Fichiers complémentaires

Table S2. Upregulated and downregulated genes between control and treated HEK-293T cells identified from microarray analysis.

ID	Gene Symbol	Description	Fold Change	HEK: Controle Avg (log2)	HEK: Peptide Avg (log2)	HEK: Controle Standard Deviation	HEK: Peptide Standard Deviation	P-val	FDR P-val	Group
TC1300008983.hg.1	INTS6	integrator complex subunit 6	10.09	12.33	9	0.06	0.73	6.15E-07	1.90E-03	Multiple_Complex
TC1700012332.hg.1	SPATA22	spermatogenesis associated 22	8.38	7.18	4.11	0.07	0.3	5.06E-07	1.90E-03	Multiple_Complex
TC0700013442.hg.1	LSMEM1	leucine-rich single-pass membrane protein 1	7.65	12.82	9.88	0.13	0.08	3.28E-07	1.90E-03	Multiple_Complex
TC2100007920.hg.1	KRTAP19-8	keratin associated protein 19-8	7.29	6.7	3.84	0.12	0.23	2.09E-06	2.80E-03	Coding
TC1100012019.hg.1	SESN3	sestrin 3	6.47	7.49	4.79	0.05	0.16	2.84E-07	1.90E-03	Multiple_Complex
TC0100008773.hg.1	MSH4	mutS homolog 4	6.24	9.77	7.13	0.05	0.79	1.51E-05	4.20E-03	Multiple_Complex
TC0900010910.hg.1	SLC35D2	solute carrier family 35 (UDP-GlcNAc/UDP-glucose transporter), member D2	6.14	5.96	3.34	0.39	0.24	7.60E-07	2.00E-03	Multiple_Complex
TC1100013189.hg.1	CFL1	cofilin 1 (non-muscle)	5.57	7.39	4.91	0.03	0.47	7.92E-06	3.50E-03	NonCoding
TC1100010222.hg.1	RPL36A	ribosomal protein L36a	5.42	13.43	10.99	0.35	0.78	3.00E-04	7.90E-03	Multiple_Complex
TC0X00008514.hg.1	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	5.18	13.32	10.94	0.15	0.45	2.69E-06	2.80E-03	Multiple_Complex
TC1200009919.hg.1	TAS2R10	taste receptor, type 2, member 10	4.96	9.62	7.3	0.31	0.65	3.10E-05	4.40E-03	Coding
TC0600011125.hg.1	HIST1H2AB	histone cluster 1, H2ab	4.92	10.28	7.98	0.09	0.04	5.81E-07	1.90E-03	Coding
TC1300007221.hg.1	SERPINE3	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 3	4.82	8.35	6.08	0.78	0.09	4.25E-05	4.90E-03	Coding
TC1100013188.hg.1	CFL1	cofilin 1 (non-muscle)	4.78	6.09	3.83	0.43	0	2.02E-06	2.80E-03	NonCoding
TC1000007641.hg.1	DKK1	dickkopf WNT signaling pathway inhibitor 1	4.64	8.16	5.95	0.06	0.6	1.56E-05	4.20E-03	Multiple_Complex

TC0600013231.hg.1	SGK1	serum/glucocorticoid regulated kinase 1	4.6	7.83	5.63	0.09	0.15	2.10E-06	2.80E-03	Multiple_Complex
TC1100009301.hg.1	TBCEL	tubulin folding cofactor E-like	4.59	13.56	11.36	0.37	0.39	6.93E-06	3.40E-03	Multiple_Complex
TC0600007377.hg.1	HIST1H2BM	histone cluster 1, H2bm	4.59	7.98	5.78	0.1	0.16	1.23E-06	2.80E-03	Coding
TC0500007966.hg.1	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	4.48	11.73	9.56	0.28	0.39	4.14E-05	4.80E-03	Multiple_Complex
TC0600007262.hg.1	HIST1H3A	histone cluster 1, H3a	4.46	7.8	5.64	0.51	0.6	2.00E-04	7.50E-03	Coding
TC0100015350.hg.1	AMPD1	adenosine monophosphate deaminase 1	4.44	6.22	4.07	0.29	0.03	2.83E-06	2.80E-03	Multiple_Complex
TC0800007370.hg.1	ADAM32	ADAM metallopeptidase domain 32	4.4	6.98	4.84	0.35	0.54	3.77E-05	4.70E-03	Multiple_Complex
TC0900009456.hg.1	RLN2	relaxin 2	4.37	10.32	8.19	0.27	0.19	2.88E-06	2.80E-03	Multiple_Complex
TC0100012219.hg.1	C1orf100	chromosome 1 open reading frame 100	4.32	7.24	5.13	0.46	0.14	1.00E-04	5.80E-03	Multiple_Complex
TC1500010090.hg.1	NRG4	neuregulin 4	4.22	10.35	8.27	0.25	0.76	2.00E-04	6.70E-03	Multiple_Complex
TC0700010355.hg.1	AGR2	anterior gradient 2, protein disulphide isomerase family member	4.22	7.11	5.03	0.63	0.35	1.40E-03	1.60E-02	Multiple_Complex
TC1200008353.hg.1	NTS	neurotensin	4.21	8.62	6.55	0.03	0.3	2.52E-06	2.80E-03	Multiple_Complex
TC0200014597.hg.1	RND3	Rho family GTPase 3	4.18	11.12	9.06	0.06	0.34	3.05E-06	2.80E-03	Multiple_Complex
TC0500013217.hg.1	COMMD10	COMM domain containing 10	4.16	11.4	9.34	0.02	0.43	3.59E-05	4.70E-03	Multiple_Complex
TC1200006771.hg.1	CLEC2D	C-type lectin domain family 2, member D	4.12	10.22	8.17	0.35	0.16	3.00E-04	8.00E-03	Multiple_Complex
TC1400008116.hg.1	GSKIP	GSK3B interacting protein	4.11	10.05	8.02	0.38	0.46	6.44E-05	5.30E-03	Multiple_Complex
TC1400010749.hg.1	LINC01599	long intergenic non-protein coding RNA 1599	4.09	7.77	5.74	0.95	0.17	2.00E-04	7.30E-03	Multiple_Complex
TC0900009685.hg.1	HACD4	3-hydroxyacyl-CoA dehydratase 4	4.07	6.7	4.68	0.01	0.55	2.99E-05	4.40E-03	Multiple_Complex
TC0200015136.hg.1	FRZB	frizzled-related protein	4	8.55	6.55	0.84	0.01	1.00E-04	5.80E-03	Coding
TC1400007039.hg.1	FANCM	Fanconi anemia complementation group M	4	13.1	11.1	0.29	0.13	1.35E-05	4.20E-03	Multiple_Complex
TC1600007524.hg.1	PYCARD-AS1	PYCARD antisense RNA 1	4	6.6	4.6	0.17	0	4.74E-06	3.40E-03	NonCoding

TC0900010390.hg.1	ABHD17B	abhydrolase domain containing 17B	3.98	9.18	7.19	0.51	0.2	1.37E-05	4.20E-03	Multiple_Complex
TC0700006928.hg.1	CCDC126	coiled-coil domain containing 126	3.98	13.38	11.39	0.07	0.52	7.39E-05	5.40E-03	Multiple_Complex
TC0100017788.hg.1	TARBP1	TAR (HIV-1) RNA binding protein 1	3.93	12.29	10.32	0.01	0.43	1.75E-05	4.30E-03	Multiple_Complex
TC1000010870.hg.1	SRGN	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_002727	3.93	8.69	6.71	0.61	0.07	2.69E-05	4.30E-03	NonCoding
TC0800011148.hg.1	CCNE2	cyclin E2	3.91	11.04	9.07	0.27	0.22	9.73E-06	3.80E-03	Multiple_Complex
TC0400007923.hg.1	MRPL1	mitochondrial ribosomal protein L1	3.9	10.36	8.39	0.01	0.12	9.71E-05	5.80E-03	Multiple_Complex
TC1000012480.hg.1	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	3.9	7.8	5.83	0.04	0.42	1.63E-05	4.20E-03	Coding
TC0200015330.hg.1	C2orf66	chromosome 2 open reading frame 66	3.89	8.15	6.19	0.12	0.03	1.97E-06	2.80E-03	Coding
TC0300012764.hg.1	HLTF	helicase-like transcription factor	3.84	11.86	9.91	0.08	0.59	6.22E-05	5.20E-03	Multiple_Complex
TC0500013298.hg.1	C1QTNF3	C1q and tumor necrosis factor related protein 3	3.84	6.51	4.57	0.01	0.22	2.53E-05	4.30E-03	Multiple_Complex
TC2000009905.hg.1	EFCAB8	EF-hand calcium binding domain 8	3.81	7.95	6.02	0.45	0.78	2.00E-04	7.30E-03	Coding
TC1200009220.hg.1	CCDC62	coiled-coil domain containing 62	3.81	8.7	6.77	0.3	0.12	1.27E-05	4.20E-03	Multiple_Complex
TC0800011259.hg.1	ANKRD46	ankyrin repeat domain 46	3.8	11.15	9.22	0.21	0.55	6.69E-05	5.30E-03	Multiple_Complex
TC0100018239.hg.1	GIPC2	GIPC PDZ domain containing family, member 2	3.79	6.99	5.07	0.57	0.1	6.00E-04	1.16E-02	Coding
TC0X00007781.hg.1	ZNF711	zinc finger protein 711	3.78	12.07	10.15	0.09	0.45	1.13E-05	4.00E-03	Multiple_Complex
TC0100014846.hg.1	GTF2B	general transcription factor IIB	3.77	11.9	9.99	0.12	0.26	4.87E-06	3.40E-03	Multiple_Complex
TC0400006930.hg.1	CPEB2	cytoplasmic polyadenylation element binding protein 2	3.77	9.35	7.43	0.41	0.16	1.55E-05	4.20E-03	Multiple_Complex
TC0500007494.hg.1	RAB3C	RAB3C, member RAS oncogene family	3.76	9.91	8	0.04	0.26	4.50E-06	3.40E-03	Multiple_Complex
TC0300007720.hg.1	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	3.75	11.64	9.73	0.2	0.49	3.39E-05	4.50E-03	Multiple_Complex
TC1000009536.hg.1	IDI1	isopentenyl-diphosphate delta isomerase 1	3.75	13.97	12.07	0.26	0.45	2.68E-05	4.30E-03	Multiple_Complex

TC0900009914.hg.1	CCL27	chemokine (C-C motif) ligand 27	3.73	11.26	9.36	0.13	0.33	9.32E-05	5.70E-03	Multiple_Complex
TC0100014626.hg.1	ASB17	ankyrin repeat and SOCS box containing 17	3.73	6.57	4.67	0.17	0.58	5.77E-05	5.20E-03	Multiple_Complex
TC0300011852.hg.1	IMPG2	interphotoreceptor matrix proteoglycan 2	3.7	7.21	5.32	0	0.28	2.75E-05	4.30E-03	Multiple_Complex
TC0900009513.hg.1	TMEM261	transmembrane protein 261	3.69	14.23	12.35	0.07	0.72	2.00E-04	7.00E-03	Multiple_Complex
TC1100010942.hg.1	OR5B2	olfactory receptor, family 5, subfamily B, member 2	3.68	6.55	4.67	1.03	0.01	5.00E-04	1.07E-02	Coding
TC0400012961.hg.1	NUDT6	nudix hydrolase 6	3.67	10.8	8.92	0.06	0.34	8.44E-06	3.70E-03	Multiple_Complex
TC0X00008097.hg.1	NXT2	nuclear transport factor 2-like export factor 2	3.66	11.62	9.75	0.14	0.37	2.84E-05	4.30E-03	Coding
TC0500010640.hg.1	C5orf28	chromosome 5 open reading frame 28	3.66	9.7	7.83	0.25	0.36	2.00E-04	6.70E-03	Multiple_Complex
TC1400006509.hg.1	OR11H7	olfactory receptor, family 11, subfamily H, member 7 (gene/pseudogene)	3.64	5.87	4.01	0.44	0.31	5.11E-05	5.10E-03	Pseudogene
TC0800012363.hg.1	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	3.64	11.68	9.81	0.38	0.45	2.00E-04	7.30E-03	NonCoding
TC0300008082.hg.1	EPHA6	EPH receptor A6	3.64	7.87	6	0.47	0.11	2.04E-05	4.30E-03	Coding
TC0100008594.hg.1	ROR1	receptor tyrosine kinase-like orphan receptor 1	3.64	12.54	10.68	0.38	0.56	2.00E-04	7.10E-03	Multiple_Complex
TC2200009352.hg.1	LOC400927; CSNK1E	TPTE and PTEN homologous inositol lipid phosphatase pseudogene; Transcript Identified by AceView, Entrez Gene ID(s) 1454; 400927	3.62	12.31	10.46	0.08	0.05	3.00E-04	8.10E-03	Multiple_Complex
TC0200015350.hg.1	RFTN2	raftlin family member 2	3.61	5.86	4.01	0.07	0.06	8.90E-06	3.80E-03	Multiple_Complex
TC0500010924.hg.1	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif 6	3.6	9.81	7.96	0.06	0.2	2.33E-05	4.30E-03	Multiple_Complex
TC1100008673.hg.1	TMEM135	transmembrane protein 135	3.58	8.54	6.7	0.2	0.46	3.69E-05	4.70E-03	Multiple_Complex
TC0400007495.hg.1	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4	3.57	13.08	11.25	0.09	0.13	4.89E-05	5.00E-03	Multiple_Complex
TC0800011064.hg.1	CALB1	calbindin 1	3.57	7.16	5.33	0.53	0.36	1.40E-03	1.65E-02	Multiple_Complex

TC0100008653.hg.1	IL12RB2	interleukin 12 receptor, beta 2	3.56	10.74	8.9	0.2	0.3	1.52E-05	4.20E-03	Multiple_Complex
TC1100012020.hg.1	SESN3	Transcript Identified by AceView, Entrez Gene ID(s) 143686	3.55	5	3.17	0.17	0.15	1.74E-05	4.30E-03	Unassigned
TC1400009108.hg.1	POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	3.55	12.71	10.88	0.21	0.3	2.35E-05	4.30E-03	Multiple_Complex
TC0300013684.hg.1	TFRC	transferrin receptor	3.53	8.59	6.77	0.13	0.78	2.00E-04	6.50E-03	Multiple_Complex
TC0800011861.hg.1	LRRC6	leucine rich repeat containing 6	3.53	8.42	6.6	0.32	0.73	7.00E-04	1.16E-02	Multiple_Complex
TC1000010827.hg.1	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	3.52	12.6	10.79	0	0.44	3.00E-04	8.00E-03	Multiple_Complex
TC0X00008516.hg.1	CT45A1	cancer/testis antigen family 45, member A1	3.51	9.67	7.86	0.11	0.17	5.31E-06	3.40E-03	Coding
TC1100006925.hg.1	PDE3B	phosphodiesterase 3B, cGMP-inhibited	3.49	7.13	5.33	0.01	0.32	4.00E-04	9.50E-03	NonCoding
TC0900007576.hg.1	ANXA1	annexin A1	3.48	11.59	9.79	0.05	0.21	1.42E-05	4.20E-03	Multiple_Complex
TC0400008390.hg.1	LRIT3	leucine-rich repeat, immunoglobulin-like and transmembrane domains 3	3.48	7.1	5.31	0.25	0.35	4.90E-05	5.00E-03	Coding
TC0500010753.hg.1	CDC20B	cell division cycle 20B	3.47	6.46	4.66	0.12	0.34	2.22E-05	4.30E-03	Coding
TC0600013033.hg.1	TBC1D32	TBC1 domain family, member 32	3.47	9.96	8.17	0.16	0.18	1.66E-05	4.20E-03	Multiple_Complex
TC0900006739.hg.1	CNTLN	Transcript Identified by AceView, Entrez Gene ID(s) 54875	3.46	6.78	4.99	0.2	1.26	3.50E-03	2.73E-02	Unassigned
TC0X00008596.hg.1	CDR1; CDR1-AS	Memczak2013 ANTISENSE, CDS, coding, downstream_end, upstream_start, UTR3, UTR5 best transcript NM_004065; CDR1 antisense RNA; CDR1 antisense RNA [Source:HGNC Symbol;Acc:HGNC:48926]	3.46	14.13	12.34	0.05	0.38	1.00E-04	6.20E-03	NonCoding
TC0100017022.hg.1	GOLT1A	golgi transport 1A	3.45	7.72	5.93	0.51	0.34	8.94E-05	5.70E-03	Multiple_Complex
TC1600007985.hg.1	CETP	cholesteryl ester transfer protein, plasma	3.45	6.56	4.77	0.27	0.06	1.64E-05	4.20E-03	Multiple_Complex

TC1600007741.hg.1	PHKB	Transcript Identified by AceView, Entrez Gene ID(s) 5257	3.45	6.49	4.7	0.75	0.19	2.10E-03	2.02E-02	Unassigned
TC0200015221.hg.1	MSTN	myostatin	3.43	5.78	4	0.61	0.09	9.46E-05	5.70E-03	Coding
TC0700012293.hg.1	TMEM168	transmembrane protein 168	3.43	10.51	8.73	0.33	0.07	1.00E-04	6.20E-03	Multiple_Complex
TC1000011025.hg.1	PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme	3.42	10.38	8.61	0.02	0.54	9.09E-05	5.70E-03	Multiple_Complex
TC1200012606.hg.1	LRMP	lymphoid-restricted membrane protein	3.4	6.64	4.88	0.44	0.38	2.00E-04	6.70E-03	Multiple_Complex
TC0200016423.hg.1	SPDYA	speedy/RINGO cell cycle regulator family member A	3.4	6.67	4.91	0.14	0.03	1.07E-05	3.90E-03	Multiple_Complex
TC1400010620.hg.1	SNAPC1	small nuclear RNA activating complex polypeptide 1	3.4	13.03	11.27	0.06	0.31	2.47E-05	4.30E-03	Multiple_Complex
TC0500007457.hg.1	SETD9	SET domain containing 9	3.38	9.87	8.11	0.25	0.41	4.90E-05	5.00E-03	Multiple_Complex
TC1000007700.hg.1	UBE2D1	ubiquitin conjugating enzyme E2D 1	3.38	11.51	9.76	0.14	0.15	1.00E-04	5.80E-03	Multiple_Complex
TC1200008318.hg.1	METTL25	methyltransferase like 25	3.35	11.12	9.38	0.07	0.27	4.06E-05	4.80E-03	Multiple_Complex
TC0200007418.hg.1	SLC3A1	solute carrier family 3 (amino acid transporter heavy chain), member 1	3.35	6.99	5.24	0.1	0.62	8.83E-05	5.70E-03	Coding
TC1000007176.hg.1	MAP3K8	mitogen-activated protein kinase kinase kinase 8	3.34	8.04	6.3	0.04	0.45	5.89E-05	5.20E-03	Multiple_Complex
TC0200009789.hg.1	07-Mar	membrane associated ring finger 7	3.33	10.59	8.86	0.03	0.68	2.00E-04	7.60E-03	Multiple_Complex
TC1200007161.hg.1	MRPS35	mitochondrial ribosomal protein S35	3.32	9.79	8.06	0.41	0.48	2.00E-04	7.10E-03	Multiple_Complex
TC0600013796.hg.1	AGPAT4	Transcript Identified by AceView, Entrez Gene ID(s) 56895	3.32	6.71	4.98	0.29	0.36	2.70E-03	2.35E-02	Unassigned
TC0100016828.hg.1	F13B	coagulation factor XIII, B polypeptide	3.32	6.15	4.42	0.79	0.02	5.00E-04	1.03E-02	Multiple_Complex
TC0200008536.hg.1	ANKRD36	Transcript Identified by AceView, Entrez Gene ID(s) 375248	3.32	11.89	10.16	0.19	0.31	4.00E-04	9.40E-03	Unassigned
TC1500007304.hg.1	C15orf65	chromosome 15 open reading frame 65	3.31	9.97	8.25	0.23	0.41	7.37E-05	5.40E-03	Multiple_Complex
TC0800010490.hg.1	TMEM68	transmembrane protein 68	3.31	10.26	8.53	0.28	0.05	2.12E-05	4.30E-03	Multiple_Complex

TC0400010609.hg.1	CORIN	corin, serine peptidase	3.31	7.96	6.23	0.53	0.08	1.00E-04	5.80E-03	Multiple_Complex
TC0100008588.hg.1	EFCAB7; DLEU2L	EF-hand calcium binding domain 7; deleted in lymphocytic leukemia 2-like	3.3	11.7	9.98	0.24	0.52	3.00E-04	8.60E-03	Multiple_Complex
TC1300007969.hg.1	ABHD13	abhydrolase domain containing 13	3.3	10.52	8.8	0.04	0.43	4.00E-04	9.60E-03	Coding
TC0200015332.hg.1	PGAP1	post-GPI attachment to proteins 1	3.3	12.19	10.47	0.01	0.19	5.77E-05	5.20E-03	Multiple_Complex
TC0800007439.hg.1	POLB	polymerase (DNA directed), beta	3.29	13.12	11.4	0.15	0.36	4.51E-05	4.90E-03	Multiple_Complex
TC1100008651.hg.1	TMEM126B	transmembrane protein 126B	3.29	13.87	12.15	0.18	0.38	6.67E-05	5.30E-03	Coding
TC0500013225.hg.1	CDC42SE2	CDC42 small effector 2	3.29	6.04	4.32	0.93	0.13	7.00E-04	1.21E-02	NonCoding
TC1200009547.hg.1	SLC6A13	solute carrier family 6 (neurotransmitter transporter), member 13	3.28	6.59	4.88	0.3	0.24	7.63E-05	5.50E-03	Multiple_Complex
TC1200006454.hg.1	WNK1	Transcript Identified by AceView, Entrez Gene ID(s) 378465; 65125	3.28	8.45	6.73	0.31	0.29	4.00E-04	9.50E-03	Unassigned
TC0800010685.hg.1	MYBL1	v-myb avian myeloblastosis viral oncogene homolog-like 1	3.28	10.69	8.97	0.29	0.17	8.47E-05	5.60E-03	Multiple_Complex
TC0400008834.hg.1	SCOC	short coiled-coil protein	3.28	11.83	10.12	0.09	0.08	3.00E-04	8.20E-03	Coding
TC0500007465.hg.1	GPBP1	GC-rich promoter binding protein 1	3.26	13.14	11.44	0.07	0.24	2.30E-05	4.30E-03	Multiple_Complex
TC0X00010914.hg.1	CT45A7; CT45A6	cancer/testis antigen family 45, member A7; cancer/testis antigen family 45, member A6	3.26	10.03	8.33	0.15	0.02	8.00E-04	1.26E-02	Coding
TC0500010731.hg.1	ARL15	ADP-ribosylation factor like GTPase 15	3.26	10.12	8.41	0.72	0.72	1.60E-03	1.74E-02	Multiple_Complex
TC1200010903.hg.1	ANKRD52	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_173595	3.25	7.91	6.21	0.46	1	2.20E-03	2.08E-02	NonCoding
TC0400009503.hg.1	PRIMPOL	primase and DNA directed polymerase	3.24	10.52	8.83	0.02	0.07	1.00E-04	5.80E-03	Multiple_Complex
TC1300007344.hg.1	TDRD3	tudor domain containing 3	3.23	9.93	8.24	0.11	0.66	4.00E-04	9.30E-03	Multiple_Complex

TC0500008568.hg.1	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporter), member 2	3.23	10.98	9.29	0.04	0.45	1.00E-04	5.80E-03	Multiple_Complex
TC0900008316.hg.1	FKTN	fukutin	3.2	10.6	8.92	0.01	0.24	1.00E-04	5.80E-03	Multiple_Complex
TC1200012804.hg.1	PRIM1	primase, DNA, polypeptide 1 (49kDa)	3.2	9.96	8.28	0.28	0.19	2.00E-04	7.30E-03	Multiple_Complex
TC0300008536.hg.1	EAF2	ELL associated factor 2	3.2	11.17	9.49	0.07	0.03	6.93E-06	3.40E-03	Multiple_Complex
TC1200011423.hg.1	TSPAN19	tetraspanin 19	3.2	8.13	6.45	0.07	0.56	3.00E-04	8.00E-03	Multiple_Complex
TC0X00010917.hg.1	CT45A8	cancer/testis antigen family 45, member A8	3.19	9.77	8.1	0.14	0.18	1.00E-04	5.80E-03	Coding
TC0X00010918.hg.1	CT45A9	cancer/testis antigen family 45, member A9	3.19	9.77	8.1	0.14	0.18	1.00E-04	5.80E-03	Coding
TC1400006965.hg.1	GEMIN2	gem nuclear organelle associated protein 2	3.19	13.12	11.44	0.1	0.3	2.00E-04	6.70E-03	Multiple_Complex
TC1200012612.hg.1	MED21	mediator complex subunit 21	3.18	12.13	10.46	0.19	0.34	2.00E-04	6.30E-03	Multiple_Complex
TC0200016757.hg.1	NCKAP1	NCK-associated protein 1	3.17	11.03	9.37	0.14	0.28	1.00E-04	6.30E-03	Multiple_Complex
TC1200012753.hg.1	KLRC2	killer cell lectin-like receptor subfamily C, member 2	3.17	6.15	4.49	0.23	0.19	1.00E-04	6.20E-03	Coding
TC0100014562.hg.1	LRRC40	leucine rich repeat containing 40	3.17	11.78	10.12	0.21	0.24	2.00E-04	7.30E-03	Multiple_Complex
TC0200011974.hg.1	SF3B6	splicing factor 3b subunit 6	3.17	15.59	13.93	0.04	0.73	1.30E-03	1.55E-02	Multiple_Complex
TC0300009597.hg.1	PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	3.16	9.2	7.54	0.29	0.01	2.47E-05	4.30E-03	Multiple_Complex
TC1100012219.hg.1	SLC35F2	solute carrier family 35, member F2	3.16	11.17	9.51	0.12	0.35	2.74E-05	4.30E-03	Multiple_Complex
TC0X00010919.hg.1	CT45A10	cancer/testis antigen family 45, member A10	3.15	10.99	9.34	0.16	0.19	1.00E-04	5.80E-03	Coding
TC1600010347.hg.1	RPGRIP1L	RPGRIP1-like	3.15	12.31	10.65	0.09	0.49	1.10E-03	1.43E-02	Multiple_Complex
TC0700009215.hg.1	EXOC4	exocyst complex component 4	3.14	6.84	5.19	0.29	0.18	2.19E-05	4.30E-03	NonCoding
TC0600008262.hg.1	TMEM14A	transmembrane protein 14A	3.14	12.52	10.87	0.16	0.12	5.70E-05	5.20E-03	Multiple_Complex
TC0400012952.hg.1	BDH2	3-hydroxybutyrate dehydrogenase, type 2	3.12	9.08	7.44	0.44	0.48	1.80E-03	1.85E-02	Multiple_Complex

TC1200007053.hg.1	SPX	spexin hormone	3.12	10.19	8.55	0.36	0.39	2.00E-04	7.60E-03	Multiple_Complex
TC0800012457.hg.1	TMEM65	transmembrane protein 65	3.11	11.66	10.02	0.19	0.18	2.00E-04	6.40E-03	Multiple_Complex
TC1200012819.hg.1	TMBIM4	transmembrane BAX inhibitor motif containing 4	3.11	11.38	9.74	0.24	0.38	1.00E-04	6.20E-03	Multiple_Complex
TC1200007105.hg.1	LYRM5	LYR motif containing 5	3.11	12.23	10.59	0.23	0.18	2.58E-05	4.30E-03	Multiple_Complex
TC0700013581.hg.1	STEAP4	STEAP family member 4	3.11	5.89	4.25	0.23	0.76	1.20E-03	1.53E-02	Coding
TC0100008897.hg.1	WDR63	WD repeat domain 63	3.08	8.57	6.95	0.53	0.62	1.10E-03	1.47E-02	Multiple_Complex
TC0100014502.hg.1	WDR78	WD repeat domain 78	3.07	8.96	7.34	0.14	0.1	1.30E-03	1.57E-02	Multiple_Complex
TC0400012068.hg.1	PRMT9	protein arginine methyltransferase 9	3.07	9.06	7.44	0.32	0.24	6.00E-04	1.15E-02	Multiple_Complex
TC0100009899.hg.1	C1orf54	chromosome 1 open reading frame 54	3.06	12.53	10.92	0.24	0.42	7.31E-05	5.40E-03	Multiple_Complex
TC0X00010910.hg.1	CT45A3; CT45A4; CT45A5	cancer/testis antigen family 45, member A3; cancer/testis antigen family 45, member A4; cancer/testis antigen family 45, member A5	3.06	9.92	8.3	0.2	0.07	2.80E-03	2.39E-02	Coding
TC1900006768.hg.1	CATSPERD	catsper channel auxiliary subunit delta	3.06	5.53	3.92	0.13	0.17	3.25E-05	4.50E-03	Multiple_Complex
TC0300012007.hg.1	CD200R1	CD200 receptor 1	3.06	5.43	3.82	0.33	0.29	5.28E-05	5.10E-03	Coding
TC1100009431.hg.1	PATE4	prostate and testis expressed 4	3.06	6.92	5.3	0.41	0.54	6.00E-04	1.10E-02	Multiple_Complex
TC1400008940.hg.1	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	3.06	8.37	6.76	0.14	0.38	5.70E-05	5.20E-03	Multiple_Complex
TC0100011549.hg.1	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	3.06	11.18	9.57	0.1	0.45	1.00E-04	5.80E-03	Multiple_Complex
TC0X00010915.hg.1	CT45A2	cancer/testis antigen family 45, member A2	3.05	9.08	7.47	0.17	0.18	2.00E-04	7.30E-03	Coding
TC1000011885.hg.1	DCLRE1A	DNA cross-link repair 1A	3.05	12.82	11.21	0.01	0.24	5.40E-05	5.20E-03	Multiple_Complex
TC1800006487.hg.1	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	3.05	10.73	9.13	0.22	0.53	1.00E-04	6.20E-03	Multiple_Complex

TC0600009445.hg.1	SMLR1	small leucine-rich protein 1	3.05	7.08	5.47	1.13	0.1	2.40E-03	2.16E-02	Multiple_Complex
TC0100009329.hg.1	FNDC7	fibronectin type III domain containing 7	3.05	6.77	5.16	0.17	0.43	6.15E-05	5.20E-03	Multiple_Complex
TC1100012961.hg.1	AMPD3	adenosine monophosphate deaminase 3	3.05	5.81	4.2	0.62	0.61	1.20E-03	1.50E-02	Multiple_Complex
TC1800007895.hg.1	METTL4	methyltransferase like 4	3.04	12.44	10.84	0.1	0.12	3.72E-05	4.70E-03	Multiple_Complex
TC0800011595.hg.1	EXT1; hunera	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_000127; Transcript Identified by AceView	3.04	7.11	5.5	0.52	0.07	2.00E-04	6.90E-03	NonCoding
TC0900008202.hg.1	TGFBR1	transforming growth factor, beta receptor 1	3.02	8.73	7.14	0.49	0.37	5.00E-04	1.00E-02	Multiple_Complex
TC0900007069.hg.1	C9orf131	chromosome 9 open reading frame 131	3.02	6.45	4.85	0.04	0.18	6.69E-05	5.30E-03	Coding
TC0300009035.hg.1	TRPC1	transient receptor potential cation channel, subfamily C, member 1	3.02	11.78	10.18	0.17	0.53	4.00E-04	9.20E-03	Multiple_Complex
TC0500011751.hg.1	FEM1C	fem-1 homolog c (C. elegans)	3.02	8.35	6.76	0.62	0.1	3.00E-04	8.10E-03	Multiple_Complex
TC1000011520.hg.1	OPALIN	oligodendrocytic myelin paranodal and inner loop protein	3.02	7.33	5.74	0.59	0.43	1.30E-03	1.56E-02	Multiple_Complex
TC0200010582.hg.1	FASTKD2	FAST kinase domains 2	3.01	10.55	8.96	0.28	0.52	3.00E-04	8.20E-03	Multiple_Complex
TC0500008586.hg.1	ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif 19	3	7.75	6.16	0.56	0.38	5.00E-04	1.04E-02	Multiple_Complex
TC0800010427.hg.1	RB1CC1	RB1-inducible coiled-coil 1	3	11.23	9.64	0.12	0.49	2.00E-04	7.10E-03	Multiple_Complex
TC1200007954.hg.1	USP15; MIR6125	ubiquitin specific peptidase 15; microRNA 6125	2.99	13.39	11.81	0.06	0.89	1.30E-03	1.54E-02	Multiple_Complex
TC0600007387.hg.1	OR2B6	olfactory receptor, family 2, subfamily B, member 6	2.99	8.13	6.55	0.24	0.13	2.65E-05	4.30E-03	Coding
TC0500009411.hg.1	RANBP17	RAN binding protein 17	2.99	14.56	12.99	0.2	0.54	7.00E-04	1.16E-02	Multiple_Complex
TC2000006631.hg.1	CRLS1	cardiolipin synthase 1	2.99	12.92	11.35	0.03	0.48	6.00E-04	1.09E-02	Multiple_Complex
TC1100008985.hg.1	ATM	ATM serine/threonine kinase	2.98	13.67	12.1	0.29	0.38	2.00E-04	7.40E-03	Multiple_Complex

TC0100014895.hg.1	ZNF644	zinc finger protein 644	2.97	11.37	9.8	0.06	0.33	7.18E-05	5.40E-03	Multiple_Complex
TC0300011853.hg.1	SENP7	SUMO1/sentrin specific peptidase 7	2.97	9.27	7.7	0.11	0.58	1.00E-04	6.20E-03	Multiple_Complex
TC1100006923.hg.1	PDE3B	phosphodiesterase 3B, cGMP-inhibited	2.97	8.96	7.39	0.27	0.32	4.00E-04	9.30E-03	Multiple_Complex
TC0500010865.hg.1	DEPDC1B	DEP domain containing 1B	2.96	12.01	10.45	0.2	0.19	7.41E-05	5.40E-03	Multiple_Complex
TC0900009692.hg.1	IFNA21	interferon, alpha 21	2.96	5.76	4.19	0.01	0.02	4.16E-05	4.80E-03	Coding
TC0900008297.hg.1	NIPSNAP3A; NIPSNAP3B	nipsnap homolog 3A (C. elegans); nipsnap homolog 3B (C. elegans)	2.96	7.26	5.7	0.23	0.12	1.00E-04	5.90E-03	Multiple_Complex
TC0X00010912.hg.1	CT45A5	cancer/testis antigen family 45, member A5	2.96	9.62	8.06	0.08	0.13	1.30E-03	1.57E-02	Coding
TC1200008026.hg.1	LEMD3	LEM domain containing 3	2.95	12.27	10.71	0.53	0.43	5.00E-04	1.06E-02	Multiple_Complex
TC0900010386.hg.1	TMEM2	transmembrane protein 2	2.95	8.86	7.3	0.14	0.14	1.87E-05	4.30E-03	Multiple_Complex
TC0800011633.hg.1	MRPL13	mitochondrial ribosomal protein L13	2.95	13.45	11.9	0.04	0.29	9.22E-05	5.70E-03	Multiple_Complex
TC0100018006.hg.1	ADSS	adenylosuccinate synthase	2.94	11.21	9.65	0.37	0.44	3.00E-04	8.00E-03	Multiple_Complex
TC1200010598.hg.1	RND1	Rho family GTPase 1	2.94	8.83	7.28	0.32	0.37	3.00E-04	7.90E-03	Multiple_Complex
TC1500007318.hg.1	TEX9	testis expressed 9	2.94	8.58	7.02	0.41	0.18	2.00E-04	6.70E-03	Multiple_Complex
TC1700006899.hg.1	MAP2K4; MIR744	mitogen-activated protein kinase kinase 4; microRNA 744	2.94	14.59	13.04	0.3	0.44	9.00E-04	1.30E-02	Multiple_Complex
TC0300008550.hg.1	CSTA	cystatin A (stefin A)	2.94	7.08	5.53	0.08	0.33	1.00E-04	5.90E-03	Multiple_Complex
TC0200007273.hg.1	RMDN2	regulator of microtubule dynamics 2	2.93	7.84	6.29	0.23	0.44	1.00E-04	6.10E-03	Multiple_Complex
TC1800008231.hg.1	ESCO1	establishment of sister chromatid cohesion N-acetyltransferase 1	2.93	11.73	10.18	0.04	0.23	8.49E-05	5.60E-03	Multiple_Complex
TC0400008376.hg.1	SEC24B	SEC24 homolog B, COPII coat complex component	2.93	10.54	8.98	0.02	0.28	3.98E-05	4.80E-03	Multiple_Complex
TC0500007667.hg.1	MRPS36	mitochondrial ribosomal protein S36	2.93	13.5	11.95	0.08	0.35	1.00E-04	5.80E-03	Multiple_Complex
TC0900011199.hg.1	OR2K2	olfactory receptor, family 2, subfamily K, member 2	2.93	6.22	4.67	0.18	0.58	2.00E-04	7.00E-03	Coding

TC0400012949.hg.1	SLC39A8	solute carrier family 39 (zinc transporter), member 8	2.93	11.55	10	0.03	0.17	2.00E-04	6.70E-03	Multiple_Complex
TC1400010776.hg.1	CATSPERB	catsper channel auxiliary subunit beta	2.93	5.61	4.06	0.16	0.12	2.20E-05	4.30E-03	Multiple_Complex
TC0600014136.hg.1	ADGRF4	adhesion G protein-coupled receptor F4	2.93	5.92	4.37	0.4	0.07	5.69E-05	5.20E-03	Coding
TC1400009579.hg.1	ADAM20	ADAM metallopeptidase domain 20	2.92	6.32	4.77	0.25	0.13	4.23E-05	4.90E-03	Coding
TC0100015180.hg.1	WDR47	WD repeat domain 47	2.92	12.47	10.92	0.21	0.26	1.00E-04	6.30E-03	Multiple_Complex
TC0100015750.hg.1	HORMAD1	HORMA domain containing 1	2.92	5.58	4.03	0.26	0.16	1.80E-03	1.88E-02	Multiple_Complex
TC1000007871.hg.1	STOX1	storkhead box 1	2.92	9.74	8.19	0.04	0.1	2.00E-04	6.60E-03	Coding
TC0400012945.hg.1	HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	2.92	13	11.46	0.14	0.08	4.52E-05	4.90E-03	Multiple_Complex
TC1200010156.hg.1	CASC1	cancer susceptibility candidate 1	2.91	6.23	4.69	0.31	0.62	6.00E-04	1.07E-02	Multiple_Complex
TC0200007132.hg.1	YPEL5	yippee like 5	2.91	12.43	10.89	0.05	0.32	3.00E-04	7.70E-03	Multiple_Complex
TC1200011722.hg.1	PMCH	pro-melanin-concentrating hormone	2.91	10.31	8.77	0.31	0.53	1.40E-03	1.62E-02	Coding
TC0X00010355.hg.1	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	2.9	8.6	7.06	0.22	0.69	1.00E-03	1.40E-02	Multiple_Complex
TC1400008622.hg.1	OR5AU1	olfactory receptor, family 5, subfamily AU, member 1	2.9	6.65	5.11	0.09	0	1.00E-04	6.10E-03	Coding
TC1200010690.hg.1	CSRNP2	cysteine-serine-rich nuclear protein 2	2.9	8.57	7.03	0.28	0.07	9.20E-05	5.70E-03	Multiple_Complex
TC0600012976.hg.1	GPRC6A	G protein-coupled receptor, class C, group 6, member A	2.9	5.05	3.52	0.47	0.21	1.00E-04	5.90E-03	Coding
TC1400006446.hg.1	OR11H12	olfactory receptor, family 11, subfamily H, member 12	2.9	7.67	6.14	0.29	0.16	8.00E-04	1.26E-02	Coding
TC1000007226.hg.1	CCDC7	coiled-coil domain containing 7	2.9	8.3	6.76	0.51	0.33	1.00E-03	1.36E-02	Multiple_Complex
TC0700006931.hg.1	FAM221A	family with sequence similarity 221, member A	2.89	10.12	8.59	0.15	0.03	4.07E-05	4.80E-03	Multiple_Complex
TC1100010156.hg.1	BTBD10	BTB (POZ) domain containing 10	2.89	10.36	8.83	0.22	0.08	6.59E-05	5.30E-03	Multiple_Complex
TC1300008424.hg.1	USP12	ubiquitin specific peptidase 12	2.89	9.71	8.18	0.08	0.31	7.71E-05	5.50E-03	Multiple_Complex
TC1200010968.hg.1	DDIT3	DNA-damage-inducible transcript 3	2.89	11.99	10.46	0.1	0.26	3.00E-04	8.00E-03	Coding

TC1600008889.hg.1	CPNE7	copine VII	2.89	7.99	6.46	0.15	0.31	1.90E-03	1.90E-02	Multiple_Complex
TC1100006812.hg.1	ZNF143	zinc finger protein 143	2.88	14.75	13.23	0.17	0.45	2.00E-04	6.30E-03	Multiple_Complex
TSUnmapped00000134.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	2.88	11.44	9.92	0.06	0.65	8.00E-04	1.27E-02	NonCoding
TC0300008539.hg.1	SLC15A2	solute carrier family 15 (oligopeptide transporter), member 2	2.87	7.75	6.23	0.45	0.11	2.00E-04	7.10E-03	Multiple_Complex
TC1400010755.hg.1	PSMA3-AS1	PSMA3 antisense RNA 1	2.87	14.07	12.55	0.01	0.21	2.00E-04	7.10E-03	Multiple_Complex
TC0400010171.hg.1	LCORL	Transcript Identified by AceView, Entrez Gene ID(s) 254251	2.87	5.64	4.11	1.14	0.06	8.70E-03	4.90E-02	Coding
TC0100014927.hg.1	EVI5	ecotropic viral integration site 5	2.87	13.97	12.45	0.05	0.14	2.00E-04	6.70E-03	Multiple_Complex
TC0800008531.hg.1	EMC2	ER membrane protein complex subunit 2	2.86	14.28	12.76	0.21	0.39	1.00E-04	5.90E-03	Multiple_Complex
TC0400012027.hg.1	ANAPC10	anaphase promoting complex subunit 10	2.86	11.41	9.89	0.1	0.43	7.00E-04	1.17E-02	Multiple_Complex
TC0800009764.hg.1	PSD3	pleckstrin and Sec7 domain containing 3	2.86	9.92	8.41	0.2	0.81	1.50E-03	1.67E-02	Multiple_Complex
TC0900008238.hg.1	MURC	muscle-related coiled-coil protein	2.85	7.28	5.77	0.19	0.06	8.00E-04	1.25E-02	Coding
TC1800009215.hg.1	ANKRD12	ankyrin repeat domain 12	2.85	11.41	9.9	0.55	0.26	8.00E-04	1.24E-02	Multiple_Complex
TC0X00010916.hg.1	CT45A6; CT45A7	cancer/testis antigen family 45, member A6; cancer/testis antigen family 45, member A7	2.84	9.53	8.02	0.01	0.14	4.30E-03	3.10E-02	Coding
TC0100010651.hg.1	LOC730159; RP11-360D2.1	uncharacterized LOC730159; putative novel transcript	2.84	6.76	5.25	0.45	0.47	5.00E-04	1.07E-02	Multiple_Complex
TC0200015601.hg.1	KANSL1L	KAT8 regulatory NSL complex subunit 1 like	2.84	11.01	9.51	0.02	0.16	5.02E-05	5.00E-03	Multiple_Complex
TC0400012856.hg.1	RAPGEF2	Rap guanine nucleotide exchange factor 2	2.84	7.81	6.3	0.21	0.29	1.00E-04	5.80E-03	NonCoding
TC0400012618.hg.1	CASP3	caspase 3	2.83	12.38	10.88	0.01	0.42	2.00E-04	6.60E-03	Multiple_Complex
TC0200016464.hg.1	APLF	aprataxin and PNKP like factor	2.83	12.35	10.85	0.05	0.4	4.40E-03	3.13E-02	Multiple_Complex
TC0X00009384.hg.1	DYNLT3	dynein, light chain, Tctex-type 3	2.82	11.21	9.71	0.04	0.47	8.00E-04	1.26E-02	Coding

TC0900011192.hg.1	LPAR1	lysophosphatidic acid receptor 1	2.82	9.89	8.39	0.55	0.69	1.40E-03	1.61E-02	Multiple_Complex
TC0300010474.hg.1	PP2D1	protein phosphatase 2C-like domain containing 1	2.82	6.87	5.38	0.02	0.03	1.82E-05	4.30E-03	Multiple_Complex
TC0600012731.hg.1	ATG5	autophagy related 5	2.82	11.28	9.78	0.01	0.24	1.00E-04	5.80E-03	Multiple_Complex
TC0600014321.hg.1	SNX14	sorting nexin 14	2.82	11.81	10.32	0.03	0.36	1.00E-04	6.20E-03	Multiple_Complex
TC0X00010880.hg.1	MOSPD1	motile sperm domain containing 1	2.82	10.97	9.47	0.12	0.33	6.00E-04	1.07E-02	Multiple_Complex
TC1100008665.hg.1	CCDC81	coiled-coil domain containing 81	2.81	7.57	6.08	0.01	0.37	6.13E-05	5.20E-03	Multiple_Complex
TC0100010674.hg.1	GPR52	G protein-coupled receptor 52	2.81	7.27	5.78	0.15	0.07	7.71E-05	5.50E-03	Coding
TC0100009116.hg.1	RWDD3; TMEM56; TMEM56-RWDD3	RWD domain containing 3; transmembrane protein 56; TMEM56-RWDD3 readthrough	2.81	9.44	7.95	0.22	0.32	1.00E-04	5.80E-03	Multiple_Complex
TC0X00010196.hg.1	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	2.81	9.56	8.07	0.3	1	3.90E-03	2.91E-02	Multiple_Complex
TC0500011554.hg.1	CHD1	chromodomain helicase DNA binding protein 1	2.81	14.01	12.52	0.15	0.49	4.00E-04	9.60E-03	Multiple_Complex
TC1200008591.hg.1	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	2.81	12.33	10.84	0.01	0.24	3.00E-04	8.00E-03	Multiple_Complex
TC0900012228.hg.1	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)	2.81	14.51	13.02	0	0.43	2.00E-04	7.20E-03	Multiple_Complex
TC1400008767.hg.1	STXBP6	syntaxin binding protein 6 (amisyn)	2.8	9.79	8.3	0.3	0.47	5.00E-04	9.90E-03	Multiple_Complex
TC0700013585.hg.1	LRRD1	leucine-rich repeats and death domain containing 1	2.8	4.92	3.43	0.64	0.18	4.00E-04	9.50E-03	Coding
TC0100018068.hg.1	TFB2M	transcription factor B2, mitochondrial	2.8	10.61	9.12	0.15	0.47	2.00E-04	6.70E-03	Multiple_Complex
TC0500007927.hg.1	RASGRF2	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_006909	2.79	5.44	3.96	0.32	0.32	1.00E-04	5.80E-03	NonCoding
TC0600009446.hg.1	AKAP7	A kinase (PRKA) anchor protein 7	2.79	7.3	5.82	0.32	0.43	1.40E-03	1.62E-02	Multiple_Complex
TC1100012000.hg.1	GPR83	G protein-coupled receptor 83	2.78	5.56	4.09	0.38	0.23	1.00E-04	6.00E-03	Multiple_Complex
TC0X00008228.hg.1	DOCK11	dedicator of cytokinesis 11	2.78	11.25	9.78	0.13	0.21	1.00E-03	1.42E-02	Multiple_Complex

TC1900011908.hg.1	PDE4C	phosphodiesterase 4C, cAMP-specific	2.78	8.4	6.92	0.05	0.57	1.20E-03	1.51E-02	Multiple_Complex
TC0400010078.hg.1	RAB28	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_004249	2.78	7.13	5.66	0.05	0.5	2.00E-04	7.60E-03	NonCoding
TC0500009424.hg.1	FGF18	fibroblast growth factor 18	2.78	7.3	5.83	0.63	0.15	9.00E-04	1.35E-02	Coding
TC1200010518.hg.1	SLC38A2	solute carrier family 38, member 2	2.78	13.27	11.8	0.12	0.09	3.10E-05	4.40E-03	Multiple_Complex
TC1000006995.hg.1	COMMD3-BMI1; BMI1; COMMD3	COMMD3-BMI1 readthrough; BMI1 proto-oncogene, polycomb ring finger; COMM domain containing 3	2.77	10.01	8.54	0.4	0.16	2.50E-03	2.26E-02	Multiple_Complex
TC0100016711.hg.1	PDC	phosducin	2.77	6.99	5.52	0.09	0.16	5.00E-04	1.02E-02	Coding
TC0700012456.hg.1	IQUB	IQ motif and ubiquitin domain containing	2.77	7.54	6.08	0.66	0.05	5.00E-04	1.07E-02	Multiple_Complex
TC0400010895.hg.1	TMPRSS11D	transmembrane protease, serine 11D	2.76	6.79	5.33	0.32	0.08	4.00E-04	9.70E-03	Multiple_Complex
TC0500008846.hg.1	IGIP	IgA-inducing protein	2.76	10.97	9.51	0.26	0.09	1.40E-03	1.60E-02	Coding
TC0200011990.hg.1	PTRHD1	peptidyl-tRNA hydrolase domain containing 1	2.76	13.39	11.92	0.01	0.38	3.00E-04	8.30E-03	Multiple_Complex
TC0100018453.hg.1	ARHGAP29	Rho GTPase activating protein 29	2.76	5.19	3.73	0.09	0.24	5.70E-05	5.20E-03	NonCoding
TC0100009402.hg.1	CEPT1	choline/ethanolamine phosphotransferase 1	2.76	12.08	10.62	0.19	0.14	1.00E-04	6.20E-03	Multiple_Complex
TC0900009694.hg.1	IFNA4	interferon, alpha 4	2.75	6.74	5.28	0.11	0.33	1.00E-04	6.00E-03	Coding
TC0900009775.hg.1	EQTN	equatorin, sperm acrosome associated	2.75	6.69	5.23	0.02	0.08	5.00E-04	1.03E-02	Multiple_Complex
TC1900010008.hg.1	KIAA1683	KIAA1683	2.75	10.72	9.26	0.09	0.11	3.17E-05	4.50E-03	Multiple_Complex
TC0100011091.hg.1	C1orf53	chromosome 1 open reading frame 53	2.75	9.67	8.21	0.16	0.08	6.00E-04	1.11E-02	Multiple_Complex
TC0800012333.hg.1	NDUFAF6	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	2.75	6.15	4.69	0	0.03	1.00E-04	5.80E-03	NonCoding
TC0500013360.hg.1	CDKL3	cyclin-dependent kinase-like 3	2.75	9.74	8.28	0.35	0.09	5.00E-04	1.07E-02	Multiple_Complex
TC2100007176.hg.1	PCP4	Purkinje cell protein 4	2.74	6.32	4.86	0.33	0.32	1.00E-04	5.80E-03	Multiple_Complex

TC0300012670.hg.1	ATR	ATR serine/threonine kinase	2.74	11.2	9.74	0.08	0.21	6.33E-05	5.30E-03	Multiple_Complex
TC0200013019.hg.1	MCEE	methylmalonyl CoA epimerase	2.74	9.07	7.62	0.27	0.34	8.00E-04	1.27E-02	Multiple_Complex
TC1700012440.hg.1	RNFT1	ring finger protein, transmembrane 1	2.74	9.94	8.49	0.45	0.57	6.00E-04	1.11E-02	Multiple_Complex
TC0700006945.hg.1	MPP6	membrane protein, palmitoylated 6	2.74	11.35	9.9	0.14	0.21	8.00E-04	1.27E-02	Multiple_Complex
TC0500010842.hg.1	PDE4D	phosphodiesterase 4D, cAMP-specific	2.74	8.85	7.39	0.03	0.33	2.00E-04	6.70E-03	Multiple_Complex
TC1300007484.hg.1	PIBF1	progesterone immunomodulatory binding factor 1	2.74	11.93	10.48	0.05	0.26	3.00E-04	8.30E-03	Multiple_Complex
TC0X00011403.hg.1	SPANXD	SPANX family, member D	2.73	6.63	5.18	0.67	0.29	7.00E-04	1.19E-02	Coding
TC0100014997.hg.1	ALG14	ALG14, UDP-N-acetylglucosaminyltransferase subunit	2.73	8.78	7.33	0.06	0.34	2.00E-04	7.40E-03	Multiple_Complex
TC0100018091.hg.1	ZNF124	zinc finger protein 124	2.73	9.26	7.81	0.15	0.02	1.00E-04	6.10E-03	Multiple_Complex
TC1400007204.hg.1	CGRRF1	cell growth regulator with ring finger domain 1	2.72	11.09	9.65	0.15	0.26	8.00E-04	1.27E-02	Multiple_Complex
TC0900012140.hg.1	PGM5	phosphoglucomutase 5	2.72	6.98	5.54	0.37	0.21	2.20E-03	2.06E-02	NonCoding
TC1900011769.hg.1	C5AR1	complement component 5a receptor 1	2.72	10	8.56	0.59	0.16	6.00E-04	1.10E-02	NonCoding
TC1200011470.hg.1	DUSP6	dual specificity phosphatase 6	2.72	7.76	6.32	0.19	0.59	5.00E-04	1.04E-02	Multiple_Complex
TC1100010055.hg.1	SCUBE2	signal peptide, CUB domain, EGF-like 2	2.71	6.09	4.65	0.01	0.48	1.40E-03	1.60E-02	Multiple_Complex
TC0700012479.hg.1	POT1	protection of telomeres 1	2.71	12.13	10.69	0.31	0.64	1.30E-03	1.58E-02	Multiple_Complex
TC0700007334.hg.1	MRPL32	mitochondrial ribosomal protein L32	2.71	13.59	12.15	0.25	0.21	2.00E-04	7.10E-03	Multiple_Complex
TC1500008023.hg.1	ZFAND6	zinc finger, AN1-type domain 6	2.71	13.34	11.91	0.08	0.27	3.00E-04	8.00E-03	Multiple_Complex
TC1700007498.hg.1	SUZ12	SUZ12 polycomb repressive complex 2 subunit	2.71	9.45	8.01	0.06	0.22	7.40E-05	5.40E-03	Multiple_Complex
TC0500011157.hg.1	GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2	2.71	7.73	6.29	0.08	0.19	7.02E-05	5.40E-03	Coding
TC0800012423.hg.1	PPP1R42	protein phosphatase 1, regulatory subunit 42	2.71	7.46	6.02	0.11	0.88	1.90E-03	1.90E-02	Multiple_Complex
TC0100011698.hg.1	DISP1	dispatched homolog 1 (Drosophila)	2.71	12.18	10.74	0	0.27	9.28E-05	5.70E-03	Multiple_Complex

TC0900010607.hg.1	AGTPBP1	ATP/GTP binding protein 1	2.7	11.34	9.9	0.15	0.04	5.00E-04	1.00E-02	Multiple_Complex
TC0700008321.hg.1	ANKIB1	ankyrin repeat and IBR domain containing 1	2.7	12.85	11.42	0.23	0.47	3.00E-04	8.50E-03	Multiple_Complex
TC0700013612.hg.1	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	2.7	14.59	13.15	0.08	0.21	7.82E-05	5.50E-03	Multiple_Complex
TC0200009927.hg.1	MYO3B	myosin IIIB	2.7	5.2	3.76	0.3	0.3	1.00E-03	1.40E-02	Multiple_Complex
TC1500009492.hg.1	RSL24D1	ribosomal L24 domain containing 1	2.7	14.23	12.79	0.17	0.31	4.00E-04	9.10E-03	Multiple_Complex
TC0400008534.hg.1	NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	2.7	8.24	6.81	0.07	0.33	1.80E-03	1.85E-02	Multiple_Complex
TC1100013094.hg.1	PTS	6-pyruvoyltetrahydropterin synthase	2.7	14.22	12.79	0.13	0.15	2.00E-04	6.60E-03	Multiple_Complex
TC0100010867.hg.1	LAMC2	laminin, gamma 2	2.7	7.37	5.94	0.34	0.08	4.00E-04	9.30E-03	Multiple_Complex
TC0900010580.hg.1	GKAP1	G kinase anchoring protein 1	2.69	12.44	11.01	0.14	0.16	4.29E-05	4.90E-03	Multiple_Complex
TC1300006481.hg.1	ZMYM2	zinc finger, MYM-type 2	2.69	11.38	9.96	0.25	0.29	1.00E-03	1.39E-02	Multiple_Complex
TC0300014074.hg.1	IFT80	intraflagellar transport 80	2.69	10.49	9.07	0.23	0.26	6.00E-04	1.15E-02	Multiple_Complex
TC0500008107.hg.1	SLF1	SMC5-SMC6 complex localization factor 1	2.69	9.53	8.1	0.11	0.29	2.00E-04	7.00E-03	Multiple_Complex
TC1200012665.hg.1	THAP2	THAP domain containing, apoptosis associated protein 2	2.69	7.63	6.2	0.49	0.2	8.00E-04	1.27E-02	Multiple_Complex
TC0600014154.hg.1	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1	2.69	13.82	12.4	0.31	0.29	8.00E-04	1.25E-02	Multiple_Complex
TC0100015060.hg.1	LRRC39	leucine rich repeat containing 39	2.68	8.01	6.59	0.04	0.26	4.10E-03	2.99E-02	Coding
TC2100008380.hg.1	KRTAP12-2	keratin associated protein 12-2	2.68	8.95	7.52	0.56	0.35	7.00E-04	1.19E-02	Coding
TC2200008704.hg.1	DMC1	DNA meiotic recombinase 1	2.68	10.31	8.88	0.32	0.19	2.00E-04	6.90E-03	Multiple_Complex
TC0800011074.hg.1	C8orf88	chromosome 8 open reading frame 88	2.68	8.87	7.44	0.14	0.54	1.20E-03	1.51E-02	Multiple_Complex
TC0100011463.hg.1	SYT14	synaptotagmin XIV	2.68	10.5	9.08	0.28	0.07	2.00E-04	7.40E-03	Multiple_Complex
TC1400007444.hg.1	PPP1R36	protein phosphatase 1, regulatory subunit 36	2.68	6.03	4.61	0.45	0.09	4.00E-04	9.20E-03	Multiple_Complex

TC0600009232.hg.1	FAM26F	family with sequence similarity 26, member F	2.68	6.39	4.97	0.16	0.15	4.74E-05	5.00E-03	Coding
TSUnmapped00000315.hg.1	OBP2B	odorant binding protein 2B	2.68	8.12	6.7	0.85	0.53	3.80E-03	2.86E-02	Coding
TC1000008364.hg.1	RP11-380G5.2; PTEN	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_000314; novel transcript, sense intronic to PTEN	2.67	11.77	10.35	0.5	0.3	8.00E-04	1.22E-02	NonCoding
TC0800012313.hg.1	SGK3; C8orf44-SGK3	serum/glucocorticoid regulated kinase family, member 3; C8orf44-SGK3 readthrough	2.67	10.22	8.81	0.19	0.04	2.00E-04	6.40E-03	Multiple_Complex
TC0100014040.hg.1	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	2.67	9.8	8.39	0.36	0.07	2.00E-04	6.70E-03	Multiple_Complex
TC1700008033.hg.1	HEXIM1	hexamethylene bis-acetamide inducible 1	2.67	11.21	9.8	0.24	0.16	9.18E-05	5.70E-03	Coding
TC0300014048.hg.1	NPHP3-ACAD11	NPHP3-ACAD11 readthrough (NMD candidate)	2.67	9.74	8.33	0.28	0.83	2.30E-03	2.12E-02	Multiple_Complex
TC2000008515.hg.1	SNX5	Jeck2013 ALT_DONOR, coding, INTERNAL, intronic best transcript NM_152227	2.67	8.88	7.47	0.52	0.3	1.50E-03	1.70E-02	NonCoding
TC0300013270.hg.1	MRPL47	mitochondrial ribosomal protein L47	2.67	14.55	13.14	0.11	0.35	2.00E-04	6.80E-03	Multiple_Complex
TC1700012361.hg.1	CDRT1	CMT1A duplicated region transcript 1	2.66	6.81	5.39	0.31	0.44	8.00E-04	1.25E-02	Multiple_Complex
TC1800007155.hg.1	PIK3C3	phosphatidylinositol 3-kinase, catalytic subunit type 3	2.66	10.15	8.74	0.24	0.21	1.00E-04	5.80E-03	Multiple_Complex
TC0400008841.hg.1	ELMOD2	ELMO/CED-12 domain containing 2	2.66	11.64	10.23	0.14	0.38	1.00E-03	1.41E-02	Multiple_Complex
TC0500007605.hg.1	TRAPPC13	trafficking protein particle complex 13	2.66	8.78	7.37	0.23	0.81	8.70E-03	4.89E-02	Multiple_Complex
TC1900008476.hg.1	SULT2B1	sulfotransferase family 2B member 1	2.65	9.41	8	0.15	0.3	9.11E-05	5.70E-03	Multiple_Complex
TC0800008478.hg.1	FZD6	frizzled class receptor 6	2.65	13.01	11.6	0.07	0.4	1.00E-04	6.00E-03	Coding
TC1700010408.hg.1	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2)	2.65	6.36	4.95	0.13	0.08	7.70E-05	5.50E-03	Multiple_Complex
TC0300013047.hg.1	ZBBX	zinc finger, B-box domain containing	2.64	7.71	6.31	0.76	0.23	5.20E-03	3.49E-02	Multiple_Complex

TC1100007184.hg.1	DNAJC24	DnaJ (Hsp40) homolog, subfamily C, member 24	2.64	12.26	10.85	0.05	0.44	2.00E-04	7.50E-03	Multiple_Complex
TC0X00010442.hg.1	TMSB15B; RP11-722G7.1	Homo sapiens thymosin beta 15B (TMSB15B), mRNA.; Thymosin beta-15B [Source:UniProtKB/Swiss-Prot;Acc:P0CG35]	2.64	9.63	8.23	0.44	0.25	1.10E-03	1.43E-02	Coding
TC0500010511.hg.1	C5orf42	chromosome 5 open reading frame 42	2.64	11.9	10.5	0.46	0.43	1.30E-03	1.55E-02	Multiple_Complex
TC0100009608.hg.1	HAO2	hydroxyacid oxidase 2 (long chain)	2.64	5.42	4.02	0.55	0.04	1.60E-03	1.74E-02	Multiple_Complex
TC0X00010387.hg.1	TMSB15A	thymosin beta 15a	2.63	12.59	11.19	0.17	0.25	7.00E-04	1.17E-02	Multiple_Complex
TC0900009779.hg.1	C9orf72	chromosome 9 open reading frame 72	2.63	10.66	9.27	0.01	0.66	9.00E-04	1.33E-02	Multiple_Complex
TC1200011453.hg.1	C12orf50	chromosome 12 open reading frame 50	2.63	8.24	6.84	0.75	0.38	1.50E-03	1.70E-02	Multiple_Complex
TC0600008350.hg.1	BAG2	BCL2-associated athanogene 2	2.63	11.25	9.85	0.03	0.26	2.00E-04	7.10E-03	Multiple_Complex
TC1000009165.hg.1	PSTK	phosphoseryl-tRNA kinase	2.63	11.76	10.37	0.42	0.24	6.00E-04	1.13E-02	Multiple_Complex
TC1200006948.hg.1	C12orf60	chromosome 12 open reading frame 60	2.63	10.71	9.32	0.06	0.3	4.00E-04	9.70E-03	Multiple_Complex
TC1400010621.hg.1	CHURC1	churchill domain containing 1	2.63	15.28	13.88	0.17	0.31	5.00E-04	1.01E-02	Multiple_Complex
TC1800007354.hg.1	POLI	polymerase (DNA directed) iota	2.63	10.31	8.92	0.26	0.13	1.00E-03	1.41E-02	Multiple_Complex
TC0700009036.hg.1	LEP	leptin	2.63	5.83	4.44	1.23	0.14	8.60E-03	4.85E-02	Coding
TC0800010987.hg.1	C8orf59	chromosome 8 open reading frame 59	2.63	12.3	10.91	0.19	0.08	1.10E-03	1.43E-02	Multiple_Complex
TC0700006656.hg.1	RSPH10B2	radial spoke head 10 homolog B2 (Chlamydomonas)	2.63	7.57	6.17	0.29	0.52	7.00E-04	1.21E-02	Multiple_Complex
TC1100008661.hg.1	EED; MIR6755	embryonic ectoderm development; microRNA 6755	2.62	13.29	11.9	0.17	0.38	2.00E-04	7.50E-03	Multiple_Complex
TC0100007514.hg.1	WASF2	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_006990	2.62	4.24	2.85	0.26	0.24	1.00E-04	5.80E-03	NonCoding
TC0400011721.hg.1	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	2.62	14.49	13.1	0.4	0.18	1.00E-03	1.36E-02	Multiple_Complex
TC0500011497.hg.1	GLRX	glutaredoxin	2.62	10.42	9.03	0.24	0.13	8.00E-04	1.23E-02	Multiple_Complex

TC0900008463.hg.1	HSDL2	hydroxysteroid dehydrogenase like 2	2.61	12.82	11.43	0.23	0.68	1.50E-03	1.69E-02	Multiple_Complex
TC0X00010465.hg.1	NUP62CL	nucleoporin 62kDa C-terminal like	2.61	8.85	7.47	0.05	0.05	8.00E-04	1.25E-02	Multiple_Complex
TC0700010716.hg.1	DPY19L1	dpy-19-like 1 (C. elegans)	2.61	12.35	10.97	0.06	0.26	1.20E-03	1.52E-02	Multiple_Complex
TSUnmapped00000474.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	2.61	10.92	9.54	0.07	0.43	3.00E-04	8.10E-03	Coding
TC1300007531.hg.1	LMO7DN	LMO7 downstream neighbor	2.6	7.5	6.12	0.36	0.38	3.00E-04	8.00E-03	Multiple_Complex
TC0400007559.hg.1	TMEM165	transmembrane protein 165	2.6	11.6	10.22	0.15	0.07	3.00E-04	7.70E-03	Multiple_Complex
TC0200012936.hg.1	FBXO48	F-box protein 48	2.6	9.01	7.63	0.22	0.35	2.00E-04	7.10E-03	Coding
TC0200012339.hg.1	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	2.6	7.11	5.73	0.49	0.28	4.00E-04	9.80E-03	Multiple_Complex
TC0600011237.hg.1	OR2B2	olfactory receptor, family 2, subfamily B, member 2	2.6	5.23	3.85	0.23	0.27	4.00E-04	9.10E-03	Multiple_Complex
TC0200016544.hg.1	RIF1	replication timing regulatory factor 1	2.6	9.31	7.93	0.08	0.13	1.60E-03	1.74E-02	NonCoding
TC0100009142.hg.1	PTBP2	polypyrimidine tract binding protein 2	2.6	11.79	10.42	0.02	0.38	5.00E-04	1.00E-02	Multiple_Complex
TC0200008285.hg.1	MRPL35	mitochondrial ribosomal protein L35	2.6	9.92	8.55	0.12	0.56	7.00E-04	1.17E-02	Multiple_Complex
TC0300009147.hg.1	RNF13	ring finger protein 13	2.6	12.58	11.2	0.3	0.1	4.00E-04	9.30E-03	Multiple_Complex
TC1400007300.hg.1	PSMA3	proteasome subunit alpha 3	2.59	15.42	14.05	0.12	0.21	1.00E-04	6.00E-03	Multiple_Complex
TC1600010780.hg.1	CMTR2	cap methyltransferase 2	2.59	9.37	8	0.27	0.48	1.00E-03	1.41E-02	Multiple_Complex
TC1700011785.hg.1	EXOC7	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001145297	2.59	9.3	7.93	0.06	0.38	2.00E-04	6.80E-03	NonCoding
TC1700011233.hg.1	MRPS23	mitochondrial ribosomal protein S23	2.59	10.98	9.61	0.7	0.51	3.10E-03	2.53E-02	Multiple_Complex
TC0200010236.hg.1	GULP1	GULP, engulfment adaptor PTB domain containing 1	2.59	9.64	8.27	0.09	0.2	3.30E-03	2.65E-02	Multiple_Complex
TC0500008232.hg.1	PPIP5K2	diphosphoinositol pentakisphosphate kinase 2	2.59	12.72	11.35	0.05	0.16	9.83E-05	5.80E-03	Multiple_Complex

TC2200007043.hg.1	HORMAD2	HORMA domain containing 2	2.59	6.59	5.22	0.42	0.26	5.00E-04	1.03E-02	Multiple_Complex
TC0700008898.hg.1	ANKRD7	ankyrin repeat domain 7	2.59	8.45	7.08	0.64	0.15	1.16E-02	5.89E-02	Multiple_Complex
TC0100011661.hg.1	MARK1	MAP/microtubule affinity-regulating kinase 1	2.58	8.25	6.88	0.05	0.3	3.00E-04	8.10E-03	Multiple_Complex
TC0700011780.hg.1	PEX1	peroxisomal biogenesis factor 1	2.58	11.08	9.71	0.02	0.09	4.00E-04	9.60E-03	Multiple_Complex
TC2000007117.hg.1	ASXL1	additional sex combs like transcriptional regulator 1	2.58	14.69	13.32	0.39	0.3	1.10E-03	1.44E-02	Multiple_Complex
TC0400011706.hg.1	FABP2	fatty acid binding protein 2, intestinal	2.58	5.31	3.94	0.56	0.36	1.60E-03	1.74E-02	Coding
TC0800011137.hg.1	RAD54B; FSBP	RAD54 homolog B (S. cerevisiae); fibrinogen silencer binding protein	2.58	12.53	11.17	0.02	0.49	8.00E-04	1.22E-02	Multiple_Complex
TC0900010797.hg.1	ASPN	asporin	2.58	5.87	4.5	0.56	0.27	1.40E-03	1.63E-02	Coding
TC1500009429.hg.1	DMXL2	Dmx-like 2	2.58	12.09	10.73	0.06	0.19	2.00E-04	6.70E-03	Multiple_Complex
TC2000009447.hg.1	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	2.58	11.41	10.05	0.12	0.01	3.00E-04	8.00E-03	Multiple_Complex
TC0800008510.hg.1	OXR1	oxidation resistance 1	2.58	10.68	9.32	0.27	0.3	5.00E-04	1.07E-02	Multiple_Complex
TC0300013933.hg.1	THUMPD3-AS1	THUMPD3 antisense RNA 1	2.57	11.73	10.37	0.07	0.12	1.00E-04	5.80E-03	Multiple_Complex
TC0600008630.hg.1	TTK	TTK protein kinase	2.57	13.04	11.68	0.2	0.32	6.00E-04	1.15E-02	Multiple_Complex
TC1500006963.hg.1	CASC5	cancer susceptibility candidate 5	2.57	9.53	8.17	0.08	0.27	2.00E-04	6.30E-03	Multiple_Complex
TC0200012318.hg.1	CDKL4	cyclin-dependent kinase-like 4	2.57	6.93	5.57	0.07	0.3	1.00E-04	5.80E-03	Multiple_Complex
TC0200007401.hg.1	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	2.57	10.74	9.38	0.17	0.25	2.00E-04	6.70E-03	Multiple_Complex
TC0800011105.hg.1	TRIQK	triple QxxK/R motif containing	2.56	12.21	10.85	0.12	0.57	8.00E-04	1.26E-02	Multiple_Complex
TC1500007097.hg.1	B2M	beta-2-microglobulin	2.56	15.53	14.17	0.12	0.35	2.00E-04	7.10E-03	Multiple_Complex
TSUnmapped00000370.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	2.56	11.22	9.86	0.06	0.39	9.00E-04	1.32E-02	Coding
TC0800007209.hg.1	WRN	Werner syndrome, RecQ helicase-like	2.56	9.28	7.93	0.06	0.23	1.00E-04	5.80E-03	Multiple_Complex

TC1400010577.hg.1	NGDN	neuroguidin, EIF4E binding protein	2.55	13.77	12.42	0.05	0.31	3.00E-04	7.70E-03	Multiple_Complex
TC0X00010990.hg.1	SPANXC; SPANXD	SPANX family, member C; SPANX family, member D	2.55	5.98	4.63	0.52	0.1	6.00E-04	1.11E-02	Coding
TC0500010579.hg.1	TTC33	tetratricopeptide repeat domain 33	2.55	8.72	7.37	0.46	0.51	1.90E-03	1.90E-02	Multiple_Complex
TC0700009222.hg.1	LRGUK	leucine-rich repeats and guanylate kinase domain containing	2.55	6.88	5.53	0.03	0.39	6.00E-04	1.10E-02	Multiple_Complex
TC0500011408.hg.1	TMEM161B	transmembrane protein 161B	2.55	10.92	9.57	0.25	0.13	8.00E-04	1.23E-02	Multiple_Complex
TC0200010572.hg.1	ZDBF2	zinc finger, DBF-type containing 2	2.55	13.07	11.72	0.19	0.65	1.70E-03	1.83E-02	Multiple_Complex
TC0800012432.hg.1	MRPS28	mitochondrial ribosomal protein S28	2.55	13.54	12.19	0.02	0.02	1.00E-04	6.10E-03	Multiple_Complex
TC0600014150.hg.1	SMIM8	small integral membrane protein 8	2.55	10.01	8.66	0.03	0.43	6.00E-04	1.12E-02	Coding
TC2200008828.hg.1	PHF5A	PHD finger protein 5A	2.55	14.65	13.3	0.15	0.28	4.00E-04	9.20E-03	Multiple_Complex
TC0400011421.hg.1	LAMTOR3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3	2.54	9.89	8.55	0.46	0.42	2.10E-03	2.01E-02	Multiple_Complex
TC0200007174.hg.1	SPAST	spastin	2.54	10.49	9.15	0.45	0.43	8.00E-04	1.27E-02	Multiple_Complex
TC0600007791.hg.1	DEF6	DEF6 guanine nucleotide exchange factor	2.54	6.29	4.95	0.96	0.13	3.70E-03	2.80E-02	Multiple_Complex
TC1000008502.hg.1	TBC1D12	TBC1 domain family, member 12	2.54	8.11	6.77	0.23	0.02	1.00E-04	6.20E-03	Multiple_Complex
TC0600009868.hg.1	ARMT1	acidic residue methyltransferase 1	2.54	11.4	10.06	0.01	0.19	8.00E-04	1.25E-02	Multiple_Complex
TC1200009198.hg.1	LRRC43	leucine rich repeat containing 43	2.53	6.51	5.17	0.07	0.11	4.00E-04	9.70E-03	Multiple_Complex
TC1200009916.hg.1	TAS2R9	taste receptor, type 2, member 9	2.53	5.75	4.41	0.31	0.22	1.60E-03	1.73E-02	Coding
TC0600009082.hg.1	C6orf183	chromosome 6 open reading frame 183	2.53	5.64	4.3	0.46	0.19	4.00E-04	9.00E-03	Multiple_Complex
TC0900006538.hg.1	JAK2	Janus kinase 2	2.53	9.1	7.76	0.11	0.31	2.00E-04	6.40E-03	Multiple_Complex
TC0100015397.hg.1	CD58	CD58 molecule	2.53	11.92	10.58	0.17	0.12	3.00E-04	7.70E-03	Multiple_Complex
TC0300013804.hg.1	OXSM	3-oxoacyl-ACP synthase, mitochondrial	2.53	10.03	8.69	0.05	0.46	4.00E-04	9.30E-03	Multiple_Complex

TC0400008362.hg.1	OSTC	oligosaccharyltransferase complex subunit (non-catalytic)	2.53	13.85	12.52	0.24	0.33	9.00E-04	1.34E-02	Multiple_Complex
TC0100010939.hg.1	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	2.53	8.86	7.52	0.01	0.05	3.00E-04	8.90E-03	Multiple_Complex
TC1000008475.hg.1	EXOC6	exocyst complex component 6	2.52	8.38	7.05	0.06	0.5	5.00E-04	1.00E-02	Multiple_Complex
TC1000006861.hg.1	MEIG1	meiosis/spermiogenesis associated 1	2.52	7.91	6.58	0.11	0.48	3.00E-03	2.48E-02	Multiple_Complex
TC1700007138.hg.1	TVP23B	trans-golgi network vesicle protein 23 homolog B (S. cerevisiae)	2.52	13.92	12.59	0.04	0.15	5.00E-04	1.00E-02	Multiple_Complex
TC1500010777.hg.1	IL16	interleukin 16	2.52	7.13	5.8	0.04	0.18	2.20E-03	2.06E-02	NonCoding
TC0500012127.hg.1	TRPC7	transient receptor potential cation channel, subfamily C, member 7	2.52	7.43	6.1	0.33	0.29	2.70E-03	2.36E-02	Multiple_Complex
TC0800011472.hg.1	NUDCD1	NudC domain containing 1	2.52	12.87	11.54	0	0.48	1.00E-03	1.36E-02	Multiple_Complex
TC0200010567.hg.1	EEF1B2; SNORA41	eukaryotic translation elongation factor 1 beta 2; small nucleolar RNA, H/ACA box 41	2.52	14.3	12.97	0.07	0.27	1.00E-04	5.90E-03	Multiple_Complex
TC0700008747.hg.1	HBP1	HMG-box transcription factor 1	2.52	11.15	9.81	0.04	0.11	9.22E-05	5.70E-03	Multiple_Complex
TC0100009572.hg.1	FAM46C	family with sequence similarity 46, member C	2.52	7.23	5.9	0.57	0.29	1.40E-03	1.61E-02	Coding
TC0400012763.hg.1	S100P	S100 calcium binding protein P	2.51	10.16	8.83	0.48	0.17	4.00E-04	9.50E-03	Multiple_Complex
TC2100006627.hg.1	MIR99AHG	mir-99a-let-7c cluster host gene	2.51	11.66	10.33	0.33	0.04	2.00E-04	7.50E-03	Multiple_Complex
TC0500008539.hg.1	GRAMD3	GRAM domain containing 3	2.51	6.37	5.04	0.31	0.07	1.00E-04	6.20E-03	Multiple_Complex
TC0400012818.hg.1	CCNG2	cyclin G2	2.51	8.9	7.57	0.32	0.36	3.00E-04	8.00E-03	Multiple_Complex
TC0200016585.hg.1	MOB4	MOB family member 4, phocein	2.51	12.1	10.77	0.2	0.15	1.00E-04	6.20E-03	Multiple_Complex
TC0200007195.hg.1	TTC27; MIR4765	tetratricopeptide repeat domain 27; microRNA 4765	2.51	8.75	7.42	0	0.19	4.00E-04	9.30E-03	Multiple_Complex
TC1000012121.hg.1	OAT	ornithine aminotransferase	2.51	11.63	10.3	0.12	0.18	3.00E-04	8.00E-03	Multiple_Complex
TC0800010944.hg.1	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	2.51	9.05	7.72	0.06	0.23	3.00E-04	8.30E-03	Multiple_Complex

TC1200007151.hg.1	SMCO2	single-pass membrane protein with coiled-coil domains 2	2.51	8.27	6.95	0.08	0.51	1.10E-03	1.47E-02	Multiple_Complex
TC1400010748.hg.1	LINC01588	long intergenic non-protein coding RNA 1588	2.51	7.28	5.95	0.3	0.01	1.80E-03	1.86E-02	Multiple_Complex
TSUnmapped00000190.hg.1	KIF15	kinesin family member 15	2.51	9.55	8.22	0.7	0.34	1.60E-03	1.73E-02	Coding
TC0100016831.hg.1	ASPM	abnormal spindle microtubule assembly	2.51	11.37	10.05	0.01	0.2	1.00E-04	5.80E-03	Multiple_Complex
TC0800008481.hg.1	CTHRC1	collagen triple helix repeat containing 1	2.5	6.66	5.34	0.43	0.58	1.30E-03	1.60E-02	Multiple_Complex
TC0400007596.hg.1	ARL9	ADP-ribosylation factor like GTPase 9	2.5	7.83	6.51	0.73	0.11	2.40E-03	2.19E-02	Coding
TC0400008287.hg.1	CISD2	CDGSH iron sulfur domain 2	2.5	13.4	12.07	0	0.17	1.60E-03	1.74E-02	Coding
TC1000006703.hg.1	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	2.5	13.38	12.06	0.09	0.46	8.00E-04	1.28E-02	Multiple_Complex
TC0300013051.hg.1	PDCD10	programmed cell death 10	2.5	14.22	12.9	0.18	0.61	1.50E-03	1.70E-02	Multiple_Complex
TC1300007483.hg.1	BORA	bora, aurora kinase A activator	2.5	8.23	6.91	0.07	0.31	2.00E-04	6.60E-03	Multiple_Complex
TC0100016833.hg.1	ZBTB41	zinc finger and BTB domain containing 41	2.5	10.68	9.36	0.18	0.05	2.00E-04	6.80E-03	Multiple_Complex
TC0400007096.hg.1	ANAPC4	anaphase promoting complex subunit 4	2.5	11.36	10.04	0.01	0.22	2.00E-04	6.80E-03	Multiple_Complex
TC0600008697.hg.1	NT5E	5-nucleotidase, ecto (CD73)	2.5	7.56	6.23	0.47	0.12	4.00E-04	9.00E-03	Multiple_Complex
TC1100009397.hg.1	SPA17	sperm autoantigenic protein 17	2.5	12.17	10.85	0.31	0.45	2.80E-03	2.41E-02	Multiple_Complex
TC1000007748.hg.1	CDK1	cyclin-dependent kinase 1	2.5	13.69	12.37	0.16	0.35	1.00E-03	1.40E-02	Multiple_Complex
TC0200013603.hg.1	MITD1	microtubule interacting and trafficking domain containing 1	2.5	13.12	11.8	0.11	0.02	6.00E-04	1.14E-02	Multiple_Complex
TC0300008524.hg.1	STXBP5L	syntaxin binding protein 5-like	2.49	9.1	7.78	0.5	0.14	2.80E-03	2.37E-02	Multiple_Complex
TC1100008886.hg.1	TMEM133	transmembrane protein 133	2.49	6.17	4.85	0.48	0.21	1.70E-03	1.79E-02	Coding
TC1100012052.hg.1	CCDC82	coiled-coil domain containing 82	2.49	11.49	10.17	0.16	0.1	2.00E-04	6.90E-03	Multiple_Complex

TC1100010451.hg.1	IMMP1L	inner mitochondrial membrane peptidase subunit 1	2.49	12.05	10.73	0.02	0.24	2.40E-03	2.16E-02	Multiple_Complex
TC0400011402.hg.1	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	2.49	10.27	8.95	0.47	0.43	1.40E-03	1.60E-02	Multiple_Complex
TC0200015397.hg.1	CLK1	CDC like kinase 1	2.49	14.81	13.49	0.43	0.04	1.40E-03	1.60E-02	Multiple_Complex
TC1800009284.hg.1	C18orf32	chromosome 18 open reading frame 32	2.49	13.94	12.62	0.27	0.3	4.00E-04	9.30E-03	Multiple_Complex
TC1900010833.hg.1	PSG5	pregnancy specific beta-1-glycoprotein 5	2.49	7.01	5.7	1.09	0.12	7.50E-03	4.43E-02	Multiple_Complex
TC0100017368.hg.1	BPNT1	3(2), 5-bisphosphate nucleotidase 1	2.49	12.43	11.11	0.05	0.26	1.30E-03	1.57E-02	Multiple_Complex
TC0400010580.hg.1	GNPDA2	glucosamine-6-phosphate deaminase 2	2.49	9.49	8.18	0.2	0.34	3.00E-04	8.10E-03	Multiple_Complex
TC0900008318.hg.1	TMEM38B	transmembrane protein 38B	2.48	12.65	11.34	0.12	0.24	2.00E-04	7.00E-03	Multiple_Complex
TC0300010975.hg.1	KIF9	kinesin family member 9	2.48	11.66	10.35	0.07	0.08	3.00E-04	7.70E-03	Multiple_Complex
TC0500012160.hg.1	NME5	NME/NM23 family member 5	2.48	6.35	5.04	0.54	0.45	1.11E-02	5.73E-02	Multiple_Complex
TC0200010275.hg.1	GLS	glutaminase	2.48	11.75	10.44	0.01	0.36	4.00E-04	9.00E-03	Multiple_Complex
TC0800010630.hg.1	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	2.48	13.04	11.73	0.14	0.4	8.00E-04	1.27E-02	Multiple_Complex
TC0700008667.hg.1	PSMC2	proteasome 26S subunit, ATPase 2	2.48	13.61	12.3	0.1	0.39	2.00E-04	7.60E-03	Multiple_Complex
TC0200009065.hg.1	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	2.47	13.66	12.35	0.08	0.39	4.00E-04	9.80E-03	Multiple_Complex
TC1000008047.hg.1	CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1	2.47	11.28	9.97	0.46	0.05	1.50E-03	1.69E-02	Multiple_Complex
TC0500008296.hg.1	MAN2A1	mannosidase, alpha, class 2A, member 1	2.47	12.12	10.81	0.05	0.24	2.00E-04	7.30E-03	Multiple_Complex
TC0200015432.hg.1	MPP4	membrane protein, palmitoylated 4	2.47	6.75	5.45	0.6	0.21	2.30E-03	2.13E-02	Multiple_Complex
TC0100010924.hg.1	C1orf27	chromosome 1 open reading frame 27	2.47	11.8	10.5	0.21	0.26	3.00E-04	7.60E-03	Multiple_Complex
TC0500011296.hg.1	ACOT12	acyl-CoA thioesterase 12	2.47	4.79	3.49	0.15	0.49	2.70E-03	2.31E-02	Multiple_Complex
TC2100006585.hg.1	RBM11	RNA binding motif protein 11	2.47	12.62	11.32	0.1	0.17	2.00E-04	6.40E-03	Multiple_Complex

TC0100018488.hg.1	TMOD4	tropomodulin 4 (muscle)	2.46	5.49	4.19	0.27	0.55	1.10E-03	1.46E-02	Multiple_Complex
TC1200007906.hg.1	XRCC6BP1	XRCC6 binding protein 1	2.46	12.84	11.54	0.22	0.41	8.00E-04	1.22E-02	Multiple_Complex
TC2000007083.hg.1	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	2.46	5.04	3.74	0.72	0.03	1.30E-03	1.57E-02	Multiple_Complex
TC0400009519.hg.1	SNX25	sorting nexin 25	2.46	10.88	9.58	0.17	0.01	1.00E-04	5.80E-03	Multiple_Complex
TC0600012358.hg.1	PHIP	pleckstrin homology domain interacting protein	2.46	11.75	10.45	0.19	0.12	9.72E-05	5.80E-03	Multiple_Complex
TC1200009524.hg.1	ZNF84	zinc finger protein 84	2.46	9.68	8.38	0.37	0.48	3.00E-03	2.48E-02	Multiple_Complex
TC1000006633.hg.1	FAM208B	family with sequence similarity 208, member B	2.46	11.45	10.15	0.27	0.01	8.00E-04	1.23E-02	Multiple_Complex
TC0400007026.hg.1	RP11-362J17.1; PACRGL	novel transcript, antisense to KCNIP4; Transcript Identified by AceView, Entrez Gene ID(s) 133015	2.45	6.05	4.76	0.54	0.59	3.40E-03	2.66E-02	NonCoding
TC0500010872.hg.1	ERCC8	excision repair cross-complementation group 8	2.45	9.51	8.21	0.07	0.21	9.00E-04	1.33E-02	Multiple_Complex
TC0300008289.hg.1	DZIP3	DAZ interacting zinc finger protein 3	2.45	10.96	9.67	0.08	0.18	5.00E-04	1.04E-02	Multiple_Complex
TC1400006521.hg.1	PNP	purine nucleoside phosphorylase	2.45	11.68	10.39	0.01	0.23	1.00E-04	5.80E-03	Multiple_Complex
TC0700008878.hg.1	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	2.45	9.33	8.03	0.26	0.44	1.80E-03	1.85E-02	Multiple_Complex
TC1600010012.hg.1	PYDC1	PYD (pyrin domain) containing 1	2.45	5.38	4.09	0.17	0.2	3.00E-04	8.10E-03	Multiple_Complex
TC1200012228.hg.1	IL31	interleukin 31	2.45	5.76	4.47	0.44	0.31	7.00E-04	1.22E-02	Coding
TC0500010670.hg.1	EMB	embigin	2.45	9.62	8.33	0.26	0.4	1.70E-03	1.82E-02	Multiple_Complex
TC1100013017.hg.1	PGA5	pepsinogen 5, group I (pepsinogen A)	2.45	7.33	6.04	0.79	0.23	1.20E-02	6.04E-02	Multiple_Complex
TC0100018238.hg.1	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	2.44	11.93	10.64	0.07	0.03	2.00E-04	6.70E-03	Multiple_Complex
TC0500010928.hg.1	CENPK	centromere protein K	2.44	12.73	11.44	0.16	0.36	1.00E-03	1.41E-02	Multiple_Complex

TC1300006699.hg.1	ATP5EP2	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2	2.44	12.15	10.87	0.48	0.37	1.20E-03	1.51E-02	Multiple_Complex
TC0300008111.hg.1	OR5K2	olfactory receptor, family 5, subfamily K, member 2	2.44	5.16	3.87	1.14	0.13	1.45E-02	6.87E-02	Coding
TC1000007132.hg.1	BAMBI	BMP and activin membrane-bound inhibitor	2.44	8.22	6.94	0.11	0.12	2.30E-03	2.14E-02	Multiple_Complex
TC0700010751.hg.1	AOAH	acyloxyacyl hydrolase (neutrophil)	2.44	6.1	4.82	0.12	0.37	8.00E-04	1.24E-02	Multiple_Complex
TC0200014402.hg.1	LCT	lactase	2.44	5.79	4.51	0.54	0.34	1.10E-03	1.48E-02	Coding
TC0500007154.hg.1	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	2.43	8.8	7.51	0.45	0.27	7.00E-04	1.20E-02	Multiple_Complex
TC0900011236.hg.1	INIP	INTS3 and NABP interacting protein	2.43	11.11	9.83	0.15	0.17	1.80E-03	1.85E-02	Multiple_Complex
TC0100006723.hg.1	VAMP3	vesicle associated membrane protein 3	2.43	8.3	7.02	0.01	0.18	2.00E-04	7.40E-03	Multiple_Complex
TC0100012732.hg.1	UTS2	urotensin 2	2.43	9.44	8.16	0	0.08	4.00E-04	9.50E-03	Coding
TC0700006669.hg.1	MIOS	missing oocyte, meiosis regulator, homolog (Drosophila)	2.43	11.41	10.13	0.08	0.51	1.70E-03	1.78E-02	Multiple_Complex
TC0500007552.hg.1	LOC100421561	family with sequence similarity 133, member A pseudogene	2.43	9.07	7.79	0.16	0.2	5.00E-04	1.02E-02	Multiple_Complex
TC1800007969.hg.1	L3MBTL4	l(3)mbt-like 4 (Drosophila)	2.42	9.88	8.6	0.04	0.05	5.00E-04	1.00E-02	Multiple_Complex
TC1200010108.hg.1	GYS2	glycogen synthase 2 (liver)	2.42	5.08	3.81	0.06	0.07	1.80E-03	1.89E-02	Coding
TC1300008025.hg.1	ING1	inhibitor of growth family member 1	2.42	6.95	5.68	0.72	0.11	2.60E-03	2.30E-02	Coding
TC0700010443.hg.1	STEAP1B	STEAP family member 1B	2.42	9.35	8.08	0.21	0.04	1.10E-03	1.47E-02	Multiple_Complex
TC0900012276.hg.1	SCAI; GOLGA1	suppressor of cancer cell invasion; golgin A1	2.42	9.77	8.5	0.4	0.54	2.70E-03	2.34E-02	Multiple_Complex
TC0600014148.hg.1	CYB5R4	cytochrome b5 reductase 4	2.42	10.13	8.85	0.3	0.41	8.00E-04	1.25E-02	Multiple_Complex
TC0500010540.hg.1	LIFR	leukemia inhibitory factor receptor alpha	2.42	9.88	8.61	0.43	0.12	6.00E-04	1.15E-02	Multiple_Complex

TC0500007604.hg.1	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	2.42	13.55	12.28	0.26	0.25	3.00E-04	8.30E-03	Multiple_Complex
TC0600014239.hg.1	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	2.41	14.24	12.97	0.16	0.31	7.00E-04	1.17E-02	Coding
TC0100017935.hg.1	RGS7	regulator of G-protein signaling 7	2.41	6.91	5.64	0.33	0.03	3.00E-04	8.20E-03	Multiple_Complex
TC1400009563.hg.1	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter), member 1	2.41	6.29	5.02	0.42	0.25	8.00E-04	1.23E-02	Coding
TC0X00007026.hg.1	USP9X	ubiquitin specific peptidase 9, X-linked	2.41	13.37	12.1	0.25	0.26	2.00E-04	7.30E-03	Multiple_Complex
TC0600009169.hg.1	FAM229B	family with sequence similarity 229, member B	2.41	14.4	13.13	0.17	0.52	5.80E-03	3.74E-02	Coding
TC0700013362.hg.1	MRPS17	mitochondrial ribosomal protein S17	2.41	14.8	13.54	0.09	0.17	3.00E-04	8.20E-03	Multiple_Complex
TC1500009393.hg.1	USP50	ubiquitin specific peptidase 50	2.41	7.31	6.04	0.21	0.01	2.00E-04	7.10E-03	Multiple_Complex
TC1100013091.hg.1	SDHD	succinate dehydrogenase complex subunit D, integral membrane protein	2.41	11.32	10.05	0.29	0.06	3.00E-04	8.00E-03	Multiple_Complex
TC0500010615.hg.1	SEPP1	selenoprotein P, plasma, 1	2.4	10.86	9.59	0.24	0.2	9.00E-04	1.32E-02	Multiple_Complex
TC1700010550.hg.1	C17orf98	chromosome 17 open reading frame 98	2.4	5.72	4.46	0	0.05	9.99E-05	5.80E-03	Coding
TC0900012159.hg.1	DNAJC25	DnaJ (Hsp40) homolog, subfamily C , member 25	2.4	10.07	8.8	0.26	0.42	2.10E-03	2.02E-02	Multiple_Complex
TC0500013167.hg.1	ZNF131	zinc finger protein 131	2.4	9.82	8.56	0.44	0.06	1.60E-03	1.76E-02	Multiple_Complex
TC0400011477.hg.1	CENPE	centromere protein E	2.4	9.69	8.43	0.35	0.09	7.00E-04	1.16E-02	Multiple_Complex
TC1100007005.hg.1	LDHC	lactate dehydrogenase C	2.4	11.35	10.08	0.01	0.06	1.80E-03	1.85E-02	Coding
TC0700010831.hg.1	MPLKIP	M-phase specific PLK1 interacting protein	2.4	14.88	13.62	0.06	0.09	4.00E-04	9.70E-03	Multiple_Complex
TC0600008209.hg.1	CENPQ	centromere protein Q	2.4	10.55	9.29	0.06	0.48	3.50E-03	2.73E-02	Coding
TC0400007361.hg.1	SLC30A9	solute carrier family 30 (zinc transporter), member 9	2.39	11.17	9.91	0.04	0.18	2.00E-04	7.10E-03	Multiple_Complex
TC1000011003.hg.1	PLA2G12B	phospholipase A2, group XIIB	2.39	7.17	5.91	0.11	0.06	1.00E-04	5.80E-03	Coding

