	5.88	5.73	6.09	5.93	5.90
TC1201717	---	8.61E-05	4	4.48	3.89	3.90	3.66	3.73	4.09	4.00	4.05
TC15r00005	---	8.75E-05	4	7.33	6.52	6.35	6.47	6.54	6.45	6.19	6.51
TC0100349	---	9.13E-05	4	6.26	5.31	5.04	5.28	5.25	5.25	5.45	5.32
TC2000018	---	9.15E-05	4	5.85	5.48	5.48	5.43	5.35	5.43	5.37	5.41

TC0101794	---	9.35E-05	4	4.76	4.53	4.31	4.25	4.22	4.34	4.41	4.48
TC0200174	---	9.46E-05	4	5.12	4.49	4.43	4.50	4.60	4.59	4.64	4.57
TC1500775	---	9.85E-05	4	5.39	4.39	4.34	4.19	4.26	4.30	4.00	4.63
TC0701338	---	0.000101	4	8.74	8.23	8.27	8.34	8.29	8.29	8.29	8.35
TC1101214	---	0.000104	4	5.15	3.33	3.72	3.53	3.40	3.78	3.87	3.76
TC0701505	---	0.000104	4	11.26	11.01	11.08	10.95	11.06	11.09	10.99	11.04
TC1900360	---	0.000106	4	9.51	9.25	9.27	9.19	9.27	9.43	9.35	9.37
TC0600964	---	0.000106	4	4.17	3.62	3.54	3.75	3.70	3.66	3.70	3.93
TC0200443	---	0.000106	4	4.15	3.53	3.59	3.54	3.65	3.66	3.64	3.72
TC0100904	---	0.000106	4	5.13	4.78	4.85	4.67	4.66	4.80	4.85	4.78
TC1101494	---	0.000107	4	4.40	3.37	3.42	3.44	3.83	3.73	3.63	3.55
TC1100188	---	0.000108	4	3.48	2.99	2.81	2.71	2.89	2.89	2.92	3.03
TC1200198	---	0.000109	4	5.97	5.19	5.14	5.00	4.87	4.97	5.10	5.18
TC1600556	---	0.00011	4	3.29	2.31	2.35	2.23	2.38	2.21	2.52	2.47
TC1400785	---	0.000114	4	5.05	4.54	4.14	4.21	4.00	4.22	4.25	4.43
TC1501116	---	0.000114	4	9.89	9.65	9.68	9.59	9.70	9.68	9.60	9.64
TC0600274	---	0.000114	4	5.21	4.31	4.27	4.24	4.27	4.32	4.55	4.51
TC1001313	---	0.000117	4	10.08	9.71	9.84	9.69	9.78	9.77	9.77	9.74
TC1300307	---	0.000118	4	3.83	2.92	2.61	2.63	2.60	2.53	2.88	2.64
TC0700250	---	0.000121	4	4.55	4.27	4.14	4.10	4.06	4.21	4.36	4.31
TC1100498	---	0.000123	4	4.90	3.83	3.89	3.87	4.04	3.84	4.14	3.80
TC1200897	---	0.000123	4	3.83	2.26	2.66	2.81	2.59	2.90	3.16	3.10
TC1500024	---	0.000123	4	7.18	6.81	6.36	6.71	6.89	6.65	6.90	6.48
TC0201336	---	0.000124	4	3.82	3.29	3.35	3.29	3.37	3.39	3.20	3.26
TC0501190	---	0.000125	4	2.84	2.56	2.48	2.28	2.47	2.54	2.49	2.42
TC0102550	---	0.000127	4	6.76	6.68	6.35	6.14	6.21	6.59	6.60	6.50
TC0501265	---	0.000128	4	4.93	4.17	4.32	4.39	4.38	4.31	4.27	4.15
TC1601014	---	0.000128	4	7.78	6.84	7.11	7.43	7.15	7.15	7.05	7.16
TC1600987	---	0.00013	4	3.77	2.91	3.02	3.19	3.23	3.23	3.00	3.21
TC1901370	---	0.000131	4	3.33	2.80	2.79	2.86	2.62	2.84	2.93	2.94
TC1901098	---	0.000133	4	6.34	5.04	4.59	4.67	4.81	4.91	5.31	4.85
TC0300890	---	0.000133	4	3.93	2.91	2.99	3.00	2.84	3.01	3.01	3.02
TC1101439	---	0.000133	4	4.30	4.05	3.86	3.82	3.97	3.92	4.03	4.05
TC0800090	---	0.00014	4	5.56	4.73	4.81	4.68	4.79	4.97	4.92	4.94

TC0600166	---	0.000159	4	2.36	1.70	1.85	1.71	1.85	1.78	1.91	1.77
TC1201052	---	0.000159	4	5.72	5.17	5.15	5.18	5.32	5.44	5.45	5.41
TC1600679	---	0.000163	4	4.67	4.23	4.03	3.93	4.15	4.18	4.04	4.07
TC0103078	---	0.000164	4	5.85	5.11	4.98	5.13	5.07	5.34	5.48	5.30
TC1700026	---	0.000166	4	4.79	4.25	4.44	4.13	4.26	4.10	4.41	4.29
TC0601242	---	0.000166	4	4.49	4.09	4.15	3.95	3.96	4.07	4.04	4.06
TC1101269	---	0.000167	4	2.87	2.67	2.69	2.53	2.62	2.68	2.72	2.74
TC0401153	---	0.000168	4	5.43	4.83	4.87	4.71	4.78	4.90	4.75	4.76
TC0X00408	---	0.000173	4	3.89	3.35	3.37	3.18	3.05	3.32	3.14	3.33
TC1200278	---	0.000174	4	6.27	5.57	5.70	5.68	5.56	5.70	5.63	5.58
TC0801053	---	0.000174	4	4.12	3.89	3.82	3.69	3.50	3.77	3.89	3.77
TC0301897	---	0.000177	4	5.57	4.77	4.85	4.80	4.88	4.72	4.55	4.81
TC1201339	---	0.000178	4	4.04	3.38	3.51	3.40	3.42	3.50	3.53	3.67
TC0301901	---	0.000179	4	11.54	11.24	11.23	11.11	11.16	11.23	11.26	11.18
TC0800853	---	0.000184	4	3.82	3.02	2.92	3.13	2.96	3.07	2.98	3.25
TC0500041	---	0.000184	4	5.53	5.13	5.12	5.13	5.12	5.18	5.09	5.23
TC1101090	---	0.000184	4	4.40	4.10	3.94	3.96	3.89	3.94	3.99	3.90
TC1900163	---	0.000187	4	5.12	4.42	4.38	4.21	4.36	4.40	4.43	4.46
TC1200076	---	0.000189	4	5.57	5.13	5.07	5.08	5.08	5.12	5.11	4.93
TC0901089	---	0.000189	4	4.94	4.07	4.19	4.16	4.08	4.23	4.43	4.53
TC1400324	---	0.00019	4	4.16	3.95	3.92	3.92	3.87	3.92	3.82	3.95
TC0102722	---	0.000197	4	7.58	6.78	6.53	6.86	6.63	7.00	6.80	7.00
TC0100658	---	0.0002	4	3.54	3.14	3.11	3.03	2.95	2.82	3.10	3.05
TC0100160	---	0.000201	4	6.78	6.31	6.51	6.20	6.20	6.20	6.36	6.30
TC0900335	---	0.000206	4	10.54	10.31	10.33	10.28	10.34	10.31	10.25	10.29
TC1000466	---	0.000206	4	3.61	3.06	3.10	3.03	2.99	3.02	3.09	3.16
TC0700130	---	0.000209	4	3.96	3.56	3.73	3.49	3.49	3.66	3.56	3.59
TC0300382	---	0.00021	4	5.74	5.32	5.31	5.35	5.36	5.35	5.30	5.45
TC1101663	---	0.000211	4	5.41	4.93	4.97	4.94	5.02	4.90	4.87	5.06
TC0501396	---	0.000213	4	5.46	4.87	4.46	4.69	4.42	4.66	4.62	4.79
TC1800326	---	0.000214	4	6.69	6.50	5.86	5.85	5.76	6.11	6.39	6.30
TC0701454	---	0.000215	4	5.80	5.28	5.12	5.20	5.14	5.46	5.63	5.56
TC1000938	---	0.00022	4	9.81	9.44	9.36	9.37	9.36	9.43	9.47	9.49
TC1700415	---	0.000224	4	5.71	5.24	5.25	5.31	5.32	5.42	5.38	5.56

TC2100090	---	0.000235	4	4.28	3.94	3.98	3.79	3.87	4.11	4.04	4.05
TC0400344	---	0.000235	4	5.22	4.46	4.41	4.56	4.42	4.57	4.64	4.62
TC0600111	---	0.000236	4	3.24	2.50	2.91	2.44	2.71	2.63	2.60	2.61
TC0201913	---	0.000243	4	4.23	3.99	4.01	3.96	4.00	3.98	3.97	4.01
TC1700469	---	0.000248	4	4.13	3.40	3.36	3.46	3.36	3.54	3.62	3.63
TC1701040	---	0.000254	4	3.86	2.91	2.78	3.08	3.12	3.24	3.18	3.28
TC1700978	---	0.000259	4	6.21	5.80	5.71	5.87	5.76	5.64	5.71	5.53
TC1900659	---	0.000263	4	6.11	5.39	5.20	4.99	5.17	5.66	5.75	5.88
TC1200125	---	0.000264	4	4.14	3.77	3.76	3.74	3.72	3.73	3.76	3.75
TC0400547	---	0.000265	4	8.31	7.74	7.20	7.22	7.20	7.30	7.34	7.33
TC1000004	---	0.000266	4	6.53	6.40	5.75	5.86	5.84	6.00	5.94	5.92
TC0200757	---	0.000266	4	3.04	2.74	2.49	2.28	2.16	2.41	2.55	2.35
TC1300477	---	0.000266	4	5.10	4.10	4.16	4.38	4.31	4.48	4.32	4.44
TC0700902	---	0.000272	4	4.63	3.50	3.23	3.14	3.08	3.44	3.26	3.50
TC0400016	---	0.000273	4	4.93	4.68	4.60	4.58	4.64	4.63	4.71	4.65
TC0401041	---	0.000274	4	9.67	9.17	9.14	9.08	9.13	9.18	9.25	9.13
TC0X01159	---	0.000275	4	8.07	7.29	7.09	7.24	7.39	7.44	7.53	7.39
TC0900220	---	0.000276	4	3.97	3.55	3.54	3.51	3.54	3.52	3.55	3.54
TC0300614	---	0.000277	4	4.27	4.01	3.96	4.00	3.92	3.90	3.90	3.98
TC0601360	---	0.00028	4	4.23	3.74	3.75	3.63	3.85	3.88	4.00	3.91
TC1201580	---	0.000281	4	5.82	5.20	5.06	5.31	5.30	5.20	5.37	5.30
TC1400212	---	0.000283	4	4.05	3.42	3.41	3.37	3.17	3.38	3.62	3.69
TC0103422	---	0.000285	4	3.70	3.43	2.99	3.13	2.88	3.04	3.05	3.03
TC2200229	---	0.000286	4	4.70	4.02	4.07	3.99	3.94	4.18	4.14	4.02
TC1000999	---	0.000287	4	3.86	3.38	3.51	3.29	3.50	3.23	3.32	3.37
TC0700694	---	0.000291	4	5.55	4.81	4.71	4.71	4.79	4.96	4.83	4.99
TC2200398	---	0.000292	4	3.33	3.14	3.17	3.09	3.15	3.08	3.10	3.16
TC1901631	---	0.000304	4	4.39	3.75	3.58	3.64	3.66	3.91	4.08	3.86
TC0X00217	---	0.000305	4	4.71	4.32	4.26	4.09	4.28	4.23	4.20	4.37
TC0102144	---	0.000311	4	10.32	9.91	10.02	9.88	9.93	9.97	9.91	9.91
TC1500035	---	0.000312	4	5.52	4.86	4.89	4.78	4.88	4.76	4.66	4.83
TC0201515	---	0.000312	4	4.62	3.96	4.08	4.11	4.20	4.07	4.20	4.28
TC1600192	---	0.000313	4	3.56	3.00	3.04	2.96	2.98	3.06	3.15	3.02
TC1001104	---	0.000325	4	6.86	6.46	6.32	6.10	6.14	6.30	6.31	6.06

TC1000291	---	0.000327	4	5.72	4.95	4.86	4.77	4.81	4.93	4.83	5.00
TC1400854	---	0.000335	4	10.26	10.00	10.04	9.91	9.99	9.98	9.96	9.95
TC1101369	---	0.000335	4	3.04	2.49	2.60	2.47	2.46	2.50	2.52	2.61
TC0200007	---	0.000335	4	4.74	4.12	4.12	4.13	4.00	4.14	3.99	4.09
TC1700412	---	0.00034	4	4.00	3.70	3.75	3.68	3.74	3.76	3.63	3.73
TC1200043	---	0.000341	4	3.62	3.21	3.24	3.21	3.25	3.26	3.18	3.21
TC0901083	---	0.000341	4	5.69	4.94	4.79	4.80	4.86	5.09	5.10	5.13
TC1200815	---	0.000342	4	3.99	3.54	3.63	3.51	3.56	3.55	3.57	3.58
TC2000176	---	0.000353	4	4.39	3.52	3.59	3.61	3.48	3.51	3.60	3.72
TC1101275	---	0.000354	4	3.81	3.41	3.49	3.39	3.40	3.48	3.48	3.62
TC1001320	---	0.000355	4	4.75	4.49	4.50	4.48	4.48	4.48	4.39	4.44
TC1701157	---	0.000355	4	9.16	8.78	8.83	8.65	8.82	8.88	8.81	8.86
TC0300043	---	0.000356	4	4.70	4.08	4.09	3.85	3.92	4.05	4.20	4.22
TC1201533	---	0.000364	4	3.93	3.36	3.62	3.30	3.25	3.27	3.35	3.52
TC1000125	---	0.000369	4	6.80	6.29	6.14	5.93	5.88	5.97	6.17	6.04
TC0X01174	---	0.000375	4	7.01	6.44	6.21	6.30	6.27	6.49	6.62	6.48
TC1701295	---	0.000386	4	6.29	5.54	5.43	5.56	5.36	5.75	5.80	5.64
TC1500746	---	0.000386	4	5.50	4.97	4.97	4.94	5.03	4.95	4.90	5.02
TC0300125	---	0.000386	4	4.25	3.86	3.77	3.60	3.62	3.60	3.67	3.68
TC0701136	---	0.000391	4	5.06	4.44	4.35	4.09	4.22	4.22	4.29	4.30
TC0301528	---	0.0004	4	5.53	5.20	5.14	5.11	5.10	5.18	5.16	5.16
TC0101977	---	0.000401	4	11.11	10.87	10.87	10.83	10.87	10.91	10.80	10.85
TC0901214	---	0.000402	4	8.51	8.13	8.07	8.01	8.06	8.19	8.20	8.13
TC0401213	---	0.000406	4	2.53	2.33	2.34	2.24	2.37	2.33	2.29	2.34
TC1400121	---	0.000406	4	5.39	4.63	4.25	4.42	4.34	4.66	4.76	4.64
TC0202169	---	0.000409	4	5.13	4.76	4.57	4.53	4.56	4.83	4.86	4.79
TC0X01110	---	0.000409	4	4.35	3.51	3.86	3.66	3.72	3.52	3.74	3.71
TC1100642	---	0.000415	4	4.96	4.66	4.63	4.65	4.60	4.53	4.58	4.53
TC2200025	---	0.000421	4	5.34	4.79	4.78	4.73	4.65	4.80	5.09	4.97
TC1700653	---	0.000435	4	8.00	7.56	7.16	7.08	6.99	7.36	7.34	7.28
TC1100762	---	0.000436	4	3.70	3.31	3.27	3.14	3.24	3.25	3.18	3.29
TC1701552	---	0.000437	4	6.14	5.01	5.10	5.03	5.19	5.51	5.65	5.44
TC1200321	---	0.000443	4	11.02	10.71	10.71	10.69	10.76	10.73	10.60	10.67
TC0201463	---	0.000448	4	3.95	3.53	3.61	3.50	3.86	3.71	3.73	3.70

TC1701583	---	0.000453	4	3.65	3.12	3.18	3.31	3.31	3.21	3.43	3.38
TC1600164	---	0.00046	4	6.68	6.39	6.15	6.21	6.24	6.39	6.28	6.30
TC1100750	---	0.000466	4	3.79	2.56	2.85	2.67	2.67	2.78	3.02	2.95
TC0600563	---	0.000468	4	5.27	4.70	4.61	4.70	4.90	4.91	5.02	4.86
TC0400384	---	0.000474	4	3.42	3.11	3.08	3.04	3.24	3.15	3.19	3.33
TC0600123	---	0.000474	4	5.06	4.55	4.80	4.49	4.58	4.69	4.55	4.68
TC0301899	---	0.000474	4	3.24	2.94	2.97	2.90	2.93	2.78	2.90	2.97
TC1601136	---	0.000474	4	10.27	9.95	9.96	9.90	10.01	9.99	9.90	9.95
TC2200755	---	0.000483	4	4.66	4.05	4.17	4.19	4.29	4.37	4.37	4.34
TC0Y00043	---	0.000489	4	2.79	2.56	2.53	2.43	2.45	2.58	2.51	2.55
TC1700910	---	0.00049	4	4.38	4.08	4.08	4.20	4.11	4.11	3.96	4.19
TC0900302	---	0.00049	4	2.63	2.30	2.26	2.10	2.07	2.22	2.16	2.42
TC0X01337	---	0.000498	4	4.80	4.31	4.27	4.20	4.17	4.17	4.26	4.26
TC1400059	---	0.000503	4	4.28	3.81	3.89	3.78	3.79	3.80	3.79	3.75
TC1500331	---	0.000505	4	10.69	10.44	10.45	10.41	10.48	10.50	10.40	10.46
TC1000059	---	0.000512	4	4.25	3.40	3.25	3.06	2.82	3.21	3.22	3.48
TC0500159	---	0.000513	4	9.79	9.43	9.52	9.43	9.47	9.54	9.47	9.52
TC0600026	---	0.000513	4	6.67	5.90	6.06	5.96	6.11	5.82	5.71	6.00
TC1901376	---	0.00052	4	4.54	3.98	4.05	3.80	4.04	3.88	3.88	3.98
TC0801239	---	0.00052	4	3.34	2.83	2.76	2.86	2.82	2.86	2.98	2.86
TC0800283	---	0.000522	4	3.57	3.13	3.39	3.20	3.11	3.24	3.24	3.33
TC1100879	---	0.000524	4	4.33	3.88	3.96	3.93	3.90	3.88	4.01	3.98
TC1201198	---	0.000526	4	12.66	12.49	12.48	12.47	12.49	12.47	12.41	12.47
TC1100336	---	0.000527	4	3.73	3.47	3.49	3.40	3.49	3.45	3.40	3.39
TC1201487	---	0.000532	4	3.53	3.17	3.19	3.10	3.25	3.27	3.15	3.25
TC1300258	---	0.000538	4	9.71	9.35	9.49	9.37	9.40	9.50	9.49	9.41
TC0102624	---	0.000551	4	4.37	3.28	3.16	3.15	3.34	3.87	3.31	3.70
TC0X00655	---	0.000578	4	3.01	2.74	2.68	2.66	2.64	2.62	2.68	2.69
TC2000731	---	0.000585	4	3.87	3.29	3.32	3.34	3.26	3.33	3.21	3.29
TC1800271	---	0.000602	4	4.01	3.46	3.40	3.54	3.45	3.52	3.65	3.52
TC0500371	---	0.000604	4	4.09	3.52	3.60	3.32	3.48	3.59	3.67	3.55
TC0102511	---	0.000606	4	12.07	11.81	11.83	11.79	11.80	11.85	11.86	11.81
TC1401132	---	0.000616	4	4.90	4.68	4.69	4.62	4.67	4.61	4.65	4.64
TC1601305	---	0.000617	4	5.92	5.38	5.38	5.33	5.30	5.40	5.52	5.39

TC0101241	---	0.000625	4	3.95	3.64	3.66	3.61	3.64	3.66	3.53	3.58
TC0300340	---	0.000626	4	9.59	9.31	9.32	9.25	9.32	9.35	9.27	9.32
TC0201494	---	0.00063	4	4.37	4.29	4.21	4.11	4.21	4.24	4.22	4.23
TC1100787	---	0.000631	4	3.55	3.20	3.17	3.26	3.01	3.17	3.25	3.25
TC0300864	---	0.000631	4	3.35	2.89	3.01	2.92	2.89	2.92	2.85	2.99
TC0101751	---	0.000635	4	7.43	7.06	7.13	7.02	7.02	7.01	7.00	7.00
TC0901142	---	0.000638	4	4.88	4.69	4.69	4.62	4.65	4.73	4.67	4.73
TC1500700	---	0.00064	4	3.29	2.76	2.65	2.75	2.78	2.82	2.85	2.84
TC1500453	---	0.00064	4	3.29	3.07	3.15	3.13	3.16	3.15	3.11	3.13
TC0600647	---	0.000641	4	4.76	4.57	4.59	4.54	4.59	4.60	4.78	4.60
TC0600642	---	0.000645	4	3.22	2.52	2.71	2.65	2.70	2.82	2.91	2.70
TC2100204	---	0.000653	4	4.80	4.42	4.34	4.36	4.24	4.46	4.53	4.50
TC0500964	---	0.000661	4	3.22	2.69	2.78	2.75	2.79	2.53	2.46	2.86
TC1300222	---	0.000662	4	10.08	9.63	9.58	9.55	9.57	9.64	9.68	9.58
TC0201774	---	0.000664	4	4.53	3.97	3.77	3.77	3.68	3.99	3.99	3.94
TC1100070	---	0.000665	4	5.50	5.57	5.12	5.05	5.16	5.42	5.53	5.40
TC2000252	---	0.00067	4	10.87	10.64	10.76	10.63	10.69	10.74	10.63	10.65
TC1000221	---	0.000679	4	4.91	4.42	4.41	4.58	4.47	4.39	4.51	4.58
TC0Xr00013	---	0.000698	4	7.52	6.95	7.35	7.29	7.03	7.32	7.27	7.45
TC1901523	---	0.000714	4	10.32	10.14	10.09	10.00	10.11	10.12	10.00	10.07
TC1000839	---	0.000717	4	9.95	9.57	9.57	9.51	9.62	9.66	9.54	9.58
TC1200580	---	0.000718	4	2.89	2.50	2.46	2.61	2.29	2.38	2.36	2.40
TC0901114	---	0.000726	4	6.76	6.37	6.37	6.41	6.36	6.40	6.28	6.34
TC0201280	---	0.000733	4	8.18	7.82	7.95	7.80	7.94	8.00	7.90	7.90
TC0600870	---	0.000735	4	7.06	6.68	6.72	6.64	6.78	6.71	6.59	6.74
TC1100818	---	0.000736	4	11.19	10.93	10.95	10.88	10.97	10.97	10.83	10.92
TC0202213	---	0.000738	4	6.95	5.85	5.55	5.84	5.66	6.09	6.10	5.95
TC0600034	---	0.00074	4	12.09	11.92	11.92	11.90	11.96	11.94	11.89	11.94
TC0101597	---	0.00074	4	2.96	2.58	2.59	2.51	2.62	2.56	2.41	2.49
TC0500895	---	0.00075	4	2.95	2.40	2.47	2.41	2.46	2.23	2.42	2.47
TC0300227	---	0.000752	4	5.20	4.31	4.38	4.43	4.73	4.63	4.54	4.62
TC0500994	---	0.000755	4	3.20	2.64	2.80	3.26	2.89	2.95	2.72	2.75
TC0700189	---	0.000756	4	6.65	5.57	5.36	5.58	5.97	5.90	6.01	5.85
TC0202219	---	0.000756	4	10.71	10.35	10.42	10.26	10.42	10.38	10.32	10.33