TC0100011022.hg.1	RGS2	regulator of G-protein signaling 2	2.39	10.83	9.57	0.03	0.63	1.20E-03	1.53E-02	Multiple_Complex
TC1400010773.hg.1	DIO2	deiodinase, iodothyronine, type II	2.39	5.57	4.32	0.58	0.52	2.70E-03	2.34E-02	Multiple_Complex
TC1400007168.hg.1	GPR137C	G protein-coupled receptor 137C	2.39	9.59	8.33	0.18	0.31	1.10E-03	1.43E-02	Multiple_Complex
TC1200009980.hg.1	GPRC5D	G protein-coupled receptor, class C, group 5, member D	2.39	5.67	4.41	0.19	0.03	4.00E-04	9.90E-03	Coding
TC1200010251.hg.1	OVCH1	ovochymase 1	2.39	5.21	3.96	0.61	0.09	1.80E-03	1.86E-02	Multiple_Complex
TC1200011961.hg.1	TMEM116	transmembrane protein 116	2.39	10.14	8.89	0.02	0.29	1.50E-03	1.71E-02	Multiple_Complex
TC0300012718.hg.1	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	2.39	12.22	10.97	0.08	0	2.00E-04	7.40E-03	Multiple_Complex
TC0200014029.hg.1	C2orf76	chromosome 2 open reading frame 76	2.39	11.27	10.01	0.41	0.44	1.40E-03	1.64E-02	Multiple_Complex
TC1700008499.hg.1	BCAS3	breast carcinoma amplified sequence 3	2.39	8.23	6.97	0.2	0.07	3.30E-03	2.62E-02	Multiple_Complex
TC0300006702.hg.1	CAPN7	calpain 7	2.39	12.16	10.91	0.09	0.2	7.00E-04	1.19E-02	Multiple_Complex
TC0100009444.hg.1	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	2.38	13.86	12.61	0.17	0.19	6.00E-04	1.15E-02	Multiple_Complex
TC0100015593.hg.1	ANKRD35	ankyrin repeat domain 35	2.38	5.41	4.16	0.52	0.57	2.70E-03	2.32E-02	Coding
TC0300009782.hg.1	EIF4A2; SNORA63; SNORD2; SNORA4; SNORA81; MIR1248	eukaryotic translation initiation factor 4A2; small nucleolar RNA, H/ACA box 63; small nucleolar RNA, C/D box 2; small nucleolar RNA, H/ACA box 4; small nucleolar RNA, H/ACA box 81; microRNA 1248	2.38	14.87	13.62	0.1	0.53	1.20E-03	1.52E-02	Multiple_Complex
TC0X00011319.hg.1	TMSB15B	thymosin beta 15B	2.38	10.23	8.98	0.06	0.09	2.10E-03	2.04E-02	Coding
TC1200012719.hg.1	WDR66	WD repeat domain 66	2.38	6.73	5.48	0.69	0.5	4.70E-03	3.29E-02	Multiple_Complex
TC0500009478.hg.1	RPL26L1	ribosomal protein L26-like 1	2.38	14.25	13	0.07	0.23	4.00E-04	9.30E-03	Coding
TC0700013371.hg.1	ZNF138	zinc finger protein 138	2.38	13.52	12.27	0.06	0.18	1.00E-04	6.30E-03	Multiple_Complex
TSUnmapped00000095.hg.1	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	2.38	11.8	10.55	0.14	0.59	1.90E-03	1.92E-02	Coding

TC0900009916.hg.1	CCL21	chemokine (C-C motif) ligand 21	2.38	7.05	5.8	0.41	0.66	2.70E-03	2.35E-02	Coding
TC1500007802.hg.1	GOLGA6B	golgin A6 family, member B	2.38	7.45	6.2	0.14	0.79	5.40E-03	3.55E-02	Multiple_Complex
TC0800008487.hg.1	RIMS2	regulating synaptic membrane exocytosis 2	2.38	9.31	8.06	0.3	0.05	7.00E-04	1.22E-02	Multiple_Complex
TC2100008545.hg.1	NRIP1	nuclear receptor interacting protein 1	2.38	10.17	8.93	0.13	0.19	2.00E-04	7.20E-03	Multiple_Complex
TC1300006861.hg.1	NBEA	neurobeachin	2.37	8.13	6.89	0.07	0.22	2.00E-04	7.10E-03	Multiple_Complex
TC0800011710.hg.1	TATDN1; MIR6844	TatD DNase domain containing 1; microRNA 6844	2.37	12.23	10.98	0.35	0.21	5.00E-04	9.90E-03	Multiple_Complex
TC0100010381.hg.1	UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1	2.37	14.45	13.2	0.08	0.27	2.00E-04	7.40E-03	Multiple_Complex
TC1200009914.hg.1	TAS2R7	taste receptor, type 2, member 7	2.37	5.61	4.36	0.88	0.76	2.16E-02	8.96E-02	Coding
TC0500013351.hg.1	FNIP1	folliculin interacting protein 1	2.37	12.23	10.99	0.15	0.15	3.00E-04	8.20E-03	Multiple_Complex
TC0200010438.hg.1	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	2.37	15.09	13.85	0.01	0.13	2.00E-04	7.50E-03	Coding
TC0500007378.hg.1	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	2.37	15.03	13.79	0.01	0.09	7.00E-04	1.20E-02	Multiple_Complex
TC0200006476.hg.1	SNTG2	syntrophin, gamma 2	2.37	7.48	6.24	1.21	0.01	1.81E-02	7.98E-02	Multiple_Complex
TC0200008680.hg.1	SLC9A2	solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2	2.37	8.83	7.59	0.2	0	5.00E-04	1.01E-02	Multiple_Complex
TC1400010759.hg.1	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	2.36	7.51	6.26	0.17	0.18	1.80E-03	1.83E-02	NonCoding
TC1500009522.hg.1	MNS1	meiosis-specific nuclear structural 1	2.36	7.9	6.66	0.52	0.41	7.00E-03	4.23E-02	Multiple_Complex
TC0700009060.hg.1	FAM71F1	family with sequence similarity 71, member F1	2.36	6.37	5.13	0.5	0.37	1.80E-03	1.89E-02	Multiple_Complex
TC0500011433.hg.1	CETN3	centrin 3	2.36	13.84	12.6	0.03	0.03	5.00E-04	1.06E-02	Multiple_Complex
TC0800009968.hg.1	CCDC25	coiled-coil domain containing 25	2.36	12.16	10.92	0.18	0.26	6.00E-04	1.13E-02	Multiple_Complex

TC0300009310.hg.1	MLF1	myeloid leukemia factor 1	2.36	11.63	10.39	0.27	0.05	6.00E-04	1.14E-02	Multiple_Complex
TSUnmapped00000275.hg.1	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	2.36	13.18	11.94	0.04	0.45	7.00E-04	1.17E-02	Coding
TC0400008283.hg.1	LOC105377348; RP11-10L12.4; UBE2D3; pugo	uncharacterized LOC105377348; Salzman2013 ANTISENSE, coding, INTERNAL, intronic, OVERLAPTX best transcript NM_181890; novel transcript, antisense UBE2D3; Transcript Identified by AceView	2.36	6.57	5.33	0.38	0.55	6.10E-03	3.84E-02	NonCoding
TC1200011460.hg.1	KITLG	KIT ligand	2.36	7.5	6.27	0.73	0.29	4.90E-03	3.36E-02	Multiple_Complex
TC0100013636.hg.1	RNF19B	ring finger protein 19B	2.36	8.53	7.29	0.01	0	4.00E-04	9.50E-03	Multiple_Complex
TC1000010239.hg.1	ARHGAP12	Rho GTPase activating protein 12	2.36	9.66	8.42	0.04	0.42	5.00E-04	1.03E-02	Multiple_Complex
TC0300008316.hg.1	PVRL3	poliovirus receptor-related 3	2.36	12.91	11.67	0.1	0.59	1.40E-03	1.63E-02	Multiple_Complex
TC0200010202.hg.1	FSIP2	fibrous sheath interacting protein 2	2.36	6.61	5.37	0.2	0.27	5.00E-04	1.03E-02	Multiple_Complex
TC0800011216.hg.1	STK3	serine/threonine kinase 3	2.36	11.7	10.46	0.03	0.45	5.00E-04	1.04E-02	Multiple_Complex
TC1100012187.hg.1	KBTBD3	kelch repeat and BTB (POZ) domain containing 3	2.36	9.2	7.96	0.13	0.42	6.70E-03	4.11E-02	Multiple_Complex
TC1000007760.hg.1	C10orf107	chromosome 10 open reading frame 107	2.36	7.66	6.43	0.16	0.67	1.90E-03	1.93E-02	Coding

TC0600013144.hg.1	C6orf191andARHGAP18; RP1-69D17.4; RP1-69D17.3; TCONS_l2_00025470; TCONS_l2_00024911; LAMA2	Transcript Identified by AceView, Entrez Gene ID(s) 93663; 253582; Jeck2013 ALT_ACCEPTOR, ALT_DONOR, downstream_end, ncRNA, OVEXON, upstream_start best transcript TCONS_l2_00025470; Jeck2013 ALT_ACCEPTOR, ncRNA, OVEXON, upstream_start best transcript TCONS_l2_00024911; Salzman2013 ANTISENSE, CDS, coding, downstream_end, intronic, OVCODE, OVEXON, UTR3 best transcript NM_000426; Salzman2013 ANNOTATED, INTERNAL, ncRNA, OVEXON best transcript TCONS_l2_00025470; putative novel transcript; novel transcript	2.35	6.74	5.51	0.13	0.19	4.00E-04	9.00E-03	NonCoding
TC0600013458.hg.1	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	2.35	7.25	6.01	0.1	0.02	4.00E-04	9.60E-03	Multiple_Complex
TC2200006450.hg.1	OR11H1	olfactory receptor, family 11, subfamily H, member 1	2.35	5.16	3.93	0.98	0.35	1.04E-02	5.50E-02	Coding
TC0200015460.hg.1	ICA1L	islet cell autoantigen 1 like	2.35	10.33	9.1	0.07	0.37	1.00E-03	1.41E-02	Multiple_Complex
TC1700007634.hg.1	ZNHIT3	zinc finger, HIT-type containing 3	2.35	8.29	7.05	0.09	0.23	6.20E-03	3.89E-02	Multiple_Complex
TC1400008683.hg.1	RBM23	RNA binding motif protein 23	2.35	12.55	11.32	0.19	0.36	1.30E-03	1.57E-02	Multiple_Complex
TC0100015258.hg.1	DRAM2	DNA-damage regulated autophagy modulator 2	2.35	13.78	12.55	0.12	0.22	5.00E-04	1.03E-02	Multiple_Complex
TC1400009355.hg.1	TRMT5	tRNA methyltransferase 5	2.35	8.63	7.4	0.05	0.29	5.00E-04	1.00E-02	Multiple_Complex
TC0100016794.hg.1	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 2	2.34	7.54	6.31	0.55	0.04	2.70E-03	2.32E-02	Coding
TC1100013165.hg.1	SLC43A3	solute carrier family 43, member 3	2.34	6.86	5.63	0.45	0.16	6.00E-04	1.09E-02	Multiple_Complex

TC0700009980.hg.1	PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	2.34	9.77	8.55	0.09	0.48	2.10E-03	2.04E-02	Multiple_Complex
TC1700006582.hg.1	OR3A3	olfactory receptor, family 3, subfamily A, member 3	2.34	6.72	5.49	1.07	0.48	1.57E-02	7.23E-02	Coding
TC0600009236.hg.1	RWDD1	RWD domain containing 1	2.34	12.82	11.6	0.06	0.26	6.00E-04	1.15E-02	Multiple_Complex
TC1200009931.hg.1	TAS2R46	taste receptor, type 2, member 46	2.34	7.15	5.93	0.11	0.82	9.60E-03	5.21E-02	Coding
TC0X00007075.hg.1	KDM6A	lysine (K)-specific demethylase 6A	2.34	10.68	9.46	0.02	0.24	2.00E-04	6.60E-03	Multiple_Complex
TC1900008456.hg.1	ELSPBP1	epididymal sperm binding protein 1	2.34	11.92	10.69	0.17	0.14	3.00E-04	7.70E-03	Coding
TC1200006616.hg.1	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	2.34	8.48	7.26	0.52	0.29	1.10E-03	1.44E-02	Multiple_Complex
TC0100018274.hg.1	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	2.34	6.39	5.17	0.68	0.43	5.10E-03	3.43E-02	NonCoding
TC1000010847.hg.1	DNA2	DNA replication helicase/nuclease 2	2.34	9.64	8.41	0.27	0.28	5.00E-04	1.04E-02	Multiple_Complex
TC0200016646.hg.1	MEMO1	mediator of cell motility 1	2.34	8.43	7.21	0.12	0.19	5.00E-04	1.07E-02	Multiple_Complex
TC1700007469.hg.1	ATAD5	ATPase family, AAA domain containing 5	2.33	10.32	9.1	0.02	0.48	6.00E-04	1.13E-02	Multiple_Complex
TC1700011451.hg.1	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	2.33	8.38	7.16	0.15	0.48	1.30E-03	1.56E-02	Multiple_Complex
TC0500013211.hg.1	APC	adenomatous polyposis coli	2.33	11.08	9.86	0.13	0.04	1.00E-04	6.00E-03	Multiple_Complex
TC1100008652.hg.1	TMEM126A	transmembrane protein 126A	2.33	13.61	12.39	0.03	0.34	7.00E-04	1.16E-02	Multiple_Complex
TC0600010008.hg.1	GTF2H5	general transcription factor IIH subunit 5	2.33	12.3	11.07	0.11	0.34	9.00E-04	1.31E-02	Coding
TC1000011964.hg.1	RAB11FIP2	RAB11 family interacting protein 2 (class I)	2.33	12.66	11.44	0.3	0.19	2.40E-03	2.17E-02	Multiple_Complex
TC0600013054.hg.1	SERINC1	serine incorporator 1	2.33	13.36	12.14	0.26	0.34	6.00E-04	1.08E-02	Multiple_Complex
TC2100007377.hg.1	KRTAP10-10	keratin associated protein 10-10	2.33	8.17	6.95	0.49	0.59	9.60E-03	5.21E-02	Coding
TC0600012740.hg.1	RTN4IP1	reticulon 4 interacting protein 1	2.33	11.65	10.44	0.05	0.09	2.00E-04	7.40E-03	Multiple_Complex
TC1600010987.hg.1	CMIP	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_198390	2.32	5.54	4.32	0.26	0.66	8.80E-03	4.93E-02	NonCoding

TC1500008328.hg.1	BLM	Bloom syndrome, RecQ helicase-like	2.32	12.53	11.31	0.03	0.04	1.00E-04	6.20E-03	Multiple_Complex
TC0100015234.hg.1	SLC16A4	solute carrier family 16, member 4	2.32	9.11	7.89	0.24	0.03	2.00E-04	6.80E-03	Multiple_Complex
TC0100014848.hg.1	CCBL2; RBMXL1	cysteine conjugate-beta lyase 2; RNA binding motif protein, X-linked-like 1	2.32	11.8	10.58	0.18	0.56	1.40E-03	1.60E-02	Multiple_Complex
TC1900011857.hg.1	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	2.32	13.02	11.81	0.19	0.38	9.00E-04	1.32E-02	Multiple_Complex
TC0800007993.hg.1	PI15	peptidase inhibitor 15	2.32	8	6.79	0.29	0.23	5.00E-04	1.02E-02	Multiple_Complex
TC0600009019.hg.1	SOBP	sine oculis binding protein homolog	2.32	9.53	8.32	0.27	0.64	2.50E-03	2.24E-02	Multiple_Complex
TC0400006773.hg.1	LOC650293	seven transmembrane helix receptor; Transcript Identified by AceView, Entrez Gene ID(s) 650293, RefSeq ID(s) NM_001040071	2.32	7.78	6.56	0.58	0.08	1.90E-03	1.89E-02	Multiple_Complex
TC0100014612.hg.1	CRYZ	crystallin zeta	2.32	10.37	9.16	0.02	0.2	5.00E-04	1.02E-02	Multiple_Complex
TC0600013186.hg.1	CTGF	connective tissue growth factor	2.32	7.3	6.09	0.29	0.2	4.00E-04	8.90E-03	Multiple_Complex
TC1400009016.hg.1	FBXO33	F-box protein 33	2.32	7.38	6.17	0.55	0.23	2.20E-03	2.07E-02	Multiple_Complex
TC0300013296.hg.1	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	2.31	14.93	13.72	0.05	0.36	1.40E-03	1.65E-02	Multiple_Complex
TC1200008642.hg.1	PARPBP	PARP1 binding protein	2.31	11.92	10.71	0.14	0.03	5.00E-04	1.07E-02	Multiple_Complex
TC1400010603.hg.1	TTC6	tetratricopeptide repeat domain 6	2.31	5.32	4.11	0.14	0.18	1.40E-03	1.63E-02	Multiple_Complex
TC0100016492.hg.1	RFWD2	ring finger and WD repeat domain 2, E3 ubiquitin protein ligase	2.31	8.63	7.42	0.69	0.19	1.20E-02	6.03E-02	Multiple_Complex
TC1400009198.hg.1	DDHD1	DDHD domain containing 1	2.31	10.34	9.13	0.23	0.34	7.00E-04	1.17E-02	Multiple_Complex
TC0100008503.hg.1	HOOK1	hook microtubule-tethering protein 1	2.31	14.04	12.83	0.11	0.07	6.20E-03	3.89E-02	Multiple_Complex
TC0200016586.hg.1	HSPE1-MOB4	HSPE1-MOB4 readthrough	2.31	11.9	10.69	0.09	0.21	2.00E-04	7.40E-03	Coding
TC0200013943.hg.1	SLC35F5	solute carrier family 35, member F5	2.31	10.25	9.05	0.04	0.29	5.00E-04	1.03E-02	Multiple_Complex

TC0200010511.hg.1	NBEAL1	neurobeachin like 1	2.31	9.95	8.74	0.28	0.06	4.00E-04	9.30E-03	Multiple_Complex
TC1600011042.hg.1	SLC38A8	Transcript Identified by AceView, Entrez Gene ID(s) 146167	2.31	8.02	6.81	0.11	0.77	1.93E-02	8.30E-02	Unassigned
TC0400010260.hg.1	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	2.31	8.59	7.38	0.34	0.56	2.70E-03	2.36E-02	Multiple_Complex
TSUnmapped00000478.hg.1	ZNF502	zinc finger protein 502	2.31	7.53	6.32	0.52	0.25	1.00E-03	1.39E-02	Coding
TC1600007739.hg.1	PHKB	phosphorylase kinase, beta	2.31	12.09	10.89	0.2	0.51	2.70E-03	2.31E-02	Multiple_Complex
TC0200007249.hg.1	GPATCH11	G-patch domain containing 11	2.31	10.77	9.56	0.05	0.13	6.00E-04	1.08E-02	Multiple_Complex
TC1300008111.hg.1	PROZ	protein Z, vitamin K-dependent plasma glycoprotein	2.3	5.29	4.09	0.09	0.16	4.80E-03	3.29E-02	Multiple_Complex
TC0600013898.hg.1	FAM103A1	Homo sapiens family with sequence similarity 103, member A1, mRNA (cDNA clone MGC:2560 IMAGE:2989772), complete cds.; Homo sapiens family with sequence similarity 103, member A1, mRNA (cDNA clone MGC:18029 IMAGE:3924570), complete cds.; Homo sapiens family with sequence similarity 103, member A1, mRNA (cDNA clone MGC:102778 IMAGE:5578103), complete cds.	2.3	12.21	11.01	0.09	0	2.00E-04	7.00E-03	Multiple_Complex
TC0500010515.hg.1	NUP155	nucleoporin 155kDa	2.3	11.59	10.38	0.1	0.07	1.00E-04	6.20E-03	Multiple_Complex
TC1900010789.hg.1	POU2F2	POU class 2 homeobox 2	2.3	7.05	5.85	0.14	0.7	3.80E-03	2.89E-02	Multiple_Complex

TC1500010914.hg.1	HDGFRP3	hepatoma-derived growth factor, related protein 3; Hepatoma-derived growth factor-related protein 3 [Source:UniProtKB/Swiss-Prot;Acc:Q9Y3E1]; Transcript Identified by AceView, Entrez Gene ID(s) 50810; Jeck2013, Memczak2013, Salzman2013 ANNOTATED, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_016073; Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_016073; Salzman2013 ANNOTATED, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_016073	2.3	8.98	7.78	0.35	0.54	3.50E-03	2.75E-02	Multiple_Complex
TC1000011017.hg.1	CFAP70	cilia and flagella associated protein 70	2.3	9.4	8.2	0.21	0.07	4.90E-03	3.37E-02	Multiple_Complex
TC0100014605.hg.1	LRRIQ3	leucine-rich repeats and IQ motif containing 3	2.3	8.59	7.39	0.3	0.49	1.50E-03	1.65E-02	Multiple_Complex
TC1600008627.hg.1	HSBP1	heat shock factor binding protein 1	2.3	14.95	13.75	0.02	0.19	2.00E-04	7.30E-03	Multiple_Complex
TC1100013160.hg.1	C11orf91	chromosome 11 open reading frame 91	2.3	6.22	5.02	0.4	0.21	6.00E-04	1.15E-02	Multiple_Complex
TC1400007321.hg.1	DACT1	Transcript Identified by AceView, Entrez Gene ID(s) 51339	2.3	5.34	4.14	0.22	0.03	1.40E-03	1.61E-02	Unassigned
TC0400008004.hg.1	MRPS18C	mitochondrial ribosomal protein S18C	2.3	14.7	13.5	0.03	0.31	7.00E-04	1.18E-02	Multiple_Complex
TC0700007244.hg.1	STARD3NL	STARD3 N-terminal like	2.3	13.05	11.85	0.06	0.19	1.80E-03	1.85E-02	Multiple_Complex
TC1700012191.hg.1	CD68	CD68 molecule	2.3	7.88	6.68	0.05	0.49	8.00E-04	1.24E-02	Coding
TC0100014218.hg.1	SCP2	Jeck2013 ANTISENSE, coding, INTERNAL, OVEXON, UTR3 best transcript NM_001007098	2.3	11.11	9.91	0.21	0.3	6.00E-04	1.15E-02	Multiple_Complex
TC0200016504.hg.1	CCDC138	coiled-coil domain containing 138	2.3	9.91	8.71	0.27	0.09	1.00E-03	1.37E-02	Multiple_Complex

TC0200010431.hg.1	NIF3L1	NIF3 NGG1 interacting factor 3-like 1	2.3	11.18	9.99	0.12	0.32	5.00E-04	1.02E-02	Multiple_Complex
TC1100007006.hg.1	LDHAL6A	lactate dehydrogenase A-like 6A	2.29	7.9	6.7	0.67	0.41	3.30E-03	2.62E-02	Coding
TC0200012734.hg.1	USP34	ubiquitin specific peptidase 34	2.29	13.69	12.49	0.19	0.34	5.00E-04	1.00E-02	Multiple_Complex
TC0X00010966.hg.1	ATP11C	ATPase, class VI, type 11C	2.29	12.06	10.86	0.12	0.12	9.00E-04	1.31E-02	Multiple_Complex
TC0200014244.hg.1	FAR2P1	fatty acyl-CoA reductase 2 pseudogene 1	2.29	8.29	7.09	0.07	0.3	1.30E-03	1.55E-02	Multiple_Complex
TC1200007822.hg.1	IKZF4	IKAROS family zinc finger 4	2.29	8.36	7.16	0.13	0.17	1.00E-02	5.35E-02	Multiple_Complex
TC1300007137.hg.1	RB1	retinoblastoma 1	2.29	10.64	9.45	0.09	0.48	1.00E-03	1.39E-02	Multiple_Complex
TC0200012639.hg.1	CLHC1	clathrin heavy chain linker domain containing 1	2.29	8.51	7.32	0.2	0.06	2.00E-04	7.20E-03	Multiple_Complex
TC1800008035.hg.1	PPP4R1	protein phosphatase 4, regulatory subunit 1	2.29	7.39	6.2	0.22	0.26	9.00E-04	1.32E-02	Multiple_Complex
TC1400007328.hg.1	DAAM1	dishevelled associated activator of morphogenesis 1	2.28	10.02	8.82	0.23	0.34	1.10E-03	1.48E-02	Multiple_Complex
TC1000007272.hg.1	CREM	cAMP responsive element modulator	2.28	12.61	11.42	0.06	0.43	1.50E-03	1.71E-02	Multiple_Complex
TC0200013567.hg.1	ANKRD36B	ankyrin repeat domain 36B	2.28	13.94	12.75	0	0.3	1.70E-03	1.80E-02	Multiple_Complex
TC1700009042.hg.1	AFMID	arylformamidase	2.28	9.39	8.2	0.28	0.31	7.00E-04	1.17E-02	Multiple_Complex
TC0400007933.hg.1	ANXA3	annexin A3	2.28	7.4	6.21	0.07	0.21	7.00E-04	1.17E-02	Multiple_Complex
TC0700008292.hg.1	STEAP1	six transmembrane epithelial antigen of the prostate 1	2.28	10.94	9.75	0.53	0.5	1.20E-02	6.04E-02	Multiple_Complex
TC1200008488.hg.1	PLXNC1	plexin C1	2.28	6.61	5.42	0.36	0.33	1.90E-03	1.89E-02	Multiple_Complex
TC0200011720.hg.1	ODC1; SNORA80B	ornithine decarboxylase 1; small nucleolar RNA, H/ACA box 80B	2.28	12.67	11.48	0.01	0.32	4.00E-04	9.30E-03	Multiple_Complex
TC1300009672.hg.1	CCDC168	coiled-coil domain containing 168	2.28	5.22	4.03	0.53	0.15	5.70E-03	3.70E-02	Coding
TC0400010606.hg.1	COMMD8	COMM domain containing 8	2.28	9.2	8.01	0.17	0.25	4.50E-03	3.20E-02	Multiple_Complex
TC1500009386.hg.1	GABPB1	GA binding protein transcription factor, beta subunit 1	2.28	11.2	10.01	0.1	0.44	6.00E-04	1.11E-02	Multiple_Complex

TC0700013395.hg.1	GTPBP10	GTP-binding protein 10 (putative)	2.28	11.51	10.32	0.13	0.04	3.00E-04	8.50E-03	Multiple_Complex
TC0100011611.hg.1	SPATA17	spermatogenesis associated 17	2.28	6.62	5.43	0.15	0.37	9.00E-04	1.28E-02	Multiple_Complex
TC0200012248.hg.1	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	2.28	5.87	4.68	0.49	0.01	7.00E-03	4.21E-02	Multiple_Complex
TC0X00008689.hg.1	MAGEA11	MAGE family member A11	2.28	7.34	6.15	0.21	0.91	7.20E-03	4.28E-02	Multiple_Complex
TC0200016499.hg.1	MRPL30	mitochondrial ribosomal protein L30	2.28	12.78	11.6	0.19	0.15	5.00E-04	9.90E-03	Multiple_Complex
TC2000008445.hg.1	FLRT3	fibronectin leucine rich transmembrane protein 3	2.27	9.15	7.96	0.24	0.42	1.43E-02	6.83E-02	Multiple_Complex
TC0X00008138.hg.1	ALG13	Transcript Identified by AceView, Entrez Gene ID(s) 79868	2.27	5.98	4.8	0.17	0.39	8.00E-04	1.23E-02	Unassigned
TC1200006959.hg.1	PTPRO	Transcript Identified by AceView, Entrez Gene ID(s) 5800	2.27	5.7	4.52	0.07	0.88	6.60E-03	4.06E-02	Unassigned
TC1000007564.hg.1	MAPK8	mitogen-activated protein kinase 8	2.27	13.16	11.98	0.18	0.05	1.30E-03	1.59E-02	Multiple_Complex
TC0500007641.hg.1	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	2.27	10.32	9.14	0.11	0.36	8.60E-03	4.85E-02	Multiple_Complex
TC1100008900.hg.1	C11orf70	chromosome 11 open reading frame 70	2.27	9.36	8.18	0.3	0.11	7.00E-04	1.19E-02	Multiple_Complex
TC0200013595.hg.1	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	2.27	10.76	9.58	0.37	0.13	1.33E-02	6.49E-02	Multiple_Complex
TC0600011234.hg.1	HIST1H4L	histone cluster 1, H4l	2.27	4.46	3.28	0.59	0.12	4.10E-03	3.02E-02	Coding
TC2200008513.hg.1	RFPL3S	RFPL3 antisense	2.27	5.44	4.26	0.36	0.19	2.70E-03	2.32E-02	Multiple_Complex
TC0400012452.hg.1	FBXO8	F-box protein 8	2.26	11.63	10.45	0.07	0.11	3.00E-04	8.30E-03	Coding
TC1200011767.hg.1	SLC41A2	solute carrier family 41 (magnesium transporter), member 2	2.26	9.76	8.58	0.06	0.22	9.00E-04	1.31E-02	Multiple_Complex
TC1000008423.hg.1	RPP30	ribonuclease P/MRP 30kDa subunit	2.26	14.75	13.57	0.04	0.17	7.00E-04	1.17E-02	Multiple_Complex
TC1000011488.hg.1	SORBS1	Transcript Identified by AceView, Entrez Gene ID(s) 10580	2.26	4.65	3.47	0.28	0.2	1.20E-03	1.51E-02	Unassigned

TC0300012252.hg.1	SNX4	sorting nexin 4	2.26	9.52	8.34	0.04	0.09	4.80E-03	3.33E-02	Multiple_Complex
TC0X00008578.hg.1	F9	coagulation factor IX	2.26	6.02	4.84	0.74	0.16	6.40E-03	3.98E-02	Multiple_Complex
TC0300010068.hg.1	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	2.26	9.69	8.51	0.17	0.2	6.00E-04	1.09E-02	Multiple_Complex
TC1500007659.hg.1	PIAS1	protein inhibitor of activated STAT 1	2.26	12.18	11	0.02	0.45	8.00E-04	1.25E-02	Multiple_Complex
TC0700010621.hg.1	FKBP14	FK506 binding protein 14	2.26	11.37	10.19	0.28	0.01	6.00E-04	1.10E-02	Multiple_Complex
TC0100016345.hg.1	NME7	NME/NM23 family member 7	2.26	9.33	8.15	0.17	0.09	1.20E-03	1.52E-02	Multiple_Complex
TC1900007826.hg.1	ZNF30	zinc finger protein 30	2.26	8.2	7.03	0.3	0.34	8.00E-04	1.27E-02	Multiple_Complex
TC1300010031.hg.1	CCDC169-SOHLH2	CCDC169-SOHLH2 readthrough	2.26	5.05	3.88	0.05	1.02	1.10E-02	5.73E-02	Coding
TC0500008540.hg.1	PHAX	phosphorylated adaptor for RNA export	2.26	12.1	10.93	0.11	0.16	6.00E-04	1.14E-02	Multiple_Complex
TC0500011448.hg.1	ARRDC3	arrestin domain containing 3	2.26	8.43	7.26	0.08	0.74	3.60E-03	2.78E-02	Multiple_Complex
TC0400008557.hg.1	USP53	ubiquitin specific peptidase 53	2.26	10.34	9.17	0.01	0.26	4.00E-04	9.60E-03	Multiple_Complex
TC1000008363.hg.1	PTEN	phosphatase and tensin homolog	2.26	10.61	9.44	0.03	0.04	2.00E-04	6.60E-03	Multiple_Complex
TC1100008979.hg.1	CUL5	cullin 5	2.25	13.37	12.2	0.23	0.19	6.00E-04	1.13E-02	Multiple_Complex
TC0200015193.hg.1	CALCRL	calcitonin receptor like receptor	2.25	5.61	4.44	0.21	0.62	3.00E-03	2.50E-02	Multiple_Complex
TC0500007912.hg.1	ZFYVE16	zinc finger, FYVE domain containing 16	2.25	9.71	8.54	0.02	0.23	9.00E-04	1.29E-02	Multiple_Complex
TC0700013605.hg.1	PNPLA8	patatin-like phospholipase domain containing 8	2.25	12.07	10.9	0.34	0.32	1.80E-03	1.86E-02	Multiple_Complex
TC1200011965.hg.1	NAA25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	2.25	7.43	6.26	0	0.61	2.70E-03	2.32E-02	Multiple_Complex
TC0600009327.hg.1	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	2.25	8.8	7.63	0.35	0.5	1.22E-02	6.11E-02	Multiple_Complex
TC1900011799.hg.1	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	2.25	6.01	4.84	0.43	0.26	1.60E-03	1.72E-02	Multiple_Complex

TC0200009922.hg.1	UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	2.25	12.74	11.58	0.07	0.02	3.00E-04	8.30E-03	Multiple_Complex
TC0600009508.hg.1	TBPL1	TBP-like 1	2.24	10.14	8.98	0.08	0.25	2.10E-03	2.04E-02	Multiple_Complex
TC0500011160.hg.1	ANKRD31	ankyrin repeat domain 31	2.24	8.33	7.16	0.04	0.39	2.64E-02	1.03E-01	Multiple_Complex
TC1400009842.hg.1	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	2.24	10.88	9.72	0.43	0.22	9.00E-04	1.29E-02	Multiple_Complex
TC1900006655.hg.1	MRPL54	mitochondrial ribosomal protein L54	2.24	9.55	8.38	0.13	0.63	3.70E-03	2.84E-02	Coding
TC0100013619.hg.1	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand	2.24	14.18	13.02	0.12	0.17	1.20E-03	1.50E-02	Multiple_Complex
TC1200011574.hg.1	FGD6	FYVE, RhoGEF and PH domain containing 6	2.24	8.07	6.9	0.08	0.16	4.00E-04	9.10E-03	Multiple_Complex
TC0200014617.hg.1	NEB	nebulin	2.24	8.92	7.76	0.03	0.12	5.80E-03	3.71E-02	Multiple_Complex
TC0600013361.hg.1	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain, 2	2.24	9.46	8.3	0.1	0.42	1.30E-03	1.57E-02	Coding
TC0300008047.hg.1	NSUN3	NOP2/Sun domain family, member 3	2.24	10.24	9.08	0.13	0.38	9.00E-04	1.30E-02	Multiple_Complex
TC0400010768.hg.1	AASDH	aminoadipate-semialdehyde dehydrogenase	2.24	8.99	7.83	0.18	0.17	1.00E-03	1.40E-02	Multiple_Complex
TC1700011364.hg.1	BRIP1	BRCA1 interacting protein C-terminal helicase 1	2.24	9.64	8.48	0	0.06	3.00E-04	8.00E-03	Multiple_Complex
TC0100014617.hg.1	SLC44A5	solute carrier family 44, member 5	2.24	11.05	9.89	0.03	0.08	5.30E-03	3.51E-02	Multiple_Complex
TC0700013472.hg.1	MGAM	maltase-glucoamylase	2.23	6.3	5.14	0.78	0.09	4.50E-03	3.18E-02	Multiple_Complex
TC0600012971.hg.1	ZUFSP	zinc finger with UFM1-specific peptidase domain	2.23	12.76	11.6	0.02	0.26	1.90E-03	1.90E-02	Multiple_Complex
TC0300013636.hg.1	ACAP2; ACAP2-IT1; AC090018.3	Transcript Identified by AceView, Entrez Gene ID(s) 23527; ACAP2 intronic transcript 1 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:41426]; novel transcript; ACAP2 intronic transcript 1 [Source:HGNC Symbol;Acc:HGNC:41426]	2.23	7.04	5.88	0.57	0.08	3.07E-02	1.13E-01	NonCoding

TC1300007251.hg.1	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone	2.23	10.62	9.46	0.14	0.35	1.30E-03	1.57E-02	Multiple_Complex
TC0400006994.hg.1	NCAPG	non-SMC condensin I complex subunit G	2.23	12.39	11.23	0.14	0.26	4.00E-04	9.30E-03	Multiple_Complex
TC0400007991.hg.1	COPS4	COP9 signalosome subunit 4	2.23	9.9	8.74	0.57	0.28	9.20E-03	5.04E-02	Multiple_Complex
TC0800010285.hg.1	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	2.23	8.69	7.53	0.7	0.13	3.60E-03	2.80E-02	Multiple_Complex
TC0300008561.hg.1	PARP14	poly(ADP-ribose) polymerase family member 14	2.23	5.63	4.47	0.02	0.37	6.00E-04	1.08E-02	Multiple_Complex
TC0100013349.hg.1	RSRP1	arginine/serine-rich protein 1	2.23	9.68	8.52	0.22	0.28	8.00E-04	1.25E-02	Multiple_Complex
TC1400007093.hg.1	KLHDC1	kelch domain containing 1	2.23	7.61	6.46	0.18	0.1	3.00E-04	8.90E-03	Multiple_Complex
TC1100007514.hg.1	OR4B1	olfactory receptor, family 4, subfamily B, member 1	2.23	4.73	3.57	0.21	0.05	1.60E-03	1.73E-02	Coding
TC0200006715.hg.1	PQLC3	PQ loop repeat containing 3	2.23	8.36	7.2	0.13	0.15	1.00E-03	1.40E-02	Multiple_Complex
TC0100018434.hg.1	MYCBP; GJA9	MYC binding protein; gap junction protein alpha 9	2.23	14.38	13.22	0.08	0.35	1.50E-03	1.69E-02	Multiple_Complex
TC0200016699.hg.1	TRABD2A	TraB domain containing 2A	2.23	7.54	6.38	0.37	0.35	1.10E-03	1.46E-02	Multiple_Complex
TC0X00009256.hg.1	KLHL15	kelch-like family member 15	2.23	12.68	11.53	0.05	0.26	3.00E-04	8.00E-03	Coding
TC2000008910.hg.1	EIF2S2	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_003908	2.23	7.4	6.24	0.47	0.73	6.70E-03	4.08E-02	NonCoding
TC1400010599.hg.1	TTC6	tetratricopeptide repeat domain 6	2.23	6.34	5.18	0.28	0.02	4.00E-03	2.98E-02	Multiple_Complex
TC1000011993.hg.1	PRDX3	peroxiredoxin 3	2.23	13.15	12	0.32	0.15	6.00E-04	1.08E-02	Multiple_Complex
TC0100011592.hg.1	KCTD3	potassium channel tetramerization domain containing 3	2.23	8.69	7.54	0.15	0.35	2.20E-03	2.06E-02	Multiple_Complex
TC0500012539.hg.1	FAM114A2	family with sequence similarity 114, member A2	2.23	10.65	9.5	0.25	0.01	6.00E-04	1.13E-02	Multiple_Complex
TC1000012585.hg.1	CHUK	conserved helix-loop-helix ubiquitous kinase	2.22	13	11.85	0.1	0.25	1.00E-03	1.39E-02	Multiple_Complex
TC1500009946.hg.1	MYO9A	myosin IXA	2.22	10.94	9.79	0.21	0.35	1.17E-02	5.95E-02	Multiple_Complex

TC0700013224.hg.1	LMBR1	Transcript Identified by AceView, Entrez Gene ID(s) 64327	2.22	8.76	7.6	0.28	0.39	1.90E-03	1.90E-02	Unassigned
TC1100010531.hg.1	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	2.22	6.52	5.37	0.54	0.26	2.10E-03	2.04E-02	Multiple_Complex
TC1200010292.hg.1	AMN1	antagonist of mitotic exit network 1 homolog	2.22	8.07	6.92	0.06	0.27	1.30E-03	1.57E-02	Multiple_Complex
TC0300007050.hg.1	C3orf35	chromosome 3 open reading frame 35	2.22	6.66	5.51	0.1	0.26	4.00E-04	9.80E-03	Multiple_Complex
TC1200007406.hg.1	IRAK4	interleukin 1 receptor associated kinase 4	2.22	10.42	9.27	0.34	0.38	1.40E-03	1.62E-02	Multiple_Complex
TC1500007121.hg.1	SPATA5L1	spermatogenesis associated 5-like 1	2.22	10.21	9.06	0	0.39	7.00E-04	1.17E-02	Multiple_Complex
TC0700007178.hg.1	07-Sep	septin 7	2.22	13.36	12.21	0.05	0.47	1.50E-03	1.67E-02	Multiple_Complex
TC0100011096.hg.1	NEK7	NIMA-related kinase 7	2.22	7.29	6.14	0.01	0.69	6.10E-03	3.84E-02	Multiple_Complex
TC0400009088.hg.1	GUCY1B3	guanylate cyclase 1, soluble, beta 3	2.22	9.78	8.63	0.2	0.08	2.50E-03	2.24E-02	Multiple_Complex
TC0X00008125.hg.1	PAK3	p21 protein (Cdc42/Rac)-activated kinase 3	2.22	8.52	7.38	0.16	0.23	8.00E-04	1.26E-02	Multiple_Complex
TC1800007037.hg.1	MEP1B	meprin A, beta	2.22	5.3	4.15	0.55	0.06	4.00E-03	2.98E-02	Multiple_Complex
TC1700008423.hg.1	OR4D2	olfactory receptor, family 4, subfamily D, member 2	2.21	6.78	5.63	0.46	0.35	1.80E-03	1.88E-02	Coding
TC0300014063.hg.1	ANKUB1	ankyrin repeat and ubiquitin domain containing 1	2.21	7.39	6.25	0.11	0.08	3.00E-04	7.90E-03	NonCoding
TC0X00010875.hg.1	PLAC1	placenta specific 1	2.21	10.67	9.52	0.66	0.34	1.83E-02	8.03E-02	Multiple_Complex
TC1000009742.hg.1	KIN	Kin17 DNA and RNA binding protein	2.21	11.44	10.3	0.06	0.08	3.00E-04	8.80E-03	Multiple_Complex
TC0200014650.hg.1	LOC100144595; AC009227.2; tikure	uncharacterized LOC100144595; novel transcript; Transcript Identified by AceView	2.21	7.4	6.26	0.17	0.22	2.00E-03	1.96E-02	Multiple_Complex
TC0200015429.hg.1	ALS2CR11	amyotrophic lateral sclerosis 2 chromosome region candidate 11	2.21	5.84	4.69	0.25	0.01	6.00E-04	1.11E-02	Multiple_Complex
TC0400012640.hg.1	CCDC110	coiled-coil domain containing 110	2.21	7.07	5.92	0.2	0.13	1.20E-03	1.54E-02	Coding

TC0X00009208.hg.1	CXorf23	chromosome X open reading frame 23	2.21	7.67	6.53	0.11	0.54	2.10E-03	2.00E-02	Multiple_Complex
TC1500009738.hg.1	KIAA0101; CSNK1G1	KIAA0101; casein kinase 1, gamma 1	2.21	13.43	12.28	0.03	0.12	2.00E-04	7.20E-03	Multiple_Complex
TC0200015721.hg.1	TMBIM1; MIR6513	transmembrane BAX inhibitor motif containing 1; microRNA 6513	2.21	8.99	7.84	0.82	0.08	8.80E-03	4.93E-02	Multiple_Complex
TC1300006974.hg.1	NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	2.21	10.53	9.39	0.11	0.1	9.00E-04	1.31E-02	Multiple_Complex
TC0100014638.hg.1	PIGK	phosphatidylinositol glycan anchor biosynthesis class K	2.21	13.84	12.7	0.19	0.15	7.00E-04	1.17E-02	Multiple_Complex
TC0400009525.hg.1	ANKRD37	ankyrin repeat domain 37	2.21	10.18	9.04	0.36	0.42	6.20E-03	3.90E-02	Multiple_Complex
TC0900006886.hg.1	TEK	TEK tyrosine kinase, endothelial	2.2	5.19	4.05	0.53	0.31	3.70E-03	2.83E-02	Multiple_Complex
TC0800011395.hg.1	LRP12	LDL receptor related protein 12	2.2	7.92	6.78	0.35	0.69	9.00E-03	4.99E-02	Multiple_Complex
TC0800007119.hg.1	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	2.2	8.69	7.55	0.4	0.38	2.00E-03	1.98E-02	Multiple_Complex
TC1200011598.hg.1	HAL	histidine ammonia-lyase	2.2	6.19	5.05	0.34	0.24	8.00E-04	1.24E-02	Multiple_Complex
TC0800012476.hg.1	JRK	Jrk helix-turn-helix protein	2.2	10.77	9.64	0.45	0.48	5.80E-03	3.74E-02	NonCoding
TC2000006894.hg.1	KIZ	kizuna centrosomal protein	2.19	11.15	10.02	0.28	0.09	6.00E-04	1.13E-02	Multiple_Complex
TC0800012424.hg.1	COPS5	COP9 signalosome subunit 5	2.19	11.34	10.21	0.13	0.4	1.00E-03	1.40E-02	Multiple_Complex
TC0500008767.hg.1	PKD2L2	polycystic kidney disease 2-like 2	2.19	5.78	4.64	0.18	0.16	4.00E-04	9.30E-03	Coding
TC0500009881.hg.1	MRPL36	mitochondrial ribosomal protein L36	2.19	12.24	11.11	0.3	0.35	2.00E-03	2.00E-02	Multiple_Complex
TC0600007512.hg.1	TRIM15	tripartite motif containing 15	2.19	4.25	3.12	0.76	0.03	1.78E-02	7.87E-02	Multiple_Complex
TC1000009919.hg.1	TRDMT1	tRNA aspartic acid methyltransferase 1	2.19	8.89	7.76	0.11	0.27	1.00E-03	1.41E-02	Multiple_Complex
TC1500009737.hg.1	PPIB	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic, OVERLAPTX, OVEXON best transcript NM_000942	2.19	7.91	6.78	1.22	0.32	3.71E-02	1.28E-01	NonCoding

TC1900011741.hg.1	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	2.19	4.86	3.73	0.15	0.59	2.00E-03	1.96E-02	Multiple_Complex
TC0300009280.hg.1	KCNAB1	Transcript Identified by AceView, Entrez Gene ID(s) 7881	2.19	6.28	5.15	0.26	0.01	1.20E-03	1.52E-02	Unassigned
TC0400007280.hg.1	WDR19	WD repeat domain 19	2.19	9.55	8.42	0.25	0.35	3.30E-03	2.62E-02	Multiple_Complex
TC0200012977.hg.1	MXD1	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001202514	2.19	7.97	6.84	0.16	0.35	6.00E-04	1.15E-02	NonCoding
TC1000008011.hg.1	OIT3	oncoprotein induced transcript 3	2.19	5.6	4.48	0.15	0.72	4.40E-03	3.16E-02	Multiple_Complex
TC0X00009498.hg.1	FUNDC1	FUN14 domain containing 1	2.19	11.75	10.62	0.02	0.15	1.60E-03	1.72E-02	Multiple_Complex
TC0100018454.hg.1	ARHGAP29	Rho GTPase activating protein 29	2.18	9.31	8.19	0.31	0.13	1.00E-03	1.40E-02	Multiple_Complex
TC1100012318.hg.1	IL18	interleukin 18	2.18	4.84	3.71	0.15	0.13	6.00E-04	1.08E-02	Multiple_Complex
TC1100012208.hg.1	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)	2.18	9.02	7.89	0.14	0.57	2.50E-03	2.25E-02	Multiple_Complex
TC0X00010356.hg.1	BTK	Bruton agammaglobulinemia tyrosine kinase	2.18	6.59	5.47	0.32	0.03	6.00E-04	1.13E-02	Multiple_Complex
TC1900008369.hg.1	HIF3A	hypoxia inducible factor 3, alpha subunit	2.18	5.72	4.59	0.83	0.18	7.20E-03	4.29E-02	Multiple_Complex
TC1200010448.hg.1	GXYLT1	glucoside xylosyltransferase 1	2.18	9.35	8.22	0.02	0.42	6.90E-03	4.17E-02	Multiple_Complex
TC1800007101.hg.1	KIAA1328	KIAA1328	2.18	10.61	9.48	0.21	0.23	3.20E-03	2.56E-02	Multiple_Complex
TC1400008642.hg.1	OR10G2	olfactory receptor, family 10, subfamily G, member 2	2.18	4.88	3.75	0.97	0.21	2.92E-02	1.10E-01	Coding
TC0500008602.hg.1	LYRM7	LYR motif containing 7	2.18	11.8	10.67	0.1	0.49	3.30E-03	2.62E-02	Multiple_Complex
TC1500007754.hg.1	THSD4	Transcript Identified by AceView, Entrez Gene ID(s) 79875	2.18	5.31	4.18	0.28	0.42	4.20E-03	3.07E-02	Unassigned
TC0700006977.hg.1	NFE2L3	nuclear factor, erythroid 2-like 3	2.18	10.33	9.2	0.11	0.09	8.00E-04	1.23E-02	Multiple_Complex
TC0100008334.hg.1	ZYG11A	zyg-11 family member A, cell cycle regulator	2.18	8.79	7.67	0.22	0.38	1.30E-03	1.57E-02	Multiple_Complex
TC1900010089.hg.1	ZNF682	zinc finger protein 682	2.18	8.41	7.28	0.22	0.42	1.10E-03	1.44E-02	Multiple_Complex

TC0100014392.hg.1	TM2D1	TM2 domain containing 1	2.18	14.17	13.05	0.38	0.26	5.30E-03	3.53E-02	Multiple_Complex
TC1000008406.hg.1	KIF20B	kinesin family member 20B	2.18	11.55	10.43	0.1	0.23	6.00E-04	1.13E-02	Multiple_Complex
TC1400007337.hg.1	JKAMP	JNK1/MAPK8-associated membrane protein	2.18	11.59	10.47	0.49	0.38	3.70E-03	2.84E-02	Multiple_Complex
TC0200008262.hg.1	RNF181	ring finger protein 181	2.18	9.04	7.92	0.65	0.36	1.51E-02	7.04E-02	Multiple_Complex
TC0100010905.hg.1	SWT1	SWT1 RNA endoribonuclease homolog	2.18	6.96	5.84	0.3	0.15	1.00E-03	1.38E-02	Multiple_Complex
TC0800008484.hg.1	DCAF13	DDB1 and CUL4 associated factor 13	2.18	12.31	11.19	0.23	0.09	1.00E-03	1.41E-02	Multiple_Complex
TC0600011184.hg.1	HIST1H2BJ	histone cluster 1, H2bj	2.18	10.69	9.56	0.23	0.34	1.10E-03	1.43E-02	Multiple_Complex
TC1700009861.hg.1	TVP23C; CDRT4; TVP23C-CDRT4	trans-golgi network vesicle protein 23 homolog C (S. cerevisiae); CMT1A duplicated region transcript 4; TVP23C-CDRT4 readthrough	2.17	13.46	12.34	0	0.04	7.00E-04	1.18E-02	Multiple_Complex
TC0800012290.hg.1	UBXN8	UBX domain protein 8	2.17	9.12	8	0.31	0.22	1.50E-03	1.66E-02	Multiple_Complex
TC0300009412.hg.1	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	2.17	13.21	12.09	0.13	0.03	4.00E-04	9.30E-03	Multiple_Complex
TC0800007870.hg.1	CSPP1	centrosome and spindle pole associated protein 1	2.17	8.71	7.59	0.21	0.32	1.10E-03	1.47E-02	Multiple_Complex
TC0300013923.hg.1	IL5RA	interleukin 5 receptor, alpha	2.17	7.32	6.2	0.44	0.05	1.30E-03	1.59E-02	Multiple_Complex
TC0400007848.hg.1	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	2.17	6.45	5.33	0.32	0.66	5.70E-03	3.71E-02	Multiple_Complex
TC2000010015.hg.1	WFDC6	WAP four-disulfide core domain 6	2.17	5.8	4.68	0.17	0.16	5.00E-04	1.00E-02	Coding
TC1000007698.hg.1	CISD1	CDGSH iron sulfur domain 1	2.17	15.09	13.97	0.04	0.24	6.00E-04	1.13E-02	Multiple_Complex
TC0400010024.hg.1	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	2.17	5.12	4	0.21	0.12	2.80E-03	2.41E-02	Multiple_Complex
TC0400008389.hg.1	RRH	retinal pigment epithelium-derived rhodopsin homolog	2.17	6.57	5.45	0.51	0.12	1.40E-03	1.60E-02	Coding
TC0500007452.hg.1	MAP3K1	mitogen-activated protein kinase kinase kinase 1, E3 ubiquitin protein ligase	2.17	6.76	5.64	0.25	0.18	8.00E-04	1.25E-02	Multiple_Complex

TC0100012221.hg.1	C1orf101	chromosome 1 open reading frame 101	2.17	8.99	7.87	0.16	0.18	1.10E-03	1.44E-02	Multiple_Complex
TC0100008114.hg.1	UROD	uroporphyrinogen decarboxylase	2.17	9.65	8.53	0.04	0.33	6.00E-04	1.10E-02	Multiple_Complex
TC0700013397.hg.1	CDK14	cyclin-dependent kinase 14	2.17	7.11	5.99	0.23	0.95	1.19E-02	6.02E-02	Multiple_Complex
TC1700009857.hg.1	TEKT3	tektin 3	2.17	6.71	5.59	0.49	0.29	2.98E-02	1.11E-01	Multiple_Complex
TC1400007307.hg.1	ARID4A	AT rich interactive domain 4A (RBP1-like)	2.17	12.16	11.04	0.15	0	5.00E-04	1.05E-02	Multiple_Complex
TC1400007442.hg.1	ZBTB1	zinc finger and BTB domain containing 1	2.17	10.34	9.23	0.41	0.3	1.60E-03	1.72E-02	Multiple_Complex
TC1900011883.hg.1	ZNF799	zinc finger protein 799	2.17	8.85	7.73	0.02	0.1	1.00E-03	1.41E-02	Multiple_Complex
TC0200010328.hg.1	SLC39A10	solute carrier family 39 (zinc transporter), member 10	2.17	13.03	11.92	0.03	0.23	1.00E-03	1.40E-02	Multiple_Complex
TC0X00011311.hg.1	ARMCX5-GPRASP2	ARMCX5-GPRASP2 readthrough	2.17	9.87	8.75	0.52	0.56	1.00E-02	5.32E-02	Multiple_Complex
TC0400011414.hg.1	TRMT10A	tRNA methyltransferase 10A	2.17	7.93	6.82	0.31	0.26	3.50E-03	2.74E-02	Multiple_Complex
TC0500007251.hg.1	FBXO4	F-box protein 4	2.17	9.42	8.31	0.61	0.36	7.20E-03	4.30E-02	Multiple_Complex
TC1600009664.hg.1	ACSM1	acyl-CoA synthetase medium-chain family member 1	2.17	4.38	3.27	0.46	0.03	1.24E-02	6.19E-02	Multiple_Complex
TC0800011086.hg.1	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	2.17	9.25	8.13	0.03	0.79	7.70E-03	4.49E-02	Multiple_Complex
TC0600010757.hg.1	SLC35B3	solute carrier family 35 (adenosine 3-phospho 5-phosphosulfate transporter), member B3	2.17	10	8.88	0.07	0.12	1.00E-03	1.39E-02	Multiple_Complex
TC1100010787.hg.1	TRIM64C	tripartite motif containing 64C	2.16	5.65	4.53	0.15	0.44	4.80E-03	3.31E-02	Coding
TC0200011361.hg.1	DUSP28	dual specificity phosphatase 28	2.16	5.11	4	0.1	0.02	5.00E-04	1.07E-02	Multiple_Complex
TC1200011535.hg.1	UBE2N	ubiquitin conjugating enzyme E2N	2.16	12.43	11.32	0.3	0.26	1.00E-03	1.42E-02	Multiple_Complex
TC1700011366.hg.1	INTS2	integrator complex subunit 2	2.16	12.84	11.73	0.32	0.16	1.00E-03	1.40E-02	Multiple_Complex
TC0600012064.hg.1	GCM1	glial cells missing homolog 1 (Drosophila)	2.16	7.19	6.08	0.27	0.23	2.80E-03	2.41E-02	Coding

TC1300007565.hg.1	SLAIN1	SLAIN motif family member 1	2.16	11.65	10.53	0.26	0.19	7.00E-04	1.17E-02	Multiple_Complex
TC1700012349.hg.1	NAA38	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	2.16	14.68	13.57	0.11	0.49	6.40E-03	3.96E-02	Multiple_Complex
TC0500013259.hg.1	MFAP3	microfibrillar associated protein 3	2.16	9.55	8.44	0.3	0.01	7.00E-04	1.20E-02	Multiple_Complex
TC1100010175.hg.1	RRAS2	related RAS viral (r-ras) oncogene homolog 2	2.16	11.94	10.83	0.05	0.3	1.90E-03	1.91E-02	Multiple_Complex
TC0600007842.hg.1	SRSF3	serine/arginine-rich splicing factor 3	2.16	13.21	12.11	0.26	0.11	5.00E-04	1.00E-02	Multiple_Complex
TC0500011219.hg.1	AP3B1	adaptor-related protein complex 3, beta 1 subunit	2.16	10.58	9.47	0.22	0.02	4.00E-04	9.80E-03	Multiple_Complex
TC1200009928.hg.1	TAS2R19	taste receptor, type 2, member 19	2.16	5.74	4.63	0.13	0.38	5.40E-03	3.54E-02	Coding
TC0800010937.hg.1	FABP9	fatty acid binding protein 9, testis	2.15	4.83	3.73	0.68	0.47	1.32E-02	6.44E-02	Coding
TC0300014076.hg.1	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	2.15	6.05	4.95	0.68	0.11	4.20E-03	3.05E-02	Multiple_Complex
TC1600007530.hg.1	ITGAM	Transcript Identified by AceView, Entrez Gene ID(s) 3684	2.15	6.72	5.62	0.37	0.58	3.13E-02	1.15E-01	Unassigned
TC0600009439.hg.1	TMEM200A	transmembrane protein 200A	2.15	8.64	7.53	0.61	0.2	3.50E-03	2.72E-02	Coding
TC1800007215.hg.1	HAUS1	HAUS augmin like complex subunit 1	2.15	14.13	13.02	0.07	0.33	1.60E-03	1.74E-02	Multiple_Complex
TC0900012216.hg.1	IFNA17	interferon, alpha 17	2.15	5.5	4.39	0.71	0.05	4.20E-03	3.04E-02	Coding
TC1500009363.hg.1	COPS2	COP9 signalosome subunit 2	2.15	12.67	11.57	0.28	0.29	2.10E-03	2.02E-02	Multiple_Complex
TC1100013016.hg.1	PGA4	pepsinogen 4, group I (pepsinogen A)	2.15	6.96	5.86	0.38	0.37	2.10E-03	2.02E-02	Multiple_Complex
TC0900007100.hg.1	NPR2	natriuretic peptide receptor 2	2.15	6.61	5.5	0.02	0.42	1.27E-02	6.28E-02	Multiple_Complex
TC1200012668.hg.1	TRHDE	thyrotropin-releasing hormone degrading enzyme	2.15	7.66	6.55	0.29	0.86	1.19E-02	6.02E-02	Multiple_Complex
TC0400011524.hg.1	TBCK	TBC1 domain containing kinase	2.15	8.76	7.66	0.2	0.53	1.05E-02	5.54E-02	Multiple_Complex
TC0600014144.hg.1	PHF3	PHD finger protein 3	2.15	6.71	5.61	0.34	0.44	2.80E-03	2.40E-02	NonCoding
TC1200012768.hg.1	RERG	RAS-like, estrogen-regulated, growth inhibitor	2.15	9.39	8.29	0.03	0.07	7.00E-04	1.16E-02	Multiple_Complex
TC0700013457.hg.1	FSCN3	fascin actin-bundling protein 3, testicular	2.15	5.48	4.37	0.08	0.29	3.00E-03	2.50E-02	Multiple_Complex

TC1100011247.hg.1	RNASEH2C	ribonuclease H2, subunit C	2.15	13.9	12.8	0.01	0.17	7.00E-04	1.21E-02	Multiple_Complex
TC1200006561.hg.1	RAD51AP1	RAD51 associated protein 1	2.15	13.52	12.42	0.15	0.31	1.90E-03	1.93E-02	Multiple_Complex
TC1600007439.hg.1	C16orf92	chromosome 16 open reading frame 92	2.14	5.2	4.1	0.52	0.08	1.80E-03	1.86E-02	Coding
TC0200010246.hg.1	WDR75	WD repeat domain 75	2.14	12.6	11.5	0.18	0.4	1.70E-03	1.78E-02	Multiple_Complex
TC0700006933.hg.1	STK31	serine/threonine kinase 31	2.14	5.26	4.16	0.3	0.11	1.50E-03	1.71E-02	Multiple_Complex
TC1700006702.hg.1	TXNDC17	thioredoxin domain containing 17	2.14	14.81	13.71	0.1	0.26	1.10E-03	1.46E-02	Multiple_Complex
TC0900007492.hg.1	PIP5K1B	Transcript Identified by AceView, Entrez Gene ID(s) 8395	2.14	5.15	4.06	0.63	0.79	2.81E-02	1.07E-01	Unassigned
TC0300008017.hg.1	ZNF654	zinc finger protein 654	2.14	9.62	8.52	0.15	0.37	1.58E-02	7.29E-02	Coding
TC0700008536.hg.1	SPDYE3	speedy/RINGO cell cycle regulator family member E3	2.14	7.37	6.27	0.09	0.04	1.10E-03	1.48E-02	Multiple_Complex
TC1300009673.hg.1	TEX30	testis expressed 30	2.14	12.48	11.38	0.18	0.31	1.30E-03	1.56E-02	Multiple_Complex
TC1200007251.hg.1	KIAA1551	KIAA1551	2.14	9.07	7.97	0.39	0.34	1.90E-03	1.89E-02	Multiple_Complex
TC0400008618.hg.1	FGF2	fibroblast growth factor 2 (basic)	2.14	9.78	8.68	0.26	0.01	1.20E-03	1.50E-02	Multiple_Complex
TC1000007846.hg.1	SIRT1	sirtuin 1	2.14	13.24	12.14	0.01	0.25	5.00E-04	1.05E-02	Multiple_Complex
TC0900007488.hg.1	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	2.14	9.65	8.55	0.05	0.29	8.00E-04	1.25E-02	Multiple_Complex
TC1900006977.hg.1	ICAM1	intercellular adhesion molecule 1	2.13	7.99	6.9	0.69	0.12	4.20E-03	3.04E-02	Multiple_Complex
TC0300012572.hg.1	CEP70	centrosomal protein 70kDa	2.13	10.32	9.22	0.37	0.12	1.50E-03	1.65E-02	Multiple_Complex
TC1100009426.hg.1	PATE1	prostate and testis expressed 1	2.13	6.06	4.96	0.5	0.61	1.46E-02	6.88E-02	Multiple_Complex
TC0800007995.hg.1	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	2.13	8.42	7.33	0.05	0.2	5.00E-04	1.02E-02	Multiple_Complex
TC2000009265.hg.1	CDH22	Transcript Identified by AceView, Entrez Gene ID(s) 64405	2.13	6.2	5.1	0.67	0.52	7.30E-03	4.32E-02	Unassigned
TC0700009411.hg.1	MGAM2	maltase-glucoamylase 2 (putative)	2.13	4.38	3.29	0.5	0.39	3.70E-03	2.83E-02	Multiple_Complex

TC1400009006.hg.1	TRAPPC6B	trafficking protein particle complex 6B	2.13	10.36	9.27	0.26	0.05	6.00E-04	1.13E-02	Multiple_Complex
TC0800008370.hg.1	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	2.13	15.04	13.95	0.15	0.45	6.60E-03	4.06E-02	Multiple_Complex
TC1100010400.hg.1	LGR4	leucine-rich repeat containing G protein-coupled receptor 4	2.13	6.55	5.46	0.17	0.2	1.20E-03	1.49E-02	Multiple_Complex
TC0200016545.hg.1	RIF1	replication timing regulatory factor 1	2.13	7.78	6.69	0.6	0.01	1.37E-02	6.61E-02	NonCoding
TC0500013350.hg.1	RAPGEF6	Rap guanine nucleotide exchange factor 6	2.13	6.64	5.55	0.07	0.09	4.00E-04	9.80E-03	Multiple_Complex
TC1200008671.hg.1	HCFC2	host cell factor C2	2.13	10.03	8.94	0.27	0.05	5.00E-04	1.04E-02	Multiple_Complex
TC0200015514.hg.1	GPR1	G protein-coupled receptor 1	2.13	5.62	4.53	0.97	0.03	1.26E-02	6.23E-02	Coding
TC0800012312.hg.1	SGK3	serum/glucocorticoid regulated kinase family, member 3	2.13	10.09	9	0.02	0.07	6.00E-04	1.13E-02	Multiple_Complex
TC0100017216.hg.1	NEK2	NIMA-related kinase 2	2.13	10.58	9.49	0.14	0.16	4.00E-04	9.40E-03	Multiple_Complex
TC0700007067.hg.1	MTURN	maturin, neural progenitor differentiation regulator homolog (Xenopus)	2.13	8.88	7.79	0.48	1.06	2.74E-02	1.05E-01	Multiple_Complex
TC1700008328.hg.1	STXBP4	syntaxin binding protein 4	2.13	10.91	9.82	0.1	0.13	8.00E-04	1.25E-02	Multiple_Complex
TC1100011182.hg.1	PYGM	phosphorylase, glycogen, muscle	2.13	7.1	6.02	0.22	0.35	1.10E-03	1.47E-02	Multiple_Complex
TC0300009471.hg.1	SKIL	SKI-like proto-oncogene	2.13	9.8	8.71	0.28	0.21	1.60E-03	1.74E-02	Multiple_Complex
TC0200010615.hg.1	CCNYL1; MIR4775	cyclin Y like 1; microRNA 4775	2.12	10.93	9.84	0	0.22	9.00E-04	1.30E-02	Multiple_Complex
TC0100013348.hg.1	SYF2	SYF2 pre-mRNA-splicing factor	2.12	12.97	11.88	0	0.25	9.00E-04	1.34E-02	Multiple_Complex
TC0300009459.hg.1	GPR160	G protein-coupled receptor 160	2.12	13.15	12.07	0.14	0.66	9.90E-03	5.32E-02	Multiple_Complex
TC0600010071.hg.1	SLC22A1	solute carrier family 22 (organic cation transporter), member 1	2.12	5.88	4.8	0.03	0.98	1.41E-02	6.75E-02	Multiple_Complex
TC0100015310.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	2.12	14.49	13.4	0.18	0.3	1.00E-03	1.42E-02	Multiple_Complex
TC2000009945.hg.1	FAM209A	family with sequence similarity 209, member A	2.12	6.3	5.22	0.36	0.3	3.20E-03	2.56E-02	Coding

TC0300010561.hg.1	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	2.12	12.75	11.67	0.31	0.1	1.20E-03	1.50E-02	Multiple_Complex
TC2100008165.hg.1	BRWD1	bromodomain and WD repeat domain containing 1	2.12	11.96	10.87	0.26	0.14	8.00E-04	1.25E-02	Multiple_Complex
TC1100010733.hg.1	SPI1	Spi-1 proto-oncogene	2.12	6.46	5.38	0.07	0.62	2.90E-03	2.45E-02	Multiple_Complex
TC0500008882.hg.1	PCDHB11	protocadherin beta 11	2.12	8.97	7.89	0.15	0.68	1.12E-02	5.76E-02	Coding
TC0200010253.hg.1	ANKAR	ankyrin and armadillo repeat containing	2.12	6.88	5.79	0.23	0.1	1.60E-03	1.74E-02	Multiple_Complex
TC1200009967.hg.1	DUSP16	dual specificity phosphatase 16	2.11	11.55	10.47	0.52	0.12	2.20E-03	2.09E-02	Multiple_Complex
TC0200012809.hg.1	PELI1	pellino E3 ubiquitin protein ligase 1	2.11	7.45	6.37	0.03	0.21	4.90E-03	3.36E-02	Multiple_Complex
TC1200012263.hg.1	MPHOSPH9	M-phase phosphoprotein 9	2.11	10.11	9.03	0.24	0.16	6.00E-04	1.16E-02	Multiple_Complex
TC1000012015.hg.1	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	2.11	12.34	11.26	0.39	0.48	4.30E-03	3.12E-02	Multiple_Complex
TC1900011690.hg.1	ZNF493	zinc finger protein 493	2.11	9.86	8.78	0.43	0.25	1.60E-03	1.74E-02	Multiple_Complex
TC0900009758.hg.1	TUSC1	tumor suppressor candidate 1	2.11	7.95	6.87	0.26	0.29	1.20E-03	1.52E-02	Coding
TC0200016770.hg.1	MIR6809; TNS1	microRNA 6809; tensin 1	2.11	5.95	4.87	0.89	0.6	2.21E-02	9.10E-02	Multiple_Complex
TC0700008147.hg.1	RSBN1L	round spermatid basic protein 1-like	2.11	11.15	10.07	0.1	0.27	1.90E-03	1.93E-02	Multiple_Complex
TC0300008284.hg.1	HHLA2	HERV-H LTR-associating 2	2.11	4.63	3.55	0.31	0.3	1.40E-03	1.61E-02	Coding
TC1500009395.hg.1	TRPM7	transient receptor potential cation channel, subfamily M, member 7	2.11	9.12	8.04	0.01	0.66	8.80E-03	4.92E-02	Multiple_Complex
TC0300013025.hg.1	BCHE	butyrylcholinesterase	2.11	9.53	8.45	0.3	0.1	1.80E-03	1.86E-02	Coding
TC1200012763.hg.1	TAS2R30; TAS2R43; PRR4	taste receptor, type 2, member 30; taste receptor, type 2, member 43; proline rich 4 (lacrimal)	2.11	7.78	6.7	0.43	0.19	2.60E-03	2.27E-02	Multiple_Complex
TC0500012166.hg.1	CDC25C	cell division cycle 25C	2.11	10	8.92	0.2	0.19	3.00E-03	2.50E-02	Multiple_Complex
TC1200007627.hg.1	HIGD1C	HIG1 hypoxia inducible domain family, member 1C	2.11	5.15	4.08	0.65	0.21	6.20E-03	3.89E-02	Coding

TC0200016454.hg.1	KIAA1841	KIAA1841	2.11	10.14	9.06	0.07	0.32	9.80E-03	5.28E-02	Multiple_Complex
TC0300013083.hg.1	LRRC34	leucine rich repeat containing 34	2.11	10.58	9.5	0.13	0.08	7.00E-04	1.22E-02	Multiple_Complex
TC0200007533.hg.1	FOXN2	forkhead box N2	2.11	9.65	8.58	0.1	0.45	2.00E-03	1.98E-02	Multiple_Complex
TC0500012371.hg.1	PLAC8L1	PLAC8-like 1	2.11	8.13	7.06	0.25	0.75	2.39E-02	9.62E-02	Coding
TC1400007665.hg.1	BBOF1	basal body orientation factor 1	2.11	6.55	5.48	0.2	0.08	9.00E-04	1.30E-02	Multiple_Complex
TC0200012608.hg.1	PSME4	proteasome activator subunit 4	2.11	12.33	11.26	0.09	0.27	7.00E-04	1.17E-02	Multiple_Complex
TC1700009592.hg.1	MED31	mediator complex subunit 31	2.11	13.01	11.93	0.02	0.22	2.80E-03	2.39E-02	Multiple_Complex
TC0300007194.hg.1	ABHD5	abhydrolase domain containing 5	2.11	6.68	5.61	0.09	0.14	7.00E-04	1.17E-02	Multiple_Complex
TC0700012296.hg.1	C7orf60	chromosome 7 open reading frame 60	2.1	8.27	7.2	0.22	0.58	4.00E-03	2.98E-02	Multiple_Complex
TC1800008399.hg.1	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	2.1	7.12	6.04	0.08	0.39	1.50E-03	1.67E-02	Multiple_Complex
TC1900011878.hg.1	ZNF625-ZNF20; ZNF625	ZNF625-ZNF20 readthrough (NMD candidate); zinc finger protein 625	2.1	6.8	5.73	0.28	0.22	9.00E-04	1.31E-02	Multiple_Complex
TC0100009394.hg.1	CD53	CD53 molecule	2.1	6.95	5.87	0.67	0.21	4.30E-03	3.10E-02	Multiple_Complex
TC0500010427.hg.1	ZFR	zinc finger RNA binding protein	2.1	13.27	12.2	0.2	0.76	9.50E-03	5.16E-02	Multiple_Complex
TC1200008184.hg.1	TBC1D15	TBC1 domain family, member 15	2.1	10.4	9.33	0.4	0.39	4.50E-03	3.20E-02	Multiple_Complex
TC0600007819.hg.1	CLPSL2	colipase-like 2	2.1	8.18	7.1	0.65	0.42	6.60E-03	4.05E-02	Multiple_Complex
TC1600010789.hg.1	TAT	tyrosine aminotransferase	2.1	5.46	4.38	0.86	0.37	1.27E-02	6.26E-02	Multiple_Complex
TC1500009370.hg.1	FAM227B	family with sequence similarity 227, member B	2.1	8.34	7.27	0.05	0.34	1.60E-03	1.74E-02	Multiple_Complex
TC1000010768.hg.1	EGR2	early growth response 2	2.1	5.69	4.61	1.31	0.18	4.21E-02	1.40E-01	Multiple_Complex
TC1000007081.hg.1	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	2.1	11.82	10.75	0.08	0.38	1.20E-03	1.51E-02	Multiple_Complex
TC0200012804.hg.1	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	2.1	9.29	8.22	0.1	0.33	9.00E-04	1.30E-02	Multiple_Complex

TC0100011696.hg.1	FAM177B	family with sequence similarity 177, member B	2.1	7.21	6.14	0.03	0.25	6.00E-04	1.13E-02	Multiple_Complex
TC0X00006924.hg.1	FAM47B	family with sequence similarity 47, member B	2.1	6.83	5.77	0.02	0.16	5.00E-04	1.00E-02	Coding
TC1900010706.hg.1	SERTAD1	SERTA domain containing 1	2.1	7.42	6.35	0.76	0.04	1.41E-02	6.73E-02	Multiple_Complex
TC1800007431.hg.1	MALT1	MALT1 paracaspase	2.1	9.09	8.02	0.17	0.45	4.40E-03	3.15E-02	Multiple_Complex
TC1400008019.hg.1	GOLGA5	golgin A5	2.1	11.82	10.75	0.01	0.22	7.00E-04	1.21E-02	Multiple_Complex
TC0600007263.hg.1	HIST1H4A	histone cluster 1, H4a	2.09	7.38	6.32	0.34	0.04	3.00E-03	2.48E-02	Coding
TC0100015896.hg.1	NUP210L; MIR5698	nucleoporin 210kDa like; microRNA 5698	2.09	6.57	5.51	0.11	0.25	4.60E-03	3.23E-02	Multiple_Complex
TC1000008489.hg.1	LGI1	leucine-rich, glioma inactivated 1	2.09	7.95	6.89	0.54	0.1	5.50E-03	3.60E-02	Multiple_Complex
TC1800006786.hg.1	RNMT	RNA (guanine-7-) methyltransferase	2.09	8.84	7.77	0.03	0.21	9.00E-04	1.29E-02	Multiple_Complex
TC0X00010375.hg.1	ZMAT1	zinc finger, matrin-type 1	2.09	8.07	7	0.07	0.05	1.60E-03	1.75E-02	Multiple_Complex
TC0500010920.hg.1	SREK1IP1	SREK1-interacting protein 1	2.09	13.5	12.43	0.15	0.32	1.20E-03	1.53E-02	Multiple_Complex
TC1900009792.hg.1	PODNL1	podocan-like 1	2.09	6.73	5.67	0.35	0.15	2.00E-03	1.96E-02	Multiple_Complex
TC0200010273.hg.1	NAB1	NGFI-A binding protein 1	2.09	9.95	8.89	0.26	0.42	5.00E-03	3.39E-02	Multiple_Complex
TC0700006715.hg.1	PHF14	PHD finger protein 14	2.09	10.68	9.62	0.09	0.18	2.60E-03	2.28E-02	Multiple_Complex
TC1900010651.hg.1	GMFG	glia maturation factor, gamma	2.09	5.61	4.55	0.04	0.25	6.00E-04	1.09E-02	Multiple_Complex
TC0200012684.hg.1	FANCL	Fanconi anemia complementation group L	2.09	10.12	9.06	0.3	0.03	4.30E-03	3.09E-02	Multiple_Complex
TC0200010252.hg.1	ASNSD1	asparagine synthetase domain containing 1	2.09	10.37	9.3	0	0.19	1.20E-03	1.51E-02	Multiple_Complex
TC1000012492.hg.1	CUTC	cutC copper transporter	2.09	9.73	8.67	0.22	0.28	1.30E-03	1.56E-02	Multiple_Complex
TC0500010493.hg.1	LMBRD2	LMBR1 domain containing 2	2.09	9.53	8.47	0.04	0.27	1.10E-03	1.48E-02	Multiple_Complex
TC0300009865.hg.1	OSTN	osteocrin	2.09	5.72	4.66	0.61	0.61	1.38E-02	6.63E-02	Coding
TC1000010621.hg.1	ASAH2	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	2.08	10.09	9.03	0.29	0.2	2.23E-02	9.18E-02	Multiple_Complex

TC0900006539.hg.1	JAK2	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_004972	2.08	7.95	6.89	0.8	0.19	1.87E-02	8.15E-02	NonCoding
TC0900008286.hg.1	SMC2	structural maintenance of chromosomes 2	2.08	11.98	10.92	0.01	0.13	6.00E-04	1.09E-02	Multiple_Complex
TC0600013125.hg.1	THEMIS	thymocyte selection associated	2.08	4.67	3.61	0.06	0.1	4.00E-04	9.30E-03	Coding
TC0700008873.hg.1	CAV1	caveolin 1	2.08	8.44	7.38	0.34	0.02	1.20E-03	1.50E-02	Multiple_Complex
TC1200008142.hg.1	FRS2	fibroblast growth factor receptor substrate 2	2.08	10.62	9.56	0	0.34	1.60E-03	1.73E-02	Multiple_Complex
TC0200015887.hg.1	CUL3	cullin 3	2.08	12.06	11	0.14	0.04	8.00E-04	1.28E-02	Multiple_Complex
TC2000007792.hg.1	PFDN4	prefoldin subunit 4	2.08	13.95	12.89	0.16	0.24	4.20E-03	3.05E-02	Multiple_Complex
TC1400008908.hg.1	EAPP	E2F-associated phosphoprotein	2.08	12.99	11.93	0.02	0.19	1.30E-03	1.58E-02	Multiple_Complex
TC0500008654.hg.1	LEAP2	liver expressed antimicrobial peptide 2	2.08	7.97	6.91	0.45	0.01	6.30E-03	3.94E-02	Multiple_Complex
TC0100015754.hg.1	CTSK	cathepsin K	2.08	5.93	4.87	0	0.18	8.00E-04	1.23E-02	Multiple_Complex
TSUnmapped00000141.hg.1	HMBS	hydroxymethylbilane synthase	2.08	8.11	7.05	0.5	0.09	2.50E-03	2.23E-02	NonCoding
TC1200009892.hg.1	OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	2.08	5.92	4.87	0.7	0.37	1.06E-02	5.56E-02	Multiple_Complex
TC1300006914.hg.1	UFM1	ubiquitin-fold modifier 1	2.08	13.02	11.97	0.05	0.1	1.10E-03	1.46E-02	Multiple_Complex
TC0100016822.hg.1	KCNT2	potassium channel, sodium activated subfamily T, member 2	2.08	11.57	10.51	0.24	0.1	2.14E-02	8.87E-02	Multiple_Complex
TC0100015445.hg.1	TBX15	T-box 15	2.08	5.17	4.12	0.61	0.03	4.50E-03	3.17E-02	Multiple_Complex
TC1400008913.hg.1	SNX6	sorting nexin 6	2.08	12.31	11.25	0.06	0.5	8.40E-03	4.81E-02	Multiple_Complex
TC2000010009.hg.1	BLCAP	bladder cancer associated protein	2.08	6.33	5.27	0.03	0.46	2.00E-03	1.99E-02	NonCoding
TC1100013088.hg.1	BIRC2	baculoviral IAP repeat containing 2	2.08	12.22	11.17	0.1	0.12	7.00E-04	1.22E-02	Multiple_Complex
TC1500010256.hg.1	BTBD1	BTB (POZ) domain containing 1	2.08	10.41	9.36	0.05	0.26	9.00E-04	1.29E-02	Multiple_Complex

TC1200012739.hg.1	PARP11	poly(ADP-ribose) polymerase family member 11	2.07	8.47	7.42	0.52	0.32	3.60E-03	2.76E-02	Multiple_Complex
TC1200011608.hg.1	CDK17	cyclin-dependent kinase 17	2.07	11.41	10.36	0.34	0.13	3.40E-03	2.66E-02	Multiple_Complex
TC0X00010982.hg.1	CDR1	cerebellar degeneration related protein 1	2.07	12.59	11.54	0.14	0.13	7.00E-04	1.17E-02	Coding
TC0900008653.hg.1	MORN5	MORN repeat containing 5	2.07	5.9	4.85	0.87	0.3	1.44E-02	6.85E-02	Multiple_Complex
TC0300012123.hg.1	CD80	CD80 molecule	2.07	6.26	5.2	0.48	0.22	3.70E-03	2.82E-02	Multiple_Complex
TC0700007285.hg.1	CDK13	cyclin-dependent kinase 13	2.07	12.28	11.23	0.03	0.39	1.60E-03	1.74E-02	Multiple_Complex
TC1100007227.hg.1	HIPK3	homeodomain interacting protein kinase 3	2.07	10.21	9.16	0.16	0.23	8.00E-04	1.25E-02	Multiple_Complex
TC0300011450.hg.1	TMF1	TATA element modulatory factor 1	2.07	10.52	9.46	0.2	0.14	1.30E-03	1.59E-02	Multiple_Complex
TC1400007086.hg.1	LRR1; RHOQP1	leucine rich repeat protein 1; ras homolog family member Q pseudogene 1	2.07	10.55	9.5	0.02	0.03	1.50E-03	1.69E-02	Multiple_Complex
TC1100010998.hg.1	MS4A4E	membrane-spanning 4-domains, subfamily A, member 4E	2.07	5.83	4.78	0.27	0.43	3.10E-03	2.53E-02	Multiple_Complex
TC1300009740.hg.1	LIG4	ligase IV, DNA, ATP-dependent	2.07	9.6	8.56	0.13	0.01	5.00E-04	1.01E-02	Coding
TC1900009583.hg.1	ZNF266	zinc finger protein 266	2.07	8.61	7.56	0.27	0.13	1.00E-03	1.37E-02	Multiple_Complex
TC0200015463.hg.1	WDR12	WD repeat domain 12	2.07	10.55	9.5	0.35	0.37	3.20E-03	2.59E-02	Multiple_Complex
TC0300008086.hg.1	ARL6	ADP-ribosylation factor like GTPase 6	2.07	8.69	7.65	0.49	0.29	3.50E-03	2.72E-02	Multiple_Complex
TC1000011892.hg.1	CCDC186; MIR2110	coiled-coil domain containing 186; microRNA 2110	2.07	9.91	8.87	0.07	0.44	2.40E-03	2.16E-02	Multiple_Complex
TC1900007950.hg.1	ZNF567	zinc finger protein 567	2.07	10.2	9.15	0.5	0.37	3.50E-03	2.72E-02	Multiple_Complex
TC1500010740.hg.1	DTWD1	DTW domain containing 1	2.07	9.04	7.99	0.26	0.21	1.70E-03	1.83E-02	Multiple_Complex
TC0200015476.hg.1	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	2.07	10.97	9.92	0.16	0	9.00E-04	1.34E-02	Multiple_Complex
TC0800008758.hg.1	FAM91A1	family with sequence similarity 91, member A1	2.07	9.23	8.18	0.34	0.03	9.00E-04	1.31E-02	Multiple_Complex

TC0200015427.hg.1	TRAK2	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_015049	2.07	8.44	7.39	0.44	0.23	2.00E-03	1.96E-02	Multiple_Complex
TC0800010417.hg.1	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	2.07	9.16	8.11	0.13	0.3	1.80E-03	1.86E-02	Multiple_Complex
TC0300012773.hg.1	TM4SF1	transmembrane 4 L six family member 1	2.06	5.21	4.16	0.32	0	8.00E-04	1.28E-02	Multiple_Complex
TC0200015214.hg.1	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	2.06	9.35	8.3	0	0.03	1.00E-03	1.40E-02	Multiple_Complex
TC1200010550.hg.1	RPAP3	RNA polymerase II associated protein 3	2.06	12.39	11.34	0.47	0.14	2.20E-03	2.08E-02	Multiple_Complex
TC0300007206.hg.1	TCAIM	T cell activation inhibitor, mitochondrial	2.06	10.79	9.75	0.13	0.68	9.30E-03	5.09E-02	Multiple_Complex
TC1600009396.hg.1	TNP2	transition protein 2 (during histone to protamine replacement)	2.06	6.02	4.97	0.14	0.28	3.90E-03	2.94E-02	Multiple_Complex
TC1100010703.hg.1	CHRM4	cholinergic receptor, muscarinic 4	2.06	6.73	5.69	0.63	0.56	1.87E-02	8.15E-02	Coding
TC0700010181.hg.1	RSPH10B2; RSPH10B	radial spoke head 10 homolog B2 (Chlamydomonas); radial spoke head 10 homolog B (Chlamydomonas)	2.06	7.64	6.6	0.21	0.48	4.80E-03	3.33E-02	Multiple_Complex
TC0300013865.hg.1	SEC22A	SEC22 homolog A, vesicle trafficking protein	2.06	8.74	7.7	0.18	0.29	1.30E-03	1.55E-02	Multiple_Complex
TC1700008820.hg.1	C17orf80	chromosome 17 open reading frame 80	2.06	10.79	9.75	0.05	0.36	2.10E-03	2.02E-02	Multiple_Complex
TC1200008764.hg.1	WSCD2	WSC domain containing 2	2.06	4.94	3.9	0.15	0.03	3.20E-03	2.61E-02	Multiple_Complex
TC1900006588.hg.1	GADD45B	growth arrest and DNA-damage-inducible, beta	2.06	11.46	10.42	0.23	0.24	1.40E-03	1.60E-02	Multiple_Complex
TC1200012181.hg.1	SPPL3	signal peptide peptidase like 3	2.06	8.85	7.81	0.38	0.47	6.60E-03	4.06E-02	Multiple_Complex
TC0800011208.hg.1	HRSP12	heat-responsive protein 12	2.06	10.53	9.49	0.05	0.06	1.30E-03	1.58E-02	Multiple_Complex
TC1000010844.hg.1	RUFY2	RUN and FYVE domain containing 2	2.06	10.65	9.61	0.47	0.25	2.80E-03	2.41E-02	Multiple_Complex
TC0800009856.hg.1	EGR3	early growth response 3	2.06	8.06	7.02	0.71	0.15	1.84E-02	8.04E-02	Multiple_Complex
TC0200007297.hg.1	GEMIN6	gem nuclear organelle associated protein 6	2.06	13.38	12.33	0.12	0.31	5.20E-03	3.46E-02	Multiple_Complex

TC0300013522.hg.1	TMEM207	transmembrane protein 207	2.06	5.16	4.11	0.16	0.03	5.00E-04	1.03E-02	Coding
TC0600013249.hg.1	ALDH8A1	aldehyde dehydrogenase 8 family, member A1	2.06	7.27	6.23	0.42	0.11	7.10E-03	4.25E-02	Multiple_Complex
TC1000012561.hg.1	JMJD1C	jumonji domain containing 1C	2.06	13.55	12.51	0.19	0.13	8.00E-04	1.27E-02	Multiple_Complex
TC0200012189.hg.1	NLRC4	NLR family, CARD domain containing 4	2.06	6.89	5.85	0.07	0.31	1.30E-03	1.55E-02	Coding
TC1000009535.hg.1	IDI2	isopentenyl-diphosphate delta isomerase 2	2.06	7.52	6.48	0.07	0.3	5.10E-03	3.45E-02	Coding
TC1700009750.hg.1	TMEM220	transmembrane protein 220	2.06	10.05	9.01	0.03	0.34	1.03E-02	5.47E-02	Multiple_Complex
TC0200008062.hg.1	ACTG2	actin, gamma 2, smooth muscle, enteric	2.06	7.29	6.25	0.59	0.3	7.10E-03	4.27E-02	Multiple_Complex
TC1000010699.hg.1	IPMK	inositol polyphosphate multikinase	2.06	11.75	10.71	0.36	0.04	2.00E-03	1.96E-02	Multiple_Complex
TC0500012079.hg.1	SAR1B	Transcript Identified by AceView, Entrez Gene ID(s) 51128	2.06	5.46	4.42	1.04	0	3.75E-02	1.29E-01	Unassigned
TC1100009412.hg.1	PKNOX2	PBX/knotted 1 homeobox 2	2.06	9.33	8.29	0.85	0.04	1.46E-02	6.89E-02	Multiple_Complex
TC0400009253.hg.1	ANXA10	annexin A10	2.05	5.11	4.08	0.19	0.01	9.00E-04	1.31E-02	Multiple_Complex
TC0X00006779.hg.1	ZNF645	zinc finger protein 645	2.05	4.64	3.6	0.04	0.16	9.00E-04	1.32E-02	Coding
TC1100013150.hg.1	TPH1	tryptophan hydroxylase 1	2.05	5.93	4.89	0.22	0.22	2.60E-03	2.31E-02	Multiple_Complex
TC0700007345.hg.1	STK17A	serine/threonine kinase 17a	2.05	10.7	9.66	0.25	0.09	7.00E-04	1.19E-02	Multiple_Complex
TC0500013200.hg.1	RFESD	Rieske (Fe-S) domain containing	2.05	9.26	8.22	0.16	0.27	3.00E-03	2.49E-02	Multiple_Complex
TC1200010415.hg.1	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	2.05	9.25	8.22	0.22	0.22	3.17E-02	1.16E-01	Multiple_Complex
TC0600012968.hg.1	TRAPPC3L	trafficking protein particle complex 3-like	2.05	5.56	4.52	0.57	0.63	2.17E-02	8.97E-02	Multiple_Complex
TC1700011448.hg.1	POLG2	polymerase (DNA directed), gamma 2, accessory subunit	2.05	9.38	8.35	0.44	0.13	1.80E-03	1.84E-02	Multiple_Complex
TC1800006655.hg.1	TXNDC2	thioredoxin domain containing 2 (spermatozoa)	2.05	7.19	6.16	0.48	0.36	7.80E-03	4.53E-02	Multiple_Complex

TC1200012178.hg.1	UNC119B	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, UTR3 best transcript NM_001080533	2.05	4.73	3.7	0.02	0.06	5.00E-04	1.00E-02	NonCoding
TC1600008330.hg.1	HPR	haptoglobin-related protein	2.05	5.18	4.15	0.01	0.27	1.50E-03	1.69E-02	Multiple_Complex
TC0800007866.hg.1	MCMDC2	minichromosome maintenance domain containing 2	2.05	5.24	4.21	0.47	0.59	1.00E-02	5.34E-02	Multiple_Complex
TC2100008487.hg.1	TPTE	transmembrane phosphatase with tensin homology	2.05	7.73	6.7	1.04	0.39	2.60E-02	1.02E-01	Multiple_Complex
TC0100009331.hg.1	STXBP3	syntaxin binding protein 3	2.05	8.57	7.53	0.24	0.16	9.00E-04	1.32E-02	Multiple_Complex
TC0X00008470.hg.1	PHF6	PHD finger protein 6	2.05	13.12	12.08	0.17	0.43	2.00E-03	1.95E-02	Multiple_Complex
TC0200015307.hg.1	DNAH7	dynein, axonemal, heavy chain 7	2.05	6	4.97	0.12	0.09	2.00E-03	1.99E-02	Multiple_Complex
TC1500007926.hg.1	RCN2	reticulocalbin 2, EF-hand calcium binding domain	2.05	12.97	11.94	0.07	0.22	2.30E-03	2.11E-02	Multiple_Complex
TC0400008106.hg.1	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	2.05	7.65	6.62	0.15	0.28	4.00E-03	2.95E-02	Multiple_Complex

TCUn_GL000195v100006435.hg.1	LOC389831; TCONS_00030034; TCONS_00030035; AC011043.1	uncharacterized LOC389831; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVEXON, UTR3 best transcript NM_001242480; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVEXON, UTR3, UTR5 best transcript NM_001242480; Salzman2013 ANNOTATED, ncRNA, OVEXON best transcript TCONS_00030034; Salzman2013 ANNOTATED, ncRNA, OVCODE, OVEXON best transcript TCONS_00030034; Salzman2013 ALT_ACCEPTOR, ncRNA, OVCODE, OVEXON, upstream_start best transcript TCONS_00030034; Salzman2013 ALT_DONOR, downstream_end, ncRNA, OVEXON best transcript TCONS_00030035; Salzman2013 ALT_DONOR, coding, intronic, OVEXON, UTR5 best transcript NM_001242480; uncharacterized protein LOC389831 [Source:RefSeq peptide;Acc:NP_001229409]	2.05	7.26	6.23	0.31	0.09	1.10E-03	1.44E-02	Multiple_Complex
TC0900008515.hg.1	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	2.05	12.93	11.89	0.4	0.1	4.40E-03	3.16E-02	Multiple_Complex
TC0600010960.hg.1	TPMT	thiopurine S-methyltransferase	2.05	11.3	10.26	0.12	0.1	1.40E-03	1.63E-02	Multiple_Complex
TC0X00009254.hg.1	APOO	apolipoprotein O	2.05	12.3	11.27	0.13	0.09	7.00E-04	1.22E-02	Multiple_Complex

TSUnmapped00000763.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	2.05	10.76	9.73	0.29	0.21	1.20E-03	1.48E-02	Coding
TC0500009671.hg.1	ZFP2	ZFP2 zinc finger protein	2.04	5.2	4.16	0.95	0.25	1.75E-02	7.80E-02	Coding
TC0600012628.hg.1	NDUFAF4	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4	2.04	13.18	12.15	0.01	0.27	1.10E-03	1.48E-02	Multiple_Complex
TC1600011466.hg.1	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	2.04	5.55	4.52	1.08	0.03	2.40E-02	9.65E-02	NonCoding
TC0900009645.hg.1	HAUS6	HAUS augmin like complex subunit 6	2.04	13.49	12.46	0.22	0.24	1.10E-03	1.48E-02	Multiple_Complex
TSUnmapped00000627.hg.1	KIF15	kinesin family member 15	2.04	9.5	8.47	0.07	0.53	2.90E-03	2.45E-02	Coding
TC1000012066.hg.1	NSMCE4A	NSE4 homolog A, SMC5-SMC6 complex component	2.04	10.61	9.58	0.14	0.17	6.50E-03	4.00E-02	Multiple_Complex
TC0700010749.hg.1	KIAA0895	KIAA0895	2.04	7.67	6.64	0.15	0.24	9.00E-04	1.34E-02	Multiple_Complex
TC1600006635.hg.1	PRSS41	protease, serine 41	2.04	7.84	6.81	0.55	0.31	4.40E-03	3.16E-02	Multiple_Complex
TC0900011461.hg.1	STRBP; MIR600HG; MIR600	spermatid perinuclear RNA binding protein; MIR600 host gene; microRNA 600	2.04	13.17	12.14	0.06	0.08	5.00E-04	1.04E-02	Multiple_Complex
TC0300008331.hg.1	ABHD10	abhydrolase domain containing 10	2.04	8.43	7.4	0.41	0.18	4.30E-03	3.10E-02	Multiple_Complex
TC0400012458.hg.1	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	2.04	7.11	6.08	0.48	0.31	4.20E-03	3.06E-02	Multiple_Complex
TC1700010254.hg.1	SSH2	slingshot protein phosphatase 2	2.04	9.86	8.83	0.41	0.43	3.30E-03	2.63E-02	Multiple_Complex
TC0100015109.hg.1	LOC101928436; RP11-153F1.1; RP11-347K2.2; teyfawbu	uncharacterized LOC101928436; novel transcript; Transcript Identified by AceView	2.04	6.02	4.99	0.61	0.21	5.30E-03	3.50E-02	Multiple_Complex
TC0400008725.hg.1	PCDH10	protocadherin 10	2.04	10.11	9.09	0.16	0.06	3.40E-03	2.71E-02	Multiple_Complex
TC0600007848.hg.1	RAB44	RAB44, member RAS oncogene family	2.03	6.42	5.39	0.14	0.03	1.30E-03	1.55E-02	Multiple_Complex
TC0200014717.hg.1	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	2.03	10.42	9.39	0.33	0.05	1.60E-03	1.74E-02	Multiple_Complex

TC2000007686.hg.1	LINC01272	long intergenic non-protein coding RNA 1272	2.03	8.26	7.24	0.31	0.12	1.40E-03	1.60E-02	Multiple_Complex
TC1600011399.hg.1	MT1X	metallothionein 1X	2.03	8.46	7.43	0.25	0.07	8.00E-04	1.26E-02	Multiple_Complex
TC0200015776.hg.1	RESP18	regulated endocrine-specific protein 18	2.03	5.55	4.53	0.67	0.25	8.30E-03	4.74E-02	Multiple_Complex
TC1800007508.hg.1	TNFRSF11A	Transcript Identified by AceView, Entrez Gene ID(s) 8792	2.03	7.11	6.09	0.26	0.06	1.40E-03	1.62E-02	Unassigned
TC0200013075.hg.1	TPRKB	TP53RK binding protein	2.03	12.45	11.43	0.34	0.06	5.70E-03	3.68E-02	Multiple_Complex
TC1600010602.hg.1	CDH16	cadherin 16, KSP-cadherin	2.03	5.83	4.8	0.3	0.26	5.50E-03	3.60E-02	Multiple_Complex
TC0800007978.hg.1	LY96	lymphocyte antigen 96	2.03	5.92	4.89	0.42	0.1	2.73E-02	1.05E-01	Coding
TC0800008916.hg.1	EFR3A	EFR3 homolog A	2.03	8.3	7.28	0.15	0.05	2.10E-03	2.00E-02	Multiple_Complex
TC0400011056.hg.1	NUP54	nucleoporin 54kDa	2.03	11.61	10.59	0.56	0.39	7.30E-03	4.32E-02	Multiple_Complex
TC1200007137.hg.1	FGFR1OP2	FGFR1 oncogene partner 2	2.03	11.12	10.1	0.23	0.06	4.40E-03	3.15E-02	Multiple_Complex
TC1100007307.hg.1	C11orf74	chromosome 11 open reading frame 74	2.03	14.86	13.83	0.14	0.26	1.10E-03	1.46E-02	Multiple_Complex
TC2000009180.hg.1	OSER1	oxidative stress responsive serine-rich 1	2.03	11.53	10.51	0.23	0.28	2.20E-03	2.08E-02	Coding
TC0100018237.hg.1	RABGGTB; SNORD45B; SNORD45A; SNORD45C	Rab geranylgeranyltransferase, beta subunit; small nucleolar RNA, C/D box 45B; small nucleolar RNA, C/D box 45A; small nucleolar RNA, C/D box 45C	2.03	12.74	11.72	0.08	0.06	7.00E-04	1.20E-02	Multiple_Complex
TC1200011301.hg.1	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	2.03	13.42	12.39	0.21	0.37	1.80E-03	1.86E-02	Multiple_Complex
TC1500009458.hg.1	ARPP19	cAMP-regulated phosphoprotein 19kDa	2.03	11.42	10.39	0.17	0.08	3.90E-03	2.91E-02	Multiple_Complex
TC0800008726.hg.1	TBC1D31	TBC1 domain family, member 31	2.03	11.66	10.64	0.06	0.17	4.00E-03	2.95E-02	Multiple_Complex
TC1100010943.hg.1	OR5B12	olfactory receptor, family 5, subfamily B, member 12	2.03	4.76	3.74	0.79	0.39	1.57E-02	7.25E-02	Coding
TC0600014234.hg.1	CAGE1	cancer antigen 1	2.03	5.02	4	0.56	0.41	7.00E-03	4.22E-02	Multiple_Complex

TC1100011404.hg.1	MRPL21	mitochondrial ribosomal protein L21	2.03	13.1	12.08	0.05	0.23	1.30E-03	1.59E-02	Multiple_Complex
TC1200011506.hg.1	BTG1; LINC01619	B-cell translocation gene 1, anti-proliferative; long intergenic non-protein coding RNA 1619	2.03	8.01	6.99	0.34	0.06	1.50E-03	1.69E-02	Multiple_Complex
TC0100015698.hg.1	HIST2H3D	histone cluster 2, H3d	2.03	9.03	8.02	0.28	0.29	2.60E-03	2.30E-02	Coding
TC0700009174.hg.1	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	2.03	12.48	11.46	0.31	0.09	2.50E-03	2.25E-02	Multiple_Complex
TC0200010165.hg.1	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	2.03	9.28	8.26	0.06	0.06	1.10E-03	1.44E-02	Multiple_Complex
TC1800008405.hg.1	TRAPPC8	trafficking protein particle complex 8	2.03	8.93	7.91	0.28	0.02	1.30E-03	1.56E-02	Multiple_Complex
TC1300008426.hg.1	USP12	Transcript Identified by AceView, Entrez Gene ID(s) 219333	2.02	6.98	5.96	0.01	0.13	2.20E-03	2.06E-02	Unassigned
TC0800008235.hg.1	FAM92A1	family with sequence similarity 92, member A1	2.02	10.53	9.51	0.24	0.35	3.30E-03	2.63E-02	Multiple_Complex
TC2000007937.hg.1	PHACTR3	Transcript Identified by AceView, Entrez Gene ID(s) 116154	2.02	8.64	7.62	0.26	0.52	9.10E-03	5.00E-02	Unassigned
TC1900008392.hg.1	FKRP	fukutin related protein	2.02	6.91	5.89	0.33	0.06	9.40E-03	5.14E-02	Multiple_Complex
TC0600009350.hg.1	RNF217	ring finger protein 217	2.02	10.02	9.01	0.47	0.29	7.10E-03	4.27E-02	Multiple_Complex
TC1500009641.hg.1	RORA	RAR-related orphan receptor A	2.02	9.51	8.5	0.06	0.41	2.30E-03	2.12E-02	Multiple_Complex
TC0100008812.hg.1	PTGFR	prostaglandin F receptor (FP)	2.02	8.3	7.29	0.01	0.43	2.80E-03	2.39E-02	Coding
TC1200007779.hg.1	OR9K2	olfactory receptor, family 9, subfamily K, member 2	2.02	5.62	4.61	0.06	0.25	1.45E-02	6.87E-02	Coding
TC1100011811.hg.1	CCDC90B	coiled-coil domain containing 90B	2.02	12.86	11.85	0.07	0.33	2.40E-03	2.18E-02	Multiple_Complex
TC0500011173.hg.1	POC5	POC5 centriolar protein	2.02	11.03	10.02	0.34	0.11	9.90E-03	5.32E-02	Multiple_Complex
TC1600011570.hg.1	CMC2	C-x(9)-C motif containing 2	2.02	14.01	12.99	0.1	0.13	1.70E-03	1.78E-02	Multiple_Complex
TC0900010618.hg.1	C9orf153	chromosome 9 open reading frame 153	2.02	5.81	4.8	0.27	0.28	2.70E-03	2.32E-02	Multiple_Complex

TC1900009891.hg.1	LOC102724279; AC004791.2; nimure	uncharacterized LOC102724279; Transcript Identified by AceView; novel transcript	2.02	9.18	8.17	0.15	0.32	6.80E-03	4.15E-02	Multiple_Complex
TC1200009881.hg.1	CLEC2B	C-type lectin domain family 2, member B	2.02	5.01	4	0.13	0.02	3.50E-03	2.74E-02	Multiple_Complex
TC0800008279.hg.1	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	2.02	8.32	7.31	0.28	0.04	2.40E-03	2.17E-02	Multiple_Complex
TC1200008003.hg.1	TBK1	TANK-binding kinase 1	2.02	10.05	9.04	0.15	0.24	1.40E-03	1.64E-02	Multiple_Complex
TC1700006877.hg.1	ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese-dependent	2.02	12.07	11.05	0.04	0.26	1.00E-02	5.33E-02	Multiple_Complex
TC0300011030.hg.1	TMEM89	transmembrane protein 89	2.01	7.03	6.02	0.44	0.03	3.30E-03	2.65E-02	Coding
TC0200015399.hg.1	PPIL3	peptidylprolyl isomerase (cyclophilin)-like 3	2.01	12.21	11.2	0.22	0.13	1.40E-03	1.61E-02	Multiple_Complex
TC0400007422.hg.1	ATP10D	ATPase, class V, type 10D	2.01	7.83	6.82	0.36	0.05	2.10E-03	2.00E-02	Multiple_Complex
TC1500010633.hg.1	SPATA41	spermatogenesis associated 41 (non-protein coding)	2.01	5.5	4.49	0.13	0.52	8.60E-03	4.85E-02	Multiple_Complex
TC1000008467.hg.1	05-Mar	membrane associated ring finger 5	2.01	11.37	10.36	0.17	0.01	1.50E-03	1.67E-02	Multiple_Complex
TC0800011021.hg.1	RMDN1	regulator of microtubule dynamics 1	2.01	13.37	12.36	0.03	0.41	4.20E-03	3.06E-02	Multiple_Complex
TC0600008562.hg.1	SENP6	SUMO1/sentrin specific peptidase 6	2.01	13.19	12.18	0.05	0.13	1.10E-03	1.42E-02	Multiple_Complex
TC0900008243.hg.1	PLPPR1	phospholipid phosphatase related 1	2.01	4.49	3.48	1.03	0.03	2.27E-02	9.28E-02	Multiple_Complex
TC0400008335.hg.1	AIMP1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	2.01	12.05	11.05	0.09	0.08	7.00E-04	1.22E-02	Multiple_Complex
TC0500009444.hg.1	EFCAB9	EF-hand calcium binding domain 9	2.01	6.55	5.54	0.6	0.5	1.14E-02	5.85E-02	Multiple_Complex
TC1500008269.hg.1	KIF7	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_198525	2.01	5.83	4.82	0.34	0.25	5.80E-03	3.73E-02	NonCoding
TC1500007711.hg.1	TLE3	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001105192	2.01	5.5	4.49	0.54	0.07	1.50E-02	7.03E-02	NonCoding

TC1200011588.hg.1	USP44	ubiquitin specific peptidase 44	2.01	8.76	7.75	0.03	0.2	1.56E-02	7.21E-02	Multiple_Complex
TC0600007559.hg.1	HCG22	HLA complex group 22	2.01	6	4.99	0.82	0.32	1.84E-02	8.05E-02	NonCoding
TC1900006930.hg.1	OR7E24	olfactory receptor, family 7, subfamily E, member 24	2.01	5	3.99	0	0.11	1.40E-03	1.60E-02	Coding
TC0800006625.hg.1	ZNF705B	zinc finger protein 705B	2.01	6.12	5.12	1.05	0.24	3.43E-02	1.22E-01	Coding
TC0400009322.hg.1	GALNT7	polypeptide N-acetylgalactosaminyltransferase 7	2.01	10.63	9.62	0.26	0.17	1.60E-03	1.72E-02	Multiple_Complex
TC0X00006669.hg.1	GLRA2	glycine receptor alpha 2	2.01	6.2	5.19	0.02	0.06	1.40E-03	1.64E-02	Coding
TC0200007194.hg.1	BIRC6	Transcript Identified by AceView, Entrez Gene ID(s) 57448	2.01	6.13	5.13	0.07	0.57	4.40E-03	3.16E-02	Unassigned
TC0900009461.hg.1	PLGRKT	plasminogen receptor, C-terminal lysine transmembrane protein	2	8.19	7.18	0.58	0.15	1.26E-02	6.23E-02	Multiple_Complex
TC1100009819.hg.1	NAP1L4	nucleosome assembly protein 1-like 4	2	12.17	11.17	0.16	0.35	5.00E-03	3.41E-02	Multiple_Complex
TC1300007052.hg.1	GTF2F2	general transcription factor IIF subunit 2	2	12.81	11.8	0.1	0.21	8.00E-04	1.25E-02	Multiple_Complex
TC2100008490.hg.1	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	2	8.89	7.88	0.3	0.07	2.30E-03	2.12E-02	Multiple_Complex
TC0400009379.hg.1	SPCS3	signal peptidase complex subunit 3	2	14	12.99	0.01	0.37	4.00E-03	2.96E-02	Multiple_Complex
TC0100006524.hg.1	MIB2	mindbomb E3 ubiquitin protein ligase 2	2	7.72	6.72	0.95	0.41	2.36E-02	9.53E-02	Multiple_Complex
TC2200009262.hg.1	EIF3L	eukaryotic translation initiation factor 3, subunit L	2	13.22	12.22	0.04	0.23	1.00E-03	1.40E-02	Multiple_Complex
TC0900012154.hg.1	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	2	10.64	9.64	0.03	0.21	8.90E-03	4.94E-02	Multiple_Complex
TC0200007184.hg.1	BIRC6	baculoviral IAP repeat containing 6	2	10.49	9.49	0.09	0.48	4.00E-03	2.99E-02	Multiple_Complex
TC1400010594.hg.1	FAM177A1	family with sequence similarity 177, member A1	2	7.96	6.96	0.16	0.33	1.12E-02	5.78E-02	Multiple_Complex
TC0700008261.hg.1	RUNDC3B	RUN domain containing 3B	2	9.36	8.36	0.26	0.34	6.80E-03	4.13E-02	Multiple_Complex
TC0200014790.hg.1	GRB14	growth factor receptor bound protein 14	2	9.18	8.18	0.13	0.35	5.20E-03	3.47E-02	Multiple_Complex

TC0X00010675.hg.1	CUL4B	cullin 4B	2	10.62	9.62	0.01	0.36	2.20E-03	2.09E-02	Multiple_Complex
TC1200010899.hg.1	MYL6	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_079423	2	7.28	6.28	0.91	0.04	2.10E-02	8.77E-02	NonCoding
TC0800007377.hg.1	ADAM18	ADAM metallopeptidase domain 18	2	4.99	3.99	0.4	0.59	8.90E-03	4.94E-02	Multiple_Complex
TC0500009377.hg.1	SPDL1	spindle apparatus coiled-coil protein 1	2	11.61	10.61	0.17	0.26	1.40E-03	1.61E-02	Multiple_Complex
TC1300006676.hg.1	RASL11A	RAS-like, family 11, member A	2	7.32	6.32	0.11	0.44	2.80E-03	2.41E-02	Multiple_Complex
TC0500011478.hg.1	KIAA0825	KIAA0825	2	5.11	4.11	0.01	0.42	3.80E-03	2.88E-02	Multiple_Complex
TC2000009912.hg.1	CNBD2	cyclic nucleotide binding domain containing 2	2	8.48	7.48	0.77	0.18	1.78E-02	7.87E-02	Coding
TC1600010375.hg.1	CRNDE	colorectal neoplasia differentially expressed (non-protein coding)	1.99	13.17	12.17	0.15	0.16	2.70E-03	2.32E-02	Multiple_Complex
TC0500011602.hg.1	GIN1	gypsy retrotransposon integrase 1	1.99	10.65	9.65	0.21	0.05	2.90E-03	2.46E-02	Multiple_Complex
TC1100008797.hg.1	PANX1	pannexin 1	1.99	7.61	6.61	0.26	0.19	2.90E-03	2.41E-02	Coding
TC0200012971.hg.1	ANXA4	Salzman2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001153	1.99	6.22	5.23	0.47	0.01	2.50E-03	2.22E-02	NonCoding
TC0300012191.hg.1	PARP9	poly(ADP-ribose) polymerase family member 9	1.99	10	9.01	0.26	0.24	2.70E-03	2.36E-02	Multiple_Complex
TC0500011352.hg.1	EDIL3	EGF-like repeats and discoidin I-like domains 3	1.99	12.03	11.04	0.06	0.25	1.10E-03	1.47E-02	Multiple_Complex
TC0100009191.hg.1	AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	1.99	9.35	8.35	0.1	0.25	2.20E-03	2.06E-02	Multiple_Complex
TC1200010201.hg.1	TM7SF3	transmembrane 7 superfamily member 3	1.99	10.23	9.24	0.33	0.32	6.90E-03	4.19E-02	Multiple_Complex
TC1000010452.hg.1	ZNF32	zinc finger protein 32	1.99	9.21	8.21	0.04	0.38	1.50E-03	1.71E-02	Multiple_Complex
TC0400011208.hg.1	FAM175A	family with sequence similarity 175, member A	1.99	10.04	9.04	0.06	0.36	2.10E-03	2.00E-02	Multiple_Complex
TC0100015049.hg.1	FRRS1	ferric-chelate reductase 1	1.99	8.77	7.77	0.19	0.61	8.60E-03	4.86E-02	Multiple_Complex
TC0200016676.hg.1	WDPCP	WD repeat containing planar cell polarity effector	1.99	9.03	8.04	0.13	0.45	3.00E-03	2.48E-02	Multiple_Complex

TC2100007850.hg.1	LTN1	listerin E3 ubiquitin protein ligase 1	1.99	11.98	10.99	0.04	0.18	2.10E-03	2.03E-02	Multiple_Complex
TC0X00007851.hg.1	FAM133A	family with sequence similarity 133, member A	1.99	6.39	5.4	0.14	0.5	7.60E-03	4.45E-02	Coding
TC1900011705.hg.1	TDRD12	tudor domain containing 12	1.99	4.75	3.76	1.02	0.23	2.61E-02	1.02E-01	Multiple_Complex
TC0500012248.hg.1	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	1.99	11.92	10.93	0.37	0.24	2.20E-03	2.06E-02	Multiple_Complex
TC0200010214.hg.1	ZC3H15	zinc finger CCCH-type containing 15	1.99	13.01	12.02	0.01	0.05	1.90E-03	1.94E-02	Multiple_Complex
TC0400007830.hg.1	ALB	albumin	1.99	7.02	6.03	0.25	0.21	1.70E-03	1.78E-02	Multiple_Complex
TC0800011830.hg.1	ASAP1	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_018482	1.99	6.5	5.51	0.42	0.07	1.23E-02	6.15E-02	NonCoding
TC0600009228.hg.1	NT5DC1	5-nucleotidase domain containing 1	1.99	8.49	7.5	0.35	0.17	2.00E-03	1.95E-02	Multiple_Complex
TC1400010760.hg.1	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	1.99	7.84	6.85	0.45	0.21	4.10E-03	3.01E-02	Multiple_Complex
TC1300007237.hg.1	ALG11; UTP14C	ALG11, alpha-1,2-mannosyltransferase; UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	1.99	10.24	9.25	0.17	0.23	3.60E-03	2.77E-02	Multiple_Complex
TC1400009388.hg.1	PPP2R5E	protein phosphatase 2, regulatory subunit B, epsilon isoform	1.98	10.92	9.93	0.34	0.46	1.55E-02	7.17E-02	Multiple_Complex
TC0300011941.hg.1	MYH15	myosin, heavy chain 15	1.98	5.69	4.7	0.51	0.56	1.92E-02	8.28E-02	Multiple_Complex
TC0200010216.hg.1	ITGAV	integrin alpha V	1.98	8.88	7.89	0.25	0.33	3.80E-03	2.86E-02	Multiple_Complex
TC1700008769.hg.1	KCNJ2	potassium channel, inwardly rectifying subfamily J, member 2	1.98	5.12	4.13	0.47	0.17	2.02E-02	8.57E-02	Coding
TC0200016637.hg.1	SMC6	structural maintenance of chromosomes 6	1.98	9.26	8.28	0.25	0.05	4.80E-03	3.31E-02	Multiple_Complex
TC2200006955.hg.1	CRYBA4	crystallin beta A4	1.98	5.26	4.27	0.35	0.23	4.60E-03	3.23E-02	Multiple_Complex
TC0200009431.hg.1	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	1.98	9.14	8.16	0.11	0.32	5.00E-03	3.38E-02	Multiple_Complex

TC0900011031.hg.1	MRPL50	mitochondrial ribosomal protein L50	1.98	11.5	10.51	0.01	0.1	1.80E-03	1.85E-02	Multiple_Complex
TC0700008818.hg.1	ZNF277	zinc finger protein 277	1.98	6.48	5.49	0.11	0.17	1.10E-03	1.42E-02	Multiple_Complex
TC0300009673.hg.1	KLHL24	kelch-like family member 24	1.98	11.97	10.98	0.06	0.29	2.40E-03	2.19E-02	Multiple_Complex
TC0200012129.hg.1	TRMT61B	tRNA methyltransferase 61B	1.98	8.27	7.29	0.04	0.37	2.70E-03	2.32E-02	Multiple_Complex
TC0500011150.hg.1	GFM2	G elongation factor, mitochondrial 2	1.98	13.24	12.26	0.14	0.34	2.40E-03	2.20E-02	Multiple_Complex
TC0600007241.hg.1	LRRC16A	Transcript Identified by AceView, Entrez Gene ID(s) 55604	1.98	5.29	4.3	0.02	0.15	2.94E-02	1.10E-01	Unassigned
TC0200013610.hg.1	REV1	REV1, DNA directed polymerase	1.98	8.57	7.58	0.02	0.14	1.00E-03	1.39E-02	Multiple_Complex
TC0100008620.hg.1	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	1.98	8.51	7.53	0.31	0.43	3.30E-03	2.61E-02	Multiple_Complex
TC1400010779.hg.1	ATXN3	ataxin 3	1.98	8.27	7.28	0.46	0.16	3.00E-03	2.47E-02	NonCoding
TC1200012743.hg.1	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	1.98	5.96	4.98	0.63	0.11	5.50E-03	3.60E-02	NonCoding
TC0200014971.hg.1	SP3	Sp3 transcription factor	1.98	12.67	11.68	0.06	0.18	2.00E-03	1.98E-02	Multiple_Complex
TC1500010865.hg.1	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	1.98	4.96	3.97	0.06	0.12	1.20E-03	1.52E-02	NonCoding
TC0700011834.hg.1	PON3	paraoxonase 3	1.98	5.49	4.51	0.02	0.48	5.50E-03	3.60E-02	Multiple_Complex
TC1100007637.hg.1	OR8U1; OR8U8	olfactory receptor, family 8, subfamily U, member 1; olfactory receptor, family 8, subfamily U, member 8	1.98	4.74	3.75	0.13	0.22	3.00E-03	2.49E-02	Coding
TC0400011241.hg.1	SLC10A6	solute carrier family 10 (sodium/bile acid cotransporter), member 6	1.98	7.63	6.65	0.51	1.08	4.11E-02	1.38E-01	Multiple_Complex
TC1700008938.hg.1	UBALD2	UBA-like domain containing 2	1.98	7.46	6.48	0.26	0.6	2.93E-02	1.10E-01	Multiple_Complex
TC0800008183.hg.1	OSGIN2	oxidative stress induced growth inhibitor family member 2	1.98	9.05	8.06	0.18	0.39	2.40E-03	2.19E-02	Multiple_Complex
TC0500009673.hg.1	ZNF454	zinc finger protein 454	1.98	6.37	5.39	0.11	0.02	2.90E-03	2.45E-02	Multiple_Complex

TC0900009404.hg.1	PUM3	pumilio RNA binding family member 3	1.98	12.28	11.3	0.01	0.02	1.20E-03	1.51E-02	Multiple_Complex
TC1100009833.hg.1	OSBPL5	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_020896	1.97	4.43	3.44	0.1	0.06	1.40E-03	1.62E-02	NonCoding
TC0300013906.hg.1	KCNMB2	potassium channel subfamily M regulatory beta subunit 2	1.97	4.95	3.97	0.36	0.41	1.53E-02	7.11E-02	Multiple_Complex
TC0200013003.hg.1	FIGLA	folliculogenesis specific bHLH transcription factor	1.97	5.95	4.97	0.09	0.33	1.80E-03	1.86E-02	Coding
TC0X00007416.hg.1	FAAH2	fatty acid amide hydrolase 2	1.97	9.83	8.85	0.04	0.15	4.90E-03	3.37E-02	Multiple_Complex
TC0100017948.hg.1	CHML	choroideremia-like (Rab escort protein 2)	1.97	7.6	6.62	0.89	0.82	4.78E-02	1.52E-01	Multiple_Complex
TSUnmapped00000074.hg.1	STKLD1	serine/threonine kinase-like domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28669]	1.97	6.02	5.04	0.98	0.09	2.74E-02	1.05E-01	NonCoding
TC0200014814.hg.1	SCN1A	sodium channel, voltage gated, type I alpha subunit	1.97	4.85	3.87	0.35	0.01	1.40E-03	1.64E-02	Multiple_Complex
TC0400007017.hg.1	SLIT2	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_004787	1.97	8.27	7.29	0.06	0.49	4.40E-03	3.13E-02	NonCoding
TC0700012444.hg.1	CADPS2	Ca++-dependent secretion activator 2	1.97	8.12	7.14	0.23	0.33	2.01E-02	8.53E-02	Multiple_Complex
TC0200008675.hg.1	IL18RAP	interleukin 18 receptor accessory protein	1.97	4.71	3.73	0.68	0.17	1.03E-02	5.43E-02	Multiple_Complex
TC1100008800.hg.1	IZUMO1R	IZUMO1 receptor, JUNO	1.97	5.9	4.93	0.22	0.17	1.70E-03	1.78E-02	Coding
TC0800010869.hg.1	PEX2	peroxisomal biogenesis factor 2	1.97	10.14	9.16	0.15	0.1	2.20E-03	2.07E-02	Multiple_Complex
TC0900006969.hg.1	CHMP5	charged multivesicular body protein 5	1.97	15.06	14.08	0.05	0.13	2.20E-03	2.09E-02	Multiple_Complex
TC0600011438.hg.1	LTB	lymphotoxin beta (TNF superfamily, member 3)	1.97	7.52	6.55	0.42	0.6	9.60E-03	5.20E-02	Multiple_Complex
TC0400007330.hg.1	NSUN7	NOP2/Sun domain family, member 7	1.97	5.05	4.07	0.23	0.12	3.30E-03	2.65E-02	Multiple_Complex
TC1400008636.hg.1	METTL3	methyltransferase like 3	1.97	10.15	9.17	0.01	0.33	9.20E-03	5.07E-02	Multiple_Complex
TC1000008908.hg.1	SHOC2	SHOC2 leucine-rich repeat scaffold protein	1.97	13.13	12.16	0.18	0.27	1.90E-03	1.93E-02	Multiple_Complex

TC0200014694.hg.1	ACVR1C	activin A receptor type IC	1.97	8.08	7.1	0.23	0.01	1.40E-03	1.61E-02	Multiple_Complex
TC0100018359.hg.1	TSNAX	translin-associated factor X	1.97	10.05	9.07	0.19	0.55	8.60E-03	4.87E-02	Multiple_Complex
TC0600006926.hg.1	PAK1IP1	PAK1 interacting protein 1	1.97	10.08	9.1	0.21	0.19	1.40E-03	1.61E-02	Multiple_Complex
TC1800006446.hg.1	CETN1	centrin 1	1.97	4.99	4.02	0.14	0.12	1.20E-03	1.52E-02	Coding
TC0300012924.hg.1	VEPH1	ventricular zone expressed PH domain containing 1	1.97	6.95	5.98	0.68	0.3	1.21E-02	6.06E-02	Multiple_Complex
TC0800012451.hg.1	EIF3E	eukaryotic translation initiation factor 3, subunit E	1.96	16.42	15.45	0.08	0.13	2.40E-03	2.18E-02	Multiple_Complex
TC1100010349.hg.1	SVIP	small VCP/p97-interacting protein	1.96	12.47	11.49	0.12	0.06	2.50E-03	2.23E-02	Multiple_Complex
TC1000008401.hg.1	IFIT5	interferon-induced protein with tetratricopeptide repeats 5	1.96	8.6	7.63	0.34	0.43	9.90E-03	5.31E-02	Coding
TC0800008730.hg.1	FAM83A	family with sequence similarity 83, member A	1.96	5.34	4.37	0.07	0.03	1.10E-03	1.44E-02	Multiple_Complex
TC0300006840.hg.1	UBE2E1	ubiquitin conjugating enzyme E2E 1	1.96	11.79	10.82	0.13	0.3	1.40E-03	1.64E-02	Multiple_Complex
TC1900011693.hg.1	ZNF429	zinc finger protein 429	1.96	7.78	6.8	0.2	0.2	1.20E-03	1.50E-02	Coding
TC1700007811.hg.1	TMEM99	transmembrane protein 99	1.96	9.19	8.22	0.07	0.25	2.30E-03	2.13E-02	Multiple_Complex
TC0700011298.hg.1	ZNF680	zinc finger protein 680	1.96	12.36	11.39	0	0.44	4.90E-03	3.36E-02	Multiple_Complex
TC0700011383.hg.1	SBDS	Shwachman-Bodian-Diamond syndrome	1.96	12.6	11.63	0.04	0.04	1.60E-03	1.74E-02	Multiple_Complex
TC0500011333.hg.1	TMEM167A	transmembrane protein 167A	1.96	12.92	11.94	0.07	0.29	1.40E-03	1.63E-02	Multiple_Complex
TC0200016719.hg.1	SNORD89; RNF149	small nucleolar RNA, C/D box 89; ring finger protein 149	1.96	8.87	7.9	0.1	0.52	4.90E-03	3.34E-02	Multiple_Complex
TC0900012215.hg.1	IFNA16	interferon, alpha 16	1.96	5.29	4.32	0.54	0.2	4.50E-03	3.16E-02	Coding
TC1300008809.hg.1	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	1.96	11.3	10.33	0.08	0.57	4.80E-03	3.29E-02	Multiple_Complex
TC0500010813.hg.1	MIER3	mesoderm induction early response 1, family member 3	1.96	9.17	8.2	0.42	0.29	4.90E-03	3.34E-02	Multiple_Complex

TC0200014414.hg.1	CXCR4	chemokine (C-X-C motif) receptor 4	1.96	10.75	9.78	0.4	0.09	2.30E-03	2.12E-02	Multiple_Complex
TC0300007106.hg.1	MOBP	myelin-associated oligodendrocyte basic protein	1.96	7.51	6.54	0.04	0.35	3.50E-03	2.73E-02	Multiple_Complex
TC0300012186.hg.1	CCDC58	coiled-coil domain containing 58	1.96	15.42	14.45	0.03	0.25	3.50E-03	2.72E-02	Multiple_Complex
TC0800012428.hg.1	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	1.96	12.42	11.45	0.03	0.34	2.00E-03	1.99E-02	Multiple_Complex
TC1200007170.hg.1	CCDC91	coiled-coil domain containing 91	1.96	14.01	13.04	0.25	0.11	1.80E-03	1.86E-02	Multiple_Complex
TC0800011260.hg.1	SNX31	sorting nexin 31	1.96	5.22	4.25	0.27	0.64	1.18E-02	5.98E-02	Multiple_Complex
TC1300008720.hg.1	MTRF1	mitochondrial translational release factor 1	1.96	9.78	8.81	0.14	0.15	3.20E-03	2.61E-02	Multiple_Complex
TC1500009002.hg.1	ACTC1	actin, alpha, cardiac muscle 1	1.96	6.28	5.31	0.06	0.04	7.00E-04	1.21E-02	Multiple_Complex
TC0700009703.hg.1	WDR86-AS1	WDR86 antisense RNA 1	1.96	5.53	4.56	0.24	0.16	9.00E-03	4.96E-02	NonCoding
TC1200007992.hg.1	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	1.96	8.1	7.13	0.43	0.34	4.70E-03	3.26E-02	Multiple_Complex
TC0200012956.hg.1	GFPT1	glutamine--fructose-6-phosphate transaminase 1	1.96	13.29	12.32	0.37	0.27	3.50E-03	2.73E-02	Multiple_Complex
TC0700012010.hg.1	TFR2	transferrin receptor 2	1.95	6.63	5.67	0.01	0.59	6.00E-03	3.82E-02	Multiple_Complex
TC0200011965.hg.1	ATAD2B	ATPase family, AAA domain containing 2B	1.95	9.53	8.57	0.21	0.78	1.58E-02	7.29E-02	Multiple_Complex
TC0X00010172.hg.1	HMGN5	high mobility group nucleosome binding domain 5	1.95	12.27	11.3	0.01	0.25	2.00E-03	2.00E-02	Multiple_Complex
TC2100007597.hg.1	HSPA13	heat shock protein 70kDa family, member 13	1.95	12.65	11.68	0.18	0.23	4.00E-03	2.98E-02	Multiple_Complex
TC1100009407.hg.1	CCDC15	coiled-coil domain containing 15	1.95	9.86	8.89	0.06	0.3	1.03E-02	5.45E-02	Multiple_Complex
TC1200012836.hg.1	C12orf73	chromosome 12 open reading frame 73	1.95	12.81	11.84	0.32	0.18	1.30E-02	6.38E-02	Multiple_Complex
TC1200008134.hg.1	YEATS4	YEATS domain containing 4	1.95	11.41	10.45	0.27	0.44	3.40E-03	2.68E-02	Multiple_Complex
TC1500009179.hg.1	PLA2G4D	phospholipase A2, group IVD (cytosolic)	1.95	5.64	4.67	0.16	0.31	2.20E-03	2.09E-02	Multiple_Complex
TC0500008588.hg.1	KIAA1024L	KIAA1024-like	1.95	5.58	4.62	0.08	0.22	5.60E-03	3.66E-02	Multiple_Complex

TC0200016718.hg.1	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	1.95	5.2	4.23	0.16	0.22	1.30E-03	1.54E-02	NonCoding
TC1600011389.hg.1	TP53TG3C	TP53 target 3C	1.95	4.93	3.97	0.43	0.25	1.35E-02	6.55E-02	Multiple_Complex
TC0600007986.hg.1	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	1.95	6.11	5.15	0.81	0.27	1.69E-02	7.62E-02	Coding
TC1100009122.hg.1	NXPE2	neurexophilin and PC-esterase domain family, member 2	1.95	5.16	4.2	0.43	0.41	1.76E-02	7.81E-02	Multiple_Complex
TC2000006625.hg.1	C20orf196	Transcript Identified by AceView, Entrez Gene ID(s) 149840	1.95	4.87	3.91	0.72	0.78	4.46E-02	1.46E-01	Unassigned
TC0500009707.hg.1	SQSTM1	Transcript Identified by AceView, Entrez Gene ID(s) 8878	1.95	7.53	6.57	0.53	0.12	2.53E-02	1.00E-01	Unassigned
TC1700012257.hg.1	KRTAP9-3	keratin associated protein 9-3	1.95	6.67	5.71	0.51	0.39	2.87E-02	1.09E-01	Coding
TC1000012565.hg.1	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	1.95	8.44	7.48	0.45	0.2	4.20E-03	3.05E-02	NonCoding
TC0100012401.hg.1	OR4F29; OR4F3; OR4F16	olfactory receptor, family 4, subfamily F, member 29; olfactory receptor, family 4, subfamily F, member 3; olfactory receptor, family 4, subfamily F, member 16	1.95	7.5	6.54	0.11	0.4	2.10E-02	8.78E-02	Coding
TC0100012410.hg.1	OR4F16; OR4F29	olfactory receptor, family 4, subfamily F, member 16; olfactory receptor, family 4, subfamily F, member 29	1.95	7.5	6.54	0.11	0.4	2.10E-02	8.78E-02	Coding
TC1000008435.hg.1	HECTD2	HECT domain containing E3 ubiquitin protein ligase 2	1.95	9.56	8.6	0.45	0.46	8.90E-03	4.95E-02	Multiple_Complex
TC1200008601.hg.1	ANO4	anoctamin 4	1.95	6.15	5.19	0.13	0.25	3.80E-03	2.86E-02	Multiple_Complex
TC1100007472.hg.1	NR1H3	nuclear receptor subfamily 1, group H, member 3	1.95	8.9	7.94	0.28	0.29	2.90E-03	2.43E-02	Multiple_Complex
TC0X00006715.hg.1	SCML1	sex comb on midleg-like 1 (Drosophila)	1.94	12.72	11.76	0.08	0.1	9.00E-04	1.34E-02	Multiple_Complex
TC0100011669.hg.1	HLX	H2.0-like homeobox	1.94	5.27	4.31	0.27	0.26	5.70E-03	3.68E-02	Multiple_Complex
TC0300013842.hg.1	SLMAP	sarcolemma associated protein	1.94	8.56	7.6	0.05	0.28	1.30E-03	1.57E-02	Multiple_Complex
TC1600006757.hg.1	SMIM22	small integral membrane protein 22	1.94	6.39	5.43	0.41	0	5.10E-03	3.43E-02	Multiple_Complex

TC0400011159.hg.1	PRKG2	protein kinase, cGMP-dependent, type II	1.94	5.94	4.98	0.49	0.17	4.70E-03	3.26E-02	Multiple_Complex
TC0X00008468.hg.1	CCDC160	coiled-coil domain containing 160	1.94	5.43	4.47	0.09	0.37	3.40E-03	2.68E-02	Multiple_Complex
TC1200010450.hg.1	YAF2	YY1 associated factor 2	1.94	10.74	9.78	0.49	0	4.10E-03	3.03E-02	Multiple_Complex
TC0600013147.hg.1	ARHGAP18	Rho GTPase activating protein 18	1.94	8.91	7.95	0.09	0.63	7.10E-03	4.24E-02	Multiple_Complex
TC0300010903.hg.1	KIAA1143	KIAA1143	1.94	11.23	10.27	0.21	0.15	7.60E-03	4.45E-02	Multiple_Complex
TC0200013376.hg.1	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	1.94	11.16	10.2	0.28	0.13	1.80E-03	1.86E-02	Multiple_Complex
TC0500011240.hg.1	HOMER1	homer scaffolding protein 1	1.94	13.87	12.91	0.18	0.06	2.60E-03	2.30E-02	Multiple_Complex
TC0500012367.hg.1	GRXCR2	glutaredoxin, cysteine rich 2	1.94	5.41	4.45	0.21	0.26	1.70E-03	1.80E-02	Coding
TC0800008540.hg.1	TRHR	thyrotropin-releasing hormone receptor	1.94	5.99	5.04	0.36	0.45	5.20E-03	3.47E-02	Coding
TC1900006586.hg.1	TMPRSS9	transmembrane protease, serine 9	1.94	4.65	3.69	0.33	0.11	2.30E-03	2.13E-02	Multiple_Complex
TC0800010506.hg.1	PLAG1	pleiomorphic adenoma gene 1	1.94	9.96	9	0.16	0.29	5.30E-03	3.53E-02	Multiple_Complex
TC0X00010351.hg.1	TAF7L	TATA box binding protein associated factor 7 like	1.94	6.04	5.08	0.15	0.5	1.63E-02	7.44E-02	Coding
TC0200015226.hg.1	HIBCH	Transcript Identified by AceView, Entrez Gene ID(s) 26275	1.94	7.77	6.81	0.02	0.2	1.50E-03	1.67E-02	Unassigned
TC1000007883.hg.1	SRGN	serglycin	1.94	4.99	4.03	0.44	0.3	2.10E-02	8.78E-02	Multiple_Complex
TC0100012828.hg.1	LZIC	leucine zipper and CTNNBIP1 domain containing	1.94	11.42	10.46	0.01	0.09	3.00E-03	2.49E-02	Multiple_Complex
TC0700007031.hg.1	JAZF1	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_175061	1.94	7.82	6.86	0.07	0.62	9.50E-03	5.17E-02	NonCoding
TC1100007762.hg.1	OOSP2	oocyte secreted protein 2	1.94	6.5	5.55	0.74	0.68	4.22E-02	1.40E-01	Multiple_Complex
TC0200015099.hg.1	CWC22	CWC22 homolog, spliceosome-associated protein	1.94	10.22	9.26	0.12	0.23	3.30E-03	2.63E-02	Multiple_Complex
TC0900008219.hg.1	NR4A3	nuclear receptor subfamily 4, group A, member 3	1.94	7.81	6.86	0.14	0.26	1.40E-03	1.64E-02	Multiple_Complex

TC1200011755.hg.1	NFYB	nuclear transcription factor Y subunit beta	1.94	8.68	7.73	0.25	0.16	5.60E-03	3.65E-02	Multiple_Complex
TC1100008983.hg.1	ACAT1	acetyl-CoA acetyltransferase 1	1.94	9.47	8.52	0.33	0.16	2.30E-03	2.12E-02	Multiple_Complex
TC0900011294.hg.1	LOC100505478; RP11-402G3.3	uncharacterized LOC100505478; putative novel transcript	1.94	6.27	5.32	0.35	0.47	6.40E-03	3.96E-02	Multiple_Complex
TC0600009240.hg.1	KPNA5	karyopherin alpha 5 (importin alpha 6)	1.94	12.7	11.74	0.13	0.33	2.50E-03	2.23E-02	Multiple_Complex
TC1100012990.hg.1	MIR670HG; HSD17B12	MIR670 host gene; hydroxysteroid (17-beta) dehydrogenase 12	1.93	7.71	6.76	0.13	0.26	1.70E-03	1.80E-02	Multiple_Complex
TC1500007735.hg.1	LRRC49	leucine rich repeat containing 49	1.93	7.88	6.93	0	0.6	1.59E-02	7.32E-02	Multiple_Complex
TC0300006942.hg.1	STT3B	STT3B, subunit of the oligosaccharyltransferase complex (catalytic)	1.93	11.08	10.13	0.85	0.33	2.12E-02	8.84E-02	Multiple_Complex
TC0100011388.hg.1	IL19	interleukin 19	1.93	5.56	4.61	0.68	0.36	1.20E-02	6.04E-02	Multiple_Complex
TC1200011671.hg.1	UHRF1BP1L	UHRF1 binding protein 1-like	1.93	12.21	11.26	0.19	0.42	6.20E-03	3.89E-02	Multiple_Complex
TC1900006804.hg.1	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	1.93	10.88	9.93	0.24	0.1	3.90E-03	2.91E-02	Multiple_Complex
TC0700009536.hg.1	ARHGEF5	Rho guanine nucleotide exchange factor 5	1.93	6.02	5.06	0.34	0.15	3.70E-03	2.80E-02	Multiple_Complex
TC0300014094.hg.1	TCTEX1D2	Tctex1 domain containing 2	1.93	13.03	12.08	0.13	0.2	4.90E-03	3.37E-02	Multiple_Complex
TC0500008054.hg.1	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	1.93	12.18	11.23	0.15	0.13	3.00E-03	2.49E-02	Multiple_Complex
TC1000007885.hg.1	SRGN	Transcript Identified by AceView, Entrez Gene ID(s) 5552	1.93	7.21	6.26	0.74	0.57	3.16E-02	1.16E-01	Coding
TC1700011131.hg.1	MBTD1	mbt domain containing 1	1.93	10.16	9.21	0.01	0.52	8.60E-03	4.85E-02	Multiple_Complex
TC2000008379.hg.1	MKKS	McKusick-Kaufman syndrome	1.93	11.31	10.36	0.11	0.3	6.80E-03	4.13E-02	Multiple_Complex
TC1000007875.hg.1	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	1.93	9.9	8.95	0	0.19	2.10E-03	2.00E-02	Multiple_Complex
TC0700006783.hg.1	TSPAN13	tetraspanin 13	1.93	13.51	12.56	0.41	0.26	4.50E-03	3.19E-02	Multiple_Complex
TC0400012875.hg.1	KLKB1	kallikrein B1	1.93	5.46	4.51	0.13	0.32	5.30E-03	3.52E-02	Multiple_Complex

TC0900009859.hg.1	AQP7	aquaporin 7	1.93	6.06	5.11	0.58	0.03	7.00E-03	4.22E-02	Multiple_Complex
TC0600008764.hg.1	ANKRD6	ankyrin repeat domain 6	1.93	7.95	7	0.28	0.48	3.02E-02	1.12E-01	Multiple_Complex
TC1200008706.hg.1	KIAA1033	KIAA1033	1.93	11.81	10.86	0.1	0.44	3.60E-03	2.79E-02	Multiple_Complex
TC0100009038.hg.1	C1orf146	chromosome 1 open reading frame 146	1.93	4.05	3.1	0.19	0.08	4.40E-03	3.14E-02	Coding
TC1500010097.hg.1	SCAPER	S-phase cyclin A-associated protein in the ER	1.93	10.43	9.49	0.3	0.42	6.40E-03	3.96E-02	Multiple_Complex
TC1600009535.hg.1	FOPNL	FGFR1OP N-terminal like	1.93	13	12.05	0.15	0.4	1.45E-02	6.86E-02	Multiple_Complex
TC0300007617.hg.1	KCTD6	potassium channel tetramerization domain containing 6	1.93	7.28	6.33	0.03	0.19	7.00E-03	4.22E-02	Multiple_Complex
TC1100009924.hg.1	OR51B4	olfactory receptor, family 51, subfamily B, member 4	1.93	7.46	6.51	0.51	0.07	4.10E-03	3.02E-02	Coding
TC0200008617.hg.1	PDCL3	phosducin like 3	1.93	9.46	8.51	0.02	0.4	8.50E-03	4.83E-02	Coding
TC2100007967.hg.1	PAXBP1	PAX3 and PAX7 binding protein 1	1.93	12.41	11.47	0.01	0.3	1.70E-03	1.78E-02	Multiple_Complex
TC1300006979.hg.1	RGCC	regulator of cell cycle	1.93	6.82	5.87	0.23	0.38	8.40E-03	4.78E-02	Multiple_Complex
TC0500013175.hg.1	IPO11; LRRC70	importin 11; leucine rich repeat containing 70	1.93	11.25	10.31	0.26	0.2	1.70E-03	1.82E-02	Multiple_Complex
TC1200008843.hg.1	FAM216A	family with sequence similarity 216, member A	1.93	12.92	11.98	0.16	0.2	1.10E-02	5.71E-02	Multiple_Complex
TC0400007282.hg.1	KLB	klotho beta	1.93	5.49	4.54	0.52	0.4	1.36E-02	6.56E-02	Coding
TC0600008674.hg.1	RIPPLY2	ripply transcriptional repressor 2	1.92	10.21	9.26	0.28	0.08	1.50E-03	1.67E-02	Multiple_Complex
TC0M00006454.hg.1	ND6	NADH dehydrogenase, subunit 6 (complex I)	1.92	14.36	13.42	0.23	0.03	1.50E-03	1.66E-02	Multiple_Complex
TC0800008080.hg.1	FABP5	fatty acid binding protein 5 (psoriasis-associated)	1.92	12.46	11.51	0.24	0.06	1.30E-03	1.55E-02	Multiple_Complex
TC0X00009664.hg.1	CACNA1F	calcium channel, voltage-dependent, L type, alpha 1F subunit	1.92	5.12	4.18	0.47	0.33	5.90E-03	3.78E-02	Multiple_Complex
TC0900009279.hg.1	TOR4A	torsin family 4, member A	1.92	7.38	6.44	0.2	0.51	9.20E-03	5.07E-02	Multiple_Complex
TC1700007478.hg.1	NF1	neurofibromin 1	1.92	9.98	9.04	0.13	0.05	4.50E-03	3.20E-02	Multiple_Complex
TC1400010595.hg.1	KIAA0391	KIAA0391	1.92	11.67	10.72	0.08	0.03	1.00E-03	1.40E-02	Multiple_Complex

TC1200011298.hg.1	CAPS2	calcyphosine 2	1.92	5.85	4.9	0.21	0.25	5.80E-03	3.71E-02	Multiple_Complex
TC0700011518.hg.1	GTF2IRD2; GTF2IRD2B	GTF2I repeat domain containing 2; GTF2I repeat domain containing 2B	1.92	8.05	7.11	0.18	0.14	1.70E-03	1.79E-02	Multiple_Complex
TC0500011579.hg.1	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	1.92	5.33	4.39	0.29	0.4	1.96E-02	8.38E-02	Multiple_Complex
TC1900011972.hg.1	ZNF404	zinc finger protein 404	1.92	6.93	5.99	0.05	0.52	5.00E-03	3.38E-02	Coding
TC1100008490.hg.1	UVRAG	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_003369	1.92	7.54	6.6	0.63	0.39	4.19E-02	1.39E-01	NonCoding
TC0300008140.hg.1	TMEM30C	transmembrane protein 30C	1.92	4.46	3.52	0.32	0.53	3.30E-02	1.19E-01	Multiple_Complex
TC0800010663.hg.1	ARMC1	armadillo repeat containing 1	1.92	9.48	8.55	0.53	0.23	5.70E-03	3.69E-02	Multiple_Complex
TC1300008289.hg.1	ZDHHC20	zinc finger, DHHC-type containing 20	1.91	11	10.06	0.38	0.5	8.00E-03	4.62E-02	Multiple_Complex
TC0300006622.hg.1	PPARG	peroxisome proliferator-activated receptor gamma	1.91	8.5	7.56	0.02	0.1	1.00E-03	1.40E-02	Multiple_Complex
TC2000009895.hg.1	LINC00493	long intergenic non-protein coding RNA 493	1.91	13.96	13.02	0.09	0.06	2.40E-03	2.16E-02	Multiple_Complex
TC2000006755.hg.1	NDUFAF5	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5	1.91	12.34	11.41	0.12	0.17	3.00E-03	2.50E-02	Multiple_Complex
TC1800008862.hg.1	PIGN	phosphatidylinositol glycan anchor biosynthesis class N	1.91	11.62	10.68	0.32	0.1	6.50E-03	4.02E-02	Multiple_Complex
TC1100006831.hg.1	ADM	adrenomedullin	1.91	8.27	7.34	0.16	0.23	3.20E-03	2.61E-02	Coding
TC0900012161.hg.1	DNAJC25-GNG10	DNAJC25-GNG10 readthrough	1.91	12.93	11.99	0.38	0.07	3.10E-03	2.55E-02	Coding
TC0800006864.hg.1	ZDHHC2	zinc finger, DHHC-type containing 2	1.91	9.68	8.74	0.26	0.12	2.20E-03	2.08E-02	Multiple_Complex
TC0200013357.hg.1	KRCC1	lysine-rich coiled-coil 1	1.91	11.55	10.61	0.29	0.05	2.60E-03	2.29E-02	Multiple_Complex
TC0600011817.hg.1	C6orf132	chromosome 6 open reading frame 132	1.91	6.49	5.56	0.22	0.16	6.20E-03	3.88E-02	Multiple_Complex
TC0X00007238.hg.1	PAGE4	P antigen family, member 4 (prostate associated)	1.91	5.54	4.61	0.18	0.05	1.90E-03	1.93E-02	Multiple_Complex

TC0200016661.hg.1	C2orf61	chromosome 2 open reading frame 61	1.91	6.25	5.31	0.04	0.53	1.38E-02	6.65E-02	Multiple_Complex
TC0200011885.hg.1	TTC32	tetratricopeptide repeat domain 32	1.91	12.82	11.88	0.34	0.07	3.50E-03	2.73E-02	Multiple_Complex
TC0900007877.hg.1	GADD45G	growth arrest and DNA-damage-inducible, gamma	1.91	6.81	5.88	0.09	0.01	2.90E-03	2.41E-02	Multiple_Complex
TC1600009326.hg.1	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	1.91	11.68	10.74	0	0.68	1.63E-02	7.43E-02	Multiple_Complex
TC0200016563.hg.1	KLHL23	kelch-like family member 23	1.91	9.65	8.71	0.01	0.49	6.00E-03	3.82E-02	Multiple_Complex
TC1200012766.hg.1	PRB1	proline-rich protein BstNI subfamily 1	1.91	6.56	5.63	0.35	0.25	1.29E-02	6.33E-02	Coding
TC0600014151.hg.1	SMIM8	small integral membrane protein 8	1.91	4.43	3.5	0.98	0.25	3.99E-02	1.35E-01	NonCoding
TC0100008955.hg.1	PKN2	protein kinase N2	1.91	14.34	13.41	0.21	0.28	3.20E-03	2.57E-02	Multiple_Complex
TC2100008143.hg.1	ERG	v-ets avian erythroblastosis virus E26 oncogene homolog	1.91	5.8	4.87	0.94	0.18	2.57E-02	1.01E-01	Multiple_Complex
TC0600012647.hg.1	FBXL4	F-box and leucine-rich repeat protein 4	1.91	9.93	9	0.22	0.36	4.10E-03	2.99E-02	Multiple_Complex
TC0200012297.hg.1	SRSF7	serine/arginine-rich splicing factor 7	1.91	14.65	13.72	0.09	0.08	1.40E-03	1.64E-02	Multiple_Complex
TC0100018344.hg.1	LYPLAL1	lysophospholipase-like 1	1.9	13.31	12.38	0.11	0.1	1.40E-03	1.61E-02	Multiple_Complex
TC1700006720.hg.1	BCL6B	B-cell CLL/lymphoma 6, member B	1.9	5.49	4.56	0.99	0.12	2.92E-02	1.10E-01	Multiple_Complex
TC1200009994.hg.1	LINC01559	long intergenic non-protein coding RNA 1559	1.9	5.55	4.62	0.44	0.06	4.40E-03	3.13E-02	Multiple_Complex
TC1000008923.hg.1	TECTB	tectorin beta	1.9	4.11	3.18	0.68	0.05	2.08E-02	8.72E-02	Multiple_Complex
TC1900007848.hg.1	HAMP	hepcidin antimicrobial peptide	1.9	5.85	4.93	0.46	0.55	1.28E-02	6.30E-02	Multiple_Complex
TC0200016742.hg.1	PLA2R1	phospholipase A2 receptor 1	1.9	4.51	3.58	0.18	0.22	5.60E-03	3.65E-02	Multiple_Complex
TC0200007038.hg.1	DRC1	dynein regulatory complex subunit 1	1.9	6.3	5.37	0.04	0.21	1.50E-03	1.71E-02	Multiple_Complex
TC1000012498.hg.1	GSTO2	glutathione S-transferase omega 2	1.9	10.27	9.34	0.01	0.48	8.60E-03	4.86E-02	Multiple_Complex
TC2000009016.hg.1	DSN1	DSN1 homolog, MIS12 kinetochore complex component	1.9	13.75	12.82	0.21	0.17	3.70E-03	2.82E-02	Multiple_Complex

TC1100010991.hg.1	GIF	gastric intrinsic factor (vitamin B synthesis)	1.9	4.88	3.95	0.31	0.14	2.90E-03	2.44E-02	Multiple_Complex
TC0100010793.hg.1	CEP350	centrosomal protein 350kDa	1.9	10.79	9.87	0.31	0.26	3.20E-03	2.59E-02	Multiple_Complex
TC1200006444.hg.1	CCDC77	coiled-coil domain containing 77	1.9	11.1	10.17	0.48	0.24	1.38E-02	6.65E-02	Multiple_Complex
TC0200016680.hg.1	SERTAD2	SERTA domain containing 2	1.9	5.6	4.67	0.78	0.32	3.21E-02	1.17E-01	NonCoding
TC1200008370.hg.1	C12orf29	chromosome 12 open reading frame 29	1.9	14.06	13.14	0.02	0.36	4.90E-03	3.33E-02	Multiple_Complex
TC0600014366.hg.1	PDE10A	phosphodiesterase 10A	1.9	9.48	8.55	0.13	0.23	2.10E-03	2.00E-02	Multiple_Complex
TC1600011322.hg.1	FAM195A	family with sequence similarity 195, member A	1.9	11.16	10.24	0.41	0.68	3.40E-02	1.21E-01	Multiple_Complex
TC1000011478.hg.1	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	1.9	4.48	3.55	0.08	0.26	9.70E-03	5.24E-02	Multiple_Complex
TC1200010024.hg.1	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	1.9	5.74	4.82	0.6	0.17	8.40E-03	4.78E-02	Multiple_Complex
TC1700007444.hg.1	NSRP1; MIR423	nuclear speckle splicing regulatory protein 1; microRNA 423	1.9	10.49	9.57	0.13	0.47	5.10E-03	3.45E-02	Multiple_Complex
TC1400007036.hg.1	PRPF39	pre-mRNA processing factor 39	1.9	7.19	6.26	0.16	0.33	3.30E-03	2.63E-02	Multiple_Complex
TC0400010612.hg.1	NFXL1	nuclear transcription factor, X-box binding-like 1	1.9	9.92	8.99	0.17	0.2	2.40E-03	2.16E-02	Multiple_Complex
TC0100012471.hg.1	AURKAIP1	aurora kinase A interacting protein 1	1.9	10.54	9.61	0.06	0.63	2.98E-02	1.11E-01	Multiple_Complex
TC0500009281.hg.1	PTTG1	pituitary tumor-transforming 1	1.9	12.33	11.4	0.14	0.05	1.10E-03	1.44E-02	Multiple_Complex
TC1000008385.hg.1	STAMBPL1	STAM binding protein-like 1	1.9	11.17	10.25	0.33	0.51	7.30E-03	4.35E-02	Multiple_Complex
TC0600008678.hg.1	MRAP2	melanocortin 2 receptor accessory protein 2	1.9	8	7.07	0.21	0.45	3.31E-02	1.19E-01	Coding
TC1000011825.hg.1	BBIP1	BBSome interacting protein 1	1.9	14.27	13.35	0.15	0.1	4.70E-03	3.25E-02	Multiple_Complex
TC0100011543.hg.1	TATDN3	TatD DNase domain containing 3	1.9	9.95	9.03	0.12	0.22	2.50E-03	2.24E-02	Multiple_Complex
TC0700010887.hg.1	COA1	cytochrome c oxidase assembly factor 1 homolog	1.9	13.16	12.23	0.3	0.46	6.40E-03	3.97E-02	Multiple_Complex
TC1300010040.hg.1	NEK5	NIMA-related kinase 5	1.9	5.37	4.45	0.42	0.59	1.20E-02	6.04E-02	Multiple_Complex
TC1400006828.hg.1	COCH	cochlin	1.9	11.05	10.12	0.35	0.12	2.81E-02	1.07E-01	Multiple_Complex

TC1900011763.hg.1	APOC4-APOC2; APOC2	APOC4-APOC2 readthrough (NMD candidate); apolipoprotein C-II	1.9	8.08	7.16	1.08	0.13	4.92E-02	1.56E-01	Multiple_Complex
TC0100009908.hg.1	ECM1	extracellular matrix protein 1	1.9	6.32	5.4	0.61	0.01	2.42E-02	9.69E-02	Multiple_Complex
TC0300010557.hg.1	NEK10	NIMA-related kinase 10	1.89	6.1	5.18	0.19	0.12	2.10E-03	2.01E-02	Multiple_Complex
TC2200008364.hg.1	TTC28	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001145418	1.89	7	6.08	0.78	0.3	3.58E-02	1.25E-01	NonCoding
TC1600007007.hg.1	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	1.89	10.7	9.78	0.16	0.21	6.40E-03	3.98E-02	Multiple_Complex
TC1000012481.hg.1	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	1.89	7.87	6.95	0.11	0.29	2.80E-03	2.37E-02	Coding
TC0200007032.hg.1	HADHB	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	1.89	11.16	10.24	0.39	0.23	4.50E-03	3.20E-02	Multiple_Complex
TC0200009596.hg.1	ACVR2A	activin A receptor type IIA	1.89	11.32	10.4	0.16	0.04	1.20E-03	1.50E-02	Multiple_Complex
TC1600010498.hg.1	SLC38A7	solute carrier family 38, member 7	1.89	4.87	3.95	0.15	0.13	2.79E-02	1.07E-01	Multiple_Complex
TC0600014329.hg.1	OSTM1	osteopetrosis associated transmembrane protein 1	1.89	11.03	10.11	0.44	0.36	7.60E-03	4.46E-02	NonCoding
TC0400012825.hg.1	HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3	1.89	5.94	5.02	0.71	0.14	1.12E-02	5.78E-02	NonCoding
TC0100008622.hg.1	boyboy; RP4-630A11.3; LEPR	Transcript Identified by AceView; Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001003679; putative novel transcript	1.89	6.27	5.34	0.24	0.36	1.27E-02	6.28E-02	NonCoding
TC0100015873.hg.1	S100A13	S100 calcium binding protein A13	1.89	12.06	11.14	0.3	0.68	1.89E-02	8.17E-02	Multiple_Complex
TC1200007182.hg.1	FAR2	fatty acyl-CoA reductase 2	1.89	8.26	7.34	0.73	0.37	2.17E-02	8.98E-02	Multiple_Complex
TC2000009236.hg.1	WFDC9	WAP four-disulfide core domain 9	1.89	5.86	4.94	0.2	0.05	4.90E-03	3.36E-02	Coding
TC0800008062.hg.1	ZBTB10	zinc finger and BTB domain containing 10	1.89	11.08	10.16	0.57	0.18	8.00E-03	4.63E-02	Coding

TC2000009242.hg.1	WFDC3	WAP four-disulfide core domain 3	1.89	8.53	7.61	0.2	0.66	3.58E-02	1.25E-01	Multiple_Complex
TC0700013401.hg.1	AC007566.10; GATAD1	Transcript Identified by AceView, Entrez Gene ID(s) 57798; novel transcript, antisense to ERVW-1 and PEX1	1.89	8.54	7.62	0.83	0.12	2.28E-02	9.29E-02	NonCoding
TC0200012260.hg.1	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta	1.89	14.53	13.61	0.01	0.05	1.40E-03	1.60E-02	Multiple_Complex
TC2200009337.hg.1	GATSL3	GATS protein-like 3	1.89	7.65	6.73	0.1	0.39	1.14E-02	5.85E-02	Multiple_Complex
TC0100016438.hg.1	ANKRD45	ankyrin repeat domain 45	1.89	5.42	4.5	0.19	0.43	4.70E-03	3.29E-02	Multiple_Complex
TC2200008796.hg.1	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	1.89	11.73	10.82	0.11	0.44	7.00E-03	4.22E-02	Multiple_Complex
TC0100011520.hg.1	PPP2R5A	protein phosphatase 2, regulatory subunit B, alpha	1.89	9.42	8.5	0.33	0.06	5.10E-03	3.43E-02	Multiple_Complex
TC1300010029.hg.1	N4BP2L1	NEDD4 binding protein 2-like 1	1.89	6.38	5.46	0.24	0.17	1.50E-02	7.03E-02	Multiple_Complex
TC0X00009262.hg.1	SUPT20HL2	SPT20 homolog, SAGA complex component-like 2	1.89	7.67	6.76	0.59	0.06	8.00E-03	4.63E-02	Multiple_Complex
TC2200007626.hg.1	ATXN10	ataxin 10	1.89	15.49	14.58	0.3	0.32	7.20E-03	4.29E-02	Multiple_Complex
TC1100007795.hg.1	PGA3; PGA4	pepsinogen 3, group I (pepsinogen A); pepsinogen 4, group I (pepsinogen A)	1.89	6.29	5.38	0.29	0.19	6.70E-03	4.09E-02	Multiple_Complex
TC1000006912.hg.1	MRC1	mannose receptor, C type 1	1.89	6.22	5.31	0.32	0.2	6.40E-03	3.96E-02	Coding
TC0800008197.hg.1	OTUD6B	OTU domain containing 6B	1.89	9.96	9.05	0.08	0.33	3.90E-03	2.92E-02	Multiple_Complex
TC0900010063.hg.1	CNTNAP3	contactin associated protein-like 3	1.89	9.38	8.47	0.33	0.27	3.50E-03	2.72E-02	Multiple_Complex
TC0300011223.hg.1	SELK	selenoprotein K; selenoprotein K [Source:EntrezGene;Acc:58515]; Transcript Identified by AceView, Entrez Gene ID(s) 58515, RefSeq ID(s) NM_021237	1.88	13.51	12.6	0.13	0.3	8.00E-03	4.63E-02	Multiple_Complex
TC1700010878.hg.1	SPATA32	spermatogenesis associated 32	1.88	5.88	4.97	0.59	0.35	1.08E-02	5.62E-02	Coding

TC1100008264.hg.1	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	1.88	9.08	8.17	0.24	0.44	4.50E-03	3.20E-02	Multiple_Complex
TC1300006767.hg.1	USPL1	ubiquitin specific peptidase like 1	1.88	11.72	10.8	0.2	0.11	1.90E-03	1.93E-02	Multiple_Complex
TC0900010439.hg.1	TRPM6	transient receptor potential cation channel, subfamily M, member 6	1.88	6.8	5.89	0.09	0.65	1.07E-02	5.58E-02	Multiple_Complex
TC0200009700.hg.1	GALNT13	polypeptide N-acetylgalactosaminyltransferase 13	1.88	10.89	9.97	0.13	0.54	9.40E-03	5.14E-02	Multiple_Complex
TC0600011615.hg.1	DEF6	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_022047	1.88	7.43	6.52	0.37	0.41	1.96E-02	8.39E-02	NonCoding
TC0700008897.hg.1	LSM8	LSM8 homolog, U6 small nuclear RNA associated	1.88	9.99	9.07	0.34	0.14	5.70E-03	3.69E-02	Multiple_Complex
TC1400008036.hg.1	COX8C	cytochrome c oxidase subunit VIIIC	1.88	8.77	7.85	0.42	0.23	4.70E-03	3.27E-02	Coding
TC0600013330.hg.1	PBOV1	prostate and breast cancer overexpressed 1	1.88	4.77	3.86	0.32	0.53	1.73E-02	7.73E-02	Coding
TC1700012442.hg.1	TBC1D3P1-DHX40P1	TBC1D3P1-DHX40P1 readthrough transcribed pseudogene	1.88	11.44	10.53	0.27	0.07	2.10E-03	2.04E-02	Multiple_Complex
TC0500009772.hg.1	OR4F3	olfactory receptor, family 4, subfamily F, member 3	1.88	7.16	6.25	0.55	0.13	4.85E-02	1.54E-01	Coding
TC1100010945.hg.1	OR5B21	olfactory receptor, family 5, subfamily B, member 21	1.88	6.52	5.61	0.01	0.03	1.40E-03	1.64E-02	Coding
TC0100013021.hg.1	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	1.88	6.18	5.27	0.7	0.55	2.59E-02	1.01E-01	Multiple_Complex
TC0500009116.hg.1	GM2A	GM2 ganglioside activator	1.88	7.02	6.11	0.86	0.49	4.76E-02	1.52E-01	Multiple_Complex
TC0800009437.hg.1	DEFA1B; DEFA1; DEFA3	defensin, alpha 1B; defensin, alpha 1; defensin, alpha 3, neutrophil-specific	1.88	5.24	4.33	0.19	0.21	1.53E-02	7.09E-02	Coding
TC0800012381.hg.1	DEFA1; DEFA1B	defensin, alpha 1; defensin, alpha 1B	1.88	5.24	4.33	0.19	0.21	1.53E-02	7.09E-02	Coding
TC1900009669.hg.1	KANK2	KN motif and ankyrin repeat domains 2	1.88	8.65	7.74	0.47	0.18	1.12E-02	5.78E-02	Multiple_Complex
TC0400010470.hg.1	SMIM14	small integral membrane protein 14	1.88	9.07	8.16	0.53	0.23	1.20E-02	6.03E-02	Multiple_Complex
TC2000009673.hg.1	SYCP2	synaptonemal complex protein 2	1.88	8	7.09	0.48	0.34	3.12E-02	1.15E-01	Multiple_Complex

TC2100006618.hg.1	USP25	ubiquitin specific peptidase 25	1.88	10.11	9.2	0.3	0.05	2.00E-03	1.99E-02	Multiple_Complex
TC0600012495.hg.1	CGA	glycoprotein hormones, alpha polypeptide	1.88	6.77	5.87	0.01	0.12	1.30E-03	1.56E-02	Multiple_Complex
TC2000007479.hg.1	PI3	peptidase inhibitor 3, skin-derived	1.88	6.52	5.61	0.5	0.28	1.55E-02	7.17E-02	Multiple_Complex
TC0400008876.hg.1	USP38	ubiquitin specific peptidase 38	1.88	8.53	7.62	0.26	0.01	4.10E-03	3.01E-02	Multiple_Complex
TC0100008584.hg.1	ALG6	ALG6, alpha-1,3-glucosyltransferase	1.88	11.22	10.31	0.26	0.32	2.61E-02	1.02E-01	Multiple_Complex
TC1300007799.hg.1	FARP1	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_005766	1.88	4.22	3.32	0.12	0.09	9.40E-03	5.13E-02	NonCoding
TC0700006651.hg.1	ZNF853	zinc finger protein 853	1.87	6.52	5.62	0.24	0.14	4.30E-03	3.09E-02	Multiple_Complex
TC0500009161.hg.1	SAP30L	SAP30-like	1.87	8.68	7.77	0.19	0.03	1.60E-03	1.73E-02	Multiple_Complex
TC0600011133.hg.1	HIST1H2BE	Memczak2013 ANTISENSE, CDS, coding, upstream_start, UTR3, UTR5 best transcript NM_003523	1.87	5.23	4.32	0.31	0.38	5.50E-03	3.60E-02	NonCoding
TC0500010788.hg.1	IL6ST	interleukin 6 signal transducer	1.87	11.49	10.58	0.03	0.24	1.80E-03	1.87E-02	Multiple_Complex
TC1700007829.hg.1	KRTAP9-7	keratin associated protein 9-7	1.87	5.11	4.2	0.45	0.29	1.49E-02	6.97E-02	Coding
TC0200015402.hg.1	FAM126B	family with sequence similarity 126, member B	1.87	10.86	9.96	0.24	0.09	5.70E-03	3.69E-02	Multiple_Complex
TC0700007807.hg.1	ZNF92	zinc finger protein 92	1.87	10.7	9.8	0.47	0.24	2.41E-02	9.68E-02	Multiple_Complex
TC0400009396.hg.1	NEIL3	nei-like DNA glycosylase 3	1.87	10.65	9.74	0.19	0	1.90E-03	1.94E-02	Multiple_Complex
TC0200015631.hg.1	IKZF2	IKAROS family zinc finger 2	1.87	6.04	5.14	0.19	0.19	3.60E-03	2.79E-02	Multiple_Complex
TC0100017058.hg.1	TMEM81	transmembrane protein 81	1.87	6.92	6.01	0.9	0.21	3.00E-02	1.12E-01	Coding
TSUnmapped00000088.hg.1	DUSP16	dual specificity phosphatase 16	1.87	10.02	9.11	0.24	0.32	6.60E-03	4.06E-02	Coding
TC0100014286.hg.1	USP24	Transcript Identified by AceView, Entrez Gene ID(s) 23358	1.87	4.37	3.47	0.54	0.3	1.52E-02	7.08E-02	Unassigned
TC0800009919.hg.1	GNRH1	gonadotropin releasing hormone 1	1.87	7.95	7.05	0.04	0.5	9.00E-03	4.99E-02	Coding

TC1600008278.hg.1	IL34	interleukin 34	1.87	6.42	5.52	0.33	0.29	7.20E-03	4.31E-02	Multiple_Complex
TC0X00009387.hg.1	RPGR	retinitis pigmentosa GTPase regulator	1.87	10.96	10.06	0.09	0.1	1.40E-03	1.60E-02	Multiple_Complex
TSUnmapped00000089.hg.1	ZNF546	zinc finger protein 546	1.87	8.06	7.16	0.04	0.07	2.30E-02	9.38E-02	Coding
TC0100018440.hg.1	STIL	SCL/TAL1 interrupting locus	1.87	10.29	9.38	0.12	0.25	2.20E-03	2.06E-02	Multiple_Complex
TC0100008308.hg.1	ZFYVE9	zinc finger, FYVE domain containing 9	1.87	9.45	8.55	0.01	0.2	1.52E-02	7.08E-02	Multiple_Complex
TC1000012495.hg.1	BORCS7	BLOC-1 related complex subunit 7	1.87	9.67	8.77	0.3	0.41	1.28E-02	6.31E-02	Multiple_Complex
TC0800012382.hg.1	DEFA3	defensin, alpha 3, neutrophil-specific	1.87	5.23	4.33	0.2	0.33	1.85E-02	8.07E-02	Coding
TC1200006718.hg.1	CLEC6A	C-type lectin domain family 6, member A	1.87	4.83	3.93	0.11	0.75	3.37E-02	1.21E-01	Multiple_Complex
TC0X00011312.hg.1	ARMCX5	armadillo repeat containing, X-linked 5	1.87	11.21	10.31	0.19	0.69	1.81E-02	7.96E-02	Multiple_Complex
TC1800009268.hg.1	DSC2	desmocollin 2	1.87	7.98	7.08	0.13	0.62	1.85E-02	8.08E-02	Multiple_Complex
TC1400007201.hg.1	CDKN3	cyclin-dependent kinase inhibitor 3	1.87	14.53	13.63	0.01	0.27	4.60E-03	3.23E-02	Multiple_Complex
TC1900009304.hg.1	PIP5K1C	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_012398	1.87	5.6	4.7	0.35	0.38	1.14E-02	5.84E-02	NonCoding
TC0X00008052.hg.1	CXorf57	chromosome X open reading frame 57	1.87	12.11	11.21	0.08	0.4	2.26E-02	9.25E-02	Multiple_Complex
TC0800012351.hg.1	WDYHV1	WDYHV motif containing 1	1.86	7.49	6.59	0.35	0.54	9.60E-03	5.21E-02	Multiple_Complex
TC0900006714.hg.1	CCDC171	coiled-coil domain containing 171	1.86	7.06	6.16	0.19	0.16	5.80E-03	3.74E-02	Multiple_Complex
TC1200008517.hg.1	METAP2	methionyl aminopeptidase 2	1.86	10.57	9.67	0.29	0.09	2.40E-03	2.16E-02	Multiple_Complex
TC0600012240.hg.1	LMBRD1	LMBR1 domain containing 1	1.86	13.54	12.64	0.12	0.09	2.60E-03	2.28E-02	Multiple_Complex
TC0500008384.hg.1	AP3S1	adaptor-related protein complex 3, sigma 1 subunit	1.86	11.21	10.31	0.22	0.08	2.60E-03	2.28E-02	Multiple_Complex
TC0X00009124.hg.1	PIGA	phosphatidylinositol glycan anchor biosynthesis class A	1.86	8.76	7.86	0.18	0.3	2.80E-03	2.41E-02	Multiple_Complex

TSUnmapped00000217.hg.1	KAT6B	K(lysine) acetyltransferase 6B	1.86	4.53	3.63	0.06	0.02	2.30E-03	2.13E-02	NonCoding
TC0400006810.hg.1	USP17L23	ubiquitin specific peptidase 17-like family member 23 [Source:HGNC Symbol;Acc:HGNC:44451]	1.86	6.67	5.77	0.37	0.18	6.90E-03	4.17E-02	Coding
TC1300010032.hg.1	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	1.86	5.87	4.97	0.09	0.39	4.30E-03	3.10E-02	Coding
TC1500010863.hg.1	SERINC4	serine incorporator 4	1.86	7.82	6.92	0.24	0.89	3.13E-02	1.15E-01	Multiple_Complex
TC0500012659.hg.1	FABP6	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001040442	1.86	5.45	4.55	0.53	0.21	1.11E-02	5.73E-02	NonCoding
TC0100009056.hg.1	CCDC18	coiled-coil domain containing 18	1.86	10.05	9.15	0.19	0.36	4.80E-03	3.29E-02	Multiple_Complex
TC2200007468.hg.1	TEF	thyrotrophic embryonic factor	1.86	6.15	5.26	0.11	0.53	8.70E-03	4.90E-02	Multiple_Complex
TC0X00010406.hg.1	TCEAL8	transcription elongation factor A (SII)-like 8	1.86	11.86	10.97	0.05	0.19	6.10E-03	3.86E-02	Multiple_Complex
TC1800006889.hg.1	RIOK3	RIO kinase 3	1.86	13.16	12.26	0.04	0.31	2.70E-03	2.32E-02	Multiple_Complex
TC1100008790.hg.1	C11orf54	chromosome 11 open reading frame 54	1.86	10.41	9.52	0.04	0.07	2.00E-03	1.97E-02	Multiple_Complex
TC1200011838.hg.1	CMKLR1	chemerin chemokine-like receptor 1	1.86	4.83	3.93	0.03	0.26	2.40E-03	2.16E-02	Multiple_Complex
TC1200010481.hg.1	TWF1	twinfilin actin binding protein 1	1.86	10.21	9.32	0.09	0.21	3.40E-03	2.66E-02	Multiple_Complex
TC0200014672.hg.1	NR4A2	nuclear receptor subfamily 4, group A, member 2	1.86	6.52	5.63	0.52	0.2	1.54E-02	7.14E-02	Multiple_Complex
TC0300009451.hg.1	MYNN	myoneurin	1.86	11.39	10.49	0.09	0.33	1.07E-02	5.60E-02	Multiple_Complex
TC0800010936.hg.1	PMP2	peripheral myelin protein 2	1.86	4.24	3.35	0.21	0.2	2.20E-03	2.10E-02	Coding
TC1500010680.hg.1	OR4F4; OR4F17	olfactory receptor, family 4, subfamily F, member 4; olfactory receptor, family 4, subfamily F, member 17	1.86	5.79	4.9	0.46	0.21	5.70E-03	3.70E-02	Coding
TC1900011884.hg.1	ZNF443	zinc finger protein 443	1.86	8.73	7.84	0.23	0.13	4.30E-03	3.09E-02	Multiple_Complex
TC0900006782.hg.1	FOCAD	focadhesin	1.86	9.71	8.82	0.38	0.25	5.40E-03	3.59E-02	Multiple_Complex

TC0800007137.hg.1	FZD3	frizzled class receptor 3	1.86	8.11	7.21	0.04	0.23	3.60E-03	2.76E-02	Multiple_Complex
TC0100008336.hg.1	SCP2	sterol carrier protein 2	1.86	12.86	11.97	0.47	0.05	6.00E-03	3.83E-02	Multiple_Complex
TC0600011354.hg.1	TRIM10	tripartite motif containing 10	1.86	6.22	5.32	0.23	0.26	5.60E-03	3.65E-02	Coding
TC1300009580.hg.1	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	1.86	7.89	7	0.02	0.25	3.32E-02	1.19E-01	Multiple_Complex
TC0X00009100.hg.1	TRAPPC2	trafficking protein particle complex 2	1.85	11.75	10.86	0.05	0.49	1.45E-02	6.86E-02	Multiple_Complex
TC0500010594.hg.1	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	1.85	5.28	4.39	0.43	0.15	2.06E-02	8.68E-02	Coding
TC0900010126.hg.1	FOXD4L6	forkhead box D4-like 6	1.85	6.76	5.87	0.43	0.05	4.30E-03	3.12E-02	Coding
TC0300008940.hg.1	ARMC8	armadillo repeat containing 8	1.85	11.16	10.27	0.18	0.24	2.50E-03	2.24E-02	Multiple_Complex
TC0600008323.hg.1	HCRTR2	hypocretin (orexin) receptor 2	1.85	4.89	4	0.08	0.13	2.80E-03	2.36E-02	Coding
TC1000012329.hg.1	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	1.85	11.61	10.72	0.13	0.02	2.60E-03	2.30E-02	Multiple_Complex
TC1000007619.hg.1	ASAH2B	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B	1.85	11.8	10.91	0.05	0.15	5.30E-03	3.53E-02	Multiple_Complex
TC0100016891.hg.1	KIF14	kinesin family member 14	1.85	8.9	8.01	0.37	0.49	1.45E-02	6.86E-02	Multiple_Complex
TC1900009394.hg.1	C19orf70	chromosome 19 open reading frame 70	1.85	14.02	13.13	0.3	0.29	1.12E-02	5.78E-02	Multiple_Complex
TC2100008171.hg.1	LCA5L	Leber congenital amaurosis 5-like	1.85	8.2	7.31	0.61	0.16	1.35E-02	6.52E-02	Multiple_Complex
TC0300007450.hg.1	IQCF2	IQ motif containing F2	1.85	5.09	4.2	0.36	0.16	2.02E-02	8.56E-02	Multiple_Complex
TC1500009377.hg.1	ATP8B4	ATPase, class I, type 8B, member 4	1.85	4.68	3.79	0	0.02	1.92E-02	8.28E-02	Multiple_Complex
TC0200014857.hg.1	FASTKD1	FAST kinase domains 1	1.85	11.14	10.26	0.44	0.21	1.90E-02	8.20E-02	Multiple_Complex
TC0600013734.hg.1	OSTCP1	oligosaccharyltransferase complex subunit pseudogene 1	1.85	7	6.12	0.27	0.11	5.10E-03	3.44E-02	Multiple_Complex
TC0100014769.hg.1	MCOLN3	mucolipin 3	1.85	11.91	11.02	0.21	0.03	2.30E-03	2.12E-02	Multiple_Complex

TC0600014360.hg.1	IPCEF1	interaction protein for cytohesin exchange factors 1	1.85	7.28	6.39	0.67	0.09	2.87E-02	1.09E-01	Multiple_Complex
TC0500007668.hg.1	CDK7	cyclin-dependent kinase 7	1.85	13.25	12.36	0.22	0.13	2.20E-03	2.08E-02	Multiple_Complex
TC0100008599.hg.1	UBE2U	ubiquitin-conjugating enzyme E2U (putative)	1.85	5.15	4.27	0.47	0.47	1.39E-02	6.67E-02	Multiple_Complex
TC1000012477.hg.1	HELLS	helicase, lymphoid-specific	1.85	11.34	10.45	0.14	0.29	3.20E-03	2.61E-02	Multiple_Complex
TC1100013148.hg.1	PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	1.85	13.3	12.41	0.23	0.29	3.10E-03	2.54E-02	Multiple_Complex
TC1300008696.hg.1	MRPS31	mitochondrial ribosomal protein S31	1.85	12.24	11.35	0.12	0.18	2.70E-03	2.32E-02	Multiple_Complex
TSUnmapped00000125.hg.1	KIAA1143	KIAA1143 [Source:HGNC Symbol;Acc:HGNC:29198]	1.85	12.12	11.23	0.18	0.35	4.70E-03	3.29E-02	NonCoding
TC0400008943.hg.1	EDNRA	endothelin receptor type A	1.85	10.72	9.83	0.15	0.36	4.80E-03	3.31E-02	Multiple_Complex
TC1900007371.hg.1	KIAA1683	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001145304	1.85	7.23	6.35	0.32	0.68	1.73E-02	7.73E-02	NonCoding
TC1000011469.hg.1	NOC3L	NOC3-like DNA replication regulator	1.85	10.51	9.63	0.06	0.57	2.02E-02	8.57E-02	Multiple_Complex
TC0400011253.hg.1	KLHL8	kelch-like family member 8	1.85	8.74	7.86	0.01	0.51	9.00E-03	4.98E-02	Multiple_Complex
TC0400008170.hg.1	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	1.85	9.6	8.72	0.07	0.26	2.40E-03	2.17E-02	Multiple_Complex
TC0X00008914.hg.1	ZBED1; DHRSX	zinc finger, BED-type containing 1; dehydrogenase/reductase (SDR family) X-linked	1.85	7.92	7.04	0.15	0.16	1.80E-03	1.85E-02	Multiple_Complex
TC2100007082.hg.1	DYRK1A	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	1.85	11.17	10.29	0.39	0.06	5.60E-03	3.66E-02	Multiple_Complex
TC1800007849.hg.1	THOC1	THO complex 1	1.85	7.36	6.47	0.52	0.44	2.72E-02	1.05E-01	Multiple_Complex
TC1000011005.hg.1	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	1.84	9.71	8.83	0.02	0.16	2.10E-03	2.04E-02	Multiple_Complex
TC1700012261.hg.1	PSME3	proteasome activator subunit 3	1.84	6.06	5.17	0.58	0.76	4.15E-02	1.39E-01	NonCoding

TC1200012161.hg.1	TRIAP1	TP53 regulated inhibitor of apoptosis 1	1.84	8.64	7.76	0.14	0.67	2.36E-02	9.52E-02	Multiple_Complex
TC0300010123.hg.1	CRBN	cereblon	1.84	11.9	11.02	0.1	0	3.30E-03	2.64E-02	Multiple_Complex
TC0900010470.hg.1	PRUNE2	prune homolog 2 (Drosophila)	1.84	6.92	6.04	0.39	0.35	2.72E-02	1.05E-01	Multiple_Complex
TC0900008847.hg.1	LCN2	lipocalin 2	1.84	5.41	4.53	0.31	0.42	1.44E-02	6.86E-02	Multiple_Complex
TC0300013960.hg.1	HIGD1A	HIG1 hypoxia inducible domain family, member 1A	1.84	14.61	13.72	0.03	0.09	2.40E-03	2.20E-02	Multiple_Complex
TC0200013607.hg.1	TXNDC9	thioredoxin domain containing 9	1.84	7.55	6.67	0.28	0.32	1.70E-02	7.65E-02	Multiple_Complex
TC0200014584.hg.1	MMADHC	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	1.84	14.27	13.39	0.18	0.24	4.30E-03	3.10E-02	Multiple_Complex
TC1500009845.hg.1	AAGAB	alpha- and gamma-adaptin binding protein	1.84	11.59	10.71	0.28	0.07	5.60E-03	3.64E-02	Multiple_Complex
TC2200009324.hg.1	DRICH1	aspartate-rich 1	1.84	5.17	4.29	0.03	0.17	2.40E-03	2.19E-02	Multiple_Complex
TC1200008344.hg.1	LRRIQ1	leucine-rich repeats and IQ motif containing 1	1.84	10.23	9.35	0.19	0.5	1.93E-02	8.32E-02	Multiple_Complex
TC0100008559.hg.1	ANGPTL3	angiopoietin like 3	1.84	6.47	5.59	0.15	0.44	7.00E-03	4.23E-02	Multiple_Complex
TSUnmapped00000455.hg.1	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	1.84	5.19	4.31	0.54	0.03	7.10E-03	4.26E-02	Coding
TC0600009333.hg.1	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	1.84	7.29	6.41	0.12	0.01	3.00E-03	2.47E-02	Multiple_Complex
TC1200012799.hg.1	SARNP	SAP domain containing ribonucleoprotein	1.84	13.75	12.87	0.07	0.08	5.60E-03	3.66E-02	Multiple_Complex
TC1000007701.hg.1	TFAM	transcription factor A, mitochondrial	1.84	14.81	13.93	0.07	0.13	2.30E-03	2.12E-02	Multiple_Complex
TC0100007920.hg.1	PPIE	peptidylprolyl isomerase E (cyclophilin E)	1.84	12.5	11.62	0.06	0.33	1.07E-02	5.59E-02	Multiple_Complex
TC1700010328.hg.1	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	1.84	13.76	12.88	0.04	0.19	2.00E-03	1.96E-02	Multiple_Complex
TSUnmapped00000372.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	1.84	8.23	7.35	0.05	0.41	5.60E-03	3.66E-02	Coding
TC1300008497.hg.1	UBL3	ubiquitin-like 3	1.84	8.85	7.97	0.47	0.06	7.50E-03	4.40E-02	Multiple_Complex

TC0200016466.hg.1	APLF	aprataxin and PNKP like factor	1.84	6.08	5.2	0.26	0.68	1.86E-02	8.10E-02	NonCoding
TC0600012656.hg.1	USP45	ubiquitin specific peptidase 45	1.84	12.57	11.69	0.08	0.13	7.10E-03	4.25E-02	Multiple_Complex
TC0600012123.hg.1	DST	dystonin	1.84	11.35	10.47	0.24	0.27	4.40E-03	3.16E-02	Multiple_Complex
TC0200012522.hg.1	FBXO11	F-box protein 11	1.84	8.93	8.05	0.02	0.29	5.00E-03	3.39E-02	Multiple_Complex
TC0200016578.hg.1	NUP35	nucleoporin 35kDa	1.84	9.99	9.11	0.1	0.25	3.00E-03	2.50E-02	Multiple_Complex
TC1200011994.hg.1	SDS	serine dehydratase	1.84	5.58	4.7	0.47	0.03	7.10E-03	4.27E-02	Multiple_Complex
TC0X00010661.hg.1	RHOXF2B; RHOXF2	Rhox homeobox family, member 2B; Rhox homeobox family, member 2	1.84	4.7	3.83	0.78	0.14	2.50E-02	9.89E-02	Multiple_Complex
TC0100016893.hg.1	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	1.84	9.77	8.9	0.04	0.41	7.50E-03	4.42E-02	Multiple_Complex
TC0900012214.hg.1	IFNA10	interferon, alpha 10	1.84	5.36	4.48	0.15	0.1	3.20E-03	2.61E-02	Coding
TC0300010033.hg.1	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	1.84	8.79	7.92	0.07	0.21	8.20E-03	4.69E-02	Multiple_Complex
TC0700012478.hg.1	C7orf77	chromosome 7 open reading frame 77	1.84	5.31	4.44	0.69	0.09	2.64E-02	1.03E-01	Multiple_Complex
TC0500012039.hg.1	ZCCHC10	zinc finger, CCHC domain containing 10	1.84	9.43	8.55	0.08	0.39	1.48E-02	6.96E-02	Multiple_Complex
TC1200008255.hg.1	ZDHHC17	zinc finger, DHHC-type containing 17	1.84	6.93	6.06	0.14	0.31	2.24E-02	9.18E-02	Multiple_Complex
TC2100008379.hg.1	KRTAP12-4	keratin associated protein 12-4	1.84	4.95	4.08	0.12	0.08	7.00E-03	4.21E-02	Multiple_Complex
TC0200007664.hg.1	VRK2	vaccinia related kinase 2	1.84	9.84	8.96	0.14	0.25	9.20E-03	5.07E-02	Multiple_Complex
TC0500011614.hg.1	NUDT12	nudix hydrolase 12	1.84	10.14	9.26	0.13	0.38	1.37E-02	6.61E-02	Multiple_Complex
TC0100010623.hg.1	SUCO	SUN domain containing ossification factor	1.84	9.6	8.73	0.04	0.48	6.40E-03	3.97E-02	Multiple_Complex
TC0500008356.hg.1	KCNN2	potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 2	1.84	5.63	4.76	0.55	0.3	1.00E-02	5.32E-02	Multiple_Complex
TC1900011904.hg.1	USHBP1	Usher syndrome 1C binding protein 1	1.83	7.82	6.94	0.56	0.36	1.74E-02	7.76E-02	Multiple_Complex

TC0700007692.hg.1	ZNF716	zinc finger protein 716	1.83	5.27	4.39	0.69	0.26	3.54E-02	1.24E-01	Coding
TC0200007176.hg.1	SLC30A6	solute carrier family 30 (zinc transporter), member 6	1.83	14.49	13.62	0.18	0.28	5.80E-03	3.75E-02	Multiple_Complex
TC0400011291.hg.1	HERC6	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001165136	1.83	7.74	6.86	0.01	0.08	2.30E-03	2.15E-02	NonCoding
TC1500010921.hg.1	MRPL46	mitochondrial ribosomal protein L46	1.83	12.44	11.57	0.12	0.09	2.60E-03	2.28E-02	Multiple_Complex
TC0300010679.hg.1	CLASP2	Transcript Identified by AceView, Entrez Gene ID(s) 23122	1.83	7.18	6.3	0.33	0.14	4.40E-03	3.16E-02	Unassigned
TC1300009273.hg.1	COMMD6	COMM domain containing 6	1.83	16.15	15.28	0.14	0.2	6.90E-03	4.18E-02	Multiple_Complex
TC0800009921.hg.1	KCTD9	potassium channel tetramerization domain containing 9	1.83	7.92	7.05	0.03	0.51	8.90E-03	4.94E-02	Multiple_Complex
TC1200007625.hg.1	TMPRSS12	transmembrane (C-terminal) protease, serine 12	1.83	6.3	5.42	1.01	0.14	4.28E-02	1.41E-01	Coding
TC2200008654.hg.1	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	1.83	7.3	6.43	0.68	0.13	1.40E-02	6.73E-02	Multiple_Complex
TC0900011246.hg.1	ZNF883	zinc finger protein 883	1.83	4.96	4.09	0.41	0.1	4.75E-02	1.51E-01	Multiple_Complex
TC0600014153.hg.1	CFAP206	cilia and flagella associated protein 206	1.83	6.3	5.43	0.5	0.02	7.50E-03	4.40E-02	Multiple_Complex
TC1700012309.hg.1	METTL23	methyltransferase like 23	1.83	14.31	13.44	0.11	0.19	2.60E-03	2.28E-02	Multiple_Complex
TC0500008541.hg.1	TEX43	testis expressed 43	1.83	6.7	5.83	0.11	0.22	1.50E-02	7.01E-02	Multiple_Complex
TC0X00008731.hg.1	VMA21	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)	1.83	12.24	11.37	0.09	0.08	2.80E-03	2.38E-02	Multiple_Complex
TC1300008439.hg.1	MTIF3	mitochondrial translational initiation factor 3	1.83	9.91	9.04	0.23	0.16	4.40E-03	3.13E-02	Multiple_Complex
TC0200009106.hg.1	GLI2	GLI family zinc finger 2	1.83	6.16	5.3	0.68	0.2	1.77E-02	7.85E-02	Multiple_Complex
TC0100011148.hg.1	CAMSAP2	calmodulin regulated spectrin-associated protein family, member 2	1.83	10.1	9.23	0.16	0.2	2.60E-03	2.27E-02	Multiple_Complex