TC0401431	---	0.000766	4	10.33	10.07	10.05	9.93	10.01	10.01	10.01	9.96
TC0601456	---	0.000769	4	11.38	11.10	11.13	11.04	11.11	11.14	11.04	11.10
TC1200655	---	0.000776	4	2.56	2.16	2.13	2.01	2.06	1.92	2.11	1.97
TC2000218	---	0.000777	4	5.88	4.58	4.54	4.67	4.60	5.03	5.15	5.00
TC1101645	---	0.000784	4	4.96	4.34	4.21	4.55	4.32	4.53	4.76	4.64
TC0800577	---	0.000791	4	3.69	3.37	3.22	3.28	3.34	3.22	3.35	3.25
TC1600866	---	0.000792	4	11.51	11.23	11.19	11.17	11.28	11.23	11.10	11.20
TC1101066	---	0.000796	4	5.47	5.17	5.03	5.17	5.38	5.09	5.01	5.20
TC1500905	---	0.000796	4	12.25	12.11	12.11	12.01	12.10	12.14	12.05	12.13
TC1100819	---	0.000801	4	10.38	10.03	10.17	10.00	10.06	10.13	10.06	10.01
TC1600855	---	0.000801	4	5.00	4.63	4.61	4.55	4.55	4.67	4.56	4.59
TC1901521	---	0.000804	4	4.17	3.57	3.48	3.69	3.63	3.63	3.51	3.52
TC1600397	---	0.000808	4	6.21	5.89	5.73	5.74	5.85	5.82	5.73	5.87
TC1901341	---	0.000822	4	4.28	3.96	3.94	3.96	3.98	3.99	3.92	3.95
TC0601705	---	0.000824	4	3.27	2.65	2.84	2.95	2.92	3.04	2.98	3.08
TC1001019	---	0.000826	4	7.52	7.07	7.06	6.98	7.03	7.15	7.20	7.11
TC2000810	---	0.000838	4	4.28	3.57	3.41	3.22	3.46	3.59	3.67	3.73
TC0701111	---	0.000848	4	10.89	10.57	10.64	10.52	10.57	10.62	10.55	10.59
TC0700571	---	0.000853	4	11.88	11.71	11.69	11.69	11.69	11.71	11.67	11.71
TC0X00249	---	0.000853	4	3.21	2.95	2.81	2.89	2.94	2.71	2.92	2.73
TC1700970	---	0.000854	4	4.38	4.23	3.95	3.83	3.88	3.95	4.20	4.08
TC0Xr00012	---	0.000856	4	5.30	4.82	5.00	4.83	4.59	4.86	5.12	5.04
TC1200227	---	0.000856	4	3.19	2.86	3.12	2.92	2.90	2.99	2.98	2.96
TC1300251	---	0.000861	4	4.73	4.07	4.41	4.29	4.02	4.22	4.20	4.46
TC1600545	---	0.000868	4	3.26	2.77	2.90	2.78	2.89	2.75	2.67	2.79
TC1200473	---	0.000872	4	6.65	6.06	6.20	6.13	6.17	5.98	5.97	6.05
TC1201202	---	0.000875	4	3.97	2.89	2.90	2.63	2.72	2.72	2.92	2.86
TC1101656	---	0.000878	4	5.16	4.65	4.51	4.50	4.26	4.54	4.44	4.53
TC1400262	---	0.00089	4	6.02	5.52	5.71	5.65	5.51	5.73	5.92	5.78
TC1701683	---	0.000892	4	6.57	6.17	6.12	6.26	6.23	6.20	6.21	6.28
TC0400993	---	0.000899	4	3.02	2.56	2.59	2.45	2.46	2.36	2.51	2.60
TC0201076	---	0.000905	4	4.58	3.87	3.99	4.06	3.92	3.88	4.02	4.00
TC1800053	---	0.000916	4	3.24	2.92	2.91	2.88	2.74	2.92	2.80	2.89
TC1500939	---	0.000923	4	4.59	3.94	3.89	3.76	3.88	3.85	4.12	4.05

TC0200609		---		0.000932	4	4.38	3.81	3.64	3.95	3.81	3.91	3.79	3.81
TC1000039		---		0.000954	4	3.56	3.20	3.16	3.18	3.32	3.22	3.49	3.11
TC0300917		---		0.000979	4	8.30	7.75	7.64	7.77	8.11	8.07	8.12	7.65
TC2200006		---		0.000993	4	4.48	4.14	4.15	4.04	3.98	4.16	4.10	4.12
TC1900672		---		0.000994	4	4.95	4.55	4.49	4.41	4.54	4.55	4.39	4.49
TC0201593	AAK1	22848	AP2 associated kinase 1	0.000111	5	5.78	5.81	5.85	5.91	5.68	5.56	5.65	5.59
TC0202293	ABCA12	26154	ATP-binding cassette, sub-family A (AB	0.000455	5	2.25	2.24	2.30	2.19	2.21	2.20	2.21	2.20
TC1701649	ABCA5	23461	ATP-binding cassette, sub-family A (AB	0.000184	5	3.17	3.16	3.09	2.84	2.86	2.96	3.00	2.93
TC1701646	ABCA9	10350	ATP-binding cassette, sub-family A (AB	0.000563	5	2.42	2.31	2.38	2.27	2.30	2.29	2.26	2.31
TC0701397	ABCB1	5243	ATP-binding cassette, sub-family B (MD	0.00077	5	2.96	2.91	2.95	2.86	2.88	2.84	2.86	2.90
TC1601083	ABCC11	85320	ATP-binding cassette, sub-family C (CFT	2.57E-06	5	3.75	3.73	3.74	3.64	3.65	3.63	3.60	3.64
TC1601082	ABCC12	94160	ATP-binding cassette, sub-family C (CFT	3.55E-05	5	3.23	3.22	3.28	3.17	3.17	3.18	3.11	3.20
TC1100915	ABCG4	64137	ATP-binding cassette, sub-family G (WH	0.00025	5	4.05	4.01	4.03	3.93	3.96	3.96	3.83	3.95
TC0801190	ABRA	137735	actin-binding Rho activating protein	0.000655	5	3.63	3.65	3.77	3.64	3.51	3.48	3.41	3.48
TC0X00785	ACE2	59272	angiotensin I converting enzyme (pepti	0.000254	5	2.39	2.44	2.47	2.34	2.39	2.34	2.30	2.33
TC0301298	ACOX2	8309	acyl-Coenzyme A oxidase 2, branched	0.000976	5	3.92	3.79	3.75	3.72	3.74	3.72	3.68	3.75
TC1900112	ACSBG2	81616	acyl-CoA synthetase bubblegum family	1.33E-05	5	3.20	3.01	3.01	2.96	2.98	2.97	2.88	2.98
TC1600232	ACSM2A	123876	acyl-CoA synthetase medium-chain fam	3.96E-05	5	3.09	2.96	2.97	2.91	2.91	2.89	2.91	2.94
TC1600919	ACSM2B	648338 //	acyl-CoA synthetase medium-chain fam	1.41E-06	5	3.80	3.67	3.73	3.63	3.65	3.66	3.59	3.64
TC0101643	ACTN2	88	actinin, alpha 2	0.00057	5	2.68	2.66	2.75	2.66	2.62	2.63	2.60	2.64
TC0800893	ADAM2	2515	ADAM metallopeptidase domain 2 (fer	0.000315	5	2.16	2.15	2.19	2.08	2.07	2.04	2.08	2.12
TC2100252	ADAMTS1	9510	ADAM metallopeptidase with thrombo	0.000197	5	3.51	3.54	3.56	3.45	3.43	3.43	3.36	3.45
TC1501270	ADAMTS17	170691	ADAM metallopeptidase with thrombo	0.000813	5	3.98	3.87	3.90	3.84	3.89	3.79	3.77	3.84
TC2100253	ADAMTS5	11096	ADAM metallopeptidase with thrombo	0.000293	5	3.38	3.29	3.31	3.19	3.19	3.18	3.19	3.26
TC1501147	ADAMTS7	11173	ADAM metallopeptidase with thrombo	0.000481	5	4.90	4.86	4.88	4.78	4.83	4.81	4.73	4.77
TC1500574	ADAMTSL3	57188	ADAMTS-like 3 /// ADAMTS-like protei	5.24E-05	5	3.34	3.28	3.30	3.19	3.21	3.26	3.18	3.26
TC0301500	ADCY5	111	adenylate cyclase 5	7.79E-06	5	4.41	4.39	4.42	4.32	4.33	4.31	4.23	4.28
TC1201153	ADCY6	112	adenylate cyclase 6	0.000188	5	3.98	4.00	4.00	3.89	3.89	3.91	3.87	3.91
TC0501279	AFF4	27125	AF4/FMR2 family, member 4 /// AF4/F	1.02E-06	5	6.56	6.84	6.50	6.49	6.32	6.45	6.54	6.54
TC1700807	AFMID	125061	arylformamidase	5.18E-05	5	3.66	3.51	3.55	3.38	3.48	3.43	3.46	3.46
TC1500596	AGBL1	731136 //	ATP/GTP binding protein-like 1	0.000212	5	3.08	2.86	2.92	2.82	2.84	2.80	2.77	2.87
TC0701030	AGR2	10551	anterior gradient homolog 2 (Xenopus	0.000105	5	2.32	2.36	2.45	2.28	2.33	2.29	2.25	2.34
TC0501541	AGXT2L2	85007	alanine-glyoxylate aminotransferase 2-	2.09E-05	5	5.47	5.30	5.22	5.17	5.24	5.21	5.19	5.09
TC0300872	AHSG	197	alpha-2-HS-glycoprotein	2.68E-06	5	3.18	3.09	3.08	2.98	2.96	2.97	2.87	3.01

TC0400309	ALB	213	albumin /// Serum albumin precursor.	6.04E-06	5	2.37	2.54	2.40	2.31	2.30	2.30	2.30	2.33
TC0901200	ALDOB	229	aldolase B, fructose-bisphosphate /// F	0.00083	5	2.82	2.85	2.83	2.76	2.74	2.76	2.71	2.75
TC0X00500	ALG13	55849	Uncharacterized protein CXorf45. [Sou	2.20E-12	5	3.77	3.79	3.90	3.62	3.54	3.54	3.63	3.61
TC1000200	ALOX5	240	arachidonate 5-lipoxygenase	7.59E-10	5	7.91	8.15	8.20	8.02	7.88	7.74	7.62	7.60
TC0103034	ANGPTL1	9068	angiopoietin-like 1	6.75E-07	5	3.00	3.15	2.97	2.82	2.78	2.82	2.80	2.81
TC0100115	ANGPTL7	10218	angiopoietin-like 7	3.42E-06	5	3.76	3.51	3.60	3.45	3.58	3.38	3.34	3.49
TC0400471	ANK2	287	ankyrin 2, neuronal /// Ankyrin-2 (Brai	4.30E-05	5	2.91	2.88	2.89	2.83	2.80	2.78	2.78	2.82
TC1000745	ANKRD16	54522	ankyrin repeat domain 16	7.41E-05	5	3.84	3.89	3.95	3.83	3.87	3.84	3.73	3.81
TC0600326	ANKS1A	23294	ankyrin repeat and sterile alpha motif	7.65E-06	5	5.74	5.95	5.98	5.87	5.75	5.60	5.62	5.61
TC0401074	ANTXR2	118429	anthrax toxin receptor 2 /// Anthrax to	0.000313	5	7.41	7.72	7.39	7.38	7.37	7.46	7.47	7.48
TC1800392	AQP4	361	aquaporin 4 /// Aquaporin-4 (AQP-4) (	3.48E-05	5	2.95	2.85	2.90	2.78	2.75	2.80	2.73	2.83
TC0200759	ARHGAP15	55843	Rho GTPase activating protein 15	1.49E-06	5	8.34	8.62	8.60	8.29	8.17	8.32	8.26	8.24
TC0X01373	ARHGAP4	393	Rho GTPase activating protein 4 /// Rh	0.000122	5	5.91	5.84	5.82	5.80	5.77	5.69	5.65	5.68
TC0300141	ARPP-21 /// AR	10777	cyclic AMP-regulated phosphoprotein,	2.56E-05	5	2.77	2.64	2.67	2.58	2.63	2.57	2.59	2.62
TC0X00326	ARR3	407	arrestin 3, retinal (X-arrestin) /// Arrest	0.000336	5	3.72	3.55	3.61	3.56	3.57	3.53	3.49	3.54
TC0X00738	ARSE	415	arylsulfatase E (chondrodysplasia punc	0.000751	5	3.48	3.54	3.59	3.43	3.48	3.49	3.40	3.48
TC0X00013	ARSF	416	arylsulfatase F	0.000798	5	2.88	2.78	2.82	2.72	2.76	2.73	2.66	2.74
TC0401419	ASB5	140458	ankyrin repeat and SOCS box-containin	0.000598	5	2.62	2.59	2.72	2.58	2.58	2.54	2.51	2.65
TC0901285	ASTN2	23245	astrotactin 2 /// astrotactin 2 isoform	6.96E-05	5	3.75	3.72	3.74	3.62	3.68	3.68	3.63	3.69
TC1300287	ATP11A	23250	ATPase, class VI, type 11A /// Probable	2.43E-08	5	6.82	7.04	6.76	6.62	6.52	6.46	6.45	6.49
TC0101187	ATP1A4	480	ATPase, Na+/K+ transporting, alpha 4 p	0.000273	5	3.24	3.26	3.28	3.19	3.18	3.16	3.12	3.17
TC1300666	ATP4B	496	ATPase, H+/K+ exchanging, beta polype	0.000628	5	3.61	3.67	3.72	3.59	3.62	3.53	3.54	3.55
TC0701671	ATP6V0A4	50617	ATPase, H+ transporting, lysosomal V0	0.000932	5	3.05	3.09	3.13	3.03	3.05	3.05	2.97	3.07
TC0103089	B3GALT2	8707	UDP-Gal:betaGlcNAc beta 1,3-galactos	5.23E-05	5	3.39	3.20	3.25	3.10	3.09	3.03	2.93	2.99
TC0601458	BACH2	60468	BTB and CNC homology 1, basic leucine	0.000141	5	3.67	3.53	3.45	3.36	3.37	3.40	3.39	3.46
TC0601129	BAT5	7920	HLA-B associated transcript 5	0.000387	5	5.60	5.61	5.45	5.47	5.51	5.49	5.35	5.46
TC1100577	BBS1 /// DPP3	10072 ///	dipeptidyl-peptidase 3 /// Bardet-Biedl	1.81E-05	5	4.27	4.21	4.26	4.29	4.28	4.16	4.16	4.15
TC0300503	BOC	91653	Boc homolog (mouse) /// Brother of C	0.000165	5	4.13	4.05	4.10	4.02	4.01	3.99	3.97	4.01
TC0601226	BTBD9	114781	BTB (POZ) domain containing 9 /// BTB	1.78E-09	5	4.91	5.14	5.02	4.97	4.78	4.77	4.89	4.85
TC0500788	BTNL3	10917	butyrophilin-like 3 /// Butyrophilin-like	2.11E-05	5	3.66	3.46	3.44	3.29	3.29	3.27	3.21	3.28
TC1701551	BZRAP1	9256	benzodiazapine receptor (peripheral) a	0.000959	5	4.65	4.53	4.53	4.49	4.52	4.48	4.48	4.48
TC1000488	C10orf65	112817	chromosome 10 open reading frame 6	0.000196	5	4.53	4.41	4.45	4.30	4.32	4.32	4.35	4.34
TC1100317	C11orf49	79096	chromosome 11 open reading frame 4	7.86E-05	5	4.40	4.33	4.47	4.46	4.41	4.33	4.27	4.29
TC1101808	C11orf65	160140	chromosome 11 open reading frame 6	0.000357	5	2.95	2.94	2.87	2.80	2.83	2.81	2.81	2.83

TC1201177	C12orf25	84070	chromosome 12 open reading frame 2	0.000299	5	4.06	3.96	4.00	3.91	3.91	3.92	3.79	3.92
TC1300462	C13orf18	731930 //	chromosome 13 open reading frame 1	6.04E-06	5	6.84	7.02	6.20	6.11	6.13	6.60	6.15	6.43
TC1501130	C15orf5	---	Uncharacterized protein C15orf5. [Sou	0.000304	5	2.84	3.12	2.85	2.70	2.92	2.88	2.72	2.79
TC1701806	C17orf62	79415	chromosome 17 open reading frame 6	1.39E-06	5	6.38	6.43	6.36	6.34	6.28	6.21	6.16	6.12
TC1701063	C17orf76	388341	chromosome 17 open reading frame 7	6.41E-06	5	5.23	5.36	5.09	4.99	5.05	5.22	5.15	5.18
TC1900502	C19orf15	57828	chromosome 19 open reading frame 1	9.54E-05	5	4.43	4.34	4.37	4.27	4.30	4.31	4.30	4.30
TC0102336	C1orf141	400757	chromosome 1 open reading frame 14	0.000811	5	2.15	2.07	2.08	2.02	2.08	2.01	1.97	2.02
TC0103147	C1orf157	284573	chromosome 1 open reading frame 15	3.17E-05	5	3.44	3.25	3.26	3.21	3.25	3.15	3.17	3.23
TC0101143	C1orf182	128229	chromosome 1 open reading frame 18	0.000117	5	3.26	3.25	3.25	3.11	3.15	3.13	3.19	3.12
TC0102853	C1orf61	10485	chromosome 1 open reading frame 61	0.000382	5	4.10	3.97	4.00	3.87	3.90	3.91	3.92	3.92
TC0101568	C1orf95	375057	chromosome 1 open reading frame 95	4.80E-05	5	4.74	4.55	4.53	4.44	4.46	4.43	4.45	4.49
TC2000699	C20orf173	---	Uncharacterized protein C20orf173. [S	0.000112	5	4.18	4.01	4.07	3.97	4.04	3.92	3.90	4.00
TC0200180	C2orf56	55471	chromosome 2 open reading frame 56	1.30E-20	5	4.71	5.42	5.31	4.77	4.73	4.55	4.63	4.44
TC0300077	C3orf20	84077	chromosome 3 open reading frame 20	0.000541	5	3.57	3.46	3.52	3.44	3.44	3.42	3.38	3.43
TC0301712	C3orf57 /// Q6	165679	chromosome 3 open reading frame 57	0.000176	5	3.43	3.35	3.39	3.22	3.38	3.23	3.22	3.25
TC0401082	C4orf11	---	---	0.000671	5	3.02	2.84	2.80	2.73	2.86	2.82	2.67	2.76
TC0600787	C6orf103	---	Uncharacterized protein C6orf103. [Sou	0.00052	5	2.22	2.28	2.32	2.23	2.21	2.18	2.19	2.21
TC0601210	C6orf222	389384	chromosome 6 open reading frame 22	0.000494	5	3.80	3.66	3.71	3.67	3.67	3.68	3.55	3.64
TC0701459	C7orf38	221786	chromosome 7 open reading frame 38	0.000233	5	4.80	4.94	4.97	4.73	4.72	4.80	4.89	4.93
TC0701495	C7orf52	375607	chromosome 7 open reading frame 52	0.000576	5	4.28	4.25	4.19	4.09	4.13	4.15	4.07	4.06
TC0102293	C8B	732	complement component 8, beta polyp	1.90E-05	5	2.92	2.83	3.04	2.83	2.82	2.84	2.77	2.77
TC0500935	C9	735	complement component 9	0.000404	5	2.58	2.56	2.59	2.48	2.49	2.47	2.46	2.49
TC0900884	C9orf144 /// Q	389715	chromosome 9 open reading frame 14	0.000356	5	3.33	3.16	3.14	3.05	3.11	3.12	3.02	3.14
TC0901249	C9orf84	158401	chromosome 9 open reading frame 84	3.37E-06	5	4.72	4.40	5.16	4.89	4.56	4.49	4.48	4.12
TC0101344	CA120_HUMA	---	Putative uncharacterized protein C1orf	0.0005	5	3.41	3.39	3.16	3.37	3.17	3.19	3.12	3.27
TC0100620	CACHD1	57685	cache domain containing 1 /// cache d	1.07E-05	5	3.30	3.39	3.43	3.31	3.27	3.23	3.24	3.29
TC0103113	CACNA1S	779	calcium channel, voltage-dependent, L	0.000302	5	3.81	3.74	3.76	3.73	3.72	3.69	3.63	3.68
TC0701382	CACNA2D1	781	calcium channel, voltage-dependent, a	0.000776	5	2.18	2.16	2.19	2.13	2.13	2.09	2.09	2.10
TC0300320	CACNA2D3	55799	calcium channel, voltage-dependent, a	3.89E-05	5	2.86	2.89	2.93	2.81	2.81	2.76	2.80	2.80
TC1600572	CALB2	794	calbindin 2	0.000536	5	3.27	3.30	3.34	3.24	3.28	3.18	3.18	3.25
TC1700947	CAMTA2	23125	calmodulin binding transcription activa	0.000922	5	6.18	6.17	6.02	6.02	6.02	5.87	5.83	5.83
TC1300655	CARS2	79587	cysteinyl-tRNA synthetase 2, mitochon	0.00011	5	5.34	5.54	5.47	5.41	5.35	5.30	5.29	5.21
TC0X00860	CASK	8573	calcium/calmodulin-dependent serine	1.70E-08	5	3.98	4.38	4.02	3.93	3.92	4.00	4.08	4.00
TC0700812	CASP2	835	caspase 2, apoptosis-related cysteine p	0.000378	5	6.27	6.15	6.36	6.38	6.24	6.21	6.13	6.07

TC0500492	CATSPER3	347732	cation channel, sperm associated 3	0.000307	5	3.52	3.24	3.34	3.26	3.20	3.21	3.22	3.21
TC0202327	CCDC108	255101	coiled-coil domain containing 108 /// C	1.24E-05	5	3.93	3.82	3.86	3.77	3.78	3.77	3.73	3.77
TC1901652	CCDC114	93233	coiled-coil domain containing 114 /// C	0.000203	5	4.87	4.86	4.84	4.72	4.80	4.83	4.75	4.78
TC0102214	CCDC17	149483	coiled-coil domain containing 17 /// co	9.04E-07	5	4.65	4.48	4.44	4.38	4.44	4.36	4.34	4.38
TC1701630	CCDC46	201134	coiled-coil domain containing 46	0.000953	5	2.44	2.48	2.51	2.44	2.44	2.39	2.39	2.41
TC1701800	CCDC57	732273 //	coiled-coil domain containing 57 /// Co	2.39E-06	5	4.67	4.63	4.53	4.51	4.50	4.49	4.43	4.45
TC1200696	CCDC63	160762	coiled-coil domain containing 63	0.000303	5	3.10	3.07	3.15	3.03	3.03	3.03	2.95	3.05
TC0400866	CCKAR	886	cholecystokinin A receptor	0.0009	5	3.55	3.45	3.42	3.32	3.34	3.30	3.31	3.27
TC0201149	CCL20	6364	chemokine (C-C motif) ligand 20	4.32E-08	5	2.87	3.25	3.17	2.83	2.87	2.85	2.78	2.82
TC0701352	CCL26	10344	chemokine (C-C motif) ligand 26	9.95E-06	5	3.71	3.66	3.63	3.48	3.52	3.61	3.48	3.41
TC1500272	CCNDBP1	23582	cyclin D-type binding-protein 1	0.000457	5	7.89	7.93	7.94	7.75	7.67	7.75	7.68	7.75
TC1200922	CD163L1	283316	CD163 molecule-like 1	0.000836	5	3.53	3.40	3.45	3.38	3.36	3.32	3.30	3.37
TC1901113	CD209	30835	CD209 molecule /// CD209 antigen (De	1.32E-05	5	3.71	3.74	3.63	3.57	3.62	3.68	3.52	3.64
TC1701676	CD300LF	146722	CD300 molecule-like family member f /	0.000226	5	7.16	6.83	7.20	7.10	6.87	6.89	6.88	6.97
TC2000617	CD93	22918	CD93 molecule	0.000106	5	9.36	8.85	8.82	8.98	8.85	8.45	8.37	8.63
TC0801123	CDH17	1015	cadherin 17, LI cadherin (liver-intestine	0.000829	5	2.46	2.48	2.56	2.44	2.43	2.40	2.42	2.40
TC2000420	CDH26	60437	cadherin-like 26 /// Cadherin-like prote	1.90E-07	5	3.86	3.74	3.69	3.62	3.58	3.55	3.56	3.54
TC0900598	CERCAM /// CE	51148	cerebral endothelial cell adhesion mole	0.000207	5	4.59	4.69	4.64	4.58	4.65	4.63	4.51	4.57
TC0200990	CFLAR	8837	CASP8 and FADD-like apoptosis regulat	0.000422	5	8.92	8.69	8.72	8.63	8.54	8.58	8.57	8.57
TC0501171	CHD1	1105	chromodomain helicase DNA binding p	4.00E-07	5	7.38	7.99	7.58	7.40	7.19	7.40	7.52	7.48
TC1700112	CHD3	1107	chromodomain helicase DNA binding p	6.10E-05	5	5.49	5.45	5.17	5.12	5.22	5.02	5.19	5.13
TC1200906	CHD4	1108	chromodomain helicase DNA binding p	1.16E-05	5	7.48	7.92	7.40	7.39	7.38	7.38	7.49	7.44
TC0800329	CHD7	55636	chromodomain helicase DNA binding p	0.000319	5	6.63	7.04	6.56	6.43	6.47	6.54	6.68	6.53
TC0100830	CHI3L2	1117	chitinase 3-like 2	3.73E-06	5	3.24	3.49	3.29	3.21	3.23	3.22	3.24	3.27
TC0201865	CLASP1	23332	cytoplasmic linker associated protein 1	6.08E-07	5	6.30	6.66	6.39	6.37	6.24	6.25	6.21	6.18
TC2100097	CLIC6	54102	chloride intracellular channel 6 /// Chlo	0.000864	5	3.22	3.18	3.12	3.05	3.11	3.08	2.98	3.09
TC0102462	CNN3	1266	calponin 3, acidic	0.000998	5	3.55	3.57	3.64	3.52	3.56	3.50	3.44	3.48
TC0300004	CNTN6	27255	contactin 6	0.000466	5	2.51	2.46	2.49	2.40	2.43	2.35	2.39	2.43
TC0102492	COL11A1	1301	collagen, type XI, alpha 1 /// Collagen a	0.000118	5	3.92	3.82	3.83	3.78	3.78	3.78	3.74	3.80
TC0800526	COL14A1	7373	collagen, type XIV, alpha 1 /// Collagen	0.000119	5	2.90	2.86	2.86	2.81	2.82	2.77	2.77	2.80
TC0102071	COL16A1	1307	collagen, type XVI, alpha 1 /// Collagen	0.000488	5	5.23	5.17	5.17	5.11	5.13	5.14	5.05	5.11
TC0601348	COL21A1	81578	collagen, type XXI, alpha 1 /// collagen,	0.000133	5	3.40	3.32	3.35	3.29	3.27	3.29	3.22	3.31
TC0102401	COL24A1	255631	collagen, type XXIV, alpha 1	1.72E-05	5	3.62	3.50	3.47	3.45	3.41	3.42	3.37	3.42
TC0401180	COL25A1	84570	collagen, type XXV, alpha 1 /// Collagen	7.88E-05	5	4.14	4.05	4.07	4.02	4.03	4.01	3.94	4.03

TC0300618	COL29A1	256076	collagen, type XXIX, alpha 1	0.000626	5	2.49	2.34	2.34	2.29	2.26	2.23	2.18	2.31
TC0200930	COL3A1	1281	collagen, type III, alpha 1 (Ehlers-Danlo	2.02E-06	5	4.38	4.28	4.26	4.20	4.22	4.22	4.16	4.22
TC1300275	COL4A2	1284	collagen, type IV, alpha 2 /// Collagen	4.35E-05	5	4.86	4.79	4.77	4.71	4.74	4.73	4.66	4.75
TC0201146	COL4A3	1285	collagen, type IV, alpha 3 (Goodpastur	0.000456	5	3.94	3.89	3.89	3.83	3.85	3.83	3.80	3.82
TC0202364	COL4A4	1286	collagen, type IV, alpha 4 /// Collagen	1.45E-05	5	3.76	3.65	3.64	3.59	3.60	3.58	3.51	3.60
TC0X00488	COL4A5	1287	collagen, type IV, alpha 5 (Alport synd	7.38E-05	5	3.53	3.42	3.41	3.35	3.39	3.37	3.34	3.38
TC0X01146	COL4A6	1288	collagen, type IV, alpha 6 /// Collagen	1.24E-06	5	3.58	3.49	3.50	3.40	3.41	3.39	3.39	3.42
TC0202171	COL5A2 /// CO	1290	collagen, type V, alpha 2 /// Collagen a	2.77E-06	5	3.94	3.85	3.86	3.78	3.77	3.76	3.73	3.79
TC1700328	CPD	1362	carboxypeptidase D	6.60E-10	5	8.99	9.62	9.35	9.11	8.92	9.00	8.90	8.99
TC0300028	CPNE9	151835	copine family member IX /// Copine-9 (	0.000179	5	3.24	3.22	3.22	3.12	3.17	3.11	3.08	3.13
TC0701108	CRHR2	1395	corticotropin releasing hormone recep	0.000504	5	4.08	4.21	4.16	4.07	4.13	4.11	4.03	4.11
TC2200147	CRYBB3	1417	crystallin, beta B3	9.99E-05	5	4.99	4.89	4.92	4.77	4.81	4.87	4.68	4.84
TC0102097	CSMD2	114784	CUB and Sushi multiple domains 2 ///	0.00011	5	3.70	3.69	3.69	3.62	3.63	3.63	3.60	3.62
TC1701801	CSNK1D	1453	casein kinase 1, delta /// Casein kinase	0.000108	5	7.37	7.39	7.03	7.11	7.07	7.03	6.93	6.99
TC0100647	CTH	1491	cystathionase (cystathionine gamma-ly	0.000439	5	2.85	2.83	2.83	2.75	2.73	2.72	2.69	2.73
TC0200378	CTNNA2	1496	catenin (cadherin-associated protein),	0.000303	5	3.27	3.17	3.18	3.14	3.14	3.09	3.10	3.10
TC0901170	CTSL2 /// CTSL	1515 ///	cathepsin L2 /// cathepsin L1	3.99E-06	5	3.35	3.15	3.15	3.08	3.06	3.10	3.04	3.13
TC1101170	CYB5R2	51700	cytochrome b5 reductase 2 /// NADH-	6.57E-06	5	3.86	3.95	3.93	3.80	3.86	3.79	3.72	3.73
TC0801302	CYP11B2	1585	cytochrome P450, family 11, subfamily	0.000106	5	5.10	4.95	4.91	4.88	4.88	4.96	4.76	4.92
TC1901525	CYP2A7 /// CY	1549 ///	cytochrome P450, family 2, subfamily	5.01E-05	5	4.27	4.17	4.17	4.08	4.10	4.14	4.07	4.13
TC1000462	CYP2C18 /// C	1562 ///	cytochrome P450, family 2, subfamily	0.000848	5	2.48	2.48	2.52	2.41	2.44	2.42	2.37	2.50
TC0601302	CYP39A1	51302	cytochrome P450, family 39, subfamily	0.000678	5	2.21	2.16	2.25	2.10	2.12	2.10	2.12	2.13
TC0700527	CYP3A43	64816	cytochrome P450, family 3, subfamily	0.000197	5	2.50	2.37	2.39	2.34	2.35	2.31	2.29	2.34
TC0200808	DAPL1	92196	death associated protein-like 1	0.000929	5	3.17	3.14	3.20	2.98	2.98	3.07	2.92	3.03
TC0101109	DCST1	149095	DC-STAMP domain containing 1 /// DC	0.000418	5	3.95	3.86	3.86	3.79	3.78	3.81	3.77	3.83
TC0701201	DDC	1644	dopa decarboxylase (aromatic L-amino	0.000299	5	3.50	3.53	3.53	3.43	3.46	3.42	3.40	3.43
TC0102800	DENND4B	---	DENN/MADD domain containing 4B. [S	0.000132	5	5.75	5.64	5.62	5.53	5.57	5.57	5.53	5.47
TC0801330	DGAT1	8694	diacylglycerol O-acyltransferase homol	8.71E-06	5	6.12	5.79	5.70	5.62	5.64	5.67	5.60	5.55
TC1200415	DGKA	1606	diacylglycerol kinase, alpha 80kDa	0.000105	5	5.66	5.60	5.48	5.39	5.45	5.36	5.40	5.27
TC1100689	DKFZp434E111	283218	hypothetical protein DKFZp434E1119	0.000615	5	2.45	2.31	2.19	2.02	2.25	2.23	2.09	2.13
TC0300421	DKFZp667G211	131544	hypothetical protein DKFZp667G2110	0.000106	5	2.78	2.84	2.89	2.77	2.70	2.76	2.73	2.73
TC1001092	DLG5	9231	discs, large homolog 5 (Drosophila) ///	0.000134	5	4.33	4.27	4.22	4.17	4.21	4.15	4.14	4.17
TC0100482	DMAP1	55929	DNA methyltransferase 1 associated pr	0.000737	5	5.06	4.91	4.95	4.92	4.98	4.88	4.88	4.84
TC0X00837	DMD	1756	dystrophin (muscular dystrophy, Duch	0.000709	5	2.45	2.48	2.51	2.45	2.44	2.44	2.41	2.43

TC1701742	DNAH17	---	CDNA FLJ44071 fis, clone TESTI403772	0.000409	5	4.48	4.51	4.50	4.51	4.46	4.43	4.36	4.38
TC1700108	DNAH2	146754	dynein, axonemal, heavy chain 2 /// dy	0.000407	5	3.31	3.32	3.32	3.25	3.27	3.25	3.22	3.28
TC1600926	DNAH3	55567	dynein, axonemal, heavy chain 3	6.84E-05	5	2.84	2.85	2.87	2.80	2.80	2.76	2.76	2.79
TC1700137	DNAH9	1770	dynein, axonemal, heavy chain 9	1.10E-05	5	3.11	3.07	3.08	3.02	3.01	3.00	2.99	3.03
TC0900146	DNAI1	27019	dynein, axonemal, intermediate chain	7.61E-05	5	3.56	3.55	3.57	3.46	3.45	3.45	3.44	3.48
TC1100133	DNHD1	144132	dynein heavy chain domain 1	3.61E-06	5	4.23	4.06	4.15	4.01	4.00	4.03	4.02	4.06
TC1000474	DNTT	1791	deoxynucleotidyltransferase, terminal	0.000817	5	3.01	2.98	2.97	2.88	2.87	2.87	2.85	2.86
TC0300290	DOCK3	1795	dedicator of cytokinesis 3	0.000289	5	3.09	3.04	3.03	2.98	2.99	2.95	2.95	2.99
TC1901175	DOCK6	57572	dedicator of cytokinesis 6	0.000477	5	4.32	4.31	4.31	4.23	4.26	4.27	4.17	4.23
TC0700909	DPP6	1804	dipeptidyl-peptidase 6 /// Dipeptidyl a	0.000776	5	3.37	3.37	3.35	3.29	3.32	3.26	3.24	3.29
TC0100979	DRD5P2	---	Seven transmembrane helix receptor. [	0.000993	5	3.72	3.62	3.62	3.76	3.74	3.61	3.44	3.49
TC0X00424	DRP2	1821	dystrophin related protein 2 /// Dystro	6.96E-05	5	3.34	3.29	3.32	3.22	3.25	3.24	3.18	3.24
TC0600053	DSP	1832	desmoplakin	0.00068	5	3.01	3.03	3.03	3.00	2.96	2.94	2.92	3.01
TC0400089	DUB3	377630	deubiquitinating enzyme 3	0.00017	5	3.29	3.24	3.28	3.10	3.07	2.76	2.75	2.92
TC1001084	DUSP13	51207	dual specificity phosphatase 13 /// Dua	3.82E-06	5	5.31	5.51	5.33	5.29	5.32	5.30	5.22	5.25
TC0800838	DUSP4	1846	dual specificity phosphatase 4	0.00069	5	3.34	3.48	3.40	3.28	3.30	3.30	3.33	3.29
TC1501103	EDC3	80153	enhancer of mRNA decapping 3 homol	4.88E-11	5	5.20	5.36	5.39	5.25	5.29	5.15	5.10	4.96
TC0400582	EDNRA	1909	endothelin receptor type A /// Endothe	1.01E-05	5	2.85	2.60	2.71	2.58	2.64	2.55	2.58	2.58
TC0800924	EFCAB1	79645	EF-hand calcium binding domain 1	4.26E-07	5	3.17	2.99	3.02	2.83	2.89	2.88	2.89	2.93
TC0201530	EFEMP1	2202	EGF-containing fibulin-like extracellula	0.000807	5	2.93	2.89	2.94	2.80	2.83	2.85	2.83	2.85
TC0100390	EIF2C4	192670	eukaryotic translation initiation factor	3.24E-07	5	8.61	8.34	8.41	8.16	8.03	8.05	8.00	8.01
TC2200647	ELFN2	114794	extracellular leucine-rich repeat and fi	7.85E-05	5	4.11	3.86	4.00	3.74	3.83	3.88	3.79	3.81
TC0200200	EML4	27436	echinoderm microtubule associated pr	0.000102	5	6.74	6.85	6.67	6.41	6.29	6.46	6.44	6.42
TC0801212	ENPP2	5168	ectonucleotide pyrophosphatase/phos	4.12E-07	5	3.03	3.31	3.04	2.92	2.89	2.96	3.00	3.06
TC0300407	EPHA3	2042	EPH receptor A3	0.000567	5	2.68	2.61	2.69	2.59	2.60	2.55	2.52	2.59
TC0202280	ERBB4	2066	v-erb-a erythroblastic leukemia viral or	0.000497	5	2.93	2.87	2.91	2.81	2.85	2.83	2.79	2.82
TC0800650	ERICH1 /// Q8	157697	glutamate-rich 1	0.000935	5	5.49	5.48	5.52	5.64	5.50	5.36	5.32	5.28
TC2000339	EYA2	2139	eyes absent homolog 2 (Drosophila) //	5.31E-05	5	4.18	4.18	4.22	4.12	4.12	4.13	4.06	4.11
TC0501528	F12	2161	coagulation factor XII (Hageman factor	0.000601	5	4.63	4.65	4.60	4.53	4.55	4.50	4.47	4.52
TC0600693	FABP7	2173	fatty acid binding protein 7, brain /// F	5.89E-05	5	2.72	2.54	2.53	2.51	2.48	2.39	2.37	2.49
TC0X00944	FAM156B /// T	727866	family with sequence similarity 156, m	3.08E-07	5	5.11	4.96	4.96	4.82	4.88	4.86	4.87	4.85
TC0500421	FAM170A ///	340069	family with sequence similarity 170, m	0.000236	5	3.91	3.67	3.71	3.63	3.65	3.59	3.59	3.63
TC1000964	FAM170B /// C	170370	family with sequence similarity 170, m	0.000363	5	4.14	4.01	4.02	3.90	4.00	3.85	3.73	3.67
TC1701644	FAM20A	54757	family with sequence similarity 20, me	0.000277	5	4.82	4.60	4.64	4.73	4.58	4.52	4.54	4.50

TC1001258	FAM26C	255022	family with sequence similarity 26, mer	5.30E-05	5	3.92	3.63	3.63	3.45	3.53	3.49	3.41	3.53
TC0301300	FAM3D	131177	family with sequence similarity 3, mem	5.85E-05	5	3.98	3.82	3.83	3.81	3.74	3.70	3.70	3.78
TC0801251	FAM49B	51571	family with sequence similarity 49, mer	3.11E-06	5	8.24	8.37	8.39	8.15	8.09	8.19	8.13	8.22
TC2000694	FAM83C	128876	family with sequence similarity 83, mer	0.000433	5	4.24	4.13	4.13	4.01	4.02	4.05	3.98	4.03
TC0401470	FAT	2195	FAT tumor suppressor homolog 1 (Dros	0.00057	5	2.88	2.85	2.88	2.82	2.80	2.80	2.76	2.80
TC0501423	FAT2	2196	FAT tumor suppressor homolog 2 (Dros	9.25E-06	5	3.78	3.72	3.74	3.65	3.64	3.63	3.59	3.64
TC0300068	FBLN2	2199	fibulin 2	0.000611	5	4.54	4.50	4.49	4.47	4.42	4.41	4.34	4.40
TC0201622	FBXO41	150726	F-box protein 41	0.000714	5	4.40	4.47	4.47	4.33	4.36	4.40	4.32	4.38
TC0300252	FBXW12	285231	F-box and WD repeat domain containi	0.000715	5	2.86	2.76	2.79	2.71	2.75	2.67	2.68	2.69
TC0103185	FCAMR	83953	Fc receptor, IgA, IgM, high affinity /// F	0.0005	5	3.67	3.54	3.59	3.48	3.48	3.48	3.48	3.56
TC0102876	FCRL2	79368	Fc receptor-like 2 /// Fc receptor-like p	3.38E-06	5	2.95	2.97	3.09	2.95	2.95	2.88	2.84	2.85
TC0800541	FER1L6	654463	fer-1-like 6 (C. elegans)	0.00053	5	3.11	3.07	3.09	3.05	3.03	3.00	2.97	3.04
TC1900443	FFAR2	2867	free fatty acid receptor 2	1.99E-06	5	7.70	8.34	7.94	7.71	7.41	7.63	7.73	7.74
TC1201463	FGD6	55785	FYVE, RhoGEF and PH domain containi	1.05E-06	5	2.73	2.76	2.84	2.69	2.69	2.67	2.72	2.73
TC0901260	FKBP15	23307	FK506 binding protein 15, 133kDa	1.51E-05	5	7.29	7.05	7.47	7.33	7.09	7.04	7.05	6.89
TC0300374	FLJ10213	55096	hypothetical protein FLJ10213	6.22E-08	5	6.21	6.70	6.27	6.30	6.28	6.14	5.99	5.77
TC1400047	FLJ10357 /// N	55701	hypothetical protein FLJ10357 /// CDN	0.000229	5	5.69	5.34	5.44	5.53	5.33	5.21	5.16	5.24
TC0901473	FLJ20433 /// N	54932	hypothetical protein FLJ20433 /// CDN	0.000238	5	5.07	5.01	4.99	4.93	4.97	4.95	4.88	4.93
TC1901262	FLJ21438	64926	hypothetical protein FLJ21438	0.000477	5	5.53	5.50	5.48	5.35	5.44	5.38	5.33	5.33
TC1601268	FLJ22167 /// C	79583 ///	hypothetical protein FLJ22167 /// carb	0.000511	5	4.18	4.14	4.23	4.11	4.10	4.12	4.08	4.13
TC0500944	FLJ40243	133558	hypothetical protein FLJ40243	0.00031	5	2.51	2.45	2.49	2.42	2.43	2.40	2.37	2.42
TC0500600	FLJ41603	389337	FLJ41603 protein	9.94E-06	5	4.24	4.10	4.13	4.06	4.03	4.04	3.92	4.04
TC0200924	FLJ44048 /// N	401024	FLJ44048 protein /// CDNA FLJ44048 fi	0.000251	5	2.02	2.08	2.11	2.09	2.02	1.98	1.93	2.08
TC1500798	FMN1	644296 //	formin 1	0.000364	5	3.24	3.34	3.35	3.26	3.22	3.16	3.17	3.18
TC0103145	FMOD	2331	fibromodulin	1.71E-05	5	3.04	3.04	3.11	2.93	2.96	2.84	2.87	2.94
TC0202295	FN1	2335	fibronectin 1	0.000244	5	3.11	3.06	3.10	3.01	3.04	3.00	2.98	3.04
TC0400339	FRAS1	80144	Fraser syndrome 1 /// Extracellular ma	1.42E-05	5	3.23	3.18	3.18	3.10	3.13	3.12	3.08	3.11
TC0900786	FREM1	158326	FRAS1 related extracellular matrix 1 ///	0.000305	5	2.67	2.67	2.69	2.60	2.61	2.58	2.58	2.61
TC1100541	FRMD8	83786	FERM domain containing 8 /// FERM d	0.000388	5	5.01	4.95	4.89	4.83	4.83	4.88	4.86	4.91
TC1000960	FRMPD2	143162	FERM and PDZ domain containing 2	5.93E-05	5	3.59	3.55	3.55	3.47	3.50	3.47	3.43	3.48
TC0401369	FSTL5	56884	follistatin-like 5 /// Follistatin-related p	0.000827	5	2.56	2.47	2.50	2.43	2.43	2.38	2.41	2.42
TC0X01395	GAB3	139716	GRB2-associated binding protein 3 ///	1.41E-08	5	6.42	5.97	5.85	5.85	5.67	5.66	5.70	5.67
TC0500665	GABRA6	2559	gamma-aminobutyric acid (GABA) A re	0.0007	5	2.45	2.46	2.56	2.39	2.46	2.39	2.38	2.43
TC0X00671	GABRQ	55879	gamma-aminobutyric acid (GABA) rece	0.000222	5	3.11	3.10	3.15	3.06	3.06	2.96	3.02	3.02