TC0500011276.hg.1	FAM151B	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_205548	1.83	5.16	4.29	0.34	0.24	1.81E-02	7.96E-02	NonCoding
TC0700008564.hg.1	ZAN	zonadhesin (gene/pseudogene)	1.83	5.37	4.5	0.18	0.42	2.59E-02	1.02E-01	Multiple_Complex
TC1700009284.hg.1	TBCD	Transcript Identified by AceView, Entrez Gene ID(s) 6904	1.83	9.5	8.63	0.06	0.27	2.07E-02	8.71E-02	Unassigned
TC1300007592.hg.1	NDFIP2	Nedd4 family interacting protein 2	1.83	10.25	9.39	0.12	0.36	6.40E-03	3.99E-02	Multiple_Complex
TC1700009037.hg.1	C17orf99	chromosome 17 open reading frame 99	1.82	5.51	4.64	0.27	0.02	3.00E-03	2.50E-02	Multiple_Complex
TC0200007886.hg.1	PNO1	partner of NOB1 homolog	1.82	8.25	7.38	0.17	0.18	2.70E-03	2.35E-02	Multiple_Complex
TC1400008669.hg.1	OR6J1	olfactory receptor, family 6, subfamily J, member 1 (gene/pseudogene)	1.82	5.34	4.47	0.28	0.31	5.00E-03	3.39E-02	Coding
TC1900010508.hg.1	CLIP3	CAP-GLY domain containing linker protein 3	1.82	6.95	6.08	0.57	0.69	3.37E-02	1.21E-01	Multiple_Complex
TC0300013984.hg.1	HYAL2	hyaluronoglucosaminidase 2	1.82	6.15	5.28	0.08	0.16	8.40E-03	4.79E-02	Multiple_Complex
TC0X00009117.hg.1	FANCB	Fanconi anemia complementation group B	1.82	9.89	9.03	0.09	0.38	1.39E-02	6.68E-02	Multiple_Complex
TC1100009159.hg.1	APOC3	apolipoprotein C-III	1.82	8.24	7.37	0.35	0.16	5.90E-03	3.78E-02	Multiple_Complex
TC0900012155.hg.1	MSANTD3-TMEFF1	MSANTD3-TMEFF1 readthrough	1.82	10.49	9.62	0.17	0.12	2.03E-02	8.60E-02	Coding
TC0200008563.hg.1	VWA3B	von Willebrand factor A domain containing 3B	1.82	4.55	3.68	0.36	0.21	5.80E-03	3.74E-02	Multiple_Complex
TC0400009221.hg.1	MSMO1	methylsterol monooxygenase 1	1.82	12.3	11.43	0.22	0.15	3.50E-03	2.72E-02	Multiple_Complex
TC1400009066.hg.1	MIS18BP1	MIS18 binding protein 1	1.82	8.85	7.98	0.18	0.02	7.20E-03	4.31E-02	Multiple_Complex
TC0400011348.hg.1	HPGDS	hematopoietic prostaglandin D synthase	1.82	4.34	3.48	0.05	0.08	1.28E-02	6.32E-02	Multiple_Complex
TC1200011720.hg.1	NUP37	nucleoporin 37kDa	1.82	9.88	9.01	0	0.07	3.90E-03	2.94E-02	Multiple_Complex
TC1700008438.hg.1	RAD51C	RAD51 paralog C	1.82	14.08	13.22	0.02	0.08	3.60E-03	2.80E-02	Multiple_Complex
TC1400009223.hg.1	CNIH1	cornichon family AMPA receptor auxiliary protein 1	1.82	11.04	10.17	0.03	0.16	1.80E-03	1.86E-02	Multiple_Complex
TC0200016604.hg.1	RBM44	RNA binding motif protein 44	1.82	5.16	4.3	0.78	0.21	3.59E-02	1.26E-01	Multiple_Complex

TC0700012847.hg.1	PRSS37	protease, serine, 37	1.82	4.71	3.84	0.07	0.81	2.42E-02	9.69E-02	Coding
TC0700012451.hg.1	TAS2R16	taste receptor, type 2, member 16	1.82	4.92	4.05	0.23	0.37	5.10E-03	3.45E-02	Coding
TC2100006974.hg.1	SON; MIR6501	SON DNA binding protein; microRNA 6501	1.82	10.78	9.91	0.3	0.07	3.00E-03	2.49E-02	Multiple_Complex
TC1300006715.hg.1	PAN3; RNU6-82P	PAN3 poly(A) specific ribonuclease subunit; RNA, U6 small nuclear 82, pseudogene	1.82	10.09	9.22	0.03	0.1	2.00E-03	1.95E-02	Multiple_Complex
TC1700010417.hg.1	SLC35G3	solute carrier family 35, member G3	1.82	5.69	4.83	0.26	0.56	1.06E-02	5.55E-02	Coding
TC2100007996.hg.1	TMEM50B	transmembrane protein 50B	1.82	12.61	11.75	0.31	0.12	1.63E-02	7.42E-02	Multiple_Complex
TC0800010802.hg.1	C8orf89	chromosome 8 open reading frame 89	1.82	5.65	4.79	0.53	0.09	9.50E-03	5.17E-02	Multiple_Complex
TC0400012916.hg.1	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	1.82	5.23	4.37	0.47	0.09	7.40E-03	4.36E-02	NonCoding
TC0800012166.hg.1	SCRIB	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_182706	1.82	6.83	5.97	0.4	0.15	3.43E-02	1.22E-01	NonCoding
TC0200007477.hg.1	SOCS5	suppressor of cytokine signaling 5	1.82	7.35	6.49	0.62	0.53	2.46E-02	9.79E-02	Coding
TC1400007112.hg.1	ATP5S	ATP synthase, H+ transporting, mitochondrial Fo complex subunit s (factor B)	1.82	11.6	10.74	0.22	0.15	5.50E-03	3.60E-02	Multiple_Complex
TC0500008156.hg.1	ERAP2	endoplasmic reticulum aminopeptidase 2	1.82	5.2	4.34	0.6	0.09	2.23E-02	9.16E-02	Multiple_Complex
TC0700008295.hg.1	CFAP69	cilia and flagella associated protein 69	1.82	7.51	6.64	0.25	0.19	3.50E-03	2.73E-02	Multiple_Complex
TC0X00011317.hg.1	TCEAL1	transcription elongation factor A (SII)-like 1	1.82	13.75	12.89	0.28	0.26	5.20E-03	3.47E-02	Multiple_Complex
TC0600014293.hg.1	CRIP3	cysteine-rich protein 3	1.82	6.72	5.86	0.31	0.1	3.90E-03	2.93E-02	Multiple_Complex
TC0600013462.hg.1	FBXO30	F-box protein 30	1.82	8.51	7.65	0.05	0.02	1.60E-03	1.74E-02	Coding
TC1100011611.hg.1	PGM2L1	phosphoglucomutase 2-like 1	1.82	9.37	8.5	0.1	0.03	2.40E-03	2.16E-02	Multiple_Complex
TC0200016455.hg.1	C2orf74	chromosome 2 open reading frame 74	1.82	10.85	9.99	0.17	0.02	4.30E-03	3.10E-02	Multiple_Complex

TC1000009725.hg.1	SFMBT2	Scm-like with four mbt domains 2	1.82	9.24	8.38	0.37	0.08	1.21E-02	6.06E-02	Multiple_Complex
TC1800007523.hg.1	PHLPP1	PH domain and leucine rich repeat protein phosphatase 1	1.82	12.27	11.41	0.38	0.11	8.40E-03	4.78E-02	Multiple_Complex
TC1000010113.hg.1	ANKRD26	ankyrin repeat domain 26	1.82	11.34	10.48	0.01	0.09	4.70E-03	3.26E-02	Multiple_Complex
TC1600007962.hg.1	MT1A	metallothionein 1A	1.82	8.99	8.13	0.26	0.17	5.40E-03	3.56E-02	Coding
TC0100018233.hg.1	FPGT	fucose-1-phosphate guanylyltransferase	1.82	10.3	9.44	0.01	0.15	1.12E-02	5.77E-02	Coding
TC0900010814.hg.1	ZNF484	zinc finger protein 484	1.81	11.38	10.52	0.24	0.35	5.10E-03	3.41E-02	Multiple_Complex
TC0600012132.hg.1	RAB23	RAB23, member RAS oncogene family	1.81	10.97	10.11	0.21	0.13	4.70E-03	3.28E-02	Multiple_Complex
TC1700008598.hg.1	MILR1	mast cell immunoglobulin-like receptor 1	1.81	6.68	5.82	0.13	0.34	1.48E-02	6.96E-02	Multiple_Complex
TC1900007458.hg.1	ZNF93	zinc finger protein 93	1.81	8.54	7.69	0.61	0.05	1.04E-02	5.49E-02	Multiple_Complex
TC0300012815.hg.1	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	1.81	4.79	3.93	0.44	0.02	6.10E-03	3.87E-02	Coding
TC0200014860.hg.1	CCDC173	coiled-coil domain containing 173	1.81	7.17	6.31	0.24	0.47	8.10E-03	4.66E-02	Coding
TC0700012044.hg.1	FIS1	fission, mitochondrial 1	1.81	14.1	13.24	0.04	0.21	7.90E-03	4.59E-02	Multiple_Complex
TC0300008532.hg.1	FBXO40	F-box protein 40	1.81	4.38	3.53	0.07	0.08	3.10E-03	2.50E-02	Coding
TC1200012735.hg.1	ZNF26	zinc finger protein 26	1.81	6.95	6.09	0.05	0	2.70E-03	2.34E-02	NonCoding
TC0100012320.hg.1	OR2G3	olfactory receptor, family 2, subfamily G, member 3	1.81	8.26	7.4	0.07	0.47	1.84E-02	8.04E-02	Coding
TC1900010164.hg.1	ZNF208	zinc finger protein 208	1.81	10.2	9.34	0.03	0.11	2.10E-03	2.00E-02	Multiple_Complex
TC1200011310.hg.1	PHLDA1	pleckstrin homology-like domain, family A, member 1	1.81	7.33	6.47	0.27	0.76	2.97E-02	1.11E-01	Multiple_Complex
TC0500008467.hg.1	SRFBP1	serum response factor binding protein 1	1.81	11.26	10.4	0.11	0.46	3.09E-02	1.14E-01	Multiple_Complex
TC0300008506.hg.1	LRRC58	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, intronic, UTR3 best transcript NM_001099678	1.81	7.47	6.61	0.05	0.35	6.80E-03	4.13E-02	NonCoding
TC0500007314.hg.1	MRPS30	mitochondrial ribosomal protein S30	1.81	13.4	12.54	0.14	0.26	5.00E-03	3.39E-02	Multiple_Complex

TC1200006951.hg.1	PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	1.81	4.77	3.92	0.56	0.13	1.73E-02	7.74E-02	Coding
TC1400007490.hg.1	FAM71D	family with sequence similarity 71, member D	1.81	6.11	5.25	0.3	0.3	2.02E-02	8.57E-02	Multiple_Complex
TC1100012516.hg.1	CCDC153	coiled-coil domain containing 153	1.81	10.2	9.34	0.09	0.22	3.10E-03	2.54E-02	Multiple_Complex
TC0800012301.hg.1	FAM110B	family with sequence similarity 110, member B	1.81	5.72	4.87	0.44	0.21	2.10E-02	8.79E-02	Multiple_Complex
TC1100008927.hg.1	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	1.81	13.67	12.81	0.06	0.09	5.70E-03	3.70E-02	Multiple_Complex
TC0500013172.hg.1	C5orf64	chromosome 5 open reading frame 64	1.81	6.32	5.47	0.36	0.04	3.70E-03	2.83E-02	Multiple_Complex
TC0100014762.hg.1	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	1.81	8.55	7.69	0.47	0.13	6.80E-03	4.15E-02	Multiple_Complex
TC1300009670.hg.1	METTL21C	methyltransferase like 21C	1.81	5.66	4.81	0.74	0.28	2.40E-02	9.64E-02	Coding
TC0600012883.hg.1	TUBE1	tubulin, epsilon 1	1.81	13.83	12.97	0	0.11	3.10E-03	2.51E-02	Multiple_Complex
TC1600007955.hg.1	MT3	metallothionein 3	1.81	7.01	6.15	0.19	0.14	3.20E-03	2.61E-02	Multiple_Complex
TC0100008885.hg.1	SPATA1	spermatogenesis associated 1	1.81	5.93	5.07	0.26	0.32	1.18E-02	5.98E-02	Multiple_Complex
TC0100012345.hg.1	OR2L3	olfactory receptor, family 2, subfamily L, member 3	1.81	4.71	3.86	0.48	0.17	7.20E-03	4.29E-02	Coding
TC1000012599.hg.1	CUZD1	CUB and zona pellucida-like domains 1	1.81	6.27	5.41	0.57	0.45	3.41E-02	1.22E-01	Multiple_Complex
TC1200010109.hg.1	LDHB	lactate dehydrogenase B	1.81	15.89	15.04	0.19	0.26	3.50E-03	2.74E-02	Multiple_Complex
TC0X00008401.hg.1	RAB33A	RAB33A, member RAS oncogene family	1.81	6.77	5.92	0.58	0.14	1.64E-02	7.46E-02	Coding
TC0600012702.hg.1	HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1	1.81	8.7	7.85	0.53	0.34	1.95E-02	8.36E-02	Multiple_Complex
TC0200016440.hg.1	TMEM247	transmembrane protein 247	1.81	4.45	3.6	0.35	0.22	7.30E-03	4.32E-02	NonCoding
TC1800007092.hg.1	MOCOS	molybdenum cofactor sulfurase	1.81	8.38	7.53	0.01	0.34	3.90E-03	2.91E-02	Multiple_Complex
TC0X00008014.hg.1	TMEM31	transmembrane protein 31	1.81	7.39	6.53	0.33	0.29	6.20E-03	3.91E-02	Coding
TC0100009974.hg.1	OAZ3	ornithine decarboxylase antizyme 3	1.81	6.08	5.22	0.39	0.37	1.56E-02	7.21E-02	Multiple_Complex

TC0100015711.hg.1	HIST2H2AB	histone cluster 2, H2ab	1.81	12.7	11.85	0	0.07	2.20E-03	2.06E-02	Coding
TC0400010205.hg.1	KCNIP4	Kv channel interacting protein 4	1.81	6.19	5.34	0.11	0.06	4.91E-02	1.55E-01	Multiple_Complex
TC1300009321.hg.1	RNF219	ring finger protein 219	1.81	10.93	10.08	0.37	0.38	9.20E-03	5.04E-02	Multiple_Complex
TC0300013601.hg.1	ATP13A3	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_024524	1.81	5.36	4.5	0.63	0.05	1.35E-02	6.54E-02	NonCoding
TC1700006580.hg.1	OR3A4P; OR3A5P	olfactory receptor, family 3, subfamily A, member 4 pseudogene; olfactory receptor, family 3, subfamily A, member 5 pseudogene	1.81	6.13	5.28	0.59	0.3	1.84E-02	8.06E-02	Multiple_Complex
TC1300007045.hg.1	GPALPP1	GPALPP motifs containing 1	1.81	9.52	8.67	0.08	0.01	2.90E-03	2.43E-02	Multiple_Complex
TC1900009625.hg.1	ICAM3	intercellular adhesion molecule 3	1.8	5.63	4.78	0.45	0.45	1.74E-02	7.76E-02	Multiple_Complex
TC0600007285.hg.1	HIST1H2AE	histone cluster 1, H2ae	1.8	7.75	6.89	0.33	0	3.40E-03	2.66E-02	Coding
TC0300012812.hg.1	GPR171	G protein-coupled receptor 171	1.8	4.93	4.08	0	0.17	1.78E-02	7.87E-02	Coding
TC2200009014.hg.1	PKDREJ	polycystin (PKD) family receptor for egg jelly	1.8	5.41	4.56	0.34	0.03	4.10E-03	3.00E-02	Coding
TC1800008235.hg.1	ABHD3	Transcript Identified by AceView, Entrez Gene ID(s) 171586	1.8	7.75	6.9	0.35	0.03	1.32E-02	6.45E-02	Unassigned
TC0700006727.hg.1	TMEM106B	transmembrane protein 106B	1.8	8.17	7.32	0.07	0.28	3.30E-03	2.64E-02	Multiple_Complex
TC0X00011289.hg.1	GAGE2B; GAGE2A; GAGE2C	G antigen 2B; G antigen 2A; G antigen 2C	1.8	6.76	5.91	0.12	0.25	1.09E-02	5.66E-02	Coding
TC0900009958.hg.1	FAM221B	family with sequence similarity 221, member B	1.8	5.79	4.94	0.67	0.16	2.98E-02	1.11E-01	Multiple_Complex
TC1100011742.hg.1	KCTD21	potassium channel tetramerization domain containing 21	1.8	7.85	7	0.37	0.14	1.69E-02	7.61E-02	Coding
TC1200010250.hg.1	ERGIC2	ERGIC and golgi 2	1.8	11.75	10.9	0.06	0.36	1.03E-02	5.45E-02	Multiple_Complex

TC0800009095.hg.1	DENND3	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_014957	1.8	5.11	4.26	0.26	0.2	9.50E-03	5.16E-02	NonCoding
TC0800011158.hg.1	C8orf37	chromosome 8 open reading frame 37	1.8	5.81	4.96	0.16	0.02	2.60E-03	2.28E-02	Coding
TC0400012386.hg.1	C4orf27	chromosome 4 open reading frame 27	1.8	10.64	9.79	0.2	0.2	3.30E-03	2.61E-02	Multiple_Complex
TC1600009068.hg.1	MEIOB; LINC00254	meiosis specific with OB domains; long intergenic non-protein coding RNA 254	1.8	5.82	4.97	0.8	0.33	3.50E-02	1.23E-01	Multiple_Complex
TC2000007430.hg.1	SRSF6	serine/arginine-rich splicing factor 6	1.8	11.03	10.18	0.25	0.11	3.60E-03	2.79E-02	Multiple_Complex
TC1900010670.hg.1	CLC	Charcot-Leyden crystal galectin	1.8	5.35	4.5	0.38	0.5	2.55E-02	1.01E-01	Coding
TC0200012489.hg.1	PIGF	phosphatidylinositol glycan anchor biosynthesis class F	1.8	12.3	11.46	0.01	0.11	2.70E-03	2.32E-02	Multiple_Complex
TC1000010912.hg.1	SAR1A	secretion associated, Ras related GTPase 1A	1.8	13.62	12.78	0.02	0.08	1.90E-03	1.92E-02	Multiple_Complex
TC0700012299.hg.1	GPR85	G protein-coupled receptor 85	1.8	6.69	5.84	0.7	0.47	3.10E-02	1.14E-01	Multiple_Complex
TC1900011150.hg.1	NOSIP	nitric oxide synthase interacting protein	1.8	12.53	11.68	0.07	0.18	7.40E-03	4.37E-02	Multiple_Complex
TC1100007805.hg.1	TMEM216	transmembrane protein 216	1.8	8.68	7.83	0.26	0.18	1.97E-02	8.42E-02	Multiple_Complex
TC1100012831.hg.1	ZBTB44	zinc finger and BTB domain containing 44	1.8	10.07	9.23	0.21	0.49	1.29E-02	6.36E-02	Multiple_Complex
TC0700012709.hg.1	FAM180A	family with sequence similarity 180, member A	1.8	5.1	4.25	0.7	0.18	1.78E-02	7.87E-02	Multiple_Complex
TC0100009176.hg.1	SNX7	sorting nexin 7	1.8	9.28	8.43	0.31	0.01	1.63E-02	7.43E-02	Multiple_Complex
TC0900012256.hg.1	CDC14B	cell division cycle 14B	1.8	12.1	11.26	0.15	0.15	2.60E-03	2.30E-02	Multiple_Complex
TC1000008926.hg.1	ACSL5	acyl-CoA synthetase long-chain family member 5	1.8	5.72	4.88	0.58	0.47	2.11E-02	8.81E-02	Multiple_Complex
TC1200012761.hg.1	TAS2R31	taste receptor, type 2, member 31	1.8	7.2	6.36	0.06	0.01	7.50E-03	4.42E-02	Coding
TC1900011926.hg.1	ZNF91	zinc finger protein 91	1.79	9.82	8.98	0.19	0.17	4.10E-03	3.02E-02	Multiple_Complex
TC1600010859.hg.1	MLKL	mixed lineage kinase domain-like	1.79	7.04	6.19	0.75	0.4	3.83E-02	1.31E-01	Multiple_Complex

TC1200012617.hg.1	FGD4	FYVE, RhoGEF and PH domain containing 4	1.79	9.62	8.78	0.25	0.35	1.01E-02	5.38E-02	Multiple_Complex
TC0800011597.hg.1	EXT1; spawla	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_000127; Transcript Identified by AceView	1.79	7.41	6.57	0.08	0.22	4.10E-03	3.02E-02	NonCoding
TC0200010586.hg.1	CPO	carboxypeptidase O	1.79	5.12	4.28	0.68	0.01	1.52E-02	7.08E-02	Coding
TC1600007255.hg.1	RBBP6	retinoblastoma binding protein 6	1.79	14.08	13.24	0.2	0.16	4.40E-03	3.14E-02	Multiple_Complex
TC1500010672.hg.1	TARSL2	threonyl-tRNA synthetase-like 2	1.79	8.58	7.74	0.04	0.76	2.27E-02	9.26E-02	Multiple_Complex
TC0200016445.hg.1	MSH6	mutS homolog 6	1.79	10.25	9.41	0.23	0.39	6.90E-03	4.19E-02	Multiple_Complex
TC0700012915.hg.1	NOBOX	NOBOX oogenesis homeobox	1.79	4.89	4.05	0.98	0.13	4.30E-02	1.42E-01	Coding
TC1300008735.hg.1	VWA8; MIR5006	von Willebrand factor A domain containing 8; microRNA 5006	1.79	12.25	11.41	0	0.23	4.40E-03	3.13E-02	Multiple_Complex
TC1400007310.hg.1	KIAA0586	KIAA0586	1.79	13.22	12.38	0.11	0.3	5.00E-03	3.41E-02	Multiple_Complex
TC0700012453.hg.1	SLC13A1	solute carrier family 13 (sodium/sulfate symporter), member 1	1.79	5.39	4.55	0.7	0.2	2.27E-02	9.27E-02	Coding
TC0900012189.hg.1	TMEM141	transmembrane protein 141	1.79	12.21	11.36	0.01	0.39	1.15E-02	5.88E-02	Multiple_Complex
TC1100011083.hg.1	AHNAK	AHNAK nucleoprotein	1.79	5.38	4.53	0.53	0.17	1.15E-02	5.88E-02	Multiple_Complex
TC0600014093.hg.1	ZNRD1	zinc ribbon domain containing 1	1.79	13.93	13.09	0.07	0.22	4.20E-03	3.04E-02	Multiple_Complex
TC1900007820.hg.1	ZNF181	zinc finger protein 181	1.79	10.59	9.74	0.11	0.08	3.60E-03	2.79E-02	Multiple_Complex
TC0600008735.hg.1	ORC3	origin recognition complex subunit 3	1.79	13.14	12.3	0.07	0.48	7.30E-03	4.34E-02	Multiple_Complex
TC0600012863.hg.1	REV3L	REV3 like, DNA directed polymerase zeta catalytic subunit	1.79	8.01	7.17	0.27	0.13	4.10E-03	3.02E-02	Multiple_Complex
TC0500007610.hg.1	ERBB2IP	erbb2 interacting protein	1.79	7.62	6.78	0.06	0.11	3.50E-03	2.72E-02	Multiple_Complex
TC0X00009981.hg.1	IL2RG	interleukin 2 receptor, gamma	1.79	5.73	4.89	0.03	0.2	2.78E-02	1.06E-01	Multiple_Complex

TC0400011659.hg.1	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	1.79	5.04	4.2	0.24	0.22	8.00E-03	4.61E-02	Multiple_Complex
TC0500010150.hg.1	DNAH5	Transcript Identified by AceView, Entrez Gene ID(s) 1767	1.79	4.4	3.56	0.21	0.69	4.49E-02	1.46E-01	Unassigned
TC0200013594.hg.1	COA5	cytochrome c oxidase assembly factor 5	1.79	13.71	12.87	0.01	0.06	5.00E-03	3.39E-02	Multiple_Complex
TC0700013349.hg.1	GHRHR	growth hormone releasing hormone receptor	1.79	6.01	5.18	0.66	0.35	3.96E-02	1.34E-01	NonCoding
TC1100010987.hg.1	FABP5	fatty acid binding protein 5 (psoriasis-associated)	1.79	13.12	12.28	0.03	0.25	3.30E-03	2.63E-02	Multiple_Complex
TC1900011797.hg.1	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	1.79	7.71	6.87	0.57	0.16	2.15E-02	8.93E-02	Multiple_Complex
TC0700012824.hg.1	MRPS33	mitochondrial ribosomal protein S33	1.79	13.73	12.89	0.05	0.02	6.50E-03	4.02E-02	Multiple_Complex
TC0800008783.hg.1	SQLE	squalene epoxidase	1.79	10.23	9.39	0.41	0.07	6.90E-03	4.20E-02	Multiple_Complex
TC1200012575.hg.1	DYRK4	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 4	1.79	9.31	8.47	0.15	0.19	4.10E-03	3.03E-02	Multiple_Complex
TC0900011385.hg.1	PSMD5	proteasome 26S subunit, non-ATPase 5	1.79	6.82	5.98	0.08	0.65	1.61E-02	7.36E-02	Multiple_Complex
TC0600008757.hg.1	PNRC1	proline-rich nuclear receptor coactivator 1	1.79	8.53	7.69	0.3	0.32	1.07E-02	5.60E-02	Multiple_Complex
TC0300013146.hg.1	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1.79	4.55	3.71	0.07	0.23	5.20E-03	3.48E-02	Multiple_Complex
TC1300008086.hg.1	ATP11A	ATPase, class VI, type 11A	1.79	7.08	6.24	0.81	0.37	3.80E-02	1.31E-01	NonCoding
TC1800008234.hg.1	ABHD3	abhydrolase domain containing 3	1.79	7.73	6.89	0.48	0.54	1.85E-02	8.09E-02	Multiple_Complex
TC0400009024.hg.1	ARFIP1	ADP-ribosylation factor interacting protein 1	1.79	9.8	8.96	0.11	0.31	4.10E-03	3.00E-02	Multiple_Complex
TC0700013441.hg.1	IFRD1	interferon-related developmental regulator 1	1.79	10.85	10.01	0.01	0.16	3.90E-03	2.93E-02	Multiple_Complex
TC0X00009727.hg.1	SPANXN5	SPANX family, member N5	1.79	5.4	4.56	0.51	0.31	1.20E-02	6.05E-02	Coding
TC0200009964.hg.1	HAT1	histone acetyltransferase 1	1.79	16.38	15.54	0.09	0.28	7.50E-03	4.40E-02	Multiple_Complex
TC0X00010382.hg.1	BEX5	brain expressed X-linked 5	1.79	12.3	11.46	0.16	0.06	2.30E-03	2.12E-02	Multiple_Complex

TC0100015752.hg.1	CTSS	cathepsin S	1.79	4.87	4.03	0.23	0.07	1.26E-02	6.24E-02	Multiple_Complex
TC1900009804.hg.1	C19orf67	chromosome 19 open reading frame 67	1.79	5.75	4.91	0.73	0.09	3.13E-02	1.15E-01	Multiple_Complex
TC0300011306.hg.1	PDHB	pyruvate dehydrogenase (lipoamide) beta	1.78	12.27	11.43	0.08	0.01	2.60E-03	2.30E-02	Multiple_Complex
TC2100008519.hg.1	WRB	tryptophan rich basic protein	1.78	7.48	6.64	0.07	0.27	8.40E-03	4.78E-02	Multiple_Complex
TC1200012754.hg.1	KLRC1	killer cell lectin-like receptor subfamily C, member 1	1.78	4.21	3.38	0.17	0.25	3.94E-02	1.34E-01	Multiple_Complex
TC1300010025.hg.1	RNF6	ring finger protein (C3H2C3 type) 6	1.78	10	9.17	0.21	0.56	1.48E-02	6.97E-02	Multiple_Complex
TC0500010497.hg.1	NADK2	NAD kinase 2, mitochondrial	1.78	8.4	7.57	0.1	0.14	2.30E-03	2.13E-02	Multiple_Complex
TC1500010853.hg.1	FSIP1	fibrous sheath interacting protein 1	1.78	5.69	4.85	0.82	0.12	3.11E-02	1.14E-01	Multiple_Complex
TC0400010251.hg.1	DHX15	DEAH (Asp-Glu-Ala-His) box helicase 15	1.78	13.84	13	0.1	0.18	3.10E-03	2.51E-02	Multiple_Complex
TC0600014060.hg.1	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	1.78	12.71	11.88	0.16	0.32	1.14E-02	5.84E-02	Multiple_Complex
TC0X00007501.hg.1	YIPF6	Yip1 domain family member 6	1.78	10.38	9.54	0.28	0.05	4.40E-03	3.16E-02	Multiple_Complex
TC0500007673.hg.1	RAD17	RAD17 checkpoint clamp loader component	1.78	11.82	10.98	0.19	0.12	4.40E-03	3.16E-02	Multiple_Complex
TC1100007865.hg.1	METTL12; SNORA57	methyltransferase like 12; small nucleolar RNA, H/ACA box 57	1.78	4.95	4.12	0.73	0.09	2.44E-02	9.73E-02	Multiple_Complex
TC0700013375.hg.1	ZNF273	zinc finger protein 273	1.78	9.28	8.45	0.03	0.05	2.50E-03	2.22E-02	Multiple_Complex
TC0700008430.hg.1	SDHAF3	succinate dehydrogenase complex assembly factor 3	1.78	14.16	13.33	0.2	0.3	8.70E-03	4.88E-02	Multiple_Complex
TC0200016669.hg.1	ASB3	ankyrin repeat and SOCS box containing 3	1.78	9.74	8.91	0.2	0.42	8.50E-03	4.83E-02	Multiple_Complex
TC0100018398.hg.1	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	1.78	8.34	7.51	0.47	0.25	4.54E-02	1.47E-01	Multiple_Complex
TC0100015478.hg.1	NBPF7	neuroblastoma breakpoint family, member 7	1.78	5.72	4.89	0.49	0.09	9.90E-03	5.32E-02	Multiple_Complex
TC1000012398.hg.1	FUOM	fucose mutarotase	1.78	9.11	8.28	0.37	0.38	2.10E-02	8.78E-02	Multiple_Complex
TC0100012242.hg.1	EFCAB2	EF-hand calcium binding domain 2	1.78	8.66	7.83	0.44	0.43	2.62E-02	1.02E-01	Multiple_Complex

TC0700011847.hg.1	SLC25A13	solute carrier family 25 (aspartate/glutamate carrier), member 13	1.78	8.85	8.02	0.04	0.32	7.80E-03	4.54E-02	Multiple_Complex
TC1300008249.hg.1	GJB2	gap junction protein beta 2	1.78	8.9	8.07	0.29	0.5	2.64E-02	1.03E-01	Coding
TC0800008352.hg.1	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	1.78	11.06	10.23	0.54	0.05	1.28E-02	6.31E-02	Multiple_Complex
TC0800009970.hg.1	PBK	PDZ binding kinase	1.78	8.74	7.91	0.13	0.29	1.40E-02	6.73E-02	Multiple_Complex
TC1500009797.hg.1	DPP8	dipeptidyl-peptidase 8	1.78	9.54	8.72	0.02	0.15	2.40E-03	2.20E-02	Multiple_Complex
TC0100018565.hg.1	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1.78	5.98	5.15	0.17	0.22	2.41E-02	9.66E-02	Multiple_Complex
TC0500009824.hg.1	ZDHHC11	Transcript Identified by AceView, Entrez Gene ID(s) 79844	1.78	6.4	5.57	0.47	0.43	3.61E-02	1.26E-01	Unassigned
TC2100008279.hg.1	ERVH48-1	endogenous retrovirus group 48, member 1	1.77	4.94	4.11	0.09	0.04	5.60E-03	3.67E-02	Multiple_Complex
TC0700008337.hg.1	VPS50	VPS50 EARP/GARPII complex subunit	1.77	6.87	6.04	0.34	0.7	3.57E-02	1.25E-01	Multiple_Complex
TC0800012390.hg.1	MSR1	macrophage scavenger receptor 1	1.77	5.03	4.2	0.81	0.05	3.09E-02	1.14E-01	NonCoding
TC0500008830.hg.1	UBE2D2	ubiquitin conjugating enzyme E2D 2	1.77	12.66	11.84	0.33	0.06	1.04E-02	5.48E-02	Multiple_Complex
TC1200012248.hg.1	HCAR3	hydroxycarboxylic acid receptor 3	1.77	5.53	4.7	0.3	0.56	2.23E-02	9.16E-02	Coding
TC0100017212.hg.1	SLC30A1	solute carrier family 30 (zinc transporter), member 1	1.77	8.36	7.54	0.38	0.33	1.52E-02	7.08E-02	Multiple_Complex
TC0X00008820.hg.1	OPN1LW	opsin 1 (cone pigments), long-wave-sensitive	1.77	6.72	5.89	0.43	0.12	5.00E-02	1.57E-01	Multiple_Complex
TC1600009244.hg.1	12-Sep	septin 12	1.77	7.89	7.07	0.15	0.2	1.08E-02	5.63E-02	Multiple_Complex
TC0600013603.hg.1	MTRF1L	mitochondrial translational release factor 1-like	1.77	9.81	8.99	0.11	0.2	7.10E-03	4.27E-02	Multiple_Complex
TC0800008786.hg.1	NSMCE2	NSE2/MMS21 homolog, SMC5-SMC6 complex SUMO ligase	1.77	10.03	9.2	0.09	0.33	1.22E-02	6.11E-02	Multiple_Complex
TC1200009734.hg.1	VAMP1	vesicle associated membrane protein 1	1.77	9.51	8.69	0.25	0.06	3.60E-03	2.79E-02	Multiple_Complex
TC1500008105.hg.1	FAM103A1	family with sequence similarity 103, member A1	1.77	12.86	12.04	0.24	0.01	4.70E-03	3.29E-02	Coding

TC1200011474.hg.1	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	1.77	11.53	10.7	0.19	0.47	8.90E-03	4.94E-02	Multiple_Complex
TC0900009275.hg.1	C9orf173	chromosome 9 open reading frame 173	1.77	8.49	7.67	0.04	0.37	6.00E-03	3.80E-02	Multiple_Complex
TC1500007975.hg.1	IREB2	iron responsive element binding protein 2	1.77	10.51	9.69	0.27	0.44	8.80E-03	4.92E-02	Multiple_Complex
TC1200008113.hg.1	NUP107	nucleoporin 107kDa	1.77	8.81	7.99	0.32	0.46	1.42E-02	6.78E-02	Multiple_Complex
TC1500009702.hg.1	RPS27L	ribosomal protein S27-like	1.77	14.84	14.02	0.01	0.37	6.20E-03	3.90E-02	Multiple_Complex
TC0X00010712.hg.1	THOC2	THO complex 2	1.77	12.25	11.42	0.23	0.16	6.60E-03	4.06E-02	Multiple_Complex
TC1200007003.hg.1	CAPZA3	capping protein (actin filament) muscle Z-line, alpha 3	1.77	4.65	3.83	0.87	0.08	4.18E-02	1.39E-01	Coding
TSUnmapped00000419.hg.1	INPP5D	inositol polyphosphate-5-phosphatase D	1.77	4.22	3.39	0.01	0	2.20E-03	2.08E-02	NonCoding
TC0400008551.hg.1	SYNPO2	synaptopodin 2	1.77	5.21	4.38	0.03	0.05	2.80E-03	2.37E-02	Multiple_Complex
TC1000012164.hg.1	DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	1.77	9.36	8.54	0.21	0.49	1.45E-02	6.88E-02	Multiple_Complex
TC0200011886.hg.1	WDR35	WD repeat domain 35	1.77	9.44	8.61	0.1	0.01	3.70E-03	2.83E-02	Multiple_Complex
TC1700012296.hg.1	PRKAR1A; ARSG	protein kinase, cAMP-dependent, regulatory, type I, alpha; arylsulfatase G	1.77	12.99	12.17	0.1	0.09	8.00E-03	4.63E-02	Multiple_Complex
TC0400007360.hg.1	DCAF4L1	DDB1 and CUL4 associated factor 4-like 1	1.77	7.34	6.52	0.27	0.4	1.11E-02	5.75E-02	Coding
TC0100015243.hg.1	KCNA10	potassium channel, voltage gated shaker related subfamily A, member 10	1.77	8.09	7.27	0.76	0.07	3.35E-02	1.20E-01	Coding
TC0400012951.hg.1	SLC9B2	solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2	1.77	7.93	7.1	0.27	0.45	1.14E-02	5.83E-02	Multiple_Complex
TC0200014907.hg.1	SLC25A12	solute carrier family 25 (aspartate/glutamate carrier), member 12	1.77	7.21	6.39	0.04	0.3	3.35E-02	1.20E-01	Multiple_Complex
TC1400006851.hg.1	ARHGAP5	Rho GTPase activating protein 5	1.77	11.06	10.24	0.2	0.63	2.01E-02	8.54E-02	Multiple_Complex
TC0800010511.hg.1	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5	1.77	4.27	3.44	0.18	0.13	7.60E-03	4.47E-02	Coding

TC2200009107.hg.1	C22orf34	chromosome 22 open reading frame 34	1.77	7.06	6.24	0.01	0.7	3.93E-02	1.33E-01	Multiple_Complex
TC1700010455.hg.1	CCL14; CCL15; CCL15-CCL14	chemokine (C-C motif) ligand 14; chemokine (C-C motif) ligand 15; CCL15-CCL14 readthrough (NMD candidate)	1.77	6.79	5.97	0.68	0.02	2.51E-02	9.92E-02	Multiple_Complex
TC0400008641.hg.1	FAT4	FAT atypical cadherin 4	1.77	9.86	9.04	0.23	0.24	5.50E-03	3.62E-02	Multiple_Complex
TC0200010112.hg.1	RBM45	RNA binding motif protein 45	1.77	11.46	10.64	0.11	0.3	6.20E-03	3.90E-02	Multiple_Complex
TC0300013914.hg.1	TPRG1	tumor protein p63 regulated 1	1.77	6.6	5.78	0.32	0.11	8.00E-03	4.62E-02	NonCoding
TC0400008882.hg.1	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	1.77	12.4	11.59	0.13	0.21	4.70E-03	3.29E-02	Multiple_Complex
TC1500010880.hg.1	TIPIN	TIMELESS interacting protein	1.77	11.27	10.45	0.08	0.21	4.50E-03	3.16E-02	Multiple_Complex
TC2100007854.hg.1	CCT8	chaperonin containing TCP1, subunit 8 (theta)	1.76	11.91	11.09	0.24	0.13	4.30E-03	3.09E-02	Multiple_Complex
TC0300006627.hg.1	TSEN2	TSEN2 tRNA splicing endonuclease subunit	1.76	11.26	10.44	0.04	0.35	5.00E-03	3.39E-02	Multiple_Complex
TC0500009356.hg.1	FBLL1	fibrillarin-like 1	1.76	5.87	5.05	0.14	0.14	4.00E-03	2.95E-02	Multiple_Complex
TC1200012534.hg.1	POLE	Transcript Identified by AceView, Entrez Gene ID(s) 5426	1.76	5.51	4.69	0.27	0.01	2.04E-02	8.61E-02	Unassigned
TC2000007627.hg.1	CSE1L	CSE1 chromosome segregation 1-like (yeast)	1.76	15.21	14.39	0.02	0.11	2.40E-03	2.19E-02	Multiple_Complex
TC1200010046.hg.1	SLC15A5	solute carrier family 15, member 5	1.76	4.83	4.01	0.25	0.36	1.49E-02	6.97E-02	Coding
TC0700009410.hg.1	OR9A4	olfactory receptor, family 9, subfamily A, member 4	1.76	4.86	4.04	0.81	0.03	3.00E-02	1.12E-01	Coding
TC1700008452.hg.1	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	1.76	12.65	11.83	0.06	0.17	1.90E-02	8.21E-02	Multiple_Complex
TC1200009672.hg.1	C12orf4	chromosome 12 open reading frame 4	1.76	14.79	13.98	0.1	0.23	7.80E-03	4.53E-02	Multiple_Complex
TC0100017024.hg.1	PLEKHA6	Transcript Identified by AceView, Entrez Gene ID(s) 22874	1.76	6.16	5.34	0.17	0.27	4.73E-02	1.51E-01	Unassigned
TC0900011257.hg.1	WDR31	WD repeat domain 31	1.76	6.35	5.54	0.26	0.48	1.99E-02	8.47E-02	Multiple_Complex

TC0300011017.hg.1	SPINK8	serine peptidase inhibitor, Kazal type 8 (putative)	1.76	5.4	4.58	0.19	0.43	1.13E-02	5.82E-02	Coding
TC0X00006631.hg.1	TMSB4X	thymosin beta 4, X-linked	1.76	12.49	11.67	0.25	0.16	5.10E-03	3.41E-02	Multiple_Complex
TC1400009924.hg.1	EML5	echinoderm microtubule associated protein like 5	1.76	6.37	5.55	0.28	0.05	8.90E-03	4.96E-02	Multiple_Complex
TC0900010933.hg.1	CTSV	cathepsin V	1.76	9.35	8.54	0.12	0.05	2.35E-02	9.52E-02	Multiple_Complex
TC0600012289.hg.1	OOEP	oocyte expressed protein	1.76	5.11	4.29	0.2	0.65	3.13E-02	1.15E-01	Coding
TC0700013343.hg.1	ZNRF2	zinc and ring finger 2, E3 ubiquitin protein ligase	1.76	9.07	8.26	0.85	0.17	4.05E-02	1.36E-01	Multiple_Complex
TC0500011523.hg.1	LNPEP	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_175920	1.76	7.01	6.19	0.01	0.08	4.00E-03	2.98E-02	NonCoding
TC2200007242.hg.1	APOL1	apolipoprotein L1	1.76	5.25	4.44	0.16	0.67	2.21E-02	9.09E-02	Multiple_Complex
TC0400012305.hg.1	NPY1R	neuropeptide Y receptor Y1	1.76	7.41	6.59	0.53	0.06	1.76E-02	7.81E-02	Coding
TC0X00007195.hg.1	RBM3	RNA binding motif (RNP1, RRM) protein 3	1.76	8.2	7.38	0.05	0.16	6.50E-03	4.00E-02	Multiple_Complex
TC1700010649.hg.1	KRTAP1-4	keratin associated protein 1-4	1.76	6.73	5.92	0.83	0.11	3.61E-02	1.26E-01	Coding
TC0800011679.hg.1	ATAD2	ATPase family, AAA domain containing 2	1.76	10.9	10.09	0.39	0.57	2.60E-02	1.02E-01	Multiple_Complex
TC0600008057.hg.1	PTCRA	pre T-cell antigen receptor alpha	1.76	6.8	5.99	0.69	0.16	4.05E-02	1.36E-01	Coding
TSUnmapped00000286.hg.1	HMBS	hydroxymethylbilane synthase	1.76	6.25	5.44	0.18	0.03	7.70E-03	4.52E-02	Coding
TC0600011464.hg.1	SLC44A4	solute carrier family 44, member 4	1.76	4.1	3.29	0.62	0.08	1.90E-02	8.20E-02	Multiple_Complex
TC0700011119.hg.1	SEC61G	Sec61 translocon gamma subunit	1.76	16.64	15.83	0.12	0.1	3.40E-03	2.70E-02	Multiple_Complex
TC0900010922.hg.1	ZNF510	zinc finger protein 510	1.76	7.61	6.8	0.32	0.01	5.80E-03	3.72E-02	Multiple_Complex
TC0600008473.hg.1	SMAP1	small ArfGAP 1	1.76	8.06	7.24	0.33	0.22	5.90E-03	3.76E-02	Multiple_Complex
TC0600014260.hg.1	ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	1.76	8.44	7.63	0.32	0.12	8.00E-03	4.60E-02	Multiple_Complex
TSUnmapped00000341.hg.1	ZNF780A	zinc finger protein 780A	1.76	6.92	6.11	0.29	0.15	1.89E-02	8.17E-02	Coding

TC1800007080.hg.1	GALNT1	polypeptide N-acetylgalactosaminyltransferase 1	1.76	6.3	5.49	0.33	0.64	2.35E-02	9.50E-02	Multiple_Complex
TC0100007832.hg.1	ZC3H12A; MIR6732	zinc finger CCCH-type containing 12A; microRNA 6732	1.76	7.76	6.95	0.66	0.08	4.70E-02	1.51E-01	Multiple_Complex
TC1000008806.hg.1	CFAP58	cilia and flagella associated protein 58	1.76	4.79	3.98	0.04	0.37	8.80E-03	4.91E-02	Coding
TC1200009985.hg.1	GSG1	germ cell associated 1	1.76	4.81	3.99	0.28	0.15	6.00E-03	3.83E-02	Coding
TC0300007220.hg.1	ZNF502	zinc finger protein 502	1.76	5.92	5.1	0.39	0.33	2.00E-02	8.50E-02	Coding
TC0100017730.hg.1	EGLN1	egl-9 family hypoxia-inducible factor 1	1.76	11.82	11.01	0.29	0.34	1.69E-02	7.61E-02	Multiple_Complex
TC1500006786.hg.1	SCG5	secretogranin V	1.76	6.1	5.29	0.56	0.2	2.66E-02	1.03E-01	Multiple_Complex
TC0300014077.hg.1	WDR49	WD repeat domain 49	1.76	6.53	5.72	0.25	0.02	5.90E-03	3.76E-02	Multiple_Complex
TC1100011190.hg.1	EHD1	EH domain containing 1	1.76	9.32	8.51	0.38	0.05	6.40E-03	3.96E-02	Multiple_Complex
TC1300008533.hg.1	HSPH1	heat shock 105kDa/110kDa protein 1	1.76	14.71	13.9	0.05	0.06	2.60E-03	2.28E-02	Multiple_Complex
TC0500010779.hg.1	SLC38A9	solute carrier family 38, member 9	1.75	8.45	7.63	0.04	0.56	4.19E-02	1.39E-01	Multiple_Complex
TC0800010142.hg.1	GOT1L1	glutamic-oxaloacetic transaminase 1-like 1	1.75	5.53	4.72	0.43	0.08	8.10E-03	4.68E-02	Coding
TC1700009398.hg.1	MIR22HG	MIR22 host gene	1.75	6.12	5.31	0.47	0.27	1.62E-02	7.41E-02	Multiple_Complex
TC1400008589.hg.1	KLHL33	kelch-like family member 33	1.75	5.62	4.81	0.23	0.24	1.31E-02	6.40E-02	Coding
TC0100017617.hg.1	HIST3H2A	histone cluster 3, H2a	1.75	11.2	10.39	0.02	0.04	3.60E-03	2.76E-02	Coding
TC0800008546.hg.1	ENY2	enhancer of yellow 2 homolog (Drosophila)	1.75	15.35	14.54	0.15	0.19	6.20E-03	3.90E-02	Multiple_Complex
TC0800011826.hg.1	ASAP1; ASAP1-IT2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1; ASAP1 intronic transcript 2	1.75	8.51	7.7	0.27	0.42	2.45E-02	9.77E-02	Multiple_Complex
TC0100015061.hg.1	DBT	dihydrolipoamide branched chain transacylase E2	1.75	10.27	9.46	0.38	0.53	1.86E-02	8.11E-02	Multiple_Complex
TC2000008295.hg.1	GPCPD1	glycerophosphocholine phosphodiesterase 1	1.75	7.69	6.88	0.08	0.06	1.07E-02	5.61E-02	Multiple_Complex

TC1700010990.hg.1	HOXB1	homeobox B1	1.75	5.74	4.93	0.45	0.29	1.92E-02	8.29E-02	Coding
TC0100011073.hg.1	CRB1	crumbs family member 1, photoreceptor morphogenesis associated	1.75	6.13	5.32	0.15	0.19	9.70E-03	5.24E-02	Multiple_Complex
TC1500010871.hg.1	ZNF280D	zinc finger protein 280D	1.75	10.68	9.87	0.14	0.26	1.24E-02	6.17E-02	Multiple_Complex
TC0300010916.hg.1	TMEM158	transmembrane protein 158 (gene/pseudogene)	1.75	5.59	4.78	0.12	0.24	6.70E-03	4.11E-02	Coding
TC0300012975.hg.1	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	1.75	5.08	4.27	0.43	0.15	8.90E-03	4.94E-02	Multiple_Complex
TC0600007143.hg.1	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	1.75	9.82	9.01	0.04	0.19	4.60E-03	3.23E-02	Multiple_Complex
TC1000008276.hg.1	CCSER2	coiled-coil serine rich protein 2	1.75	12.6	11.8	0.1	0.16	4.80E-03	3.29E-02	Multiple_Complex
TC1900012055.hg.1	VN1R1	vomeronasal 1 receptor 1	1.75	7.64	6.84	0.2	0.22	7.90E-03	4.58E-02	Multiple_Complex
TC1400010616.hg.1	SLC38A6	solute carrier family 38, member 6	1.75	8.51	7.7	0.17	0.12	3.80E-03	2.88E-02	Multiple_Complex
TC1200007052.hg.1	GOLT1B	golgi transport 1B	1.75	12.15	11.35	0.07	0.21	3.90E-03	2.94E-02	Multiple_Complex
TC1600007103.hg.1	CLEC19A	C-type lectin domain family 19, member A	1.75	4.7	3.9	0.12	0.61	3.07E-02	1.13E-01	Multiple_Complex
TC1100011311.hg.1	PC	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_022172	1.75	5.43	4.62	0.18	0.55	3.14E-02	1.15E-01	NonCoding
TC0500007804.hg.1	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	1.75	8.46	7.65	0.12	0.26	4.90E-03	3.36E-02	Multiple_Complex
TC1000007092.hg.1	MASTL	microtubule associated serine/threonine kinase-like	1.75	12.87	12.07	0.17	0.29	5.50E-03	3.59E-02	Multiple_Complex
TC0200014899.hg.1	METTL8	methyltransferase like 8	1.75	10.72	9.92	0.16	0.45	1.02E-02	5.39E-02	Multiple_Complex
TC1600008329.hg.1	HP	haptoglobin	1.75	6.09	5.29	0.39	0.18	2.57E-02	1.01E-01	Multiple_Complex
TC1400009386.hg.1	GPHB5	glycoprotein hormone beta 5	1.75	5.27	4.47	0.39	0.43	1.53E-02	7.11E-02	Multiple_Complex
TC1200012767.hg.1	PRB2	proline-rich protein BstNI subfamily 2	1.75	7.33	6.52	0.63	0	3.61E-02	1.26E-01	Multiple_Complex

TC0300010540.hg.1	TOP2B; MIR4442	topoisomerase (DNA) II beta; microRNA 4442	1.75	9.76	8.96	0.24	0.45	1.89E-02	8.20E-02	Multiple_Complex
TC0300012345.hg.1	LINC01565	long intergenic non-protein coding RNA 1565	1.75	5.42	4.61	0.67	0.46	4.16E-02	1.39E-01	Multiple_Complex
TC1900011965.hg.1	PSG2	pregnancy specific beta-1-glycoprotein 2	1.75	5.01	4.21	0.61	0.06	1.85E-02	8.07E-02	Multiple_Complex
TC0900011160.hg.1	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	1.75	7.48	6.68	0.43	0.26	1.24E-02	6.19E-02	Multiple_Complex
TC0300012943.hg.1	LXN	latexin	1.75	8.53	7.73	0.04	0.39	2.46E-02	9.80E-02	Multiple_Complex
TC1100006676.hg.1	OR51L1	olfactory receptor, family 51, subfamily L, member 1	1.75	4.35	3.55	0.27	0.09	1.02E-02	5.40E-02	Coding
TC1400010649.hg.1	VRK1	vaccinia related kinase 1	1.75	14.8	14	0.24	0.01	4.60E-03	3.21E-02	Multiple_Complex
TC0600014202.hg.1	FGFR1OP	FGFR1 oncogene partner	1.74	8.59	7.79	0.04	0.34	5.80E-03	3.73E-02	Multiple_Complex
TC0300007223.hg.1	KIF15	kinesin family member 15	1.74	9.51	8.71	0.14	0.22	5.90E-03	3.79E-02	Multiple_Complex
TC0700009083.hg.1	AHCYL2	adenosylhomocysteinase-like 2	1.74	7.24	6.44	0.63	0.14	3.16E-02	1.16E-01	Multiple_Complex
TC0600012293.hg.1	MB21D1	Mab-21 domain containing 1	1.74	4.35	3.55	0.18	0.24	4.70E-03	3.26E-02	Multiple_Complex
TC1700011519.hg.1	HELZ	helicase with zinc finger	1.74	9.92	9.12	0.15	0.74	3.81E-02	1.31E-01	Multiple_Complex
TSUnmapped00000335.hg.1	HMBS	hydroxymethylbilane synthase	1.74	4.52	3.72	0.44	0.37	3.47E-02	1.23E-01	NonCoding
TC0X00010211.hg.1	CHM	choroideremia (Rab escort protein 1)	1.74	11.58	10.78	0.07	0.45	9.00E-03	4.98E-02	Multiple_Complex
TC0500008785.hg.1	EGR1	early growth response 1	1.74	8.82	8.02	0.31	0.04	6.60E-03	4.04E-02	Coding
TC0300011651.hg.1	GBE1	glucan (1,4-alpha-), branching enzyme 1	1.74	5.16	4.36	0.17	0.35	9.60E-03	5.21E-02	Multiple_Complex
TC0X00011010.hg.1	SPANXN3	SPANX family, member N3	1.74	7.39	6.59	0.78	0.22	3.82E-02	1.31E-01	Coding
TC0300006618.hg.1	SYN2	synapsin II	1.74	8.41	7.61	0.21	0.24	1.80E-02	7.94E-02	Multiple_Complex
TC1000008063.hg.1	ADK; MRPL35P3	adenosine kinase; mitochondrial ribosomal protein L35 pseudogene 3	1.74	12.71	11.91	0.12	0.14	4.00E-03	2.95E-02	Multiple_Complex
TC1300008614.hg.1	SPG20	spastic paraplegia 20 (Troyer syndrome)	1.74	11.99	11.19	0.19	0.17	7.20E-03	4.31E-02	Multiple_Complex
TC0100014008.hg.1	MUTYH	mutY DNA glycosylase	1.74	6.29	5.49	0.5	0	2.30E-02	9.38E-02	Multiple_Complex

TC1000006466.hg.1	WDR37	WD repeat domain 37	1.74	9.96	9.16	0.11	0.06	1.20E-02	6.04E-02	Multiple_Complex
TC1400007232.hg.1	FBXO34	F-box protein 34	1.74	6.97	6.17	0.07	0.12	6.50E-03	4.01E-02	Multiple_Complex
TC1900010067.hg.1	PBX4	pre-B-cell leukemia homeobox 4	1.74	7.62	6.82	0.07	0.07	3.10E-03	2.51E-02	Multiple_Complex
TC0200014620.hg.1	CACNB4	calcium channel, voltage-dependent, beta 4 subunit	1.74	9.76	8.96	0.51	0.3	2.29E-02	9.33E-02	Multiple_Complex
TC0600008447.hg.1	ADGRB3	adhesion G protein-coupled receptor B3	1.74	5.87	5.08	0.5	0.4	4.06E-02	1.37E-01	Multiple_Complex
TC1900010528.hg.1	ZNF260	zinc finger protein 260	1.74	7.37	6.57	0.03	0.17	3.10E-03	2.54E-02	Multiple_Complex
TC1000009057.hg.1	NANOS1	nanos homolog 1 (Drosophila)	1.74	7.44	6.64	0.34	0.46	1.93E-02	8.32E-02	Coding
TC0300010521.hg.1	THRB	thyroid hormone receptor, beta	1.74	6.66	5.86	0.65	0.07	3.49E-02	1.23E-01	Multiple_Complex
TC2000008950.hg.1	ACSS2	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001076552	1.74	4.87	4.08	0.32	0.16	2.74E-02	1.05E-01	NonCoding
TC0X00011126.hg.1	GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3	1.74	5.43	4.63	0.19	0.1	3.50E-03	2.73E-02	Multiple_Complex
TC1800006937.hg.1	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	1.74	7.6	6.8	0.43	0.46	4.52E-02	1.47E-01	Multiple_Complex
TC0700008450.hg.1	LMTK2	lemur tyrosine kinase 2	1.74	10.06	9.26	0.2	0.35	2.31E-02	9.40E-02	Multiple_Complex
TC0400011749.hg.1	BBS7	Bardet-Biedl syndrome 7	1.74	12.41	11.61	0.19	0.19	1.15E-02	5.88E-02	Multiple_Complex
TC0200010474.hg.1	KIAA2012	KIAA2012	1.74	5.95	5.15	0.02	0.2	4.33E-02	1.42E-01	Multiple_Complex
TC1900011963.hg.1	PSG6	pregnancy specific beta-1-glycoprotein 6	1.74	6.82	6.02	0.46	0.2	3.25E-02	1.18E-01	Multiple_Complex
TC1900009823.hg.1	GIPC1	GIPC PDZ domain containing family, member 1	1.74	8.34	7.55	0.11	0.37	9.50E-03	5.19E-02	Multiple_Complex
TC0200006671.hg.1	GRHL1	grainyhead-like transcription factor 1	1.74	7.29	6.49	0.05	0.35	1.50E-02	7.03E-02	Multiple_Complex
TC0100012089.hg.1	GPR137B	G protein-coupled receptor 137B	1.74	8.95	8.16	0.45	0.22	2.25E-02	9.23E-02	Multiple_Complex
TC0500011529.hg.1	RIOK2	RIO kinase 2	1.74	8.17	7.37	0.07	0.33	4.03E-02	1.36E-01	Multiple_Complex
TC2000008029.hg.1	MRGBP	MRG/MORF4L binding protein	1.74	7.44	6.65	0.12	0.19	5.80E-03	3.74E-02	Multiple_Complex

TC1400009391.hg.1	WDR89	WD repeat domain 89	1.74	7.74	6.95	0.67	0.35	4.76E-02	1.52E-01	Multiple_Complex
TC0500012605.hg.1	SOX30	SRY box 30	1.74	6.08	5.29	0.65	0.03	4.00E-02	1.35E-01	Coding
TC0300013855.hg.1	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.74	12.11	11.32	0.28	0.18	8.80E-03	4.92E-02	Multiple_Complex
TC0400011043.hg.1	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	1.74	11.45	10.65	0.17	0.21	6.10E-03	3.86E-02	Multiple_Complex
TC0600007657.hg.1	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	1.74	7.26	6.47	0.33	0.47	2.67E-02	1.04E-01	Multiple_Complex
TC0100010269.hg.1	SLAMF8	SLAM family member 8	1.74	5.49	4.69	0.72	0.27	4.20E-02	1.40E-01	Multiple_Complex
TC0200007998.hg.1	ZNF638	zinc finger protein 638	1.74	13.8	13.01	0.39	0.03	7.90E-03	4.59E-02	Multiple_Complex
TC0100014964.hg.1	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	1.74	13.1	12.3	0.11	0.14	3.50E-03	2.75E-02	Multiple_Complex
TC1400007244.hg.1	KTN1	kinectin 1 (kinesin receptor)	1.74	11.7	10.91	0.1	0.04	4.10E-03	2.99E-02	Multiple_Complex
TC1000009920.hg.1	VIM-AS1	VIM antisense RNA 1	1.73	5.9	5.11	0.18	0.06	8.70E-03	4.88E-02	NonCoding
TC0100008026.hg.1	YBX1	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_004559	1.73	10.57	9.78	0.59	0.2	2.97E-02	1.11E-01	NonCoding
TC0200015082.hg.1	FKBP7	FK506 binding protein 7	1.73	9.96	9.16	0.17	0.28	6.50E-03	4.02E-02	Multiple_Complex
TC2100008549.hg.1	KRTAP13-3	keratin associated protein 13-3	1.73	5.28	4.49	0.34	0.31	1.56E-02	7.19E-02	Coding
TC1800007201.hg.1	SIGLEC15	sialic acid binding Ig-like lectin 15	1.73	8.77	7.97	0.19	0.3	7.00E-03	4.22E-02	Multiple_Complex
TC0800011075.hg.1	TMEM55A	transmembrane protein 55A	1.73	6.71	5.92	0.28	0.37	3.34E-02	1.20E-01	Multiple_Complex
TC0300011028.hg.1	COL7A1; MIR711	collagen, type VII, alpha 1; microRNA 711	1.73	8.93	8.14	0.23	0.52	1.46E-02	6.89E-02	Multiple_Complex
TC1000007462.hg.1	ZNF22	zinc finger protein 22	1.73	9.92	9.13	0.05	0.24	1.56E-02	7.20E-02	Multiple_Complex
TC0500013322.hg.1	NAIP	NLR family, apoptosis inhibitory protein	1.73	8.6	7.81	0.12	0.11	1.14E-02	5.86E-02	Multiple_Complex
TC0600012709.hg.1	POPDC3	popeye domain containing 3	1.73	12.94	12.15	0.16	0.04	1.89E-02	8.18E-02	Multiple_Complex

TC0100016709.hg.1	TPR	translocated promoter region, nuclear basket protein	1.73	11.24	10.45	0.1	0.02	5.60E-03	3.64E-02	Multiple_Complex
TC0300013878.hg.1	NCK1	NCK adaptor protein 1	1.73	9.3	8.51	0.17	0	4.10E-03	3.01E-02	Multiple_Complex
TC1800006749.hg.1	CEP192	centrosomal protein 192kDa	1.73	8.89	8.1	0.09	0.22	4.00E-03	2.97E-02	Multiple_Complex
TC1100013145.hg.1	COPB1	coatomer protein complex subunit beta 1	1.73	8.06	7.27	0.68	0.19	2.47E-02	9.82E-02	Multiple_Complex
TC0100010082.hg.1	TDRD10	tudor domain containing 10	1.73	5.07	4.28	0.33	0.38	1.08E-02	5.63E-02	Multiple_Complex
TC1100012712.hg.1	ACRV1	acrosomal vesicle protein 1	1.73	6.7	5.91	0.34	0.04	3.38E-02	1.21E-01	Coding
TC1600006530.hg.1	TPSD1	tryptase delta 1	1.73	5.21	4.42	0.81	0.09	4.57E-02	1.48E-01	Multiple_Complex
TC1900009546.hg.1	PRAM1	PML-RARA regulated adaptor molecule 1	1.73	7.25	6.46	0.5	0.19	2.20E-02	9.09E-02	Multiple_Complex
TC0500011752.hg.1	FEM1C	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_020177	1.73	7.28	6.49	0.32	0.06	1.02E-02	5.41E-02	NonCoding
TC0400008664.hg.1	PLK4	polo-like kinase 4	1.73	10.2	9.41	0.23	0.28	2.05E-02	8.63E-02	Multiple_Complex
TC1500007699.hg.1	KIF23	kinesin family member 23	1.73	11.69	10.9	0.17	0.18	4.70E-03	3.29E-02	Multiple_Complex
TC1200008592.hg.1	SCYL2	SCY1-like, kinase-like 2	1.73	10.6	9.81	0.16	0.12	5.70E-03	3.71E-02	Multiple_Complex
TC0700007112.hg.1	PPP1R17	protein phosphatase 1, regulatory subunit 17	1.73	5.03	4.24	0.08	0.27	1.28E-02	6.32E-02	Multiple_Complex
TC0300009726.hg.1	VPS8	Transcript Identified by AceView, Entrez Gene ID(s) 23355	1.73	4.07	3.28	0.54	0.17	2.09E-02	8.74E-02	Unassigned
TC0X00006823.hg.1	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	1.73	10.78	9.99	0.18	0.2	4.70E-03	3.25E-02	Multiple_Complex
TC0600007270.hg.1	HIST1H2AC	histone cluster 1, H2ac	1.73	11.75	10.96	0.01	0.36	1.66E-02	7.54E-02	Multiple_Complex
TC0X00009340.hg.1	FTHL17	ferritin, heavy polypeptide-like 17	1.73	7.05	6.26	0.13	0.23	1.24E-02	6.19E-02	Coding
TC2200006985.hg.1	PITPNB	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_012399	1.73	5.93	5.14	0.54	0.06	2.58E-02	1.01E-01	NonCoding
TC0100009097.hg.1	ABCD3	ATP binding cassette subfamily D member 3	1.73	10.5	9.71	0.08	0.44	8.60E-03	4.85E-02	Multiple_Complex

TC0200016673.hg.1	RTN4	reticulon 4	1.73	8.02	7.23	0.13	0.05	5.80E-03	3.75E-02	Multiple_Complex
TC0700011318.hg.1	ERV3-1; ZNF117	endogenous retrovirus group 3, member 1; zinc finger protein 117	1.73	9.72	8.93	0.03	0.03	9.60E-03	5.20E-02	Multiple_Complex
TC0400009352.hg.1	CEP44	centrosomal protein 44kDa	1.73	7.93	7.14	0.34	0.14	1.30E-02	6.36E-02	Multiple_Complex
TC0200008103.hg.1	POLE4	polymerase (DNA-directed), epsilon 4, accessory subunit	1.73	13.96	13.17	0.16	0.16	5.30E-03	3.50E-02	Multiple_Complex
TC0200015009.hg.1	ATF2	activating transcription factor 2	1.73	14.66	13.88	0.22	0.14	4.80E-03	3.29E-02	Multiple_Complex
TC1900008257.hg.1	ZNF227	zinc finger protein 227	1.73	7.96	7.17	0.03	0.08	4.40E-03	3.14E-02	Multiple_Complex
TC0100013013.hg.1	UQCRHL	ubiquinol-cytochrome c reductase hinge protein like	1.73	12.45	11.66	0.22	0.03	7.00E-03	4.21E-02	Multiple_Complex
TC1700010763.hg.1	BRCA1	breast cancer 1, early onset	1.73	10.27	9.48	0.28	0.4	2.98E-02	1.11E-01	Multiple_Complex
TC0400009855.hg.1	TMEM128	transmembrane protein 128	1.73	11.23	10.44	0.34	0.11	1.87E-02	8.16E-02	Multiple_Complex
TC0500009269.hg.1	TTC1	Transcript Identified by AceView, Entrez Gene ID(s) 7265	1.72	7.25	6.47	0.31	0.25	3.48E-02	1.23E-01	Unassigned
TC1600007811.hg.1	PAPD5	PAP associated domain containing 5	1.72	11.76	10.98	0.08	0.07	5.20E-03	3.47E-02	Multiple_Complex
TC1700007520.hg.1	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	1.72	6.91	6.12	0.07	0.11	8.20E-03	4.72E-02	Multiple_Complex
TC0500008766.hg.1	MYOT	myotilin	1.72	5.16	4.38	0.23	0.07	6.50E-03	4.01E-02	Multiple_Complex
TC0200009813.hg.1	PSMD14	proteasome 26S subunit, non-ATPase 14	1.72	14.3	13.51	0.16	0.1	4.40E-03	3.16E-02	Multiple_Complex
TC0600012801.hg.1	SESN1	sestrin 1	1.72	7.22	6.43	0.17	0.21	1.31E-02	6.40E-02	Multiple_Complex
TC0M00006434.hg.1	ND2	MTND2	1.72	12.85	12.06	0.07	0.04	3.70E-03	2.84E-02	Multiple_Complex
TC1100009097.hg.1	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B, ionotropic	1.72	4.58	3.79	0.4	0.18	1.55E-02	7.18E-02	Coding
TC0400006988.hg.1	LAP3	Transcript Identified by AceView, Entrez Gene ID(s) 51056	1.72	5.02	4.23	0.21	0.44	1.93E-02	8.30E-02	Unassigned
TC1600010171.hg.1	VPS35	VPS35 retromer complex component	1.72	8.53	7.75	0.26	0.25	3.56E-02	1.25E-01	Multiple_Complex

TC0X00011308.hg.1	RPL36A	ribosomal protein L36a	1.72	15.33	14.55	0.33	0.14	7.60E-03	4.45E-02	Multiple_Complex
TC1700007916.hg.1	CNTD1	cyclin N-terminal domain containing 1	1.72	5.7	4.92	0.29	0.31	1.41E-02	6.73E-02	Multiple_Complex
TC1400007172.hg.1	STYX	serine/threonine/tyrosine interacting protein	1.72	10.68	9.9	0.14	0.04	8.80E-03	4.92E-02	Multiple_Complex
TC1200007526.hg.1	LINC00935	long intergenic non-protein coding RNA 935	1.72	4.61	3.83	0.75	0.02	3.19E-02	1.16E-01	Multiple_Complex
TC1900009917.hg.1	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	1.72	5.42	4.64	0.81	0.15	4.35E-02	1.43E-01	Multiple_Complex
TC0300013912.hg.1	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	1.72	14	13.21	0.15	0.01	4.80E-03	3.30E-02	Coding
TC1900006833.hg.1	MBD3L5	methyl-CpG binding domain protein 3-like 5	1.72	5.45	4.67	0.41	0.16	2.19E-02	9.05E-02	Coding
TSUnmapped00000255.hg.1	KIF15	kinesin family member 15	1.72	7.87	7.09	0.24	0.37	1.00E-02	5.32E-02	Coding
TC2000009913.hg.1	CNBD2	cyclic nucleotide binding domain containing 2	1.72	4.12	3.33	0.05	0.12	2.98E-02	1.11E-01	Multiple_Complex
TC2200007973.hg.1	DGCR14	Transcript Identified by AceView, Entrez Gene ID(s) 8220	1.72	9.62	8.84	0.58	0.05	2.09E-02	8.76E-02	Unassigned
TC0500011125.hg.1	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	1.72	10.12	9.34	0.01	0.14	1.09E-02	5.65E-02	Multiple_Complex
TC0700009398.hg.1	TAS2R3	taste receptor, type 2, member 3	1.72	6.62	5.84	0.17	0.31	1.24E-02	6.18E-02	Coding
TC1500010738.hg.1	CTXN2	cortexin 2	1.72	4.29	3.51	0.46	0.31	1.92E-02	8.29E-02	Coding
TC0900010903.hg.1	RP11-569G13.3; LOC158434; setora	uncharacterized protein LOC158434 [Source:RefSeq peptide;Acc:NP_001243337]; uncharacterized LOC158434; Protein LOC158434 [Source:UniProtKB/TrEMBL;Acc:A0A087X204]; novel transcript; Transcript Identified by AceView	1.72	6.52	5.74	0.7	0.05	4.02E-02	1.36E-01	Multiple_Complex
TC0700011601.hg.1	TMEM60	transmembrane protein 60	1.72	11.84	11.06	0.27	0.31	1.30E-02	6.37E-02	Multiple_Complex
TC0300011103.hg.1	HYAL1	hyaluronoglucosaminidase 1	1.72	7.75	6.97	0.27	0.46	1.27E-02	6.29E-02	Multiple_Complex

TC1600011320.hg.1	WFIKKN1	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	1.72	7.37	6.59	0.29	0.44	1.83E-02	8.03E-02	Coding
TSUnmapped00000060.hg.1	TGM4	transglutaminase 4	1.72	5.5	4.72	0.55	0.32	2.17E-02	8.99E-02	NonCoding
TC0900012168.hg.1	MRRF	mitochondrial ribosome recycling factor	1.72	10.07	9.29	0.03	0.29	1.16E-02	5.92E-02	Multiple_Complex
TC0100018045.hg.1	SMYD3	SET and MYND domain containing 3	1.72	9.6	8.82	0.01	0.4	9.40E-03	5.14E-02	Multiple_Complex
TC0800006718.hg.1	C8orf74	chromosome 8 open reading frame 74	1.72	5.8	5.01	0.52	0.19	2.59E-02	1.02E-01	Multiple_Complex
TC1200012598.hg.1	MGST1	microsomal glutathione S-transferase 1	1.72	4.56	3.78	0.73	0.35	4.35E-02	1.43E-01	NonCoding
TC0600008168.hg.1	ANKRD66	ankyrin repeat domain 66	1.72	4.92	4.14	0.39	0.47	2.57E-02	1.01E-01	Multiple_Complex
TC1000010758.hg.1	RTKN2	rhotekin 2	1.72	11.28	10.5	0.12	0.1	2.02E-02	8.57E-02	Coding
TC0600013004.hg.1	MCM9	minichromosome maintenance 9 homologous recombination repair factor	1.72	6.23	5.45	0.24	0.55	3.05E-02	1.13E-01	Multiple_Complex
TC0400012903.hg.1	PROM1	prominin 1	1.72	5.7	4.92	0.06	0.21	6.00E-03	3.81E-02	Multiple_Complex
TC1300009895.hg.1	PCID2	PCI domain containing 2	1.72	10.35	9.57	0.17	0.21	6.50E-03	4.00E-02	Multiple_Complex
TC1700012408.hg.1	KRTAP4-5	keratin associated protein 4-5	1.72	7.04	6.26	0.52	0.02	1.95E-02	8.37E-02	Coding
TC1600007263.hg.1	SLC5A11	solute carrier family 5 (sodium/inositol cotransporter), member 11	1.71	5.05	4.28	0.08	0.18	5.40E-03	3.58E-02	Multiple_Complex
TC0100018406.hg.1	HNRNPCL1	heterogeneous nuclear ribonucleoprotein C-like 1	1.71	9.7	8.92	0.29	0.33	1.84E-02	8.06E-02	Coding
TC0100012787.hg.1	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	1.71	6	5.22	0.44	0.22	4.63E-02	1.49E-01	Multiple_Complex
TC0800010043.hg.1	PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme	1.71	11.23	10.45	0.05	0.19	4.80E-03	3.29E-02	Multiple_Complex
TC1600007528.hg.1	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	1.71	6.25	5.47	0.55	0.18	3.71E-02	1.28E-01	Multiple_Complex

TC0600007196.hg.1	MRS2	MRS2 magnesium transporter	1.71	7.43	6.65	0.03	0.61	4.04E-02	1.36E-01	Multiple_Complex
TC0100018236.hg.1	ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	1.71	12.78	12	0.06	0.06	4.30E-03	3.12E-02	Multiple_Complex
TC0600014193.hg.1	SCAF8; TIAM2	SR-related CTD-associated factor 8; T-cell lymphoma invasion and metastasis 2	1.71	11.24	10.46	0.33	0.15	1.11E-02	5.75E-02	Multiple_Complex
TC0800007957.hg.1	RDH10	retinol dehydrogenase 10 (all-trans)	1.71	9.87	9.09	0.29	0.29	9.30E-03	5.09E-02	Multiple_Complex
TC1300009492.hg.1	TGDS	TDP-glucose 4,6-dehydratase	1.71	11.52	10.75	0.09	0.19	8.80E-03	4.92E-02	Multiple_Complex
TC0600011225.hg.1	HIST1H2AJ	histone cluster 1, H2aj	1.71	14.15	13.37	0.09	0.12	3.80E-03	2.86E-02	Multiple_Complex
TC0200016582.hg.1	NABP1	nucleic acid binding protein 1	1.71	9.62	8.84	0.51	0.1	1.28E-02	6.30E-02	Multiple_Complex
TC0400009376.hg.1	WDR17	WD repeat domain 17	1.71	10.93	10.15	0.01	0.2	3.00E-02	1.12E-01	Multiple_Complex
TC0300009357.hg.1	NMD3	NMD3 ribosome export adaptor	1.71	12.94	12.17	0	0.17	6.90E-03	4.19E-02	Multiple_Complex
TC2200009140.hg.1	TTLL8	tubulin tyrosine ligase-like family member 8	1.71	4.55	3.78	0.09	0.58	1.72E-02	7.71E-02	Multiple_Complex
TC0600010921.hg.1	ATXN1	ataxin 1	1.71	7.7	6.92	0.11	0.12	8.30E-03	4.77E-02	Multiple_Complex
TC1300009979.hg.1	UCHL3	ubiquitin C-terminal hydrolase L3	1.71	14.28	13.51	0.07	0.16	5.00E-03	3.38E-02	Multiple_Complex
TC2200007904.hg.1	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	1.71	12.54	11.77	0.04	0.35	1.11E-02	5.73E-02	Multiple_Complex
TC0200016662.hg.1	CALM2	calmodulin 2 (phosphorylase kinase, delta)	1.71	15.69	14.92	0.06	0.01	3.40E-03	2.69E-02	Multiple_Complex
TC0200016700.hg.1	TRABD2A	TraB domain containing 2A	1.71	6.39	5.61	0.61	0.14	2.78E-02	1.06E-01	NonCoding
TC0600009667.hg.1	VTA1	vesicle (multivesicular body) trafficking 1	1.71	12.48	11.71	0.3	0.13	1.11E-02	5.76E-02	Multiple_Complex
TC0100008874.hg.1	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	1.71	9.59	8.82	0.28	0.18	4.48E-02	1.46E-01	Multiple_Complex
TC0300012857.hg.1	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	1.71	12.12	11.35	0.1	0.1	6.20E-03	3.91E-02	Multiple_Complex
TC2000007085.hg.1	COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung)	1.71	6.31	5.53	0.26	0.13	1.71E-02	7.66E-02	Multiple_Complex
TC1100008340.hg.1	FOLR1	folate receptor 1 (adult)	1.71	4.24	3.47	0.68	0.02	3.49E-02	1.23E-01	Multiple_Complex

TC1400007563.hg.1	SLC10A1	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, intronic best transcript NM_003049	1.71	6.62	5.85	0.18	0.71	4.33E-02	1.42E-01	NonCoding
TC0500008202.hg.1	FAM174A	family with sequence similarity 174, member A	1.71	10.26	9.49	0.38	0.11	7.70E-03	4.52E-02	Multiple_Complex
TC1300010033.hg.1	CCDC169	coiled-coil domain containing 169	1.71	6.77	5.99	0.12	0.12	4.40E-03	3.16E-02	Multiple_Complex
TC1100010405.hg.1	LIN7C	lin-7 homolog C (C. elegans)	1.71	14.6	13.82	0.08	0.19	7.90E-03	4.59E-02	Multiple_Complex
TC0900011453.hg.1	ZBTB6	zinc finger and BTB domain containing 6	1.71	10.6	9.82	0.16	0.64	2.85E-02	1.08E-01	Coding
TC1300006989.hg.1	AKAP11	A kinase (PRKA) anchor protein 11	1.71	11.77	11	0.28	0.05	1.01E-02	5.37E-02	Multiple_Complex
TC1400008945.hg.1	RALGAPA1	Ral GTPase activating protein, alpha subunit 1 (catalytic)	1.71	12.18	11.41	0.14	0.35	8.90E-03	4.96E-02	Multiple_Complex
TC2100008534.hg.1	PCBP3	poly(rC) binding protein 3	1.71	8.08	7.31	0.37	0.11	8.90E-03	4.94E-02	NonCoding
TC0200013870.hg.1	LIMS3L	LIM and senescent cell antigen-like domains 3-like	1.71	4.4	3.62	0.17	0.01	4.00E-03	2.95E-02	Multiple_Complex
TC1100008727.hg.1	TRIM64	tripartite motif containing 64	1.71	4.04	3.26	0.34	0.12	2.42E-02	9.68E-02	Coding
TC0100012200.hg.1	SDCCAG8	serologically defined colon cancer antigen 8	1.71	11.69	10.91	0.04	0.14	2.04E-02	8.61E-02	Multiple_Complex
TC1900011709.hg.1	FXYD1	FXYD domain containing ion transport regulator 1	1.71	5.85	5.08	0.23	0.38	3.90E-02	1.33E-01	Multiple_Complex
TC0200011745.hg.1	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	1.71	11.46	10.69	0.06	0.05	3.80E-03	2.86E-02	Multiple_Complex
TC1700007454.hg.1	GOSR1	golgi SNAP receptor complex member 1	1.71	11.01	10.24	0.13	0.49	1.23E-02	6.13E-02	Multiple_Complex
TC0100008052.hg.1	CFAP57	cilia and flagella associated protein 57	1.71	4.85	4.08	0.21	0.46	1.82E-02	7.99E-02	Multiple_Complex
TC0100009035.hg.1	KIAA1107	KIAA1107	1.71	7.59	6.82	0.02	0.45	1.69E-02	7.61E-02	Coding
TC0900009895.hg.1	C9orf24	chromosome 9 open reading frame 24	1.71	4.89	4.12	0.24	0.15	5.90E-03	3.78E-02	Multiple_Complex
TC2100008496.hg.1	SLC5A3; MRPS6	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3; mitochondrial ribosomal protein S6	1.71	9.87	9.1	0.4	0.2	1.25E-02	6.22E-02	Multiple_Complex
TC0200011097.hg.1	ALPPL2	alkaline phosphatase, placental like 2	1.71	6.71	5.94	0.58	0.17	1.84E-02	8.04E-02	Coding

TC1500010945.hg.1	LINS1	lines homolog 1	1.71	9.62	8.85	0.15	0.02	7.30E-03	4.34E-02	Multiple_Complex
TC0900010271.hg.1	FOXD4L5	forkhead box D4-like 5	1.71	5.22	4.45	0.29	0.13	6.30E-03	3.93E-02	Coding
TC1100007863.hg.1	ROM1	retinal outer segment membrane protein 1	1.71	8.57	7.8	0.36	0.23	3.16E-02	1.16E-01	Multiple_Complex
TC1100013204.hg.1	ZNF705E	zinc finger protein 705E	1.71	6.43	5.66	0.5	0.19	3.40E-02	1.21E-01	Multiple_Complex
TC1500007303.hg.1	PIGB	phosphatidylinositol glycan anchor biosynthesis class B	1.71	8.05	7.28	0.14	0.43	1.11E-02	5.74E-02	Multiple_Complex
TC0X00006803.hg.1	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	1.71	13.7	12.93	0.24	0.5	1.85E-02	8.08E-02	Multiple_Complex
TC0800008663.hg.1	MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene)	1.7	8.01	7.24	0.04	0.41	1.02E-02	5.39E-02	Multiple_Complex
TC1200012787.hg.1	PUS7L	pseudouridylate synthase 7-like	1.7	9.16	8.39	0.11	0.2	5.10E-03	3.43E-02	Multiple_Complex
TC1300008938.hg.1	DLEU2; MIR15A; MIR16-1; MIR3613	deleted in lymphocytic leukemia 2 (non-protein coding); microRNA 15a; microRNA 16-1; microRNA 3613	1.7	8.11	7.34	0.06	0.14	3.71E-02	1.28E-01	Multiple_Complex
TC0400011727.hg.1	PRDM5	PR domain containing 5	1.7	8.77	8	0.17	0.1	5.00E-03	3.41E-02	Multiple_Complex
TC1100008847.hg.1	CEP57	centrosomal protein 57kDa	1.7	11.93	11.16	0.22	0.16	6.30E-03	3.95E-02	Multiple_Complex
TC1100006437.hg.1	ODF3	outer dense fiber of sperm tails 3	1.7	6.03	5.26	0.24	0.39	1.45E-02	6.87E-02	Multiple_Complex
TC0100017435.hg.1	HHIPL2	HHIP-like 2	1.7	4.77	4	0.4	0.42	1.64E-02	7.46E-02	Multiple_Complex
TC0600009406.hg.1	C6orf58	chromosome 6 open reading frame 58	1.7	4.65	3.88	0.7	0.18	4.05E-02	1.36E-01	Multiple_Complex
TC1900007127.hg.1	IER2	immediate early response 2	1.7	10.48	9.71	0.17	0.18	5.00E-03	3.39E-02	Coding
TC0100017984.hg.1	AKT3	v-akt murine thymoma viral oncogene homolog 3	1.7	11.79	11.02	0.33	0.13	8.20E-03	4.70E-02	Multiple_Complex
TC1400010698.hg.1	INF2	inverted formin, FH2 and WH2 domain containing	1.7	9.1	8.33	0.32	0.41	2.60E-02	1.02E-01	Multiple_Complex
TC0200016559.hg.1	BBS5	Bardet-Biedl syndrome 5	1.7	6.24	5.47	0.11	0.12	1.16E-02	5.89E-02	Multiple_Complex

TC0400006714.hg.1	TADA2B	Transcript Identified by AceView, Entrez Gene ID(s) 93624	1.7	4.63	3.86	0.15	0.07	5.10E-03	3.45E-02	Unassigned
TC0100015795.hg.1	POGZ	Transcript Identified by AceView, Entrez Gene ID(s) 23126	1.7	5.89	5.13	0.27	0.17	8.70E-03	4.90E-02	Unassigned
TC1800008162.hg.1	FAM210A	family with sequence similarity 210, member A	1.7	9.71	8.95	0.25	0.19	1.42E-02	6.78E-02	Multiple_Complex
TC0600009753.hg.1	STXBP5	syntaxin binding protein 5 (tomosyn)	1.7	8.49	7.72	0.46	0.2	2.90E-02	1.09E-01	Multiple_Complex
TC0400008861.hg.1	IL15	interleukin 15	1.7	5.64	4.87	0.23	0.03	1.27E-02	6.28E-02	Multiple_Complex
TC0100012020.hg.1	COA6	cytochrome c oxidase assembly factor 6	1.7	13.78	13.01	0.08	0.13	4.00E-03	2.98E-02	Multiple_Complex
TC0100011755.hg.1	DNAH14	dynein, axonemal, heavy chain 14	1.7	12.73	11.96	0.04	0.35	1.08E-02	5.63E-02	Multiple_Complex
TC1900007819.hg.1	ZNF302	zinc finger protein 302	1.7	13.48	12.71	0.08	0.23	9.00E-03	4.98E-02	Multiple_Complex
TC0100017020.hg.1	REN	renin	1.7	4.9	4.13	0.06	0.18	6.00E-03	3.83E-02	Multiple_Complex
TC0700009230.hg.1	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	1.7	4.79	4.03	0.5	0.26	1.60E-02	7.34E-02	Multiple_Complex
TC1600010685.hg.1	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	1.7	5.51	4.74	0.41	0.14	1.62E-02	7.39E-02	Multiple_Complex
TC1700010314.hg.1	EVI2A; EVI2B	ecotropic viral integration site 2A; ecotropic viral integration site 2B	1.7	4.99	4.23	0.29	0.14	1.00E-02	5.32E-02	Coding
TC0X00006671.hg.1	MOSPD2	motile sperm domain containing 2	1.7	10.79	10.03	0.24	0.42	2.48E-02	9.83E-02	Multiple_Complex
TC1600009256.hg.1	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	1.7	7.31	6.54	0.78	0.15	4.26E-02	1.41E-01	Multiple_Complex
TC1100010992.hg.1	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	1.7	4.85	4.09	0.21	0.01	1.48E-02	6.96E-02	Multiple_Complex
TC0100008190.hg.1	CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	1.7	6.89	6.13	0.43	0.01	1.25E-02	6.20E-02	Multiple_Complex
TC1100013018.hg.1	SDHAF2	succinate dehydrogenase complex assembly factor 2	1.7	10.33	9.57	0.32	0.54	3.14E-02	1.15E-01	Multiple_Complex
TC0X00010329.hg.1	TSPAN6	tetraspanin 6	1.7	14.23	13.47	0.01	0.06	5.00E-03	3.40E-02	Multiple_Complex

TC0100018229.hg.1	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	1.7	5.73	4.97	0.32	0.1	8.50E-03	4.83E-02	Multiple_Complex
TC1400009776.hg.1	NGB	neuroglobin	1.7	5.22	4.46	0.3	0.35	1.65E-02	7.49E-02	Coding
TC0400011040.hg.1	RCHY1	ring finger and CHY zinc finger domain containing 1, E3 ubiquitin protein ligase	1.69	9.25	8.49	0.21	0.31	1.22E-02	6.12E-02	Multiple_Complex
TC0600008468.hg.1	FAM135A	family with sequence similarity 135, member A	1.69	9.78	9.02	0.51	0.09	3.69E-02	1.28E-01	Multiple_Complex
TC2200007021.hg.1	RFPL1	ret finger protein-like 1	1.69	5.12	4.36	0.16	0.61	4.33E-02	1.42E-01	Coding
TC1100011980.hg.1	TAF1D; SNORA8; SNORA18; SNORA40; SNORA1; SNORA25; SNORA32; SNORD5; MIR1304	TATA box binding protein associated factor 1D; small nucleolar RNA, H/ACA box 8; small nucleolar RNA, H/ACA box 18; small nucleolar RNA, H/ACA box 40; small nucleolar RNA, H/ACA box 1; small nucleolar RNA, H/ACA box 25; small nucleolar RNA, H/ACA box 32; small nucleolar RNA, C/D box 5; microRNA 1304	1.69	15.8	15.04	0.16	0.1	5.20E-03	3.47E-02	Multiple_Complex
TC0900011454.hg.1	ZBTB26	zinc finger and BTB domain containing 26	1.69	7.78	7.02	0.05	0.03	7.90E-03	4.59E-02	Coding
TC1200012789.hg.1	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	1.69	14.77	14.01	0.11	0.15	4.80E-03	3.32E-02	Multiple_Complex
TC0X00007668.hg.1	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	1.69	8.74	7.98	0.18	0.47	1.43E-02	6.83E-02	Multiple_Complex
TC0300007445.hg.1	GRM2	glutamate receptor, metabotropic 2	1.69	5.96	5.2	0.29	0.11	1.69E-02	7.61E-02	Multiple_Complex
TC0X00011310.hg.1	RPL36A-HNRNPH2	RPL36A-HNRNPH2 readthrough	1.69	12.53	11.77	0.21	0.19	7.80E-03	4.53E-02	Coding
TC0100008772.hg.1	RABGGTB	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_004582	1.69	9.66	8.9	0.16	0.29	1.41E-02	6.75E-02	NonCoding
TC0400011973.hg.1	CLGN	calmegin	1.69	10.65	9.89	0.35	0.2	3.06E-02	1.13E-01	Multiple_Complex

TC0400010780.hg.1	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	1.69	8.88	8.12	0.34	0.07	2.68E-02	1.04E-01	Multiple_Complex
TC1200012667.hg.1	TPH2	tryptophan hydroxylase 2	1.69	4.91	4.15	0.23	0.25	2.74E-02	1.05E-01	Multiple_Complex
TC0700010345.hg.1	ISPD	isoprenoid synthase domain containing	1.69	4.17	3.41	0.54	0.21	2.70E-02	1.04E-01	Multiple_Complex
TC0100010009.hg.1	LCE1D	late cornified envelope 1D	1.69	6.46	5.7	0.59	0.16	2.13E-02	8.85E-02	Coding
TC1700009479.hg.1	OR1E2	olfactory receptor, family 1, subfamily E, member 2	1.69	6.89	6.13	0.21	0.21	7.60E-03	4.46E-02	Coding
TC0200011673.hg.1	MBOAT2	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_138799	1.69	5.29	4.53	0.12	0.32	9.70E-03	5.23E-02	NonCoding
TC1400007466.hg.1	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	1.69	9.56	8.8	0.09	0.29	8.30E-03	4.76E-02	Multiple_Complex
TC0400008620.hg.1	SPATA5	spermatogenesis associated 5	1.69	10.37	9.61	0.1	0.21	9.20E-03	5.04E-02	Multiple_Complex
TC0800010021.hg.1	MBOAT4	membrane bound O-acyltransferase domain containing 4	1.69	4.4	3.64	0.03	0.57	2.59E-02	1.01E-01	Coding
TC0700008246.hg.1	DMTF1	cyclin D binding myb-like transcription factor 1	1.69	11.46	10.7	0.46	0.25	1.65E-02	7.48E-02	Multiple_Complex
TC1900011755.hg.1	ZNF226	zinc finger protein 226	1.69	10.34	9.59	0.06	0.37	9.50E-03	5.18E-02	Multiple_Complex
TC1400006729.hg.1	TSSK4	testis-specific serine kinase 4	1.69	6.28	5.53	0.35	0.07	1.12E-02	5.78E-02	Multiple_Complex
TC0800012331.hg.1	NDUFAF6	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	1.69	10.79	10.03	0.35	0.13	1.60E-02	7.33E-02	Multiple_Complex
TC2100008095.hg.1	PIGP	phosphatidylinositol glycan anchor biosynthesis class P	1.69	12.51	11.75	0.35	0.12	1.25E-02	6.20E-02	Multiple_Complex
TC0700010687.hg.1	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	1.69	9	8.24	0.2	0.26	1.60E-02	7.34E-02	Multiple_Complex
TC0900007520.hg.1	SMC5	structural maintenance of chromosomes 5	1.69	12.05	11.29	0.12	0.03	4.00E-03	2.95E-02	Multiple_Complex
TC0700008961.hg.1	ASB15	ankyrin repeat and SOCS box containing 15	1.69	5.54	4.78	0.5	0.04	1.94E-02	8.34E-02	Coding
TC0100015851.hg.1	SPRR2E	small proline-rich protein 2E	1.69	6.42	5.67	0.55	0.44	2.98E-02	1.11E-01	Coding

TC0100014566.hg.1	ANKRD13C	ankyrin repeat domain 13C	1.69	9.02	8.26	0.4	0.29	1.59E-02	7.31E-02	Multiple_Complex
TC0300014032.hg.1	POPDC2	popeye domain containing 2	1.69	7.92	7.16	0.01	0.07	1.42E-02	6.77E-02	Multiple_Complex
TC1700012310.hg.1	MFSD11	major facilitator superfamily domain containing 11	1.69	8.56	7.81	0.35	0.09	3.56E-02	1.25E-01	Multiple_Complex
TC1800009283.hg.1	SMAD2	SMAD family member 2	1.69	9.68	8.93	0.27	0.09	7.00E-03	4.21E-02	Multiple_Complex
TC0500009521.hg.1	CPEB4	cytoplasmic polyadenylation element binding protein 4	1.68	8.52	7.77	0.27	0.49	2.06E-02	8.67E-02	Multiple_Complex
TC0100009913.hg.1	ADAMTSL4	ADAMTS like 4	1.68	5.6	4.85	0.41	0.27	2.53E-02	9.99E-02	Multiple_Complex
TC0500007831.hg.1	F2R	coagulation factor II (thrombin) receptor	1.68	8.35	7.6	0.36	0.24	2.65E-02	1.03E-01	Multiple_Complex
TC1100007899.hg.1	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	1.68	6.49	5.74	0.15	0.46	1.74E-02	7.76E-02	Multiple_Complex
TC0X00008674.hg.1	AFF2	AF4/FMR2 family, member 2	1.68	4.78	4.03	0.12	0.03	4.80E-03	3.33E-02	Multiple_Complex
TC0200015194.hg.1	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	1.68	8.17	7.42	0.07	0.07	1.28E-02	6.31E-02	Multiple_Complex
TC0700010005.hg.1	ZFAND2A	zinc finger, AN1-type domain 2A	1.68	13.83	13.08	0.04	0.2	7.10E-03	4.27E-02	Multiple_Complex
TC0300009126.hg.1	GYG1	glycogenin 1	1.68	8.67	7.92	0.18	0.01	1.18E-02	5.98E-02	Multiple_Complex
TC1700011277.hg.1	TRIM37	Transcript Identified by AceView, Entrez Gene ID(s) 4591	1.68	8.27	7.52	0.32	0.06	1.34E-02	6.49E-02	Unassigned
TC0100015058.hg.1	SASS6	SAS-6 centriolar assembly protein	1.68	13.18	12.43	0.03	0.04	4.10E-03	3.03E-02	Multiple_Complex
TC1900011713.hg.1	PSENEN	presenilin enhancer gamma secretase subunit	1.68	15.03	14.29	0.03	0.06	9.90E-03	5.29E-02	Multiple_Complex
TC2100006784.hg.1	JAM2	junctional adhesion molecule 2	1.68	10.64	9.89	0.14	0.29	2.33E-02	9.44E-02	Multiple_Complex
TC1200010336.hg.1	YARS2	tyrosyl-tRNA synthetase 2, mitochondrial	1.68	11.05	10.3	0.14	0.16	5.20E-03	3.48E-02	Multiple_Complex
TC0400012777.hg.1	SOD3	superoxide dismutase 3, extracellular	1.68	5.97	5.22	0.46	0.49	3.50E-02	1.24E-01	NonCoding

TC0800012362.hg.1	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	1.68	10.04	9.29	0.29	0.37	1.88E-02	8.16E-02	Multiple_Complex
TC1800006748.hg.1	SEH1L	SEH1-like nucleoporin	1.68	9.54	8.79	0.28	0.5	2.23E-02	9.15E-02	Multiple_Complex
TC0800008770.hg.1	RNF139	ring finger protein 139	1.68	8.02	7.27	0.06	0.31	9.00E-03	4.98E-02	Multiple_Complex
TC1000008269.hg.1	GHITM	growth hormone inducible transmembrane protein	1.68	15.3	14.56	0	0.02	4.60E-03	3.23E-02	Multiple_Complex
TC0100014768.hg.1	MCOLN2	mucolipin 2	1.68	6.26	5.51	0.08	0.29	3.14E-02	1.15E-01	Multiple_Complex
TC0500007531.hg.1	PDE4D	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001165899	1.68	4.21	3.47	0.11	0.61	3.53E-02	1.24E-01	NonCoding
TC0700008765.hg.1	DLD	dihydrolipoamide dehydrogenase	1.68	9.76	9.02	0.36	0.21	1.55E-02	7.17E-02	Multiple_Complex
TC0600008343.hg.1	BEND6	BEN domain containing 6	1.68	6.06	5.31	0.09	0.27	4.17E-02	1.39E-01	Multiple_Complex
TC1200006966.hg.1	STRAP	serine/threonine kinase receptor associated protein	1.68	14.67	13.92	0.15	0.1	5.00E-03	3.39E-02	Multiple_Complex
TC0200007803.hg.1	LGALSL	lectin, galactoside-binding-like	1.68	11.38	10.63	0.29	0.4	3.00E-02	1.12E-01	Multiple_Complex
TC0400008972.hg.1	DCLK2	doublecortin-like kinase 2	1.68	7.98	7.23	0.48	0.13	1.50E-02	7.01E-02	Multiple_Complex
TC0X00010374.hg.1	NXF5	nuclear RNA export factor 5	1.68	4.93	4.18	0.4	0.4	4.34E-02	1.43E-01	Multiple_Complex
TC1400006833.hg.1	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	1.68	6.46	5.71	0.08	0	4.51E-02	1.47E-01	Multiple_Complex
TC1400010777.hg.1	TC2N	tandem C2 domains, nuclear	1.68	10.15	9.4	0.43	0.37	3.19E-02	1.16E-01	Multiple_Complex
TC1400009655.hg.1	HEATR4	HEAT repeat containing 4	1.68	7.16	6.41	0.52	0.28	1.96E-02	8.39E-02	Multiple_Complex
TC0400007520.hg.1	RASL11B	RAS-like, family 11, member B	1.68	5.53	4.79	0.09	0.14	1.22E-02	6.11E-02	Multiple_Complex
TC1400006549.hg.1	RNASE8	ribonuclease, RNase A family, 8	1.68	5.11	4.37	0.33	0.07	1.01E-02	5.37E-02	Coding
TC0800008371.hg.1	SPAG1	sperm associated antigen 1	1.68	6.29	5.54	0.2	0.74	4.75E-02	1.52E-01	Multiple_Complex
TC0X00007138.hg.1	ZNF157	zinc finger protein 157	1.68	6.31	5.57	0.21	0.13	1.69E-02	7.61E-02	Coding
TC1700012275.hg.1	EFCAB13	EF-hand calcium binding domain 13	1.68	4.76	4.02	0.28	0.1	1.24E-02	6.19E-02	Multiple_Complex

TC1000009684.hg.1	GDI2	GDP dissociation inhibitor 2	1.68	11.76	11.02	0.1	0.22	8.30E-03	4.75E-02	Multiple_Complex
TC1400006506.hg.1	OR11G2	olfactory receptor, family 11, subfamily G, member 2	1.68	4.69	3.95	0.51	0.29	2.30E-02	9.36E-02	Coding
TC1000010724.hg.1	MRLN	myoregulin	1.67	5.92	5.18	0.35	0.03	1.70E-02	7.62E-02	Multiple_Complex
TC2100008576.hg.1	KRTAP10-5	keratin associated protein 10-5	1.67	5.6	4.85	0.63	0.17	2.79E-02	1.06E-01	Multiple_Complex
TC0600009142.hg.1	RPF2	ribosome production factor 2 homolog	1.67	15.48	14.73	0.08	0.08	7.60E-03	4.46E-02	Multiple_Complex
TC1400009998.hg.1	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	1.67	16.28	15.54	0.13	0.33	9.00E-03	4.97E-02	Multiple_Complex
TC0100012149.hg.1	FMN2; ADH5P3	formin 2; alcohol dehydrogenase 5 (class III), chi polypeptide, pseudogene 3	1.67	6.24	5.5	0.52	0.25	3.45E-02	1.22E-01	Multiple_Complex
TSUnmapped00000382.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	1.67	4.5	3.76	0.66	0	2.84E-02	1.08E-01	NonCoding
TC1200011811.hg.1	MTERF2	mitochondrial transcription termination factor 2	1.67	9.81	9.07	0.39	0.25	1.33E-02	6.49E-02	Multiple_Complex
TC1100012197.hg.1	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	1.67	5.41	4.66	0.07	0.22	7.00E-03	4.21E-02	Multiple_Complex
TC0200013095.hg.1	BOLA3	bolA family member 3	1.67	14.13	13.39	0.08	0.33	8.20E-03	4.70E-02	Multiple_Complex
TC0200007746.hg.1	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	1.67	9.97	9.23	0.1	0.08	5.30E-03	3.50E-02	Coding
TC0500008055.hg.1	ADGRV1	adhesion G protein-coupled receptor V1	1.67	6.61	5.87	0.14	0.36	1.03E-02	5.45E-02	Multiple_Complex
TC0100017713.hg.1	TTC13	tetratricopeptide repeat domain 13	1.67	9.72	8.98	0.02	0.4	1.34E-02	6.51E-02	Multiple_Complex
TC0800012435.hg.1	ZFAND1	zinc finger, AN1-type domain 1	1.67	15.25	14.51	0.17	0.13	3.31E-02	1.19E-01	Multiple_Complex
TC0300009306.hg.1	RSRC1	arginine/serine-rich coiled-coil 1	1.67	11.09	10.35	0.22	0.32	2.19E-02	9.03E-02	Multiple_Complex
TC0900007547.hg.1	C9orf85	chromosome 9 open reading frame 85	1.67	11.85	11.11	0.11	0.25	6.60E-03	4.04E-02	Coding
TC1000009345.hg.1	GLRX3	glutaredoxin 3	1.67	11.57	10.82	0.48	0.18	1.71E-02	7.67E-02	Multiple_Complex

TC1900011907.hg.1	PDE4C	phosphodiesterase 4C, cAMP-specific	1.67	5.18	4.43	0.68	0.17	4.05E-02	1.36E-01	Multiple_Complex
TC1000011323.hg.1	GLUD1	glutamate dehydrogenase 1	1.67	11.46	10.72	0.01	0.09	5.90E-03	3.77E-02	Multiple_Complex
TC0600008211.hg.1	GLYATL3	glycine-N-acyltransferase-like 3	1.67	5.93	5.19	0.24	0.07	3.82E-02	1.31E-01	Coding
TC0600012413.hg.1	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1.67	11.63	10.89	0.03	0.16	7.30E-03	4.31E-02	Multiple_Complex
TC0200015073.hg.1	PDE11A	phosphodiesterase 11A	1.67	4.58	3.84	0.49	0.04	2.42E-02	9.69E-02	Multiple_Complex
TC1700007557.hg.1	CCL2	chemokine (C-C motif) ligand 2	1.67	5.71	4.97	0.66	0.03	4.06E-02	1.36E-01	Multiple_Complex
TC0800012446.hg.1	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	1.67	13.02	12.28	0.12	0.06	5.00E-03	3.41E-02	Multiple_Complex
TC0100017523.hg.1	LIN9	lin-9 DREAM MuvB core complex component	1.67	10.74	10	0.03	0.49	3.98E-02	1.35E-01	Multiple_Complex
TC1400010604.hg.1	MIA2	melanoma inhibitory activity 2	1.67	4.53	3.79	0.1	0.02	1.63E-02	7.42E-02	Multiple_Complex
TC1000007020.hg.1	OTUD1	OTU deubiquitinase 1	1.67	10.32	9.58	0.25	0.14	3.44E-02	1.22E-01	Coding
TC0400012940.hg.1	SEC31A	SEC31 homolog A, COPII coat complex component	1.67	10.52	9.78	0.09	0.23	1.01E-02	5.38E-02	Multiple_Complex
TC0800012316.hg.1	XKR9	X-linked Kx blood group related 9	1.67	4.22	3.48	0.14	0.04	7.50E-03	4.42E-02	Coding
TC0X00010664.hg.1	RHOXF1	Rhox homeobox family, member 1	1.67	5.7	4.96	0.22	0.68	3.19E-02	1.16E-01	Coding
TC0400007775.hg.1	ODAM	odontogenic, ameloblast asssociated	1.67	5.08	4.34	0.44	0	2.65E-02	1.03E-01	Multiple_Complex
TC1100009981.hg.1	TPP1	tripeptidyl peptidase I	1.67	9.48	8.74	0.32	0.6	4.70E-02	1.51E-01	Multiple_Complex
TC2000009646.hg.1	CTSZ	cathepsin Z	1.67	9.07	8.33	0.19	0.36	1.39E-02	6.66E-02	Multiple_Complex
TC0100009611.hg.1	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	1.67	5.08	4.34	0.28	0.05	8.70E-03	4.90E-02	Multiple_Complex
TC0600014328.hg.1	OSTM1	osteopetrosis associated transmembrane protein 1	1.67	13.72	12.99	0.27	0.01	2.82E-02	1.07E-01	Multiple_Complex
TC0600011130.hg.1	HIST1H4C	Jeck2013 ANTISENSE, CDS, coding, INTERNAL, OVCODE, OVEXON, UTR3 best transcript NM_003542	1.67	14.66	13.93	0.07	0.32	9.50E-03	5.18E-02	NonCoding

TC0800011312.hg.1	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	1.67	10.92	10.19	0.14	0.24	6.90E-03	4.17E-02	Multiple_Complex
TC0700011586.hg.1	GSAP	gamma-secretase activating protein	1.67	7.07	6.33	0.02	0.48	2.09E-02	8.74E-02	Multiple_Complex
TC1000011546.hg.1	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	1.67	6.28	5.55	0.35	0.48	2.78E-02	1.06E-01	Coding
TC0600007274.hg.1	HIST1H2BD	histone cluster 1, H2bd	1.67	10.17	9.44	0.3	0.07	7.70E-03	4.51E-02	Coding
TC0100016351.hg.1	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	1.67	7.56	6.83	0.25	0.17	8.90E-03	4.94E-02	Multiple_Complex
TC0300013687.hg.1	TFRC	Transcript Identified by AceView, Entrez Gene ID(s) 7037	1.67	4.99	4.26	0.24	0.44	1.85E-02	8.08E-02	Unassigned
TC0500007075.hg.1	SUB1	SUB1 homolog, transcriptional regulator	1.67	15.72	14.98	0.12	0.27	9.50E-03	5.18E-02	Multiple_Complex
TC1700009730.hg.1	RCVRN	recoverin	1.67	5.82	5.08	0.01	0.32	9.20E-03	5.07E-02	Multiple_Complex
TC1200009834.hg.1	MFAP5	microfibrillar associated protein 5	1.67	4.65	3.91	0.19	0.27	9.90E-03	5.31E-02	Multiple_Complex
TC0900009579.hg.1	ZDHHC21	zinc finger, DHHC-type containing 21	1.66	9.31	8.57	0.38	0.12	1.96E-02	8.38E-02	Multiple_Complex
TC1200012664.hg.1	MYRFL	myelin regulatory factor-like	1.66	6.06	5.32	0.4	0.48	3.89E-02	1.33E-01	Multiple_Complex
TC0600009370.hg.1	TRMT11	tRNA methyltransferase 11 homolog	1.66	12.29	11.55	0.1	0.2	9.10E-03	5.00E-02	Multiple_Complex
TC2100006852.hg.1	USP16	ubiquitin specific peptidase 16	1.66	14.75	14.02	0.01	0.16	1.52E-02	7.07E-02	Multiple_Complex
TC1100010254.hg.1	SAAL1	serum amyloid A-like 1	1.66	13.04	12.31	0.06	0.2	6.10E-03	3.87E-02	Multiple_Complex
TC1200007795.hg.1	OR6C2	olfactory receptor, family 6, subfamily C, member 2	1.66	4.78	4.05	0.16	0.14	2.91E-02	1.10E-01	Coding
TC1500008170.hg.1	ALPK3	alpha kinase 3	1.66	5.78	5.05	0.18	0.2	9.60E-03	5.20E-02	Multiple_Complex
TC0X00007424.hg.1	ZXDB	zinc finger, X-linked, duplicated B	1.66	4.65	3.92	0.04	0.19	9.10E-03	5.00E-02	Coding
TC0300012566.hg.1	A4GNT	alpha-1,4-N-acetylglucosaminyltransferase	1.66	4.63	3.9	0.04	0.19	6.30E-03	3.94E-02	Coding
TC0400012857.hg.1	RAPGEF2	Rap guanine nucleotide exchange factor 2	1.66	8.75	8.01	0.46	0.6	4.30E-02	1.42E-01	Multiple_Complex
TC1700012412.hg.1	KRT33B	keratin 33B, type I	1.66	4.76	4.03	0.24	0.26	1.32E-02	6.43E-02	Coding

TC1000008927.hg.1	VTI1A	vesicle transport through interaction with t-SNAREs 1A	1.66	8.91	8.18	0.24	0.38	1.94E-02	8.34E-02	Multiple_Complex
TC1700007859.hg.1	KLHL10	kelch-like family member 10	1.66	5.54	4.8	0.55	0.12	3.62E-02	1.26E-01	Multiple_Complex
TC0500013289.hg.1	LOC285692; CTD-2143L24.1; TAS2R1	uncharacterized LOC285692; novel transcript; Transcript Identified by AceView, Entrez Gene ID(s) 285692; 50834	1.66	5.05	4.32	0.37	0.08	1.01E-02	5.36E-02	NonCoding
TC0X00006626.hg.1	TLR8	toll-like receptor 8	1.66	4.52	3.79	0.23	0.08	9.40E-03	5.15E-02	Coding
TC0600009080.hg.1	CEP57L1	centrosomal protein 57kDa-like 1	1.66	10.56	9.83	0.32	0.1	1.61E-02	7.36E-02	Multiple_Complex
TC2100008517.hg.1	WRB	tryptophan rich basic protein	1.66	12.4	11.67	0.1	0.09	1.88E-02	8.17E-02	Multiple_Complex
TC0200015401.hg.1	ORC2	origin recognition complex subunit 2	1.66	10.47	9.73	0.43	0.01	1.26E-02	6.23E-02	Multiple_Complex
TC1800007015.hg.1	TTR	transthyretin	1.66	5.63	4.9	0.5	0.19	2.93E-02	1.10E-01	Multiple_Complex
TC1600007217.hg.1	SCNN1B	sodium channel, non voltage gated 1 beta subunit	1.66	5.82	5.09	0.57	0.08	5.00E-02	1.57E-01	Multiple_Complex
TC1100008779.hg.1	CCDC67	coiled-coil domain containing 67	1.66	4.47	3.74	0.33	0.35	1.66E-02	7.54E-02	Multiple_Complex
TC0600007207.hg.1	GMNN	geminin, DNA replication inhibitor	1.66	12.31	11.57	0.12	0.09	8.80E-03	4.92E-02	Multiple_Complex
TC0500008835.hg.1	CXXC5	CXXC finger protein 5	1.66	6.89	6.16	0.14	0.18	7.10E-03	4.27E-02	Multiple_Complex
TC0400011130.hg.1	PAQR3	progestin and adipoQ receptor family member III	1.66	9.92	9.19	0.46	0.09	1.88E-02	8.17E-02	Multiple_Complex
TC1100008991.hg.1	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	1.66	9.06	8.32	0.21	0.32	1.06E-02	5.57E-02	Multiple_Complex
TC1700011984.hg.1	NPTX1	neuronal pentraxin I	1.66	7.03	6.3	0.6	0.05	3.16E-02	1.16E-01	Multiple_Complex
TC1900011261.hg.1	SIGLEC6	sialic acid binding Ig-like lectin 6	1.66	5.8	5.07	0.51	0.21	2.02E-02	8.56E-02	Multiple_Complex
TC1600007557.hg.1	ZNF267	zinc finger protein 267	1.66	11.84	11.11	0.07	0.16	9.60E-03	5.22E-02	Multiple_Complex
TC0800008126.hg.1	CA2	carbonic anhydrase II	1.66	8.13	7.4	0.36	0.12	2.64E-02	1.03E-01	Multiple_Complex
TC1400007155.hg.1	C14orf166	chromosome 14 open reading frame 166	1.66	14.69	13.96	0.07	0.07	8.30E-03	4.74E-02	Multiple_Complex

TC1300007884.hg.1	TPP2	tripeptidyl peptidase II	1.66	9.2	8.47	0.27	0.54	2.53E-02	1.00E-01	Multiple_Complex
TC0200009687.hg.1	ARL6IP6	ADP-ribosylation factor like GTPase 6 interacting protein 6	1.66	10.77	10.04	0	0.16	6.90E-03	4.20E-02	Multiple_Complex
TC0800012297.hg.1	SMIM19	small integral membrane protein 19	1.66	13.84	13.11	0.02	0.01	6.60E-03	4.06E-02	Multiple_Complex
TC0300009651.hg.1	ATP11B	ATPase, class VI, type 11B	1.66	12.3	11.57	0.09	0.2	2.02E-02	8.57E-02	Multiple_Complex
TC0800011241.hg.1	RGS22	regulator of G-protein signaling 22	1.66	4.36	3.63	0.23	0.04	1.75E-02	7.80E-02	Multiple_Complex
TC0200009041.hg.1	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	1.66	12.57	11.84	0.17	0	9.10E-03	5.04E-02	Multiple_Complex
TC0600012540.hg.1	GABRR2	gamma-aminobutyric acid (GABA) A receptor, rho 2	1.66	6.1	5.37	0.66	0.23	3.52E-02	1.24E-01	Multiple_Complex
TC1500010906.hg.1	RP11-351M8.2; MESDC2; RP11-351M8.1	Transcript Identified by AceView, Entrez Gene ID(s) 23184; novel transcript, antisense to CEMIP	1.66	7.13	6.4	0.49	0.04	4.02E-02	1.36E-01	Multiple_Complex
TC0400007095.hg.1	ZCCHC4	zinc finger, CCHC domain containing 4	1.66	8.01	7.28	0.16	0.19	1.39E-02	6.68E-02	Multiple_Complex
TC0900006945.hg.1	TOPORS-AS1; GVQW1	TOPORS antisense RNA 1; GVQW motif containing 1	1.66	6.92	6.19	0.58	0.22	2.48E-02	9.83E-02	Multiple_Complex
TC0300012598.hg.1	RBP1	retinol binding protein 1, cellular	1.66	6.13	5.4	0.53	0.15	2.00E-02	8.49E-02	Multiple_Complex
TC0900006653.hg.1	TYRP1	tyrosinase-related protein 1	1.66	4.7	3.97	0.1	0.16	3.22E-02	1.17E-01	Multiple_Complex
TC1200007425.hg.1	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	1.66	11.75	11.02	0.06	0.55	2.80E-02	1.07E-01	Multiple_Complex
TC1600009766.hg.1	LINC01567	long intergenic non-protein coding RNA 1567	1.66	4.3	3.57	0.48	0.14	2.28E-02	9.32E-02	NonCoding
TC0300008147.hg.1	LNP1	leukemia NUP98 fusion partner 1	1.66	8.54	7.81	0.14	0.11	7.80E-03	4.54E-02	Coding
TC1100012677.hg.1	OR8B12	olfactory receptor, family 8, subfamily B, member 12	1.66	4.87	4.14	0.62	0.28	4.53E-02	1.47E-01	Coding
TC0700012099.hg.1	RASA4	Salzman2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_006989	1.66	9.02	8.29	0.43	0.01	1.39E-02	6.67E-02	NonCoding
TC1900011160.hg.1	TSKS	testis-specific serine kinase substrate	1.66	5.3	4.57	0.34	0.11	2.21E-02	9.09E-02	Multiple_Complex

TC0700010019.hg.1	TMEM184A	transmembrane protein 184A	1.66	5.49	4.76	0.28	0.12	3.38E-02	1.21E-01	Multiple_Complex
TC0600014058.hg.1	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	1.66	5.39	4.66	0.38	0.12	1.18E-02	5.98E-02	NonCoding
TC0100018100.hg.1	OR2B11	olfactory receptor, family 2, subfamily B, member 11	1.66	4	3.27	0.55	0.07	2.58E-02	1.01E-01	Coding
TC1100008626.hg.1	PCF11	PCF11 cleavage and polyadenylation factor subunit	1.65	13.85	13.13	0.04	0.32	8.90E-03	4.94E-02	Multiple_Complex
TC2000009169.hg.1	GTSF1L	gametocyte specific factor 1-like	1.65	6.55	5.82	0	0.04	2.08E-02	8.73E-02	Coding
TC1200007859.hg.1	NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	1.65	8.31	7.59	0.18	0.18	1.08E-02	5.63E-02	Multiple_Complex
TC1400006905.hg.1	INSM2	insulinoma-associated 2	1.65	5.49	4.76	0.26	0.38	1.42E-02	6.77E-02	Coding
TC0300014050.hg.1	NPHP3	nephronophthisis 3 (adolescent)	1.65	8.85	8.13	0.08	0.41	1.82E-02	8.01E-02	Multiple_Complex
TC1400007504.hg.1	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	1.65	5.18	4.45	0.02	0.07	2.30E-02	9.36E-02	Multiple_Complex
TC0100010755.hg.1	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	1.65	7.76	7.04	0.25	0.07	1.85E-02	8.07E-02	Multiple_Complex
TC0900008667.hg.1	OR1N2	olfactory receptor, family 1, subfamily N, member 2	1.65	4.06	3.33	0.39	0.29	1.67E-02	7.56E-02	Coding
TC0900011440.hg.1	OR1J1	olfactory receptor, family 1, subfamily J, member 1	1.65	5.36	4.64	0.38	0.09	2.19E-02	9.03E-02	Coding
TC0400012102.hg.1	LRBA	LPS-responsive vesicle trafficking, beach and anchor containing	1.65	11.76	11.04	0.25	0.02	8.80E-03	4.90E-02	Multiple_Complex
TC0300012166.hg.1	HCLS1	hematopoietic cell-specific Lyn substrate 1	1.65	6.88	6.16	0.67	0.13	3.96E-02	1.34E-01	Multiple_Complex
TC0500007725.hg.1	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	1.65	10.6	9.87	0.21	0.55	2.37E-02	9.57E-02	Multiple_Complex
TC1700008191.hg.1	B4GALNT2	beta-1,4-N-acetyl-galactosaminyl transferase 2	1.65	4.69	3.96	0.34	0.41	2.03E-02	8.60E-02	Multiple_Complex
TC1000010655.hg.1	DKK1	Jeck2013 ANTISENSE, CDS, coding, INTERNAL, intronic, OVCODE, OVEXON best transcript NM_012242	1.65	6.16	5.44	0.62	0.06	4.34E-02	1.43E-01	NonCoding
TC0100011554.hg.1	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	1.65	7.06	6.34	0.18	0.43	2.99E-02	1.12E-01	Multiple_Complex

TC0500011490.hg.1	TTC37	tetratricopeptide repeat domain 37	1.65	10.99	10.27	0.1	0.15	8.10E-03	4.68E-02	Multiple_Complex
TC0600007203.hg.1	ACOT13	acyl-CoA thioesterase 13	1.65	14.17	13.44	0.25	0.07	9.00E-03	5.00E-02	Multiple_Complex
TC0X00011396.hg.1	USP26	ubiquitin specific peptidase 26	1.65	5.22	4.5	0.16	0.61	3.81E-02	1.31E-01	NonCoding
TC0400012057.hg.1	SLC10A7	solute carrier family 10, member 7	1.65	8.5	7.77	0.02	0.51	1.75E-02	7.80E-02	Multiple_Complex
TC0200016543.hg.1	RIF1	replication timing regulatory factor 1	1.65	9.88	9.16	0.27	0.08	1.69E-02	7.61E-02	Multiple_Complex
TC0600009392.hg.1	RSPO3	R-spondin 3	1.65	4.05	3.33	0.67	0.29	4.00E-02	1.35E-01	Multiple_Complex
TC1100012997.hg.1	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	1.65	11.97	11.25	0.31	0.13	1.68E-02	7.60E-02	Multiple_Complex
TC0500008014.hg.1	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1.65	8.07	7.35	0.12	0.37	1.23E-02	6.13E-02	Multiple_Complex
TC1300009232.hg.1	DIS3	DIS3 homolog, exosome endoribonuclease and 3-5 exoribonuclease	1.65	11.34	10.62	0.03	0.15	1.00E-02	5.34E-02	Multiple_Complex
TC1200007147.hg.1	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	1.65	8.37	7.64	0.47	0.3	4.94E-02	1.56E-01	Multiple_Complex
TC0500010760.hg.1	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	1.65	10.37	9.65	0.32	0.35	1.61E-02	7.36E-02	Multiple_Complex
TC0X00007013.hg.1	MPC1L	mitochondrial pyruvate carrier 1-like	1.65	4.8	4.08	0.7	0.03	3.53E-02	1.24E-01	Multiple_Complex
TC0100012898.hg.1	NPPB	natriuretic peptide B	1.65	5.93	5.21	0.31	0.11	1.51E-02	7.05E-02	Coding
TC0600013602.hg.1	FBXO5	F-box protein 5	1.65	11.03	10.31	0.2	0.03	6.40E-03	3.96E-02	Multiple_Complex
TC0700010247.hg.1	RPA3	replication protein A3	1.65	15.3	14.58	0.16	0.11	9.20E-03	5.04E-02	Multiple_Complex
TC0600014068.hg.1	TMEM14C	transmembrane protein 14C	1.65	14.72	14	0.17	0.03	8.50E-03	4.83E-02	Multiple_Complex
TC1300007070.hg.1	COG3	component of oligomeric golgi complex 3	1.65	13.11	12.39	0.23	0.42	1.83E-02	8.03E-02	Multiple_Complex
TC0800012468.hg.1	HHLA1	HERV-H LTR-associating 1	1.65	4.86	4.14	0.29	0.21	1.78E-02	7.87E-02	Multiple_Complex
TC0700008265.hg.1	ADAM22	ADAM metallopeptidase domain 22	1.65	10.8	10.08	0.21	0.27	2.94E-02	1.10E-01	Multiple_Complex
TC0800007653.hg.1	MRPL15	mitochondrial ribosomal protein L15	1.65	10.07	9.35	0.54	0.03	3.98E-02	1.35E-01	Coding

TC0200010791.hg.1	PNKD; MIR6810	paroxysmal nonkinesigenic dyskinesia; microRNA 6810	1.65	7.8	7.08	0.21	0.38	1.83E-02	8.04E-02	Multiple_Complex
TC0600009238.hg.1	RSPH4A	radial spoke head 4 homolog A (Chlamydomonas)	1.65	5.88	5.17	0.17	0.03	1.22E-02	6.11E-02	Coding
TC0900007863.hg.1	CKS2	CDC28 protein kinase regulatory subunit 2	1.65	14.58	13.86	0.42	0.08	1.72E-02	7.70E-02	Multiple_Complex
TC0700013468.hg.1	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	1.65	14.14	13.42	0.03	0.06	8.90E-03	4.94E-02	Multiple_Complex
TC1000007056.hg.1	THNSL1	threonine synthase-like 1	1.65	8.67	7.95	0.04	0.23	7.20E-03	4.28E-02	Multiple_Complex
TC1600008643.hg.1	WFDC1	WAP four-disulfide core domain 1	1.65	5.72	5.01	0.52	0.38	3.24E-02	1.18E-01	Multiple_Complex
TC0700011603.hg.1	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	1.65	5.91	5.19	0.04	0.26	8.60E-03	4.86E-02	Multiple_Complex
TC0300010821.hg.1	ULK4	unc-51 like kinase 4	1.65	8.66	7.95	0.17	0.25	1.10E-02	5.70E-02	Multiple_Complex
TC1800006728.hg.1	CIDEA	cell death-inducing DFFA-like effector a	1.65	5.56	4.84	0.37	0.1	2.79E-02	1.06E-01	Multiple_Complex
TC1200007640.hg.1	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	1.65	7.44	6.72	0.43	0.4	2.53E-02	1.00E-01	Multiple_Complex
TC1400010615.hg.1	MNAT1	MNAT CDK-activating kinase assembly factor 1	1.65	14.57	13.85	0.02	0.25	1.19E-02	6.02E-02	Multiple_Complex
TC1700007757.hg.1	GRB7	growth factor receptor bound protein 7	1.64	5.49	4.78	0.32	0.23	1.92E-02	8.28E-02	Multiple_Complex
TC1400007653.hg.1	DNAL1	dynein, axonemal, light chain 1	1.64	8.93	8.22	0.13	0.04	5.70E-03	3.69E-02	Coding
TC0900012288.hg.1	LCN10	lipocalin 10	1.64	4.77	4.05	0.58	0.1	2.74E-02	1.05E-01	Multiple_Complex
TC0300009602.hg.1	MFN1	mitofusin 1	1.64	8.4	7.68	0.42	0.16	2.10E-02	8.78E-02	Multiple_Complex
TC1000011899.hg.1	AFAP1L2	actin filament associated protein 1-like 2	1.64	4.93	4.21	0.7	0.14	4.75E-02	1.52E-01	Multiple_Complex
TC0500007044.hg.1	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	1.64	4.81	4.09	0.03	0.51	4.18E-02	1.39E-01	Multiple_Complex
TC1500006822.hg.1	NUTM1	NUT midline carcinoma, family member 1	1.64	5.7	4.98	0.3	0.31	1.97E-02	8.43E-02	Coding
TC0200009903.hg.1	G6PC2	glucose-6-phosphatase, catalytic, 2	1.64	4.72	4	0.53	0.31	3.02E-02	1.12E-01	Multiple_Complex
TC1100008881.hg.1	ARHGAP42	Rho GTPase activating protein 42	1.64	5.53	4.81	0.39	0.47	2.78E-02	1.06E-01	Multiple_Complex

TC1000008508.hg.1	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	1.64	4.26	3.54	0.19	0.11	1.12E-02	5.76E-02	Multiple_Complex
TC0100010532.hg.1	XCL1	chemokine (C motif) ligand 1	1.64	7.37	6.65	0.02	0.08	8.60E-03	4.86E-02	Coding
TC0200014385.hg.1	CCNT2-AS1	CCNT2 antisense RNA 1	1.64	8.41	7.69	0.67	0.3	4.14E-02	1.38E-01	Multiple_Complex
TC0200010507.hg.1	CARF	calcium responsive transcription factor	1.64	10.96	10.24	0.31	0.25	3.25E-02	1.18E-01	Multiple_Complex
TC0200016581.hg.1	C2orf88	chromosome 2 open reading frame 88	1.64	8.18	7.47	0.06	0.16	1.34E-02	6.51E-02	Multiple_Complex
TC0100009696.hg.1	LOC388692; FAM231D; RP11-403I13.7; RP11-403I13.8	Homo sapiens uncharacterized LOC388692 (LOC388692), long non-coding RNA.; Homo sapiens family with sequence similarity 231, member D (FAM231D), long non-coding RNA.; novel transcript	1.64	6.3	5.59	0.69	0.23	4.57E-02	1.48E-01	NonCoding
TC0400009467.hg.1	TRAPPC11	trafficking protein particle complex 11	1.64	7.1	6.38	0.02	0.57	3.35E-02	1.20E-01	Multiple_Complex
TC0600013341.hg.1	GVQW2	GVQW motif containing 2	1.64	8.73	8.02	0.08	0.29	1.57E-02	7.25E-02	Multiple_Complex
TC0X00008223.hg.1	WDR44	WD repeat domain 44	1.64	11.22	10.51	0.13	0.12	7.60E-03	4.45E-02	Multiple_Complex
TC1000008315.hg.1	BMPR1A	bone morphogenetic protein receptor type IA	1.64	10.98	10.26	0.34	0.29	1.48E-02	6.96E-02	Multiple_Complex
TC0800010045.hg.1	TEX15	testis expressed 15	1.64	6.71	5.99	0.11	0.24	7.90E-03	4.58E-02	Multiple_Complex
TC0200009889.hg.1	B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 1	1.64	8.39	7.67	0.52	0.07	2.03E-02	8.60E-02	Coding
TC0200007506.hg.1	EPCAM	epithelial cell adhesion molecule	1.64	7.33	6.62	0.38	0.34	2.40E-02	9.64E-02	Multiple_Complex
TC1700011083.hg.1	SAMD14	sterile alpha motif domain containing 14	1.64	5.45	4.74	0.39	0.1	1.62E-02	7.39E-02	Multiple_Complex
TC0100017028.hg.1	PPP1R15B	protein phosphatase 1, regulatory subunit 15B	1.64	11.88	11.16	0.14	0.39	1.31E-02	6.41E-02	Coding
TC0700013367.hg.1	ZNF679	zinc finger protein 679	1.64	6.39	5.67	0.71	0.07	4.04E-02	1.36E-01	Coding
TC1000008670.hg.1	TLX1	T-cell leukemia homeobox 1	1.64	4.6	3.88	0.38	0.2	2.62E-02	1.02E-01	Multiple_Complex
TC1900012038.hg.1	LILRA6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	1.64	5.4	4.69	0.03	0.28	4.53E-02	1.47E-01	Multiple_Complex

TC2000009275.hg.1	OCSTAMP	osteoclast stimulatory transmembrane protein	1.64	5.21	4.5	0.44	0.07	2.70E-02	1.04E-01	Coding
TC1200007597.hg.1	COX14	COX14 cytochrome c oxidase assembly factor	1.64	12.75	12.04	0.22	0.11	8.20E-03	4.72E-02	Multiple_Complex
TC0X00011292.hg.1	PAGE5	P antigen family, member 5 (prostate associated)	1.64	6.03	5.31	0.28	0.41	2.71E-02	1.05E-01	Multiple_Complex
TC1200011699.hg.1	ARL1	ADP-ribosylation factor like GTPase 1	1.64	13.37	12.65	0.04	0.14	1.51E-02	7.05E-02	Multiple_Complex
TC0900007680.hg.1	TLE4	transducin-like enhancer of split 4	1.64	7.53	6.82	0.05	0.27	3.02E-02	1.12E-01	Multiple_Complex
TC1700011922.hg.1	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	1.64	9.53	8.81	0.03	0.01	1.69E-02	7.61E-02	Multiple_Complex
TC2000007202.hg.1	ACSS2	acyl-CoA synthetase short-chain family member 2	1.64	8.11	7.4	0.05	0.21	2.15E-02	8.92E-02	Multiple_Complex
TC1600011513.hg.1	BOLA2; BOLA2B	bolA family member 2; bolA family member 2B	1.64	13.64	12.93	0.38	0.3	2.91E-02	1.10E-01	Multiple_Complex
TC0200016507.hg.1	LIMS3L; LIMS3	LIM and senescent cell antigen-like domains 3-like; LIM and senescent cell antigen-like domains 3	1.64	4.1	3.39	0.6	0.28	3.29E-02	1.19E-01	Multiple_Complex
TC0700011675.hg.1	SEMA3D	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	1.64	6.06	5.35	0.05	0.32	1.49E-02	6.98E-02	Multiple_Complex
TC0700013329.hg.1	AMZ1	archaelysin family metallopeptidase 1	1.64	6.9	6.19	0.29	0.29	1.69E-02	7.61E-02	Multiple_Complex
TSUnmapped00000479.hg.1	STKLD1	serine/threonine kinase-like domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28669]	1.64	6.78	6.07	0.17	0.42	1.95E-02	8.36E-02	NonCoding
TC1200012813.hg.1	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	1.64	7.08	6.37	0.37	0.54	3.56E-02	1.25E-01	Multiple_Complex
TC0100010397.hg.1	NUF2	NUF2, NDC80 kinetochore complex component	1.64	11.42	10.71	0.43	0.02	3.74E-02	1.29E-01	Multiple_Complex
TC0200016442.hg.1	MSH2	mutS homolog 2	1.64	11.01	10.3	0.28	0.06	2.03E-02	8.59E-02	Multiple_Complex
TC1200009875.hg.1	CLECL1	C-type lectin-like 1	1.64	5.21	4.5	0.42	0.01	1.78E-02	7.86E-02	Coding
TC1300006503.hg.1	IFT88	intraflagellar transport 88	1.64	5.6	4.89	0.2	0.15	1.65E-02	7.50E-02	Multiple_Complex
TSUnmapped00000628.hg.1	STKLD1	serine/threonine kinase-like domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28669]	1.64	5.57	4.86	0.15	0.36	1.41E-02	6.74E-02	NonCoding

TC1200008675.hg.1	TXNRD1	thioredoxin reductase 1	1.64	9.84	9.13	0.13	0.55	2.30E-02	9.38E-02	Multiple_Complex
TC0200014550.hg.1	ORC4	origin recognition complex subunit 4	1.64	15.16	14.45	0.02	0.23	1.21E-02	6.08E-02	Multiple_Complex
TC0300009856.hg.1	IL1RAP	interleukin 1 receptor accessory protein	1.63	5.32	4.61	0.59	0.02	4.68E-02	1.50E-01	NonCoding
TC1700011442.hg.1	PECAM1	platelet/endothelial cell adhesion molecule 1	1.63	4.83	4.13	0.02	0.05	6.10E-03	3.86E-02	Multiple_Complex
TC0700013394.hg.1	CCDC146	coiled-coil domain containing 146	1.63	7.25	6.54	0.67	0.2	3.90E-02	1.33E-01	Multiple_Complex
TC1200008920.hg.1	OAS3	2-5-oligoadenylate synthetase 3	1.63	5.84	5.13	0.29	0.31	2.79E-02	1.07E-01	Multiple_Complex
TC1100011183.hg.1	SF1	splicing factor 1	1.63	7.49	6.78	0.26	0.59	3.53E-02	1.24E-01	Multiple_Complex
TC1700009701.hg.1	CCDC42	coiled-coil domain containing 42	1.63	6.06	5.35	0.24	0.14	1.30E-02	6.36E-02	Coding
TC1900007695.hg.1	URI1	URI1, prefoldin-like chaperone	1.63	11.81	11.1	0.1	0.15	7.60E-03	4.47E-02	Multiple_Complex
TC1600009137.hg.1	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.63	14.26	13.55	0.17	0.35	1.31E-02	6.39E-02	Multiple_Complex
TC0800010949.hg.1	SNX16	sorting nexin 16	1.63	8.96	8.25	0.03	0.34	1.34E-02	6.50E-02	Multiple_Complex
TC1700010653.hg.1	KRTAP2-3	keratin associated protein 2-3	1.63	8.37	7.66	0.48	0.29	2.59E-02	1.02E-01	Coding
TC1900012025.hg.1	ZNF28	zinc finger protein 28	1.63	6.67	5.96	0.12	0.04	1.14E-02	5.85E-02	Multiple_Complex
TC0900007050.hg.1	DNAI1	Transcript Identified by AceView, Entrez Gene ID(s) 27019	1.63	9.08	8.38	0.09	0.13	1.12E-02	5.78E-02	Coding
TC0200013351.hg.1	RGPD1; RGPD2	RANBP2-like and GRIP domain containing 1; RANBP2-like and GRIP domain containing 2	1.63	6.77	6.06	0.22	0.18	1.10E-02	5.71E-02	Multiple_Complex
TC1400009973.hg.1	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	1.63	7.67	6.97	0.21	0.39	2.80E-02	1.07E-01	Multiple_Complex
TC2000009433.hg.1	FAM65C	family with sequence similarity 65, member C	1.63	5.26	4.55	0.3	0.22	1.21E-02	6.06E-02	Multiple_Complex
TSUnmapped00000757.hg.1	SLC25A26	solute carrier family 25 (S-adenosylmethionine carrier), member 26	1.63	5.77	5.06	0.51	0.08	2.12E-02	8.82E-02	Coding
TC0100016676.hg.1	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	1.63	10.2	9.49	0.04	0.23	1.72E-02	7.69E-02	Multiple_Complex

TC0300010770.hg.1	CSRNP1	cysteine-serine-rich nuclear protein 1	1.63	6.65	5.94	0.03	0.28	1.81E-02	7.96E-02	Multiple_Complex
TC1000009472.hg.1	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	1.63	5.86	5.15	0.51	0.17	2.35E-02	9.51E-02	Multiple_Complex
TC0900008679.hg.1	OR1K1	olfactory receptor, family 1, subfamily K, member 1	1.63	4.15	3.45	0.39	0.19	2.24E-02	9.19E-02	Coding
TC0X00011238.hg.1	CLIC2	chloride intracellular channel 2	1.63	6.56	5.86	0.32	0.46	2.71E-02	1.04E-01	Multiple_Complex
TC1000009244.hg.1	BCCIP	BRCA2 and CDKN1A interacting protein	1.63	12.45	11.75	0.19	0.03	1.12E-02	5.78E-02	Multiple_Complex
TC0300014039.hg.1	TXNRD3	thioredoxin reductase 3	1.63	9.81	9.11	0.38	0.36	4.35E-02	1.43E-01	Multiple_Complex
TC1500010870.hg.1	DYX1C1	dyslexia susceptibility 1 candidate 1	1.63	7.16	6.46	0.42	0.53	4.43E-02	1.45E-01	Multiple_Complex
TC0500010822.hg.1	ACTBL2	actin, beta-like 2	1.63	4.96	4.26	0.6	0.23	3.36E-02	1.20E-01	Multiple_Complex
TC1200010842.hg.1	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	1.63	7.44	6.73	0.43	0.03	2.10E-02	8.79E-02	Coding
TC0500011759.hg.1	ATG12	autophagy related 12	1.63	12.4	11.7	0.05	0.15	9.90E-03	5.32E-02	Multiple_Complex
TC0100009386.hg.1	PROK1	prokineticin 1	1.63	5.99	5.29	0.16	0.43	1.88E-02	8.16E-02	Coding
TC0100008102.hg.1	KIF2C	Jeck2013 ALT_DONOR, coding, INTERNAL, intronic best transcript NM_006845	1.63	5.02	4.31	0.66	0.19	3.74E-02	1.29E-01	NonCoding
TC0600011840.hg.1	PRPH2	peripherin 2 (retinal degeneration, slow)	1.63	5.74	5.04	0.32	0.1	1.18E-02	5.98E-02	Multiple_Complex
TC16_KI270728v1_random00006438.hg.1	TP53TG3D; LOC102723655; TP53TG3; AC136612.1	Homo sapiens TP53 target 3D (TP53TG3D), transcript variant 2, non-coding RNA.; TP53-target gene 3 protein; Homo sapiens TP53 target 3, mRNA (cDNA clone MGC:119889 IMAGE:40015196), complete cds.; Homo sapiens TP53 target 3, mRNA (cDNA clone MGC:119888 IMAGE:40015195), complete cds.	1.63	4.61	3.9	0.1	0.23	1.00E-02	5.34E-02	Multiple_Complex
TC1600009184.hg.1	ZNF200	Transcript Identified by AceView, Entrez Gene ID(s) 7752	1.63	6.44	5.74	0.1	0.32	2.06E-02	8.67E-02	Unassigned

TC1700012460.hg.1	ABCA5	ATP binding cassette subfamily A member 5	1.63	9.75	9.04	0.08	0.1	1.48E-02	6.96E-02	Multiple_Complex
TC0900011148.hg.1	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	1.63	11.69	10.99	0.15	0.29	1.59E-02	7.32E-02	Multiple_Complex
TC2100007917.hg.1	KRTAP11-1	keratin associated protein 11-1	1.63	5.63	4.93	0.56	0.35	4.54E-02	1.47E-01	Coding
TC0800012415.hg.1	PENK	proenkephalin	1.63	5.08	4.38	0.26	0.45	2.72E-02	1.05E-01	Multiple_Complex
TC1600011473.hg.1	NMRAL1	NmrA-like family domain containing 1	1.63	6.08	5.38	0.14	0.02	1.31E-02	6.40E-02	NonCoding
TC0600010028.hg.1	C6orf99	chromosome 6 open reading frame 99	1.63	6.66	5.96	0.07	0.03	7.00E-03	4.21E-02	Multiple_Complex
TC1200012778.hg.1	LMNTD1	lamin tail domain containing 1	1.63	6.43	5.73	0.2	0.36	2.45E-02	9.76E-02	Coding
TC1900012033.hg.1	ZNF347	zinc finger protein 347	1.63	5.26	4.56	0.11	0.01	7.90E-03	4.60E-02	Multiple_Complex
TC2000009957.hg.1	LINC00266-1	long intergenic non-protein coding RNA 266-1	1.63	10.89	10.19	0.22	0.02	9.40E-03	5.14E-02	Multiple_Complex
TC0300012143.hg.1	LRRC58	leucine rich repeat containing 58	1.63	9.05	8.35	0.48	0.21	3.41E-02	1.22E-01	Multiple_Complex
TC1400008748.hg.1	TGM1	transglutaminase 1	1.63	7.55	6.85	0.52	0.24	3.06E-02	1.13E-01	Multiple_Complex
TC0200012459.hg.1	SRBD1	S1 RNA binding domain 1	1.63	9.11	8.41	0.18	0.1	3.68E-02	1.27E-01	Multiple_Complex
TC1100010090.hg.1	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	1.63	5.13	4.43	0.02	0.16	7.40E-03	4.38E-02	Multiple_Complex
TC0X00007381.hg.1	FOXR2	forkhead box R2	1.62	4.2	3.5	0.47	0.05	1.98E-02	8.46E-02	Coding
TC1900009984.hg.1	UNC13A	unc-13 homolog A (C. elegans)	1.62	3.96	3.26	0.19	0.49	3.34E-02	1.20E-01	Multiple_Complex
TC1200007522.hg.1	C12orf54	chromosome 12 open reading frame 54	1.62	5.37	4.67	0.25	0.13	9.50E-03	5.16E-02	Multiple_Complex
TC1900009455.hg.1	MBD3L4	methyl-CpG binding domain protein 3-like 4	1.62	4.98	4.28	0.5	0.23	3.50E-02	1.24E-01	Coding
TC0X00010204.hg.1	SATL1	spermidine/spermine N1-acetyl transferase-like 1	1.62	5.56	4.86	0.38	0.14	2.27E-02	9.27E-02	Coding
TC1900011034.hg.1	ZNF541	zinc finger protein 541	1.62	5.32	4.62	0.51	0.37	3.36E-02	1.20E-01	Multiple_Complex
TC0800008467.hg.1	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	1.62	11.81	11.11	0.15	0.16	1.30E-02	6.37E-02	Multiple_Complex

TC0600011372.hg.1	PPP1R10	protein phosphatase 1, regulatory subunit 10	1.62	12.61	11.91	0.18	0.39	1.86E-02	8.12E-02	Multiple_Complex
TC0600014251.hg.1	ZBED9	zinc finger, BED-type containing 9	1.62	5.87	5.17	0.55	0.21	4.18E-02	1.39E-01	NonCoding
TC1500010184.hg.1	BCL2A1	BCL2-related protein A1	1.62	4.82	4.12	0.06	0.22	2.27E-02	9.28E-02	Coding
TC0400011518.hg.1	INTS12	integrator complex subunit 12	1.62	12.36	11.66	0.24	0.02	8.50E-03	4.81E-02	Multiple_Complex
TC1900008946.hg.1	GALP	galanin-like peptide	1.62	6.83	6.13	0.33	0.47	4.65E-02	1.49E-01	Coding
TC1200012698.hg.1	CHPT1	choline phosphotransferase 1	1.62	11.17	10.47	0.17	0.37	2.17E-02	8.97E-02	Multiple_Complex
TC1000011605.hg.1	CWF19L1; SNORA12	CWF19-like 1, cell cycle control (S. pombe); small nucleolar RNA, H/ACA box 12	1.62	8.92	8.22	0.5	0.28	4.30E-02	1.42E-01	Multiple_Complex
TC1900007885.hg.1	ARHGAP33	Rho GTPase activating protein 33	1.62	8.9	8.2	0.38	0.02	4.12E-02	1.38E-01	Multiple_Complex
TC0600009597.hg.1	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	1.62	8.84	8.14	0.15	0.06	7.50E-03	4.40E-02	Multiple_Complex
TC0Y00006775.hg.1	BPY2C; BPY2	basic charge, Y-linked, 2C; basic charge, Y-linked, 2	1.62	4.19	3.49	0.36	0.2	4.06E-02	1.37E-01	Multiple_Complex
TC1100011684.hg.1	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	1.62	9.71	9.01	0.07	0.02	1.68E-02	7.58E-02	Multiple_Complex
TC1500009353.hg.1	CEP152	centrosomal protein 152kDa	1.62	9.48	8.78	0.15	0.37	2.24E-02	9.18E-02	Multiple_Complex
TC0300008133.hg.1	CMSS1	cms1 ribosomal small subunit homolog (yeast)	1.62	12.11	11.41	0.1	0.04	1.15E-02	5.88E-02	Multiple_Complex
TC0100013889.hg.1	ZMYND12	zinc finger, MYND-type containing 12	1.62	5.03	4.34	0.21	0.38	2.01E-02	8.55E-02	Multiple_Complex
TC0700011710.hg.1	SLC25A40	solute carrier family 25, member 40	1.62	10.77	10.07	0.2	0.11	1.89E-02	8.18E-02	Multiple_Complex
TC0300008171.hg.1	TRMT10C	tRNA methyltransferase 10C, mitochondrial RNase P subunit	1.62	12.92	12.23	0.02	0.07	1.00E-02	5.32E-02	Coding
TC0500010265.hg.1	CDH18	cadherin 18, type 2	1.62	5.92	5.22	0.49	0.26	4.37E-02	1.43E-01	Multiple_Complex
TC0400011503.hg.1	PPA2	pyrophosphatase (inorganic) 2	1.62	7.3	6.6	0.48	0.08	4.22E-02	1.40E-01	Multiple_Complex
TC1200007380.hg.1	PPHLN1	periphilin 1	1.62	11.86	11.16	0.17	0.1	8.30E-03	4.75E-02	Multiple_Complex

TC1400007639.hg.1	C14orf169	chromosome 14 open reading frame 169	1.62	5.31	4.62	0.19	0.15	1.04E-02	5.47E-02	Multiple_Complex
TC0500007808.hg.1	POLK	polymerase (DNA directed) kappa	1.62	13.96	13.26	0.16	0.4	2.73E-02	1.05E-01	Multiple_Complex
TC1400007298.hg.1	ACTR10	actin-related protein 10 homolog (S. cerevisiae)	1.62	14.31	13.61	0.21	0.22	2.67E-02	1.04E-01	Multiple_Complex
TC0300010424.hg.1	DPH3	diphthamide biosynthesis 3	1.62	12.46	11.76	0.1	0.08	1.48E-02	6.96E-02	Multiple_Complex
TC0300008346.hg.1	SLC35A5	solute carrier family 35, member A5	1.62	11.04	10.35	0.32	0.19	1.31E-02	6.42E-02	Multiple_Complex
TC1600011494.hg.1	ARL6IP1	ADP-ribosylation factor like GTPase 6 interacting protein 1	1.62	14.69	14	0.29	0.19	1.64E-02	7.46E-02	Multiple_Complex
TC1700007409.hg.1	SEZ6	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, intronic best transcript NM_178860	1.62	6.49	5.8	0.1	0.14	7.50E-03	4.43E-02	NonCoding
TC1000008955.hg.1	PLEKHS1	pleckstrin homology domain containing, family S member 1	1.62	4.33	3.64	0.02	0.44	1.96E-02	8.39E-02	Coding
TC2000009243.hg.1	TNNC2	troponin C type 2 (fast)	1.62	5.23	4.54	0.02	0.63	4.29E-02	1.42E-01	Coding
TC2200007088.hg.1	LIMK2	LIM domain kinase 2	1.62	8.91	8.22	0.01	0.42	2.99E-02	1.12E-01	Multiple_Complex
TC0800007738.hg.1	SDCBP	syndecan binding protein	1.61	13.06	12.36	0.22	0.12	1.04E-02	5.49E-02	Multiple_Complex
TC1700007704.hg.1	ARHGAP23	Rho GTPase activating protein 23	1.61	7.01	6.32	0.25	0.37	2.20E-02	9.08E-02	Multiple_Complex
TC0100018403.hg.1	ERRFI1	ERBB receptor feedback inhibitor 1	1.61	10.56	9.87	0.06	0.42	1.72E-02	7.71E-02	Multiple_Complex
TC0400012496.hg.1	AGA	aspartylglucosaminidase	1.61	10.38	9.69	0.21	0.2	1.11E-02	5.75E-02	Multiple_Complex
TC0Y00006807.hg.1	BPY2B	basic charge, Y-linked, 2B	1.61	4.2	3.51	0.27	0.22	3.28E-02	1.19E-01	Multiple_Complex
TC0400012620.hg.1	CENPU	centromere protein U	1.61	12.26	11.57	0.22	0.13	1.01E-02	5.36E-02	Multiple_Complex
TC1100009004.hg.1	FDX1	ferredoxin 1	1.61	9.56	8.87	0.28	0.11	1.20E-02	6.04E-02	Coding
TC1700010223.hg.1	SEZ6	seizure related 6 homolog (mouse)	1.61	6.42	5.73	0.11	0.61	4.02E-02	1.36E-01	Multiple_Complex
TC0400008668.hg.1	LARP1B	La ribonucleoprotein domain family, member 1B	1.61	11.05	10.36	0.24	0.1	1.44E-02	6.85E-02	Multiple_Complex
TC1900011877.hg.1	ZNF625	zinc finger protein 625	1.61	7.4	6.71	0.3	0.13	1.53E-02	7.09E-02	Multiple_Complex

TC1900011925.hg.1	ZNF91	zinc finger protein 91	1.61	7.83	7.14	0.19	0.18	1.04E-02	5.48E-02	NonCoding
TC2000008975.hg.1	C20orf173	chromosome 20 open reading frame 173	1.61	6.08	5.4	0.02	0.37	1.37E-02	6.60E-02	Multiple_Complex
TC1300007085.hg.1	LRRC63	leucine rich repeat containing 63	1.61	6.28	5.59	0.18	0.16	9.70E-03	5.24E-02	Coding
TC0300008964.hg.1	MRPS22	mitochondrial ribosomal protein S22	1.61	11.84	11.15	0.06	0.28	1.33E-02	6.49E-02	Multiple_Complex
TC1000009221.hg.1	ZRANB1	zinc finger, RAN-binding domain containing 1	1.61	8.92	8.23	0.06	0.11	8.90E-03	4.94E-02	Multiple_Complex
TC1300008338.hg.1	MIPEP	mitochondrial intermediate peptidase	1.61	11.31	10.62	0.09	0.19	9.30E-03	5.12E-02	Multiple_Complex
TSUnmapped00000638.hg.1	DYRK1B	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	1.61	7.61	6.92	0.17	0.19	1.32E-02	6.44E-02	Coding
TC1900009568.hg.1	OR7D4	olfactory receptor, family 7, subfamily D, member 4	1.61	6.7	6.01	0.26	0.26	1.57E-02	7.25E-02	Coding
TC1500007939.hg.1	HMG20A	high mobility group 20A	1.61	11.59	10.9	0.22	0.02	9.60E-03	5.22E-02	Multiple_Complex
TC0600013536.hg.1	RAET1E	retinoic acid early transcript 1E	1.61	5.59	4.9	0.25	0.01	3.80E-02	1.31E-01	Multiple_Complex
TC0800010696.hg.1	TCF24	transcription factor 24	1.61	5.41	4.73	0.01	0.39	1.81E-02	7.96E-02	Multiple_Complex
TC0700012203.hg.1	COG5	component of oligomeric golgi complex 5	1.61	10.36	9.68	0.35	0.09	2.41E-02	9.67E-02	Multiple_Complex
TC0400011620.hg.1	ZGRF1	zinc finger, GRF-type containing 1	1.61	10.58	9.89	0.37	0.08	1.64E-02	7.46E-02	Multiple_Complex
TC0600012036.hg.1	IL17F	interleukin 17F	1.61	8.27	7.58	0.22	0.3	3.41E-02	1.22E-01	Multiple_Complex
TC1900009456.hg.1	MBD3L3	methyl-CpG binding domain protein 3-like 3	1.61	5.25	4.57	0.43	0.16	1.86E-02	8.11E-02	Coding
TC2000008802.hg.1	DEFB116	defensin, beta 116	1.61	5.38	4.7	0.69	0.02	4.74E-02	1.51E-01	Coding
TC0300011267.hg.1	DNAH12	dynein, axonemal, heavy chain 12	1.61	5.62	4.93	0.28	0.19	1.21E-02	6.07E-02	Multiple_Complex
TSUnmapped00000492.hg.1	KAT6B	K(lysine) acetyltransferase 6B	1.61	9.49	8.81	0.03	0.21	9.00E-03	4.97E-02	Coding
TC0100015023.hg.1	DPYD	dihydropyrimidine dehydrogenase	1.61	7.28	6.6	0.16	0.24	1.59E-02	7.30E-02	Multiple_Complex
TC0900006762.hg.1	ACER2	alkaline ceramidase 2	1.61	6.55	5.87	0.45	0.21	3.74E-02	1.29E-01	Multiple_Complex

TC0500007933.hg.1	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	1.61	5.82	5.14	0.08	0.28	1.24E-02	6.18E-02	Multiple_Complex
TC1700010186.hg.1	KRT18P55	keratin 18 pseudogene 55	1.61	4.63	3.94	0.01	0.07	1.14E-02	5.84E-02	Multiple_Complex
TC0600011773.hg.1	TREML2	triggering receptor expressed on myeloid cells-like 2	1.61	4.75	4.07	0.16	0.06	2.00E-02	8.50E-02	Coding
TC1700010050.hg.1	LGALS9B	lectin, galactoside-binding, soluble, 9B	1.61	6.57	5.89	0.51	0.02	4.68E-02	1.50E-01	Multiple_Complex
TC0600011228.hg.1	HIST1H2AK	histone cluster 1, H2ak	1.61	7.25	6.57	0.13	0.05	1.37E-02	6.61E-02	Coding
TC0300013896.hg.1	MFSD1	major facilitator superfamily domain containing 1	1.6	9.27	8.59	0.14	0.41	2.25E-02	9.23E-02	Multiple_Complex
TC0600007629.hg.1	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	1.6	5.22	4.54	0.12	0.32	1.60E-02	7.35E-02	Multiple_Complex
TC1700010638.hg.1	KRT28	keratin 28, type I	1.6	4.16	3.48	0.03	0.54	3.08E-02	1.14E-01	Coding
TC1900011655.hg.1	PET100	PET100 homolog	1.6	15.77	15.09	0.13	0.11	8.30E-03	4.75E-02	Multiple_Complex
TC0200012742.hg.1	XPO1	exportin 1	1.6	10.1	9.41	0.18	0.12	1.00E-02	5.34E-02	Multiple_Complex
TC1900011207.hg.1	JOSD2	Josephin domain containing 2	1.6	9.71	9.03	0.5	0.28	3.81E-02	1.31E-01	Multiple_Complex
TC0300008604.hg.1	UMPS	uridine monophosphate synthetase	1.6	10.75	10.07	0.2	0.36	2.18E-02	9.00E-02	Multiple_Complex
TC1700009397.hg.1	TLCD2	TLC domain containing 2	1.6	5.22	4.54	0.11	0.16	1.71E-02	7.66E-02	Coding
TC0700008677.hg.1	LHFPL3	lipoma HMGIC fusion partner-like 3	1.6	5.12	4.44	0.37	0.24	2.36E-02	9.53E-02	Coding
TC0600007628.hg.1	C4B	complement component 4B (Chido blood group)	1.6	8.1	7.42	0.41	0.48	3.83E-02	1.31E-01	Multiple_Complex
TC0600014108.hg.1	C4A	complement component 4A (Rodgers blood group)	1.6	8.1	7.42	0.41	0.48	3.83E-02	1.31E-01	Multiple_Complex
TC0200014390.hg.1	ZRANB3	zinc finger, RAN-binding domain containing 3	1.6	9.05	8.37	0.12	0.24	1.66E-02	7.50E-02	Multiple_Complex
TC1600006519.hg.1	SSTR5	somatostatin receptor 5	1.6	6.78	6.1	0.45	0.33	3.54E-02	1.24E-01	Coding
TC0600012379.hg.1	ELOVL4	ELOVL fatty acid elongase 4	1.6	8.84	8.16	0.06	0.15	1.59E-02	7.32E-02	Multiple_Complex
TC1000009894.hg.1	FAM188A	family with sequence similarity 188, member A	1.6	9.83	9.15	0.39	0.26	4.09E-02	1.37E-01	Multiple_Complex

TC1300008855.hg.1	ESD	esterase D	1.6	14.07	13.39	0.08	0.06	8.60E-03	4.86E-02	Multiple_Complex
TC1100010207.hg.1	SOX6; MIR6073	SRY box 6; microRNA 6073	1.6	6.79	6.11	0.03	0.38	3.00E-02	1.12E-01	Multiple_Complex
TC1000009930.hg.1	HACD1	3-hydroxyacyl-CoA dehydratase 1	1.6	11.55	10.87	0.14	0.1	1.70E-02	7.62E-02	Multiple_Complex
TC1500010745.hg.1	POLR2M	polymerase (RNA) II (DNA directed) polypeptide M	1.6	5.65	4.97	0.1	0.19	3.99E-02	1.35E-01	NonCoding
TC0500009353.hg.1	RARS	arginyl-tRNA synthetase	1.6	14.89	14.21	0.23	0.33	4.03E-02	1.36E-01	Multiple_Complex
TC0800007888.hg.1	C8orf34	chromosome 8 open reading frame 34	1.6	6.79	6.11	0.39	0.02	2.32E-02	9.43E-02	Multiple_Complex
TC2000008123.hg.1	NRSN2-AS1	NRSN2 antisense RNA 1	1.6	8.89	8.22	0.34	0.09	1.59E-02	7.31E-02	NonCoding
TC1300008292.hg.1	MICU2	mitochondrial calcium uptake 2	1.6	10.41	9.73	0.12	0.29	1.88E-02	8.17E-02	Multiple_Complex
TC0800006739.hg.1	SLC35G5	solute carrier family 35, member G5	1.6	5.73	5.05	0.17	0.45	4.51E-02	1.47E-01	Coding
TC0700006984.hg.1	SNX10	sorting nexin 10	1.6	8.03	7.35	0.09	0.2	1.29E-02	6.36E-02	Multiple_Complex
TC0900010773.hg.1	ROR2	receptor tyrosine kinase-like orphan receptor 2	1.6	5.73	5.05	0.39	0.07	3.14E-02	1.15E-01	Multiple_Complex
TC0600012829.hg.1	METTL24	methyltransferase like 24	1.6	5.69	5.01	0.04	0.26	1.35E-02	6.55E-02	Multiple_Complex
TC1700007451.hg.1	CPD	carboxypeptidase D	1.6	7.52	6.84	0.24	0.18	4.82E-02	1.53E-01	Multiple_Complex
TC0700006795.hg.1	AHR	aryl hydrocarbon receptor	1.6	11.89	11.22	0.01	0.18	9.50E-03	5.17E-02	Multiple_Complex
TC0500007919.hg.1	MSH3	mutS homolog 3	1.6	8.88	8.2	0.18	0.06	9.60E-03	5.21E-02	Multiple_Complex
TC0500013361.hg.1	SAR1B	secretion associated, Ras related GTPase 1B	1.6	13.07	12.39	0.11	0.22	1.34E-02	6.49E-02	Multiple_Complex
TC1200009941.hg.1	PRB3	proline-rich protein BstNI subfamily 3	1.6	6.97	6.3	0.27	0.24	3.49E-02	1.23E-01	Multiple_Complex
TC1600008867.hg.1	LOC400558; RP11-46C24.3	uncharacterized LOC400558; Transcript Identified by AceView, Entrez Gene ID(s) 400558; novel transcript	1.6	7.26	6.58	0.05	0.02	1.99E-02	8.49E-02	Multiple_Complex
TC0800006837.hg.1	TUSC3	tumor suppressor candidate 3	1.6	13.86	13.18	0.05	0.13	1.98E-02	8.44E-02	Multiple_Complex
TC0100011320.hg.1	CNTN2	contactin 2 (axonal)	1.6	5.84	5.17	0.4	0.19	3.03E-02	1.12E-01	Multiple_Complex

TC0700008963.hg.1	LMOD2	leiomodin 2 (cardiac)	1.6	4.39	3.71	0.42	0.15	1.91E-02	8.25E-02	Coding
TC0500007115.hg.1	RAI14	Transcript Identified by AceView, Entrez Gene ID(s) 26064	1.6	8	7.33	0.22	0.27	2.54E-02	1.00E-01	Unassigned
TC0700012449.hg.1	RNF148	ring finger protein 148	1.6	4.2	3.52	0.43	0.02	1.91E-02	8.26E-02	Coding
TC1500010093.hg.1	ETFA	electron-transfer-flavoprotein, alpha polypeptide	1.6	12.63	11.96	0.09	0.17	9.70E-03	5.22E-02	Multiple_Complex
TC1100013157.hg.1	DCDC1	doublecortin domain containing 1	1.6	7.19	6.52	0.05	0.12	2.24E-02	9.20E-02	Coding
TC0100007127.hg.1	ACTL8	actin-like 8	1.6	5.7	5.03	0.5	0.05	3.78E-02	1.30E-01	Multiple_Complex
TC1600008567.hg.1	CENPN	centromere protein N	1.6	14.17	13.49	0	0.04	9.90E-03	5.32E-02	Multiple_Complex
TSUnmapped00000241.hg.1	ZNF502	zinc finger protein 502	1.6	5.33	4.66	0.27	0.06	1.25E-02	6.21E-02	Coding
TC0600007244.hg.1	SCGN	secretagogin, EF-hand calcium binding protein	1.59	4.85	4.18	0.24	0.23	1.76E-02	7.81E-02	Coding
TC0700010352.hg.1	ANKMY2	ankyrin repeat and MYND domain containing 2	1.59	8.48	7.81	0.13	0.12	8.80E-03	4.92E-02	Multiple_Complex
TC0600013914.hg.1	GPR31	G protein-coupled receptor 31	1.59	6.65	5.98	0.5	0.14	2.56E-02	1.01E-01	Multiple_Complex
TC0200013602.hg.1	TSGA10	testis specific 10	1.59	8.93	8.25	0.15	0.28	2.44E-02	9.73E-02	Multiple_Complex
TC0100016115.hg.1	SLAMF9	SLAM family member 9	1.59	4.6	3.93	0.39	0.13	2.29E-02	9.34E-02	Multiple_Complex
TC0100013623.hg.1	SYNC	syncoilin, intermediate filament protein	1.59	4.96	4.29	0.36	0.03	4.66E-02	1.50E-01	Multiple_Complex
TSUnmapped00000622.hg.1	GREM1	gremlin 1, DAN family BMP antagonist [Source:HGNC Symbol;Acc:HGNC:2001]	1.59	4.34	3.67	0.1	0.32	1.44E-02	6.85E-02	Coding
TC0200007446.hg.1	PRKCE	protein kinase C, epsilon	1.59	9.37	8.7	0.04	0.16	4.55E-02	1.47E-01	Multiple_Complex
TC0X00006935.hg.1	MAGEB16	MAGE family member B16	1.59	4.58	3.91	0.49	0.39	4.29E-02	1.42E-01	Coding
TC0100018483.hg.1	HIST2H2BE	histone cluster 2, H2be	1.59	6.8	6.12	0.28	0.16	2.15E-02	8.91E-02	Coding
TC0300013639.hg.1	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.59	7.2	6.52	0.31	0.35	2.42E-02	9.69E-02	Multiple_Complex

TC0900009704.hg.1	IFNA6	interferon, alpha 6	1.59	4.33	3.66	0.41	0.25	2.25E-02	9.23E-02	Coding
TC1200009209.hg.1	KNTC1	kinetochore associated 1	1.59	11.25	10.58	0.16	0.08	9.70E-03	5.25E-02	Multiple_Complex
TC0100017365.hg.1	EPRS	glutamyl-prolyl-tRNA synthetase	1.59	14.55	13.88	0	0.35	1.68E-02	7.60E-02	Multiple_Complex
TC0100011621.hg.1	TGFB2; TGFB2-OT1	transforming growth factor beta 2; TGFB2 overlapping transcript 1	1.59	6.7	6.03	0.14	0.04	1.18E-02	5.98E-02	Multiple_Complex
TC0300010413.hg.1	ANKRD28	ankyrin repeat domain 28	1.59	9.76	9.09	0.33	0.05	3.09E-02	1.14E-01	Multiple_Complex
TC0700009253.hg.1	NUP205	nucleoporin 205kDa	1.59	12.8	12.13	0.07	0.07	9.40E-03	5.16E-02	Multiple_Complex
TC1600009746.hg.1	PALB2	partner and localizer of BRCA2	1.59	11.62	10.95	0.21	0.22	1.67E-02	7.55E-02	Multiple_Complex
TC1500010399.hg.1	PLIN1	perilipin 1	1.59	4.61	3.94	0.32	0.42	3.04E-02	1.12E-01	Multiple_Complex
TC1900008561.hg.1	AKT1S1	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001098633	1.59	6.45	5.78	0.32	0.2	2.41E-02	9.67E-02	NonCoding
TC1200011496.hg.1	DCN	decorin	1.59	7.04	6.37	0.22	0.19	1.32E-02	6.43E-02	Multiple_Complex
TC2000008747.hg.1	NINL	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_025176	1.59	4.61	3.94	0.17	0.21	2.66E-02	1.03E-01	NonCoding
TC0100013368.hg.1	PAQR7	progestin and adipoQ receptor family member VII	1.59	5.16	4.49	0.14	0.22	1.31E-02	6.40E-02	Multiple_Complex
TC0200009949.hg.1	DCAF17	DDB1 and CUL4 associated factor 17	1.59	10.44	9.77	0.33	0.04	3.42E-02	1.22E-01	Multiple_Complex
TC0X00010366.hg.1	ARMCX6	armadillo repeat containing, X-linked 6	1.59	10.99	10.32	0.34	0.41	2.94E-02	1.10E-01	Multiple_Complex
TC0400010884.hg.1	CENPC	centromere protein C	1.59	10.73	10.06	0.39	0.15	2.59E-02	1.02E-01	Multiple_Complex
TC0100014794.hg.1	ODF2L	outer dense fiber of sperm tails 2-like	1.59	12.39	11.72	0.18	0.32	2.55E-02	1.00E-01	Multiple_Complex
TSUnmapped00000248.hg.1	BCL2L14	BCL2-like 14 (apoptosis facilitator)	1.59	4.55	3.88	0.06	0.31	4.86E-02	1.54E-01	Coding
TC0800012299.hg.1	HOOK3	hook microtubule-tethering protein 3	1.59	11.17	10.51	0.18	0.24	1.30E-02	6.36E-02	Multiple_Complex
TC0X00006607.hg.1	AMELX	amelogenin, X-linked	1.59	6.42	5.75	0.35	0.18	1.74E-02	7.77E-02	Coding

TC0600011948.hg.1	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	1.59	7.58	6.91	0.09	0.19	4.78E-02	1.52E-01	Multiple_Complex
TC0600011235.hg.1	HIST1H2AM; HIST1H3J	histone cluster 1, H2am; histone cluster 1, H3j	1.59	7.66	6.99	0.38	0.1	1.99E-02	8.49E-02	Multiple_Complex
TC0200013912.hg.1	CKAP2L	cytoskeleton associated protein 2-like	1.59	9.96	9.29	0.29	0.28	1.97E-02	8.41E-02	Multiple_Complex
TC0300013458.hg.1	RPL39L	ribosomal protein L39-like	1.59	15.34	14.67	0.05	0.25	1.97E-02	8.41E-02	Coding
TC0600011564.hg.1	MLN	motilin	1.59	4.95	4.28	0.06	0.13	8.70E-03	4.90E-02	Coding
TC1700008313.hg.1	KIF2B	kinesin family member 2B	1.59	4.45	3.78	0.25	0.21	3.33E-02	1.20E-01	Coding
TC1400009225.hg.1	GMFB	glia maturation factor, beta	1.59	11.71	11.04	0	0.16	2.18E-02	8.99E-02	Multiple_Complex
TC1100013082.hg.1	PIWIL4	piwi-like RNA-mediated gene silencing 4	1.59	5.28	4.62	0.01	0	7.70E-03	4.51E-02	Multiple_Complex
TC0X00010136.hg.1	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	1.59	12.78	12.11	0.16	0.03	1.20E-02	6.03E-02	Multiple_Complex
TC1100011966.hg.1	SLC36A4	solute carrier family 36 (proton/amino acid symporter), member 4	1.59	11.29	10.62	0.03	0.02	1.17E-02	5.93E-02	Multiple_Complex
TC0600010056.hg.1	WTAP	Wilms tumor 1 associated protein	1.59	8.38	7.71	0.15	0.32	1.72E-02	7.71E-02	Multiple_Complex
TC0900011260.hg.1	ALAD	aminolevulinate dehydratase	1.59	6.52	5.85	0.3	0.28	3.61E-02	1.26E-01	Multiple_Complex
TSUnmapped00000242.hg.1	KIF15	kinesin family member 15	1.59	7.38	6.71	0.04	0.11	1.42E-02	6.77E-02	Coding
TC0900009829.hg.1	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	1.59	14.55	13.88	0.01	0.24	2.16E-02	8.96E-02	Coding
TC1300009008.hg.1	NEK3	NIMA-related kinase 3	1.59	10.41	9.75	0.29	0.15	1.88E-02	8.17E-02	Multiple_Complex
TC0800006557.hg.1	MCPH1	microcephalin 1	1.59	9.72	9.05	0.31	0.09	3.02E-02	1.12E-01	Multiple_Complex
TC1900011770.hg.1	C5AR1	complement component 5a receptor 1	1.58	7.03	6.36	0.07	0.14	2.68E-02	1.04E-01	Multiple_Complex
TC0X00010804.hg.1	ZNF280C	zinc finger protein 280C	1.58	11.81	11.14	0.07	0.16	9.90E-03	5.31E-02	Multiple_Complex
TC1400010612.hg.1	PCNXL4	pecanex-like 4 (Drosophila)	1.58	12.59	11.93	0.03	0.31	1.45E-02	6.86E-02	Multiple_Complex

TC1000006880.hg.1	PTER	phosphotriesterase related	1.58	9.89	9.22	0.27	0.3	2.34E-02	9.48E-02	Multiple_Complex
TC0500013088.hg.1	MAPK9	mitogen-activated protein kinase 9	1.58	12.79	12.12	0.1	0.11	2.34E-02	9.49E-02	Multiple_Complex
TC1300008892.hg.1	LPAR6	lysophosphatidic acid receptor 6	1.58	5.45	4.79	0.23	0.23	1.46E-02	6.88E-02	Multiple_Complex
TC0100008641.hg.1	MIER1	mesoderm induction early response 1, transcriptional regulator	1.58	12.28	11.62	0.16	0.3	1.53E-02	7.09E-02	Multiple_Complex
TC0800008145.hg.1	WWP1	WW domain containing E3 ubiquitin protein ligase 1	1.58	8.89	8.23	0.03	0.3	1.60E-02	7.33E-02	Multiple_Complex
TC0400009644.hg.1	DUX4L7	double homeobox 4 like 7	1.58	6.74	6.07	0.5	0.25	3.73E-02	1.29E-01	Multiple_Complex
TC1900012020.hg.1	ZNF432	zinc finger protein 432	1.58	7.64	6.98	0.32	0	3.41E-02	1.22E-01	Multiple_Complex
TC0500008278.hg.1	FER	fer (fps/fes related) tyrosine kinase	1.58	8.71	8.05	0	0.28	1.78E-02	7.87E-02	Multiple_Complex
TC1100006744.hg.1	OR2AG1	olfactory receptor, family 2, subfamily AG, member 1 (gene/pseudogene)	1.58	4.65	3.98	0.38	0.19	3.12E-02	1.15E-01	Multiple_Complex
TC0600007400.hg.1	ZSCAN16	zinc finger and SCAN domain containing 16	1.58	10.75	10.09	0.07	0.2	1.09E-02	5.64E-02	Coding
TC0300012392.hg.1	EFCAB12	EF-hand calcium binding domain 12	1.58	4.4	3.74	0.12	0.37	2.69E-02	1.04E-01	Multiple_Complex
TC1600007966.hg.1	MT1H	metallothionein 1H	1.58	6.1	5.44	0.09	0.17	4.06E-02	1.37E-01	Multiple_Complex
TC0400011974.hg.1	MGAT4D	MGAT4 family, member D	1.58	6.37	5.71	0.22	0.36	1.96E-02	8.40E-02	Multiple_Complex
TC0700011835.hg.1	PON2	paraoxonase 2	1.58	9.26	8.6	0.17	0.25	1.45E-02	6.86E-02	Multiple_Complex
TC1200010205.hg.1	C12orf71	chromosome 12 open reading frame 71	1.58	4.67	4.01	0.08	0.32	1.66E-02	7.52E-02	Coding
TC0100008845.hg.1	ADGRL2	adhesion G protein-coupled receptor L2	1.58	11.45	10.79	0.02	0.24	1.26E-02	6.23E-02	Multiple_Complex
TC1000009905.hg.1	C1QL3	complement component 1, q subcomponent-like 3	1.58	5.94	5.28	0.19	0	1.22E-02	6.11E-02	Multiple_Complex
TC1000008580.hg.1	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	1.58	6.06	5.4	0.03	0.13	2.45E-02	9.76E-02	Multiple_Complex
TC1400006714.hg.1	CPNE6	copine VI (neuronal)	1.58	4.34	3.67	0.11	0.58	4.05E-02	1.36E-01	Multiple_Complex
TC0700012448.hg.1	RNF133	ring finger protein 133	1.58	3.76	3.1	0.03	0.18	1.05E-02	5.52E-02	Coding
TC1400008616.hg.1	RNASE13	ribonuclease, RNase A family, 13 (non-active)	1.58	4.01	3.35	0.17	0.16	1.94E-02	8.34E-02	Coding

TC2100007175.hg.1	IGSF5	immunoglobulin superfamily, member 5	1.58	4.13	3.47	0.29	0.03	1.73E-02	7.74E-02	Multiple_Complex
TC0600014270.hg.1	GPSM3	G-protein signaling modulator 3	1.58	8.05	7.39	0.35	0.17	2.41E-02	9.66E-02	Coding
TC1200008685.hg.1	CHST11	Transcript Identified by AceView, Entrez Gene ID(s) 50515	1.58	5.47	4.81	0.1	0.34	2.06E-02	8.66E-02	Unassigned
TC0300006446.hg.1	CNTN6	contactin 6	1.58	4.93	4.27	0.08	0.33	1.76E-02	7.81E-02	Multiple_Complex
TC0500010549.hg.1	RICTOR	RPTOR independent companion of MTOR, complex 2	1.58	9.32	8.66	0.03	0.19	2.82E-02	1.07E-01	Multiple_Complex
TC1700007852.hg.1	GAST	gastrin	1.58	7	6.34	0.08	0.06	1.52E-02	7.08E-02	Multiple_Complex
TC1500007174.hg.1	EID1	EP300 interacting inhibitor of differentiation 1	1.58	11.17	10.51	0.04	0.36	2.98E-02	1.11E-01	Multiple_Complex
TSUnmapped00000289.hg.1	RPL7A	ribosomal protein L7a	1.58	7.15	6.49	0.09	0.23	1.17E-02	5.94E-02	NonCoding
TC0300010411.hg.1	HACL1	2-hydroxyacyl-CoA lyase 1	1.58	12.41	11.75	0.35	0.15	1.71E-02	7.66E-02	Multiple_Complex
TC0600009623.hg.1	ECT2L	epithelial cell transforming 2 like	1.58	4.1	3.44	0.49	0.26	4.94E-02	1.56E-01	Multiple_Complex
TC0500012206.hg.1	PROB1	proline-rich basic protein 1	1.58	8	7.35	0.46	0.03	2.89E-02	1.09E-01	Coding
TC0800012447.hg.1	AZIN1	antizyme inhibitor 1	1.58	10.96	10.3	0.23	0.16	1.60E-02	7.35E-02	Multiple_Complex
TC0600009002.hg.1	C6orf203	chromosome 6 open reading frame 203	1.58	10.1	9.44	0.14	0.16	1.25E-02	6.22E-02	Multiple_Complex
TC1500007980.hg.1	CHRNA5	cholinergic receptor, nicotinic alpha 5	1.58	10.08	9.42	0.11	0.32	2.67E-02	1.04E-01	Multiple_Complex
TC1100012638.hg.1	ZNF202	zinc finger protein 202	1.58	9.69	9.03	0.53	0.2	3.48E-02	1.23E-01	Multiple_Complex
TC1100006436.hg.1	SCGB1C1	secretoglobin, family 1C, member 1	1.58	8.16	7.5	0.22	0.09	1.30E-02	6.36E-02	Coding
TC0100013561.hg.1	FABP3	fatty acid binding protein 3, muscle and heart	1.58	4.82	4.17	0.15	0.45	3.82E-02	1.31E-01	Multiple_Complex
TC0500012153.hg.1	FAM13B	family with sequence similarity 13, member B	1.58	7.55	6.89	0.31	0.02	1.49E-02	6.98E-02	Multiple_Complex
TC1500008982.hg.1	KATNBL1	katanin p80 subunit B-like 1	1.58	8.44	7.78	0.36	0.06	2.98E-02	1.11E-01	Multiple_Complex
TC0100016437.hg.1	SLC9C2	solute carrier family 9, member C2 (putative)	1.58	3.57	2.91	0.16	0.09	1.47E-02	6.93E-02	Multiple_Complex

TC0200006912.hg.1	TDRD15	tudor domain containing 15	1.58	3.95	3.29	0.16	0.11	1.08E-02	5.63E-02	Multiple_Complex
TC0100008549.hg.1	L1TD1	LINE-1 type transposase domain containing 1	1.58	4.78	4.12	0.35	0.04	2.35E-02	9.50E-02	Multiple_Complex
TC0500008494.hg.1	CSNK1G3	casein kinase 1, gamma 3	1.58	10.51	9.86	0.45	0.16	3.27E-02	1.18E-01	Multiple_Complex
TC1700011813.hg.1	ST6GALNAC1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1	1.58	5.53	4.87	0.04	0.39	2.05E-02	8.65E-02	Multiple_Complex
TC2000006580.hg.1	RASSF2	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_014737	1.58	5.11	4.45	0.09	0.43	2.26E-02	9.23E-02	NonCoding
TC1700006679.hg.1	RPAIN	RPA interacting protein	1.58	12.78	12.12	0.22	0.31	2.31E-02	9.41E-02	Multiple_Complex
TC0800011372.hg.1	SLC25A32	solute carrier family 25 (mitochondrial folate carrier), member 32	1.58	9.64	8.99	0.03	0.17	4.23E-02	1.40E-01	Multiple_Complex
TC1600011368.hg.1	LAT	linker for activation of T-cells	1.58	6.64	5.98	0.43	0.36	4.05E-02	1.36E-01	Multiple_Complex
TC0700008190.hg.1	CD36	CD36 molecule (thrombospondin receptor)	1.58	4.6	3.94	0.07	0.14	3.32E-02	1.20E-01	Multiple_Complex
TC1200007430.hg.1	SCAF11	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_004719	1.58	11.72	11.06	0.13	0.04	1.54E-02	7.14E-02	NonCoding
TC0600007595.hg.1	LTA	lymphotoxin alpha	1.58	5.18	4.53	0.24	0.28	1.74E-02	7.76E-02	Multiple_Complex
TC0200006833.hg.1	GEN1	GEN1 Holliday junction 5 flap endonuclease	1.58	8.67	8.02	0.46	0.37	3.80E-02	1.31E-01	Multiple_Complex
TC0700011645.hg.1	CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	1.58	6.72	6.07	0.29	0.1	2.90E-02	1.09E-01	Multiple_Complex
TC0700006913.hg.1	GPNMB	glycoprotein (transmembrane) nmb	1.58	6.71	6.05	0.18	0.16	3.05E-02	1.13E-01	Multiple_Complex
TC0800012288.hg.1	DCTN6	dynactin 6	1.58	12.05	11.39	0.07	0.14	1.24E-02	6.19E-02	Multiple_Complex
TC0100008414.hg.1	TMEM61	transmembrane protein 61	1.58	7.47	6.81	0.08	0.16	1.65E-02	7.48E-02	Coding
TC0300007164.hg.1	SS18L2	synovial sarcoma translocation gene on chromosome 18-like 2	1.57	13.15	12.49	0.3	0.26	3.22E-02	1.17E-01	Multiple_Complex

TC0900009970.hg.1	OR13C7	olfactory receptor, family 13, subfamily C, member 7 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:15102]	1.57	4.75	4.09	0.53	0.22	4.85E-02	1.54E-01	Pseudogene
TC1700008703.hg.1	NOL11	nucleolar protein 11	1.57	13.42	12.77	0.1	0.16	1.18E-02	5.97E-02	Multiple_Complex
TC1400007608.hg.1	RGS6	regulator of G-protein signaling 6	1.57	4.22	3.56	0.17	0.28	1.67E-02	7.56E-02	NonCoding
TC0900011029.hg.1	BAAT	bile acid-CoA:amino acid N-acyltransferase	1.57	5.71	5.06	0.54	0.37	4.36E-02	1.43E-01	Coding
TC0600011315.hg.1	ZFP57	ZFP57 zinc finger protein	1.57	4.02	3.36	0.03	0.13	1.83E-02	8.03E-02	Multiple_Complex
TC1100008786.hg.1	CEP295	centrosomal protein 295kDa	1.57	10.01	9.36	0.12	0.05	1.41E-02	6.73E-02	Multiple_Complex
TC0600010017.hg.1	TMEM181	transmembrane protein 181	1.57	9.27	8.62	0.34	0.25	2.28E-02	9.31E-02	Multiple_Complex
TC0600011067.hg.1	TDP2	tyrosyl-DNA phosphodiesterase 2	1.57	9.24	8.59	0.61	0.06	4.05E-02	1.36E-01	Multiple_Complex
TC0X00006775.hg.1	PHEX	phosphate regulating endopeptidase homolog, X-linked	1.57	5.95	5.3	0.1	0.38	2.63E-02	1.02E-01	Multiple_Complex
TC0200010219.hg.1	FAM171B	family with sequence similarity 171, member B	1.57	10.19	9.53	0.16	0.13	2.11E-02	8.82E-02	Multiple_Complex
TC0300014049.hg.1	ACAD11	acyl-CoA dehydrogenase family, member 11	1.57	9.59	8.94	0.1	0.12	4.81E-02	1.53E-01	Multiple_Complex
TC1600007424.hg.1	ZG16	zymogen granule protein 16	1.57	6.86	6.21	0.39	0.17	3.17E-02	1.16E-01	Multiple_Complex
TC1800008550.hg.1	SYT4	synaptotagmin IV	1.57	4.54	3.89	0.5	0.36	4.22E-02	1.40E-01	Multiple_Complex
TC0400008902.hg.1	ABCE1	ATP binding cassette subfamily E member 1	1.57	12.82	12.17	0.2	0.15	1.76E-02	7.82E-02	Multiple_Complex
TC1900006436.hg.1	OR4F17	olfactory receptor, family 4, subfamily F, member 17	1.57	5.56	4.9	0.01	0.03	8.70E-03	4.88E-02	Multiple_Complex
TC1500007180.hg.1	GALK2	galactokinase 2	1.57	7.45	6.8	0.29	0.29	2.75E-02	1.06E-01	Multiple_Complex
TC0400007769.hg.1	CSN1S1	casein alpha s1	1.57	4.5	3.85	0.37	0.12	2.17E-02	8.97E-02	Coding
TC0X00011402.hg.1	SPANXA1	sperm protein associated with the nucleus, X-linked, family member A1	1.57	8.07	7.42	0.67	0.06	4.61E-02	1.49E-01	Coding

TC1700006939.hg.1	COX10	COX10 heme A:farnesyltransferase cytochrome c oxidase assembly factor	1.57	10.77	10.12	0.58	0.26	5.00E-02	1.57E-01	Multiple_Complex
TSUnmapped00000050.hg.1	MLXIP	MLX interacting protein	1.57	6.18	5.53	0.25	0.14	4.30E-02	1.42E-01	Coding
TC1100011930.hg.1	CHORDC1	cysteine and histidine rich domain containing 1	1.57	12.68	12.03	0.2	0.08	1.48E-02	6.97E-02	Multiple_Complex
TC1000012025.hg.1	MCMBP	minichromosome maintenance complex binding protein	1.57	11.03	10.38	0.12	0.09	1.50E-02	7.02E-02	Multiple_Complex
TC1200007959.hg.1	MON2	MON2 homolog, regulator of endosome-to-Golgi trafficking	1.57	11.25	10.6	0.11	0.23	2.93E-02	1.10E-01	Multiple_Complex
TC0700006632.hg.1	OCM	oncomodulin	1.57	5.65	5	0.49	0.04	4.57E-02	1.48E-01	Coding
TC0500011984.hg.1	HINT1	histidine triad nucleotide binding protein 1	1.57	13.88	13.23	0.59	0.02	4.17E-02	1.39E-01	Multiple_Complex
TC0100008023.hg.1	PPIH	peptidylprolyl isomerase H (cyclophilin H)	1.57	11.56	10.91	0.39	0.12	2.87E-02	1.09E-01	Multiple_Complex
TC0100008697.hg.1	CTH	cystathionine gamma-lyase	1.57	11.86	11.21	0.1	0.02	9.50E-03	5.19E-02	Multiple_Complex
TC0200010580.hg.1	LOC200726; AC010731.4	hCG1657980; Transcript Identified by AceView, Entrez Gene ID(s) 200726, RefSeq ID(s) NM_001102659; novel transcript	1.57	4.65	4	0.51	0.1	2.96E-02	1.11E-01	Multiple_Complex
TC1700007419.hg.1	TAOK1; MIR4523	TAO kinase 1; microRNA 4523	1.57	13.52	12.87	0.21	0.4	2.63E-02	1.03E-01	Multiple_Complex
TC0700013421.hg.1	ZNF789	zinc finger protein 789	1.57	8.94	8.29	0.2	0.16	2.77E-02	1.06E-01	Multiple_Complex
TC0500007890.hg.1	PAPD4	PAP associated domain containing 4	1.57	11.11	10.46	0.02	0	9.30E-03	5.10E-02	Multiple_Complex
TC1700006432.hg.1	SCGB1C2	secretoglobin, family 1C, member 2	1.57	8.12	7.47	0.33	0.12	1.93E-02	8.32E-02	Coding
TC0Y00006487.hg.1	ZFY	zinc finger protein, Y-linked	1.57	7.94	7.29	0.15	0.05	1.32E-02	6.43E-02	Multiple_Complex
TC1600007958.hg.1	MT1L	metallothionein 1L (gene/pseudogene)	1.57	9.11	8.46	0.14	0.01	1.31E-02	6.40E-02	Multiple_Complex
TC1900012051.hg.1	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	1.57	4.51	3.87	0.37	0.06	2.52E-02	9.95E-02	Multiple_Complex

TC1700010670.hg.1	KRT38	keratin 38, type I	1.57	5.19	4.54	0.04	0.04	1.19E-02	6.02E-02	Coding
TC0400008119.hg.1	TIGD2	tigger transposable element derived 2	1.57	7.25	6.61	0.39	0.07	4.00E-02	1.35E-01	Multiple_Complex
TC1400010768.hg.1	MED6	mediator complex subunit 6	1.57	12.75	12.11	0.19	0.23	1.69E-02	7.62E-02	Multiple_Complex
TC1400010628.hg.1	YLPM1	YLP motif containing 1	1.56	5.32	4.67	0.1	0.04	2.45E-02	9.76E-02	NonCoding
TC1700012333.hg.1	TRPV3	transient receptor potential cation channel, subfamily V, member 3	1.56	5.37	4.72	0.15	0.08	1.15E-02	5.88E-02	Multiple_Complex
TC0200014703.hg.1	CCDC148	coiled-coil domain containing 148	1.56	8.12	7.48	0.22	0.33	2.21E-02	9.09E-02	Multiple_Complex
TC0200010966.hg.1	RHBDD1	rhomboid domain containing 1	1.56	9.24	8.59	0.08	0.06	2.02E-02	8.56E-02	Multiple_Complex
TC0600011287.hg.1	ZNF311	zinc finger protein 311	1.56	4.4	3.75	0.35	0.11	2.33E-02	9.44E-02	Multiple_Complex
TC0500009400.hg.1	KCNIP1	Kv channel interacting protein 1	1.56	4.61	3.96	0.26	0.03	4.29E-02	1.42E-01	Multiple_Complex
TC0100017059.hg.1	RBBP5	retinoblastoma binding protein 5	1.56	10.82	10.17	0.2	0	1.35E-02	6.55E-02	Multiple_Complex
TC1500009204.hg.1	UBR1	ubiquitin protein ligase E3 component n-recognin 1	1.56	12.65	12.01	0.01	0.14	1.04E-02	5.49E-02	Multiple_Complex
TC0400012366.hg.1	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	1.56	4.94	4.3	0.22	0.08	3.44E-02	1.22E-01	Multiple_Complex
TC0800011621.hg.1	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.56	5.14	4.49	0.56	0.35	4.80E-02	1.53E-01	NonCoding
TC0900011176.hg.1	C9orf152	chromosome 9 open reading frame 152	1.56	6.62	5.98	0.09	0.23	1.34E-02	6.51E-02	Multiple_Complex
TC1700008573.hg.1	DDX42	DEAD (Asp-Glu-Ala-Asp) box helicase 42	1.56	12.2	11.55	0.32	0.06	2.39E-02	9.61E-02	Multiple_Complex
TC1500010390.hg.1	RHCG	Rh family, C glycoprotein	1.56	4.49	3.84	0.23	0.04	1.76E-02	7.81E-02	Multiple_Complex
TC1000007986.hg.1	ANAPC16	anaphase promoting complex subunit 16	1.56	14.72	14.08	0.14	0.13	1.55E-02	7.17E-02	Multiple_Complex
TC1600011566.hg.1	TMEM170A	transmembrane protein 170A	1.56	11.71	11.07	0.21	0.2	2.78E-02	1.06E-01	Multiple_Complex
TC2200009278.hg.1	RBX1	ring-box 1, E3 ubiquitin protein ligase	1.56	16.12	15.47	0.08	0.14	2.05E-02	8.64E-02	Multiple_Complex
TC0900006451.hg.1	DMRT1	doublesex and mab-3 related transcription factor 1	1.56	4.83	4.19	0.34	0.17	2.11E-02	8.79E-02	Multiple_Complex