TC1400321	GALNTL1	57452	UDP-N-acetyl-alpha-D-galactosamine:p	0.000451	5	3.39	3.41	3.42	3.32	3.39	3.33	3.25	3.31
TC1900904	GALP	85569	galanin-like peptide	0.000923	5	4.07	3.94	3.91	3.88	3.81	3.87	3.77	3.85
TC0300516	GAP43	2596	growth associated protein 43	0.000559	5	3.67	3.51	3.52	3.43	3.44	3.40	3.45	3.41
TC0900564	GAPVD1	26130	GTPase activating protein and VPS9 do	0.00046	5	6.81	7.01	6.83	6.76	6.70	6.69	6.75	6.69
TC1800098	GATA6	2627	GATA binding protein 6	0.0005	5	3.42	3.52	3.56	3.40	3.43	3.49	3.35	3.47
TC0X00703	GDI1	2664	GDP dissociation inhibitor 1	0.000715	5	7.66	7.48	7.33	7.26	7.28	7.23	7.15	7.17
TC1200456	GEFT /// SLC26	115557 //	RhoA/RAC/CDC42 exchange factor ///	0.000212	5	3.94	3.94	3.96	3.83	3.86	3.85	3.83	3.88
TC0600315	GGNB1_HUMA	---	Gametogenetin-binding protein 1. [Sou	1.69E-05	5	4.23	3.92	3.98	3.95	3.88	3.78	3.80	3.99
TC0100382	GJB3	2707	gap junction protein, beta 3, 31kDa	0.000155	5	4.01	3.77	3.87	3.77	3.67	3.63	3.75	3.73
TC0X00121	GK /// GK3P	2710	glycerol kinase /// Glycerol kinase (EC	0.000422	5	8.32	8.57	8.26	8.18	7.96	8.13	8.05	8.07
TC0202332	GLB1L	79411	galactosidase, beta 1-like /// galactosid	0.000188	5	3.55	3.60	3.46	3.51	3.57	3.51	3.44	3.42
TC1101018	GLB1L3 /// Q8	112937	galactosidase, beta 1-like 3 /// galactos	0.00023	5	3.20	3.11	3.14	3.06	3.06	3.05	3.02	3.03
TC0300306	GLYCTK /// GL	132158	glycerate kinase /// Glycerate kinase (E	0.000813	5	4.89	4.96	4.96	4.90	4.93	4.84	4.86	4.81
TC1200063	GNB3	2784	guanine nucleotide binding protein (G	0.000783	5	4.27	4.16	4.20	4.10	4.07	4.13	4.08	4.08
TC0901327	GOLGA1	2800	golgi autoantigen, golgin subfamily a, 1	2.39E-07	5	5.59	5.68	5.84	5.64	5.42	5.32	5.36	5.24
TC1600916	GP2	2813	glycoprotein 2 (zymogen granule mem	9.10E-05	5	3.48	3.42	3.46	3.34	3.31	3.32	3.28	3.35
TC1300230	GPC6	10082	glypican 6	0.000516	5	3.22	3.20	3.18	3.08	3.13	3.08	3.07	3.08
TC1200319	GPD1	2819	glycerol-3-phosphate dehydrogenase 1	5.04E-05	5	3.82	3.69	3.64	3.59	3.61	3.54	3.52	3.53
TC0X00778	GPM6B	2824	glycoprotein M6B	0.000183	5	4.07	3.95	3.97	3.90	3.95	3.92	3.84	3.90
TC1200829	GPR133	283383	G protein-coupled receptor 133 /// Pro	0.000541	5	3.73	3.78	3.80	3.70	3.69	3.71	3.66	3.69
TC1600478	GPR56	9289	G protein-coupled receptor 56 /// G-pr	0.00056	5	4.90	4.77	4.76	4.68	4.70	4.71	4.67	4.72
TC1200348	GRASP	160622	GRP1 (general receptor for phosphoin	0.000137	5	4.36	4.43	4.42	4.35	4.30	4.30	4.23	4.27
TC0200047	GREB1 /// NP_	9687	GREB1 protein /// GREB1 protein isofo	0.000291	5	3.66	3.65	3.69	3.62	3.62	3.60	3.54	3.60
TC2100266	GRIK1	2897	glutamate receptor, ionotropic, kainat	0.000181	5	3.41	3.25	3.34	3.22	3.21	3.21	3.22	3.23
TC0600590	GRIK2	2898	glutamate receptor, ionotropic, kainat	0.000629	5	2.64	2.61	2.61	2.55	2.59	2.56	2.49	2.52
TC1701678	GRIN2C	2905	glutamate receptor, ionotropic, N-met	0.00013	5	4.21	4.19	4.17	4.09	4.11	4.08	4.04	4.06
TC0301030	GRIP2	80852	glutamate receptor interacting protein	0.000547	5	4.57	4.49	4.45	4.43	4.47	4.46	4.37	4.43
TC1000629	GRK5	2869	G protein-coupled receptor kinase 5 //	1.13E-08	5	4.96	5.29	4.65	4.75	4.75	4.87	4.86	5.06
TC0300017	GRM7	2917	glutamate receptor, metabotropic 7	0.000382	5	2.83	2.86	2.91	2.77	2.78	2.84	2.74	2.81
TC0701608	GRM8	652292 //	glutamate receptor, metabotropic 8	9.94E-05	5	2.80	2.83	2.92	2.80	2.79	2.78	2.74	2.77
TC0800604	GSDMDC1	79792	gasdermin domain containing 1	0.000286	5	5.49	5.48	5.41	5.35	5.34	5.36	5.31	5.35
TC1400393	GSTZ1	2954	glutathione transferase zeta 1 (maleyla	8.31E-06	5	4.14	4.19	4.22	4.06	4.09	4.04	3.95	4.05
TC2200278	GTPBP1	9567	GTP binding protein 1	2.69E-09	5	6.80	7.42	7.05	6.96	6.88	6.80	6.67	6.70
TC1300496	GUCY1B2	---	Guanylate cyclase soluble subunit beta	0.000622	5	2.70	2.63	2.67	2.56	2.58	2.56	2.53	2.59

TC1201013	GUCY2C	2984	guanylate cyclase 2C (heat stable enter	0.000249	5	3.24	3.40	3.37	3.22	3.22	3.08	3.12	3.11
TC1700114	GUCY2D	3000	guanylate cyclase 2D, membrane (retin	0.000196	5	4.66	4.69	4.72	4.61	4.63	4.61	4.54	4.60
TC0X01149	GUCY2F	2986	guanylate cyclase 2F, retinal	2.67E-05	5	2.65	2.55	2.55	2.45	2.46	2.44	2.47	2.48
TC1900437	HAMP	57817	hepcidin antimicrobial peptide	4.21E-05	5	5.44	5.59	5.35	5.29	5.27	5.29	5.17	5.30
TC1701363	HAP1	9001	huntingtin-associated protein 1	0.000565	5	4.26	4.27	4.29	4.22	4.17	4.19	4.13	4.12
TC0501345	HBEGF	1839	heparin-binding EGF-like growth factor	3.26E-09	5	4.17	4.67	4.35	4.28	4.17	4.14	4.08	4.07
TC0X00214	HDAC6	10013	histone deacetylase 6 /// Histone deac	0.00032	5	4.54	4.48	4.46	4.45	4.49	4.44	4.43	4.39
TC1400770	HEATR5A	---	HEAT repeat containing 5A [Source:Ref	0.000911	5	4.84	4.80	4.92	4.59	4.44	4.72	4.86	4.99
TC1701633	HELZ	9931	helicase with zinc finger	0.000946	5	6.81	7.09	6.88	6.86	6.69	6.69	6.77	6.72
TC0X00307	HEPH	9843	hephaestin	0.000153	5	3.26	3.15	3.18	3.06	3.09	3.10	3.07	3.13
TC0301132	HHATL	57467	hedgehog acyltransferase-like /// Glyc	1.23E-05	5	4.31	4.16	4.14	4.08	4.06	4.08	4.02	4.08
TC0103256	HHIPL2 /// KIA	79802	HHIP-like 2 /// CDNA FLJ13840 fis, clon	0.000344	5	3.19	3.06	3.08	2.96	3.01	3.01	2.97	2.97
TC0600078	HIVEP1	3096	human immunodeficiency virus type I	0.000154	5	6.96	7.11	6.64	6.62	6.52	6.64	6.80	6.79
TC0800180	HMBOX1	79618	homeobox containing 1 /// Homeobox-	2.09E-06	5	5.72	5.55	5.36	5.23	5.19	5.23	5.39	5.29
TC0101361	HMCN1	83872	hemicentin 1 /// Hemicentin-1 precurs	3.73E-07	5	2.66	2.65	2.65	2.54	2.58	2.55	2.52	2.57
TC0102151	HPCAL4	51440	hippocalcin like 4	5.24E-06	5	4.74	4.75	4.77	4.62	4.65	4.66	4.52	4.62
TC1701757	HRNBP3 /// NP	146713	hexaribonucleotide binding protein 3	1.71E-06	5	4.25	4.33	4.39	4.27	4.28	4.26	4.18	4.28
TC0202384	HTR2B	3357	5-hydroxytryptamine (serotonin) recep	0.000999	5	3.24	3.07	3.23	2.90	3.00	2.99	2.93	2.89
TC0300847	HTR3E	285242	5-hydroxytryptamine (serotonin) recep	0.00033	5	3.04	3.08	3.04	2.94	3.00	3.00	2.88	2.95
TC0500645	ICHTHYIN	348938	ichthyin protein	0.000834	5	4.25	4.22	4.13	4.17	4.16	4.09	4.04	4.04
TC1500663	IGF1R	3480	insulin-like growth factor 1 receptor	1.43E-05	5	8.15	8.05	7.82	7.85	7.73	7.59	7.48	7.55
TC1101247	IGSF22	283284	immunoglobulin superfamily, member	0.000141	5	3.86	3.83	3.84	3.74	3.73	3.72	3.74	3.78
TC0200534	IL1R1	3554	interleukin 1 receptor, type I	2.76E-11	5	5.39	5.67	5.23	5.13	5.24	4.93	4.77	4.46
TC0300896	IL1RAP /// Q8N	3556	interleukin 1 receptor accessory protei	1.02E-11	5	7.28	7.81	7.51	7.08	6.55	6.74	6.74	7.04
TC0500187	IL31RA	133396	interleukin 31 receptor A /// Interleuki	0.000177	5	2.78	2.79	2.83	2.71	2.71	2.68	2.69	2.71
TC1901294	INSL3 /// JAK3	3718 ///	Janus kinase 3 (a protein tyrosine kinas	3.30E-06	5	5.96	6.21	6.17	6.03	6.03	5.90	5.82	5.75
TC0900764	INSL6	11172	insulin-like 6	0.000334	5	4.21	4.26	4.21	4.15	4.09	4.13	4.05	4.05
TC0202416	IQCA	79781	IQ motif containing with AAA domain /	2.69E-05	5	3.03	2.97	3.06	2.96	2.96	2.92	2.87	2.93
TC0103202	IRF6	3664	interferon regulatory factor 6	0.000235	5	4.04	3.89	3.88	3.81	3.80	3.84	3.79	3.85
TC0100934	ITGA10	8515	integrin, alpha 10	0.000181	5	3.65	3.56	3.63	3.50	3.53	3.52	3.51	3.50
TC1201279	ITGA7	3679	integrin, alpha 7 /// Integrin alpha-7 pr	0.000165	5	4.44	4.43	4.45	4.49	4.45	4.37	4.31	4.34
TC0102927	ITLN2	142683	intelectin 2 /// Intelectin-2 precursor (	0.000402	5	3.67	3.48	3.56	3.44	3.40	3.42	3.37	3.52
TC1901711	JOSD2	126119	Josephin domain containing 2	0.000172	5	5.20	5.27	5.33	5.19	5.27	5.16	5.16	5.09
TC1800169	KATNAL2	83473	katanin p60 subunit A-like 2 /// katani	7.38E-05	5	3.20	3.12	3.17	3.09	3.11	3.07	3.05	3.08

TC1401048	KCNK10	54207	potassium channel, subfamily K, memb	0.000774	5	4.02	3.96	3.91	3.83	3.90	3.88	3.81	3.83
TC1501264	KCNN2	3781	potassium intermediate/small conduct	0.000128	5	4.01	3.76	3.82	3.72	3.77	3.68	3.64	3.68
TC1901570	KCNN4	3783	potassium intermediate/small conduct	0.000544	5	3.63	3.73	3.72	3.66	3.58	3.67	3.57	3.63
TC0400958	KDR	3791	kinase insert domain receptor (a type I	0.000108	5	2.70	2.61	2.61	2.53	2.60	2.50	2.54	2.55
TC0400063	KIAA0232	9778	KIAA0232	2.67E-05	5	7.04	6.88	6.60	6.55	6.50	6.57	6.60	6.64
TC1000316	KIAA1274	27143	KIAA1274 /// Paladin. [Source:Uniprot/	0.000831	5	4.49	4.52	4.56	4.46	4.50	4.44	4.38	4.46
TC1400128	KIAA1305 /// C	57523	KIAA1305 /// CDNA FLJ11811 fis, clone	0.000303	5	4.00	3.88	3.92	3.81	3.87	3.82	3.73	3.84
TC1400458	KIAA1409	57578	KIAA1409 /// CDNA FLJ43337 fis, clone	0.000301	5	2.64	2.65	2.71	2.63	2.61	2.61	2.58	2.61
TC1900871	KIR3DL1 /// KI	3812 ///	killer cell immunoglobulin-like recepto	0.000272	5	4.19	4.28	4.31	4.25	4.21	4.13	4.12	4.09
TC1400613	KLC1	3831	kinesin light chain 1 /// Kinesin light ch	0.000259	5	6.70	6.76	6.58	6.55	6.42	6.39	6.51	6.38
TC0X00397	KLHL4	56062	kelch-like 4 (Drosophila)	0.000649	5	2.76	2.80	2.80	2.69	2.69	2.70	2.67	2.69
TC1901729	KLK10	5655	kallikrein-related peptidase 10	8.33E-05	5	6.00	6.05	6.04	5.94	6.04	5.97	5.91	5.91
TC1901733	KLK14	43847	kallikrein-related peptidase 14	0.000196	5	4.51	4.55	4.60	4.50	4.44	4.46	4.37	4.46
TC1900752	KLK2	3817	kallikrein-related peptidase 2	0.000768	5	4.37	4.24	4.23	4.15	4.18	4.19	4.11	4.18
TC1901727	KLK7	5650	kallikrein-related peptidase 7 /// Kallik	1.22E-05	5	3.96	3.93	3.90	3.76	3.79	3.77	3.78	3.76
TC1901728	KLK9 /// KLK8	284366 //	kallikrein-related peptidase 9 /// kallik	0.000755	5	4.23	4.15	4.19	4.10	4.10	4.08	4.04	4.10
TC1200971	KLRC1	3821	killer cell lectin-like receptor subfamily	0.000545	5	2.76	2.59	2.64	2.49	2.53	2.52	2.49	2.56
TC0700863	KRBA1	84626	KRAB-A domain containing 1 /// KRAB-	0.000569	5	5.00	4.95	4.95	4.85	4.90	4.87	4.83	4.88
TC1201232	KRT2	3849	keratin 2 (epidermal ichthyosis bullosa	2.30E-05	5	3.49	3.34	3.33	3.28	3.32	3.24	3.19	3.29
TC1201238	KRT78	196374	keratin 78 /// keratin 5b [Source:RefSe	2.11E-05	5	3.95	3.88	3.87	3.78	3.77	3.79	3.73	3.82
TC1201221	KRT85	3891	keratin 85	0.000166	5	4.32	4.27	4.34	4.19	4.19	4.18	4.17	4.18
TC1701358	KRT9	3857	keratin 9 (epidermolytic palmoplantar	0.00075	5	3.11	3.04	3.07	2.93	2.99	2.94	2.89	2.99
TC2100398	KRTAP10-5	386680	keratin associated protein 10-5 /// Kera	0.00047	5	5.06	4.92	4.90	4.77	4.79	4.87	4.80	4.85
TC1800320	LAMA1	284217	laminin, alpha 1 /// Laminin subunit al	2.66E-06	5	3.31	3.33	3.33	3.27	3.25	3.23	3.22	3.27
TC0600715	LAMA2	3908	laminin, alpha 2 (merosin, congenital	0.000575	5	2.69	2.65	2.66	2.60	2.58	2.61	2.57	2.61
TC0601537	LAMA4	3910	laminin, alpha 4 /// Laminin subunit al	0.000528	5	2.91	2.78	2.82	2.78	2.78	2.75	2.72	2.79
TC0701547	LAMB1	3912	laminin, beta 1	1.96E-05	5	3.58	3.51	3.53	3.46	3.47	3.45	3.45	3.41
TC0103199	LAMB3	3914	laminin, beta 3	1.30E-13	5	4.27	4.45	4.40	4.21	4.22	4.18	4.12	4.17
TC0101349	LAMC2	3918	laminin, gamma 2	0.000963	5	3.55	3.48	3.49	3.41	3.40	3.42	3.37	3.48
TC1100220	LDHC	3948	lactate dehydrogenase C	0.000523	5	2.92	2.83	2.88	2.71	2.80	2.72	2.76	2.74
TC0601376	LMBRD1	55788	LMBR1 domain containing 1 /// LMBR1	1.35E-08	5	7.45	7.32	7.57	7.22	6.88	7.22	7.21	7.47
TC1201025	LMO3	55885	LIM domain only 3 (rhombotin-like 2) /	0.000473	5	3.12	2.98	3.07	2.95	2.96	2.93	2.97	2.93
TC1201180	LOC283331	283331	hypothetical protein LOC283331	2.05E-07	5	4.84	4.92	4.89	4.79	4.72	4.69	4.64	4.70
TC0301003	LOC401052	401052	hypothetical LOC401052	0.000258	5	5.36	5.20	5.21	5.16	5.21	5.19	5.13	5.13