TC0700009068.hg.1	LOC100130705; RP11-309L24.4	uncharacterized LOC100130705; putative novel transcript	1.56	6.28	5.64	0.19	0.33	2.77E-02	1.06E-01	Multiple_Complex
TC0100011487.hg.1	TRAF5	TNF receptor-associated factor 5	1.56	6.61	5.97	0.39	0.06	3.49E-02	1.23E-01	Multiple_Complex
TC0500007754.hg.1	TNPO1	transportin 1	1.56	10.92	10.28	0.33	0.21	2.09E-02	8.74E-02	Multiple_Complex
TC2100007968.hg.1	C21orf62	chromosome 21 open reading frame 62	1.56	5.15	4.51	0.07	0.4	2.81E-02	1.07E-01	Multiple_Complex
TC1700007645.hg.1	CTB-75G16.3; MRM1	Transcript Identified by AceView, Entrez Gene ID(s) 79922; novel transcript	1.56	6.23	5.58	0.42	0.03	2.42E-02	9.68E-02	Multiple_Complex
TC0100013920.hg.1	C1orf210	chromosome 1 open reading frame 210	1.56	6.9	6.26	0.48	0.13	3.77E-02	1.30E-01	Coding
TC1500010910.hg.1	RPS17	ribosomal protein S17	1.56	15.34	14.69	0.14	0.02	1.56E-02	7.19E-02	Multiple_Complex
TC0700008659.hg.1	NFE4	nuclear factor, erythroid 4	1.56	6.17	5.53	0.41	0.11	2.33E-02	9.44E-02	Multiple_Complex
TC0900008441.hg.1	UGCG	UDP-glucose ceramide glucosyltransferase	1.56	6.01	5.36	0.3	0.09	4.37E-02	1.43E-01	Multiple_Complex
TC0500013388.hg.1	HAVCR2	hepatitis A virus cellular receptor 2	1.56	5.41	4.77	0.24	0.21	4.00E-02	1.35E-01	Multiple_Complex
TC0400012934.hg.1	SDAD1	SDA1 domain containing 1	1.56	11.12	10.47	0.14	0.04	1.08E-02	5.63E-02	Multiple_Complex
TC1100013000.hg.1	CLP1; AP000662.4	Transcript Identified by AceView, Entrez Gene ID(s) 10978; novel transcript, sense overlapping CLP1	1.56	4.77	4.12	0.13	0.05	3.68E-02	1.28E-01	NonCoding
TC0400009198.hg.1	APELA	apelin receptor early endogenous ligand	1.56	5.8	5.16	0.08	0.08	2.60E-02	1.02E-01	Multiple_Complex
TC0300007051.hg.1	ITGA9	integrin alpha 9	1.56	4.76	4.12	0.05	0.02	1.52E-02	7.07E-02	Multiple_Complex
TC0600007284.hg.1	HIST1H4E	histone cluster 1, H4e	1.56	15.38	14.74	0.1	0	1.22E-02	6.11E-02	Multiple_Complex
TC1200012696.hg.1	MRPL42	mitochondrial ribosomal protein L42	1.56	15.55	14.91	0.01	0.17	1.47E-02	6.93E-02	Multiple_Complex
TC1500007529.hg.1	USP3	ubiquitin specific peptidase 3	1.56	11.94	11.31	0.02	0.17	1.69E-02	7.62E-02	Multiple_Complex
TC0900006961.hg.1	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	1.56	14	13.36	0.2	0.05	1.50E-02	7.03E-02	Multiple_Complex
TC0300007711.hg.1	SLC25A26	solute carrier family 25 (S-adenosylmethionine carrier), member 26	1.56	12.72	12.08	0.22	0.18	2.81E-02	1.07E-01	Multiple_Complex

TC1700007262.hg.1	MAP2K3	mitogen-activated protein kinase kinase 3	1.56	5.7	5.06	0.44	0.01	4.56E-02	1.47E-01	Multiple_Complex
TC1000008447.hg.1	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	1.56	11.47	10.84	0.1	0.04	1.37E-02	6.62E-02	Multiple_Complex
TC1100013164.hg.1	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	1.56	6.35	5.71	0.16	0.4	3.41E-02	1.22E-01	Multiple_Complex
TC1200008541.hg.1	CFAP54	cilia and flagella associated 54	1.56	6.91	6.27	0.29	0.03	2.73E-02	1.05E-01	Multiple_Complex
TC1600006577.hg.1	RNF151	ring finger protein 151	1.56	5.69	5.05	0.3	0.45	3.56E-02	1.25E-01	Coding
TC0500011754.hg.1	TMED7-TICAM2; TICAM2; TMED7	TMED7-TICAM2 readthrough; toll-like receptor adaptor molecule 2; transmembrane p24 trafficking protein 7	1.56	12.87	12.24	0.25	0.07	1.56E-02	7.20E-02	Multiple_Complex
TC0800012452.hg.1	EIF3E	eukaryotic translation initiation factor 3, subunit E	1.56	4.72	4.09	0.2	0.37	4.32E-02	1.42E-01	Multiple_Complex
TC0800006866.hg.1	VPS37A	vacuolar protein sorting 37 homolog A (S. cerevisiae)	1.56	9.92	9.28	0.12	0.27	3.81E-02	1.31E-01	Multiple_Complex
TC1500007056.hg.1	ADAL	adenosine deaminase-like	1.55	10.72	10.08	0.22	0.37	2.86E-02	1.08E-01	Multiple_Complex
TC0200014719.hg.1	BAZ2B	bromodomain adjacent to zinc finger domain 2B	1.55	10.3	9.66	0.06	0.23	4.25E-02	1.41E-01	Multiple_Complex
TC0500013399.hg.1	PANK3	pantothenate kinase 3	1.55	10.3	9.66	0.17	0.36	2.39E-02	9.61E-02	Multiple_Complex
TC0900007047.hg.1	DNAI1	dynein, axonemal, intermediate chain 1	1.55	6.02	5.38	0.41	0.13	3.10E-02	1.14E-01	Multiple_Complex
TC1900009404.hg.1	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	1.55	6.75	6.11	0.56	0.21	4.48E-02	1.46E-01	Multiple_Complex
TC1900011916.hg.1	ZNF626	zinc finger protein 626	1.55	8.74	8.1	0.3	0.26	2.33E-02	9.46E-02	Multiple_Complex
TC0300014052.hg.1	RYK	receptor-like tyrosine kinase	1.55	13.05	12.42	0.13	0.44	3.40E-02	1.21E-01	Multiple_Complex
TC0300011171.hg.1	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	1.55	7.31	6.68	0.37	0.27	3.10E-02	1.14E-01	Multiple_Complex
TC1100007026.hg.1	ZDHHC13	zinc finger, DHHC-type containing 13	1.55	11.91	11.28	0.01	0.11	1.98E-02	8.45E-02	Multiple_Complex

TC1900011697.hg.1	ZNF730	zinc finger protein 730	1.55	7.2	6.56	0.21	0.07	2.59E-02	1.02E-01	Multiple_Complex
TC1200011367.hg.1	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	1.55	10.82	10.18	0.32	0.1	3.67E-02	1.27E-01	Multiple_Complex
TC1000007067.hg.1	MYO3A	myosin IIIA	1.55	11	10.36	0.02	0.15	3.37E-02	1.21E-01	Multiple_Complex
TC1100011605.hg.1	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	1.55	6.17	5.53	0.11	0.11	3.74E-02	1.29E-01	Multiple_Complex
TC0100014152.hg.1	FAF1	Fas (TNFRSF6) associated factor 1	1.55	11.66	11.03	0.45	0.24	4.69E-02	1.50E-01	Multiple_Complex
TC1200010983.hg.1	AVIL	advillin	1.55	5.98	5.35	0.06	0.45	4.75E-02	1.52E-01	Multiple_Complex
TC1700010830.hg.1	ITGA2B	integrin alpha 2b	1.55	6.08	5.45	0.31	0.09	4.96E-02	1.56E-01	Multiple_Complex
TC0600013258.hg.1	AHI1	Abelson helper integration site 1	1.55	11.35	10.72	0.19	0.07	2.16E-02	8.94E-02	Multiple_Complex
TC0200015424.hg.1	ALS2CR12	amyotrophic lateral sclerosis 2 chromosome region candidate 12	1.55	5.66	5.03	0.28	0.07	2.19E-02	9.05E-02	Multiple_Complex
TC1200012599.hg.1	AEBP2	AE binding protein 2	1.55	13.26	12.62	0.09	0.15	1.36E-02	6.57E-02	Multiple_Complex
TC0300008804.hg.1	TRH	thyrotropin-releasing hormone	1.55	5.67	5.03	0.01	0.08	2.06E-02	8.68E-02	Coding
TC2100007796.hg.1	MRPL39	mitochondrial ribosomal protein L39	1.55	13.23	12.59	0.05	0.09	1.34E-02	6.49E-02	Multiple_Complex
TC0500012523.hg.1	ATOX1	antioxidant 1 copper chaperone	1.55	10.79	10.16	0.07	0.39	2.56E-02	1.01E-01	Multiple_Complex
TC1400010169.hg.1	SETD3	SET domain containing 3	1.55	12.04	11.4	0.01	0.27	1.97E-02	8.41E-02	Multiple_Complex
TC0400009223.hg.1	CPE	carboxypeptidase E	1.55	9.48	8.84	0.33	0.34	3.53E-02	1.24E-01	Coding
TC0X00010525.hg.1	TRPC5	transient receptor potential cation channel, subfamily C, member 5	1.55	4.81	4.17	0.58	0.17	4.34E-02	1.43E-01	Coding
TC0Y00006954.hg.1	AMELY	amelogenin, Y-linked	1.55	5.35	4.72	0.04	0.51	3.67E-02	1.27E-01	Coding
TC0500013224.hg.1	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	1.55	6.49	5.86	0	0.5	3.54E-02	1.24E-01	Coding
TC1000008769.hg.1	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	1.55	9.31	8.67	0.22	0.32	2.26E-02	9.24E-02	Multiple_Complex

TC0400010681.hg.1	LRRC66	leucine rich repeat containing 66	1.55	5.29	4.66	0.38	0.32	4.94E-02	1.56E-01	Coding
TC0600011903.hg.1	MRPL14	mitochondrial ribosomal protein L14	1.55	13.86	13.23	0.08	0.14	2.13E-02	8.87E-02	Multiple_Complex
TC0700010396.hg.1	TWISTNB	TWIST neighbor	1.55	12.52	11.89	0.05	0.1	1.26E-02	6.26E-02	Multiple_Complex
TC0400012381.hg.1	NEK1	NIMA-related kinase 1	1.55	10.5	9.87	0.15	0.18	2.76E-02	1.06E-01	Multiple_Complex
TC0100016316.hg.1	ADCY10	adenylate cyclase 10 (soluble)	1.55	5.51	4.88	0.45	0.02	3.51E-02	1.24E-01	Multiple_Complex
TC0700011813.hg.1	BET1	Bet1 golgi vesicular membrane trafficking protein	1.55	13.27	12.64	0.04	0.23	4.19E-02	1.39E-01	Multiple_Complex
TC1000008088.hg.1	SAMD8	sterile alpha motif domain containing 8	1.55	8.59	7.96	0.21	0.5	4.43E-02	1.45E-01	Multiple_Complex
TC1300008894.hg.1	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	1.55	5.72	5.09	0.02	0.26	1.71E-02	7.67E-02	Multiple_Complex
TC0400012902.hg.1	FGFBP2	fibroblast growth factor binding protein 2	1.55	4.53	3.9	0.37	0.05	3.02E-02	1.12E-01	Coding
TC1200012267.hg.1	SBNO1; MIR8072	strawberry notch homolog 1 (Drosophila); microRNA 8072	1.55	9.53	8.9	0.18	0.15	1.48E-02	6.96E-02	Multiple_Complex
TC0600013425.hg.1	ADAT2	adenosine deaminase, tRNA-specific 2	1.55	11.68	11.05	0.02	0.11	2.30E-02	9.36E-02	Multiple_Complex
TC1900009442.hg.1	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	1.55	4.72	4.09	0.19	0.36	4.43E-02	1.45E-01	Multiple_Complex
TC0X00008198.hg.1	PLS3	plastin 3	1.55	14.49	13.86	0.03	0.04	1.50E-02	7.01E-02	Multiple_Complex
TC1400006571.hg.1	OR4E2	olfactory receptor, family 4, subfamily E, member 2	1.55	4.11	3.48	0.04	0.02	2.14E-02	8.88E-02	Coding
TC0500010780.hg.1	SLC38A9	Transcript Identified by AceView, Entrez Gene ID(s) 153129	1.55	6.46	5.84	0.21	0.13	2.10E-02	8.78E-02	Unassigned
TC1700009489.hg.1	ITGAE	integrin alpha E	1.55	15.27	14.64	0.02	0.06	2.20E-02	9.06E-02	Multiple_Complex
TC0400007831.hg.1	AFP	alpha-fetoprotein	1.55	4.14	3.51	0.14	0.24	3.81E-02	1.31E-01	Multiple_Complex
TC0200007907.hg.1	GKN1	gastrokine 1	1.54	4.24	3.61	0.33	0.03	3.06E-02	1.13E-01	Multiple_Complex
TC0X00010962.hg.1	MCF2	MCF.2 cell line derived transforming sequence	1.54	5.52	4.89	0.44	0.15	3.82E-02	1.31E-01	Multiple_Complex

TC1700011574.hg.1	ABCA8	ATP binding cassette subfamily A member 8	1.54	5.87	5.24	0.05	0.12	2.88E-02	1.09E-01	Multiple_Complex
TC0400010618.hg.1	TEC	tec protein tyrosine kinase	1.54	6.42	5.79	0.32	0.25	2.47E-02	9.80E-02	Multiple_Complex
TC0200008819.hg.1	SOWAHC	sosondowah ankyrin repeat domain family member C	1.54	5.61	4.99	0.07	0.59	4.43E-02	1.45E-01	Coding
TC0300012164.hg.1	POLQ	polymerase (DNA directed), theta	1.54	9.95	9.33	0.02	0.19	1.38E-02	6.65E-02	Multiple_Complex
TC0600010512.hg.1	LINC01600	long intergenic non-protein coding RNA 1600	1.54	5.42	4.8	0.44	0.05	3.39E-02	1.21E-01	Multiple_Complex
TC0400012780.hg.1	PI4K2B	phosphatidylinositol 4-kinase type 2 beta	1.54	7.52	6.9	0.36	0.21	3.87E-02	1.32E-01	Multiple_Complex
TC1700011281.hg.1	SKA2	spindle and kinetochore associated complex subunit 2	1.54	14.51	13.88	0.03	0.12	1.38E-02	6.65E-02	Multiple_Complex
TC1000006859.hg.1	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	1.54	12	11.38	0.11	0.19	1.70E-02	7.64E-02	Multiple_Complex
TC1200006862.hg.1	BCL2L14	BCL2-like 14 (apoptosis facilitator)	1.54	6.02	5.39	0.23	0.22	1.98E-02	8.46E-02	Multiple_Complex
TC1200010635.hg.1	FAM186B	family with sequence similarity 186, member B	1.54	5.93	5.31	0.43	0.26	4.43E-02	1.45E-01	Multiple_Complex
TC0700012590.hg.1	ZC3HC1	zinc finger, C3HC-type containing 1	1.54	9.37	8.74	0.02	0.21	2.17E-02	8.99E-02	Multiple_Complex
TC0200007348.hg.1	PKDCC	protein kinase domain containing, cytoplasmic	1.54	6.96	6.33	0.03	0.2	1.43E-02	6.83E-02	Multiple_Complex
TC2100008200.hg.1	PLAC4	placenta specific 4	1.54	5.72	5.1	0.17	0.3	4.67E-02	1.50E-01	Multiple_Complex
TC1700010190.hg.1	IFT20	intraflagellar transport 20	1.54	11.36	10.74	0.21	0.21	2.67E-02	1.04E-01	Multiple_Complex
TC1400009256.hg.1	ATG14	autophagy related 14	1.54	9.78	9.16	0.23	0.13	4.52E-02	1.47E-01	Multiple_Complex
TC0100010672.hg.1	RABGAP1L	RAB GTPase activating protein 1-like	1.54	8.44	7.82	0.25	0	3.19E-02	1.16E-01	Multiple_Complex
TC0100014428.hg.1	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	1.54	15.62	15	0.01	0.01	3.63E-02	1.26E-01	Multiple_Complex
TC1100009302.hg.1	TECTA	tectorin alpha	1.54	6.74	6.12	0.27	0.37	4.74E-02	1.51E-01	Multiple_Complex
TC1300007167.hg.1	PHF11	PHD finger protein 11	1.54	7.12	6.5	0.11	0.16	3.25E-02	1.18E-01	Multiple_Complex
TC1000008452.hg.1	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa	1.54	7.96	7.34	0.45	0.23	3.72E-02	1.29E-01	Multiple_Complex

TC0200006648.hg.1	IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog	1.54	13.54	12.92	0.01	0.07	4.92E-02	1.55E-01	Multiple_Complex
TC1300009505.hg.1	ABCC4	ATP binding cassette subfamily C member 4	1.54	8.53	7.91	0.08	0.07	1.38E-02	6.65E-02	Multiple_Complex
TC1700009417.hg.1	SMG6	SMG6 nonsense mediated mRNA decay factor	1.54	7.51	6.88	0.33	0.02	2.68E-02	1.04E-01	Multiple_Complex
TC0200012643.hg.1	CCDC88A	coiled-coil domain containing 88A	1.54	12.87	12.25	0.1	0.18	2.08E-02	8.74E-02	Multiple_Complex
TC0100011272.hg.1	ZBED6; ZC3H11A	zinc finger, BED-type containing 6; zinc finger CCCH-type containing 11A	1.54	13.61	12.99	0.09	0.35	2.31E-02	9.38E-02	Multiple_Complex
TC1100006840.hg.1	CTR9	CTR9 homolog, Paf1/RNA polymerase II complex component	1.54	11.96	11.34	0.27	0.12	1.82E-02	8.01E-02	Multiple_Complex
TC0100013902.hg.1	SVBP	small vasohibin binding protein	1.54	7.55	6.93	0.16	0.13	3.43E-02	1.22E-01	Multiple_Complex
TC1400010636.hg.1	SLIRP	SRA stem-loop interacting RNA binding protein	1.54	16.76	16.14	0.05	0.15	1.64E-02	7.46E-02	Multiple_Complex
TC0100016263.hg.1	TMCO1	transmembrane and coiled-coil domains 1	1.54	13.18	12.56	0.32	0.16	3.19E-02	1.16E-01	Multiple_Complex
TC1000012536.hg.1	MPP7	membrane protein, palmitoylated 7	1.54	7.29	6.67	0.29	0.36	3.79E-02	1.30E-01	Multiple_Complex
TC0500013236.hg.1	FAM53C	family with sequence similarity 53, member C	1.54	5.97	5.35	0.21	0.21	3.10E-02	1.14E-01	NonCoding
TC1000008471.hg.1	KIF11	kinesin family member 11	1.54	10.7	10.08	0.04	0.18	1.47E-02	6.95E-02	Multiple_Complex
TC2000007864.hg.1	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	1.54	6.64	6.02	0.11	0.1	1.51E-02	7.04E-02	Multiple_Complex
TC1200008629.hg.1	DRAM1	DNA-damage regulated autophagy modulator 1	1.53	8.03	7.41	0.54	0.09	4.08E-02	1.37E-01	Multiple_Complex
TC0600006870.hg.1	SNRNP48	small nuclear ribonucleoprotein, U11/U12 48KDa subunit	1.53	11.41	10.79	0.1	0.3	2.94E-02	1.10E-01	Multiple_Complex
TC0800012277.hg.1	SFTPC	surfactant protein C	1.53	6.12	5.5	0.02	0.29	1.88E-02	8.17E-02	Multiple_Complex
TC0400007617.hg.1	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	1.53	13.86	13.24	0.02	0.12	1.53E-02	7.10E-02	Multiple_Complex
TC0200016444.hg.1	MSH6	mutS homolog 6	1.53	4.98	4.36	0.01	0.11	1.46E-02	6.88E-02	NonCoding
TC0500013231.hg.1	CATSPER3	cation channel, sperm associated 3	1.53	6.12	5.5	0.17	0.26	2.12E-02	8.83E-02	Multiple_Complex

TC0300009167.hg.1	EIF2A	eukaryotic translation initiation factor 2A, 65kDa	1.53	9.35	8.73	0.07	0.21	2.57E-02	1.01E-01	Multiple_Complex
TC0X00010800.hg.1	ELF4	Memczak2013 ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001421	1.53	6.91	6.29	0.41	0.32	4.55E-02	1.47E-01	NonCoding
TC0200013298.hg.1	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1.53	7.89	7.27	0.01	0.13	3.56E-02	1.25E-01	Multiple_Complex
TC1900011920.hg.1	ZNF98	zinc finger protein 98	1.53	10.16	9.54	0.2	0.05	3.33E-02	1.20E-01	Multiple_Complex
TC0400007466.hg.1	CWH43	cell wall biogenesis 43 C-terminal homolog	1.53	4.3	3.69	0.1	0.24	1.76E-02	7.82E-02	Multiple_Complex
TC0600008875.hg.1	FHL5	four and a half LIM domains 5	1.53	4.41	3.79	0.3	0.27	4.88E-02	1.54E-01	Coding
TC0600011642.hg.1	CLPS	colipase, pancreatic	1.53	6.46	5.84	0.28	0.16	2.63E-02	1.03E-01	Multiple_Complex
TC0900009910.hg.1	ARID3C	AT rich interactive domain 3C (BRIGHT-like)	1.53	4.58	3.97	0.43	0.02	2.99E-02	1.11E-01	Coding
TC0200008573.hg.1	UNC50	unc-50 homolog (C. elegans)	1.53	13.35	12.73	0.26	0.2	2.43E-02	9.69E-02	Multiple_Complex
TC1800007446.hg.1	SEC11C	SEC11 homolog C, signal peptidase complex subunit	1.53	10.01	9.4	0.32	0.23	3.64E-02	1.27E-01	Multiple_Complex
TC0600008050.hg.1	UBR2	ubiquitin protein ligase E3 component n-recognin 2	1.53	9.38	8.76	0.14	0.02	1.48E-02	6.96E-02	Multiple_Complex
TC1400008645.hg.1	OR4E1	olfactory receptor family 4 subfamily E member 1 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:8296]	1.53	5.06	4.45	0.18	0.08	4.12E-02	1.38E-01	Pseudogene
TC1100012140.hg.1	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5	1.53	12.62	12	0.2	0.1	2.16E-02	8.94E-02	Multiple_Complex
TC2200006432.hg.1	BAGE5	Synthetic construct Homo sapiens clone IMAGE:100062553, MGC:190557 B melanoma antigen family, member 5 (BAGE5) mRNA, encodes complete protein.; B melanoma antigen family, member 5 [Source:EntrezGene;Acc:85316]	1.53	7.8	7.19	0.07	0.09	2.82E-02	1.07E-01	Multiple_Complex
TC1300008873.hg.1	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	1.53	7.84	7.22	0.07	0.37	2.82E-02	1.07E-01	Multiple_Complex

TC0500012526.hg.1	GLRA1	glycine receptor alpha 1	1.53	4.33	3.71	0.14	0.19	2.62E-02	1.02E-01	Multiple_Complex
TC1100013066.hg.1	KRTAP5-10	keratin associated protein 5-10	1.53	6.31	5.7	0.28	0.07	3.80E-02	1.31E-01	Coding
TC0300011943.hg.1	KIAA1524	KIAA1524	1.53	10.85	10.23	0.27	0.43	4.38E-02	1.44E-01	Multiple_Complex
TC1500007392.hg.1	CCNB2	cyclin B2	1.53	12.32	11.71	0.15	0.12	1.50E-02	7.01E-02	Multiple_Complex
TC0600007169.hg.1	HDGFL1	hepatoma derived growth factor-like 1	1.53	4.58	3.97	0.03	0.15	1.45E-02	6.87E-02	Coding
TC0700011886.hg.1	OCM2	oncomodulin 2	1.53	8.15	7.54	0.37	0.21	4.65E-02	1.50E-01	Multiple_Complex
TC0X00007562.hg.1	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	1.53	5.23	4.62	0.06	0.12	3.96E-02	1.34E-01	Multiple_Complex
TC0500012631.hg.1	EBF1	early B-cell factor 1	1.53	5.68	5.07	0.37	0.16	3.00E-02	1.12E-01	Multiple_Complex
TC1600007183.hg.1	UQCRC2	ubiquinol-cytochrome c reductase core protein II	1.53	13.33	12.72	0.36	0.07	2.48E-02	9.84E-02	Multiple_Complex
TC1000011740.hg.1	COL17A1; MIR936	collagen, type XVII, alpha 1; microRNA 936	1.53	5.25	4.64	0.18	0.4	3.05E-02	1.13E-01	Multiple_Complex
TC1700006770.hg.1	DNAH2	dynein, axonemal, heavy chain 2	1.53	4.24	3.63	0.12	0.04	2.13E-02	8.85E-02	Multiple_Complex
TC0700013525.hg.1	FAM126A	family with sequence similarity 126, member A	1.53	4.49	3.88	0.04	0.06	1.35E-02	6.54E-02	NonCoding
TC0900010444.hg.1	CARNMT1	carnosine N-methyltransferase 1	1.53	13.57	12.96	0.14	0.09	2.27E-02	9.28E-02	Multiple_Complex
TC0100007789.hg.1	AGO3	argonaute RISC catalytic component 3	1.53	11.31	10.7	0.01	0.02	1.52E-02	7.09E-02	Multiple_Complex
TC0900012246.hg.1	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	1.53	3.81	3.2	0.13	0.09	1.85E-02	8.08E-02	NonCoding
TC2000007325.hg.1	ADIG	adipogenin	1.53	4.56	3.95	0.34	0.15	4.44E-02	1.45E-01	Multiple_Complex
TC0100014250.hg.1	TMEM59	transmembrane protein 59	1.53	15.53	14.92	0.02	0.11	2.32E-02	9.44E-02	Multiple_Complex
TC0500013366.hg.1	LECT2	leukocyte cell-derived chemotaxin 2	1.52	4.34	3.73	0.24	0.18	2.85E-02	1.08E-01	Multiple_Complex
TC1700012339.hg.1	NUP88	nucleoporin 88kDa	1.52	6.18	5.57	0.05	0.12	2.16E-02	8.95E-02	Multiple_Complex
TC0900010804.hg.1	IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	1.52	8.47	7.86	0.47	0.27	4.66E-02	1.50E-01	Multiple_Complex
TC1000007421.hg.1	ZNF487	zinc finger protein 487	1.52	7.05	6.44	0.25	0.25	3.21E-02	1.17E-01	Multiple_Complex

TC0800008324.hg.1	MATN2	matrilin 2	1.52	6.14	5.54	0.28	0.23	2.50E-02	9.91E-02	Multiple_Complex
TC1700009162.hg.1	C17orf89	chromosome 17 open reading frame 89	1.52	12.36	11.75	0.06	0.17	3.09E-02	1.14E-01	Multiple_Complex
TC0200016424.hg.1	LBH	limb bud and heart development	1.52	8.56	7.95	0.03	0.23	3.84E-02	1.31E-01	Multiple_Complex
TC0800012470.hg.1	TMEM71	transmembrane protein 71	1.52	4.54	3.94	0.43	0.18	3.71E-02	1.28E-01	Multiple_Complex
TC1900009692.hg.1	ZNF823	zinc finger protein 823	1.52	10.17	9.56	0.05	0	1.96E-02	8.39E-02	Multiple_Complex
TC0200006788.hg.1	DDX1	DEAD (Asp-Glu-Ala-Asp) box helicase 1	1.52	11.32	10.71	0.35	0.09	3.61E-02	1.26E-01	Multiple_Complex
TC2000009026.hg.1	RBL1	retinoblastoma-like 1	1.52	10.88	10.28	0.15	0.22	3.21E-02	1.17E-01	Multiple_Complex
TC0X00010481.hg.1	TEX13B	testis expressed 13B	1.52	4.01	3.41	0.48	0	3.51E-02	1.24E-01	Coding
TC2100007898.hg.1	KRTAP19-5	keratin associated protein 19-5	1.52	6.18	5.58	0.25	0.18	2.75E-02	1.06E-01	Coding
TC0300013908.hg.1	FXR1	fragile X mental retardation, autosomal homolog 1	1.52	10.57	9.97	0.1	0.1	2.65E-02	1.03E-01	Multiple_Complex
TC0500010651.hg.1	FGF10	fibroblast growth factor 10	1.52	4.7	4.09	0.09	0.18	2.65E-02	1.03E-01	Coding
TC0100013632.hg.1	FNDC5	fibronectin type III domain containing 5	1.52	8.27	7.66	0.13	0.11	4.22E-02	1.40E-01	Multiple_Complex
TC1700011117.hg.1	LINC00483	long intergenic non-protein coding RNA 483	1.52	4.07	3.46	0.03	0.12	2.95E-02	1.10E-01	Multiple_Complex
TC1200009432.hg.1	LOC338797; RP13-507P19.2; RP13-507P19.1	uncharacterized LOC338797; novel transcript	1.52	5.16	4.56	0.37	0.07	3.34E-02	1.20E-01	Multiple_Complex
TC2000007670.hg.1	SNAI1	snail family zinc finger 1	1.52	5.4	4.79	0.16	0.04	3.87E-02	1.32E-01	Coding
TC0100014650.hg.1	ZZZ3	zinc finger, ZZ-type containing 3	1.52	12.93	12.33	0.05	0.03	1.49E-02	7.00E-02	Multiple_Complex
TC1100011048.hg.1	TMEM258; MIR611	transmembrane protein 258; microRNA 611	1.52	15.06	14.46	0.14	0.02	1.95E-02	8.36E-02	Multiple_Complex
TC0100014247.hg.1	HSPB11	heat shock protein family B (small), member 11	1.52	13.16	12.55	0.11	0.13	2.39E-02	9.61E-02	Multiple_Complex
TC1100013009.hg.1	GLYATL1	glycine-N-acyltransferase-like 1	1.52	3.8	3.19	0.09	0.11	1.76E-02	7.81E-02	Multiple_Complex
TC0800012406.hg.1	TTI2	TELO2 interacting protein 2	1.52	10.76	10.16	0.17	0.09	3.60E-02	1.26E-01	Multiple_Complex

TC0400006668.hg.1	LINC01587	long intergenic non-protein coding RNA 1587	1.52	5.37	4.77	0.1	0.18	3.15E-02	1.15E-01	Multiple_Complex
TC1500009451.hg.1	BCL2L10	BCL2-like 10 (apoptosis facilitator)	1.52	6.04	5.44	0.03	0.45	4.45E-02	1.45E-01	Coding
TC0300006719.hg.1	BTD	biotinidase	1.52	11.59	10.98	0.08	0.36	3.60E-02	1.26E-01	Multiple_Complex
TC1100010472.hg.1	CCDC73	coiled-coil domain containing 73	1.52	6.72	6.12	0.2	0.33	4.89E-02	1.55E-01	Multiple_Complex
TC0900009966.hg.1	OR2S2	olfactory receptor, family 2, subfamily S, member 2 (gene/pseudogene)	1.52	5.53	4.93	0.4	0.1	2.98E-02	1.11E-01	Multiple_Complex
TC0600012512.hg.1	RARS2	arginyl-tRNA synthetase 2, mitochondrial	1.52	10.93	10.33	0.11	0.09	1.47E-02	6.93E-02	Multiple_Complex
TC0600012502.hg.1	GJB7	gap junction protein beta 7	1.52	4.97	4.37	0.08	0.24	1.95E-02	8.36E-02	Multiple_Complex
TC1700011319.hg.1	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1.52	7.67	7.07	0.14	0.1	1.62E-02	7.40E-02	Multiple_Complex
TC0900011067.hg.1	OR13C2	olfactory receptor, family 13, subfamily C, member 2	1.52	4.63	4.03	0.14	0.27	3.23E-02	1.17E-01	Coding
TC1200008322.hg.1	TMTC2	transmembrane and tetratricopeptide repeat containing 2	1.52	7.2	6.6	0.52	0.12	4.87E-02	1.54E-01	Multiple_Complex
TC2200009236.hg.1	GGT1	gamma-glutamyltransferase 1	1.52	9.05	8.45	0.24	0.34	3.31E-02	1.19E-01	Multiple_Complex
TC1500009951.hg.1	GRAMD2	GRAM domain containing 2	1.52	4.66	4.06	0.1	0.11	2.02E-02	8.56E-02	Multiple_Complex
TC1200011471.hg.1	POC1B; POC1B-GALNT4; GALNT4	POC1 centriolar protein B; POC1B-GALNT4 readthrough; polypeptide N-acetylgalactosaminyltransferase 4	1.52	8.6	8	0.42	0.01	4.71E-02	1.51E-01	Multiple_Complex
TC0400010449.hg.1	TLR10	toll-like receptor 10	1.52	4.64	4.04	0.21	0.09	2.68E-02	1.04E-01	Multiple_Complex
TC0100018226.hg.1	RP5-1198O20.4; KLF17	Transcript Identified by AceView, Entrez Gene ID(s) 128209; novel transcript	1.52	4.08	3.47	0.33	0.24	3.12E-02	1.15E-01	NonCoding
TC1100010971.hg.1	OR5A2	olfactory receptor, family 5, subfamily A, member 2	1.52	6.06	5.46	0.48	0.19	4.20E-02	1.40E-01	Coding
TC1500007091.hg.1	CTDSPL2	CTD small phosphatase like 2	1.52	12.81	12.21	0.45	0.1	4.19E-02	1.39E-01	Multiple_Complex
TC1200011812.hg.1	CRY1	cryptochrome circadian clock 1	1.52	7.94	7.33	0.24	0.03	2.04E-02	8.61E-02	Multiple_Complex

TC0100018567.hg.1	RBM34	RNA binding motif protein 34	1.52	14.23	13.63	0.21	0.01	3.15E-02	1.15E-01	Multiple_Complex
TC0800009579.hg.1	XKR6	X-linked Kx blood group related 6	1.52	6.76	6.16	0.19	0.38	3.96E-02	1.34E-01	Coding
TC2200009204.hg.1	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	1.52	10.77	10.17	0.14	0.02	3.51E-02	1.24E-01	Multiple_Complex
TC0300013994.hg.1	ITIH4	inter-alpha-trypsin inhibitor heavy chain family, member 4	1.52	6.95	6.35	0.04	0.05	1.70E-02	7.63E-02	Multiple_Complex
TC1200010119.hg.1	C2CD5	C2 calcium-dependent domain containing 5	1.52	11.55	10.95	0.12	0.03	2.51E-02	9.93E-02	Multiple_Complex
TC0500013235.hg.1	FAM53C	family with sequence similarity 53, member C	1.52	11.32	10.72	0.1	0.23	4.04E-02	1.36E-01	Multiple_Complex
TC1300010030.hg.1	N4BP2L2	NEDD4 binding protein 2-like 2	1.52	16.24	15.64	0.04	0.04	2.38E-02	9.58E-02	Multiple_Complex
TC1700007671.hg.1	C17orf78	chromosome 17 open reading frame 78	1.52	5.06	4.46	0.27	0.1	3.48E-02	1.23E-01	Coding
TC0X00009842.hg.1	SPIN2A	spindlin family, member 2A	1.51	7.56	6.97	0.02	0.39	3.38E-02	1.21E-01	Coding
TC0600012257.hg.1	B3GAT2	beta-1,3-glucuronyltransferase 2	1.51	7.33	6.73	0.33	0.07	2.87E-02	1.09E-01	Coding
TC0300006599.hg.1	SLC6A1	solute carrier family 6 (neurotransmitter transporter), member 1	1.51	5.98	5.38	0.02	0.05	1.59E-02	7.30E-02	Multiple_Complex
TC1100007733.hg.1	OR5A1	olfactory receptor, family 5, subfamily A, member 1	1.51	4.45	3.85	0.04	0.07	2.92E-02	1.10E-01	Coding
TC1000011522.hg.1	TM9SF3	transmembrane 9 superfamily member 3	1.51	8.77	8.17	0.18	0.05	2.85E-02	1.08E-01	Multiple_Complex
TC1100011694.hg.1	LRRC32	leucine rich repeat containing 32	1.51	6.3	5.71	0.01	0.03	4.99E-02	1.57E-01	Multiple_Complex
TC0100016318.hg.1	MPC2	mitochondrial pyruvate carrier 2	1.51	13.45	12.85	0.09	0.08	2.03E-02	8.59E-02	Multiple_Complex
TC1400008007.hg.1	CPSF2	cleavage and polyadenylation specific factor 2	1.51	8.61	8.01	0.01	0.46	4.73E-02	1.51E-01	Multiple_Complex
TC0100015476.hg.1	HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	1.51	4.38	3.79	0.32	0.09	3.81E-02	1.31E-01	Multiple_Complex
TC1800008549.hg.1	RIT2	Ras-like without CAAX 2	1.51	4.54	3.94	0.14	0.29	2.47E-02	9.81E-02	Multiple_Complex
TC0900008842.hg.1	SLC25A25	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001006641	1.51	7.39	6.79	0.1	0.14	4.81E-02	1.53E-01	NonCoding

TC1100009950.hg.1	OR56A5	olfactory receptor, family 56, subfamily A, member 5	1.51	4.8	4.2	0.2	0.1	2.13E-02	8.85E-02	Coding
TC1700007266.hg.1	KCNJ12	potassium channel, inwardly rectifying subfamily J, member 12	1.51	6.93	6.34	0.01	0.12	2.54E-02	1.00E-01	Multiple_Complex
TC0X00009963.hg.1	P2RY4	pyrimidinergic receptor P2Y, G-protein coupled, 4	1.51	7.76	7.16	0.48	0.21	4.91E-02	1.55E-01	Coding
TC0200006540.hg.1	DCDC2C	doublecortin domain containing 2C	1.51	4.3	3.7	0.25	0.27	2.92E-02	1.10E-01	Multiple_Complex
TC0400012824.hg.1	HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3	1.51	12.3	11.71	0.28	0.13	4.80E-02	1.53E-01	NonCoding
TC1900011933.hg.1	ZNF585A	zinc finger protein 585A	1.51	13.66	13.06	0.29	0.25	3.25E-02	1.18E-01	Multiple_Complex
TC1700008344.hg.1	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	1.51	4.24	3.64	0.21	0.38	3.42E-02	1.22E-01	Multiple_Complex
TC0400008443.hg.1	LARP7	La ribonucleoprotein domain family, member 7	1.51	12.22	11.63	0.2	0.15	3.43E-02	1.22E-01	Multiple_Complex
TC1000007199.hg.1	ZEB1	zinc finger E-box binding homeobox 1	1.51	10.36	9.77	0.22	0.27	3.54E-02	1.24E-01	Multiple_Complex
TC0300014034.hg.1	COX17	COX17 cytochrome c oxidase copper chaperone	1.51	16.02	15.43	0.01	0.05	1.63E-02	7.42E-02	Multiple_Complex
TC0100009355.hg.1	GPR61	G protein-coupled receptor 61	1.51	4.8	4.21	0.08	0.26	2.73E-02	1.05E-01	Multiple_Complex
TC2100008530.hg.1	KRTAP10-11; KRTAP12-3; KRTAP10-12	keratin associated protein 10-11; keratin associated protein 12-3; keratin associated protein 10-12	1.51	10.57	9.98	0.12	0.2	3.43E-02	1.22E-01	Multiple_Complex
TC0200008047.hg.1	ALMS1	Alstrom syndrome protein 1	1.51	8.2	7.61	0.17	0.32	3.49E-02	1.23E-01	Multiple_Complex
TC1700011656.hg.1	CPSF4L	cleavage and polyadenylation specific factor 4-like	1.51	4.28	3.68	0.04	0.3	2.46E-02	9.78E-02	Coding
TC1700009236.hg.1	SLC16A3; MIR6787	solute carrier family 16 (monocarboxylate transporter), member 3; microRNA 6787	1.51	6.56	5.97	0.35	0.25	3.59E-02	1.26E-01	Multiple_Complex
TC1100007670.hg.1	P2RX3	purinergic receptor P2X, ligand gated ion channel, 3	1.51	5.5	4.91	0.5	0.05	4.70E-02	1.51E-01	Multiple_Complex
TC1000008988.hg.1	TRUB1	TruB pseudouridine (psi) synthase family member 1	1.51	11.59	11	0.32	0.04	2.63E-02	1.03E-01	Multiple_Complex
TC0100009800.hg.1	GPR89B	G protein-coupled receptor 89B	1.51	10.37	9.78	0.14	0.14	1.87E-02	8.16E-02	Multiple_Complex

TC0X00008136.hg.1	ALG13	ALG13, UDP-N-acetylglucosaminyltransferase subunit	1.51	13.44	12.85	0.42	0.06	3.79E-02	1.30E-01	Multiple_Complex
TC1500010726.hg.1	TMEM62	transmembrane protein 62	1.51	6.96	6.36	0.17	0.02	4.65E-02	1.50E-01	Multiple_Complex
TC0900012167.hg.1	GSN	gelsolin	1.51	7.84	7.25	0.26	0.23	3.14E-02	1.15E-01	Multiple_Complex
TC1600011351.hg.1	CARHSP1	Jeck2013 ANTISENSE, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_001042476	1.51	8.08	7.48	0.32	0.08	3.69E-02	1.28E-01	NonCoding
TC1500007409.hg.1	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	1.51	4.4	3.81	0.25	0.35	4.44E-02	1.45E-01	Multiple_Complex
TC0200008900.hg.1	TMEM87B	transmembrane protein 87B	1.51	6.92	6.32	0.14	0.02	2.56E-02	1.01E-01	Multiple_Complex
TC0300014090.hg.1	ATP13A3	ATPase type 13A3	1.51	14.06	13.47	0.06	0.15	2.09E-02	8.76E-02	Multiple_Complex
TC0X00009718.hg.1	XAGE1E; XAGE1B	X antigen family, member 1E; X antigen family, member 1B	1.51	4.84	4.25	0.03	0.12	1.68E-02	7.58E-02	Multiple_Complex
TC1900010523.hg.1	ZFP82	ZFP82 zinc finger protein	1.51	5.09	4.5	0.17	0.07	4.59E-02	1.48E-01	Multiple_Complex
TC1100007734.hg.1	OR4D6	olfactory receptor, family 4, subfamily D, member 6	1.51	4.03	3.44	0.08	0.06	1.88E-02	8.16E-02	Coding
TC1000011490.hg.1	SORBS1	Transcript Identified by AceView, Entrez Gene ID(s) 10580	1.51	3.98	3.39	0.1	0.16	1.91E-02	8.25E-02	Coding
TC0900008207.hg.1	SEC61B	Sec61 translocon beta subunit	1.51	13.59	13	0.05	0.43	3.59E-02	1.25E-01	Multiple_Complex
TC2000006622.hg.1	C20orf196	chromosome 20 open reading frame 196	1.51	7.35	6.76	0	0.02	2.81E-02	1.07E-01	Multiple_Complex
TC0300006513.hg.1	GRM7	glutamate receptor, metabotropic 7	1.51	4.48	3.89	0.1	0.29	3.87E-02	1.32E-01	Multiple_Complex
TC1400009106.hg.1	DNAAF2	dynein, axonemal, assembly factor 2	1.51	8.78	8.19	0.18	0	1.78E-02	7.87E-02	Coding
TC1900010646.hg.1	IFNL3	interferon, lambda 3	1.51	6.34	5.75	0.21	0.28	3.29E-02	1.19E-01	Coding
TC1900008726.hg.1	ERVV-1	endogenous retrovirus group V, member 1	1.51	4.98	4.39	0.02	0.35	3.96E-02	1.34E-01	Coding
TC0X00011226.hg.1	F8	coagulation factor VIII, procoagulant component	1.51	5.54	4.95	0.24	0.01	4.55E-02	1.47E-01	Multiple_Complex
TC1100010091.hg.1	MRVI1	murine retrovirus integration site 1 homolog	1.51	6.62	6.03	0.18	0.01	4.50E-02	1.46E-01	Multiple_Complex

TC0500013020.hg.1	CLK4	CDC like kinase 4	1.51	11.5	10.91	0.13	0.1	3.42E-02	1.22E-01	Multiple_Complex
TC1200008734.hg.1	RIC8B	RIC8 guanine nucleotide exchange factor B	1.5	8.14	7.55	0.06	0.02	1.65E-02	7.49E-02	Multiple_Complex
TC1100012610.hg.1	BSX	brain-specific homeobox	1.5	5.95	5.36	0.01	0.27	2.57E-02	1.01E-01	Multiple_Complex
TC1500009405.hg.1	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	1.5	5.25	4.67	0.35	0.14	3.10E-02	1.14E-01	Multiple_Complex
TC2100008494.hg.1	IFNAR2	interferon (alpha, beta and omega) receptor 2	1.5	11.45	10.86	0.13	0.3	4.95E-02	1.56E-01	Multiple_Complex
TC0100013057.hg.1	FAM231A; FAM231C; RP5-1182A14.6	Homo sapiens family with sequence similarity 231, member A (FAM231A), mRNA.; Homo sapiens family with sequence similarity 231, member C (FAM231C), mRNA.; Protein FAM231A/C [Source:UniProtKB/Swiss-Prot;Acc:A6NEA5]	1.5	6.68	6.09	0.25	0.14	4.51E-02	1.47E-01	Coding
TC1000010744.hg.1	TMEM26	transmembrane protein 26	1.5	4.22	3.64	0.11	0.08	2.98E-02	1.11E-01	Multiple_Complex
TC1300007780.hg.1	RAP2A	RAP2A, member of RAS oncogene family	1.5	7.95	7.36	0.02	0.32	4.22E-02	1.40E-01	Coding
TC1100006748.hg.1	OR2D3	olfactory receptor, family 2, subfamily D, member 3	1.5	4.94	4.36	0.15	0.21	3.24E-02	1.18E-01	Coding
TC0600014300.hg.1	GCLC	glutamate-cysteine ligase, catalytic subunit	1.5	7.72	7.13	0.01	0.44	3.94E-02	1.34E-01	Multiple_Complex
TC0600009476.hg.1	TAAR9	trace amine associated receptor 9 (gene/pseudogene)	1.5	4.82	4.24	0.1	0.02	1.88E-02	8.16E-02	Coding
TC2000008439.hg.1	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	1.5	12.51	11.92	0.16	0.08	2.59E-02	1.02E-01	Multiple_Complex
TC0100008120.hg.1	HPDL	4-hydroxyphenylpyruvate dioxygenase-like	1.5	5.48	4.9	0.07	0.1	2.16E-02	8.94E-02	Coding
TC1200010229.hg.1	PTHLH	parathyroid hormone-like hormone	1.5	7.1	6.52	0.35	0.16	3.21E-02	1.17E-01	Multiple_Complex
TSUnmapped00000600.hg.1	SURF1	surfeit 1	1.5	8.57	7.98	0.23	0.22	2.73E-02	1.05E-01	NonCoding
TC0800007554.hg.1	UBE2V2	ubiquitin conjugating enzyme E2 variant 2	1.5	12.92	12.33	0.09	0.21	2.08E-02	8.72E-02	Multiple_Complex

TC2200007327.hg.1	POLR2F; MIR4534; MIR6820	polymerase (RNA) II (DNA directed) polypeptide F; microRNA 4534; microRNA 6820	-1.5	14.47	15.06	0.13	0.09	1.93E-02	8.29E-02	Multiple_Complex
TC1200009164.hg.1	RNF34	ring finger protein 34, E3 ubiquitin protein ligase	-1.5	12.92	13.51	0	0.03	1.83E-02	8.02E-02	Multiple_Complex
TC1200006850.hg.1	ETV6	ets variant 6	-1.5	7.74	8.33	0.16	0.37	3.42E-02	1.22E-01	Multiple_Complex
TC1900011987.hg.1	NOVA2	neuro-oncological ventral antigen 2	-1.5	6.67	7.26	0.05	0.35	3.01E-02	1.12E-01	Multiple_Complex
TC0100013758.hg.1	INPP5B	inositol polyphosphate-5-phosphatase B	-1.5	8.61	9.2	0.35	0.33	4.01E-02	1.36E-01	Multiple_Complex
TC2100008465.hg.1	MCM3AP	minichromosome maintenance complex component 3 associated protein	-1.5	9.39	9.97	0.23	0.14	2.28E-02	9.30E-02	Multiple_Complex
TC1600009742.hg.1	EARS2	glutamyl-tRNA synthetase 2, mitochondrial	-1.5	3.51	4.09	0.26	0.11	3.98E-02	1.35E-01	Multiple_Complex
TC1700011917.hg.1	USP36	ubiquitin specific peptidase 36	-1.5	11.18	11.76	0.45	0.09	4.17E-02	1.39E-01	Multiple_Complex
TC0900012212.hg.1	PLIN2	perilipin 2	-1.5	6.73	7.32	0.12	0.19	2.58E-02	1.01E-01	Multiple_Complex
TSUnmapped00000085.hg.1	CCDC84	coiled-coil domain containing 84	-1.5	5.6	6.18	0.35	0.02	3.68E-02	1.28E-01	NonCoding
TC0100017075.hg.1	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	-1.5	15.26	15.85	0.07	0.04	1.67E-02	7.56E-02	Multiple_Complex
TSUnmapped00000310.hg.1	HYOU1	hypoxia up-regulated 1	-1.5	9.53	10.12	0.04	0.09	1.64E-02	7.46E-02	Coding
TC1000012584.hg.1	ERLIN1	ER lipid raft associated 1	-1.5	11.97	12.56	0.04	0.15	1.82E-02	7.99E-02	Multiple_Complex
TC1600010809.hg.1	TXNL4B	thioredoxin-like 4B	-1.5	9.63	10.22	0.22	0.25	4.43E-02	1.45E-01	Multiple_Complex
TC1500010106.hg.1	TSPAN3	tetraspanin 3	-1.5	10.2	10.79	0.16	0.2	2.44E-02	9.73E-02	Multiple_Complex
TC0600011466.hg.1	ZBTB12	zinc finger and BTB domain containing 12	-1.51	4.19	4.78	0.07	0.37	2.95E-02	1.11E-01	Coding
TC2200007083.hg.1	INPP5J	inositol polyphosphate-5-phosphatase J	-1.51	7.14	7.73	0.26	0.11	2.24E-02	9.19E-02	Multiple_Complex
TC0800008330.hg.1	POP1	POP1 homolog, ribonuclease P/MRP subunit	-1.51	6.42	7.01	0.36	0.02	2.88E-02	1.09E-01	Multiple_Complex

TC0700006634.hg.1	AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	-1.51	11.33	11.92	0	0.08	1.72E-02	7.70E-02	Multiple_Complex
TC1100009657.hg.1	IFITM3	interferon induced transmembrane protein 3	-1.51	6.89	7.48	0.43	0.35	4.95E-02	1.56E-01	Multiple_Complex
TC1900007830.hg.1	SCN1B	sodium channel, voltage gated, type I beta subunit	-1.51	3.84	4.43	0.2	0.18	3.35E-02	1.20E-01	Multiple_Complex
TC0300013609.hg.1	LSG1	large 60S subunit nuclear export GTPase 1	-1.51	10.53	11.12	0.32	0.03	3.26E-02	1.18E-01	Multiple_Complex
TC1900011677.hg.1	IL27RA	interleukin 27 receptor, alpha	-1.51	5.95	6.54	0.01	0.44	4.34E-02	1.43E-01	Multiple_Complex
TC1600011221.hg.1	MVD	mevalonate (diphospho) decarboxylase	-1.51	8.57	9.17	0.05	0.04	1.48E-02	6.96E-02	Multiple_Complex
TC1400010715.hg.1	AJUBA	ajuba LIM protein	-1.51	8.75	9.35	0.26	0.45	4.87E-02	1.54E-01	Multiple_Complex
TC0200012031.hg.1	HADHA	Transcript Identified by AceView, Entrez Gene ID(s) 3030	-1.51	5.64	6.23	0.15	0.21	3.69E-02	1.28E-01	Unassigned
TC1600009966.hg.1	DCTPP1	dCTP pyrophosphatase 1	-1.51	11.58	12.17	0.06	0.15	1.72E-02	7.68E-02	Multiple_Complex
TC1900007888.hg.1	APLP1	amyloid beta (A4) precursor-like protein 1	-1.51	8.76	9.35	0.08	0.06	1.93E-02	8.32E-02	Multiple_Complex
TC0200007064.hg.1	SNX17	sorting nexin 17	-1.51	7.85	8.44	0.35	0.23	3.78E-02	1.30E-01	Multiple_Complex
TC1700010826.hg.1	SLC25A39	solute carrier family 25, member 39	-1.51	6.71	7.3	0.21	0.15	3.65E-02	1.27E-01	Multiple_Complex
TC1900011825.hg.1	ZNF587	zinc finger protein 587	-1.51	6.64	7.24	0.35	0.07	3.48E-02	1.23E-01	Multiple_Complex
TC0100014203.hg.1	ZCCHC11	zinc finger, CCHC domain containing 11	-1.51	7.46	8.05	0.48	0.17	4.43E-02	1.45E-01	Multiple_Complex
TC1600009861.hg.1	CLN3; NPIPB7	ceroid-lipofuscinosis, neuronal 3; nuclear pore complex interacting protein family, member B7	-1.51	8.97	9.57	0.12	0.09	2.03E-02	8.60E-02	Multiple_Complex
TC1100012906.hg.1	IGSF9B	immunoglobulin superfamily, member 9B	-1.51	7.06	7.66	0.38	0.17	4.28E-02	1.41E-01	Multiple_Complex
TC1600009865.hg.1	NUPR1	nuclear protein 1, transcriptional regulator	-1.51	11.29	11.89	0.07	0.34	2.78E-02	1.06E-01	Multiple_Complex
TC1600006826.hg.1	ABAT	4-aminobutyrate aminotransferase	-1.51	4.57	5.16	0.31	0.43	4.67E-02	1.50E-01	Multiple_Complex
TC1100013097.hg.1	REXO2	RNA exonuclease 2	-1.51	11.93	12.52	0.26	0.2	2.75E-02	1.06E-01	Multiple_Complex
TC1200012635.hg.1	PRR13	proline rich 13	-1.51	10.11	10.71	0.24	0.1	2.10E-02	8.79E-02	Multiple_Complex

TC1500010045.hg.1	ULK3	unc-51 like kinase 3	-1.51	7.33	7.93	0.2	0.17	2.90E-02	1.09E-01	Multiple_Complex
TC0100006773.hg.1	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	-1.51	6.74	7.33	0.07	0.08	1.51E-02	7.06E-02	Multiple_Complex
TC0500013166.hg.1	ZNF131	zinc finger protein 131	-1.51	5.53	6.13	0	0.22	3.08E-02	1.14E-01	NonCoding
TC0700007977.hg.1	FZD9	frizzled class receptor 9	-1.51	7.73	8.33	0.42	0.08	4.50E-02	1.46E-01	Coding
TC0100012454.hg.1	SDF4	stromal cell derived factor 4	-1.51	7.02	7.61	0.04	0.17	2.32E-02	9.43E-02	Multiple_Complex
TC1700012347.hg.1	GPS2	G protein pathway suppressor 2	-1.51	10.31	10.91	0.29	0.06	4.79E-02	1.53E-01	Multiple_Complex
TC1100007445.hg.1	CREB3L1	cAMP responsive element binding protein 3-like 1	-1.51	4.46	5.06	0.1	0.09	3.80E-02	1.31E-01	Multiple_Complex
TC0500009996.hg.1	NSUN2	NOP2/Sun RNA methyltransferase family, member 2	-1.51	7.97	8.57	0.12	0.19	3.20E-02	1.17E-01	Multiple_Complex
TC1900011593.hg.1	ZNF418	zinc finger protein 418	-1.51	6.71	7.31	0.29	0.11	3.31E-02	1.19E-01	Multiple_Complex
TSUnmapped00000162.hg.1	FBL	fibrillarin	-1.51	15.11	15.71	0.03	0.01	1.59E-02	7.31E-02	Coding
TC0100010193.hg.1	PRCC	papillary renal cell carcinoma (translocation-associated)	-1.51	11.01	11.6	0.3	0.1	2.72E-02	1.05E-01	Multiple_Complex
TC1900010478.hg.1	KRTDAP	keratinocyte differentiation-associated protein	-1.51	5.55	6.15	0.08	0.02	2.04E-02	8.61E-02	Multiple_Complex
TC2200008611.hg.1	EIF3D	eukaryotic translation initiation factor 3, subunit D	-1.51	11.52	12.12	0.01	0.13	1.68E-02	7.58E-02	Multiple_Complex
TSUnmapped00000394.hg.1	ATG16L1	autophagy related 16-like 1	-1.51	7.63	8.23	0.17	0.23	3.65E-02	1.27E-01	Coding
TC1300009597.hg.1	GPR18	G protein-coupled receptor 18	-1.51	4.07	4.67	0.08	0.35	3.73E-02	1.29E-01	Coding
TC0900006603.hg.1	KDM4C	Transcript Identified by AceView, Entrez Gene ID(s) 23081	-1.51	5.46	6.06	0.18	0.48	4.32E-02	1.42E-01	Unassigned
TC0900007953.hg.1	CENPP	centromere protein P	-1.52	9.64	10.24	0.29	0.11	3.91E-02	1.33E-01	Multiple_Complex
TC0500012760.hg.1	SLIT3	slit guidance ligand 3	-1.52	6.57	7.17	0.12	0.06	2.68E-02	1.04E-01	Multiple_Complex

TC1400010634.hg.1	CIPC	CLOCK-interacting pacemaker	-1.52	6.72	7.32	0.09	0.26	2.10E-02	8.78E-02	Multiple_Complex
TC1100006477.hg.1	PHRF1	PHD and ring finger domains 1	-1.52	7.61	8.21	0.22	0.21	4.51E-02	1.47E-01	Multiple_Complex
TC0X00009877.hg.1	AMER1	APC membrane recruitment protein 1	-1.52	4.44	5.04	0.15	0.05	1.60E-02	7.32E-02	Multiple_Complex
TC0100016476.hg.1	KIAA0040	KIAA0040	-1.52	8.54	9.14	0.18	0.29	3.09E-02	1.14E-01	Multiple_Complex
TC1100010757.hg.1	MTCH2	mitochondrial carrier 2	-1.52	13.33	13.93	0.05	0.12	1.90E-02	8.23E-02	Multiple_Complex
TC0300007383.hg.1	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	-1.52	7.93	8.53	0.03	0.19	2.84E-02	1.08E-01	Multiple_Complex
TC2200009353.hg.1	SUN2	Sad1 and UNC84 domain containing 2	-1.52	5.98	6.58	0.14	0.08	3.23E-02	1.17E-01	Multiple_Complex
TC2000008097.hg.1	DNAJC5; MIR941-1; MIR941-2; MIR941-3; MIR941-4; MIR941-5	DnaJ (Hsp40) homolog, subfamily C, member 5; microRNA 941-1; microRNA 941-2; microRNA 941-3; microRNA 941-4; microRNA 941-5	-1.52	7.8	8.4	0.1	0.22	2.68E-02	1.04E-01	Multiple_Complex
TSUnmapped00000427.hg.1	FBL	fibrillarin	-1.52	14.7	15.3	0.03	0.12	2.25E-02	9.21E-02	Coding
TC0900009908.hg.1	RPP25L	ribonuclease P/MRP 25kDa subunit-like	-1.52	9.36	9.96	0.01	0.02	1.83E-02	8.03E-02	Coding
TC1600010889.hg.1	KARS	lysyl-tRNA synthetase	-1.52	13.16	13.76	0.23	0.1	2.07E-02	8.71E-02	Multiple_Complex
TC1700009490.hg.1	NCBP3	nuclear cap binding subunit 3	-1.52	7.89	8.5	0.38	0.08	2.84E-02	1.08E-01	Multiple_Complex
TC0100007006.hg.1	SPEN	spen family transcriptional repressor	-1.52	10.42	11.02	0.25	0.22	2.74E-02	1.05E-01	Multiple_Complex
TC0100006577.hg.1	RER1	retention in endoplasmic reticulum sorting receptor 1	-1.52	10.56	11.16	0.01	0.18	2.62E-02	1.02E-01	Multiple_Complex
TC1000009276.hg.1	DOCK1	dedicator of cytokinesis 1	-1.52	8.29	8.89	0.46	0.09	4.43E-02	1.45E-01	Multiple_Complex
TC1000009677.hg.1	ASB13	ankyrin repeat and SOCS box containing 13	-1.52	4.04	4.64	0.05	0.34	2.42E-02	9.69E-02	Multiple_Complex
TC0100011871.hg.1	HIST3H2BB	histone cluster 3, H2bb	-1.52	9.38	9.98	0.4	0.28	3.78E-02	1.30E-01	Coding
TC1000007471.hg.1	ALOX5	arachidonate 5-lipoxygenase	-1.52	4.41	5.01	0.22	0.27	3.53E-02	1.24E-01	Multiple_Complex
TC1700010214.hg.1	FAM222B	family with sequence similarity 222, member B	-1.52	6.95	7.55	0.1	0.01	2.14E-02	8.87E-02	Multiple_Complex

TC0400011920.hg.1	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	-1.52	10.29	10.89	0.43	0.1	3.43E-02	1.22E-01	Multiple_Complex
TC1300008793.hg.1	TSC22D1	TSC22 domain family, member 1	-1.52	8.7	9.3	0.08	0.12	2.04E-02	8.61E-02	Multiple_Complex
TC1200008269.hg.1	NAV3	neuron navigator 3	-1.52	4.45	5.05	0.13	0.5	4.31E-02	1.42E-01	Multiple_Complex
TC0100009934.hg.1	ANXA9	annexin A9	-1.52	4.91	5.51	0.26	0.33	3.59E-02	1.26E-01	Multiple_Complex
TSUnmapped00000154.hg.1	LRP6	LDL receptor related protein 6	-1.52	9.22	9.82	0.26	0.01	2.01E-02	8.55E-02	Coding
TC1000008961.hg.1	NHLRC2	NHL repeat containing 2	-1.52	12.93	13.53	0.02	0.06	1.38E-02	6.64E-02	Multiple_Complex
TSUnmapped00000477.hg.1	SURF4	surfeit 4	-1.52	12.31	12.91	0.21	0.02	1.83E-02	8.02E-02	Coding
TC0600010777.hg.1	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	-1.52	7.58	8.19	0.47	0.04	3.63E-02	1.26E-01	Multiple_Complex
TC1700008868.hg.1	TMEM104	transmembrane protein 104	-1.52	7.36	7.96	0	0.07	1.89E-02	8.17E-02	Multiple_Complex
TC0800010575.hg.1	CA8	carbonic anhydrase VIII	-1.52	7.8	8.4	0.04	0.24	3.85E-02	1.32E-01	Multiple_Complex
TC0800009432.hg.1	DEFA6	defensin, alpha 6, Paneth cell-specific	-1.52	3.88	4.49	0.24	0.35	4.26E-02	1.41E-01	Coding
TC1100010054.hg.1	NRIP3	nuclear receptor interacting protein 3	-1.52	7.33	7.93	0.19	0.23	2.45E-02	9.77E-02	Multiple_Complex
TC0300013839.hg.1	ACY1	aminoacylase 1	-1.52	7.44	8.05	0.18	0.25	3.02E-02	1.12E-01	Multiple_Complex
TC1000012586.hg.1	SEC31B	SEC31 homolog B, COPII coat complex component	-1.52	7.18	7.79	0.28	0.08	2.65E-02	1.03E-01	Multiple_Complex
TC1100013191.hg.1	POLD4	polymerase (DNA-directed), delta 4, accessory subunit	-1.52	9.21	9.82	0.08	0.25	3.39E-02	1.21E-01	Multiple_Complex
TC1900011871.hg.1	ZNF653	zinc finger protein 653	-1.52	5.22	5.83	0.33	0.27	3.62E-02	1.26E-01	Multiple_Complex
TC0100006954.hg.1	KAZN	kazrin, periplakin interacting protein	-1.52	5.01	5.62	0.07	0.08	2.35E-02	9.49E-02	Multiple_Complex
TC0200010972.hg.1	MFF	mitochondrial fission factor	-1.52	11.98	12.59	0.14	0.11	1.71E-02	7.67E-02	Multiple_Complex
TC0900012295.hg.1	TMEM203	transmembrane protein 203	-1.53	9.72	10.33	0.05	0.28	2.03E-02	8.60E-02	Coding

TC0100018219.hg.1	PPCS; CCDC30	phosphopantothenoylcysteine synthetase; coiled-coil domain containing 30	-1.53	11.28	11.89	0.36	0.28	3.50E-02	1.24E-01	Multiple_Complex
TC0500012568.hg.1	GEMIN5	gem nuclear organelle associated protein 5	-1.53	7.02	7.63	0.03	0.1	2.05E-02	8.65E-02	Multiple_Complex
TC0100018081.hg.1	ZNF670; ZNF695; ZNF670-ZNF695	zinc finger protein 670; zinc finger protein 695; ZNF670-ZNF695 readthrough (NMD candidate)	-1.53	9.5	10.11	0.05	0.04	1.48E-02	6.96E-02	Multiple_Complex
TC2200007998.hg.1	C22orf29; GNB1L	chromosome 22 open reading frame 29; guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-1.53	6.92	7.53	0	0.25	1.85E-02	8.07E-02	Multiple_Complex
TC1600011374.hg.1	SPN	sialophorin	-1.53	6.62	7.23	0.08	0.27	2.23E-02	9.18E-02	Multiple_Complex
TC0300009693.hg.1	AP2M1	adaptor-related protein complex 2, mu 1 subunit	-1.53	8.01	8.62	0.2	0.24	2.05E-02	8.63E-02	Multiple_Complex
TC0100009788.hg.1	BCL9	B-cell CLL/lymphoma 9	-1.53	9.49	10.1	0.02	0.02	1.60E-02	7.32E-02	Multiple_Complex
TC0100009621.hg.1	PHGDH	phosphoglycerate dehydrogenase	-1.53	10.59	11.2	0.33	0.17	2.57E-02	1.01E-01	Multiple_Complex
TC1800006493.hg.1	EMILIN2	elastin microfibril interfacer 2	-1.53	5.46	6.07	0.21	0.2	2.87E-02	1.09E-01	Multiple_Complex
TC1600009646.hg.1	KNOP1	lysine-rich nucleolar protein 1	-1.53	11.31	11.92	0.02	0.05	3.47E-02	1.23E-01	Multiple_Complex
TC0200011106.hg.1	EIF4E2	eukaryotic translation initiation factor 4E family member 2	-1.53	11.22	11.83	0.01	0.07	1.45E-02	6.87E-02	Multiple_Complex
TC0300006580.hg.1	IRAK2	interleukin 1 receptor associated kinase 2	-1.53	7.47	8.09	0.35	0.15	3.46E-02	1.23E-01	Multiple_Complex
TC0X00010131.hg.1	PGAM4	phosphoglycerate mutase family member 4	-1.53	5.34	5.95	0.13	0.15	2.34E-02	9.47E-02	Coding
TC0100018387.hg.1	CDK11B	cyclin-dependent kinase 11B	-1.53	8.14	8.75	0.17	0.29	2.84E-02	1.08E-01	Multiple_Complex
TC1100006492.hg.1	PNPLA2	patatin-like phospholipase domain containing 2	-1.53	5.1	5.72	0.12	0.3	4.79E-02	1.53E-01	Multiple_Complex
TC1700012242.hg.1	LOC101060389; TBC1D3D	TBC1 domain family member-like; TBC1 domain family, member 3D [Source:HGNC Symbol;Acc:HGNC:28944]	-1.53	6.28	6.89	0.2	0.3	2.96E-02	1.11E-01	Coding
TC1400007494.hg.1	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	-1.53	9.83	10.44	0.28	0.04	1.86E-02	8.10E-02	Multiple_Complex

TC0600014233.hg.1	SSR1	signal sequence receptor, alpha	-1.53	10.3	10.91	0.15	0.02	1.54E-02	7.13E-02	Multiple_Complex
TC1000011398.hg.1	HTR7	5-hydroxytryptamine (serotonin) receptor 7, adenylate cyclase-coupled	-1.53	4.1	4.71	0.04	0.17	3.83E-02	1.31E-01	Multiple_Complex
TC1000009841.hg.1	PHYH	phytanoyl-CoA 2-hydroxylase	-1.53	9.3	9.91	0.01	0.05	3.53E-02	1.24E-01	Multiple_Complex
TC1100009395.hg.1	TBRG1	transforming growth factor beta regulator 1	-1.53	10.04	10.65	0.13	0.05	1.97E-02	8.41E-02	Multiple_Complex
TC1900007363.hg.1	MAST3	microtubule associated serine/threonine kinase 3	-1.53	4.19	4.8	0.54	0.04	4.36E-02	1.43E-01	Multiple_Complex
TSUnmapped00000440.hg.1	HYOU1	hypoxia up-regulated 1	-1.53	9.19	9.8	0.04	0.09	2.08E-02	8.72E-02	Coding
TC0100009373.hg.1	SLC6A17	solute carrier family 6 (neutral amino acid transporter), member 17	-1.53	6.52	7.13	0.31	0.09	3.94E-02	1.34E-01	Multiple_Complex
TC0300012073.hg.1	LSAMP	limbic system-associated membrane protein	-1.53	6.38	7	0.3	0.21	4.23E-02	1.40E-01	Multiple_Complex
TC0300008863.hg.1	CDV3	CDV3 homolog (mouse)	-1.53	13.13	13.74	0.06	0.09	1.31E-02	6.40E-02	Multiple_Complex
TC0600013883.hg.1	MPC1	mitochondrial pyruvate carrier 1	-1.53	12.1	12.71	0.53	0.01	4.02E-02	1.36E-01	Multiple_Complex
TC1600008845.hg.1	CDT1	chromatin licensing and DNA replication factor 1	-1.53	5.85	6.46	0.07	0.24	3.54E-02	1.24E-01	Multiple_Complex
TSUnmapped00000018.hg.1	ZNF35	zinc finger protein 35	-1.53	7.39	8.01	0.27	0.27	2.63E-02	1.02E-01	Coding
TC2000008111.hg.1	MYT1	myelin transcription factor 1	-1.53	5.51	6.13	0.12	0.04	3.01E-02	1.12E-01	Multiple_Complex
TC1600011355.hg.1	NPIPA1	nuclear pore complex interacting protein family, member A1	-1.53	10.89	11.5	0.4	0.18	3.00E-02	1.12E-01	Multiple_Complex
TC1400009980.hg.1	CCDC88C	coiled-coil domain containing 88C	-1.53	5.35	5.96	0.05	0.08	2.31E-02	9.39E-02	Multiple_Complex
TC1900008409.hg.1	SAE1	SUMO1 activating enzyme subunit 1	-1.53	11.74	12.35	0.06	0.19	2.24E-02	9.18E-02	Multiple_Complex
TC0X00011415.hg.1	NAA10	N(alpha)-acetyltransferase 10, NatA catalytic subunit	-1.53	11.85	12.46	0.1	0.19	1.66E-02	7.51E-02	Multiple_Complex
TC2100007935.hg.1	SCAF4	SR-related CTD-associated factor 4	-1.53	11.04	11.66	0.05	0.05	1.75E-02	7.79E-02	Multiple_Complex
TC1400009922.hg.1	PTPN21	protein tyrosine phosphatase, non-receptor type 21	-1.53	6.75	7.37	0.04	0.07	1.58E-02	7.29E-02	Multiple_Complex

TSUnmapped00000247.hg.1	REXO4	REX4 homolog, 3'-5' exonuclease [Source:HGNC Symbol;Acc:HGNC:12820]	-1.53	7.92	8.54	0.04	0.18	3.18E-02	1.16E-01	Coding
TC1000011975.hg.1	CACUL1	CDK2-associated, cullin domain 1	-1.53	12.68	13.29	0.07	0.08	1.44E-02	6.85E-02	Multiple_Complex
TC0100018267.hg.1	KCNC4	potassium channel, voltage gated Shaw related subfamily C, member 4	-1.53	4.46	5.08	0.01	0.39	4.99E-02	1.57E-01	Multiple_Complex
TSUnmapped00000433.hg.1	ATG16L1	autophagy related 16-like 1	-1.53	6.71	7.33	0.24	0.05	2.47E-02	9.81E-02	Coding
TC0600013326.hg.1	PERP	PERP, TP53 apoptosis effector	-1.53	13.31	13.92	0.23	0.07	1.71E-02	7.67E-02	Coding
TC1900012058.hg.1	ZNF417	zinc finger protein 417	-1.53	8.73	9.35	0.41	0.19	3.60E-02	1.26E-01	Multiple_Complex
TC0300013882.hg.1	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	-1.53	7.93	8.55	0.24	0.13	2.57E-02	1.01E-01	Coding
TSUnmapped00000258.hg.1	SURF4	surfeit 4	-1.53	8.71	9.32	0.17	0.29	2.51E-02	9.92E-02	NonCoding
TC1100007387.hg.1	ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (inactive)	-1.53	5.03	5.65	0.17	0.09	2.18E-02	9.00E-02	Multiple_Complex
TC1000011596.hg.1	DNMBP	dynamin binding protein	-1.53	9.64	10.26	0.24	0.05	2.05E-02	8.64E-02	Multiple_Complex
TC2000009748.hg.1	CABLES2	Cdk5 and Abl enzyme substrate 2	-1.54	6.16	6.78	0.11	0.25	2.65E-02	1.03E-01	Multiple_Complex
TC2000006721.hg.1	BTBD3	BTB (POZ) domain containing 3	-1.54	9.51	10.13	0.37	0.03	2.65E-02	1.03E-01	Multiple_Complex
TC0200011040.hg.1	ITM2C	integral membrane protein 2C	-1.54	15.1	15.72	0.03	0.01	1.89E-02	8.18E-02	Multiple_Complex
TC1100012350.hg.1	DRD2	dopamine receptor D2	-1.54	3.87	4.49	0.03	0.21	4.09E-02	1.37E-01	Multiple_Complex
TC0200007975.hg.1	VAX2	ventral anterior homeobox 2	-1.54	4.17	4.79	0.29	0.27	3.69E-02	1.28E-01	Coding
TC2100007341.hg.1	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	-1.54	6.77	7.39	0.1	0.35	2.33E-02	9.45E-02	Multiple_Complex
TC0600007544.hg.1	TUBB	tubulin, beta class I	-1.54	13.43	14.05	0.23	0.05	1.58E-02	7.27E-02	Multiple_Complex
TSUnmapped00000244.hg.1	HYOU1	hypoxia up-regulated 1	-1.54	14.06	14.68	0.13	0.08	1.58E-02	7.27E-02	Coding

TC1100011155.hg.1	TRPT1	tRNA phosphotransferase 1	-1.54	10.16	10.78	0.19	0.07	1.47E-02	6.92E-02	Multiple_Complex
TC1200009416.hg.1	RAN	RAN, member RAS oncogene family	-1.54	14.44	15.06	0.27	0.12	2.41E-02	9.66E-02	Multiple_Complex
TC0400012396.hg.1	AADAT	aminoadipate aminotransferase	-1.54	10.16	10.78	0.1	0.01	3.47E-02	1.23E-01	Multiple_Complex
TC0800011713.hg.1	MTSS1	metastasis suppressor 1	-1.54	6.85	7.48	0.11	0.01	2.97E-02	1.11E-01	Multiple_Complex
TC0100018288.hg.1	PLEKHO1	pleckstrin homology domain containing, family O member 1	-1.54	8.99	9.61	0.19	0.28	2.04E-02	8.61E-02	Multiple_Complex
TC0300011135.hg.1	VPRBP	Vpr (HIV-1) binding protein	-1.54	7.76	8.38	0.03	0.33	2.96E-02	1.11E-01	Multiple_Complex
TC0600007627.hg.1	STK19	Homo sapiens serine/threonine kinase 19 (STK19), transcript variant 1, mRNA.; Homo sapiens serine/threonine kinase 19 (STK19), transcript variant 2, mRNA.; Homo sapiens serine/threonine kinase 19 (STK19), transcript variant 3, non-coding RNA.; Homo sapiens serine/threonine kinase 19, mRNA (cDNA clone MGC:117388 IMAGE:5165123), complete cds.	-1.54	7.9	8.53	0.24	0.02	1.91E-02	8.25E-02	Multiple_Complex
TC2200008411.hg.1	ASCC2	activating signal cointegrator 1 complex subunit 2	-1.54	10.14	10.77	0.1	0.08	2.32E-02	9.44E-02	Multiple_Complex
TC1800008906.hg.1	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	-1.54	9.36	9.98	0.04	0.03	2.72E-02	1.05E-01	Multiple_Complex
TC1700012193.hg.1	NDEL1	nudE neurodevelopment protein 1-like 1	-1.54	7.25	7.87	0.07	0.11	1.44E-02	6.84E-02	Multiple_Complex
TC1800008301.hg.1	OSBPL1A	oxysterol binding protein-like 1A	-1.54	8.08	8.7	0.03	0.09	1.96E-02	8.39E-02	Multiple_Complex
TC0200016516.hg.1	TMEM177	transmembrane protein 177	-1.54	6.8	7.42	0.34	0.31	3.93E-02	1.34E-01	Multiple_Complex
TC1900009254.hg.1	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	-1.54	11.81	12.44	0.03	0.21	1.81E-02	7.98E-02	Multiple_Complex
TC1000009090.hg.1	BAG3	BCL2-associated athanogene 3	-1.54	6.77	7.39	0.06	0.16	1.86E-02	8.13E-02	Coding

TC1200012717.hg.1	GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C	-1.54	14.25	14.87	0.13	0.08	1.53E-02	7.10E-02	Multiple_Complex
TSUnmapped00000405.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	-1.54	7.25	7.88	0.03	0.07	1.75E-02	7.80E-02	Coding
TC1100007844.hg.1	ASRGL1	asparaginase like 1	-1.54	7.92	8.55	0.42	0.06	2.69E-02	1.04E-01	Multiple_Complex
TC0500009108.hg.1	GPX3	glutathione peroxidase 3	-1.54	6.72	7.34	0.34	0.01	2.60E-02	1.02E-01	Multiple_Complex
TC0200007954.hg.1	PCYOX1	prenylcysteine oxidase 1	-1.54	8.6	9.23	0.05	0.22	2.15E-02	8.94E-02	Multiple_Complex
TC1100010092.hg.1	EIF4G2; SNORD97	eukaryotic translation initiation factor 4 gamma, 2; small nucleolar RNA, C/D box 97	-1.54	9.77	10.4	0.23	0.04	1.50E-02	7.02E-02	Multiple_Complex
TC2200008620.hg.1	IFT27	intraflagellar transport 27	-1.54	9.46	10.08	0.05	0.02	2.39E-02	9.61E-02	Multiple_Complex
TC1700012287.hg.1	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.54	8.51	9.13	0.4	0.08	3.36E-02	1.20E-01	Multiple_Complex
TC0300011023.hg.1	SHISA5	shisa family member 5	-1.54	14.41	15.03	0.12	0.23	2.23E-02	9.15E-02	Multiple_Complex
TC0700012230.hg.1	NRCAM	neuronal cell adhesion molecule	-1.54	11.26	11.88	0.34	0.01	2.44E-02	9.73E-02	Multiple_Complex
TC2100007467.hg.1	DIP2A	disco-interacting protein 2 homolog A	-1.54	7.06	7.68	0.21	0.2	2.04E-02	8.61E-02	Multiple_Complex
TC2000007105.hg.1	TM9SF4	transmembrane 9 superfamily protein member 4	-1.54	13.89	14.52	0.06	0.05	1.25E-02	6.22E-02	Multiple_Complex
TC0600012040.hg.1	TRAM2	translocation associated membrane protein 2	-1.54	9.19	9.82	0.34	0.12	2.47E-02	9.82E-02	Multiple_Complex
TC0200011051.hg.1	PSMD1	proteasome 26S subunit, non-ATPase 1	-1.54	9.14	9.77	0.27	0.15	1.94E-02	8.34E-02	Multiple_Complex
TC2000009821.hg.1	GMEB2	glucocorticoid modulatory element binding protein 2	-1.54	6.18	6.8	0.62	0.07	4.85E-02	1.54E-01	Multiple_Complex
TC1600011412.hg.1	SLC9A5	solute carrier family 9, subfamily A (NHE5, cation proton antiporter 5), member 5	-1.54	7.26	7.88	0.15	0.02	1.52E-02	7.09E-02	Multiple_Complex
TC1700008216.hg.1	KAT7	K(lysine) acetyltransferase 7	-1.55	7.01	7.63	0.14	0.1	2.14E-02	8.87E-02	Multiple_Complex
TC0X00011368.hg.1	SSX2; SSX2B	synovial sarcoma, X breakpoint 2; synovial sarcoma, X breakpoint 2B	-1.55	5.41	6.04	0.16	0.3	2.02E-02	8.56E-02	Multiple_Complex

TC0900011713.hg.1	FNBP1	formin binding protein 1	-1.55	8.85	9.48	0.12	0.44	3.48E-02	1.23E-01	Multiple_Complex
TC0100018338.hg.1	NAV1	neuron navigator 1	-1.55	8.1	8.73	0.17	0.14	1.62E-02	7.41E-02	Multiple_Complex
TC1600007030.hg.1	NPIPA7; NPIPA8; PKD1P1	nuclear pore complex interacting protein family, member A7; nuclear pore complex interacting protein family, member A8; polycystic kidney disease 1 (autosomal dominant) pseudogene 1	-1.55	11.28	11.91	0.46	0.17	3.42E-02	1.22E-01	Multiple_Complex
TC0700012684.hg.1	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	-1.55	11.87	12.5	0.03	0.03	1.28E-02	6.30E-02	Multiple_Complex
TC2200008781.hg.1	MKL1	megakaryoblastic leukemia (translocation) 1	-1.55	9.23	9.86	0.18	0.23	2.66E-02	1.03E-01	Multiple_Complex
TC1400010699.hg.1	CEP170B	centrosomal protein 170B	-1.55	7.69	8.32	0.08	0.36	2.41E-02	9.67E-02	Multiple_Complex
TC0100013641.hg.1	AK2	adenylate kinase 2	-1.55	13.59	14.22	0.21	0.03	1.42E-02	6.78E-02	Multiple_Complex
TC1400009410.hg.1	ZBTB25	zinc finger and BTB domain containing 25	-1.55	9.17	9.8	0.23	0.19	1.95E-02	8.37E-02	Multiple_Complex
TC0900011864.hg.1	VAV2	vav 2 guanine nucleotide exchange factor	-1.55	6.33	6.96	0.31	0.01	2.09E-02	8.75E-02	Multiple_Complex
TC1200010341.hg.1	PKP2	plakophilin 2	-1.55	10.37	11	0.3	0.13	2.13E-02	8.86E-02	Multiple_Complex
TC0500009097.hg.1	SYNPO	synaptopodin	-1.55	6.55	7.18	0.06	0.34	4.77E-02	1.52E-01	Multiple_Complex
TC0700009996.hg.1	C7orf50	chromosome 7 open reading frame 50	-1.55	6.95	7.58	0.22	0.28	2.81E-02	1.07E-01	Multiple_Complex
TC1900007869.hg.1	RBM42	RNA binding motif protein 42	-1.55	10.29	10.92	0.11	0.39	2.39E-02	9.61E-02	Multiple_Complex
TC1400008631.hg.1	CHD8	chromodomain helicase DNA binding protein 8	-1.55	10.14	10.77	0.04	0.01	1.44E-02	6.85E-02	Multiple_Complex
TC1600007465.hg.1	ZNF48	zinc finger protein 48	-1.55	5.24	5.87	0.17	0.36	2.25E-02	9.23E-02	Multiple_Complex
TC2000008030.hg.1	OGFR	opioid growth factor receptor	-1.55	7.55	8.18	0.13	0.12	1.31E-02	6.40E-02	Multiple_Complex
TC1000007936.hg.1	SGPL1	sphingosine-1-phosphate lyase 1	-1.55	7.26	7.9	0.14	0.22	2.41E-02	9.66E-02	Multiple_Complex
TC0300008768.hg.1	HMCES	5-hydroxymethylcytosine (hmC) binding, ES cell-specific	-1.55	9.64	10.27	0.33	0.06	1.82E-02	8.01E-02	Multiple_Complex

TC0600009744.hg.1	RAB32	RAB32, member RAS oncogene family	-1.55	10.36	10.99	0.16	0.13	1.50E-02	7.01E-02	Multiple_Complex
TC0900007472.hg.1	ANKRD20A1	ankyrin repeat domain 20 family, member A1	-1.55	6.48	7.12	0.09	0.01	1.26E-02	6.25E-02	Multiple_Complex
TC1400007495.hg.1	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	-1.55	11.64	12.27	0.21	0.01	1.61E-02	7.36E-02	Multiple_Complex
TC0100013574.hg.1	PEF1	penta-EF-hand domain containing 1	-1.55	7.88	8.51	0.4	0.37	4.79E-02	1.53E-01	Multiple_Complex
TC0500012025.hg.1	08-Sep	septin 8	-1.55	7.27	7.9	0.11	0.34	2.49E-02	9.86E-02	Multiple_Complex
TC1900007279.hg.1	C19orf44	chromosome 19 open reading frame 44	-1.55	8.14	8.77	0.11	0.06	1.31E-02	6.40E-02	Multiple_Complex
TC0200016421.hg.1	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.55	11.46	12.1	0.38	0.14	2.38E-02	9.61E-02	Multiple_Complex
TC2100007336.hg.1	TRAPPC10	trafficking protein particle complex 10	-1.55	7.94	8.57	0.44	0.13	2.85E-02	1.08E-01	Multiple_Complex
TC0200013284.hg.1	C2orf68	chromosome 2 open reading frame 68	-1.55	10.67	11.3	0.07	0.39	2.38E-02	9.58E-02	Multiple_Complex
TC1200012654.hg.1	TSFM	Ts translation elongation factor, mitochondrial	-1.55	9.03	9.66	0.47	0.15	3.39E-02	1.21E-01	Multiple_Complex
TC1900011982.hg.1	OPA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	-1.55	5.07	5.71	0.35	0.26	4.14E-02	1.38E-01	Coding
TC1700009694.hg.1	MYH10	myosin, heavy chain 10, non-muscle	-1.55	13.32	13.95	0.14	0.03	1.62E-02	7.41E-02	Multiple_Complex
TC0200013578.hg.1	TMEM131	transmembrane protein 131	-1.55	7.66	8.3	0.51	0.03	3.78E-02	1.30E-01	Multiple_Complex
TC0400006579.hg.1	ADD1	adducin 1 (alpha)	-1.55	8.11	8.74	0.6	0.03	4.86E-02	1.54E-01	Multiple_Complex
TC1100007233.hg.1	KIAA1549L	KIAA1549-like	-1.55	7.04	7.67	0.47	0.11	3.70E-02	1.28E-01	Multiple_Complex
TC0400009764.hg.1	HAUS3; POLN	HAUS augmin like complex subunit 3; polymerase (DNA directed) nu	-1.55	5.33	5.96	0.19	0.37	2.57E-02	1.01E-01	Multiple_Complex

TC0Y00006476.hg.1	CD99	Homo sapiens CD99 molecule (CD99), transcript variant 2, mRNA.; Homo sapiens CD99 molecule (CD99), transcript variant 3, mRNA.; Homo sapiens CD99 molecule (CD99), transcript variant 1, mRNA.; CD99 molecule [Source:HGNC Symbol;Acc:HGNC:7082]; Homo sapiens CD99 molecule, mRNA (cDNA clone MGC:2282 IMAGE:3161673), complete cds.; Homo sapiens CD99 molecule, mRNA (cDNA clone MGC:3938 IMAGE:2906143), complete cds.; Homo sapiens CD99 molecule, mRNA (cDNA clone MGC:19734 IMAGE:3606974), complete cds.; Homo sapiens CD99 molecule, mRNA (cDNA clone MGC:4214 IMAGE:2957883), complete cds.; Homo sapiens CD99 molecule, mRNA (cDNA clone MGC:14521 IMAGE:4094268), complete cds.; Salzman2013 ANNOTATED, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_002414; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVEXON, UTR3 best transcript NM_002414	-1.55	12.3	12.94	0.2	0.1	1.52E-02	7.07E-02	Multiple_Complex
TC2000007224.hg.1	SPAG4	sperm associated antigen 4	-1.55	5.97	6.61	0.25	0.15	1.63E-02	7.42E-02	Multiple_Complex
TC1000012589.hg.1	MRPL43	mitochondrial ribosomal protein L43	-1.55	10.05	10.69	0.1	0.25	1.52E-02	7.08E-02	Multiple_Complex
TC2000009800.hg.1	YTHDF1	YTH N(6)-methyladenosine RNA binding protein 1	-1.55	8.94	9.58	0.12	0.08	2.31E-02	9.40E-02	Multiple_Complex

TC1700012218.hg.1	SARM1	sterile alpha and TIR motif containing 1	-1.55	5.14	5.78	0.27	0.28	4.73E-02	1.51E-01	Multiple_Complex
TC0100014228.hg.1	LRP8	LDL receptor related protein 8	-1.55	7.43	8.06	0.16	0.27	2.09E-02	8.74E-02	Multiple_Complex
TC1600010752.hg.1	AARS	alanyl-tRNA synthetase	-1.55	14.57	15.21	0	0.11	1.19E-02	6.00E-02	Multiple_Complex
TC1700008378.hg.1	MSI2	musashi RNA binding protein 2	-1.55	9.45	10.09	0.03	0.38	2.57E-02	1.01E-01	Multiple_Complex
TC0700011658.hg.1	SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	-1.55	5.48	6.12	0.14	0.39	3.33E-02	1.20E-01	Coding
TC1900009062.hg.1	TRIM28	tripartite motif containing 28	-1.55	11.04	11.68	0.05	0.15	1.54E-02	7.13E-02	Multiple_Complex
TC1900006991.hg.1	SLC44A2	solute carrier family 44 (choline transporter), member 2	-1.55	6.36	7	0.15	0.25	2.62E-02	1.02E-01	Multiple_Complex
TC1900007260.hg.1	TPM4	tropomyosin 4	-1.55	9.84	10.48	0	0.3	1.90E-02	8.20E-02	Multiple_Complex
TC0200013261.hg.1	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	-1.56	10.32	10.96	0.47	0.01	3.61E-02	1.26E-01	Multiple_Complex
TC1900011856.hg.1	CD320	CD320 molecule	-1.56	12.06	12.7	0.28	0.32	3.00E-02	1.12E-01	Multiple_Complex
TC1400009147.hg.1	PYGL	phosphorylase, glycogen, liver	-1.56	12.14	12.77	0.32	0.14	2.07E-02	8.71E-02	Multiple_Complex
TC1600011460.hg.1	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	-1.56	5.9	6.53	0.41	0.3	4.14E-02	1.38E-01	Multiple_Complex
TC1200011968.hg.1	HECTD4; MIR6861	HECT domain containing E3 ubiquitin protein ligase 4; microRNA 6861	-1.56	9.4	10.03	0.48	0.1	4.04E-02	1.36E-01	Multiple_Complex
TC1000008221.hg.1	TMEM254	transmembrane protein 254	-1.56	8.49	9.13	0.25	0.13	3.13E-02	1.15E-01	Multiple_Complex
TC0200012022.hg.1	KIF3C	kinesin family member 3C	-1.56	7.18	7.82	0.13	0.1	3.63E-02	1.26E-01	Multiple_Complex
TC1900011745.hg.1	ARHGEF1	Rho guanine nucleotide exchange factor 1	-1.56	4.77	5.41	0.08	0.09	1.12E-02	5.76E-02	Multiple_Complex
TC1900007882.hg.1	PROSER3	proline and serine rich 3	-1.56	6.31	6.95	0.38	0.26	3.14E-02	1.15E-01	Multiple_Complex
TC1900008999.hg.1	ZNF549	zinc finger protein 549	-1.56	4.23	4.87	0.01	0.21	4.39E-02	1.44E-01	Coding
TC1600010593.hg.1	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	-1.56	10.15	10.79	0.03	0.1	1.25E-02	6.22E-02	Multiple_Complex