TC0700872	LOC643641	643641	hypothetical protein LOC643641	1.88E-05	5	4.94	4.78	4.87	4.92	4.80	4.74	4.78	4.69
TC0500955	LOC644010	644010	hypothetical LOC644010	0.000323	5	3.92	3.51	3.80	3.53	3.45	3.53	3.61	3.40
TC1101604	LOC645332	645332	hypothetical protein LOC645332	9.22E-06	5	4.52	4.51	4.46	4.31	4.37	4.44	4.28	4.31
TC0X01407	LOC648605 ///	648605 //	similar to Trimethyllysine dioxygenase,	0.000828	5	6.89	6.75	7.04	6.94	6.64	6.70	6.75	6.69
TC1100824	LOC651610 ///	651610 //	similar to Serine-protein kinase ATM (A	1.48E-06	5	6.53	6.71	6.30	6.11	6.16	6.11	6.05	6.15
TC1601228	LOC652737	652737	similar to hydrocephalus inducing	0.000219	5	2.83	2.76	2.87	2.73	2.72	2.75	2.68	2.74
TC0801169	LOC730429 ///	730429 //	similar to E3 ubiquitin protein ligase, H	3.24E-06	5	6.95	7.04	6.78	6.82	6.62	6.53	6.63	6.56
TC1200255	LOC730517	730517	similar to MUC19	7.78E-06	5	3.18	3.08	3.09	3.01	3.03	3.00	3.01	3.02
TC0900984	LOC730908	730908	similar to Aquaporin-7 (AQP-7) (Aquap	0.000846	5	3.59	3.51	3.60	3.50	3.50	3.45	3.46	3.50
TC0800802	LOXL2	4017	lysyl oxidase-like 2	0.000344	5	4.21	4.18	4.20	4.14	4.12	4.13	4.04	4.11
TC1001206	LOXL4	84171	lysyl oxidase-like 4	0.000847	5	4.73	4.68	4.66	4.61	4.64	4.62	4.55	4.57
TC0601730	LPAL2 /// LPA /	732058 //	lipoprotein, Lp(a)-like 2 /// lipoprotein,	2.68E-08	5	3.42	3.26	3.31	3.23	3.21	3.19	3.17	3.22
TC0400260	LPHN3	23284	latrophilin 3 /// Latrophilin-3 precursor	0.000112	5	2.42	2.42	2.48	2.36	2.41	2.36	2.31	2.37
TC2000271	LPIN3	64900	lipin 3 /// Lipin-3 (Lipin 3-like). [Source:	0.000492	5	4.35	4.24	4.22	4.16	4.19	4.16	4.13	4.21
TC1201341	LRIG3	121227	leucine-rich repeats and immunoglobu	0.000157	5	2.56	2.63	2.59	2.51	2.51	2.53	2.50	2.53
TC0201973	LRP1B	53353	low density lipoprotein-related protein	7.84E-05	5	2.58	2.47	2.52	2.45	2.45	2.42	2.41	2.46
TC0202080	LRP2	4036	low density lipoprotein-related protein	7.97E-06	5	2.89	2.83	2.87	2.77	2.76	2.77	2.74	2.77
TC1200994	LRP6	4040	low density lipoprotein receptor-relate	1.73E-06	5	3.02	3.04	3.16	3.03	3.04	2.95	2.94	2.96
TC1901057	LSDP5 /// LRG1	440503 //	lipid storage droplet protein 5 /// leuci	3.44E-08	5	5.82	5.96	5.78	5.80	5.77	5.69	5.58	5.57
TC1100239	LUZP2	338645	leucine zipper protein 2	0.000758	5	2.62	2.61	2.58	2.51	2.51	2.47	2.48	2.50
TC0800590	LY6K	54742	lymphocyte antigen 6 complex, locus K	0.000417	5	3.50	3.40	3.47	3.29	3.41	3.32	3.36	3.39
TC0X01359	MAGEA2	4101	melanoma antigen family A, 2	5.23E-06	5	5.47	5.37	5.35	5.26	5.22	5.29	5.20	5.27
TC0701374	MAGI2	9863	membrane associated guanylate kinase	2.95E-05	5	3.12	3.02	3.02	2.93	2.95	2.92	2.93	2.96
TC1500632	MAN2A2	4122	mannosidase, alpha, class 2A, member	4.44E-05	5	6.09	5.98	5.61	5.65	5.86	5.71	5.59	5.57
TC1501113	MAN2C1	4123	mannosidase, alpha, class 2C, member	9.52E-05	5	4.79	4.72	4.67	4.63	4.64	4.67	4.60	4.63
TC0500048	MAR6	10299	membrane-associated ring finger (C3H	0.000125	5	7.44	7.30	7.20	7.11	7.08	7.17	7.10	7.07
TC2200619	MB	4151	myoglobin	0.000641	5	4.20	4.05	4.09	4.00	4.02	3.99	3.94	4.05
TC0200776	MBD5	55777	methyl-CpG binding domain protein 5	5.75E-08	5	4.97	5.27	5.31	4.90	4.77	4.98	5.05	5.11
TC0501215	MCC	4163	mutated in colorectal cancers	1.62E-06	5	4.48	4.25	4.26	4.22	4.23	4.20	4.15	4.20
TC0301801	MCF2L2	23101	MCF.2 cell line derived transforming se	2.01E-05	5	3.01	3.07	3.03	2.95	2.95	2.94	2.92	2.96
TC0102393	MCOLN2	255231	mucolipin 2 /// Mucolipin-2. [Source:U	0.000913	5	2.42	2.37	2.40	2.31	2.26	2.28	2.34	2.29
TC0100254	MDS2	---	Myelodysplastic syndrome 2 translocat	9.87E-05	5	3.96	3.78	3.81	3.77	3.77	3.71	3.69	3.76
TC0X00334	MED12	9968	mediator complex subunit 12 /// Medi	0.000125	5	7.04	6.92	6.88	6.84	6.73	6.58	6.65	6.56
TC0500443	MEGF10	84466	multiple EGF-like-domains 10	8.19E-07	5	3.36	3.26	3.29	3.19	3.19	3.19	3.18	3.20

TC2200323	MEI1	150365	meiosis inhibitor 1	7.59E-16	5	3.97	4.16	4.13	4.05	3.98	3.94	3.88	3.90
TC0700629	MET	4233	met proto-oncogene (hepatocyte grow	4.31E-06	5	2.59	2.50	2.54	2.44	2.45	2.46	2.41	2.45
TC0601514	MICAL1	64780	microtubule associated monoxygenase	2.82E-10	5	6.24	5.99	5.99	5.91	5.89	5.76	5.75	5.62
TC0301390	MINA	84864	MYC induced nuclear antigen /// MYC i	3.89E-05	5	4.12	4.22	4.43	4.17	4.07	4.00	4.02	4.03
TC0102225	MKNK1	8569	MAP kinase interacting serine/threoni	8.59E-21	5	6.62	7.49	7.50	6.92	6.69	6.48	6.43	6.21
TC1601258	MLKL	197259	mixed lineage kinase domain-like /// M	0.000787	5	7.41	7.68	7.69	7.61	7.29	7.19	7.34	7.27
TC1900453	MLL4 /// WBP7	9757	myeloid/lymphoid or mixed-lineage le	6.83E-05	5	5.47	5.34	5.19	5.19	5.18	5.18	5.16	5.21
TC1700406	MLLT6	4302	myeloid/lymphoid or mixed-lineage le	0.000561	5	5.53	5.64	5.38	5.49	5.36	5.28	5.47	5.49
TC1200777	MLXIP	22877	MLX interacting protein /// MLX intera	3.27E-08	5	5.59	5.58	5.79	5.82	5.58	5.34	5.40	5.31
TC1101770	MMP7	4316	matrix metallopeptidase 7 (matrilysin,	0.000448	5	2.55	2.51	2.52	2.39	2.36	2.39	2.45	2.38
TC1101875	MPZL2	10205	myelin protein zero-like 2	6.37E-05	5	5.10	5.14	4.84	4.53	4.52	4.97	4.83	4.98
TC1101874	MPZL3	196264	myelin protein zero-like 3	1.14E-07	5	8.69	9.06	8.71	8.33	8.28	8.72	8.52	8.68
TC1101205	MRVI1	10335	murine retrovirus integration site 1 ho	0.000725	5	5.20	5.25	5.32	5.15	5.09	5.21	5.13	5.17
TC0X00659	MTMR1	8776	myotubularin related protein 1 /// My	1.54E-14	5	5.15	5.62	5.96	5.27	4.92	5.00	5.07	5.03
TC2200184	MTMR3	8897	myotubularin related protein 3	0.000453	5	8.25	8.35	8.28	8.30	8.18	8.08	8.00	8.03
TC0800772	MTMR7	9108	myotubularin related protein 7	3.03E-06	5	3.76	3.57	3.57	3.54	3.57	3.52	3.48	3.52
TC0700561	MUC17	140453	mucin 17, cell surface associated /// m	0.000421	5	2.95	2.87	2.94	2.83	2.84	2.84	2.76	2.84
TC0501525	MXD3 /// RAB2	83463 ///	MAX dimerization protein 3 /// RAB24,	1.29E-07	5	6.74	6.76	6.59	6.42	6.39	6.48	6.43	6.41
TC1200633	MYBPC1	4604	myosin binding protein C, slow type	0.000454	5	2.75	2.79	2.83	2.76	2.76	2.72	2.69	2.73
TC1101347	MYBPC3	4607	myosin binding protein C, cardiac ///	1.35E-06	5	5.15	5.01	4.95	4.97	4.98	4.92	4.85	4.89
TC1701029	MYH1	4619	myosin, heavy chain 1, skeletal muscle,	0.000616	5	2.90	2.84	2.89	2.80	2.82	2.78	2.77	2.82
TC1701026	MYH13	8735	myosin, heavy chain 13, skeletal muscl	0.000301	5	3.38	3.33	3.33	3.26	3.27	3.26	3.21	3.29
TC0701504	MYLC2PL	93408	myosin light chain 2, precursor lympho	0.000621	5	4.36	4.27	4.31	4.22	4.27	4.25	4.16	4.27
TC1601073	MYLK3 /// MYL	91807	myosin light chain kinase 3 /// Putative	3.02E-05	5	3.76	3.85	3.77	3.74	3.69	3.63	3.66	3.69
TC0800011	MYOM2	9172	myomesin (M-protein) 2, 165kDa	0.00064	5	3.35	3.28	3.28	3.23	3.26	3.23	3.21	3.22
TC0101990	MYOM3	127294	myomesin family, member 3 /// myom	0.000604	5	3.58	3.56	3.54	3.47	3.49	3.47	3.46	3.49
TC0300177	MYRIP	25924	myosin VIIA and Rab interacting protei	6.57E-06	5	3.84	3.74	3.74	3.64	3.65	3.64	3.59	3.65
TC0800902	MYST3	7994	MYST histone acetyltransferase (mono	1.33E-05	5	8.16	8.35	8.14	8.00	7.83	7.95	7.95	7.95
TC1300625	NALCN	259232	sodium leak channel, non-selective ///	0.000335	5	2.99	2.98	3.00	2.90	2.91	2.91	2.88	2.92
TC0500325	NBPF22P	285622	neuroblastoma breakpoint family, me	0.000656	5	2.75	2.77	2.70	2.66	2.62	2.57	2.61	2.61
TC1700122	NDEL1	81565	nudE nuclear distribution gene E homo	3.18E-08	5	7.95	7.66	7.40	7.27	7.21	7.41	7.23	7.41
TC0400484	NDST3	9348	N-deacetylase/N-sulfotransferase (hep	0.000645	5	2.43	2.45	2.56	2.42	2.45	2.40	2.36	2.43
TC0102357	NEGR1	257194	neuronal growth regulator 1 /// Neuro	6.69E-07	5	3.43	3.59	3.43	3.33	3.36	3.44	3.37	3.37
TC1800541	NETO1	81832	neuropilin (NRP) and tolloid (TLL)-like 1	0.000313	5	2.49	2.38	2.38	2.31	2.34	2.30	2.25	2.35

TC0101446	NFASC	23114	neurofascin homolog (chicken) /// Neu	0.000574	5	3.54	3.49	3.49	3.45	3.44	3.45	3.39	3.42
TC0X00755	NLGN4X	57502	neuroligin 4, X-linked /// Neuroligin-4,	3.18E-05	5	3.22	3.29	3.31	3.22	3.24	3.18	3.10	3.19
TC1900900	NLRP8	126205	NLR family, pyrin domain containing 8	6.22E-05	5	3.12	3.03	2.96	2.91	2.90	2.91	2.93	2.90
TC1701391	NM_207388	---	CDNA FLJ31222 fis, clone KIDNE20042	5.26E-09	5	4.73	4.60	4.69	4.56	4.62	4.53	4.39	4.35
TC1501043	NOPE /// NP_0	57722	neighbor of Punc E11 /// neighbor of P	1.49E-06	5	4.42	4.38	4.41	4.33	4.32	4.31	4.24	4.28
TC0201814	NPHP1	4867	nephronophthisis 1 (juvenile) /// Neph	0.000746	5	2.64	2.59	2.60	2.50	2.55	2.52	2.48	2.52
TC2000700	NR_001442.2	---	fer-1-like 4 (C. elegans) (FER1L4) on chr	3.45E-05	5	4.01	4.02	4.02	3.91	3.94	3.93	3.89	3.94
TC1400550	NR_003214.1	---	small nucleolar RNA, C/D box 114-21 (S	1.80E-05	5	2.80	2.35	2.57	2.20	2.18	2.13	2.38	2.38
TC0900435	NR4A3	8013	nuclear receptor subfamily 4, group A,	0.000128	5	3.20	3.48	3.20	3.17	3.18	3.19	3.19	3.28
TC1001285	NRAP	4892	nebulin-related anchoring protein /// N	3.04E-05	5	3.31	3.28	3.26	3.20	3.22	3.18	3.17	3.22
TC0102252	NRD1	4898	nardilysin (N-arginine dibasic converta	0.000587	5	8.56	8.49	8.59	8.50	8.37	8.40	8.35	8.30
TC0201507	NRXN1	9378	neurexin 1 /// Neurexin-1-alpha precur	1.12E-09	5	3.15	3.11	2.98	2.89	2.94	2.92	2.89	2.94
TC1400400	NRXN3	9369	neurexin 3 /// Neurexin-3-alpha precur	2.17E-05	5	2.98	2.93	2.99	2.87	2.91	2.88	2.85	2.87
TC1701189	NUFIP2	57532	nuclear fragile X mental retardation pr	2.48E-08	5	7.82	7.92	7.61	7.60	7.41	7.57	7.63	7.63
TC1600967	NUPR1	26471	nuclear protein 1	0.000393	5	5.15	4.87	4.97	4.81	4.82	4.87	4.80	4.90
TC1900060	O75863_HUM	---	Fos39347_1. [Source:Uniprot/SPTREM	0.000131	5	2.89	2.50	2.51	2.45	2.43	2.23	2.37	2.47
TC0200945	OBFC2A	64859	oligonucleotide/oligosaccharide-bindin	1.39E-09	5	9.21	9.05	9.05	8.71	8.57	8.83	8.61	8.66
TC1001188	OPALIN	93377	oligodendrocytic myelin paranodal and	7.69E-05	5	3.91	3.81	3.80	3.69	3.75	3.81	3.70	3.73
TC0103457	OR2T35	403244	olfactory receptor, family 2, subfamily	0.000312	5	3.61	3.73	3.67	3.21	3.20	3.43	3.31	3.28
TC1100085	OR51E1	143503	olfactory receptor, family 51, subfamily	0.00011	5	3.33	3.27	3.30	3.12	3.24	3.15	3.10	3.11
TC1901136	OR7G1	125962	olfactory receptor, family 7, subfamily	0.000798	5	10.73	10.58	10.58	10.52	10.57	10.57	10.43	10.55
TC0X00147	OTC	5009	ornithine carbamoyltransferase	0.000318	5	2.28	2.24	2.34	2.24	2.21	2.15	2.20	2.24
TC1600248	OTOA	146183	otoancorin /// Otoancorin precursor. [	0.000266	5	3.23	3.21	3.23	3.13	3.14	3.16	3.14	3.16
TC0201375	OTOF	9381	otoferlin	5.85E-05	5	3.82	3.87	3.87	3.81	3.82	3.79	3.71	3.80
TC2000091	OTOR	56914	otoraplin	0.000781	5	2.78	2.57	2.60	2.50	2.49	2.46	2.51	2.51
TC1500779	OTUD7A	161725	OTU domain containing 7A	2.56E-05	5	3.83	3.89	3.89	3.83	3.82	3.79	3.77	3.71
TC1101657	P4HA3	283208	procollagen-proline, 2-oxoglutarate 4-	0.000866	5	3.74	3.72	3.65	3.64	3.60	3.59	3.58	3.64
TC0100195	PADI1	29943	peptidyl arginine deiminase, type I	0.000591	5	3.88	3.81	3.84	3.73	3.77	3.72	3.67	3.73
TC0900510	PAPPA	5069	pregnancy-associated plasma protein	0.000271	5	3.67	3.60	3.61	3.55	3.57	3.54	3.48	3.52
TC0600404	PARC /// PARC	23113	p53-associated parkin-like cytoplasmic	1.81E-07	5	4.74	4.62	4.59	4.53	4.55	4.55	4.53	4.53
TC0601737	PARK2	5071	Parkinson disease (autosomal recessive	0.000244	5	3.86	3.83	3.84	3.78	3.78	3.75	3.68	3.76
TC1101288	PAX6	5080	paired box 6 /// Paired box protein Pax	0.000455	5	3.26	3.31	3.34	3.26	3.28	3.24	3.18	3.28
TC1300256	PCCA	5095	propionyl Coenzyme A carboxylase, alp	0.000249	5	3.01	3.04	2.98	2.96	2.91	2.90	2.94	2.96
TC0500739	PCDH24	54825	protocadherin 24	0.000474	5	4.16	4.12	4.11	4.07	4.10	4.06	3.97	4.04

TC0500546	PCDHB5	26167	protocadherin beta 5	0.000342	5	2.86	2.73	3.06	2.71	2.67	2.63	2.72	2.58
TC0500559	############	56114 ///	protocadherin gamma subfamily A, 1 /,	3.40E-05	5	2.78	2.77	2.83	2.71	2.76	2.72	2.71	2.73
TC0400009	PCGF3	10336	polycomb group ring finger 3	9.85E-15	5	5.33	5.69	5.59	5.35	5.29	5.17	5.17	5.05
TC2000406	PCK1	5105	phosphoenolpyruvate carboxykinase 1	7.89E-06	5	3.42	3.44	3.43	3.37	3.35	3.35	3.28	3.33
TC0800110	PCM1	5108	pericentriolar material 1 /// Pericentric	1.62E-05	5	6.48	6.84	6.36	6.16	6.15	6.25	6.54	6.44
TC1400337	PCNX	22990	pecanex homolog (Drosophila) /// Peca	4.00E-06	5	8.02	8.32	8.11	8.11	8.02	7.94	7.79	7.77
TC0501159	PCSK1	5122	proprotein convertase subtilisin/kexin t	0.000221	5	3.21	3.19	3.18	3.10	3.10	3.07	3.08	3.07
TC0301892	PCYT1A	5130	phosphate cytidylyltransferase 1, cholir	2.57E-13	5	7.32	7.63	7.76	7.41	7.21	7.14	6.97	6.97
TC1200391	PDE1B	5153	phosphodiesterase 1B, calmodulin-dep	2.34E-05	5	4.47	4.40	4.49	4.40	4.40	4.32	4.29	4.31
TC1901297	PDE4C	5143	phosphodiesterase 4C, cAMP-specific (|	0.000347	5	4.41	4.41	4.43	4.31	4.34	4.32	4.29	4.31
TC1200080	PEX5	5830	peroxisomal biogenesis factor 5 /// Per	1.80E-06	5	4.15	4.26	4.24	4.12	4.08	4.15	4.10	4.07
TC0601255	PGC	5225	progastricsin (pepsinogen C) /// Gastric	0.000426	5	3.59	3.57	3.52	3.47	3.44	3.44	3.37	3.44
TC1700810	PGS1	9489	phosphatidylglycerophosphate synthas	5.53E-12	5	6.52	6.90	6.86	6.71	6.57	6.38	6.31	6.18
TC0X00952	PHF8	731069 //	PHD finger protein 8 /// PHD finger pro	2.40E-10	5	5.68	5.98	5.80	5.62	5.52	5.56	5.54	5.53
TC0X00801	PHKA2	5256	phosphorylase kinase, alpha 2 (liver)	2.06E-13	5	6.13	6.00	6.28	6.14	6.00	5.79	5.74	5.67
TC0901353	PIP5KL1	138429	phosphatidylinositol-4-phosphate 5-kir	0.000831	5	4.59	4.67	4.62	4.60	4.64	4.63	4.50	4.51
TC0701195	PKD1L1	168507	polycystic kidney disease 1 like 1	8.61E-06	5	3.31	3.23	3.23	3.15	3.18	3.16	3.13	3.20
TC1601286	PKD1L2 /// NP_	114780	polycystic kidney disease 1-like 2 /// pc	0.000352	5	3.93	3.90	3.92	3.83	3.83	3.83	3.83	3.85
TC0601326	PKHD1	5314	polycystic kidney and hepatic disease 1	4.07E-06	5	2.78	2.74	2.74	2.68	2.67	2.64	2.64	2.68
TC1501231	PLIN	5346	perilipin	0.00041	5	4.39	4.42	4.37	4.29	4.27	4.28	4.27	4.28
TC0100491	PLK3	1263	polo-like kinase 3 (Drosophila)	1.58E-10	5	5.40	5.67	5.49	5.32	5.37	5.32	5.19	5.27
TC0301636	PLSCR4	57088	phospholipid scramblase 4 /// Phosphc	8.73E-06	5	3.33	3.50	3.41	3.28	3.34	3.32	3.27	3.42
TC0X01368	PNCK	139728	pregnancy up-regulated non-ubiquitou	3.25E-05	5	5.06	5.00	4.97	4.89	4.94	4.96	4.89	4.92
TC1000612	PNLIPRP1	5407	pancreatic lipase-related protein 1 /// I	0.000451	5	3.20	3.09	3.13	3.06	3.03	3.04	2.99	3.05
TC0X00678	PNMA3	29944	paraneoplastic antigen MA3 /// Parane	0.000198	5	5.12	5.03	4.98	4.90	4.92	4.91	4.87	4.90
TC0102748	POGZ	23126	pogo transposable element with ZNF d	5.90E-05	5	6.83	7.15	6.73	6.74	6.77	6.76	6.82	6.79
TC1601033	POL3S	339105	polyserase 3	2.66E-05	5	5.21	5.04	5.03	4.98	4.98	4.99	4.94	5.01
TC0400772	POLN	353497	polymerase (DNA directed) nu /// DNA	0.000215	5	3.09	2.97	3.07	3.00	2.99	2.95	2.92	3.01
TC0701429	PON1	5444	paraoxonase 1	0.000744	5	2.90	2.88	2.90	2.76	2.78	2.83	2.74	2.76
TC0600330	PPARD	5467	peroxisome proliferator-activated rece	3.03E-08	5	5.66	5.55	5.28	5.31	5.21	5.29	5.28	5.35
TC1201420	PPFIA2	8499	protein tyrosine phosphatase, receptor	0.00055	5	2.57	2.53	2.57	2.49	2.50	2.45	2.47	2.53
TC0100058	PRDM16	647868 //	PR domain containing 16 /// PR domair	0.000769	5	4.48	4.50	4.48	4.40	4.43	4.39	4.36	4.41
TC0400350	PRDM8	56978	PR domain containing 8 /// PR domain	8.38E-09	5	4.65	4.88	4.48	4.42	4.45	4.60	4.55	4.57
TC2000906	PRIC285 /// PR	85441	peroxisomal proliferator-activated rece	3.54E-05	5	4.97	5.06	4.89	4.86	4.83	4.88	4.85	4.95