TC0200010713.hg.1	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	-1.56	12.95	13.59	0.31	0.04	2.50E-02	9.90E-02	Multiple_Complex
TC0500006523.hg.1	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	-1.56	13.14	13.78	0.05	0.08	1.01E-02	5.36E-02	Multiple_Complex
TC0700008023.hg.1	GATSL2	GATS protein-like 2	-1.56	7	7.64	0.08	0.26	2.42E-02	9.69E-02	Multiple_Complex
TC1300009638.hg.1	RPS26	Homo sapiens ribosomal protein S26, mRNA (cDNA clone MGC:104291 IMAGE:4287636), complete cds.	-1.56	12.2	12.84	0.34	0.1	2.56E-02	1.01E-01	Multiple_Complex
TC0900011523.hg.1	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	-1.56	12.98	13.62	0.06	0.14	1.17E-02	5.93E-02	Multiple_Complex
TC0X00008874.hg.1	F8A2	coagulation factor VIII-associated 2	-1.56	9.17	9.81	0.24	0.05	2.32E-02	9.42E-02	Coding
TC0600011478.hg.1	FKBPL	FK506 binding protein like	-1.56	7.01	7.65	0.4	0.17	2.56E-02	1.01E-01	Coding
TC0900011286.hg.1	DFNB31	deafness, autosomal recessive 31	-1.56	8.05	8.69	0.11	0.2	2.74E-02	1.05E-01	Multiple_Complex
TC2200008706.hg.1	FAM227A	family with sequence similarity 227, member A	-1.56	7.06	7.71	0.02	0.19	2.30E-02	9.38E-02	Multiple_Complex
TSUnmapped00000343.hg.1	ATG16L1	autophagy related 16-like 1	-1.56	8.44	9.08	0.55	0.24	4.91E-02	1.55E-01	NonCoding
TC1100011054.hg.1	RAB3IL1	RAB3A interacting protein (rabin3)-like 1	-1.56	8.54	9.18	0.13	0.11	1.20E-02	6.03E-02	Multiple_Complex
TC2200007361.hg.1	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	-1.56	9.42	10.06	0.17	0.06	1.38E-02	6.65E-02	Multiple_Complex
TC1500010830.hg.1	OR4F6	olfactory receptor, family 4, subfamily F, member 6	-1.56	3.78	4.42	0.06	0.01	2.63E-02	1.03E-01	Coding
TC1600007099.hg.1	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	-1.56	7.39	8.04	0.19	0.11	2.33E-02	9.46E-02	Multiple_Complex
TC1400009791.hg.1	ALKBH1	alkB homolog 1, histone H2A dioxygenase	-1.56	8.24	8.88	0.14	0.29	2.17E-02	8.97E-02	Multiple_Complex
TC0X00007302.hg.1	FAM156B; FAM156A	family with sequence similarity 156, member B; family with sequence similarity 156, member A	-1.56	5.95	6.6	0.03	0.08	3.70E-02	1.28E-01	Multiple_Complex

TC1900011057.hg.1	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	-1.56	5.51	6.15	0.19	0.11	1.45E-02	6.86E-02	Multiple_Complex
TC0100009383.hg.1	RBM15	RNA binding motif protein 15	-1.56	9.97	10.61	0.15	0.01	1.46E-02	6.88E-02	Coding
TC2200007544.hg.1	BIK	BCL2-interacting killer (apoptosis-inducing)	-1.56	6.46	7.1	0.36	0.09	2.54E-02	1.00E-01	Coding
TC0100017500.hg.1	TMEM63A	transmembrane protein 63A	-1.56	9.27	9.92	0.15	0.09	1.14E-02	5.85E-02	Multiple_Complex
TC1100010738.hg.1	PSMC3	proteasome 26S subunit, ATPase 3	-1.56	9.92	10.57	0.03	0.01	1.87E-02	8.15E-02	Multiple_Complex
TC2000009469.hg.1	ZFP64	ZFP64 zinc finger protein	-1.56	5.78	6.42	0.4	0.19	2.67E-02	1.04E-01	Multiple_Complex
TC2000008001.hg.1	ADRM1	adhesion regulating molecule 1	-1.56	10.01	10.65	0.34	0.36	3.40E-02	1.22E-01	Multiple_Complex
TC0100013189.hg.1	KIF17	kinesin family member 17	-1.57	5.95	6.6	0.08	0.45	3.47E-02	1.23E-01	Multiple_Complex
TC0300011110.hg.1	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	-1.57	4.25	4.9	0.21	0.02	1.25E-02	6.22E-02	Multiple_Complex
TC2100008222.hg.1	RIPK4	receptor-interacting serine-threonine kinase 4	-1.57	7.45	8.1	0.05	0.07	1.52E-02	7.09E-02	Coding
TC0300007290.hg.1	KLHL18	kelch-like family member 18	-1.57	7.27	7.91	0.01	0.22	2.21E-02	9.11E-02	Multiple_Complex
TC2000007016.hg.1	GINS1	GINS complex subunit 1 (Psf1 homolog)	-1.57	10.89	11.54	0.03	0.09	1.06E-02	5.55E-02	Multiple_Complex
TC2200008226.hg.1	GUCD1	guanylyl cyclase domain containing 1	-1.57	10.56	11.21	0.12	0.12	2.39E-02	9.62E-02	Multiple_Complex
TC1900011743.hg.1	TMEM91	transmembrane protein 91	-1.57	6.16	6.81	0.02	0.35	2.30E-02	9.37E-02	Multiple_Complex
TC1300008044.hg.1	ARHGEF7	Rho guanine nucleotide exchange factor 7	-1.57	6.95	7.6	0.11	0.21	4.32E-02	1.42E-01	Multiple_Complex
TC1100011539.hg.1	NUMA1	nuclear mitotic apparatus protein 1	-1.57	7.1	7.74	0.32	0.05	2.13E-02	8.87E-02	Multiple_Complex
TC1100010762.hg.1	NUP160	nucleoporin 160kDa	-1.57	8.77	9.42	0.22	0.09	1.45E-02	6.88E-02	Multiple_Complex
TC0900009040.hg.1	C9orf9	chromosome 9 open reading frame 9	-1.57	5.81	6.46	0.09	0.06	1.34E-02	6.51E-02	Multiple_Complex
TC0300008467.hg.1	ARHGAP31	Rho GTPase activating protein 31	-1.57	4.35	4.99	0.43	0.03	4.52E-02	1.47E-01	Multiple_Complex
TC1900009361.hg.1	DPP9	dipeptidyl-peptidase 9	-1.57	9.16	9.81	0.04	0.31	1.69E-02	7.61E-02	Multiple_Complex
TC0200011980.hg.1	ITSN2	intersectin 2	-1.57	9.32	9.97	0.06	0.35	1.83E-02	8.01E-02	Multiple_Complex

TC0600009862.hg.1	AKAP12	A kinase (PRKA) anchor protein 12	-1.57	11.43	12.08	0	0.01	1.19E-02	6.00E-02	Multiple_Complex
TC1200012705.hg.1	TCHP	trichoplein, keratin filament binding	-1.57	5.97	6.62	0.19	0.31	1.96E-02	8.40E-02	NonCoding
TC0700009643.hg.1	KRBA1	KRAB-A domain containing 1	-1.57	6.1	6.75	0.11	0.22	1.24E-02	6.17E-02	Multiple_Complex
TC0300007512.hg.1	PRKCD	protein kinase C, delta	-1.57	7.34	7.99	0.2	0.08	2.10E-02	8.79E-02	Multiple_Complex
TC0100016971.hg.1	ADIPOR1	adiponectin receptor 1	-1.57	11.78	12.43	0.11	0.1	1.10E-02	5.70E-02	Multiple_Complex
TC0500009470.hg.1	ERGIC1	endoplasmic reticulum-golgi intermediate compartment 1	-1.57	11.83	12.48	0.14	0.1	1.31E-02	6.40E-02	Multiple_Complex
TC1600010794.hg.1	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	-1.57	7.4	8.05	0.01	0.1	1.15E-02	5.88E-02	Multiple_Complex
TC1500006969.hg.1	ZFYVE19	zinc finger, FYVE domain containing 19	-1.57	8.43	9.08	0.56	0.03	4.14E-02	1.38E-01	Multiple_Complex
TC0900008967.hg.1	EXOSC2	exosome component 2	-1.57	13.57	14.23	0.04	0.05	9.70E-03	5.26E-02	Multiple_Complex
TC1700006703.hg.1	C17orf100	chromosome 17 open reading frame 100	-1.57	4.8	5.45	0.02	0.41	2.02E-02	8.56E-02	Multiple_Complex
TC1200012543.hg.1	ANKLE2	ankyrin repeat and LEM domain containing 2	-1.57	7.32	7.97	0.07	0.03	1.20E-02	6.05E-02	Multiple_Complex
TC1200012327.hg.1	SCARB1	scavenger receptor class B, member 1	-1.57	6.57	7.22	0.08	0.32	1.76E-02	7.81E-02	Multiple_Complex
TC0100018480.hg.1	NBPF14	neuroblastoma breakpoint family, member 14	-1.57	10.94	11.59	0.28	0.34	2.26E-02	9.23E-02	Coding
TC1700012401.hg.1	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	-1.57	11.36	12.01	0.36	0.14	2.11E-02	8.79E-02	Multiple_Complex
TC0900011769.hg.1	FAM78A	family with sequence similarity 78, member A	-1.57	3.79	4.44	0.42	0.26	4.11E-02	1.38E-01	Multiple_Complex
TC2000008750.hg.1	NANP	N-acetylneuraminic acid phosphatase	-1.57	9.91	10.56	0.04	0.07	9.70E-03	5.24E-02	Coding
TC0X00008776.hg.1	ZNF275	zinc finger protein 275	-1.57	8.22	8.87	0.09	0.22	3.70E-02	1.28E-01	Multiple_Complex
TC0200016618.hg.1	RNASEH1	ribonuclease H1	-1.57	8.48	9.14	0.04	0.28	1.65E-02	7.50E-02	Multiple_Complex
TC2200009282.hg.1	SAMM50	SAMM50 sorting and assembly machinery component	-1.57	13.34	13.99	0.15	0.03	1.26E-02	6.23E-02	Multiple_Complex

TC0100011364.hg.1	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	-1.57	9.34	9.99	0.04	0.17	1.52E-02	7.08E-02	Multiple_Complex
TC1900010957.hg.1	SYMPK	symplekin	-1.57	14.18	14.83	0.06	0.02	9.00E-03	4.97E-02	Multiple_Complex
TC1900007026.hg.1	SWSAP1	SWIM-type zinc finger 7 associated protein 1	-1.57	5.16	5.81	0.21	0.37	3.34E-02	1.20E-01	Coding
TC1900006985.hg.1	PDE4A	phosphodiesterase 4A, cAMP-specific	-1.57	6.04	6.7	0.4	0.43	3.84E-02	1.31E-01	Multiple_Complex
TC0100007949.hg.1	ZMPSTE24	zinc metallopeptidase STE24	-1.57	10.26	10.91	0.05	0.04	1.32E-02	6.45E-02	Multiple_Complex
TC1000009414.hg.1	INPP5A	inositol polyphosphate-5-phosphatase A	-1.57	6.05	6.7	0.45	0.21	3.64E-02	1.27E-01	Multiple_Complex
TC1400008355.hg.1	RCOR1	REST corepressor 1	-1.57	6.97	7.63	0.12	0.3	1.79E-02	7.91E-02	Multiple_Complex
TC0600011943.hg.1	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	-1.57	7.08	7.74	0.41	0.02	2.83E-02	1.08E-01	Multiple_Complex
TC1200010038.hg.1	EPS8	epidermal growth factor receptor pathway substrate 8	-1.57	7	7.65	0.26	0.16	1.88E-02	8.17E-02	Multiple_Complex
TC1200009913.hg.1	YBX3	Y box binding protein 3	-1.57	14.41	15.07	0.03	0.03	1.28E-02	6.31E-02	Multiple_Complex
TC0300006687.hg.1	CCDC174	coiled-coil domain containing 174	-1.57	6.76	7.41	0.21	0.04	2.55E-02	1.01E-01	Multiple_Complex
TC0100011847.hg.1	ARF1; MIR3620	ADP-ribosylation factor 1; microRNA 3620	-1.57	14.97	15.62	0.06	0.18	1.29E-02	6.36E-02	Multiple_Complex
TC1100013004.hg.1	CTNND1	catenin (cadherin-associated protein), delta 1	-1.57	9.32	9.98	0.19	0.01	1.66E-02	7.51E-02	Multiple_Complex
TC1600011467.hg.1	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-1.58	8.2	8.86	0.32	0.4	2.86E-02	1.08E-01	Multiple_Complex
TC1900011752.hg.1	ZNF223	zinc finger protein 223	-1.58	6.45	7.11	0.13	0.02	4.43E-02	1.45E-01	Multiple_Complex
TC0200012062.hg.1	PREB	prolactin regulatory element binding	-1.58	7.55	8.21	0.27	0.35	2.23E-02	9.15E-02	Multiple_Complex
TC0200008263.hg.1	USP39	ubiquitin specific peptidase 39	-1.58	13.54	14.2	0.04	0.03	1.29E-02	6.36E-02	Multiple_Complex
TC1600009545.hg.1	ABCC6	ATP binding cassette subfamily C member 6	-1.58	8.17	8.82	0.28	0.38	4.61E-02	1.49E-01	Multiple_Complex
TC1900011866.hg.1	RAB3D	RAB3D, member RAS oncogene family	-1.58	6.72	7.38	0.22	0.37	2.34E-02	9.47E-02	Multiple_Complex
TC1100011058.hg.1	FTH1	ferritin, heavy polypeptide 1	-1.58	13.89	14.54	0.13	0.06	1.16E-02	5.91E-02	Multiple_Complex

TC1600009722.hg.1	USP31	ubiquitin specific peptidase 31	-1.58	5.8	6.45	0.18	0.06	1.42E-02	6.78E-02	Multiple_Complex
TC1900011061.hg.1	CARD8	caspase recruitment domain family, member 8	-1.58	8.16	8.82	0.16	0.43	3.57E-02	1.25E-01	Multiple_Complex
TC0300010845.hg.1	SEC22C	SEC22 homolog C, vesicle trafficking protein	-1.58	7.12	7.78	0.01	0.35	3.62E-02	1.26E-01	Multiple_Complex
TC1900007425.hg.1	RFXANK	regulatory factor X-associated ankyrin-containing protein	-1.58	9.71	10.36	0.36	0.38	3.16E-02	1.16E-01	Multiple_Complex
TC1600009777.hg.1	ARHGAP17	Rho GTPase activating protein 17	-1.58	8.1	8.76	0.07	0.36	1.99E-02	8.47E-02	Multiple_Complex
TC0600010060.hg.1	MRPL18	mitochondrial ribosomal protein L18	-1.58	11.14	11.8	0.15	0.25	1.42E-02	6.77E-02	Multiple_Complex
TC0X00008495.hg.1	FAM127A	family with sequence similarity 127, member A	-1.58	9.37	10.02	0.06	0.35	1.71E-02	7.66E-02	Multiple_Complex
TC2100008559.hg.1	C21orf59	chromosome 21 open reading frame 59	-1.58	14.01	14.67	0.07	0.14	1.27E-02	6.29E-02	Multiple_Complex
TC0100008121.hg.1	TOE1	target of EGR1, member 1 (nuclear)	-1.58	8.67	9.33	0.08	0.06	8.70E-03	4.90E-02	Multiple_Complex
TC0700012898.hg.1	TCAF1	TRPM8 channel-associated factor 1	-1.58	6.05	6.71	0.47	0.21	3.52E-02	1.24E-01	Multiple_Complex
TC0100018442.hg.1	CYB5RL	cytochrome b5 reductase-like	-1.58	7.85	8.51	0.15	0.34	2.68E-02	1.04E-01	Multiple_Complex
TC2000006559.hg.1	CDC25B	cell division cycle 25B	-1.58	8.19	8.85	0.15	0.12	1.21E-02	6.08E-02	Multiple_Complex
TC0100007240.hg.1	NBPF3	neuroblastoma breakpoint family, member 3	-1.58	5.57	6.23	0.28	0.08	1.92E-02	8.27E-02	Multiple_Complex
TSUnmapped00000546.hg.1	RCC2	regulator of chromosome condensation 2	-1.58	10.8	11.46	0.34	0.04	1.61E-02	7.38E-02	Coding
TC1800007960.hg.1	ZBTB14	zinc finger and BTB domain containing 14	-1.58	5.55	6.21	0.28	0.6	4.65E-02	1.49E-01	Multiple_Complex
TSUnmapped00000267.hg.1	LRP6	LDL receptor related protein 6	-1.58	8.77	9.43	0.19	0.02	1.73E-02	7.72E-02	Coding
TC1400009784.hg.1	VIPAS39	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog	-1.58	9.72	10.38	0.12	0.05	2.74E-02	1.05E-01	Multiple_Complex
TC0100015810.hg.1	MRPL9	mitochondrial ribosomal protein L9	-1.58	10.41	11.07	0.15	0.35	1.74E-02	7.74E-02	Multiple_Complex
TC0100012211.hg.1	ZBTB18	zinc finger and BTB domain containing 18	-1.58	4.88	5.54	0.23	0.37	2.32E-02	9.42E-02	Multiple_Complex

TC0700009693.hg.1	AGAP3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	-1.58	12.37	13.03	0.19	0.07	1.04E-02	5.47E-02	Multiple_Complex
TC1200007615.hg.1	DIP2B	disco-interacting protein 2 homolog B	-1.58	10.64	11.3	0.12	0.16	1.15E-02	5.88E-02	Multiple_Complex
TC0100012870.hg.1	EXOSC10	exosome component 10	-1.58	9.16	9.82	0.18	0	9.80E-03	5.28E-02	Multiple_Complex
TC1700010565.hg.1	FBXL20	F-box and leucine-rich repeat protein 20	-1.58	9.01	9.67	0.22	0.24	1.65E-02	7.50E-02	Multiple_Complex
TC0800009231.hg.1	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	-1.58	6.02	6.68	0.02	0.05	1.11E-02	5.75E-02	Multiple_Complex
TC0600010936.hg.1	ATXN1	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_000332	-1.58	5.84	6.5	0.12	0.01	2.61E-02	1.02E-01	NonCoding
TC2200008018.hg.1	TRMT2A	tRNA methyltransferase 2 homolog A	-1.58	12.41	13.08	0.04	0.27	1.29E-02	6.34E-02	Multiple_Complex
TC0X00010813.hg.1	ENOX2	ecto-NOX disulfide-thiol exchanger 2	-1.58	9.09	9.75	0.12	0.39	2.52E-02	9.95E-02	Multiple_Complex
TC1800009056.hg.1	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	-1.58	6.14	6.8	0.32	0.34	2.81E-02	1.07E-01	Coding
TC2000009263.hg.1	CDH22	cadherin 22, type 2	-1.58	4.24	4.9	0.58	0.26	3.93E-02	1.34E-01	Multiple_Complex
TC0200009270.hg.1	RAB6C	RAB6C, member RAS oncogene family	-1.58	6.79	7.45	0.39	0.4	3.26E-02	1.18E-01	Coding
TC1700010748.hg.1	BECN1	beclin 1, autophagy related	-1.58	9.35	10.01	0.2	0.28	1.92E-02	8.27E-02	Multiple_Complex
TC1400008173.hg.1	CCNK	cyclin K	-1.58	11.42	12.09	0.13	0.17	1.54E-02	7.14E-02	Multiple_Complex
TC0X00008108.hg.1	TMEM164	transmembrane protein 164	-1.58	6.19	6.85	0.57	0.27	3.92E-02	1.33E-01	Multiple_Complex
TC0300006714.hg.1	EAF1	ELL associated factor 1	-1.58	7.85	8.52	0.14	0.19	1.57E-02	7.25E-02	Multiple_Complex
TC1700012286.hg.1	SMG8	SMG8 nonsense mediated mRNA decay factor	-1.58	6.45	7.11	0.17	0.02	3.66E-02	1.27E-01	Multiple_Complex
TC0300012281.hg.1	ZXDC	ZXD family zinc finger C	-1.58	9.62	10.29	0.06	0.29	1.84E-02	8.06E-02	Multiple_Complex
TC0900009930.hg.1	FANCG	Fanconi anemia complementation group G	-1.58	5.26	5.92	0	0.31	2.03E-02	8.60E-02	Multiple_Complex

TC0700010170.hg.1	RNF216	ring finger protein 216	-1.58	9.55	10.21	0.03	0.24	1.93E-02	8.32E-02	Multiple_Complex
TC1300008113.hg.1	CUL4A	cullin 4A	-1.58	6.92	7.59	0.03	0.46	3.28E-02	1.19E-01	Multiple_Complex
TC0100014775.hg.1	BCL10	B-cell CLL/lymphoma 10	-1.58	8.47	9.13	0.52	0.17	3.46E-02	1.23E-01	Coding
TC1700012260.hg.1	COASY	CoA synthase	-1.59	9.22	9.88	0.11	0.2	1.11E-02	5.73E-02	Multiple_Complex
TC1600007234.hg.1	DCTN5	dynactin 5 (p25)	-1.59	9.17	9.83	0.13	0.38	2.69E-02	1.04E-01	Multiple_Complex
TC0100015743.hg.1	ENSA	endosulfine alpha	-1.59	11.48	12.14	0.48	0.19	2.81E-02	1.07E-01	Multiple_Complex
TC0100007469.hg.1	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	-1.59	5.06	5.72	0.05	0.25	1.35E-02	6.55E-02	Multiple_Complex
TC0300011264.hg.1	IL17RD	interleukin 17 receptor D	-1.59	4.97	5.64	0.15	0.51	3.80E-02	1.31E-01	Multiple_Complex
TC0600014099.hg.1	GTF2H4	general transcription factor IIH subunit 4	-1.59	9.33	10	0.58	0.3	4.06E-02	1.36E-01	Multiple_Complex
TC1900011849.hg.1	DUS3L	dihydrouridine synthase 3-like	-1.59	7.92	8.59	0.29	0.49	4.63E-02	1.49E-01	Multiple_Complex
TC1200012642.hg.1	BLOC1S1-RDH5; RP11-644F5.10	BLOC1S1-RDH5 readthrough; Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F8VNQ1]	-1.59	9.59	10.26	0.3	0.18	1.76E-02	7.81E-02	Multiple_Complex
TC0900012231.hg.1	SHB	Src homology 2 domain containing adaptor protein B	-1.59	8.19	8.86	0.1	0.03	8.50E-03	4.83E-02	Multiple_Complex
TC0700009337.hg.1	C7orf55-LUC7L2; LUC7L2; C7orf55	C7orf55-LUC7L2 readthrough; LUC7-like 2 pre-mRNA splicing factor; chromosome 7 open reading frame 55	-1.59	7.59	8.26	0.14	0	1.02E-02	5.40E-02	Multiple_Complex
TC0100007463.hg.1	HMGN2	high mobility group nucleosomal binding domain 2	-1.59	11.14	11.81	0.04	0.04	7.90E-03	4.59E-02	Multiple_Complex
TC1200007536.hg.1	CCDC65	coiled-coil domain containing 65	-1.59	4.64	5.31	0.24	0.13	2.21E-02	9.11E-02	Multiple_Complex
TC0200015231.hg.1	NEMP2	nuclear envelope integral membrane protein 2	-1.59	6.1	6.77	0.51	0.46	4.52E-02	1.47E-01	Multiple_Complex
TC0100014210.hg.1	COA7	cytochrome c oxidase assembly factor 7 (putative)	-1.59	8.09	8.76	0.03	0.11	8.70E-03	4.90E-02	Multiple_Complex

TC1100012473.hg.1	MPZL3	myelin protein zero-like 3	-1.59	9.06	9.73	0.27	0.05	2.89E-02	1.09E-01	Multiple_Complex
TC0600014188.hg.1	PHACTR2	phosphatase and actin regulator 2	-1.59	8.64	9.31	0.07	0.02	1.02E-02	5.39E-02	Multiple_Complex
TC0600010901.hg.1	DTNBP1	dystrobrevin binding protein 1	-1.59	8.34	9.01	0.53	0.23	4.70E-02	1.51E-01	Multiple_Complex
TC1200012639.hg.1	HOXC6; HOXC4; HOXC5	homeobox C6; homeobox C4; homeobox C5	-1.59	5.33	6	0.21	0.06	1.32E-02	6.44E-02	Multiple_Complex
TC0700011929.hg.1	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	-1.59	8.15	8.82	0.18	0.16	1.55E-02	7.16E-02	Multiple_Complex
TC1100011192.hg.1	ATG2A	autophagy related 2A	-1.59	8.21	8.88	0.11	0.26	1.54E-02	7.13E-02	Multiple_Complex
TC0600011537.hg.1	ZBTB22	zinc finger and BTB domain containing 22	-1.59	5.67	6.35	0.28	0.3	2.45E-02	9.77E-02	Coding
TC0400006584.hg.1	GRK4	G protein-coupled receptor kinase 4	-1.59	6.8	7.47	0.11	0.28	3.31E-02	1.19E-01	NonCoding
TC0400009936.hg.1	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	-1.59	11.26	11.93	0.06	0	1.00E-02	5.32E-02	Multiple_Complex
TC0600014130.hg.1	RRP36	ribosomal RNA processing 36	-1.59	7.6	8.27	0.55	0.02	2.79E-02	1.07E-01	NonCoding
TC0200007363.hg.1	MTA3	metastasis associated 1 family member 3	-1.59	9.59	10.26	0.12	0.19	1.03E-02	5.45E-02	Multiple_Complex
TSUnmapped00000207.hg.1	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	-1.59	11.88	12.55	0.01	0.13	8.70E-03	4.90E-02	NonCoding
TC1500010907.hg.1	MESDC2	mesoderm development candidate 2	-1.59	5.86	6.53	0.11	0.18	1.13E-02	5.81E-02	Multiple_Complex
TC1700012468.hg.1	HN1	hematological and neurological expressed 1	-1.59	12.78	13.45	0.23	0.07	1.35E-02	6.55E-02	Multiple_Complex
TC1100011241.hg.1	MAP3K11	mitogen-activated protein kinase kinase kinase 11	-1.59	10.85	11.52	0.45	0.22	2.61E-02	1.02E-01	Multiple_Complex
TC1000010980.hg.1	ASCC1	activating signal cointegrator 1 complex subunit 1	-1.59	8.31	8.98	0.44	0.09	1.96E-02	8.39E-02	Multiple_Complex
TC0800007311.hg.1	ADGRA2	adhesion G protein-coupled receptor A2	-1.59	7.09	7.77	0.28	0.44	3.67E-02	1.27E-01	Multiple_Complex
TC1400010796.hg.1	JAG2	jagged 2	-1.59	8.56	9.23	0.23	0.43	2.37E-02	9.57E-02	Multiple_Complex
TC1000010602.hg.1	ERCC6; ERCC6-PGBD3; PGBD3	excision repair cross-complementation group 6; ERCC6-PGBD3 readthrough; piggyBac transposable element derived 3	-1.59	8.13	8.8	0.32	0.1	1.95E-02	8.36E-02	Multiple_Complex

TC1600009088.hg.1	PKD1; MIR6511B2; MIR6511B1	polycystic kidney disease 1 (autosomal dominant); microRNA 6511b-2; microRNA 6511b-1	-1.59	7.9	8.57	0.14	0.52	2.70E-02	1.04E-01	Multiple_Complex
TC1900008433.hg.1	GLTSCR2; SNORD23	glioma tumor suppressor candidate region gene 2; small nucleolar RNA, C/D box 23	-1.6	11.11	11.78	0.03	0.07	7.90E-03	4.59E-02	Multiple_Complex
TC1900008904.hg.1	KMT5C	lysine (K)-specific methyltransferase 5C	-1.6	6.71	7.38	0.21	0.15	1.51E-02	7.05E-02	Multiple_Complex
TC0200010838.hg.1	STK16	serine/threonine kinase 16	-1.6	6.69	7.37	0.47	0.29	3.43E-02	1.22E-01	Multiple_Complex
TC1100009864.hg.1	RHOG	ras homolog family member G	-1.6	7.39	8.06	0.12	0.13	9.50E-03	5.16E-02	Multiple_Complex
TSUnmapped00000268.hg.1	CCDC84	coiled-coil domain containing 84	-1.6	6.01	6.68	0.04	0.13	9.30E-03	5.11E-02	NonCoding
TC1700010738.hg.1	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit	-1.6	9.65	10.33	0.06	0.15	1.06E-02	5.58E-02	Multiple_Complex
TC1000011499.hg.1	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	-1.6	10.7	11.37	0.03	0.07	8.90E-03	4.93E-02	Multiple_Complex
TSUnmapped00000437.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	-1.6	7.33	8.01	0.28	0.02	2.12E-02	8.85E-02	Coding
TC1400007691.hg.1	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	-1.6	9.14	9.82	0.21	0.07	1.51E-02	7.04E-02	Multiple_Complex
TC1900009628.hg.1	CDC37; MIR1181	cell division cycle 37; microRNA 1181	-1.6	13.05	13.72	0.29	0.32	1.89E-02	8.17E-02	Multiple_Complex
TC1500007791.hg.1	ARIH1; MIR630	ariadne RBR E3 ubiquitin protein ligase 1; microRNA 630	-1.6	12.69	13.37	0.45	0.15	2.33E-02	9.46E-02	Multiple_Complex
TC1500010707.hg.1	ARHGAP11B	Rho GTPase activating protein 11B	-1.6	8.87	9.55	0.11	0.04	2.69E-02	1.04E-01	Multiple_Complex
TC0100015352.hg.1	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	-1.6	14.33	15.01	0.13	0	7.90E-03	4.57E-02	Multiple_Complex
TC1400008705.hg.1	SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8	-1.6	8.51	9.19	0.6	0.34	4.29E-02	1.42E-01	Multiple_Complex
TC0600008095.hg.1	POLR1C	polymerase (RNA) I polypeptide C	-1.6	11.53	12.2	0.35	0.23	1.89E-02	8.18E-02	Multiple_Complex

TC1600010864.hg.1	WDR59	WD repeat domain 59	-1.6	12.38	13.06	0.16	0.08	8.70E-03	4.88E-02	Multiple_Complex
TSUnmapped00000034.hg.1	TRAPPC4	trafficking protein particle complex 4	-1.6	5.04	5.71	0.34	0.3	2.87E-02	1.09E-01	Coding
TC1300008668.hg.1	LHFP	lipoma HMGIC fusion partner	-1.6	7.84	8.52	0.28	0.34	3.50E-02	1.24E-01	Multiple_Complex
TC1900011935.hg.1	ZFP30	ZFP30 zinc finger protein	-1.6	7	7.68	0.3	0.03	3.51E-02	1.24E-01	Multiple_Complex
TC1600011545.hg.1	PLLP	plasmolipin	-1.6	8.98	9.66	0.05	0.16	1.34E-02	6.50E-02	NonCoding
TC1500010691.hg.1	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	-1.6	9.18	9.86	0.13	0.42	3.91E-02	1.33E-01	Multiple_Complex
TC1700010816.hg.1	ATXN7L3	ataxin 7-like 3	-1.6	5.44	6.12	0.01	0.7	4.64E-02	1.49E-01	Multiple_Complex
TC0300009632.hg.1	SOX2	SRY box 2	-1.6	8.81	9.49	0.35	0.47	4.21E-02	1.40E-01	Coding
TC0900011305.hg.1	TNC	tenascin C	-1.6	4.47	5.15	0.39	0.05	2.04E-02	8.61E-02	Multiple_Complex
TC1200012068.hg.1	C12orf49	chromosome 12 open reading frame 49	-1.6	7.9	8.58	0.06	0.34	2.34E-02	9.49E-02	Multiple_Complex
TC0300007454.hg.1	PARP3	poly(ADP-ribose) polymerase family member 3	-1.6	3.79	4.47	0.33	0.08	2.03E-02	8.59E-02	Multiple_Complex
TC1800009289.hg.1	ACAA2	acetyl-CoA acyltransferase 2	-1.6	9.54	10.22	0.3	0.11	1.46E-02	6.89E-02	Multiple_Complex
TC1500009508.hg.1	NEDD4	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase	-1.6	8.07	8.75	0.59	0.05	3.03E-02	1.12E-01	Multiple_Complex
TC1100008039.hg.1	MUS81	MUS81 structure-specific endonuclease subunit	-1.6	8.1	8.78	0.18	0.16	1.20E-02	6.05E-02	Multiple_Complex
TC1700009623.hg.1	PHF23	PHD finger protein 23	-1.6	7.05	7.73	0.1	0.22	9.90E-03	5.31E-02	Multiple_Complex
TC0100013718.hg.1	LSM10	LSM10, U7 small nuclear RNA associated	-1.6	9.55	10.23	0.35	0.22	1.88E-02	8.16E-02	Multiple_Complex
TC0100013455.hg.1	RPA2	replication protein A2	-1.6	12.05	12.73	0.56	0.09	3.23E-02	1.17E-01	Multiple_Complex
TC0100011920.hg.1	GALNT2	polypeptide N-acetylgalactosaminyltransferase 2	-1.6	5.19	5.87	0.21	0.53	2.86E-02	1.08E-01	Multiple_Complex
TC1800009206.hg.1	TXNL4A	thioredoxin-like 4A	-1.6	11.43	12.11	0.1	0.05	8.00E-03	4.64E-02	Multiple_Complex

TC1200007710.hg.1	C12orf10	chromosome 12 open reading frame 10	-1.6	11.8	12.48	0.25	0.01	9.80E-03	5.28E-02	Multiple_Complex
TC0900011613.hg.1	FAM102A	family with sequence similarity 102, member A	-1.6	5.98	6.66	0.21	0.17	1.36E-02	6.58E-02	Multiple_Complex
TC1700008867.hg.1	SLC9A3R1; MIR3615	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1; microRNA 3615	-1.6	8.2	8.88	0.62	0.33	4.39E-02	1.44E-01	Multiple_Complex
TC1200012016.hg.1	TBX3	T-box 3	-1.6	11.37	12.05	0.08	0.11	1.18E-02	5.97E-02	Multiple_Complex
TC0600011282.hg.1	TRIM27	tripartite motif containing 27	-1.6	9	9.68	0.22	0.25	1.77E-02	7.83E-02	Multiple_Complex
TC1400006732.hg.1	GMPR2	guanosine monophosphate reductase 2	-1.6	10.03	10.71	0.4	0.27	2.19E-02	9.03E-02	Multiple_Complex
TC0600009436.hg.1	L3MBTL3	l(3)mbt-like 3 (Drosophila)	-1.6	6.48	7.16	0.45	0.33	3.05E-02	1.13E-01	Multiple_Complex
TC1200009461.hg.1	EP400; SNORA49	E1A binding protein p400; small nucleolar RNA, H/ACA box 49	-1.6	8.25	8.93	0.13	0.04	2.03E-02	8.59E-02	Multiple_Complex
TC1900007844.hg.1	LSR	lipolysis stimulated lipoprotein receptor	-1.6	6	6.68	0.03	0.42	1.74E-02	7.74E-02	Multiple_Complex
TC1900007795.hg.1	LSM14A	LSM14A mRNA processing body assembly factor	-1.6	9.66	10.34	0.23	0.06	1.15E-02	5.88E-02	Multiple_Complex
TC0700009667.hg.1	LRRC61	leucine rich repeat containing 61	-1.6	7.08	7.76	0.33	0.13	2.55E-02	1.01E-01	Multiple_Complex
TC0300012527.hg.1	MSL2	male-specific lethal 2 homolog (Drosophila)	-1.6	11.67	12.35	0.17	0.17	1.27E-02	6.29E-02	Coding
TC0100006476.hg.1	SAMD11	sterile alpha motif domain containing 11	-1.6	5.15	5.84	0.15	0.3	3.31E-02	1.19E-01	Multiple_Complex
TC1700009888.hg.1	CENPV	centromere protein V	-1.6	10	10.68	0.09	0.07	9.90E-03	5.29E-02	Multiple_Complex
TC1200008597.hg.1	GAS2L3	growth arrest-specific 2 like 3	-1.6	10.04	10.72	0.16	0.26	2.06E-02	8.68E-02	Multiple_Complex
TC0800011561.hg.1	EIF3H	eukaryotic translation initiation factor 3, subunit H	-1.6	13.24	13.92	0.07	0.09	7.60E-03	4.45E-02	Multiple_Complex
TC0X00008246.hg.1	SLC25A43	solute carrier family 25, member 43	-1.6	8.36	9.04	0.23	0.02	2.01E-02	8.55E-02	Multiple_Complex
TC0500010766.hg.1	PLPP1; RNF138P1	phospholipid phosphatase 1; ring finger protein 138, E3 ubiquitin protein ligase pseudogene 1	-1.6	8.39	9.07	0.03	0.39	4.61E-02	1.49E-01	Multiple_Complex

TC0200013516.hg.1	TMEM127	transmembrane protein 127	-1.6	7.91	8.59	0.02	0.17	1.00E-02	5.33E-02	Coding
TC0300006489.hg.1	ARL8B	ADP-ribosylation factor like GTPase 8B	-1.6	10.19	10.87	0.12	0.15	1.05E-02	5.54E-02	Multiple_Complex
TC1700012120.hg.1	OGFOD3	2-oxoglutarate and iron-dependent oxygenase domain containing 3	-1.61	6.35	7.04	0.54	0.17	4.28E-02	1.41E-01	Multiple_Complex
TC0500009093.hg.1	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.61	7.76	8.45	0.25	0	1.75E-02	7.77E-02	Multiple_Complex
TC0X00010512.hg.1	CHRDL1	chordin-like 1	-1.61	6.13	6.81	0.06	0.07	3.73E-02	1.29E-01	Coding
TC0600012875.hg.1	FYN	FYN proto-oncogene, Src family tyrosine kinase	-1.61	7.84	8.52	0.09	0.29	1.33E-02	6.49E-02	Multiple_Complex
TC0800010360.hg.1	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	-1.61	12.25	12.94	0.01	0.01	8.50E-03	4.83E-02	Multiple_Complex
TC0200009994.hg.1	CDCA7	cell division cycle associated 7	-1.61	6.84	7.53	0.48	0.22	3.03E-02	1.12E-01	Multiple_Complex
TC0400007345.hg.1	LIMCH1	LIM and calponin homology domains 1	-1.61	4.5	5.18	0.33	0.32	2.10E-02	8.78E-02	Multiple_Complex
TC0100010148.hg.1	LAMTOR2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	-1.61	11.66	12.34	0.35	0.21	2.22E-02	9.15E-02	Multiple_Complex
TC0500011924.hg.1	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	-1.61	8.54	9.23	0.34	0.52	3.79E-02	1.30E-01	Multiple_Complex
TC1700011798.hg.1	UBE2O	ubiquitin-conjugating enzyme E2O	-1.61	6.6	7.28	0.33	0.07	1.67E-02	7.55E-02	Multiple_Complex
TC0700011938.hg.1	PDAP1	PDGFA associated protein 1	-1.61	7.27	7.95	0.43	0.06	3.59E-02	1.25E-01	Multiple_Complex
TC1000006819.hg.1	MCM10	minichromosome maintenance 10 replication initiation factor	-1.61	6.74	7.43	0.29	0.3	2.38E-02	9.58E-02	Multiple_Complex
TC1100008502.hg.1	LOC100506127; RP11-111M22.2; LOC387790	putative uncharacterized protein FLJ37770-like; Transcript Identified by AceView, Entrez Gene ID(s) 387790; novel transcript	-1.61	5.81	6.49	0.32	0.27	3.09E-02	1.14E-01	Multiple_Complex
TC1500010429.hg.1	CIB1	calcium and integrin binding 1 (calmyrin)	-1.61	10.1	10.79	0.24	0.01	9.70E-03	5.26E-02	Multiple_Complex
TC0100009475.hg.1	MAGI3	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_152900	-1.61	6.79	7.47	0.2	0.31	1.87E-02	8.15E-02	Multiple_Complex

TC1100007943.hg.1	PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	-1.61	6.96	7.65	0.23	0.36	1.76E-02	7.81E-02	Multiple_Complex
TC1100013040.hg.1	TM7SF2	transmembrane 7 superfamily member 2	-1.61	9.03	9.72	0.06	0.11	8.30E-03	4.77E-02	Multiple_Complex
TC0100013323.hg.1	STPG1	sperm-tail PG-rich repeat containing 1	-1.61	10	10.68	0.13	0.03	8.10E-03	4.66E-02	Multiple_Complex
TC0100016003.hg.1	IQGAP3	IQ motif containing GTPase activating protein 3	-1.61	8.65	9.34	0.11	0.22	1.73E-02	7.72E-02	Multiple_Complex
TC1600006610.hg.1	CCNF	cyclin F	-1.61	7.25	7.94	0.22	0.22	3.72E-02	1.28E-01	Multiple_Complex
TC1000012423.hg.1	PFKP	phosphofructokinase, platelet	-1.61	12.74	13.42	0.17	0.33	1.39E-02	6.67E-02	Multiple_Complex
TC0200016624.hg.1	KIDINS220	kinase D-interacting substrate 220kDa	-1.61	8.41	9.1	0.08	0.31	1.59E-02	7.32E-02	Multiple_Complex
TC1200012199.hg.1	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-1.61	6.85	7.54	0.22	0.19	1.83E-02	8.02E-02	Multiple_Complex
TC0600007535.hg.1	ABCF1	ATP binding cassette subfamily F member 1	-1.61	8.73	9.42	0.47	0.04	2.36E-02	9.54E-02	Multiple_Complex
TC1200012737.hg.1	ZNF268	zinc finger protein 268	-1.61	8.62	9.31	0.19	0.02	1.79E-02	7.89E-02	Multiple_Complex
TC1100007818.hg.1	DAGLA	diacylglycerol lipase, alpha	-1.61	5.43	6.12	0.16	0.05	2.27E-02	9.27E-02	Multiple_Complex
TC1700010599.hg.1	MED24; MIR6884	mediator complex subunit 24; microRNA 6884	-1.61	8.47	9.15	0.13	0.2	1.01E-02	5.38E-02	Multiple_Complex
TC1900011594.hg.1	ZNF256	zinc finger protein 256	-1.61	5.36	6.05	0.06	0.14	7.70E-03	4.51E-02	Coding
TC0500013414.hg.1	THOC3	THO complex 3	-1.61	12.56	13.25	0.07	0.07	1.37E-02	6.60E-02	Multiple_Complex
TC1100010905.hg.1	MED19	mediator complex subunit 19	-1.61	6.91	7.6	0.15	0.05	1.30E-02	6.39E-02	Multiple_Complex
TC0200015963.hg.1	TRIP12	thyroid hormone receptor interactor 12	-1.61	7.61	8.3	0.29	0.06	1.22E-02	6.12E-02	Multiple_Complex
TC0300011152.hg.1	DUSP7	dual specificity phosphatase 7	-1.61	5.61	6.29	0.34	0.06	1.60E-02	7.34E-02	Multiple_Complex
TC1000006937.hg.1	PLXDC2	plexin domain containing 2	-1.61	8.61	9.3	0.39	0.05	2.84E-02	1.08E-01	Multiple_Complex
TC1600011448.hg.1	CDK10	cyclin-dependent kinase 10	-1.61	7.23	7.92	0.08	0.35	1.44E-02	6.85E-02	Multiple_Complex
TC1600011402.hg.1	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	-1.61	8.18	8.87	0.02	0.41	2.08E-02	8.73E-02	Multiple_Complex

TC0X00009341.hg.1	DMD	dystrophin	-1.61	5.36	6.05	0.51	0.18	2.43E-02	9.69E-02	Multiple_Complex
TC2100007949.hg.1	MIS18A	MIS18 kinetochore protein A	-1.61	14.17	14.86	0.24	0.1	1.00E-02	5.33E-02	Multiple_Complex
TC1100007684.hg.1	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	-1.61	4.16	4.85	0.39	0.08	1.59E-02	7.32E-02	Multiple_Complex
TC2200007419.hg.1	TNRC6B	trinucleotide repeat containing 6B	-1.61	10.07	10.76	0.19	0.12	8.50E-03	4.83E-02	Multiple_Complex
TC0900007077.hg.1	UNC13B	unc-13 homolog B (C. elegans)	-1.61	8.74	9.43	0.02	0.1	7.30E-03	4.35E-02	Multiple_Complex
TC1700011171.hg.1	COX11	COX11 cytochrome c oxidase copper chaperone	-1.61	11.35	12.04	0.48	0.08	2.16E-02	8.94E-02	Multiple_Complex
TC1600006738.hg.1	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	-1.61	9.16	9.85	0.34	0.36	2.46E-02	9.79E-02	Multiple_Complex
TC1100007216.hg.1	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	-1.62	10.69	11.38	0.44	0.14	2.21E-02	9.09E-02	Multiple_Complex
TC2100008272.hg.1	WDR4	WD repeat domain 4	-1.62	6.09	6.78	0.06	0.02	9.90E-03	5.32E-02	Multiple_Complex
TC0500013301.hg.1	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	-1.62	5.95	6.64	0.42	0.24	3.40E-02	1.21E-01	Multiple_Complex
TC2200008189.hg.1	DERL3	derlin 3	-1.62	6.68	7.37	0.03	0.25	1.26E-02	6.23E-02	Multiple_Complex
TC0700012780.hg.1	HIPK2	homeodomain interacting protein kinase 2	-1.62	8.8	9.49	0.06	0.13	1.12E-02	5.78E-02	Multiple_Complex
TC1100011234.hg.1	LTBP3	latent transforming growth factor beta binding protein 3	-1.62	6.61	7.31	0.06	0.05	6.50E-03	4.01E-02	Multiple_Complex
TC0600011594.hg.1	C6orf106	chromosome 6 open reading frame 106	-1.62	7.93	8.62	0.16	0.62	3.78E-02	1.30E-01	Multiple_Complex
TC0100010686.hg.1	CACYBP	calcyclin binding protein	-1.62	12.91	13.61	0	0.06	7.90E-03	4.57E-02	Multiple_Complex
TC1700012073.hg.1	P4HB	prolyl 4-hydroxylase, beta polypeptide	-1.62	10.14	10.83	0.23	0.09	9.40E-03	5.15E-02	Multiple_Complex
TC1100009616.hg.1	ACAD8	acyl-CoA dehydrogenase family, member 8	-1.62	6.03	6.72	0.01	0.08	1.40E-02	6.69E-02	Multiple_Complex
TC1600010772.hg.1	VAC14	Vac14 homolog (S. cerevisiae)	-1.62	7.68	8.37	0.03	0.55	2.50E-02	9.90E-02	Multiple_Complex
TC1000011948.hg.1	PDZD8	PDZ domain containing 8	-1.62	11.26	11.95	0.16	0.16	1.27E-02	6.28E-02	Multiple_Complex
TC1900011172.hg.1	VRK3	vaccinia related kinase 3	-1.62	12.88	13.58	0.3	0.02	1.13E-02	5.82E-02	Multiple_Complex

TC1900011689.hg.1	YJEFN3	YjeF N-terminal domain containing 3	-1.62	8.06	8.75	0.12	0.26	1.78E-02	7.86E-02	Coding
TC0900009163.hg.1	PPP1R26	protein phosphatase 1, regulatory subunit 26	-1.62	8.52	9.21	0.09	0.11	9.20E-03	5.07E-02	Multiple_Complex
TC0300006856.hg.1	RARB	retinoic acid receptor, beta	-1.62	5.28	5.97	0.37	0.21	2.53E-02	1.00E-01	Multiple_Complex
TC0700009488.hg.1	CASP2	caspase 2	-1.62	10.43	11.12	0.14	0.35	1.36E-02	6.57E-02	Multiple_Complex
TC0100013752.hg.1	EPHA10	EPH receptor A10	-1.62	4.09	4.79	0.4	0.42	3.31E-02	1.19E-01	Multiple_Complex
TC0900008793.hg.1	ZBTB34	zinc finger and BTB domain containing 34	-1.62	6.25	6.94	0.42	0.06	2.32E-02	9.44E-02	Multiple_Complex
TC0900008851.hg.1	DNM1	dynamin 1	-1.62	10.83	11.53	0.09	0.15	1.74E-02	7.74E-02	Multiple_Complex
TC1100011035.hg.1	CPSF7	cleavage and polyadenylation specific factor 7	-1.62	9.1	9.79	0.46	0.13	2.47E-02	9.81E-02	Multiple_Complex
TC0200007976.hg.1	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	-1.62	5.48	6.18	0.28	0.02	1.36E-02	6.56E-02	Multiple_Complex
TC0100006787.hg.1	PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta	-1.62	6.84	7.54	0.33	0.2	2.49E-02	9.85E-02	Multiple_Complex
TC2100008233.hg.1	ZBTB21	zinc finger and BTB domain containing 21	-1.62	12.89	13.59	0.01	0.08	7.10E-03	4.27E-02	Multiple_Complex
TC0500009077.hg.1	HMGXB3	HMG box domain containing 3	-1.62	8.27	8.97	0.22	0.12	1.23E-02	6.14E-02	Multiple_Complex
TC1600006578.hg.1	TBL3	transducin (beta)-like 3	-1.62	10.04	10.74	0.16	0.11	8.80E-03	4.90E-02	Multiple_Complex
TC1700011761.hg.1	RECQL5	RecQ helicase-like 5	-1.62	7.08	7.78	0.31	0.16	1.20E-02	6.05E-02	Multiple_Complex
TC1100012422.hg.1	APOA4	apolipoprotein A-IV	-1.62	7.56	8.25	0.15	0.01	3.07E-02	1.13E-01	Coding
TC1200012043.hg.1	MED13L	mediator complex subunit 13-like	-1.62	11.36	12.06	0.16	0.02	1.16E-02	5.90E-02	Multiple_Complex
TC0100015786.hg.1	POGZ	pogo transposable element with ZNF domain	-1.62	10.47	11.17	0.05	0.05	1.28E-02	6.30E-02	Multiple_Complex
TC0100007303.hg.1	KDM1A; MIR3115	lysine (K)-specific demethylase 1A; microRNA 3115	-1.62	9.15	9.85	0.16	0.1	8.70E-03	4.90E-02	Multiple_Complex
TC0100007841.hg.1	CDCA8	cell division cycle associated 8	-1.62	8.56	9.25	0.3	0.21	1.70E-02	7.65E-02	Multiple_Complex
TC0300013727.hg.1	NCBP2	nuclear cap binding protein subunit 2	-1.62	8.93	9.63	0.35	0.44	2.68E-02	1.04E-01	Multiple_Complex

TC0300010040.hg.1	NCBP2-AS2	NCBP2 antisense RNA 2 (head to head)	-1.62	6.26	6.96	0.17	0.13	1.07E-02	5.58E-02	Multiple_Complex
TSUnmapped00000706.hg.1	HYOU1	hypoxia up-regulated 1	-1.62	9.44	10.13	0.17	0.46	1.91E-02	8.24E-02	NonCoding
TC0200016347.hg.1	HDLBP	high density lipoprotein binding protein	-1.62	12.26	12.96	0.05	0.1	1.16E-02	5.90E-02	Multiple_Complex
TC0600014258.hg.1	HLA-B	major histocompatibility complex, class I, B	-1.62	12.37	13.07	0.01	0.26	9.70E-03	5.25E-02	Multiple_Complex
TC2000007502.hg.1	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	-1.62	11.21	11.91	0.35	0.01	1.44E-02	6.84E-02	Multiple_Complex
TC0500006442.hg.1	SDHA	succinate dehydrogenase complex subunit A, flavoprotein (Fp)	-1.62	13.48	14.18	0.1	0.01	8.50E-03	4.83E-02	Multiple_Complex
TC0200016727.hg.1	IWS1	IWS1 homolog (S. cerevisiae)	-1.62	9.84	10.54	0.06	0.14	9.50E-03	5.16E-02	Multiple_Complex
TC1000007333.hg.1	ZNF33A	zinc finger protein 33A	-1.62	7.84	8.54	0.19	0.13	1.15E-02	5.88E-02	Multiple_Complex
TC0300011050.hg.1	QARS; MIR6890	glutaminyl-tRNA synthetase; microRNA 6890	-1.63	13.95	14.65	0.25	0.02	8.60E-03	4.85E-02	Multiple_Complex
TC1000008092.hg.1	VDAC2	voltage-dependent anion channel 2	-1.63	12.95	13.65	0.03	0.02	6.30E-03	3.95E-02	Multiple_Complex
TC0300012807.hg.1	SIAH2	siah E3 ubiquitin protein ligase 2	-1.63	6.59	7.29	0.24	0.2	1.39E-02	6.67E-02	Multiple_Complex
TC1900010360.hg.1	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	-1.63	6.77	7.47	0.39	0.05	1.89E-02	8.17E-02	Multiple_Complex
TC1600009954.hg.1	MAPK3	mitogen-activated protein kinase 3	-1.63	10.94	11.64	0.15	0.02	8.60E-03	4.86E-02	Multiple_Complex
TC0100012272.hg.1	CNST	consortin, connexin sorting protein	-1.63	5.73	6.43	0.25	0.11	1.10E-02	5.72E-02	Multiple_Complex
TC1100008144.hg.1	GSTP1	glutathione S-transferase pi 1	-1.63	14.09	14.79	0.19	0	7.70E-03	4.49E-02	Multiple_Complex
TC0400012178.hg.1	DCHS2	dachsous cadherin-related 2	-1.63	5.77	6.47	0.1	0.59	2.74E-02	1.05E-01	Multiple_Complex
TC1100013012.hg.1	STX3	syntaxin 3	-1.63	9.79	10.49	0.51	0.18	2.30E-02	9.36E-02	Multiple_Complex
TC0X00007251.hg.1	CCNB3	cyclin B3	-1.63	5.06	5.76	0.71	0.32	4.68E-02	1.50E-01	Multiple_Complex
TC1900011863.hg.1	FDX1L	ferredoxin 1-like	-1.63	9.53	10.24	0.27	0.14	1.17E-02	5.93E-02	Multiple_Complex
TC0600007792.hg.1	PPARD	peroxisome proliferator-activated receptor delta	-1.63	7	7.7	0.12	0.22	8.30E-03	4.76E-02	Multiple_Complex

TC1400006718.hg.1	PSME1	proteasome activator subunit 1	-1.63	8.57	9.28	0.24	0.05	8.60E-03	4.85E-02	Multiple_Complex
TC0700009485.hg.1	GSTK1	glutathione S-transferase kappa 1	-1.63	7.49	8.2	0.37	0.31	1.82E-02	7.99E-02	Multiple_Complex
TC1900006532.hg.1	RPS15	ribosomal protein S15	-1.63	15.21	15.91	0.36	0.11	1.22E-02	6.10E-02	Multiple_Complex
TC2000008130.hg.1	TBC1D20	TBC1 domain family, member 20	-1.63	8.29	8.99	0.12	0.28	1.07E-02	5.58E-02	Multiple_Complex
TC1100006455.hg.1	B4GALNT4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-1.63	6.69	7.39	0.24	0.05	2.12E-02	8.82E-02	Multiple_Complex
TC0700007949.hg.1	POM121	POM121 transmembrane nucleoporin	-1.63	13.95	14.66	0.17	0.12	8.80E-03	4.93E-02	Multiple_Complex
TC0100006497.hg.1	SCNN1D	sodium channel, non voltage gated 1 delta subunit	-1.63	4.58	5.29	0.59	0.08	2.71E-02	1.04E-01	Multiple_Complex
TC1700010209.hg.1	TLCD1	TLC domain containing 1	-1.63	8.95	9.66	0.12	0.09	7.40E-03	4.37E-02	Multiple_Complex
TC0300007797.hg.1	GPR27	G protein-coupled receptor 27	-1.63	6.45	7.16	0.08	0.38	3.01E-02	1.12E-01	Coding
TC0700010435.hg.1	CDCA7L	cell division cycle associated 7-like	-1.63	11.28	11.99	0.27	0.13	1.20E-02	6.03E-02	Multiple_Complex
TC1700010721.hg.1	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.63	9.01	9.72	0.36	0.31	1.81E-02	7.96E-02	Multiple_Complex
TC0700006648.hg.1	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	-1.63	15.12	15.83	0.17	0	8.80E-03	4.92E-02	Multiple_Complex
TSUnmapped00000128.hg.1	ZNF852	zinc finger protein 852	-1.63	5.58	6.29	0.29	0.23	1.75E-02	7.79E-02	NonCoding
TC0100007954.hg.1	SMAP2	small ArfGAP2	-1.63	13.13	13.83	0.26	0.04	9.70E-03	5.23E-02	Multiple_Complex
TC1900010748.hg.1	ATP5SL	ATP5S-like	-1.63	7.7	8.41	0.11	0.22	7.80E-03	4.54E-02	Multiple_Complex
TSUnmapped00000819.hg.1	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	-1.63	8.42	9.13	0.13	0.05	8.80E-03	4.90E-02	Coding
TC1500010756.hg.1	RAB11A	RAB11A, member RAS oncogene family	-1.63	4.3	5.01	0.09	0.29	1.79E-02	7.89E-02	NonCoding
TC2000007300.hg.1	RPRD1B	regulation of nuclear pre-mRNA domain containing 1B	-1.63	10.09	10.8	0	0.27	1.61E-02	7.35E-02	Multiple_Complex

TC0400007868.hg.1	PARM1	prostate androgen-regulated mucin-like protein 1	-1.63	5.06	5.77	0.17	0.01	9.90E-03	5.31E-02	Multiple_Complex
TC0300013812.hg.1	TRAK1	trafficking protein, kinesin binding 1	-1.63	7.63	8.33	0.19	0.13	1.73E-02	7.72E-02	Multiple_Complex
TC1700010349.hg.1	C17orf75	chromosome 17 open reading frame 75	-1.63	7.33	8.04	0.17	0.13	2.13E-02	8.87E-02	Multiple_Complex
TC1200009239.hg.1	KMT5A	lysine (K)-specific methyltransferase 5A	-1.63	9.64	10.35	0.07	0.19	9.10E-03	5.00E-02	Multiple_Complex
TC1600009260.hg.1	EEF2KMT	eukaryotic elongation factor 2 lysine methyltransferase	-1.64	8.24	8.95	0.16	0.29	1.66E-02	7.52E-02	Multiple_Complex
TC1100012526.hg.1	USP2	ubiquitin specific peptidase 2	-1.64	5.38	6.09	0.29	0.47	4.67E-02	1.50E-01	Multiple_Complex
TC1200009252.hg.1	TCTN2	tectonic family member 2	-1.64	9.86	10.57	0.07	0.2	9.70E-03	5.22E-02	Multiple_Complex
TC0300008173.hg.1	PCNP	PEST proteolytic signal containing nuclear protein	-1.64	13.13	13.84	0.28	0.09	9.60E-03	5.20E-02	Multiple_Complex
TC1900011012.hg.1	TMEM160	transmembrane protein 160	-1.64	8.58	9.3	0.08	0.01	3.77E-02	1.30E-01	Multiple_Complex
TC0500009725.hg.1	CNOT6	CCR4-NOT transcription complex subunit 6	-1.64	10.55	11.27	0.24	0.02	7.70E-03	4.49E-02	Multiple_Complex
TC2000008815.hg.1	BCL2L1	BCL2-like 1	-1.64	6.03	6.75	0.19	0.04	1.93E-02	8.29E-02	Multiple_Complex
TC1000008731.hg.1	RPARP-AS1	RPARP antisense RNA 1	-1.64	11.61	12.32	0.03	0.03	1.53E-02	7.10E-02	Multiple_Complex
TC0700011139.hg.1	VOPP1	vesicular, overexpressed in cancer, prosurvival protein 1	-1.64	7.66	8.38	0.24	0.07	1.84E-02	8.04E-02	Multiple_Complex
TC0600014096.hg.1	TRIM39-RPP21	TRIM39-RPP21 readthrough	-1.64	8.84	9.56	0.61	0.18	3.48E-02	1.23E-01	Coding
TC0200014250.hg.1	SMPD4	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	-1.64	10.5	11.21	0.22	0.06	8.30E-03	4.73E-02	Multiple_Complex
TSUnmapped00000333.hg.1	SURF4	surfeit 4	-1.64	12.26	12.97	0.13	0.09	6.80E-03	4.16E-02	Coding
TC1000010006.hg.1	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	-1.64	10.21	10.92	0.08	0.01	8.20E-03	4.71E-02	Multiple_Complex
TC1900011096.hg.1	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	-1.64	5.56	6.28	0.25	0.36	1.76E-02	7.81E-02	Multiple_Complex

TC1700008851.hg.1	GPRC5C	G protein-coupled receptor, class C, group 5, member C	-1.64	5.02	5.74	0.46	0.12	2.36E-02	9.54E-02	Multiple_Complex
TC1000011660.hg.1	MGEA5	Salzman2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_012215	-1.64	7.02	7.73	0.12	0.14	7.80E-03	4.55E-02	NonCoding
TC0600007687.hg.1	RING1	ring finger protein 1	-1.64	7	7.72	0.08	0.38	1.17E-02	5.96E-02	Multiple_Complex
TC0900010825.hg.1	NINJ1	ninjurin 1	-1.64	4.52	5.23	0	0	7.10E-03	4.27E-02	Multiple_Complex
TC1200012576.hg.1	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	-1.64	9.68	10.4	0.22	0.1	1.72E-02	7.70E-02	Multiple_Complex
TC0800009244.hg.1	MROH1	maestro heat-like repeat family member 1	-1.64	5.76	6.48	0.03	0.48	4.57E-02	1.48E-01	Multiple_Complex
TC1200012080.hg.1	TESC	tescalcin	-1.64	5.52	6.23	0.23	0.06	2.68E-02	1.04E-01	Multiple_Complex
TC1100010397.hg.1	CCDC34	coiled-coil domain containing 34	-1.64	12.15	12.86	0.05	0.08	6.10E-03	3.86E-02	Multiple_Complex
TC1500007077.hg.1	WDR76	WD repeat domain 76	-1.64	9.16	9.88	0.07	0.05	7.80E-03	4.54E-02	Multiple_Complex
TC2200009161.hg.1	LMF2	lipase maturation factor 2	-1.64	6.36	7.07	0.6	0.1	3.16E-02	1.16E-01	Multiple_Complex
TC1600011047.hg.1	HSDL1	hydroxysteroid dehydrogenase like 1	-1.64	8.42	9.13	0.62	0	3.45E-02	1.23E-01	Multiple_Complex
TC0300010228.hg.1	FANCD2OS	FANCD2 opposite strand	-1.64	6.52	7.24	0.26	0.37	1.70E-02	7.62E-02	Multiple_Complex
TC1100013003.hg.1	TMX2; C11orf31	thioredoxin-related transmembrane protein 2; chromosome 11 open reading frame 31	-1.64	11.71	12.43	0.25	0.1	9.80E-03	5.28E-02	Multiple_Complex
TC0X00009929.hg.1	OPHN1	oligophrenin 1	-1.64	8.42	9.14	0.62	0.07	3.94E-02	1.34E-01	Multiple_Complex
TC0X00008009.hg.1	TCEAL4	transcription elongation factor A (SII)-like 4	-1.64	5.11	5.82	0.12	0.01	1.17E-02	5.96E-02	Multiple_Complex
TC1100011010.hg.1	PRPF19	pre-mRNA processing factor 19	-1.64	9.19	9.91	0.35	0.23	2.11E-02	8.81E-02	Multiple_Complex
TC0900009073.hg.1	RPL7A; SNORD36C; SNORD36B; SNORD24; SNORD36A	ribosomal protein L7a; small nucleolar RNA, C/D box 36C; small nucleolar RNA, C/D box 36B; small nucleolar RNA, C/D box 24; small nucleolar RNA, C/D box 36A	-1.64	13.8	14.51	0.14	0.09	7.00E-03	4.23E-02	Multiple_Complex

TC0100018464.hg.1	PPM1J	protein phosphatase, Mg2+/Mn2+ dependent, 1J	-1.64	5.52	6.24	0.33	0.14	1.63E-02	7.43E-02	Multiple_Complex
TC0800006913.hg.1	SH2D4A	SH2 domain containing 4A	-1.64	6.1	6.81	0.29	0.43	2.10E-02	8.78E-02	Multiple_Complex
TC0200015912.hg.1	IRS1	insulin receptor substrate 1	-1.64	4.55	5.26	0.14	0.38	3.08E-02	1.14E-01	Multiple_Complex
TC0600011546.hg.1	CUTA	cutA divalent cation tolerance homolog (E. coli)	-1.64	14.78	15.5	0.08	0.06	5.30E-03	3.53E-02	Multiple_Complex
TC0500007761.hg.1	TMEM171	transmembrane protein 171	-1.65	7.86	8.58	0.16	0.25	2.02E-02	8.56E-02	Coding
TC0300013357.hg.1	PARL	presenilin associated, rhomboid-like	-1.65	12.02	12.73	0.25	0.36	1.92E-02	8.28E-02	Multiple_Complex
TC0Y00006882.hg.1	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	-1.65	12.5	13.22	0.08	0.37	1.25E-02	6.21E-02	Multiple_Complex
TC1700009877.hg.1	ZSWIM7	zinc finger, SWIM-type containing 7	-1.65	11.35	12.07	0	0.06	6.00E-03	3.82E-02	Multiple_Complex
TC1900008993.hg.1	ZNF304	zinc finger protein 304	-1.65	6.45	7.17	0.02	0.05	7.60E-03	4.45E-02	Multiple_Complex
TC1100012981.hg.1	RCN1	reticulocalbin 1, EF-hand calcium binding domain	-1.65	10.89	11.61	0.06	0.09	5.50E-03	3.61E-02	Multiple_Complex
TC2000008217.hg.1	SLC4A11	solute carrier family 4, sodium borate transporter, member 11	-1.65	5.83	6.55	0.65	0.39	4.46E-02	1.45E-01	Multiple_Complex
TC1200008466.hg.1	NUDT4	nudix hydrolase 4	-1.65	11.55	12.27	0.25	0.2	9.60E-03	5.20E-02	Multiple_Complex
TC1100012794.hg.1	ARHGAP32	Rho GTPase activating protein 32	-1.65	8.32	9.04	0.12	0.02	1.26E-02	6.24E-02	Multiple_Complex
TC0700010565.hg.1	HOXA11	homeobox A11	-1.65	4.95	5.67	0.55	0.3	2.69E-02	1.04E-01	Coding
TC1100006487.hg.1	TALDO1	transaldolase 1	-1.65	8.61	9.33	0.14	0.02	6.80E-03	4.13E-02	Multiple_Complex
TC0200016348.hg.1	HDLBP	Transcript Identified by AceView, Entrez Gene ID(s) 3069	-1.65	5.24	5.97	0.05	0.2	1.82E-02	8.01E-02	Unassigned
TC1900011007.hg.1	AP2S1	adaptor-related protein complex 2 sigma 1 subunit	-1.65	11.52	12.25	0.27	0.11	8.80E-03	4.91E-02	Multiple_Complex
TSUnmapped00000282.hg.1	KAT6B	K(lysine) acetyltransferase 6B	-1.65	7.7	8.43	0.06	0.46	1.70E-02	7.64E-02	Coding
TC1700009372.hg.1	CRK	v-crk avian sarcoma virus CT10 oncogene homolog	-1.65	8.44	9.16	0.27	0.01	8.00E-03	4.62E-02	Multiple_Complex

TC1200008182.hg.1	RAB21	RAB21, member RAS oncogene family	-1.65	7.16	7.88	0.33	0.1	2.46E-02	9.79E-02	Multiple_Complex
TC1900011707.hg.1	GPI	glucose-6-phosphate isomerase	-1.65	5.68	6.4	0.26	0.56	4.16E-02	1.39E-01	Multiple_Complex
TC1200007687.hg.1	EIF4B	eukaryotic translation initiation factor 4B	-1.65	11.76	12.48	0.5	0.16	1.79E-02	7.92E-02	Multiple_Complex
TC0700012602.hg.1	CEP41	centrosomal protein 41kDa	-1.65	8.11	8.83	0.07	0.04	9.90E-03	5.31E-02	Multiple_Complex
TC1700006585.hg.1	CTNS	cystinosin, lysosomal cystine transporter	-1.65	5.13	5.86	0.16	0.33	3.31E-02	1.19E-01	Multiple_Complex
TC1600010617.hg.1	KIAA0895L	KIAA0895-like	-1.65	4.9	5.62	0.24	0.02	1.11E-02	5.74E-02	Multiple_Complex
TC1600011398.hg.1	MMP2	matrix metallopeptidase 2	-1.65	5.45	6.17	0.21	0.15	2.25E-02	9.22E-02	Multiple_Complex
TC0700010563.hg.1	HOXA7	homeobox A7	-1.65	7.19	7.92	0.14	0.18	1.08E-02	5.63E-02	Multiple_Complex
TC1100013175.hg.1	HNRNPUL2-BSCL2	HNRNPUL2-BSCL2 readthrough (NMD candidate)	-1.65	9.59	10.31	0.23	0.05	7.30E-03	4.34E-02	Multiple_Complex
TC0100018478.hg.1	NBPF10	neuroblastoma breakpoint family, member 10	-1.65	9.69	10.42	0.26	0.18	8.60E-03	4.87E-02	Multiple_Complex
TC1600008169.hg.1	PARD6A	par-6 family cell polarity regulator alpha	-1.65	4.02	4.75	0.15	0.06	1.29E-02	6.34E-02	Multiple_Complex
TC1200007832.hg.1	NABP2	nucleic acid binding protein 2	-1.65	11.12	11.84	0.11	0.14	6.70E-03	4.10E-02	Multiple_Complex
TC2000007473.hg.1	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	-1.65	13.36	14.09	0	0.03	4.80E-03	3.33E-02	Multiple_Complex
TC1200012622.hg.1	SLC48A1	solute carrier family 48 (heme transporter), member 1	-1.65	6.93	7.66	0.68	0.17	3.65E-02	1.27E-01	Multiple_Complex
TC0800009641.hg.1	FAM86B1	family with sequence similarity 86, member B1	-1.65	11.64	12.36	0.04	0.15	9.40E-03	5.16E-02	Multiple_Complex
TC0600014215.hg.1	GMDS	GDP-mannose 4,6-dehydratase	-1.65	10.75	11.47	0.11	0.67	3.29E-02	1.19E-01	Multiple_Complex
TC0X00009750.hg.1	KDM5C	lysine (K)-specific demethylase 5C	-1.65	11.27	11.99	0.01	0.05	5.60E-03	3.66E-02	Multiple_Complex
TC1200010901.hg.1	RNF41	ring finger protein 41, E3 ubiquitin protein ligase	-1.65	10.25	10.98	0.02	0.03	4.70E-03	3.29E-02	Multiple_Complex
TC0500012100.hg.1	H2AFY	H2A histone family, member Y	-1.65	13.1	13.83	0.02	0.08	4.90E-03	3.34E-02	Multiple_Complex
TC0900012124.hg.1	POLR1E	polymerase (RNA) I polypeptide E	-1.65	9.59	10.32	0.01	0.21	9.10E-03	5.00E-02	Multiple_Complex

TC1600011286.hg.1	CHMP1A	charged multivesicular body protein 1A	-1.65	5.81	6.54	0.67	0.1	3.83E-02	1.31E-01	Multiple_Complex
TC1900011789.hg.1	EMC10	ER membrane protein complex subunit 10	-1.65	8.45	9.17	0.11	0.45	2.24E-02	9.18E-02	Multiple_Complex
TC0300013847.hg.1	PPP4R2	protein phosphatase 4, regulatory subunit 2	-1.66	8.41	9.14	0.22	0.17	2.15E-02	8.93E-02	Multiple_Complex
TC1200012308.hg.1	NCOR2	nuclear receptor corepressor 2	-1.66	7.96	8.69	0.24	0.15	9.10E-03	5.04E-02	Multiple_Complex
TC1600008128.hg.1	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	-1.66	6.13	6.85	0.32	0.53	4.07E-02	1.37E-01	Multiple_Complex
TC0400012933.hg.1	NAAA	N-acylethanolamine acid amidase	-1.66	6.47	7.2	0.13	0.07	6.40E-03	3.98E-02	Multiple_Complex
TC0500012044.hg.1	FSTL4	follistatin-like 4	-1.66	7.63	8.36	0.08	0.12	6.90E-03	4.20E-02	Multiple_Complex
TC0700011504.hg.1	WBSCR27	Williams Beuren syndrome chromosome region 27	-1.66	4.32	5.04	0.27	0.08	7.60E-03	4.47E-02	Multiple_Complex
TC1700012230.hg.1	ZNF207; MIR632	zinc finger protein 207; microRNA 632	-1.66	12.96	13.68	0.19	0.05	7.80E-03	4.54E-02	Multiple_Complex
TC1900011843.hg.1	SLC39A3	solute carrier family 39 (zinc transporter), member 3	-1.66	9.47	10.2	0.22	0.41	2.11E-02	8.81E-02	Multiple_Complex
TC0700008104.hg.1	LOC100133091	uncharacterized LOC100133091; Salzman2013 ANNOTATED, INTERNAL, ncRNA, OVEXON best transcript NR_029411; Transcript Identified by AceView, Entrez Gene ID(s) 554248; 100133091, RefSeq ID(s) NR_029411	-1.66	10.93	11.66	0.16	0.12	7.10E-03	4.27E-02	Multiple_Complex
TC1700009681.hg.1	CTC1	CTS telomere maintenance complex component 1	-1.66	6.31	7.03	0.06	0.09	1.28E-02	6.32E-02	Multiple_Complex
TC1900007331.hg.1	COLGALT1	collagen beta(1-O)galactosyltransferase 1	-1.66	10.69	11.42	0.01	0.19	6.00E-03	3.80E-02	Multiple_Complex
TC0300013822.hg.1	EXOSC7	exosome component 7	-1.66	11.14	11.87	0.04	0.25	7.40E-03	4.37E-02	Multiple_Complex
TC2200007356.hg.1	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	-1.66	11.26	11.99	0.21	0.25	1.00E-02	5.32E-02	Multiple_Complex
TC1900006510.hg.1	GPX4	glutathione peroxidase 4	-1.66	10.11	10.84	0.61	0.02	3.05E-02	1.13E-01	Multiple_Complex
TC1900011796.hg.1	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	-1.66	5.65	6.38	0.14	0.04	1.63E-02	7.43E-02	NonCoding

TC1400010617.hg.1	PRKCH	protein kinase C, eta	-1.66	5.57	6.3	0.08	0.62	2.77E-02	1.06E-01	Multiple_Complex
TC0500013237.hg.1	HARS2	histidyl-tRNA synthetase 2, mitochondrial	-1.66	6.08	6.81	0.37	0.31	4.13E-02	1.38E-01	Multiple_Complex
TC1100007285.hg.1	FJX1	four jointed box 1	-1.66	7.73	8.46	0	0.01	9.30E-03	5.11E-02	Multiple_Complex
TC0100006479.hg.1	KLHL17	kelch-like family member 17	-1.66	8.15	8.88	0.22	0.61	3.79E-02	1.30E-01	Multiple_Complex
TC0X00009057.hg.1	MID1	midline 1	-1.66	11.14	11.87	0.36	0.04	1.12E-02	5.76E-02	Multiple_Complex
TC0600007636.hg.1	RNF5	ring finger protein 5, E3 ubiquitin protein ligase	-1.66	10.76	11.49	0.26	0.26	1.02E-02	5.39E-02	Multiple_Complex
TC0900006970.hg.1	NFX1	nuclear transcription factor, X-box binding 1	-1.66	11.49	12.23	0.45	0.11	1.48E-02	6.96E-02	Multiple_Complex
TC1100007384.hg.1	ALKBH3; SEC14L1P1	alkB homolog 3, alpha-ketoglutarate-dependent dioxygenase; SEC14-like 1 pseudogene 1	-1.66	9.52	10.25	0.43	0.03	2.21E-02	9.11E-02	Multiple_Complex
TC1400010020.hg.1	C14orf142	chromosome 14 open reading frame 142	-1.66	7.95	8.68	0.18	0.16	6.50E-03	4.00E-02	Coding
TC1900009603.hg.1	OLFM2	olfactomedin 2	-1.66	6.41	7.14	0.32	0.03	1.06E-02	5.56E-02	Multiple_Complex
TC0600011470.hg.1	NELFE; MIR1236	negative elongation factor complex member E; microRNA 1236	-1.66	7.08	7.81	0.15	0.35	1.58E-02	7.27E-02	Multiple_Complex
TC1200011820.hg.1	PRDM4	PR domain containing 4	-1.66	10.72	11.46	0.28	0.02	7.90E-03	4.59E-02	Multiple_Complex
TC1100009240.hg.1	C2CD2L	C2CD2-like	-1.66	7.39	8.12	0.08	0.4	4.53E-02	1.47E-01	Multiple_Complex
TC1100007876.hg.1	TMEM179B; MIR6748	transmembrane protein 179B; microRNA 6748	-1.66	13.88	14.61	0.01	0.1	6.20E-03	3.89E-02	Multiple_Complex
TC0500012497.hg.1	TNIP1	TNFAIP3 interacting protein 1	-1.66	8.17	8.91	0.04	0.03	5.40E-03	3.55E-02	Multiple_Complex
TC0900006527.hg.1	CDC37L1	cell division cycle 37-like 1	-1.66	5.06	5.79	0.11	0.22	3.28E-02	1.19E-01	Multiple_Complex
TC0100010514.hg.1	MPZL1	myelin protein zero-like 1	-1.66	8.99	9.73	0.15	0.07	5.60E-03	3.65E-02	Multiple_Complex
TC0700010189.hg.1	CYTH3	cytohesin 3	-1.66	9.53	10.26	0.37	0.18	1.42E-02	6.78E-02	Multiple_Complex
TC0800008845.hg.1	MYC	v-myc avian myelocytomatosis viral oncogene homolog	-1.66	10.92	11.66	0.05	0.16	5.80E-03	3.71E-02	Multiple_Complex
TC0200011400.hg.1	02-Sep	septin 2	-1.66	10.31	11.05	0.32	0.06	8.50E-03	4.81E-02	Multiple_Complex

TC0100010112.hg.1	SLC50A1	solute carrier family 50 (sugar efflux transporter), member 1	-1.66	8.73	9.47	0.38	0.04	1.13E-02	5.79E-02	Multiple_Complex
TC1400006890.hg.1	SRP54	signal recognition particle 54kDa	-1.66	10.78	11.52	0.54	0.01	1.98E-02	8.45E-02	Multiple_Complex
TC1100012722.hg.1	CDON	cell adhesion associated, oncogene regulated	-1.66	8.93	9.67	0.16	0.29	1.50E-02	7.02E-02	Multiple_Complex
TC1600010500.hg.1	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial	-1.66	13.42	14.15	0.05	0.12	5.60E-03	3.64E-02	Multiple_Complex
TC0X00008055.hg.1	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)	-1.66	5.79	6.52	0.21	0.72	4.60E-02	1.48E-01	Multiple_Complex
TC1100011568.hg.1	FCHSD2	FCH and double SH3 domains 2	-1.66	8.54	9.27	0.06	0.06	1.61E-02	7.36E-02	Multiple_Complex
TC0600009102.hg.1	FIG4	FIG4 phosphoinositide 5-phosphatase	-1.66	8.3	9.04	0.06	0.24	2.06E-02	8.67E-02	Multiple_Complex
TC0100010134.hg.1	DAP3	death associated protein 3	-1.67	11.73	12.46	0.35	0.1	1.32E-02	6.43E-02	Multiple_Complex
TC0700007822.hg.1	VKORC1L1	vitamin K epoxide reductase complex subunit 1 like 1	-1.67	10.23	10.96	0.12	0.47	1.52E-02	7.08E-02	Multiple_Complex
TC0300013719.hg.1	CEP19	centrosomal protein 19kDa	-1.67	6.96	7.7	0.04	0.35	9.60E-03	5.21E-02	Multiple_Complex
TC1000006794.hg.1	DHTKD1	dehydrogenase E1 and transketolase domain containing 1	-1.67	11.06	11.8	0.31	0.16	9.80E-03	5.29E-02	Multiple_Complex
TC1200007895.hg.1	OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin	-1.67	10.19	10.92	0.02	0.2	6.30E-03	3.93E-02	Multiple_Complex
TC0500011255.hg.1	MTX3	metaxin 3	-1.67	6.81	7.55	0.49	0.44	2.76E-02	1.06E-01	Multiple_Complex
TC1200012574.hg.1	TULP3	tubby like protein 3	-1.67	11.69	12.42	0.05	0.05	6.20E-03	3.91E-02	Multiple_Complex
TC0900011396.hg.1	RAB14	RAB14, member RAS oncogene family	-1.67	12.83	13.56	0.41	0.19	1.71E-02	7.66E-02	Coding
TC1000010725.hg.1	CCDC6	coiled-coil domain containing 6	-1.67	11.89	12.63	0.17	0.03	7.50E-03	4.42E-02	Multiple_Complex
TC1200008568.hg.1	TMPO	thymopoietin	-1.67	10.96	11.7	0.42	0.08	1.21E-02	6.05E-02	Multiple_Complex
TC0200008734.hg.1	C2orf49	chromosome 2 open reading frame 49	-1.67	9.52	10.26	0.32	0.14	9.70E-03	5.24E-02	Coding
TC0X00006477.hg.1	CD99	CD99 molecule	-1.67	12.46	13.2	0.16	0.12	6.30E-03	3.93E-02	Multiple_Complex

TC0800012206.hg.1	DGAT1; MIR6848	diacylglycerol O-acyltransferase 1; microRNA 6848	-1.67	10.42	11.16	0.04	0.41	1.22E-02	6.11E-02	Multiple_Complex
TC0500007586.hg.1	RGS7BP	regulator of G-protein signaling 7 binding protein	-1.67	6.52	7.26	0.19	0.14	1.79E-02	7.92E-02	Multiple_Complex
TC0100015789.hg.1	POGZ	Transcript Identified by AceView, Entrez Gene ID(s) 23126	-1.67	4.68	5.42	0.11	0.59	3.56E-02	1.25E-01	Unassigned
TC1900011098.hg.1	BCAT2	branched chain amino-acid transaminase 2, mitochondrial	-1.67	8.27	9.01	0.05	0.1	2.44E-02	9.73E-02	Multiple_Complex
TC1100012717.hg.1	PUS3	pseudouridylate synthase 3	-1.67	9.57	10.31	0.03	0.19	1.29E-02	6.35E-02	Coding
TC1900006688.hg.1	MPND	MPN domain containing	-1.67	7.8	8.53	0.26	0.35	1.97E-02	8.40E-02	Multiple_Complex
TC0200010046.hg.1	HOXD12	homeobox D12	-1.67	5.63	6.37	0.17	0.54	3.03E-02	1.12E-01	Coding
TC1400010605.hg.1	CTAGE5	CTAGE family, member 5	-1.67	9.05	9.79	0.06	0.31	9.80E-03	5.28E-02	Multiple_Complex
TC1900007906.hg.1	TBCB	tubulin folding cofactor B	-1.67	11.54	12.28	0	0.05	5.80E-03	3.71E-02	Multiple_Complex
TC2200006947.hg.1	ASPHD2	aspartate beta-hydroxylase domain containing 2	-1.67	5.95	6.69	0.46	0.06	2.11E-02	8.79E-02	Multiple_Complex
TC1600010453.hg.1	CCDC102A	coiled-coil domain containing 102A	-1.67	7.05	7.79	0.69	0.07	3.05E-02	1.13E-01	Multiple_Complex
TC1900011675.hg.1	C19orf53	chromosome 19 open reading frame 53	-1.67	11.52	12.26	0.06	0.07	4.50E-03	3.20E-02	Coding
TC0100015401.hg.1	IGSF3	immunoglobulin superfamily, member 3	-1.67	6.63	7.37	0.21	0.17	6.50E-03	4.03E-02	Multiple_Complex
TC1200007866.hg.1	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	-1.67	14.25	14.99	0.1	0	4.50E-03	3.17E-02	Multiple_Complex
TC0600011912.hg.1	SLC35B2; MIR4647	solute carrier family 35 (adenosine 3-phospho 5-phosphosulfate transporter), member B2; microRNA 4647	-1.67	11.15	11.9	0.16	0.18	6.20E-03	3.91E-02	Multiple_Complex
TC1200011269.hg.1	TRHDE-AS1	TRHDE antisense RNA 1	-1.67	4.79	5.54	0.3	0.19	9.90E-03	5.31E-02	NonCoding
TC2100006659.hg.1	CXADR	coxsackie virus and adenovirus receptor	-1.67	9.6	10.34	0.43	0.18	1.68E-02	7.61E-02	Multiple_Complex
TC0600007700.hg.1	KIFC1	kinesin family member C1	-1.67	6.94	7.68	0.05	0.33	8.60E-03	4.85E-02	Multiple_Complex

TC0100006627.hg.1	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	-1.67	7.06	7.8	0.17	0.09	1.16E-02	5.89E-02	Multiple_Complex
TC0900009164.hg.1	MRPS2	mitochondrial ribosomal protein S2	-1.67	11.89	12.63	0.01	0.01	4.20E-03	3.05E-02	Multiple_Complex
TC2200007614.hg.1	FAM118A	family with sequence similarity 118, member A	-1.67	6.53	7.27	0.17	0.52	4.35E-02	1.43E-01	Multiple_Complex
TC1000006648.hg.1	RBM17	RNA binding motif protein 17	-1.67	9.53	10.27	0.42	0.05	1.16E-02	5.89E-02	Multiple_Complex
TC1100011094.hg.1	UBXN1	UBX domain protein 1	-1.67	10.67	11.41	0.1	0.15	6.30E-03	3.95E-02	Multiple_Complex
TC0600009851.hg.1	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	-1.67	8.07	8.81	0.73	0.11	3.89E-02	1.33E-01	Multiple_Complex
TC0800012190.hg.1	SHARPIN	SHANK-associated RH domain interactor	-1.67	6.77	7.51	0.43	0.28	2.78E-02	1.06E-01	Multiple_Complex
TC1900009002.hg.1	ZNF530	zinc finger protein 530	-1.68	5.31	6.06	0.63	0.11	2.61E-02	1.02E-01	Multiple_Complex
TC1700007907.hg.1	TUBG2	tubulin, gamma 2	-1.68	13.59	14.34	0.06	0.07	4.70E-03	3.25E-02	Multiple_Complex
TC1200007759.hg.1	COPZ1	coatomer protein complex subunit zeta 1	-1.68	10.95	11.69	0.16	0.05	5.30E-03	3.53E-02	Multiple_Complex
TSUnmapped00000461.hg.1	ZNF35	zinc finger protein 35	-1.68	8.18	8.93	0.42	0.28	1.57E-02	7.23E-02	Coding
TC1600010452.hg.1	DOK4	docking protein 4	-1.68	7.37	8.11	0.57	0.13	4.51E-02	1.47E-01	Multiple_Complex
TC1900011860.hg.1	DNMT1	DNA (cytosine-5-)-methyltransferase 1	-1.68	8.02	8.77	0.03	0.02	1.69E-02	7.61E-02	Multiple_Complex
TC0900011650.hg.1	WDR34	WD repeat domain 34	-1.68	9.73	10.48	0.57	0.43	4.44E-02	1.45E-01	Multiple_Complex
TC0800009735.hg.1	MTUS1	microtubule associated tumor suppressor 1	-1.68	7.61	8.36	0.32	0.25	1.12E-02	5.77E-02	Multiple_Complex
TC1300009570.hg.1	STK24	serine/threonine kinase 24	-1.68	4.82	5.56	0.2	0.05	3.48E-02	1.23E-01	Multiple_Complex
TC1200012626.hg.1	PRPF40B	PRP40 homolog, pre-mRNA processing factor B	-1.68	7	7.74	0.11	0.65	2.60E-02	1.02E-01	Multiple_Complex
TC1600010470.hg.1	ZNF319	zinc finger protein 319	-1.68	5.38	6.12	0.49	0.39	2.51E-02	9.93E-02	Coding
TC0600006873.hg.1	BMP6	bone morphogenetic protein 6	-1.68	8.2	8.95	0.18	0.22	7.50E-03	4.42E-02	Multiple_Complex
TC0500013354.hg.1	P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	-1.68	7.78	8.53	0.13	0.08	8.30E-03	4.75E-02	Multiple_Complex

TC2000006464.hg.1	FAM110A	family with sequence similarity 110, member A	-1.68	6.17	6.91	0.4	0.07	1.05E-02	5.53E-02	Multiple_Complex
TSUnmapped00000061.hg.1	FBL	fibrillarin	-1.68	13.45	14.2	0.07	0.09	4.60E-03	3.22E-02	Coding
TC0700013065.hg.1	ABCF2	ATP binding cassette subfamily F member 2	-1.68	5.49	6.24	0.13	0.4	1.83E-02	8.03E-02	Multiple_Complex
TC0300013807.hg.1	XYLB	xylulokinase homolog (H. influenzae)	-1.68	8.62	9.37	0.39	0.07	1.00E-02	5.32E-02	Multiple_Complex
TC0900011872.hg.1	BRD3	bromodomain containing 3	-1.68	8.71	9.46	0.42	0.27	1.45E-02	6.86E-02	Multiple_Complex
TC0600012871.hg.1	TRAF3IP2	TRAF3 interacting protein 2	-1.68	7.5	8.25	0.26	0.09	8.70E-03	4.90E-02	Multiple_Complex
TC0200013021.hg.1	PAIP2B	poly(A) binding protein interacting protein 2B	-1.68	8.88	9.63	0.51	0.19	2.03E-02	8.60E-02	Coding
TC1500010501.hg.1	RGMA	repulsive guidance molecule family member a	-1.68	7.66	8.41	0.17	0.29	8.30E-03	4.75E-02	Multiple_Complex
TC1600007374.hg.1	NFATC2IP; MIR4517	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein; microRNA 4517	-1.68	8.81	9.56	0.06	0.13	5.10E-03	3.43E-02	Multiple_Complex
TC1000009527.hg.1	LARP4B	La ribonucleoprotein domain family, member 4B	-1.68	8.86	9.61	0.01	0.52	2.08E-02	8.72E-02	Multiple_Complex
TC1600009063.hg.1	MRPS34	mitochondrial ribosomal protein S34	-1.68	8.44	9.19	0.04	0.23	7.80E-03	4.54E-02	Multiple_Complex
TC0400011175.hg.1	TMEM150C	transmembrane protein 150C	-1.68	5.54	6.29	0.13	0.01	3.12E-02	1.15E-01	Multiple_Complex
TC0300011044.hg.1	DALRD3	DALR anticodon binding domain containing 3	-1.68	9.51	10.26	0.18	0.17	1.08E-02	5.61E-02	Multiple_Complex
TC0600013794.hg.1	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	-1.68	7.51	8.26	0.46	0.19	4.44E-02	1.45E-01	Multiple_Complex
TC0700013337.hg.1	UMAD1	UBAP1-MVB12-associated (UMA) domain containing 1	-1.68	10.36	11.12	0.13	0.05	8.90E-03	4.93E-02	Multiple_Complex
TC2000007133.hg.1	MAPRE1	microtubule-associated protein, RP/EB family, member 1	-1.68	10.84	11.59	0.18	0.02	5.20E-03	3.46E-02	Multiple_Complex
TC1700006644.hg.1	PSMB6	proteasome subunit beta 6	-1.68	12.73	13.48	0.15	0.06	4.60E-03	3.23E-02	Multiple_Complex
TC1900011910.hg.1	HOMER3	homer scaffolding protein 3	-1.68	6.45	7.2	0.23	0.22	2.39E-02	9.62E-02	Multiple_Complex
TC1400010580.hg.1	DHRS4L2	dehydrogenase/reductase (SDR family) member 4 like 2	-1.68	9.13	9.88	0.38	0.44	2.99E-02	1.11E-01	Multiple_Complex

TC0500009620.hg.1	RGS14	regulator of G-protein signaling 14	-1.68	7.97	8.72	0.17	0.11	6.00E-03	3.82E-02	Multiple_Complex
TC0500009585.hg.1	ARL10	ADP-ribosylation factor like GTPase 10	-1.68	11.19	11.94	0.19	0.18	7.90E-03	4.58E-02	Multiple_Complex
TC0100012101.hg.1	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	-1.69	11.14	11.89	0.16	0.25	7.70E-03	4.52E-02	Multiple_Complex
TC0X00009250.hg.1	ACOT9	acyl-CoA thioesterase 9	-1.69	8.51	9.26	0.44	0.06	1.10E-02	5.71E-02	Multiple_Complex
TC1400009426.hg.1	MAX	MYC associated factor X	-1.69	11.81	12.56	0.21	0.14	6.30E-03	3.94E-02	Multiple_Complex
TC1400010723.hg.1	TM9SF1	transmembrane 9 superfamily member 1	-1.69	9.09	9.84	0.52	0.22	1.84E-02	8.06E-02	Multiple_Complex
TC0X00009882.hg.1	MTMR8	myotubularin related protein 8	-1.69	5.03	5.79	0.4	0.5	2.41E-02	9.67E-02	Multiple_Complex
TC1300007104.hg.1	LRCH1	leucine-rich repeats and calponin homology (CH) domain containing 1	-1.69	6.38	7.14	0.37	0.22	1.52E-02	7.08E-02	Multiple_Complex
TC2200009170.hg.1	ARSA	arylsulfatase A	-1.69	8.16	8.92	0.21	0.36	1.08E-02	5.63E-02	Multiple_Complex
TC1700007319.hg.1	WSB1	WD repeat and SOCS box containing 1	-1.69	12.29	13.04	0.13	0.18	5.50E-03	3.60E-02	Multiple_Complex
TC1100007874.hg.1	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G	-1.69	11.97	12.72	0.35	0.17	1.06E-02	5.58E-02	Multiple_Complex
TC1700011038.hg.1	ZNF652	zinc finger protein 652	-1.69	11.21	11.97	0.03	0.02	4.00E-03	2.97E-02	Multiple_Complex
TC1600006733.hg.1	GLIS2	GLIS family zinc finger 2	-1.69	4.72	5.48	0.07	0.01	4.10E-03	3.00E-02	Multiple_Complex
TC0700007392.hg.1	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-1.69	10.75	11.5	0.18	0.14	1.07E-02	5.60E-02	Multiple_Complex
TC1500010659.hg.1	SNRPA1	small nuclear ribonucleoprotein polypeptide A	-1.69	12.92	13.68	0.54	0.07	1.85E-02	8.08E-02	Multiple_Complex
TC1900011827.hg.1	ZNF8	zinc finger protein 8	-1.69	7.53	8.29	0.13	0.27	4.97E-02	1.57E-01	Multiple_Complex
TC0900009929.hg.1	VCP	valosin containing protein	-1.69	8.27	9.03	0.18	0.01	5.50E-03	3.62E-02	Multiple_Complex
TC0200013765.hg.1	UXS1	UDP-glucuronate decarboxylase 1	-1.69	9.36	10.12	0.26	0.41	2.71E-02	1.05E-01	Multiple_Complex
TC1600011376.hg.1	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	-1.69	11.95	12.71	0.08	0.26	6.40E-03	3.97E-02	Multiple_Complex