TC1400281	PRKCH	5583	protein kinase C, eta	0.000418	5	4.43	4.53	4.29	4.13	4.07	4.10	4.21	4.26
TC0500912	PRLR	5618	prolactin receptor /// Prolactin recept	0.000651	5	2.70	2.61	2.65	2.55	2.60	2.56	2.55	2.58
TC1300314	PSPC1	55269	paraspeckle component 1 /// paraspec	8.72E-05	5	6.44	6.51	6.65	6.51	6.41	6.26	6.36	6.20
TC0901023	PTAR1	375743	protein prenyltransferase alpha subuni	0.000122	5	5.33	5.41	5.57	5.40	5.22	5.27	5.24	5.19
TC1000683	PTPRE	5791	protein tyrosine phosphatase, recepto	0.000604	5	8.18	8.13	7.87	7.96	7.92	7.98	7.83	7.90
TC2000749	PTPRT	11122	protein tyrosine phosphatase, recepto	0.000258	5	4.03	4.03	4.02	3.93	3.98	3.97	3.87	3.96
TC0100338	PTPRU	10076	protein tyrosine phosphatase, recepto	0.000892	5	4.30	4.38	4.36	4.30	4.33	4.34	4.23	4.30
TC1200948	PZP	5858	pregnancy-zone protein /// Pregnancy	3.47E-05	5	3.04	2.91	2.93	2.86	2.88	2.85	2.85	2.84
TC0101690	Q495C9_HUM	---	CDNA FLJ43187 fis, clone FCBBF302344	0.000299	5	4.59	4.43	4.44	4.36	4.33	4.38	4.25	4.41
TC0201893	Q499Y1_HUM	---	---	0.000264	5	2.51	2.62	2.53	2.48	2.45	2.37	2.45	2.45
TC0400720	Q5BLP7_HUM	---	CH41746 (Fragment). [Source:Uniprot/	0.000604	5	2.72	2.71	2.75	2.67	2.64	2.63	2.62	2.60
TC1500038	Q5HYA3_HUM	---	---	0.000151	5	3.10	3.00	3.03	2.94	2.97	2.95	2.95	2.96
TC1300123	Q5SVS6_HUM	---	OTTHUMP00000018350. [Source:Unip	0.000221	5	4.31	4.29	4.38	4.24	4.23	4.24	4.25	4.20
TC0900248	Q5VV11_HUM	---	Family with sequence similarity 88, me	0.000895	5	3.87	3.69	3.72	3.60	3.62	3.63	3.59	3.64
TC0300620	Q69YT0_HUM	---	---	1.41E-05	5	3.62	3.47	3.45	3.41	3.41	3.37	3.34	3.42
TC0701121	Q6EIF5_HUMA	---	AAA1 variant XI. [Source:Uniprot/SPTR	0.000954	5	2.47	2.45	2.50	2.36	2.40	2.37	2.38	2.44
TC1901374	Q6NUH5_HUM	---	---	0.000117	5	3.76	3.53	3.60	3.51	3.46	3.44	3.41	3.53
TC0103039	Q6NWZ2_HU	---	---	0.000621	5	3.98	4.13	3.98	3.68	3.86	3.71	3.81	3.81
TC2200509	Q6P575_HUM	---	---	0.000524	5	5.67	5.43	5.37	5.25	5.29	5.34	5.26	5.26
TC1600253	Q6UTX4_HUM	---	CDNA FLJ46765 fis, clone TRACH30245	0.00084	5	3.05	3.03	3.05	2.96	2.99	2.97	2.96	2.98
TC0300241	Q6UX91_HUM	---	SQFE253. [Source:Uniprot/SPTREMBL;	4.57E-09	5	6.64	6.33	6.28	6.21	6.18	5.97	5.87	5.83
TC0200535	Q6UXP0_HUM	---	AHPA9419. [Source:Uniprot/SPTREMB	9.76E-05	5	4.57	3.85	4.13	4.32	4.27	4.09	3.87	3.71
TC0200300	Q6ZNG6_HUM	---	CDNA FLJ16124 fis, clone BRACE20116	0.000268	5	2.59	2.55	2.55	2.46	2.52	2.49	2.46	2.49
TC0901120	Q6ZQV3_HUM	---	CDNA FLJ46870 fis, clone UTERU30125	0.000659	5	3.40	3.30	3.31	3.17	3.11	3.17	3.21	3.22
TC2000447	Q6ZRC6_HUM	---	CDNA FLJ46471 fis, clone THYMU3023	5.56E-05	5	4.37	4.34	4.34	4.14	4.20	4.20	4.16	4.19
TC0800651	Q6ZRD0_HUM	---	CDNA FLJ46459 fis, clone THYMU3020	2.49E-05	5	5.00	4.43	4.51	4.53	4.46	4.37	4.30	4.24
TC2000422	Q6ZRE1_HUM	---	CDNA FLJ46426 fis, clone THYMU3013	2.63E-14	5	4.20	4.52	4.22	4.03	4.04	4.07	3.96	3.87
TC1900189	Q6ZSN3_HUM	---	CDNA FLJ45351 fis, clone BRHIP301183	0.000342	5	4.76	4.73	4.65	4.74	4.70	4.62	4.63	4.58
TC0400807	Q6ZU05_HUM	---	CDNA FLJ44077 fis, clone TESTI403881	0.000366	5	5.45	5.25	5.14	5.05	4.99	5.05	5.02	4.98
TC0400601	Q6ZUS2_HUM	---	CDNA FLJ43373 fis, clone NTONG2007	2.07E-06	5	2.81	3.01	2.95	2.83	2.84	2.76	2.75	2.71
TC2200550	Q6ZVA3_HUM	---	CDNA FLJ42830 fis, clone BRCAN2017	4.07E-05	5	4.72	4.57	4.73	4.78	4.64	4.45	4.44	4.18
TC1200098	Q6ZVH2_HUM	---	CDNA FLJ42583 fis, clone BRACE3009	0.000184	5	3.12	3.80	3.44	3.34	3.09	3.12	2.99	3.10
TC0500840	Q6ZVT4_HUM	---	CDNA FLJ42124 fis, clone TESTI200947	0.000305	5	4.31	4.11	4.10	4.04	4.03	3.98	3.94	4.07
TC0800154	Q71JB2_HUMA	---	---	1.41E-05	5	9.21	9.18	9.24	9.00	8.84	8.92	8.72	8.69

TC1800414	Q86W11_HUM	---	Zinc finger protein. [Source:Uniprot/SP	3.98E-07	5	3.59	3.55	3.69	3.51	3.48	3.46	3.47	3.46
TC0600629	Q8N1W0_HUN	---	CDNA FLJ37396 fis, clone BRAMY20273	1.47E-05	5	3.24	3.12	3.18	3.06	3.05	3.03	3.04	3.09
TC0X01403	Q8N793_HUM.	---	CDNA FLJ25895 fis, clone CBR03553. [S	0.000583	5	5.71	5.62	5.93	5.65	5.50	5.75	5.77	5.56
TC1901100	Q8TCW6_HUM	---	---	0.000324	5	3.08	2.83	2.85	2.73	2.73	2.73	2.64	2.71
TC0900267	Q8WX68_HUM	---	BA251O17.4 (Similar to methylenetetra	0.000505	5	3.53	3.67	3.65	3.53	3.54	3.46	3.50	3.55
TC1100745	Q96AU6_HUM.	---	FAT3 protein (Fragment). [Source:Unip	4.50E-05	5	3.11	3.01	3.04	2.94	2.95	2.96	2.91	2.97
TC2200508	Q99919_HUM/	---	F<lambda>8 protein (Fragment). [Sourc	1.90E-09	5	5.14	4.98	4.78	4.63	4.73	4.71	4.67	4.56
TC2000762	Q9BVX4_HUM.	---	---	0.000589	5	4.06	4.07	4.01	3.90	3.94	4.06	3.97	3.98
TC2200045	Q9BYA7_HUM/	---	---	0.000665	5	4.26	4.13	4.09	3.98	4.10	4.01	3.99	4.06
TC0301843	Q9BZK4_HUM/	---	Ovarian cancer-related protein 2. [Sour	0.000379	5	2.93	3.08	2.83	2.59	2.63	2.50	2.72	2.87
TC0800804	Q9P1G9_HUM.	---	---	0.000229	5	6.58	6.17	5.79	5.82	5.63	5.75	5.57	5.64
TC0X00492	Q9P1I9_HUMA	---	---	1.38E-09	5	7.87	8.03	7.47	7.25	6.98	7.12	7.29	7.29
TC0101557	Q9UI51_HUMA	---	---	0.00055	5	6.79	6.57	6.39	6.21	6.20	6.39	6.31	6.24
TC1900180	QTRT1 /// DNN	81890 ///	queuine tRNA-ribosyltransferase 1 (tRN	7.94E-05	5	6.48	6.40	6.32	6.31	6.28	6.20	6.14	6.17
TC0202245	RAPH1	65059	Ras association (RalGDS/AF-6) and plec	0.000895	5	3.19	3.07	3.17	3.06	3.04	3.07	3.10	3.11
TC1201583	RASAL1	8437	RAS protein activator like 1 (GAP1 like)	0.000985	5	3.87	3.94	3.90	3.85	3.87	3.86	3.76	3.81
TC0800932	RB1CC1	9821	RB1-inducible coiled-coil 1	0.000496	5	7.23	7.29	7.09	6.99	6.82	6.96	7.04	7.04
TC0X00208	RBM3	5935	RNA binding motif (RNP1, RRM) protei	0.000198	5	4.79	5.10	4.88	4.69	4.77	4.85	4.81	4.78
TC1101508	RCOR2	283248	REST corepressor 2	6.25E-05	5	4.77	4.69	4.61	4.58	4.56	4.57	4.54	4.55
TC1400317	RDH12	145226	retinol dehydrogenase 12 (all-trans/9-c	6.29E-06	5	4.09	4.00	4.00	3.91	3.92	3.99	3.81	3.94
TC1901810	RDH13	112724	retinol dehydrogenase 13 (all-trans/9-c	0.000809	5	4.65	4.55	4.59	4.51	4.54	4.54	4.46	4.51
TC1201310	RDH16	8608	retinol dehydrogenase 16 (all-trans) ///	0.000476	5	3.76	3.59	3.47	3.49	3.52	3.52	3.38	3.49
TC0102602	REG4	83998	regenerating islet-derived family, mem	0.000964	5	3.01	2.97	3.02	2.93	2.92	2.90	2.86	2.94
TC0701525	RELN	5649	reelin	5.55E-07	5	2.83	2.77	2.83	2.69	2.70	2.71	2.70	2.71
TC2000162	REM1	28954	RAS (RAD and GEM)-like GTP-binding 1	0.000738	5	4.80	4.75	4.75	4.73	4.73	4.66	4.54	4.66
TC0201804	RGPD3	653489	RANBP2-like and GRIP domain containi	0.000872	5	3.87	3.84	3.80	3.65	3.63	3.67	3.78	3.71
TC1000396	RGR	5995	retinal G protein coupled receptor /// F	0.000783	5	4.44	4.33	4.33	4.26	4.25	4.31	4.27	4.23
TC1600710	RGS11	8786	regulator of G-protein signaling 11 /// I	0.000672	5	4.61	4.61	4.64	4.60	4.66	4.57	4.48	4.58
TC1501227	RHCG	51458	Rh family, C glycoprotein	0.000148	5	3.48	3.30	3.35	3.29	3.30	3.26	3.22	3.31
TC1201165	RHEBL1	121268	Ras homolog enriched in brain like 1	0.000743	5	3.23	3.24	3.30	3.14	3.18	3.12	3.27	3.18
TC1400746	RIPK3	11035	receptor-interacting serine-threonine k	1.20E-10	5	5.88	5.47	5.55	5.49	5.37	5.32	5.35	5.31
TC2100361	RIPK4	54101	receptor-interacting serine-threonine k	3.87E-05	5	4.16	4.26	4.16	4.17	4.13	4.13	4.04	4.09
TC1500372	RNF111	54778	ring finger protein 111 /// E3 ubiquitin-	0.000176	5	6.72	6.92	6.88	6.84	6.63	6.70	6.69	6.75
TC1101203	RNF141	50862	ring finger protein 141	1.21E-05	5	8.28	8.47	8.64	8.36	8.15	8.24	8.09	8.23

TC0201787	RNF149	284996	ring finger protein 149	0.000407	5	9.42	9.65	9.52	9.42	9.29	9.50	9.42	9.49
TC0901262	RNF183	138065	ring finger protein 183	0.000554	5	3.51	3.45	3.52	3.41	3.34	3.41	3.32	3.40
TC0300386	ROBO2	6092	roundabout, axon guidance receptor, h	1.47E-06	5	2.94	2.86	2.88	2.77	2.82	2.77	2.75	2.79
TC0601559	ROS1	6098	c-ros oncogene 1 , receptor tyrosine kir	3.93E-06	5	2.54	2.43	2.49	2.40	2.37	2.38	2.38	2.41
TC2200380	RP3-402G11.5 /	83642	selenoprotein O /// Selenoprotein O. [S	7.73E-07	5	4.85	4.62	4.68	4.60	4.63	4.62	4.57	4.57
TC2000539	RP5-1022P6.2 /	56261	hypothetical protein KIAA1434 /// Puta	2.68E-06	5	7.84	7.53	7.44	7.18	6.97	7.18	7.14	7.02
TC0X01207	RP6-166C19.1	728096	cancer/testis CT47 family, member 1	0.000128	5	6.51	6.51	6.54	6.29	6.28	6.36	6.30	6.47
TC0201635	RTKN	6242	rhotekin	1.47E-05	5	4.40	4.29	4.35	4.26	4.28	4.23	4.14	4.22
TC0201088	RUFY4	285180	RUN and FYVE domain containing 4 ///	5.72E-06	5	4.65	4.56	4.54	4.46	4.47	4.47	4.41	4.48
TC1101242	SAA2	6289	serum amyloid A2	0.000257	5	4.57	4.50	4.55	4.41	4.40	4.40	4.34	4.38
TC1900992	SBNO2	22904	strawberry notch homolog 2 (Drosophi	0.000547	5	5.64	5.79	5.71	5.69	5.64	5.61	5.50	5.56
TC0301112	SCN11A	11280	sodium channel, voltage-gated, type XI	0.00095	5	2.64	2.64	2.63	2.53	2.57	2.55	2.52	2.58
TC1200900	SCNN1A	6337	sodium channel, nonvoltage-gated 1 al	0.000537	5	3.85	3.80	3.77	3.69	3.76	3.72	3.72	3.77
TC0600327	SCUBE3	222663	signal peptide, CUB domain, EGF-like 3	6.98E-05	5	4.26	4.12	4.17	4.11	4.05	4.08	4.04	4.08
TC0700029	SDK1	221935	sidekick homolog 1, cell adhesion mole	1.20E-05	5	3.81	3.87	3.88	3.81	3.82	3.79	3.72	3.74
TC1201309	SDR-O	121214	orphan short-chain dehydrogenase / re	0.000224	5	3.98	3.83	3.90	3.78	3.81	3.76	3.68	3.78
TC0701386	SEMA3E	9723	sema domain, immunoglobulin domain	1.31E-05	5	2.22	2.15	2.25	2.13	2.15	2.09	2.07	2.07
TC0102739	SEMA6C	10500	sema domain, transmembrane domain	0.000652	5	4.34	4.21	4.22	4.15	4.17	4.21	4.13	4.15
TC0500951	SEPP1	6414	selenoprotein P, plasma, 1	0.000637	5	2.76	2.62	2.70	2.62	2.62	2.62	2.58	2.60
TC1401097	SERPINA9	327657	serpin peptidase inhibitor, clade A (alpl	0.000184	5	3.45	3.31	3.35	3.23	3.31	3.23	3.19	3.27
TC1800236	SERPINB13	5275	serpin peptidase inhibitor, clade B (ova	0.000748	5	2.45	2.50	2.55	2.38	2.43	2.42	2.41	2.44
TC1800238	SERPINB7	8710	serpin peptidase inhibitor, clade B (ova	0.000401	5	2.29	2.26	2.38	2.28	2.21	2.20	2.25	2.30
TC0300026	SETD5	55209	SET domain containing 5	7.95E-05	5	6.94	6.85	6.68	6.64	6.56	6.50	6.64	6.51
TC1101520	SF1	7536	splicing factor 1 /// Splicing factor 1 (Zi	2.81E-06	5	7.71	7.57	7.29	7.32	7.36	7.34	7.31	7.25
TC0800897	SFRP1	6422	secreted frizzled-related protein 1 /// S	1.99E-05	5	3.19	3.40	3.11	3.03	3.12	3.37	3.21	3.11
TC0800766	SGCZ	137868	sarcoglycan zeta /// Zeta-sarcoglycan (:	0.000418	5	2.79	2.61	2.66	2.59	2.59	2.53	2.51	2.52
TC1000318	SGPL1	8879	sphingosine-1-phosphate lyase 1	0.000388	5	6.16	6.39	6.20	6.14	5.84	6.12	6.12	6.23
TC1700023	SGSM2	9905	small G protein signaling modulator 2	2.06E-06	5	4.82	4.65	4.64	4.59	4.57	4.60	4.54	4.56
TC2200299	SGSM3	27352	small G protein signaling modulator 3 /	1.12E-05	5	4.75	4.62	4.65	4.62	4.63	4.59	4.53	4.56
TC1900755	SIGLEC7	27036	sialic acid binding Ig-like lectin 7	2.89E-07	5	6.06	5.69	5.89	5.90	5.51	5.48	5.46	5.68
TC0201096	SLC11A1	6556	solute carrier family 11 (proton-couple	0.000434	5	8.16	8.09	7.96	7.92	7.85	7.67	7.45	7.51
TC2000333	SLC12A5	57468	solute carrier family 12, (potassium-chl	0.000433	5	3.78	3.78	3.78	3.70	3.71	3.68	3.67	3.73
TC0700554	SLC12A9	56996	solute carrier family 12 (potassium/chl	7.50E-09	5	5.43	5.39	5.43	5.21	5.17	5.20	5.10	5.08
TC1101457	SLC15A3	51296	solute carrier family 15, member 3	2.59E-05	5	6.37	6.61	6.53	6.33	6.18	6.32	6.31	6.42

TC1100492	SLC22A9	114571	solute carrier family 22 (organic anion	0.000817	5	3.04	3.10	3.06	2.97	2.95	2.95	2.93	2.97
TC1001212	SLC25A28	81894	solute carrier family 25, member 28	5.48E-07	5	5.41	5.60	5.64	5.32	5.23	5.18	5.25	5.19
TC0800153	SLC25A37	51312	solute carrier family 25, member 37 ///	0.000605	5	10.29	10.12	10.15	10.10	9.96	10.02	9.95	9.89
TC1901088	SLC25A41	284427	solute carrier family 25, member 41 ///	0.000266	5	4.08	4.02	4.08	3.94	3.96	3.98	3.91	4.00
TC0701546	SLC26A3	1811	solute carrier family 26, member 3 ///	0.000542	5	2.38	2.33	2.40	2.29	2.31	2.28	2.27	2.33
TC0301186	SLC26A6 /// CE	65010 ///	solute carrier family 26, member 6 ///	9.42E-10	5	4.53	4.64	4.59	4.54	4.62	4.53	4.45	4.46
TC0800427	SLC26A7 /// Q	115111	solute carrier family 26, member 7 ///	0.000354	5	2.39	2.30	2.37	2.28	2.26	2.26	2.27	2.28
TC0500449	SLC27A6	28965	solute carrier family 27 (fatty acid tran	8.92E-05	5	2.96	2.84	2.93	2.84	2.84	2.80	2.78	2.83
TC1500589	SLC28A1	9154	solute carrier family 28 (sodium-couple	0.000796	5	3.75	3.74	3.80	3.68	3.69	3.66	3.65	3.72
TC0800514	SLC30A8	169026	solute carrier family 30 (zinc transporte	4.22E-05	5	2.94	2.83	2.87	2.75	2.78	2.68	2.75	2.77
TC1701119	SLC47A2	146802	solute carrier family 47, member 2 ///	0.000938	5	4.08	4.06	4.10	3.98	4.01	3.98	3.98	3.97
TC0200820	SLC4A10	57282	solute carrier family 4, sodium bicarbo	0.000266	5	2.82	2.70	2.72	2.65	2.66	2.66	2.65	2.68
TC0201632	SLC4A5	57835	solute carrier family 4, sodium bicarbo	1.80E-09	5	3.59	3.43	3.39	3.38	3.31	3.34	3.34	3.35
TC0500529	SLC4A9	83697	solute carrier family 4, sodium bicarbo	0.000304	5	4.23	4.20	4.19	4.11	4.12	4.13	4.12	4.10
TC2200608	SLC5A4	6527	solute carrier family 5 (low affinity gluc	0.00027	5	3.30	3.27	3.28	3.14	3.18	3.19	3.16	3.22
TC0301744	SLC7A14	57709	solute carrier family 7 (cationic amino	0.000378	5	3.71	3.69	3.75	3.59	3.62	3.56	3.56	3.65
TC0701451	SMURF1	731429 //	SMAD specific E3 ubiquitin protein liga	9.26E-05	5	5.57	5.58	5.31	5.39	5.32	5.33	5.40	5.42
TC0300832	SOX2	6657	SRY (sex determining region Y)-box 2	0.000732	5	3.02	2.61	2.65	2.49	2.51	2.48	2.40	2.52
TC2000666	SPAG4L	140732	sperm associated antigen 4-like /// Spe	0.000129	5	3.66	3.60	3.67	3.55	3.53	3.55	3.57	3.60
TC0300324	SPATA12	353324	spermatogenesis associated 12	0.000377	5	3.23	3.20	3.34	3.20	2.99	3.17	2.95	3.16
TC0900125	SPINK4	27290	serine peptidase inhibitor, Kazal type 4	0.000132	5	4.83	4.66	4.71	4.59	4.66	4.70	4.60	4.61
TC0401386	SPOCK3	50859	sparc/osteonectin, cwcv and kazal-like	0.000775	5	2.55	2.44	2.43	2.38	2.39	2.34	2.31	2.35
TC0400381	SPP1	6696	secreted phosphoprotein 1 (osteopont	1.85E-18	5	3.71	5.80	3.56	3.18	3.55	3.98	3.99	4.13
TC1200477	SRGAP1	57522	SLIT-ROBO Rho GTPase activating prote	3.22E-05	5	3.05	2.92	2.94	2.88	2.85	2.84	2.84	2.86
TC1600810	SRL	---	Sarcalumenin precursor. [Source:Unipr	0.000784	5	3.75	3.59	3.65	3.54	3.55	3.55	3.48	3.61
TC0X00252	SSX2B /// SSX4	727837 //	synovial sarcoma, X breakpoint 2B ///	0.000981	5	3.61	3.50	3.51	3.47	3.45	3.38	3.33	3.40
TC1501157	ST20	400410	suppressor of tumorigenicity 20	7.30E-05	5	8.73	8.27	8.34	8.24	8.16	8.08	8.06	8.14
TC1300391	STARD13	90627	StAR-related lipid transfer (START) dom	0.000249	5	2.91	3.02	3.01	2.92	2.94	2.89	2.86	2.90
TC0X00313	STARD8	9754	StAR-related lipid transfer (START) dom	0.00064	5	4.13	4.24	4.17	4.07	4.14	4.11	4.08	4.08
TC1500270	STARD9	57519	StAR-related lipid transfer (START) dom	0.000622	5	3.62	3.58	3.60	3.52	3.49	3.50	3.47	3.50
TC1701379	STAT5B	6777	signal transducer and activator of trans	5.77E-06	5	8.25	8.30	8.35	8.38	8.18	8.09	8.04	7.94
TC0501500	STC2	8614	stanniocalcin 2	0.000793	5	3.77	3.67	3.71	3.53	3.60	3.56	3.54	3.61
TC1300607	STK24	8428	serine/threonine kinase 24 (STE20 hom	0.000128	5	6.28	6.40	6.30	6.36	6.23	6.09	6.14	6.19
TC0500577	STK32A	202374	serine/threonine kinase 32A /// Serine,	0.000632	5	2.51	2.43	2.55	2.42	2.43	2.39	2.37	2.44

TC0201104	STK36	27148	serine/threonine kinase 36, fused hom	2.29E-06	5	4.04	3.93	3.95	3.85	3.84	3.91	3.88	3.90
TC0301383	STX19	415117	syntaxin 19	0.000986	5	2.62	2.58	2.50	2.33	2.24	2.36	2.23	2.43
TC1900133	STXBP2	6813	syntaxin binding protein 2 /// Syntaxin-	3.16E-07	5	7.00	7.08	7.16	7.16	7.12	6.84	6.80	6.73
TC1500637	SV2B	9899	synaptic vesicle glycoprotein 2B	0.000314	5	3.14	3.08	3.11	3.02	3.07	3.09	2.96	3.05
TC0100800	SYPL2	284612	synaptophysin-like 2	0.000412	5	4.32	4.43	4.43	4.30	4.30	4.27	4.27	4.28
TC1200537	SYT1	6857	synaptotagmin I	4.19E-05	5	2.77	2.83	2.92	2.77	2.81	2.77	2.73	2.78
TC0600850	SYTL3	94120	synaptotagmin-like 3 /// synaptotagmi	6.20E-15	5	6.89	7.60	7.05	6.54	6.44	6.62	6.48	6.55
TC1700318	TAOK1	57551	TAO kinase 1	1.91E-06	5	7.61	7.87	7.70	7.61	7.52	7.55	7.52	7.51
TC0X00701	TAZ	6901	tafazzin (cardiomyopathy, dilated 3A (X	2.10E-09	5	5.41	5.51	5.47	5.33	5.47	5.37	5.27	5.20
TC1601007	TBC1D10B	26000	TBC1 domain family, member 10B /// T	0.000744	5	4.52	4.59	4.48	4.49	4.46	4.45	4.37	4.41
TC0400065	TBC1D14	57533	TBC1 domain family, member 14	2.49E-07	5	8.57	8.83	8.81	8.68	8.46	8.44	8.35	8.35
TC1200483	TBC1D30	23329	TBC1 domain family, member 30	5.17E-13	5	4.04	4.19	3.67	3.61	3.43	3.59	3.58	3.75
TC1700868	TBCD	6904	tubulin folding cofactor D /// Tubulin-s	3.81E-06	5	4.90	4.97	4.92	4.84	4.86	4.87	4.82	4.82
TC0X00383	TBX22	50945	T-box 22 /// T-box transcription factor	0.000257	5	2.86	2.94	2.93	2.80	2.86	2.81	2.84	2.82
TC0701475	tcag7.1177	352954	opposite strand transcription unit to ST	0.000754	5	5.57	5.65	5.48	5.42	5.45	5.39	5.46	5.43
TC0101103	TDRD10	126668	tudor domain containing 10 /// Tudor	4.25E-07	5	3.44	3.26	3.29	3.14	3.20	3.23	3.18	3.22
TC0601201	TEAD3	7005	TEA domain family member 3 /// Trans	9.40E-05	5	4.50	4.59	4.53	4.51	4.54	4.47	4.41	4.44
TC1701050	TEKT3	64518	tektin 3	0.000277	5	2.37	2.41	2.46	2.38	2.42	2.36	2.28	2.34
TC1701558	TEX14	56155	testis expressed 14 /// Testis-expresse	0.000105	5	2.92	2.91	2.95	2.84	2.85	2.83	2.81	2.83
TC0X01380	TEX28P1	728447	testis expressed 28 pseudogene 1	0.000771	5	3.21	3.23	3.09	3.17	3.11	3.07	3.05	3.04
TC2100367	TFF2	7032	trefoil factor 2 (spasmolytic protein 1)	0.000942	5	3.49	3.31	3.37	3.31	3.19	3.36	3.19	3.22
TC0800566	TG	7038	thyroglobulin /// Thyroglobulin precurs	5.59E-10	5	4.06	3.84	3.92	4.05	4.02	3.86	3.77	3.82
TC1401006	TGFB3	7043	transforming growth factor, beta 3	0.000829	5	4.03	4.00	4.07	3.95	3.89	3.96	3.89	3.96
TC0300221	TGM4	7047	transglutaminase 4 (prostate)	7.02E-05	5	3.98	3.86	3.83	3.77	3.83	3.82	3.74	3.80
TC1500885	TGM5	9333	transglutaminase 5	0.000407	5	3.44	3.45	3.47	3.38	3.39	3.35	3.26	3.38
TC1501071	TLE3	7090	transducin-like enhancer of split 3 (E(s	3.36E-05	5	8.15	8.18	7.72	7.74	7.56	7.75	7.51	7.79
TC1500392	TLN2	83660	talin 2	6.37E-05	5	3.63	3.61	3.60	3.54	3.55	3.53	3.49	3.54
TC1701534	TMEM100	55273	transmembrane protein 100	0.000103	5	2.71	2.51	2.54	2.48	2.42	2.41	2.39	2.48
TC1700365	TMEM132E	124842	transmembrane protein 132E	0.000999	5	4.69	4.66	4.61	4.56	4.54	4.55	4.46	4.56
TC0801262	TMEM71	137835	transmembrane protein 71 /// Transm	2.86E-08	5	8.78	8.36	8.37	8.07	7.99	8.18	8.02	8.24
TC1701310	TNS4	84951	tensin 4 /// Tensin-4 precursor (C-term	0.000856	5	4.04	4.10	4.06	3.96	4.01	4.00	3.90	3.98
TC1400051	TOX4	9878	TOX high mobility group box family me	4.16E-05	5	7.65	7.93	7.70	7.68	7.53	7.69	7.62	7.68
TC1100616	TPCN2	219931	two pore segment channel 2 /// Two-p	0.000603	5	4.88	4.87	4.74	4.72	4.74	4.78	4.76	4.73
TC0300893	TPRG1	285386	tumor protein p63 regulated 1	8.39E-05	5	2.95	2.89	2.93	2.87	2.84	2.76	2.69	2.85

TC0101117	TRIM46	80128	tripartite motif-containing 46 /// Tripar	0.00013	5	5.10	5.01	5.01	4.92	4.96	4.99	4.91	4.95
TC0700555	TRIP6	7205	thyroid hormone receptor interactor 6	0.000877	5	4.78	4.66	4.60	4.55	4.62	4.61	4.60	4.52
TC1500776	TRPM1	4308	transient receptor potential cation cha	5.70E-05	5	3.06	3.14	3.15	3.04	3.04	3.07	3.04	3.06
TC1101076	TRPM5	29850	transient receptor potential cation cha	0.000754	5	4.91	4.98	4.97	4.91	4.92	4.91	4.82	4.89
TC1700920	TRPV3	162514	transient receptor potential cation cha	7.77E-05	5	3.36	3.39	3.42	3.29	3.31	3.28	3.27	3.29
TC1100052	TSPAN32	10077	tetraspanin 32 /// Tetraspanin-32 (Prot	0.000853	5	5.55	5.55	5.46	5.44	5.55	5.57	5.45	5.48
TC0202140	TTN	7273	titin /// titin isoform novex-3 [Source:R	3.03E-07	5	3.57	3.49	3.43	3.34	3.39	3.40	3.39	3.35
TC0Y00156	TTTY9B	---	Transcript Y 9A protein. [Source:Uniprc	0.000942	5	2.11	2.01	2.03	1.98	1.85	1.88	1.85	1.92
TC2100380	U2AF1	7307	U2 small nuclear RNA auxiliary factor 1	0.000751	5	6.68	6.91	6.79	6.68	6.59	6.70	6.68	6.70
TC1100890	UBE4A	9354	ubiquitination factor E4A (UFD2 homol	3.67E-06	5	7.55	7.12	7.12	7.12	6.93	6.94	7.00	6.94
TC0500915	UGT3A2 /// UG	167127 //	UDP glycosyltransferase 3 family, polyp	0.000471	5	2.51	2.56	2.54	2.48	2.50	2.45	2.39	2.45
TC2100149	UMODL1	89766	uromodulin-like 1 /// Uromodulin-like	0.000923	5	4.06	4.03	4.02	3.96	3.98	3.96	3.92	3.97
TC1500633	UNC45A	55898	unc-45 homolog A (C. elegans)	0.000183	5	4.70	4.76	4.71	4.70	4.76	4.69	4.62	4.64
TC0103228	USH2A	7399	Usher syndrome 2A (autosomal recessi	0.000213	5	2.56	2.53	2.56	2.48	2.50	2.45	2.46	2.51
TC1701580	USP32	84669	ubiquitin specific peptidase 32	0.000229	5	8.92	8.67	8.55	8.54	8.40	8.48	8.48	8.49
TC0201546	USP34	9736	ubiquitin specific peptidase 34 /// Ubiq	6.49E-06	5	7.21	7.09	6.95	6.72	6.67	6.77	6.87	6.81
TC1100700	USP35	57558	ubiquitin specific peptidase 35	0.000174	5	4.45	4.28	4.25	4.20	4.22	4.24	4.14	4.23
TC1700064	USP6	9098	ubiquitin specific peptidase 6 (Tre-2 on	0.000273	5	3.89	3.85	3.86	3.78	3.75	3.75	3.76	3.78
TC0X00156	USP9X	8239	ubiquitin specific peptidase 9, X-linked	3.47E-06	5	7.77	7.92	7.73	7.62	7.39	7.48	7.48	7.51
TC1000703	VENTX	27287	VENT homeobox homolog (Xenopus la	0.000433	5	4.18	4.36	4.29	4.12	4.11	4.10	4.06	4.13
TC0100133	VPS13D	55187	vacuolar protein sorting 13 homolog D	2.81E-05	5	5.64	5.41	5.16	5.27	5.20	5.13	5.17	5.10
TC0700364	WBSCR17	64409	Williams-Beuren syndrome chromoso	9.45E-06	5	3.33	3.26	3.27	3.18	3.15	3.12	3.12	3.12
TC0401097	WDFY3	23001	WD repeat and FYVE domain containin	6.78E-16	5	8.14	8.77	8.69	8.31	8.16	8.13	7.94	7.85
TC1000229	WDFY4	159491	Uncharacterized protein C10orf64. [Sou	2.83E-05	5	5.93	5.61	5.65	5.51	5.38	5.44	5.34	5.33
TC0201339	WDR35	57539	WD repeat domain 35	2.48E-07	5	3.40	3.43	3.53	3.37	3.12	3.13	3.31	3.27
TC2000784	WFDC10B	280664	WAP four-disulfide core domain 10B	0.000657	5	3.75	3.80	3.91	3.68	3.80	3.71	3.65	3.71
TC0X00955	WNK3	65267	WNK lysine deficient protein kinase 3 /	0.000507	5	2.52	2.49	2.52	2.45	2.49	2.41	2.41	2.42
TC1000511	WNT8B	7479	wingless-type MMTV integration site fa	0.000124	5	3.22	3.01	3.05	2.89	2.97	3.01	2.87	2.99
TC1700273	WSB1	26118	WD repeat and SOCS box-containing 1	1.35E-13	5	8.54	9.00	9.09	8.61	8.48	8.40	8.28	8.14
TC0X00557	XPNPEP2	7512	X-prolyl aminopeptidase (aminopeptid	0.00025	5	3.91	3.92	3.91	3.80	3.84	3.83	3.77	3.83
TC0101329	XPR1	9213	xenotropic and polytropic retrovirus re	0.000122	5	5.70	5.97	5.55	5.66	5.58	5.71	5.77	5.76
TC0301464	ZBTB20	26137	zinc finger and BTB domain containing	4.73E-10	5	5.16	5.46	5.54	4.97	5.07	4.97	5.08	5.01
TC1900452	ZBTB32	27033	zinc finger and BTB domain containing	0.000568	5	4.78	4.58	4.72	4.62	4.57	4.48	4.47	4.56
TC1600861	ZC3H7A	29066	zinc finger CCCH-type containing 7A	1.74E-05	5	6.36	6.70	6.38	6.39	6.28	6.28	6.43	6.32

TC1200534	ZDHHC17	23390	zinc finger, DHHC-type containing 17 //	0.000331	5	6.04	6.12	6.15	6.03	6.03	5.97	5.93	5.74
TC0500307	ZFYVE16	9765	zinc finger, FYVE domain containing 16	5.68E-06	5	6.60	6.34	6.26	5.99	5.99	6.12	6.14	6.04
TC1300012	ZMYM2	7750	zinc finger, MYM-type 2 /// MYM-type	2.84E-05	5	6.55	6.61	6.50	6.44	6.29	6.32	6.30	6.24
TC1900682	ZNF114	163071	zinc finger protein 114	0.000851	5	3.77	3.67	3.70	3.61	3.60	3.51	3.54	3.56
TC0X00677	ZNF185	7739	zinc finger protein 185 (LIM domain) //	1.52E-05	5	5.78	5.45	5.52	5.99	5.74	5.42	5.40	5.58
TC1400681	ZNF219	51222	zinc finger protein 219	0.000536	5	4.33	4.11	4.13	4.22	4.18	4.03	3.98	4.07
TC1900607	ZNF227	7770	zinc finger protein 227 /// Zinc finger p	4.21E-06	5	5.26	5.38	5.36	5.08	4.93	5.17	5.38	5.43
TC1200855	ZNF268 /// NM	10795	zinc finger protein 268 /// zinc finger p	4.91E-05	5	4.39	4.32	4.33	4.16	4.15	4.26	4.30	4.30
TC1600690	ZNF276	92822	zinc finger protein 276	1.49E-08	5	5.81	6.05	5.62	5.61	5.51	5.61	5.62	5.56
TC0202146	ZNF385B	151126	zinc finger protein 385B	0.000885	5	2.70	2.67	2.68	2.60	2.61	2.59	2.60	2.58
TC1800264	ZNF407 /// NM	55628	zinc finger protein 407 /// zinc finger p	2.49E-06	5	6.11	6.16	6.05	5.93	5.84	5.80	5.83	5.79
TC1901197	ZNF44	51710	zinc finger protein 44 /// Zinc finger pr	2.30E-05	5	4.50	4.37	4.40	4.32	4.26	4.23	4.29	4.32
TC1901199	ZNF442	79973	zinc finger protein 442	0.000326	5	4.62	4.62	4.76	4.58	4.64	4.61	4.56	4.65
TC1900912	ZNF471	57573	zinc finger protein 471	2.10E-05	5	2.72	2.52	2.63	2.56	2.43	2.48	2.47	2.48
TC1900489	ZNF540	163255	zinc finger protein 540 /// Zinc finger p	0.000462	5	2.84	2.73	2.78	2.71	2.72	2.68	2.61	2.72
TC1901448	ZNF585B	92285	zinc finger protein 585B	0.000123	5	4.11	4.08	4.11	3.91	3.92	3.91	4.10	4.13
TC0X00893	ZNF630	57232	zinc finger protein 630	0.000866	5	3.33	3.30	3.39	3.33	3.26	3.23	3.20	3.11
TC0900932	ZNF658B	401509	zinc finger protein 658B	1.78E-06	5	3.25	3.22	3.24	3.14	2.99	2.85	2.93	2.89
TC0900925	ZNF658B	401509	zinc finger protein 658B	5.75E-05	5	3.90	3.74	3.73	3.57	3.64	3.43	3.46	3.48
TC0X00195	ZNF81	347344	zinc finger protein 81 /// Zinc finger pr	1.45E-05	5	5.06	5.08	5.11	4.98	4.81	4.93	4.95	4.93
TC0102208	ZSWIM5	57643	zinc finger, SWIM-type containing 5	0.000767	5	3.46	3.34	3.29	3.28	3.29	3.23	3.20	3.29
TC0500203	ZSWIM6	57688	zinc finger, SWIM-type containing 6	3.83E-06	5	7.84	8.17	8.00	8.05	7.79	7.78	7.75	7.74
TC1900973		---		2.61E-14	5	8.56	7.97	7.86	7.76	7.70	7.69	7.70	7.57
TC0201977		---		3.59E-13	5	5.94	4.82	3.90	3.28	3.53	3.53	3.85	3.51
TC0300954		---		1.41E-12	5	10.31	9.61	9.49	9.17	9.14	9.19	9.25	9.08
TC0300897		---		1.44E-12	5	6.08	5.65	5.24	4.77	4.36	4.57	4.57	4.80
TC0300892		---		5.31E-12	5	2.21	2.63	2.41	2.16	2.15	2.21	2.11	2.18
TC0X01040		---		6.63E-12	5	7.60	7.22	7.06	6.83	6.66	6.62	6.60	6.53
TC0300838		---		2.60E-11	5	3.54	4.66	4.06	3.62	3.60	3.51	3.54	3.49
TC0201981		---		6.10E-11	5	5.69	4.96	4.17	3.16	3.36	3.70	4.20	3.35
TC0300951		---		2.96E-10	5	7.42	6.68	6.71	6.43	6.31	6.39	6.37	6.30
TC0101470		---		5.48E-10	5	8.49	9.05	8.63	8.34	8.16	7.93	7.78	7.64
TC1600702		---		6.46E-10	5	9.89	9.23	9.18	8.95	8.93	8.91	8.99	8.78
TC0103337		---		1.25E-09	5	4.62	4.77	4.89	4.73	4.57	4.40	4.28	4.40

TC0X01037	---	1.49E-09	5	5.57	5.96	5.95	5.44	5.30	5.42	5.45	5.36
TC0900737	---	2.55E-09	5	7.37	6.97	6.80	6.53	6.45	6.53	6.30	6.24
TC0103255	---	3.22E-09	5	10.36	9.78	9.76	9.67	9.62	9.62	9.58	9.46
TC0101738	---	4.03E-09	5	8.80	8.09	8.01	7.77	7.86	7.77	7.67	7.56
TC1101027	---	5.20E-09	5	10.61	9.74	9.75	9.46	9.56	9.45	9.40	9.38
TC0900856	---	5.62E-09	5	10.72	10.78	10.72	10.54	10.50	10.55	10.39	10.39
TC0300082	---	1.01E-08	5	6.00	5.72	5.38	5.06	5.02	5.04	5.21	4.83
TC0700936	---	1.31E-08	5	9.47	8.83	8.90	8.62	8.65	8.60	8.60	8.48
TC0201982	---	1.61E-08	5	3.77	3.86	3.34	2.76	2.58	2.66	2.75	2.91
TC0101734	---	1.83E-08	5	10.95	10.40	10.41	10.12	10.18	10.15	10.20	9.96
TC1900382	---	2.18E-08	5	4.37	4.73	4.77	4.53	4.86	4.10	3.70	3.74
TC0103410	---	2.72E-08	5	9.92	9.49	9.38	9.22	9.20	9.24	9.22	9.10
TC0103413	---	3.57E-08	5	8.21	7.70	7.71	7.49	7.56	7.48	7.35	7.34
TC17r00020	---	4.91E-08	5	10.34	9.83	9.82	9.55	9.55	9.54	9.60	9.39
TC0X01039	---	8.86E-08	5	10.44	9.30	9.15	9.00	8.87	8.86	8.89	8.63
TC0400489	---	9.12E-08	5	8.64	8.18	8.14	7.97	7.95	8.01	8.00	7.82
TC0401380	---	1.06E-07	5	5.63	5.90	5.69	5.54	5.21	5.23	5.09	5.20
TC1600699	---	1.34E-07	5	7.79	7.52	7.53	7.29	7.17	7.23	7.09	6.97
TC1300406	---	1.68E-07	5	4.59	4.61	4.68	3.95	3.75	3.95	3.72	3.59
TC1901210	---	1.82E-07	5	3.88	3.18	3.53	3.20	3.48	3.11	2.69	2.87
TC1300331	---	2.24E-07	5	8.62	8.55	8.76	8.63	8.62	8.50	8.39	8.35
TC1900381	---	2.29E-07	5	4.86	5.35	5.34	4.77	5.22	4.72	4.48	4.54
TC0200904	---	2.37E-07	5	5.26	5.67	5.48	5.23	5.36	5.24	5.06	4.96
TC0301615	---	3.80E-07	5	3.83	4.48	3.84	3.73	3.77	3.65	3.50	3.60
TC0201978	---	3.94E-07	5	6.44	5.94	5.31	5.07	5.04	5.40	5.23	5.20
TC1500708	---	5.50E-07	5	2.96	3.21	3.09	2.97	2.88	2.93	2.90	2.89
TC0900414	---	7.35E-07	5	3.55	3.48	3.39	3.30	3.35	3.37	3.35	3.34
TC1101020	---	7.92E-07	5	4.76	4.55	4.56	4.46	4.50	4.51	4.40	4.46
TC0501433	---	9.30E-07	5	10.57	10.45	10.50	10.12	10.19	10.22	10.01	9.95
TC0102582	---	9.77E-07	5	4.58	4.54	4.19	4.04	4.04	3.98	4.05	4.10
TC2200161	---	1.43E-06	5	4.02	3.99	4.09	4.04	3.93	3.87	3.77	3.77
TC17r00018	---	1.76E-06	5	5.58	5.27	5.29	5.08	4.96	4.88	4.88	4.83
TC1300647	---	1.77E-06	5	6.11	6.60	6.00	5.65	5.28	5.52	5.81	5.51
TC0103431	---	2.14E-06	5	7.29	6.67	6.58	6.27	6.20	6.33	6.39	6.25

TC0100515	---	2.49E-06	5	5.40	5.42	5.54	5.37	5.17	5.27	5.19	5.13
TC1200518	---	2.98E-06	5	6.06	5.52	5.52	5.18	5.37	5.32	5.19	5.52
TC1701749	---	3.09E-06	5	3.80	3.48	3.55	3.37	3.50	3.45	3.39	3.44
TC0103409	---	3.37E-06	5	7.70	7.12	7.11	6.90	6.93	6.84	6.96	6.80
TC1200074	---	3.61E-06	5	6.01	5.86	5.66	5.65	5.65	5.73	5.62	5.68
TC1101169	---	4.09E-06	5	3.54	3.40	3.33	3.21	3.24	3.23	3.26	3.32
TC0201975	---	4.46E-06	5	3.23	3.35	3.29	2.71	2.79	2.81	2.77	2.84
TC0103142	---	5.06E-06	5	4.76	5.14	4.78	4.53	4.63	4.51	4.56	4.51
TC1501254	---	5.34E-06	5	4.80	4.59	4.68	4.40	4.41	4.38	4.41	4.42
TC1900005	---	6.10E-06	5	6.04	5.71	5.79	5.63	5.64	5.58	5.62	5.65
TC0102955	---	6.17E-06	5	2.97	2.76	2.78	2.66	2.68	2.67	2.67	2.66
TC0102057	---	6.19E-06	5	3.31	3.13	3.21	2.94	2.96	3.04	2.93	3.07
TC0500202	---	7.09E-06	5	6.80	7.09	6.86	6.93	6.70	6.64	6.63	6.58
TC0X00654	---	1.09E-05	5	4.65	4.42	4.42	4.33	4.40	4.36	4.28	4.37
TC1101025	---	1.17E-05	5	10.13	9.78	9.71	9.53	9.58	9.56	9.61	9.47
TC1300652	---	1.19E-05	5	6.24	6.00	6.04	5.91	5.98	5.89	5.81	5.95
TC2200670	---	1.28E-05	5	4.76	5.04	4.34	4.41	4.30	4.25	4.14	4.24
TC0600737	---	1.31E-05	5	5.71	5.23	5.31	5.07	5.25	4.99	5.03	5.13
TC0500616	---	1.41E-05	5	2.10	2.36	2.14	2.02	2.02	2.17	2.11	2.07
TC0200191	---	1.71E-05	5	2.67	2.56	2.64	2.47	2.57	2.54	2.47	2.47
TC0500070	---	1.78E-05	5	2.56	2.38	2.47	2.35	2.33	2.30	2.22	2.26
TC0600027	---	1.78E-05	5	5.09	5.20	4.95	4.77	4.88	4.87	4.73	4.75
TC0100847	---	1.97E-05	5	6.88	6.62	6.58	6.24	6.17	6.35	6.33	6.25
TC0500680	---	2.03E-05	5	3.61	3.56	3.58	3.47	3.47	3.45	3.43	3.51
TC0800946	---	2.04E-05	5	4.82	4.98	5.26	4.86	4.77	4.75	4.83	4.84
TC0500597	---	2.35E-05	5	3.34	3.29	3.28	3.21	3.16	3.14	3.17	3.17
TC1300463	---	2.35E-05	5	5.85	6.24	4.94	4.63	5.00	5.58	4.94	5.45
TC0102096	---	2.37E-05	5	7.76	7.37	7.03	6.95	6.89	6.97	6.90	6.98
TC0300513	---	2.39E-05	5	4.56	4.21	4.37	4.12	4.00	4.14	4.00	4.24
TC1701062	---	2.52E-05	5	4.17	4.56	4.31	4.25	4.17	4.00	3.84	4.11
TC1600962	---	2.60E-05	5	3.33	3.16	3.16	2.89	3.11	2.98	2.99	3.02
TC0401468	---	2.68E-05	5	3.02	2.93	2.98	2.84	2.85	2.85	2.78	2.85
TC0700200	---	2.90E-05	5	6.58	6.28	6.31	6.20	6.21	6.23	6.21	6.14
TC0103073	---	3.02E-05	5	2.05	2.41	2.07	1.98	1.99	2.03	2.02	2.11

TC1100674	---	3.03E-05	5	3.42	2.95	3.18	2.80	2.79	2.94	2.85	3.02
TC1100170	---	3.03E-05	5	3.75	3.46	3.28	3.21	2.94	3.23	3.12	3.02
TC2100326	---	3.19E-05	5	3.99	3.93	3.91	3.75	3.79	3.84	3.67	3.77
TC0700617	---	3.55E-05	5	2.82	3.23	2.71	2.68	2.79	2.77	2.96	2.79
TC2200010	---	3.59E-05	5	4.00	3.79	3.80	3.76	3.78	3.66	3.76	3.72
TC0X00506	---	4.11E-05	5	6.31	6.33	6.25	6.04	6.14	6.18	6.03	5.91
TC1200940	---	4.26E-05	5	5.39	5.49	5.40	5.33	5.26	5.21	5.17	5.16
TC1600701	---	4.88E-05	5	9.16	8.73	8.74	8.53	8.55	8.56	8.42	8.36
TC0401218	---	5.05E-05	5	7.30	6.95	6.81	6.71	6.71	6.75	6.71	6.66
TC0102461	---	5.13E-05	5	3.58	3.39	3.40	3.33	3.32	3.34	3.30	3.25
TC0401360	---	5.18E-05	5	3.85	3.97	4.08	4.07	3.68	3.80	3.76	3.66
TC1000038	---	5.18E-05	5	4.80	5.17	4.58	4.55	4.57	4.53	4.25	4.12
TC0X01288	---	5.24E-05	5	3.45	3.35	3.65	3.17	3.56	3.24	3.18	3.16
TC1200252	---	5.25E-05	5	2.88	2.86	3.11	2.90	2.84	2.81	2.82	2.83
TC0200761	---	5.38E-05	5	3.90	3.80	3.98	3.73	3.76	3.74	3.63	3.49
TC1901165	---	5.88E-05	5	7.39	6.98	6.66	6.21	6.29	6.61	6.67	6.32
TC0400505	---	5.90E-05	5	4.05	4.32	4.59	4.15	3.74	3.80	3.68	3.84
TC0701795	---	6.24E-05	5	5.81	6.22	5.64	5.63	5.70	5.65	5.64	5.51
TC0500107	---	6.41E-05	5	2.23	2.05	2.33	2.10	1.99	1.93	1.98	2.05
TC0100224	---	6.81E-05	5	4.38	4.50	4.29	4.13	4.05	4.31	4.20	4.46
TC0X01099	---	7.44E-05	5	7.40	7.89	7.55	7.28	7.09	7.24	7.21	7.33
TC0100547	---	8.73E-05	5	4.55	4.34	4.37	3.97	4.17	4.12	4.09	4.18
TC0103253	---	9.63E-05	5	7.85	7.26	7.19	6.75	6.95	6.80	7.03	6.81
TC0200758	---	9.70E-05	5	2.81	2.64	2.52	2.06	2.09	2.21	2.16	2.14
TC05r00001	---	9.76E-05	5	5.73	5.65	5.55	5.17	5.18	5.44	5.39	5.53
TC0300344	---	0.000106	5	2.80	2.62	2.67	2.60	2.56	2.59	2.60	2.56
TC1101868	---	0.000115	5	4.38	4.21	4.27	4.12	4.16	4.26	4.10	4.12
TC1901358	---	0.000118	5	3.22	3.31	3.20	3.07	3.11	3.10	2.99	3.08
TC0300514	---	0.000127	5	3.42	3.24	3.48	3.07	3.14	3.00	3.06	2.98
TC0801278	---	0.000134	5	6.59	7.40	6.90	5.98	5.89	6.41	6.63	6.47
TC0201987	---	0.000138	5	5.35	5.22	5.33	5.38	4.96	5.02	5.00	4.89
TC0400500	---	0.000145	5	4.73	4.76	4.64	4.50	4.28	4.36	4.25	4.23
TC1400786	---	0.00015	5	5.71	6.20	5.94	5.55	5.64	5.72	5.84	5.37
TC0500833	---	0.000152	5	2.84	2.56	2.56	2.53	2.45	2.37	2.38	2.44

TC0202343	---	0.000157	5	4.43	4.20	4.26	4.00	4.13	4.06	3.95	4.11
TC0600957	---	0.000157	5	5.24	5.08	4.85	4.81	4.77	4.91	4.80	4.89
TC0500796	---	0.000169	5	6.57	6.12	6.05	5.81	5.69	5.81	5.68	5.54
TC0300792	---	0.000171	5	5.33	5.56	5.00	5.04	4.71	4.97	4.87	4.77
TC0500795	---	0.000179	5	10.82	10.48	10.55	10.26	10.29	10.42	10.36	10.32
TC0701734	---	0.000181	5	8.52	8.07	8.42	8.02	8.24	7.83	7.77	7.59
TC2000698	---	0.000183	5	3.43	3.26	3.43	3.26	3.27	3.24	3.17	3.25
TC0201983	---	0.000189	5	4.75	4.67	4.30	4.20	3.94	4.10	3.91	4.00
TC0201992	---	0.000192	5	3.35	3.48	3.41	3.18	3.16	3.09	3.05	3.13
TC0301698	---	0.000205	5	4.10	3.81	3.96	3.56	3.73	3.84	3.53	3.64
TC0900555	---	0.000207	5	4.68	3.99	4.27	3.83	4.02	4.00	3.89	3.94
TC2200625	---	0.000212	5	4.82	4.69	4.64	4.33	4.27	4.36	4.48	4.37
TC1000848	---	0.000213	5	4.29	4.00	3.98	3.87	3.66	3.63	3.78	3.79
TC0501189	---	0.000215	5	4.91	4.64	4.54	4.48	4.48	4.29	4.40	4.35
TC1200538	---	0.00024	5	2.90	2.62	2.79	2.54	2.67	2.57	2.55	2.58
TC1701056	---	0.000254	5	5.47	5.11	5.20	5.18	5.04	5.02	4.99	5.12
TC2000249	---	0.000256	5	5.33	5.11	5.15	5.10	5.12	5.10	4.96	5.08
TC0700852	---	0.000259	5	4.13	3.78	3.90	3.57	3.49	3.48	3.45	3.52
TC0Y00137	---	0.000266	5	3.34	2.82	2.96	2.90	2.69	2.67	2.53	2.91
TC1800435	---	0.000266	5	3.79	3.82	3.91	3.62	3.73	3.59	3.47	3.58
TC0601546	---	0.00027	5	4.21	3.72	3.76	3.59	3.53	3.52	3.45	3.54
TC1700509	---	0.000285	5	5.85	5.87	6.04	5.70	5.60	5.78	5.79	5.80
TC1100062	---	0.000304	5	4.49	4.61	4.26	4.39	4.23	4.37	4.15	4.31
TC0900241	---	0.000304	5	2.94	2.96	2.83	2.75	2.85	2.69	2.74	2.83
TC0500583	---	0.000307	5	4.83	4.09	4.52	4.19	4.16	4.23	3.98	4.32
TC0102078	---	0.00031	5	4.57	4.68	4.60	4.50	4.49	4.58	4.50	4.52
TC0Y00164	---	0.000335	5	3.43	3.32	3.33	3.20	3.23	3.26	3.22	3.27
TC0300517	---	0.000338	5	4.22	3.98	4.00	3.69	3.89	3.65	3.72	3.80
TC0900763	---	0.000338	5	4.38	4.22	4.18	3.94	3.71	3.87	3.76	3.97
TC0500561	---	0.000345	5	4.82	4.75	4.36	4.30	4.28	4.37	4.36	4.29
TC0701682	---	0.000347	5	5.30	4.85	5.20	4.76	4.71	4.84	4.97	4.88
TC1600290	---	0.000352	5	3.16	2.86	2.85	2.88	2.80	2.86	2.75	2.47
TC0301896	---	0.000354	5	5.08	4.74	4.54	4.54	4.17	4.38	4.38	4.41
TC0700813	---	0.000355	5	6.14	5.80	5.76	5.65	5.63	5.51	5.72	5.63

TC1400440	---	0.000357	5	3.46	3.30	3.21	3.09	3.07	3.06	3.02	3.21
TC0701224	---	0.000365	5	3.76	3.84	3.82	3.41	3.31	3.48	3.13	3.32
TC1000559	---	0.000376	5	4.54	4.32	4.43	4.28	4.23	4.28	4.12	4.27
TC1000985	---	0.000392	5	4.64	4.44	4.48	4.38	4.31	4.42	4.35	4.33
TC1201240	---	0.000406	5	4.65	4.46	4.50	4.38	4.38	4.44	4.38	4.47
TC1000371	---	0.000407	5	2.96	2.86	3.08	2.86	2.98	2.92	2.74	2.71
TC0400646	---	0.000433	5	2.72	2.53	2.71	2.60	2.54	2.56	2.62	2.48
TC1500818	---	0.000439	5	11.42	11.17	11.21	11.11	11.15	11.15	11.02	11.13
TC0601494	---	0.000442	5	2.73	2.73	2.73	2.60	2.68	2.63	2.59	2.61
TC2200333	---	0.000443	5	5.44	5.28	5.33	5.21	5.28	5.29	5.21	5.27
TC1601174	---	0.000455	5	2.23	2.16	2.18	2.01	2.25	1.99	1.93	1.97
TC0600866	---	0.000473	5	1.83	1.82	2.14	1.78	1.86	1.87	1.73	1.91
TC0102842	---	0.000474	5	2.79	2.40	2.53	2.46	2.30	2.19	2.27	2.41
TC1800227	---	0.00048	5	3.73	3.57	3.69	3.54	3.47	3.54	3.34	3.50
TC1500664	---	0.000481	5	8.38	8.18	8.09	8.04	7.75	7.79	7.83	7.71
TC0701801	---	0.000484	5	3.84	3.37	3.61	3.35	3.33	3.29	3.24	3.34
TC0301687	---	0.000499	5	2.69	2.40	2.57	2.52	2.28	2.35	2.23	2.23
TC0200532	---	0.00052	5	5.75	5.67	5.64	5.45	5.18	5.05	5.29	5.38
TC1000410	728122	0.00052	5	6.30	6.11	6.13	6.03	5.99	6.00	6.01	6.05
TC1700673	---	0.000522	5	5.22	5.60	5.26	5.31	5.30	5.19	5.11	5.06
TC1600038	---	0.000534	5	3.52	3.36	3.26	3.25	3.21	3.15	3.08	3.27
TC1000195	---	0.000547	5	5.03	4.93	4.92	4.81	4.87	4.75	4.79	4.84
TC0102478	---	0.000549	5	3.30	3.45	3.35	3.17	3.19	3.32	3.18	3.15
TC0301778	---	0.00055	5	5.59	5.17	5.25	5.22	5.13	5.27	4.84	5.10
TC1101973	---	0.000553	5	7.61	7.02	6.89	6.80	6.77	6.69	6.51	6.81
TC0101892	---	0.000572	5	4.48	4.62	4.62	4.45	4.48	4.55	4.44	4.47
TC1100757	---	0.000577	5	2.52	2.15	2.52	2.15	2.04	2.19	2.05	2.17
TC1001102	---	0.00058	5	6.65	6.38	6.24	6.17	6.19	6.12	6.10	6.14
TC1201073	---	0.000591	5	3.80	3.39	3.48	3.30	3.24	3.36	3.28	3.16
TC0400066	---	0.000597	5	5.26	5.26	4.93	4.85	4.62	4.80	4.71	4.69
TC0400145	---	0.000606	5	5.00	4.44	4.70	4.51	4.42	4.28	4.34	4.30
TC1101909	---	0.000616	5	2.06	1.97	2.20	1.92	2.18	1.79	1.87	1.92
TC1201456	---	0.000621	5	3.75	3.32	3.27	3.21	2.89	3.09	3.10	3.08
TC1800102	---	0.000639	5	5.23	4.88	5.07	4.88	4.88	4.71	4.83	5.02

TC1500308	---	0.000653	5	3.64	3.42	3.57	3.33	3.41	3.33	3.37	3.36
TC0800829	---	0.000659	5	5.18	4.71	4.78	4.52	4.42	4.68	4.52	4.60
TC1401157	---	0.000659	5	8.41	8.18	8.29	7.92	7.99	7.99	8.07	8.05
TC0X00632	---	0.000661	5	2.35	2.18	2.08	2.04	2.05	1.86	1.99	1.98
TC0601364	730504	0.000664	5	2.54	2.47	2.49	2.32	2.36	2.32	2.27	2.31
TC1000803	---	0.000666	5	3.13	2.93	3.09	2.94	2.90	2.92	2.85	2.84
TC2100036	---	0.000682	5	3.01	2.94	2.93	2.83	2.82	2.75	2.77	2.81
TC0400492	---	0.000682	5	7.63	7.41	7.43	7.29	7.31	7.38	7.32	7.26
TC1900386	---	0.000684	5	4.38	4.12	4.33	4.04	4.09	4.15	4.07	4.07
TC0100084	---	0.000688	5	3.97	3.40	3.60	3.42	3.48	3.44	2.99	3.30
TC1400132	---	0.000699	5	2.90	2.62	2.88	2.76	2.73	2.77	2.51	2.70
TC0102453	---	0.000699	5	1.93	2.27	2.00	1.86	2.10	1.76	1.94	1.71
TC0X01301	---	0.000746	5	3.56	3.35	3.24	3.12	3.24	3.19	3.25	3.11
TC0401024	---	0.000767	5	2.60	2.71	2.93	2.69	2.55	2.49	2.50	2.57
TC0400992	---	0.000768	5	2.95	2.88	2.94	2.79	2.76	2.86	2.73	2.74
TC0103420	---	0.000777	5	3.20	3.05	3.01	2.99	3.00	2.99	2.92	2.94
TC0X00853	---	0.000783	5	4.95	4.97	5.02	4.80	4.79	5.00	4.83	5.00
TC2000592	---	0.000788	5	2.95	2.83	2.85	2.74	2.78	2.73	2.73	2.79
TC1600385	---	0.000798	5	2.74	2.63	2.69	2.53	2.42	2.51	2.52	2.58
TC0201843	---	0.0008	5	3.11	2.56	2.80	2.76	2.57	2.49	2.45	2.62
TC1300282	---	0.000802	5	2.77	2.29	2.30	2.25	2.40	2.15	2.05	2.08
TC1100814	---	0.000805	5	2.79	2.61	2.52	2.40	2.47	2.46	2.34	2.52
TC1300531	---	0.000807	5	5.23	5.25	5.32	5.16	5.03	5.14	5.13	5.05
TC1401144	---	0.000827	5	2.79	2.45	2.59	2.40	2.49	2.39	2.38	2.43
TC0200795	---	0.000833	5	2.30	2.24	2.14	2.06	2.04	1.77	2.01	1.89
TC0900926	---	0.000833	5	7.08	6.48	6.34	6.38	6.34	6.00	5.93	5.87
TC1600788	---	0.000837	5	4.86	4.66	4.63	4.52	4.62	4.52	4.49	4.64
TC0900222	---	0.000843	5	10.86	10.54	10.57	10.45	10.54	10.50	10.36	10.44
TC0400930	---	0.000846	5	4.35	4.21	4.24	4.00	4.18	4.06	4.12	4.18
TC0800719	---	0.000846	5	2.98	2.81	2.79	2.70	2.65	2.55	2.63	2.83
TC0701266	---	0.000851	5	3.55	3.46	3.56	3.45	3.47	3.44	3.47	3.55
TC0200647	---	0.000851	5	5.06	5.08	5.39	4.58	5.39	4.90	4.44	4.91
TC1000242	---	0.000862	5	5.71	5.45	5.69	5.75	5.58	5.55	5.59	5.54
TC0901043	---	0.000871	5	2.02	1.82	1.80	1.84	1.81	1.68	1.67	1.87

TC1800486	---	0.000879	5	3.61	3.63	3.43	3.29	3.07	3.27	3.02	3.22
TC1600780	---	0.000883	5	4.60	4.45	4.44	4.38	4.37	4.37	4.31	4.45
TC0X01044	---	0.000886	5	7.42	7.70	7.38	7.40	7.14	7.34	7.26	7.16
TC0101316	---	0.000886	5	4.68	4.93	4.82	4.61	4.59	4.53	4.44	4.47
TC0300809	---	0.000892	5	11.28	11.11	11.19	11.07	11.12	11.13	11.08	11.04
TC0X00718	---	0.000895	5	6.62	6.50	6.86	6.74	6.23	6.42	6.69	6.54
TC1400009	---	0.000899	5	2.85	2.76	2.75	2.50	2.37	2.41	2.50	2.28
TC0600364	---	0.000899	5	2.88	2.71	2.61	2.50	2.48	2.62	2.41	2.51
TC1201195	---	0.000908	5	12.42	12.24	12.22	12.19	12.27	12.19	12.09	12.17
TC1300128	---	0.000916	5	3.07	2.91	3.34	2.92	2.84	2.89	2.83	3.04
TC0801223	---	0.000926	5	2.54	2.22	2.26	2.11	2.20	2.05	2.10	1.99
TC0102854	---	0.000928	5	6.06	5.57	5.69	5.41	5.40	5.38	5.45	5.43
TC2200132	---	0.000942	5	4.01	4.09	4.15	3.92	3.95	3.97	3.96	4.02
TC1100069	---	0.000948	5	3.95	3.59	3.13	3.06	3.06	2.81	3.30	3.07
TC0700676	---	0.000984	5	5.52	5.11	5.20	5.10	5.13	5.00	4.90	5.03
TC1100205	---	0.000994	5	4.89	4.78	4.83	4.69	4.75	4.70	4.65	4.73
TC2000526	---	0.000997	5	3.16	2.94	3.05	2.95	2.82	2.83	2.64	2.83