TC1100010990.hg.1	MRPL16	mitochondrial ribosomal protein L16	-1.69	7.2	7.96	0.13	0.53	1.55E-02	7.17E-02	Multiple_Complex
TC2200007792.hg.1	SELO	selenoprotein O; selenoprotein O [Source:EntrezGene;Acc:83642]; Salzman2013 ANNOTATED, CDS, coding, INTERNAL, OVCODE, OVERLAPTX, OVEXON best transcript NM_031454; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVERLAPTX, OVEXON, UTR3 best transcript NM_031454; Transcript Identified by AceView, Entrez Gene ID(s) 83642, RefSeq ID(s) NM_031454	-1.69	8.53	9.29	0.12	0.01	5.20E-03	3.49E-02	Multiple_Complex
TC1600010711.hg.1	CHTF8	chromosome transmission fidelity factor 8	-1.69	11.13	11.89	0.39	0.06	1.89E-02	8.18E-02	Multiple_Complex
TC0200016597.hg.1	SPEG	SPEG complex locus	-1.69	5.77	6.53	0.72	0.11	3.36E-02	1.20E-01	Multiple_Complex
TC1800009222.hg.1	RNF125	ring finger protein 125, E3 ubiquitin protein ligase	-1.69	5.9	6.66	0.77	0.33	4.96E-02	1.56E-01	Multiple_Complex
TC1200012573.hg.1	RHNO1	RAD9-HUS1-RAD1 interacting nuclear orphan 1	-1.69	6.86	7.61	0.01	0.05	1.22E-02	6.12E-02	Multiple_Complex
TC1700009274.hg.1	FN3KRP	fructosamine 3 kinase related protein	-1.69	6.46	7.22	0.04	0.45	1.46E-02	6.89E-02	Multiple_Complex
TC0900011819.hg.1	TSC1	tuberous sclerosis 1	-1.69	11.4	12.16	0.14	0.26	1.24E-02	6.19E-02	Multiple_Complex
TC0600006993.hg.1	NOL7	nucleolar protein 7	-1.69	12.72	13.48	0.34	0.45	1.85E-02	8.09E-02	Multiple_Complex
TC1900011756.hg.1	PVR	poliovirus receptor	-1.69	10.08	10.84	0.06	0.15	6.00E-03	3.79E-02	Multiple_Complex
TC1200010110.hg.1	KCNJ8	potassium channel, inwardly rectifying subfamily J, member 8	-1.69	7.91	8.67	0.21	0.35	3.35E-02	1.20E-01	Coding
TC2100007331.hg.1	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	-1.69	8.11	8.87	0.63	0.61	4.62E-02	1.49E-01	Multiple_Complex
TC2000007169.hg.1	CHMP4B	charged multivesicular body protein 4B	-1.69	9.11	9.87	0.21	0.11	5.50E-03	3.62E-02	Multiple_Complex
TC2000007503.hg.1	UBE2C	ubiquitin-conjugating enzyme E2C	-1.69	12.12	12.88	0.11	0.01	4.10E-03	3.01E-02	Multiple_Complex

TC1100010730.hg.1	ACP2	acid phosphatase 2, lysosomal	-1.69	6.51	7.27	0.15	0.43	1.44E-02	6.85E-02	Multiple_Complex
TC0700013510.hg.1	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	-1.69	11.28	12.04	0	0.11	4.10E-03	3.00E-02	Multiple_Complex
TC2200006623.hg.1	COMT; MIR4761	catechol-O-methyltransferase; microRNA 4761	-1.69	11.99	12.75	0	0.11	3.80E-03	2.89E-02	Multiple_Complex
TC1200009868.hg.1	DDX12P; DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12, pseudogene; DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11	-1.7	9.36	10.12	0.02	0.18	3.48E-02	1.23E-01	Multiple_Complex
TC0900008178.hg.1	NANS	N-acetylneuraminic acid synthase	-1.7	11.63	12.39	0.07	0.02	3.90E-03	2.93E-02	Multiple_Complex
TSUnmapped00000243.hg.1	MANSC1	MANSC domain containing 1	-1.7	5.47	6.23	0.04	0.09	4.70E-03	3.27E-02	Coding
TC0100010284.hg.1	PEA15	phosphoprotein enriched in astrocytes 15	-1.7	12.34	13.11	0.18	0.09	5.50E-03	3.60E-02	Multiple_Complex
TC1600011360.hg.1	SYT17	synaptotagmin XVII	-1.7	7.46	8.23	0.54	0.07	1.65E-02	7.48E-02	Multiple_Complex
TC0600011508.hg.1	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.7	6.51	7.27	0.15	0.18	7.20E-03	4.30E-02	Multiple_Complex
TC0500011725.hg.1	MCC	mutated in colorectal cancers	-1.7	6.66	7.43	0.1	0.5	2.20E-02	9.08E-02	Multiple_Complex
TC1000009065.hg.1	FAM45A	Transcript Identified by AceView, Entrez Gene ID(s) 404636	-1.7	5.87	6.63	0.17	0.61	2.28E-02	9.32E-02	Unassigned
TC1800008281.hg.1	TMEM241	transmembrane protein 241	-1.7	8.44	9.2	0.19	0.1	2.36E-02	9.52E-02	Multiple_Complex
TC1500010893.hg.1	PTPN9	protein tyrosine phosphatase, non-receptor type 9	-1.7	5.86	6.62	0.36	0.05	2.15E-02	8.92E-02	Multiple_Complex
TC1400008714.hg.1	SLC22A17	solute carrier family 22, member 17	-1.7	9.49	10.25	0.67	0.18	2.64E-02	1.03E-01	Multiple_Complex
TC1500010892.hg.1	MAN2C1	mannosidase, alpha, class 2C, member 1	-1.7	6.78	7.54	0.4	0.64	3.29E-02	1.19E-01	Multiple_Complex
TC1000012235.hg.1	MKI67	marker of proliferation Ki-67	-1.7	11.63	12.4	0.03	0.02	3.70E-03	2.81E-02	Multiple_Complex
TC0900011388.hg.1	PHF19	PHD finger protein 19	-1.7	8.01	8.77	0.18	0.35	1.26E-02	6.26E-02	Multiple_Complex
TC0X00010921.hg.1	MMGT1	membrane magnesium transporter 1	-1.7	10.95	11.71	0.5	0.15	3.78E-02	1.30E-01	Multiple_Complex

TC1400010584.hg.1	IRF9	interferon regulatory factor 9	-1.7	6.68	7.45	0.19	0.4	1.15E-02	5.88E-02	Multiple_Complex
TC1900011703.hg.1	ZNF536	zinc finger protein 536	-1.7	4.38	5.14	0.46	0.26	1.90E-02	8.23E-02	NonCoding
TC0100018569.hg.1	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	-1.7	11.08	11.85	0.04	0.05	4.40E-03	3.16E-02	Multiple_Complex
TC1400008155.hg.1	C14orf177	chromosome 14 open reading frame 177	-1.7	5.63	6.4	0.51	0.64	5.00E-02	1.57E-01	Multiple_Complex
TC0500008845.hg.1	PURA	purine-rich element binding protein A	-1.7	12.93	13.69	0.14	0.13	5.30E-03	3.54E-02	Multiple_Complex
TC0600011534.hg.1	WDR46; MIR6873	WD repeat domain 46; microRNA 6873	-1.7	6.87	7.63	0.12	0.14	4.30E-03	3.12E-02	Multiple_Complex
TC2200009345.hg.1	C1QTNF6	C1q and tumor necrosis factor related protein 6	-1.7	6.92	7.69	0.05	0.12	4.70E-03	3.25E-02	Multiple_Complex
TC1100008101.hg.1	RCE1; C11orf80	Ras converting CAAX endopeptidase 1; chromosome 11 open reading frame 80	-1.7	7.06	7.82	0.36	0.45	2.68E-02	1.04E-01	Multiple_Complex
TC1600008932.hg.1	LUC7L	LUC7-like	-1.7	7.18	7.95	0.28	0.21	1.27E-02	6.28E-02	Multiple_Complex
TC1000011713.hg.1	PCGF6	polycomb group ring finger 6	-1.7	9.39	10.16	0.25	0.05	5.70E-03	3.69E-02	Multiple_Complex
TC1100007922.hg.1	NAA40	N(alpha)-acetyltransferase 40, NatD catalytic subunit	-1.7	8.15	8.91	0.14	0.08	1.18E-02	5.98E-02	Multiple_Complex
TC0X00009569.hg.1	ZNF41	zinc finger protein 41	-1.7	9.33	10.09	0.25	0.13	1.37E-02	6.59E-02	Multiple_Complex
TC2000008993.hg.1	SCAND1	SCAN domain containing 1	-1.7	9.4	10.16	0.07	0.18	4.50E-03	3.17E-02	Coding
TC0900011805.hg.1	TTF1	transcription termination factor, RNA polymerase I	-1.7	5.54	6.31	0.63	0.2	2.74E-02	1.05E-01	Multiple_Complex
TC0500013100.hg.1	FLT4	fms-related tyrosine kinase 4	-1.7	6.63	7.4	0.64	0.31	2.96E-02	1.11E-01	Multiple_Complex
TC0100008554.hg.1	USP1	ubiquitin specific peptidase 1	-1.7	9.91	10.68	0.45	0.3	1.67E-02	7.55E-02	Multiple_Complex
TC1900007305.hg.1	MYO9B	myosin IXB	-1.7	8.22	8.99	0.38	0.31	2.55E-02	1.01E-01	Multiple_Complex
TC0700010926.hg.1	TMED4	transmembrane p24 trafficking protein 4	-1.7	12.14	12.9	0.49	0.31	1.76E-02	7.82E-02	Multiple_Complex
TC1200012647.hg.1	MYL6B	myosin light chain 6B	-1.7	10.85	11.62	0.18	0.24	7.10E-03	4.24E-02	Multiple_Complex
TC1600007001.hg.1	NOMO1	NODAL modulator 1	-1.7	15.6	16.37	0.16	0.05	4.10E-03	3.02E-02	Multiple_Complex

TC0200012076.hg.1	PPM1G	protein phosphatase, Mg2+/Mn2+ dependent, 1G	-1.7	9.71	10.48	0.08	0.19	1.05E-02	5.52E-02	Multiple_Complex
TC1200012273.hg.1	RILPL1	Rab interacting lysosomal protein-like 1	-1.7	7.62	8.39	0.35	0.22	9.60E-03	5.20E-02	Multiple_Complex
TC1200012003.hg.1	RBM19	RNA binding motif protein 19	-1.7	8.6	9.37	0.29	0.07	6.00E-03	3.80E-02	Multiple_Complex
TC0700007065.hg.1	PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	-1.7	6.65	7.42	0.4	0.22	1.41E-02	6.75E-02	Multiple_Complex
TC1700010084.hg.1	TMEM11	transmembrane protein 11	-1.7	9.44	10.21	0.38	0.09	1.75E-02	7.79E-02	Multiple_Complex
TC1100007786.hg.1	TMEM132A	transmembrane protein 132A	-1.7	10.11	10.88	0.15	0.36	1.41E-02	6.74E-02	Multiple_Complex
TC0X00010793.hg.1	ZDHHC9	zinc finger, DHHC-type containing 9	-1.7	10.79	11.56	0.1	0.25	1.65E-02	7.48E-02	Multiple_Complex
TC0900011378.hg.1	CDK5RAP2	CDK5 regulatory subunit associated protein 2	-1.7	11.73	12.49	0.61	0.07	2.22E-02	9.14E-02	Multiple_Complex
TC2000007320.hg.1	RALGAPB	Ral GTPase activating protein, beta subunit (non-catalytic)	-1.7	10.08	10.85	0.24	0.03	4.80E-03	3.33E-02	Multiple_Complex
TC0400012252.hg.1	PPID	peptidylprolyl isomerase D	-1.7	7.22	7.99	0.23	0.14	5.90E-03	3.75E-02	Multiple_Complex
TC2000009896.hg.1	DTD1	D-tyrosyl-tRNA deacylase 1	-1.7	10.51	11.28	0.1	0.05	1.58E-02	7.27E-02	Multiple_Complex
TC1700007189.hg.1	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	-1.7	8.04	8.81	0.21	0.18	8.20E-03	4.69E-02	Multiple_Complex
TC1500010041.hg.1	EDC3	enhancer of mRNA decapping 3	-1.71	10.66	11.43	0.11	0.04	4.20E-03	3.04E-02	Multiple_Complex
TC0500013143.hg.1	EXOC3	exocyst complex component 3	-1.71	6.5	7.27	0.78	0.29	4.46E-02	1.46E-01	NonCoding
TC0400008388.hg.1	GAR1	GAR1 homolog, ribonucleoprotein	-1.71	9.88	10.65	0.31	0.13	1.69E-02	7.61E-02	Multiple_Complex
TC1100009674.hg.1	RNH1	ribonuclease/angiogenin inhibitor 1	-1.71	6.29	7.06	0.03	0.26	4.52E-02	1.47E-01	Multiple_Complex
TC0700008574.hg.1	MUC3A	mucin 3A, cell surface associated	-1.71	6.25	7.02	0.04	0.2	9.60E-03	5.21E-02	Multiple_Complex
TC0X00006581.hg.1	TBL1X	transducin (beta)-like 1X-linked	-1.71	8.77	9.54	0.03	0.24	7.80E-03	4.53E-02	Multiple_Complex
TC0X00007191.hg.1	EBP	emopamil binding protein (sterol isomerase)	-1.71	13.26	14.03	0.04	0.08	4.90E-03	3.34E-02	Multiple_Complex
TC0600009961.hg.1	ARID1B	AT rich interactive domain 1B (SWI1-like)	-1.71	8.78	9.55	0.32	0.03	6.90E-03	4.17E-02	Multiple_Complex

TC0100011901.hg.1	RAB4A; SPHAR	RAB4A, member RAS oncogene family; S-phase response (cyclin related)	-1.71	11.22	11.99	0	0.01	3.20E-03	2.61E-02	Multiple_Complex
TC0900009855.hg.1	BAG1	BCL2-associated athanogene	-1.71	8.44	9.21	0.43	0.06	2.15E-02	8.92E-02	Multiple_Complex
TC1000008716.hg.1	GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	-1.71	12.04	12.81	0.16	0.08	6.30E-03	3.93E-02	Multiple_Complex
TC0100012602.hg.1	CEP104	centrosomal protein 104kDa	-1.71	7.32	8.09	0.04	0.01	3.90E-03	2.91E-02	Multiple_Complex
TC1200008126.hg.1	CPSF6	cleavage and polyadenylation specific factor 6	-1.71	9.03	9.8	0.24	0.23	1.17E-02	5.93E-02	Multiple_Complex
TC0500009856.hg.1	CLPTM1L	CLPTM1-like	-1.71	8.69	9.46	0.12	0.06	3.50E-03	2.75E-02	Multiple_Complex
TC0100017587.hg.1	MRPL55	mitochondrial ribosomal protein L55	-1.71	11.8	12.57	0.51	0.41	2.93E-02	1.10E-01	Multiple_Complex
TC0900009776.hg.1	MOB3B	MOB kinase activator 3B	-1.71	8.03	8.8	0.41	0.08	1.35E-02	6.55E-02	Multiple_Complex
TC0700013055.hg.1	CDK5	cyclin-dependent kinase 5	-1.71	7.39	8.16	0.04	0.06	4.30E-03	3.10E-02	Multiple_Complex
TC1300008688.hg.1	FOXO1	forkhead box O1	-1.71	6.89	7.67	0.14	0.22	9.60E-03	5.20E-02	Multiple_Complex
TC0X00008492.hg.1	SMIM10	small integral membrane protein 10	-1.71	7.05	7.82	0.13	0.19	6.30E-03	3.93E-02	Multiple_Complex
TC0500012271.hg.1	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	-1.71	8.92	9.69	0.79	0.04	4.12E-02	1.38E-01	Multiple_Complex
TC1600009870.hg.1	SULT1A1	sulfotransferase family 1A member 1	-1.71	6.44	7.22	0.27	0.19	6.10E-03	3.85E-02	Multiple_Complex
TC0800007985.hg.1	GDAP1	ganglioside induced differentiation associated protein 1	-1.71	8.36	9.14	0.36	0.11	2.98E-02	1.11E-01	Multiple_Complex
TC1900010011.hg.1	LSM4	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated	-1.71	10.86	11.64	0.09	0.05	3.30E-03	2.63E-02	Multiple_Complex
TC0600011145.hg.1	HIST1H4H	histone cluster 1, H4h	-1.71	8.68	9.45	0.52	0.34	1.89E-02	8.18E-02	Coding
TC1400009793.hg.1	SNW1	SNW domain containing 1	-1.71	9.43	10.2	0.57	0.2	1.70E-02	7.65E-02	Multiple_Complex
TC0800012225.hg.1	ARHGAP39	Rho GTPase activating protein 39	-1.71	5.14	5.92	0.07	0.32	8.80E-03	4.92E-02	Multiple_Complex

TC1900007829.hg.1	GRAMD1A	GRAM domain containing 1A	-1.71	7.12	7.89	0.03	0.21	8.70E-03	4.88E-02	Multiple_Complex
TC0600010542.hg.1	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	-1.71	10.44	11.21	0.12	0.19	7.00E-03	4.22E-02	Multiple_Complex
TC0500012070.hg.1	CDKN2AIPNL	CDKN2A interacting protein N-terminal like	-1.71	10.91	11.69	0.07	0.12	4.90E-03	3.36E-02	Coding
TC1200007767.hg.1	NCKAP1L	NCK-associated protein 1-like	-1.71	3.66	4.44	0.36	0.68	4.32E-02	1.42E-01	Multiple_Complex
TC1700009928.hg.1	COPS3	COP9 signalosome subunit 3	-1.71	14.53	15.3	0.16	0.31	1.69E-02	7.62E-02	Multiple_Complex
TC0400010033.hg.1	WDR1	WD repeat domain 1	-1.71	9.17	9.95	0.05	0.01	4.60E-03	3.22E-02	Multiple_Complex
TC0100011413.hg.1	CR2	complement component (3d/Epstein Barr virus) receptor 2	-1.71	7.14	7.91	0.05	0.19	2.80E-02	1.07E-01	Multiple_Complex
TC1300007248.hg.1	CKAP2	cytoskeleton associated protein 2	-1.71	12.24	13.01	0.11	0.05	6.30E-03	3.95E-02	Multiple_Complex
TC1700011523.hg.1	PSMD12	proteasome 26S subunit, non-ATPase 12	-1.71	10.14	10.92	0.17	0.04	7.60E-03	4.45E-02	Multiple_Complex
TC0X00006739.hg.1	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	-1.71	10.47	11.25	0.07	0.01	3.60E-03	2.79E-02	Multiple_Complex
TC0300011060.hg.1	RHOA	ras homolog family member A	-1.71	10.31	11.09	0.41	0.2	1.16E-02	5.90E-02	Multiple_Complex
TC0100015885.hg.1	GATAD2B	GATA zinc finger domain containing 2B	-1.71	11.41	12.18	0.04	0.04	6.00E-03	3.81E-02	Multiple_Complex
TC0500013186.hg.1	PTCD2	pentatricopeptide repeat domain 2	-1.71	6.84	7.62	0.3	0.08	1.02E-02	5.41E-02	Multiple_Complex
TC1600010291.hg.1	SALL1	spalt-like transcription factor 1	-1.71	5.91	6.69	0.68	0.51	3.97E-02	1.35E-01	Multiple_Complex
TC0300009500.hg.1	FNDC3B	fibronectin type III domain containing 3B	-1.71	11.35	12.13	0.04	0.06	5.80E-03	3.72E-02	Multiple_Complex
TC1000008758.hg.1	CNNM2	cyclin and CBS domain divalent metal cation transport mediator 2	-1.71	10.47	11.25	0.1	0.05	3.60E-03	2.79E-02	Multiple_Complex
TC1200011891.hg.1	GIT2	G protein-coupled receptor kinase interacting ArfGAP 2	-1.71	10.32	11.09	0.51	0.4	2.93E-02	1.10E-01	Multiple_Complex
TC0100006982.hg.1	EFHD2	EF-hand domain family member D2	-1.71	6.32	7.1	0.77	0.09	3.32E-02	1.19E-01	Coding
TC1700006638.hg.1	ARRB2	arrestin, beta 2	-1.72	8.66	9.44	0.24	0.26	2.35E-02	9.52E-02	Multiple_Complex
TC1900007155.hg.1	MIR1199	microRNA 1199	-1.72	4.32	5.1	0.37	0.22	8.50E-03	4.81E-02	Multiple_Complex

TC2100007474.hg.1	PRMT2	protein arginine methyltransferase 2	-1.72	10.29	11.07	0.08	0.06	3.70E-03	2.81E-02	Multiple_Complex
TC1600009134.hg.1	PRSS27	protease, serine 27	-1.72	10.57	11.35	0.4	0.15	3.58E-02	1.25E-01	Multiple_Complex
TC1700006533.hg.1	DPH1; OVCA2	diphthamide biosynthesis 1; ovarian tumor suppressor candidate 2	-1.72	6.61	7.39	0.3	0.19	1.12E-02	5.78E-02	Multiple_Complex
TC1100013230.hg.1	BCL9L	B-cell CLL/lymphoma 9-like	-1.72	7.28	8.06	0.19	0.19	7.00E-03	4.23E-02	Multiple_Complex
TC0100015627.hg.1	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	-1.72	10.14	10.92	0.01	0.08	5.50E-03	3.60E-02	Multiple_Complex
TC1400008343.hg.1	WDR20	WD repeat domain 20	-1.72	6.65	7.43	0.07	0.2	5.50E-03	3.60E-02	Multiple_Complex
TC0700010697.hg.1	RP9	retinitis pigmentosa 9 (autosomal dominant)	-1.72	8.91	9.69	0.07	0.31	6.90E-03	4.20E-02	Multiple_Complex
TC0100007791.hg.1	ADPRHL2	ADP-ribosylhydrolase like 2	-1.72	6.45	7.23	0.47	0.28	1.73E-02	7.72E-02	Multiple_Complex
TC1900008292.hg.1	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	-1.72	7.97	8.75	0.19	0.17	7.30E-03	4.33E-02	Multiple_Complex
TC1200007809.hg.1	GDF11	growth differentiation factor 11	-1.72	5.86	6.64	0.13	0.21	5.70E-03	3.68E-02	Coding
TC0100015891.hg.1	CRTC2	CREB regulated transcription coactivator 2	-1.72	10.18	10.96	0.3	0.4	1.60E-02	7.32E-02	Multiple_Complex
TC2000007992.hg.1	SS18L1	synovial sarcoma translocation gene on chromosome 18-like 1	-1.72	6.56	7.34	0.15	0.03	7.90E-03	4.57E-02	Multiple_Complex
TC1900006578.hg.1	SF3A2	splicing factor 3a subunit 2	-1.72	9.13	9.91	0.16	0.11	5.00E-03	3.38E-02	Multiple_Complex
TC1700010747.hg.1	COA3	cytochrome c oxidase assembly factor 3	-1.72	10.86	11.64	0.45	0.02	9.60E-03	5.22E-02	Multiple_Complex
TC1900011124.hg.1	C19orf73	chromosome 19 open reading frame 73	-1.72	5.66	6.44	0.03	0.13	1.78E-02	7.87E-02	Coding
TC0700011499.hg.1	DNAJC30	DnaJ (Hsp40) homolog, subfamily C, member 30	-1.72	4.89	5.68	0.43	0.52	2.65E-02	1.03E-01	Coding
TC0900008716.hg.1	NEK6	NIMA-related kinase 6	-1.72	8.75	9.54	0.05	0.13	3.90E-03	2.91E-02	Multiple_Complex
TC0X00008908.hg.1	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	-1.72	12.46	13.25	0.15	0.37	7.90E-03	4.59E-02	Multiple_Complex
TC0200012452.hg.1	SIX2	SIX homeobox 2	-1.72	7.79	8.57	0.08	0.23	1.37E-02	6.59E-02	Coding

TC2200007114.hg.1	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta	-1.72	14.42	15.21	0.04	0.03	3.90E-03	2.94E-02	Multiple_Complex
TC0200008059.hg.1	STAMBP	STAM binding protein	-1.72	9.58	10.36	0.02	0.23	1.05E-02	5.54E-02	Multiple_Complex
TC0600011938.hg.1	CLIC5	chloride intracellular channel 5	-1.72	5.79	6.57	0.26	0.16	7.90E-03	4.59E-02	Multiple_Complex
TC0100013969.hg.1	ERI3; ERI3-IT1	ERI1 exoribonuclease family member 3; ERI3 intronic transcript 1	-1.72	10.13	10.91	0.19	0.04	4.60E-03	3.22E-02	Multiple_Complex
TC0100013038.hg.1	FBXO42	F-box protein 42	-1.72	8.23	9.01	0.07	0.1	1.05E-02	5.52E-02	Multiple_Complex
TC0200016418.hg.1	ZNF512	zinc finger protein 512	-1.72	7.45	8.23	0.28	0.04	7.00E-03	4.21E-02	Multiple_Complex
TC0800011532.hg.1	TRPS1	trichorhinophalangeal syndrome I	-1.72	4.4	5.18	0.07	0.41	1.13E-02	5.82E-02	Multiple_Complex
TC1900010301.hg.1	C19orf12	chromosome 19 open reading frame 12	-1.72	6.47	7.26	0.15	0.09	4.10E-03	3.02E-02	Multiple_Complex
TC1700006630.hg.1	SMTNL2	smoothelin-like 2	-1.72	3.92	4.71	0.01	0.18	3.60E-03	2.80E-02	Multiple_Complex
TC1100010639.hg.1	TP53I11	tumor protein p53 inducible protein 11	-1.72	7.77	8.55	0.22	0.27	6.40E-03	3.96E-02	Multiple_Complex
TC0100013305.hg.1	FUCA1	fucosidase, alpha-L- 1, tissue	-1.72	6.21	7	0.43	0.28	1.20E-02	6.05E-02	Coding
TSUnmapped00000517.hg.1	HYOU1	hypoxia up-regulated 1	-1.72	9.84	10.62	0.14	0.1	3.90E-03	2.90E-02	Coding
TC0600009310.hg.1	GJA1	gap junction protein alpha 1	-1.72	5.94	6.72	0.12	0.12	5.80E-03	3.71E-02	Multiple_Complex
TC1400007663.hg.1	COQ6	coenzyme Q6 monooxygenase	-1.72	7.63	8.42	0.29	0.26	8.70E-03	4.90E-02	Multiple_Complex
TC1400009714.hg.1	TMED10	transmembrane p24 trafficking protein 10	-1.72	12.7	13.49	0.1	0.03	4.40E-03	3.15E-02	Multiple_Complex
TC2200008576.hg.1	RBFOX2	RNA binding protein, fox-1 homolog (C. elegans) 2	-1.72	10.32	11.1	0.37	0.1	1.14E-02	5.82E-02	Multiple_Complex
TC0600013177.hg.1	MED23	mediator complex subunit 23	-1.72	8.31	9.1	0.54	0.03	1.31E-02	6.40E-02	Multiple_Complex
TC1900008188.hg.1	MEGF8	multiple EGF-like-domains 8	-1.72	4.79	5.58	0.02	0.58	3.22E-02	1.17E-01	Multiple_Complex
TC1900009443.hg.1	C3	complement component 3	-1.72	9.93	10.72	0.24	0.07	6.00E-03	3.82E-02	Multiple_Complex
TC0100017612.hg.1	TRIM11; MIR6742	tripartite motif containing 11; microRNA 6742	-1.73	5.99	6.77	0.69	0.07	2.48E-02	9.85E-02	Multiple_Complex

TC0700007905.hg.1	AUTS2	autism susceptibility candidate 2	-1.73	9.37	10.15	0.5	0.29	1.98E-02	8.44E-02	Multiple_Complex
TC0600006976.hg.1	PHACTR1	phosphatase and actin regulator 1	-1.73	5.63	6.42	0.39	0.03	8.40E-03	4.78E-02	Multiple_Complex
TC0600009819.hg.1	ULBP2	UL16 binding protein 2	-1.73	10.23	11.01	0.03	0.11	2.72E-02	1.05E-01	Coding
TC0X00010473.hg.1	TSC22D3	TSC22 domain family, member 3	-1.73	12.38	13.17	0.36	0.14	7.50E-03	4.41E-02	Coding
TC0400007344.hg.1	UCHL1	ubiquitin C-terminal hydrolase L1	-1.73	14.4	15.19	0.08	0.08	2.89E-02	1.09E-01	Multiple_Complex
TC1300009330.hg.1	RBM26	RNA binding motif protein 26	-1.73	8.92	9.71	0.11	0.13	3.50E-03	2.74E-02	Multiple_Complex
TSUnmapped00000683.hg.1	MLXIP	MLX interacting protein	-1.73	5.5	6.29	0.11	0.5	2.12E-02	8.82E-02	NonCoding
TC0900012192.hg.1	PHPT1	phosphohistidine phosphatase 1	-1.73	13.25	14.04	0.35	0.16	7.10E-03	4.27E-02	Multiple_Complex
TC1000012117.hg.1	CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	-1.73	9.22	10.01	0.22	0.34	7.50E-03	4.42E-02	Multiple_Complex
TC2000009604.hg.1	PMEPA1	prostate transmembrane protein, androgen induced 1	-1.73	9.02	9.81	0.08	0.25	7.20E-03	4.31E-02	Multiple_Complex
TC1900008549.hg.1	SCAF1	SR-related CTD-associated factor 1	-1.73	6.42	7.21	0.14	0.16	5.50E-03	3.62E-02	Multiple_Complex
TC0500007694.hg.1	GTF2H2; GTF2H2B	general transcription factor IIH subunit 2; general transcription factor IIH subunit 2B (pseudogene)	-1.73	11.92	12.71	0.1	0.26	4.80E-03	3.31E-02	Multiple_Complex
TC0X00007298.hg.1	SSX2B	synovial sarcoma, X breakpoint 2B	-1.73	3.59	4.38	0.15	0.71	3.41E-02	1.22E-01	Multiple_Complex

TC1900006700.hg.1	HDGFRP2	hepatoma-derived growth factor-related protein 2; Hepatoma-derived growth factor-related protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q7Z4V5]; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVEXON, UTR5 best transcript NM_001001520; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVERLAPTX, OVEXON, UTR3, UTR5 best transcript NM_001001520; Salzman2013 ANNOTATED, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_001001520; Salzman2013 ALT_ACCEPTOR, CDS, coding, INTERNAL, intronic, OVCODE, OVEXON best transcript NM_001001520; Salzman2013 ANNOTATED, CDS, coding, OVCODE, OVERLAPTX, OVEXON, UTR3 best transcript NM_001001520; Salzman2013 ALT_DONOR, CDS, coding, INTERNAL, OVCODE, OVERLAPTX, OVEXON, UTR3 best transcript NM_001001520	-1.73	8.89	9.68	0.11	0.08	4.20E-03	3.09E-02	Multiple_Complex
TC0100017815.hg.1	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.73	13.47	14.26	0.21	0.05	4.70E-03	3.25E-02	Multiple_Complex
TC0600012437.hg.1	SNAP91	synaptosome associated protein 91kDa	-1.73	6.57	7.36	0.27	0.06	2.07E-02	8.69E-02	Multiple_Complex
TC0100016903.hg.1	TMEM9	transmembrane protein 9	-1.73	10.91	11.7	0.12	0.12	3.30E-03	2.63E-02	Multiple_Complex
TC1700012078.hg.1	ALYREF	Aly/REF export factor	-1.73	8.93	9.72	0.01	0.11	5.00E-03	3.39E-02	Multiple_Complex
TC0X00011244.hg.1	F8A3	coagulation factor VIII-associated 3	-1.73	8.8	9.59	0.27	0.3	7.20E-03	4.29E-02	Coding

TC0100018519.hg.1	F11R	F11 receptor	-1.73	11.52	12.31	0.02	0.26	6.00E-03	3.80E-02	Multiple_Complex
TC0500013391.hg.1	PWWP2A	PWWP domain containing 2A	-1.73	6.4	7.2	0.32	0.17	8.20E-03	4.70E-02	Multiple_Complex
TC1600006493.hg.1	FAM173A	family with sequence similarity 173, member A	-1.73	9.24	10.03	0.3	0.43	1.20E-02	6.05E-02	Multiple_Complex
TC0100008450.hg.1	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	-1.73	9.21	10	0.59	0.12	1.95E-02	8.37E-02	Multiple_Complex
TC0600007825.hg.1	MAPK14	mitogen-activated protein kinase 14	-1.73	7.43	8.22	0.57	0.11	1.77E-02	7.83E-02	Multiple_Complex
TC2000009949.hg.1	STX16	syntaxin 16	-1.73	10.31	11.11	0.29	0.22	8.20E-03	4.70E-02	Multiple_Complex
TC1700012285.hg.1	PRR11	proline rich 11	-1.73	7.58	8.37	0.35	0.03	6.10E-03	3.85E-02	Multiple_Complex
TC0400007245.hg.1	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	-1.73	8.23	9.02	0.52	0.05	1.13E-02	5.82E-02	Multiple_Complex
TC0600014112.hg.1	ZBTB9	zinc finger and BTB domain containing 9	-1.73	6.45	7.24	0.28	0.13	2.59E-02	1.02E-01	Multiple_Complex
TC1800007091.hg.1	ELP2	elongator acetyltransferase complex subunit 2	-1.73	6.85	7.65	0.75	0.05	3.52E-02	1.24E-01	Multiple_Complex
TC0100014188.hg.1	NRDC; MIR761	nardilysin convertase; microRNA 761	-1.73	10.16	10.96	0.37	0.09	6.60E-03	4.03E-02	Multiple_Complex
TC0100007570.hg.1	YTHDF2	YTH N(6)-methyladenosine RNA binding protein 2	-1.73	9.79	10.58	0.41	0.05	8.50E-03	4.83E-02	Multiple_Complex
TC2200007464.hg.1	L3MBTL2	l(3)mbt-like 2 (Drosophila)	-1.73	6.49	7.28	0.01	0.34	7.30E-03	4.35E-02	Multiple_Complex
TC1900011722.hg.1	HKR1	HKR1, GLI-Kruppel zinc finger family member	-1.73	7.58	8.37	0.19	0.24	1.36E-02	6.58E-02	Multiple_Complex
TC0500008919.hg.1	RNF14	ring finger protein 14	-1.73	8.22	9.02	0.02	0.03	2.70E-03	2.34E-02	Multiple_Complex
TC1000011050.hg.1	AP3M1	adaptor-related protein complex 3, mu 1 subunit	-1.73	11.66	12.46	0.42	0.06	1.11E-02	5.73E-02	Multiple_Complex
TC1900006561.hg.1	SCAMP4; ADAT3	secretory carrier membrane protein 4; adenosine deaminase, tRNA-specific 3	-1.73	6.51	7.31	0.15	0.58	1.61E-02	7.35E-02	Multiple_Complex
TC0500008777.hg.1	KIF20A	kinesin family member 20A	-1.73	8.02	8.81	0.12	0.26	1.00E-02	5.34E-02	Multiple_Complex
TC1500010460.hg.1	HDDC3	HD domain containing 3	-1.73	9.27	10.06	0.12	0.11	5.00E-03	3.41E-02	Multiple_Complex
TC0X00007709.hg.1	PGK1	phosphoglycerate kinase 1	-1.73	8.89	9.68	0.24	0.11	4.60E-03	3.23E-02	Multiple_Complex

TC1100008111.hg.1	SYT12	synaptotagmin XII	-1.74	5.96	6.76	0.49	0.1	1.59E-02	7.30E-02	Multiple_Complex
TC1000008587.hg.1	ZFYVE27	zinc finger, FYVE domain containing 27	-1.74	10.24	11.03	0.18	0.25	6.50E-03	4.02E-02	Multiple_Complex
TC0600014283.hg.1	NUDT3	nudix hydrolase 3	-1.74	9.28	10.07	0.15	0.16	4.30E-03	3.10E-02	Multiple_Complex
TSUnmapped00000383.hg.1	HYOU1	hypoxia up-regulated 1	-1.74	10.51	11.31	0.3	0	5.20E-03	3.48E-02	Coding
TC2000007448.hg.1	GDAP1L1	ganglioside induced differentiation associated protein 1-like 1	-1.74	7.36	8.16	0.17	0.19	1.46E-02	6.91E-02	Multiple_Complex
TC1700008418.hg.1	DYNLL2	dynein, light chain, LC8-type 2	-1.74	11.05	11.85	0.1	0.15	3.60E-03	2.79E-02	Multiple_Complex
TC1800008680.hg.1	CXXC1	CXXC finger protein 1	-1.74	7.97	8.77	0.29	0.32	1.00E-02	5.32E-02	Multiple_Complex
TC1900009102.hg.1	RNF126	ring finger protein 126	-1.74	7.02	7.82	0.28	0.7	3.92E-02	1.33E-01	Multiple_Complex
TC1100011032.hg.1	CYB561A3	cytochrome b561 family, member A3	-1.74	7.92	8.72	0.54	0.15	1.94E-02	8.34E-02	Multiple_Complex
TC0600011678.hg.1	MTCH1	mitochondrial carrier 1	-1.74	13.52	14.32	0.12	0.01	2.90E-03	2.45E-02	Multiple_Complex
TSUnmapped00000406.hg.1	ZNF660	zinc finger protein 660	-1.74	5.71	6.5	0.48	0.3	1.42E-02	6.77E-02	Coding
TC0500013373.hg.1	SRA1	steroid receptor RNA activator 1	-1.74	10.16	10.96	0.14	0.07	4.10E-03	3.00E-02	Multiple_Complex
TC1600007504.hg.1	SETD1A	SET domain containing 1A	-1.74	9.35	10.15	0.27	0.02	4.50E-03	3.18E-02	Multiple_Complex
TC0500007337.hg.1	PARP8	poly(ADP-ribose) polymerase family member 8	-1.74	8.4	9.2	0.52	0.13	3.05E-02	1.13E-01	Multiple_Complex
TC1000010497.hg.1	08-Mar	membrane associated ring finger 8	-1.74	6.13	6.93	0.04	0.38	1.08E-02	5.63E-02	Multiple_Complex
TC0600011870.hg.1	DNPH1	2-deoxynucleoside 5-phosphate N-hydrolase 1	-1.74	13.83	14.63	0.23	0.19	4.60E-03	3.23E-02	Multiple_Complex
TC0300013405.hg.1	C3orf70	chromosome 3 open reading frame 70	-1.74	4.14	4.94	0.04	0.73	2.93E-02	1.10E-01	Coding
TC1400009351.hg.1	SIX1	SIX homeobox 1	-1.74	9.93	10.73	0.1	0.33	5.40E-03	3.58E-02	Multiple_Complex
TC2200009349.hg.1	CSNK1E	casein kinase 1, epsilon	-1.74	13.36	14.16	0.25	0.06	4.80E-03	3.31E-02	Multiple_Complex
TC1100008126.hg.1	ANKRD13D	ankyrin repeat domain 13 family, member D	-1.74	7.42	8.21	0	0.27	1.99E-02	8.49E-02	Multiple_Complex

TC1600007521.hg.1	FUS	FUS RNA binding protein	-1.74	10.33	11.13	0.22	0.35	9.30E-03	5.11E-02	Multiple_Complex
TC0700012043.hg.1	CLDN15	claudin 15	-1.74	8.48	9.28	0.23	0.07	6.30E-03	3.93E-02	Multiple_Complex
TC0X00007205.hg.1	HDAC6	histone deacetylase 6	-1.74	9.23	10.03	0.2	0.2	4.70E-03	3.29E-02	Multiple_Complex
TC0900008865.hg.1	CERCAM	cerebral endothelial cell adhesion molecule	-1.74	9.42	10.22	0.14	0.05	3.10E-03	2.51E-02	Multiple_Complex
TC0800006989.hg.1	CCAR2	cell cycle and apoptosis regulator 2	-1.74	8.25	9.05	0.22	0.05	5.90E-03	3.75E-02	Multiple_Complex
TC2000009053.hg.1	TTI1	TELO2 interacting protein 1	-1.74	10.15	10.95	0.14	0.04	5.30E-03	3.53E-02	Multiple_Complex
TC0900011612.hg.1	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	-1.74	10.85	11.65	0.27	0.19	5.90E-03	3.76E-02	Multiple_Complex
TC0500012870.hg.1	STC2	stanniocalcin 2	-1.74	10.89	11.69	0.06	0.08	3.90E-03	2.93E-02	Multiple_Complex
TC0100013153.hg.1	TMCO4	transmembrane and coiled-coil domains 4	-1.74	4.5	5.3	0.19	0.33	7.60E-03	4.45E-02	Multiple_Complex
TC1700009539.hg.1	PFN1	profilin 1	-1.74	14.13	14.94	0.06	0.03	3.10E-03	2.52E-02	Multiple_Complex
TC0300010388.hg.1	MRPS25	mitochondrial ribosomal protein S25	-1.74	10.21	11.02	0.02	0.01	3.60E-03	2.79E-02	Multiple_Complex
TC0X00009205.hg.1	SH3KBP1	SH3-domain kinase binding protein 1	-1.74	9.56	10.36	0.03	0.01	4.00E-03	2.97E-02	Multiple_Complex
TC2200007331.hg.1	PICK1	protein interacting with PRKCA 1	-1.74	8.24	9.04	0.1	0.02	4.50E-03	3.16E-02	Multiple_Complex
TC1700006738.hg.1	EIF5A	eukaryotic translation initiation factor 5A	-1.74	14.99	15.79	0.05	0.07	2.80E-03	2.41E-02	Multiple_Complex
TC0200013103.hg.1	RTKN	rhotekin	-1.74	7.28	8.08	0.46	0.07	9.30E-03	5.11E-02	Multiple_Complex
TC11_KI270721v1_random00006432.hg.1	MRPL23; LOC102724828; AC004556.1	Homo sapiens mitochondrial ribosomal protein L23 (MRPL23), mRNA.; 39S ribosomal protein L23, mitochondrial-like; Homo sapiens mitochondrial ribosomal protein L23, mRNA (cDNA clone MGC:12795 IMAGE:4298000), complete cds.	-1.74	6.7	7.5	0.57	0.47	2.51E-02	9.92E-02	Coding
TC0500009223.hg.1	THG1L	tRNA-histidine guanylyltransferase 1-like	-1.74	6.68	7.48	0.01	0.61	3.87E-02	1.32E-01	Multiple_Complex

TC1700010831.hg.1	GPATCH8	G-patch domain containing 8	-1.74	10.03	10.83	0.11	0.27	5.40E-03	3.57E-02	Multiple_Complex
TC0800011041.hg.1	MMP16	matrix metallopeptidase 16 (membrane-inserted)	-1.74	5.63	6.43	0.09	0.71	2.72E-02	1.05E-01	Multiple_Complex
TC0300010476.hg.1	SGOL1	shugoshin-like 1 (S. pombe)	-1.74	10.18	10.98	0.08	0.02	3.30E-03	2.65E-02	Multiple_Complex
TC1600011432.hg.1	MON1B	MON1 secretory trafficking family member B	-1.74	5.72	6.53	0.18	0.25	4.70E-03	3.25E-02	Multiple_Complex
TC1700009123.hg.1	RNF213	ring finger protein 213	-1.74	5.82	6.62	0.11	0.49	1.07E-02	5.60E-02	Multiple_Complex
TC2000008218.hg.1	C20orf194	chromosome 20 open reading frame 194	-1.74	7.88	8.69	0.76	0.34	3.60E-02	1.26E-01	Multiple_Complex
TC0600013762.hg.1	TCP1; SNORA20; SNORA29	t-complex 1; small nucleolar RNA, H/ACA box 20; small nucleolar RNA, H/ACA box 29	-1.74	10.81	11.62	0.61	0.02	1.64E-02	7.45E-02	Multiple_Complex
TC1200011993.hg.1	SLC8B1	solute carrier family 8 (sodium/lithium/calcium exchanger), member B1	-1.75	8.55	9.35	0.02	0.24	8.20E-03	4.71E-02	Multiple_Complex
TC0700012165.hg.1	ATXN7L1	ataxin 7-like 1	-1.75	4.84	5.64	0.59	0.08	1.45E-02	6.88E-02	Multiple_Complex
TC0100016020.hg.1	ISG20L2	interferon stimulated exonuclease gene 20kDa like 2	-1.75	10.49	11.29	0.05	0.13	4.70E-03	3.25E-02	Multiple_Complex
TC1700006751.hg.1	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	-1.75	12.51	13.32	0.17	0.07	4.80E-03	3.32E-02	Multiple_Complex
TC0200008811.hg.1	SH3RF3	SH3 domain containing ring finger 3	-1.75	5.74	6.55	0.07	0.26	1.50E-02	7.03E-02	Multiple_Complex
TC0200012095.hg.1	SUPT7L	SPT7-like STAGA complex gamma subunit	-1.75	12.71	13.51	0.43	0.13	1.15E-02	5.87E-02	Multiple_Complex
TC1400009422.hg.1	RAB15	RAB15, member RAS oncogene family	-1.75	7.08	7.88	0.34	0.12	9.00E-03	4.97E-02	Multiple_Complex
TC1100011265.hg.1	EIF1AD	eukaryotic translation initiation factor 1A domain containing	-1.75	8.13	8.94	0.08	0	3.00E-03	2.49E-02	Multiple_Complex
TC1600011367.hg.1	SPNS1	spinster homolog 1 (Drosophila)	-1.75	9.43	10.23	0.15	0.11	5.70E-03	3.70E-02	Multiple_Complex
TC1700008879.hg.1	ICT1	immature colon carcinoma transcript 1	-1.75	9.21	10.01	0.19	0.29	1.35E-02	6.53E-02	Multiple_Complex
TC0X00009645.hg.1	GRIPAP1	GRIP1 associated protein 1	-1.75	5.51	6.31	0.33	0.28	1.49E-02	7.00E-02	Multiple_Complex
TC0600006611.hg.1	WRNIP1	Werner helicase interacting protein 1	-1.75	8.08	8.89	0.7	0.15	2.84E-02	1.08E-01	Multiple_Complex

TC1600009837.hg.1	GTF3C1	general transcription factor IIIC subunit 1	-1.75	11	11.8	0.07	0.28	4.70E-03	3.29E-02	Multiple_Complex
TC0900007981.hg.1	WNK2	WNK lysine deficient protein kinase 2	-1.75	7.05	7.85	0.08	0.48	1.18E-02	5.97E-02	Multiple_Complex
TC1900006727.hg.1	UHRF1	ubiquitin-like with PHD and ring finger domains 1	-1.75	8.85	9.65	0.06	0.1	3.80E-03	2.88E-02	Multiple_Complex
TC1100007833.hg.1	INCENP	inner centromere protein	-1.75	9.63	10.44	0.12	0.2	3.50E-03	2.74E-02	Multiple_Complex
TC0900010284.hg.1	ANKRD20A1; ANKRD20A3	ankyrin repeat domain 20 family, member A1; ankyrin repeat domain 20 family, member A3	-1.75	7.22	8.02	0.21	0.02	4.00E-03	2.98E-02	Multiple_Complex
TC1000007976.hg.1	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	-1.75	5.7	6.51	0.05	0.27	6.20E-03	3.91E-02	Multiple_Complex
TC0100018430.hg.1	SMIM12	small integral membrane protein 12	-1.75	11.83	12.64	0.01	0.09	4.30E-03	3.12E-02	Coding
TC0900009978.hg.1	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	-1.75	7.43	8.24	0.36	0	6.30E-03	3.96E-02	Multiple_Complex
TC1400009538.hg.1	DCAF5	DDB1 and CUL4 associated factor 5	-1.75	9.44	10.25	0.02	0.09	3.90E-03	2.92E-02	Multiple_Complex
TC0100018199.hg.1	SRRM1	serine/arginine repetitive matrix 1	-1.75	11.93	12.74	0.31	0.09	5.60E-03	3.65E-02	Multiple_Complex
TC0200008063.hg.1	DGUOK	deoxyguanosine kinase	-1.75	12.5	13.31	0.42	0.19	8.10E-03	4.65E-02	Multiple_Complex
TC1700009622.hg.1	DVL2	dishevelled segment polarity protein 2	-1.75	8.74	9.55	0.05	0.2	3.40E-03	2.66E-02	Multiple_Complex
TC1900007839.hg.1	FXYD5	FXYD domain containing ion transport regulator 5	-1.75	8.48	9.29	0.78	0.13	2.76E-02	1.06E-01	Multiple_Complex
TC0100013897.hg.1	P3H1	prolyl 3-hydroxylase 1	-1.75	11.56	12.37	0.05	0.05	3.80E-03	2.89E-02	Multiple_Complex
TC0200008742.hg.1	NCK2	NCK adaptor protein 2	-1.75	6.46	7.26	0.22	0.21	1.06E-02	5.54E-02	Multiple_Complex
TC0700011066.hg.1	COBL	cordon-bleu WH2 repeat protein	-1.75	10.78	11.59	0	0.19	4.90E-03	3.34E-02	Multiple_Complex
TC2000007191.hg.1	DYNLRB1	dynein, light chain, roadblock-type 1	-1.75	13.33	14.14	0.03	0.11	4.50E-03	3.16E-02	Multiple_Complex
TC1100006726.hg.1	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	-1.75	4.62	5.43	0.27	0.08	4.00E-03	2.95E-02	Multiple_Complex
TC0800007416.hg.1	GINS4	GINS complex subunit 4 (Sld5 homolog)	-1.75	7.93	8.74	0.03	0.23	1.32E-02	6.43E-02	Multiple_Complex
TC2000007857.hg.1	RAE1	ribonucleic acid export 1	-1.75	7.98	8.79	0.7	0.4	2.87E-02	1.09E-01	Multiple_Complex

TC1200009036.hg.1	FBXW8	F-box and WD repeat domain containing 8	-1.75	8.9	9.71	0.06	0.55	2.19E-02	9.04E-02	Multiple_Complex
TC0900008173.hg.1	ANP32B	acidic nuclear phosphoprotein 32 family member B	-1.75	11.61	12.42	0.37	0.02	6.20E-03	3.89E-02	Multiple_Complex
TC1700008133.hg.1	KPNB1	karyopherin (importin) beta 1	-1.75	11.82	12.63	0.37	0.16	6.20E-03	3.90E-02	Multiple_Complex
TSUnmapped00000342.hg.1	TCF20	transcription factor 20 (AR1)	-1.75	8.28	9.09	0.41	0.13	8.50E-03	4.81E-02	Coding
TSUnmapped00000362.hg.1	TCF20	transcription factor 20 (AR1)	-1.75	8.28	9.09	0.41	0.13	8.50E-03	4.81E-02	Coding
TC1100013186.hg.1	SYVN1	synovial apoptosis inhibitor 1, synoviolin	-1.75	10.7	11.51	0.01	0.04	2.60E-03	2.31E-02	Multiple_Complex
TC0700012224.hg.1	LAMB1	laminin, beta 1	-1.75	6.53	7.34	0.32	0.25	9.10E-03	5.03E-02	Multiple_Complex
TC1700011476.hg.1	GNA13	guanine nucleotide binding protein (G protein), alpha 13	-1.75	11.2	12.01	0.27	0.12	8.20E-03	4.72E-02	Multiple_Complex
TC1200012637.hg.1	HOXC10	homeobox C10	-1.75	8.07	8.88	0.16	0.2	3.60E-03	2.79E-02	Multiple_Complex
TC2000009401.hg.1	SPATA2	spermatogenesis associated 2	-1.75	6.39	7.2	0.04	0.05	8.10E-03	4.66E-02	Coding
TC1200012788.hg.1	RAPGEF3	Rap guanine nucleotide exchange factor 3	-1.75	5.66	6.47	0.05	0.25	4.50E-03	3.16E-02	Multiple_Complex
TC0900009957.hg.1	HINT2	histidine triad nucleotide binding protein 2	-1.75	13.17	13.99	0.07	0.01	3.60E-03	2.77E-02	Multiple_Complex
TC0100018208.hg.1	ZBTB8B	zinc finger and BTB domain containing 8B	-1.76	8.31	9.12	0.38	0.33	1.76E-02	7.82E-02	Coding
TC0100007672.hg.1	EIF3I	eukaryotic translation initiation factor 3, subunit I	-1.76	11.12	11.93	0.39	0.21	7.80E-03	4.53E-02	Multiple_Complex
TC0X00008405.hg.1	RBMX2	RNA binding motif protein, X-linked 2	-1.76	11.56	12.38	0.05	0.07	4.90E-03	3.37E-02	Multiple_Complex
TC0X00009638.hg.1	OTUD5	OTU deubiquitinase 5	-1.76	10.9	11.71	0.47	0.19	1.40E-02	6.72E-02	Multiple_Complex
TC1400007547.hg.1	EXD2	exonuclease 3-5 domain containing 2	-1.76	5.81	6.63	0.12	0.13	4.00E-03	2.95E-02	Multiple_Complex
TC1900012000.hg.1	TEAD2	TEA domain family member 2	-1.76	7.51	8.32	0.08	0.11	3.50E-03	2.73E-02	Multiple_Complex
TC1000009612.hg.1	KLF6	Kruppel-like factor 6	-1.76	11.81	12.63	0.04	0.3	5.20E-03	3.49E-02	Multiple_Complex
TC1000011726.hg.1	SH3PXD2A	SH3 and PX domains 2A	-1.76	7.02	7.83	0.51	0.04	1.06E-02	5.57E-02	Multiple_Complex

TC1400006663.hg.1	LRP10	LDL receptor related protein 10	-1.76	6.71	7.52	0.53	0.17	1.69E-02	7.62E-02	Multiple_Complex
TC1600008164.hg.1	FAM65A	family with sequence similarity 65, member A	-1.76	9.37	10.18	0.39	0.08	1.45E-02	6.86E-02	Multiple_Complex
TC0100015902.hg.1	C1orf43	chromosome 1 open reading frame 43	-1.76	12.72	13.53	0.57	0.08	1.32E-02	6.45E-02	Multiple_Complex
TC1700007858.hg.1	FKBP10	FK506 binding protein 10	-1.76	14.31	15.13	0.27	0.06	5.20E-03	3.49E-02	Multiple_Complex
TC2000008955.hg.1	TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	-1.76	9.97	10.78	0.5	0.25	1.19E-02	6.00E-02	Multiple_Complex
TC1900010961.hg.1	IRF2BP1	interferon regulatory factor 2 binding protein 1	-1.76	6.16	6.98	0.77	0.15	2.78E-02	1.06E-01	Coding
TC0700013400.hg.1	GATAD1	GATA zinc finger domain containing 1	-1.76	9.83	10.65	0.09	0.19	3.10E-03	2.54E-02	Multiple_Complex
TC1400008193.hg.1	EVL	Enah/Vasp-like	-1.76	7.89	8.71	0.15	0.18	3.90E-03	2.94E-02	Multiple_Complex
TC0600008092.hg.1	TJAP1	tight junction associated protein 1 (peripheral)	-1.76	9.18	10	0.16	0.2	8.90E-03	4.93E-02	Multiple_Complex
TC0700013601.hg.1	RASA4B; RASA4	RAS p21 protein activator 4B; RAS p21 protein activator 4	-1.76	6.7	7.52	0.02	0.11	4.00E-03	2.97E-02	Multiple_Complex
TC0100010543.hg.1	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-1.76	7.46	8.28	0.85	0.24	3.93E-02	1.33E-01	Multiple_Complex
TC0600013528.hg.1	LATS1	large tumor suppressor kinase 1	-1.76	12	12.81	0.2	0.06	6.40E-03	3.99E-02	Multiple_Complex
TC0200009060.hg.1	STEAP3	STEAP family member 3, metalloreductase	-1.76	6.41	7.22	0.43	0.12	1.39E-02	6.67E-02	Multiple_Complex
TC0900007844.hg.1	SPIN1	spindlin 1	-1.76	11.2	12.02	0.1	0.01	3.00E-03	2.48E-02	Multiple_Complex
TC2000009813.hg.1	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	-1.76	10.14	10.96	0.36	0.08	5.90E-03	3.77E-02	Multiple_Complex
TC2100007362.hg.1	LRRC3	leucine rich repeat containing 3	-1.76	5.39	6.21	0.5	0.07	1.07E-02	5.60E-02	Coding
TC0900010808.hg.1	BICD2	bicaudal D homolog 2 (Drosophila)	-1.76	5.95	6.77	0.03	0.04	1.41E-02	6.75E-02	Multiple_Complex
TC0800007328.hg.1	BAG4	BCL2-associated athanogene 4	-1.76	8.01	8.82	0.03	0.5	1.23E-02	6.15E-02	Multiple_Complex
TC1700008923.hg.1	UNK	unkempt family zinc finger	-1.76	8.41	9.23	0.11	0.26	7.20E-03	4.29E-02	Multiple_Complex
TC1700012100.hg.1	CSNK1D	casein kinase 1, delta	-1.76	11.83	12.65	0.17	0.07	3.40E-03	2.69E-02	Multiple_Complex

TC1700007865.hg.1	CNP	2,3-cyclic nucleotide 3 phosphodiesterase	-1.76	6	6.81	0.35	0.05	8.00E-03	4.64E-02	Multiple_Complex
TC0900008860.hg.1	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	-1.76	8.03	8.84	0.79	0.05	2.63E-02	1.02E-01	Multiple_Complex
TC2200009289.hg.1	TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	-1.76	7.3	8.12	0.12	0.47	9.30E-03	5.10E-02	Multiple_Complex
TC1400008684.hg.1	PRMT5	protein arginine methyltransferase 5	-1.76	11.25	12.07	0.22	0.2	5.20E-03	3.48E-02	Multiple_Complex
TC1900009491.hg.1	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	-1.76	4.66	5.47	0.17	0.07	4.70E-03	3.25E-02	Multiple_Complex
TC1400009617.hg.1	DPF3	D4, zinc and double PHD fingers, family 3	-1.76	6.98	7.8	0.33	0.1	1.61E-02	7.35E-02	Multiple_Complex
TC1100011973.hg.1	SMCO4	single-pass membrane protein with coiled-coil domains 4	-1.76	6.29	7.11	0.26	0.6	1.80E-02	7.92E-02	Multiple_Complex
TC0200007067.hg.1	NRBP1	nuclear receptor binding protein 1	-1.76	11.26	12.08	0.07	0.1	2.60E-03	2.28E-02	Multiple_Complex
TC1900011844.hg.1	MFSD12	major facilitator superfamily domain containing 12	-1.77	7.07	7.89	0.17	0.15	7.00E-03	4.21E-02	Multiple_Complex
TC2000006534.hg.1	MRPS26	mitochondrial ribosomal protein S26	-1.77	8.34	9.16	0.46	0.01	1.03E-02	5.43E-02	Multiple_Complex
TC1400010709.hg.1	TTC5	tetratricopeptide repeat domain 5	-1.77	7.18	8	0.65	0.05	1.93E-02	8.32E-02	Multiple_Complex
TC1400009829.hg.1	CEP128	centrosomal protein 128kDa	-1.77	6.56	7.38	0.53	0.24	2.17E-02	8.99E-02	Multiple_Complex
TC0400006692.hg.1	MRFAP1	Morf4 family associated protein 1	-1.77	12.72	13.54	0.2	0.01	5.50E-03	3.60E-02	Multiple_Complex
TC0100018282.hg.1	POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	-1.77	6.78	7.6	0.14	0	4.60E-03	3.23E-02	Multiple_Complex
TC0800008772.hg.1	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	-1.77	14.34	15.16	0.08	0.04	2.90E-03	2.42E-02	Multiple_Complex
TC1100009403.hg.1	ROBO3	roundabout guidance receptor 3	-1.77	5.94	6.76	0.6	0.55	3.11E-02	1.14E-01	Multiple_Complex
TC0X00008910.hg.1	ASMTL	acetylserotonin O-methyltransferase-like	-1.77	4.18	5	0.15	0.56	1.30E-02	6.38E-02	Multiple_Complex
TC0Y00006884.hg.1	ASMTL	acetylserotonin O-methyltransferase-like	-1.77	4.18	5	0.15	0.56	1.30E-02	6.38E-02	Multiple_Complex

TC0800012444.hg.1	PABPC1; MIR7705	poly(A) binding protein, cytoplasmic 1; microRNA 7705	-1.77	7.28	8.1	0.28	0.85	4.09E-02	1.37E-01	Multiple_Complex
TC1700008539.hg.1	MRC2	mannose receptor, C type 2	-1.77	8.96	9.78	0.09	0.22	8.00E-03	4.62E-02	Multiple_Complex
TC1100008067.hg.1	RAB1B	RAB1B, member RAS oncogene family	-1.77	10.97	11.79	0.09	0.02	2.40E-03	2.16E-02	Multiple_Complex
TC2000009909.hg.1	RALY	RALY heterogeneous nuclear ribonucleoprotein	-1.77	9.98	10.8	0.02	0.07	2.30E-03	2.12E-02	Multiple_Complex
TC1200008525.hg.1	SNRPF	small nuclear ribonucleoprotein polypeptide F	-1.77	8.83	9.65	0.55	0.29	1.80E-02	7.92E-02	Multiple_Complex
TC1800007850.hg.1	COLEC12	collectin sub-family member 12	-1.77	9.29	10.11	0.53	0.12	1.15E-02	5.88E-02	Multiple_Complex
TC1300008449.hg.1	CDX2	caudal type homeobox 2	-1.77	8.41	9.24	0.38	0.11	5.70E-03	3.70E-02	Multiple_Complex
TC0100016156.hg.1	ARHGAP30	Rho GTPase activating protein 30	-1.77	3.77	4.6	0.08	0.24	1.20E-02	6.04E-02	Multiple_Complex
TC0700009061.hg.1	CALU	calumenin	-1.77	12.47	13.3	0.19	0.01	4.60E-03	3.22E-02	Multiple_Complex
TC0200015764.hg.1	CNPPD1	cyclin Pas1/PHO80 domain containing 1	-1.77	6.84	7.67	0.54	0.09	1.04E-02	5.48E-02	Multiple_Complex
TC0100011384.hg.1	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	-1.77	9.73	10.55	0.14	0.05	7.20E-03	4.29E-02	Multiple_Complex
TC0300013336.hg.1	LAMP3	lysosomal-associated membrane protein 3	-1.77	5.7	6.53	0.09	0.01	5.70E-03	3.68E-02	Multiple_Complex
TC1400007647.hg.1	ACOT2	acyl-CoA thioesterase 2	-1.77	7.21	8.04	0.23	0.32	1.51E-02	7.06E-02	Multiple_Complex
TC1300008125.hg.1	LAMP1	lysosomal-associated membrane protein 1	-1.77	5.44	6.27	0.06	0.05	2.30E-03	2.13E-02	Multiple_Complex
TC1200009580.hg.1	FBXL14	F-box and leucine-rich repeat protein 14	-1.77	10.19	11.02	0.09	0.09	3.90E-03	2.91E-02	Multiple_Complex
TC1900010701.hg.1	C19orf47	chromosome 19 open reading frame 47	-1.77	9.54	10.37	0.05	0.15	2.70E-03	2.32E-02	Multiple_Complex
TC0200009680.hg.1	FMNL2	formin like 2	-1.77	7.7	8.53	0.55	0.05	1.24E-02	6.18E-02	Multiple_Complex
TC0100014776.hg.1	DDAH1	dimethylarginine dimethylaminohydrolase 1	-1.77	12.13	12.96	0.07	0.08	4.20E-03	3.04E-02	Multiple_Complex
TC1200008800.hg.1	UBE3B	ubiquitin protein ligase E3B	-1.77	6.69	7.52	0.25	0.1	5.00E-03	3.38E-02	Multiple_Complex

TSUnmapped00000363.hg.1	EIF3F	Eukaryotic translation initiation factor 3 subunit F [Source:UniProtKB/Swiss-Prot;Acc:O00303]	-1.77	10.45	11.28	0.31	0.43	1.05E-02	5.53E-02	Coding
TC1600011427.hg.1	IST1	increased sodium tolerance 1 homolog (yeast)	-1.77	12.46	13.29	0.05	0.12	2.40E-03	2.20E-02	Multiple_Complex
TC0100007378.hg.1	CLIC4	chloride intracellular channel 4	-1.77	11.83	12.66	0.09	0.01	6.40E-03	3.96E-02	Multiple_Complex
TC0700009827.hg.1	RBM33	RNA binding motif protein 33	-1.77	8.97	9.79	0.08	0.25	5.70E-03	3.68E-02	Multiple_Complex
TC1400006715.hg.1	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-1.77	6.31	7.14	0.26	0.15	4.40E-03	3.15E-02	Multiple_Complex
TC1900011932.hg.1	ALKBH6	alkB homolog 6	-1.77	6.98	7.81	0.58	0.22	4.01E-02	1.36E-01	Multiple_Complex
TC0800006980.hg.1	SLC39A14	solute carrier family 39 (zinc transporter), member 14	-1.77	5.87	6.69	0.48	0.68	3.16E-02	1.16E-01	Multiple_Complex
TSUnmapped00000618.hg.1	REXO4	REX4 homolog, 3'-5' exonuclease [Source:HGNC Symbol;Acc:HGNC:12820]	-1.77	7.65	8.48	0.51	0.08	1.03E-02	5.44E-02	Coding
TC1200012572.hg.1	ITFG2	integrin alpha FG-GAP repeat containing 2	-1.77	6.83	7.65	0.16	0.4	1.45E-02	6.87E-02	NonCoding
TC0100015971.hg.1	GON4L	gon-4-like (C. elegans)	-1.77	12.44	13.27	0.16	0.12	2.90E-03	2.46E-02	Multiple_Complex
TC1900009100.hg.1	POLRMT	polymerase (RNA) mitochondrial (DNA directed)	-1.77	10.82	11.65	0.19	0.02	2.90E-03	2.42E-02	Multiple_Complex
TC1300009856.hg.1	TUBGCP3	tubulin, gamma complex associated protein 3	-1.77	6.94	7.76	0.15	0.21	3.90E-03	2.93E-02	Multiple_Complex
TC0500012957.hg.1	UIMC1	ubiquitin interaction motif containing 1	-1.77	7.27	8.1	0.42	0.08	8.20E-03	4.70E-02	Multiple_Complex
TC1600011383.hg.1	TMEM265; SRCAP	transmembrane protein 265; Snf2-related CREBBP activator protein	-1.77	9.76	10.59	0.01	0.09	2.30E-03	2.15E-02	Multiple_Complex
TC0100010332.hg.1	NIT1	nitrilase 1	-1.77	8.47	9.3	0.13	0.07	5.20E-03	3.46E-02	Multiple_Complex
TC0700011162.hg.1	PSPH	phosphoserine phosphatase	-1.78	9.57	10.4	0.51	0.61	2.54E-02	1.00E-01	Multiple_Complex
TC0X00008273.hg.1	ZBTB33	zinc finger and BTB domain containing 33	-1.78	9.12	9.95	0.11	0.02	3.50E-03	2.72E-02	Multiple_Complex
TC1000010065.hg.1	ARHGAP21	Rho GTPase activating protein 21	-1.78	8.2	9.03	0.5	0.09	1.04E-02	5.50E-02	Multiple_Complex

TC1900011029.hg.1	MEIS3	Meis homeobox 3	-1.78	7.22	8.05	0.5	0.27	2.92E-02	1.10E-01	Multiple_Complex
TC1100009678.hg.1	HRAS	Harvey rat sarcoma viral oncogene homolog	-1.78	8.72	9.55	0.31	0.07	6.90E-03	4.19E-02	Multiple_Complex
TC0700013512.hg.1	CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated	-1.78	10.57	11.4	0.01	0.12	2.10E-03	2.04E-02	Multiple_Complex
TC0700008522.hg.1	COPS6	COP9 signalosome subunit 6	-1.78	12.01	12.84	0.09	0.28	6.50E-03	4.02E-02	Multiple_Complex
TC1000011938.hg.1	SHTN1	shootin 1	-1.78	10.98	11.81	0.09	0.19	3.30E-03	2.65E-02	Multiple_Complex
TC0600007862.hg.1	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	-1.78	6.83	7.66	0.57	0.04	1.23E-02	6.14E-02	Multiple_Complex
TC0500007349.hg.1	ISL1	ISL LIM homeobox 1	-1.78	4.7	5.53	0.26	0.03	6.20E-03	3.89E-02	Multiple_Complex
TC0300012029.hg.1	NAA50	N(alpha)-acetyltransferase 50, NatE catalytic subunit	-1.78	14.21	15.04	0.01	0.09	2.80E-03	2.41E-02	Multiple_Complex
TSUnmapped00000711.hg.1	ATG16L1	autophagy related 16-like 1	-1.78	8.5	9.33	0.66	0.1	2.06E-02	8.67E-02	Coding
TC1400010195.hg.1	WARS	tryptophanyl-tRNA synthetase	-1.78	12.77	13.6	0.08	0.08	2.20E-03	2.09E-02	Multiple_Complex
TC1900010988.hg.1	PNMAL1	paraneoplastic Ma antigen family-like 1	-1.78	4.39	5.22	0.35	0.08	6.40E-03	3.97E-02	Coding
TC2200009261.hg.1	SFI1	SFI1 centrin binding protein	-1.78	6.59	7.42	0.81	0.26	3.15E-02	1.15E-01	Multiple_Complex
TC0200010045.hg.1	HOXD13	homeobox D13	-1.78	8.59	9.42	0.25	0.32	6.80E-03	4.13E-02	Coding
TC0800009239.hg.1	CYC1	cytochrome c-1	-1.78	13.62	14.45	0.03	0.04	2.20E-03	2.06E-02	Multiple_Complex
TC1700009679.hg.1	AURKB	aurora kinase B	-1.78	12.75	13.58	0.08	0.14	2.60E-03	2.28E-02	Multiple_Complex
TC0600011379.hg.1	MDC1	mediator of DNA-damage checkpoint 1	-1.78	7.07	7.91	0.29	0.07	8.80E-03	4.92E-02	Multiple_Complex
TC0200012009.hg.1	DTNB	dystrobrevin beta	-1.78	7.59	8.43	0.38	0.11	8.70E-03	4.90E-02	Multiple_Complex
TC1200012163.hg.1	SRSF9	serine/arginine-rich splicing factor 9	-1.78	9.86	10.69	0.08	0.17	2.60E-03	2.28E-02	Multiple_Complex
TC0500012947.hg.1	GPRIN1	G protein regulated inducer of neurite outgrowth 1	-1.78	7.11	7.94	0.25	0.16	6.80E-03	4.16E-02	Multiple_Complex
TC1700012231.hg.1	TMEM98	transmembrane protein 98	-1.78	10.08	10.91	0.07	0.7	2.88E-02	1.09E-01	Multiple_Complex

TC0900012190.hg.1	CCDC183; RABL6	coiled-coil domain containing 183; RAB, member RAS oncogene family-like 6	-1.78	11.53	12.36	0.27	0.08	3.20E-03	2.56E-02	Multiple_Complex
TC0600007635.hg.1	PPT2; EGFL8; PPT2-EGFL8	palmitoyl-protein thioesterase 2; EGF-like-domain, multiple 8; PPT2-EGFL8 readthrough (NMD candidate)	-1.79	9.4	10.24	0.61	0.14	1.68E-02	7.60E-02	Multiple_Complex
TC1700007904.hg.1	TUBG1	tubulin, gamma 1	-1.79	14.73	15.57	0.04	0.06	2.10E-03	2.02E-02	Multiple_Complex
TC0X00011401.hg.1	RBMX; SNORD61	RNA binding motif protein, X-linked; small nucleolar RNA, C/D box 61	-1.79	12.24	13.07	0.24	0.06	3.70E-03	2.83E-02	Multiple_Complex
TC2000007015.hg.1	PYGB	phosphorylase, glycogen; brain	-1.79	9.28	10.11	0.16	0.39	6.40E-03	3.96E-02	Multiple_Complex
TC1300006886.hg.1	RFXAP	regulatory factor X-associated protein	-1.79	7.03	7.87	0.25	0.05	1.45E-02	6.86E-02	Multiple_Complex
TC2200008866.hg.1	TCF20	transcription factor 20 (AR1)	-1.79	8.59	9.43	0.31	0.15	6.10E-03	3.85E-02	Multiple_Complex
TC0500013321.hg.1	GTF2H2	general transcription factor IIH subunit 2	-1.79	12.14	12.98	0.32	0.24	6.00E-03	3.82E-02	Multiple_Complex
TC1600009102.hg.1	RNPS1	RNA binding protein S1, serine-rich domain	-1.79	13.04	13.88	0.17	0.03	4.40E-03	3.16E-02	Multiple_Complex
TC0600007508.hg.1	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	-1.79	11.12	11.96	0.3	0.14	4.00E-03	2.97E-02	Coding
TC1200010182.hg.1	BHLHE41	basic helix-loop-helix family, member e41	-1.79	7.64	8.48	0.15	0.06	2.80E-03	2.37E-02	Multiple_Complex
TC1900009769.hg.1	STX10	syntaxin 10	-1.79	9.16	10	0.45	0.79	3.62E-02	1.26E-01	Multiple_Complex
TC2200006517.hg.1	CECR2	cat eye syndrome chromosome region, candidate 2	-1.79	8.56	9.39	0	0.42	2.77E-02	1.06E-01	Multiple_Complex
TC2100007241.hg.1	ABCG1	ATP binding cassette subfamily G member 1	-1.79	7.1	7.94	0.21	0.21	1.59E-02	7.30E-02	Multiple_Complex
TC2200009206.hg.1	BMS1P20; IGLV1-51; IGLV5-52	BMS1 ribosome biogenesis factor pseudogene 20; immunoglobulin lambda variable 1-51; immunoglobulin lambda variable 5-52	-1.79	8.24	9.08	0.07	0.4	1.27E-02	6.28E-02	Multiple_Complex
TC1900010529.hg.1	ZNF529	zinc finger protein 529	-1.79	5.24	6.08	0	0.08	4.90E-03	3.36E-02	Multiple_Complex

TC1100012269.hg.1	ARHGAP20	Rho GTPase activating protein 20	-1.79	6.95	7.79	0.48	0.15	1.32E-02	6.43E-02	Coding
TC0X00008844.hg.1	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	-1.79	4.81	5.65	0.74	0.1	3.65E-02	1.27E-01	Multiple_Complex
TC1200010900.hg.1	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	-1.79	13.48	14.32	0.12	0.02	2.10E-03	2.02E-02	Multiple_Complex
TC1000006785.hg.1	PROSER2	proline and serine rich 2	-1.79	8.77	9.61	0.03	0.51	8.80E-03	4.92E-02	Multiple_Complex
TC0X00010409.hg.1	BEX2	brain expressed X-linked 2	-1.79	10.41	11.25	0.54	0.18	1.43E-02	6.83E-02	Coding
TC1700007402.hg.1	FLOT2	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_004475	-1.79	8.08	8.92	0.14	0.03	6.60E-03	4.03E-02	NonCoding
TC2100007032.hg.1	CBR1	carbonyl reductase 1	-1.79	8.97	9.81	0.36	0.07	5.40E-03	3.55E-02	Multiple_Complex
TC0600007864.hg.1	TBC1D22B	TBC1 domain family, member 22B	-1.79	7.76	8.6	0.13	0.05	4.30E-03	3.10E-02	Multiple_Complex
TC1400008760.hg.1	SDR39U1	short chain dehydrogenase/reductase family 39U, member 1	-1.79	11.92	12.76	0.23	0.13	3.00E-03	2.47E-02	Multiple_Complex
TC0900008109.hg.1	HABP4	hyaluronan binding protein 4	-1.79	8.43	9.27	0.08	0.23	3.90E-03	2.94E-02	Multiple_Complex
TC0100010335.hg.1	USP21	ubiquitin specific peptidase 21	-1.79	9.1	9.95	0.12	0.47	7.20E-03	4.31E-02	Multiple_Complex
TC0100015984.hg.1	UBQLN4	ubiquilin 4	-1.79	9.4	10.25	0.17	0.14	5.00E-03	3.41E-02	Multiple_Complex
TC1900010632.hg.1	SIRT2	sirtuin 2	-1.79	8.52	9.37	0.54	0.17	1.36E-02	6.56E-02	Multiple_Complex
TC1000011649.hg.1	POLL	polymerase (DNA directed), lambda	-1.79	7.11	7.95	0.13	0.55	1.06E-02	5.58E-02	Multiple_Complex
TC1700012263.hg.1	DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	-1.79	10.69	11.53	0.53	0.1	1.07E-02	5.60E-02	Multiple_Complex

TC1200011543.hg.1	PGAM1	Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:8462 IMAGE:2821567), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:19732 IMAGE:3604026), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:15086 IMAGE:4299008), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:61519 IMAGE:5787678), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:71323 IMAGE:6584466), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:87445 IMAGE:5262935), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:88744 IMAGE:6297173), complete cds.; Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone MGC:189702 IMAGE:8862699), complete cds.	-1.79	13.53	14.37	0.28	0.09	3.50E-03	2.72E-02	Multiple_Complex
TC0300013846.hg.1	GXYLT2	glucoside xylosyltransferase 2	-1.79	6.69	7.53	0.5	0.54	2.40E-02	9.63E-02	Multiple_Complex
TC0X00010670.hg.1	TMEM255A	transmembrane protein 255A	-1.8	9.49	10.34	0.85	0.05	3.45E-02	1.22E-01	Multiple_Complex

TC0300008152.hg.1	TFG	TRK-fused gene	-1.8	11.71	12.55	0.01	0.03	1.90E-03	1.90E-02	Multiple_Complex
TC0300006631.hg.1	MKRN2	makorin ring finger protein 2	-1.8	9.86	10.7	0.11	0.13	3.20E-03	2.61E-02	Multiple_Complex
TC1400009834.hg.1	GTF2A1	general transcription factor IIA 1	-1.8	7.67	8.52	0.51	0.18	8.70E-03	4.90E-02	Multiple_Complex
TC2100006960.hg.1	IFNAR1	interferon (alpha, beta and omega) receptor 1	-1.8	8.43	9.28	0.04	0.06	2.20E-03	2.05E-02	Multiple_Complex
TC1100013037.hg.1	ARL2	ADP-ribosylation factor like GTPase 2	-1.8	11.32	12.16	0.02	0.09	2.50E-03	2.24E-02	Multiple_Complex
TC0900007098.hg.1	RGP1	RGP1 homolog, RAB6A GEF complex partner 1	-1.8	8.59	9.43	0.71	0.15	1.89E-02	8.17E-02	Multiple_Complex
TC1600008011.hg.1	KATNB1	katanin p80 (WD repeat containing) subunit B 1	-1.8	9.06	9.91	0.12	0.19	4.40E-03	3.16E-02	Multiple_Complex
TC1500008135.hg.1	UBE2Q2L	ubiquitin conjugating enzyme E2Q family member 2-like	-1.8	10.09	10.94	0.44	0.08	9.30E-03	5.11E-02	Coding
TC0100009480.hg.1	HIPK1	homeodomain interacting protein kinase 1	-1.8	11.81	12.66	0.07	0.05	3.10E-03	2.51E-02	Multiple_Complex
TC1900007802.hg.1	KIAA0355	KIAA0355	-1.8	8.57	9.42	0.42	0.15	1.45E-02	6.88E-02	Multiple_Complex
TC1800006639.hg.1	RALBP1	ralA binding protein 1	-1.8	8.68	9.52	0.6	0.2	1.39E-02	6.67E-02	Multiple_Complex
TC1200009103.hg.1	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-1.8	11.63	12.48	0.09	0.11	5.70E-03	3.67E-02	Multiple_Complex
TSUnmapped00000445.hg.1	FBL	fibrillarin	-1.8	13.22	14.07	0.22	0.12	4.80E-03	3.33E-02	Coding
TC1700010248.hg.1	GIT1	G protein-coupled receptor kinase interacting ArfGAP 1	-1.8	8.23	9.08	0.3	0.38	1.78E-02	7.87E-02	Multiple_Complex
TC1900011947.hg.1	LRFN1	leucine rich repeat and fibronectin type III domain containing 1	-1.8	4.7	5.54	0.28	0.4	9.40E-03	5.13E-02	Multiple_Complex
TC0500013039.hg.1	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif 2	-1.8	5.87	6.71	0.16	0.31	4.40E-03	3.13E-02	Multiple_Complex
TC1400009585.hg.1	MAP3K9	mitogen-activated protein kinase kinase kinase 9	-1.8	7.4	8.24	0.02	0.22	4.70E-03	3.29E-02	Multiple_Complex
TC0600011859.hg.1	MRPL2	mitochondrial ribosomal protein L2	-1.8	7.28	8.13	0.13	0.51	8.90E-03	4.94E-02	Multiple_Complex
TC1100013176.hg.1	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	-1.8	7.97	8.82	0.12	0.07	8.60E-03	4.85E-02	Multiple_Complex

TC1500009904.hg.1	TLE3	transducin-like enhancer of split 3	-1.8	9.11	9.96	0.19	0.08	3.90E-03	2.94E-02	Multiple_Complex
TC0500006648.hg.1	PAPD7	PAP associated domain containing 7	-1.8	9.61	10.46	0.62	0.03	1.44E-02	6.85E-02	Multiple_Complex
TC2000008035.hg.1	GID8	GID complex subunit 8	-1.8	8.81	9.66	0.14	0.17	3.20E-03	2.57E-02	Multiple_Complex
TC1100011888.hg.1	CTSC	cathepsin C	-1.8	8.14	8.99	0.13	0.09	2.60E-03	2.29E-02	Multiple_Complex
TC1700010859.hg.1	DCAKD	dephospho-CoA kinase domain containing	-1.8	10.01	10.86	0.43	0.25	7.10E-03	4.27E-02	Multiple_Complex
TC0200014772.hg.1	IFIH1	interferon induced, with helicase C domain 1	-1.8	4.99	5.84	0.66	0.12	1.77E-02	7.85E-02	Multiple_Complex
TC1900011071.hg.1	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-1.8	11.03	11.88	0.14	0.11	2.30E-03	2.14E-02	Multiple_Complex
TC0600009831.hg.1	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	-1.8	5.99	6.84	0.04	0.65	1.89E-02	8.18E-02	Coding
TC1100009982.hg.1	DCHS1	dachsous cadherin-related 1	-1.8	4.9	5.75	0.22	0.63	2.40E-02	9.65E-02	Multiple_Complex
TC1400007942.hg.1	TDP1	tyrosyl-DNA phosphodiesterase 1	-1.8	10.17	11.02	0.38	0	4.90E-03	3.35E-02	Multiple_Complex
TC0200016702.hg.1	POLR1A	polymerase (RNA) I polypeptide A	-1.8	8.33	9.18	0.63	0.5	2.35E-02	9.50E-02	Multiple_Complex
TC1200008573.hg.1	SLC25A3; SNORA53	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3; small nucleolar RNA, H/ACA box 53	-1.8	11.7	12.55	0.19	0.1	3.10E-03	2.52E-02	Multiple_Complex
TC1100006440.hg.1	RIC8A; MIR6743	RIC8 guanine nucleotide exchange factor A; microRNA 6743	-1.8	6.96	7.81	0.62	0.36	2.76E-02	1.06E-01	Multiple_Complex
TC0900012221.hg.1	APTX	aprataxin	-1.81	9.69	10.54	0.07	0.16	2.30E-03	2.12E-02	Multiple_Complex
TC1200012629.hg.1	DAZAP2	DAZ associated protein 2	-1.81	8.51	9.36	0.16	0.07	3.10E-03	2.55E-02	Multiple_Complex
TC0100012601.hg.1	LRRC47	leucine rich repeat containing 47	-1.81	10.47	11.33	0.32	0.41	1.14E-02	5.85E-02	Multiple_Complex
TC1100008139.hg.1	AIP	aryl hydrocarbon receptor interacting protein	-1.81	10.92	11.77	0.24	0.15	4.40E-03	3.15E-02	Multiple_Complex
TC2000006541.hg.1	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	-1.81	10.71	11.56	0.56	0.25	1.09E-02	5.65E-02	Multiple_Complex

TC0600011874.hg.1	DLK2	delta-like 2 homolog (Drosophila)	-1.81	4.12	4.97	0.16	0.04	5.00E-03	3.38E-02	Multiple_Complex
TC0100012487.hg.1	SSU72	SSU72 homolog, RNA polymerase II CTD phosphatase	-1.81	9.57	10.42	0.24	0.04	2.80E-03	2.41E-02	Multiple_Complex
TC1200009242.hg.1	SNRNP35	small nuclear ribonucleoprotein, U11/U12 35kDa subunit	-1.81	7.81	8.66	0.21	0.18	3.80E-03	2.88E-02	Multiple_Complex
TC0800009208.hg.1	ZNF623	zinc finger protein 623	-1.81	4.28	5.13	0.89	0.44	4.21E-02	1.40E-01	Coding
TC1400008452.hg.1	ADSSL1	adenylosuccinate synthase like 1	-1.81	8.72	9.58	0.38	0.02	4.30E-03	3.12E-02	Multiple_Complex
TC0300009731.hg.1	MAP3K13	mitogen-activated protein kinase kinase kinase 13	-1.81	5.63	6.49	0.71	0.44	2.78E-02	1.06E-01	Multiple_Complex
TC0600010066.hg.1	IGF2R	insulin-like growth factor 2 receptor	-1.81	8.38	9.24	0.06	0.14	4.00E-03	2.98E-02	Multiple_Complex
TC0X00007190.hg.1	PORCN	porcupine homolog (Drosophila)	-1.81	7.06	7.91	0.42	0.26	1.11E-02	5.74E-02	Multiple_Complex
TC1000006796.hg.1	SEC61A2	Sec61 translocon alpha 2 subunit	-1.81	9.17	10.02	0.57	0.15	2.20E-02	9.08E-02	Multiple_Complex
TC1600007441.hg.1	PPP4C	protein phosphatase 4, catalytic subunit	-1.81	11.71	12.56	0.13	0.13	3.70E-03	2.82E-02	Multiple_Complex
TC0500007303.hg.1	NNT	nicotinamide nucleotide transhydrogenase	-1.81	11.16	12.02	0.31	0.1	3.30E-03	2.65E-02	Multiple_Complex
TC1700008564.hg.1	TACO1	translational activator of mitochondrially encoded cytochrome c oxidase I	-1.81	7.52	8.38	0.14	0.24	7.60E-03	4.46E-02	Multiple_Complex
TC0100011770.hg.1	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	-1.81	8.98	9.84	0.05	0.1	1.80E-03	1.85E-02	Multiple_Complex
TC0800010138.hg.1	RAB11FIP1	RAB11 family interacting protein 1 (class I)	-1.81	8.46	9.32	0.35	0.32	6.10E-03	3.86E-02	Multiple_Complex
TC1700011815.hg.1	MXRA7	matrix-remodelling associated 7	-1.81	12.81	13.67	0.32	0.15	4.20E-03	3.04E-02	Multiple_Complex
TC1500007510.hg.1	TPM1	tropomyosin 1 (alpha)	-1.81	6.89	7.75	0.68	0.01	1.52E-02	7.09E-02	Multiple_Complex
TC0600007869.hg.1	CMTR1	cap methyltransferase 1	-1.81	7.21	8.07	0.03	0.03	1.15E-02	5.88E-02	Multiple_Complex
TC1900010798.hg.1	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	-1.81	8.59	9.45	0.44	0.02	5.70E-03	3.67E-02	Multiple_Complex
TC2000008499.hg.1	RRBP1	ribosome binding protein 1	-1.81	9.59	10.45	0.63	0.02	1.47E-02	6.93E-02	Multiple_Complex
TC0200009626.hg.1	LYPD6	LY6/PLAUR domain containing 6	-1.81	5.51	6.37	0.36	0.03	3.80E-03	2.88E-02	Multiple_Complex

TC1400007222.hg.1	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	-1.81	7.48	8.34	0.15	0.09	3.00E-03	2.49E-02	Multiple_Complex
TC1700009137.hg.1	RPTOR	regulatory associated protein of MTOR, complex 1	-1.81	8.05	8.91	0.26	0.43	3.35E-02	1.20E-01	Multiple_Complex
TC1100012954.hg.1	TRIM6	tripartite motif containing 6	-1.82	5.73	6.59	0.26	0.22	3.60E-03	2.79E-02	Multiple_Complex
TC1100012308.hg.1	CRYAB	crystallin alpha B	-1.82	3.9	4.76	0.2	0.14	1.42E-02	6.77E-02	Coding
TC1800008458.hg.1	ZNF24	zinc finger protein 24	-1.82	9.8	10.66	0.48	0.08	6.20E-03	3.89E-02	Coding
TC1500008286.hg.1	ZNF710	zinc finger protein 710	-1.82	6.07	6.93	0.33	0.33	1.45E-02	6.86E-02	Multiple_Complex
TC0900006708.hg.1	SNAPC3	small nuclear RNA activating complex polypeptide 3	-1.82	9.14	10	0.11	0.14	1.90E-03	1.92E-02	Multiple_Complex
TSUnmapped00000597.hg.1	PSMC4	proteasome 26S subunit, ATPase 4 [Source:HGNC Symbol;Acc:HGNC:9551]	-1.82	12.98	13.84	0.08	0.24	2.70E-03	2.33E-02	Coding
TC0500013415.hg.1	RAB24	RAB24, member RAS oncogene family	-1.82	8.13	8.99	0.3	0.08	7.90E-03	4.58E-02	Multiple_Complex
TC0200014004.hg.1	CCDC93	coiled-coil domain containing 93	-1.82	8.79	9.65	0.58	0.4	1.64E-02	7.46E-02	Multiple_Complex
TC1900009393.hg.1	SAFB2	scaffold attachment factor B2	-1.82	8	8.86	0.61	0.04	1.53E-02	7.09E-02	Multiple_Complex
TC1500008971.hg.1	AVEN	apoptosis, caspase activation inhibitor	-1.82	7.33	8.19	0.15	0.19	2.30E-03	2.14E-02	Multiple_Complex
TC1900008372.hg.1	PPP5C	protein phosphatase 5, catalytic subunit	-1.82	12.15	13.01	0.28	0.18	4.50E-03	3.16E-02	Multiple_Complex
TC0600008059.hg.1	CNPY3	canopy FGF signaling regulator 3	-1.82	9.75	10.61	0.14	0.2	2.40E-03	2.18E-02	Multiple_Complex
TC1100010290.hg.1	E2F8	E2F transcription factor 8	-1.82	9.26	10.12	0.31	0.03	5.90E-03	3.75E-02	Multiple_Complex
TC1900006507.hg.1	CNN2	calponin 2	-1.82	4.69	5.56	0.16	0.18	3.00E-03	2.48E-02	Multiple_Complex
TC1000008713.hg.1	NOLC1	nucleolar and coiled-body phosphoprotein 1	-1.82	13.07	13.93	0.01	0.08	2.30E-03	2.11E-02	Multiple_Complex
TC0100008124.hg.1	MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	-1.82	8.82	9.68	0.17	0.45	7.30E-03	4.35E-02	Multiple_Complex
TC0300007166.hg.1	ZBTB47	zinc finger and BTB domain containing 47	-1.82	5.54	6.4	0.4	0.19	1.98E-02	8.46E-02	Coding
TC1900008090.hg.1	MAP3K10	mitogen-activated protein kinase kinase kinase 10	-1.82	8.16	9.02	0.48	0.21	8.20E-03	4.72E-02	Multiple_Complex

TC0100018182.hg.1	SZRD1	SUZ RNA binding domain containing 1	-1.82	9.16	10.02	0.06	0.11	1.70E-03	1.78E-02	Multiple_Complex
TC0800009988.hg.1	INTS9	integrator complex subunit 9	-1.82	7.38	8.24	0.61	0.07	1.06E-02	5.57E-02	Multiple_Complex
TC1600011341.hg.1	ZNF174	zinc finger protein 174	-1.82	9.09	9.96	0.13	0.13	2.00E-03	1.96E-02	Multiple_Complex
TC1400010377.hg.1	AKT1	v-akt murine thymoma viral oncogene homolog 1	-1.82	11.88	12.75	0.04	0.16	5.70E-03	3.69E-02	Multiple_Complex
TC1700011743.hg.1	GGA3	golgi-associated, gamma adaptin ear containing, ARF binding protein 3	-1.82	7.74	8.61	0.21	0.28	3.90E-03	2.93E-02	Multiple_Complex
TC0100007798.hg.1	THRAP3	thyroid hormone receptor associated protein 3	-1.82	9.92	10.78	0.54	0.25	9.70E-03	5.24E-02	Multiple_Complex
TC1500008545.hg.1	ASB7	ankyrin repeat and SOCS box containing 7	-1.82	8.46	9.33	0.37	0.16	5.10E-03	3.45E-02	Multiple_Complex
TC0400006540.hg.1	FGFR3	fibroblast growth factor receptor 3	-1.82	3.84	4.7	0.38	0.47	2.74E-02	1.05E-01	Multiple_Complex
TC1700012437.hg.1	SRSF1	serine/arginine-rich splicing factor 1	-1.82	8.26	9.13	0.25	0.05	3.00E-03	2.48E-02	Multiple_Complex
TC0700006652.hg.1	ZNF316	zinc finger protein 316	-1.82	5.46	6.32	0.25	0.29	1.00E-02	5.32E-02	Multiple_Complex
TC2000007658.hg.1	SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	-1.82	7.42	8.28	0.02	0.02	8.80E-03	4.91E-02	Multiple_Complex
TC0500013371.hg.1	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	-1.82	6.35	7.21	0.03	0.21	5.20E-03	3.46E-02	Multiple_Complex
TC1900006526.hg.1	MUM1	melanoma associated antigen (mutated) 1	-1.82	6.18	7.04	0.31	0.39	7.60E-03	4.47E-02	Multiple_Complex
TC0100006550.hg.1	PRKCZ	protein kinase C, zeta	-1.82	6.18	7.04	0.02	0.22	4.30E-03	3.09E-02	Multiple_Complex
TC0700007361.hg.1	UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	-1.82	9.14	10	0.1	0.09	4.40E-03	3.15E-02	Multiple_Complex
TC0700013458.hg.1	HILPDA	hypoxia inducible lipid droplet-associated	-1.82	7.89	8.75	0.12	0.35	4.60E-03	3.23E-02	Multiple_Complex
TC1900011984.hg.1	DMPK	dystrophia myotonica-protein kinase	-1.82	7.72	8.58	0.32	0.28	8.60E-03	4.86E-02	Multiple_Complex
TC0100016658.hg.1	ARPC5	actin related protein 2/3 complex subunit 5	-1.82	10.94	11.8	0.2	0.21	2.70E-03	2.34E-02	Multiple_Complex
TC0200013531.hg.1	KANSL3	KAT8 regulatory NSL complex subunit 3	-1.82	10.67	11.53	0.07	0.13	2.30E-03	2.11E-02	Multiple_Complex
TC0300013786.hg.1	ARPC4	actin related protein 2/3 complex subunit 4	-1.82	7.26	8.13	0.16	0.45	6.20E-03	3.90E-02	Multiple_Complex

TC2200008091.hg.1	PI4KAP2	phosphatidylinositol 4-kinase, catalytic, alpha pseudogene 2	-1.82	10.02	10.89	0.11	0.35	1.02E-02	5.41E-02	Multiple_Complex
TC1900009382.hg.1	PTPRS	protein tyrosine phosphatase, receptor type, S	-1.82	10.07	10.93	0.19	0.14	2.90E-03	2.44E-02	Multiple_Complex
TC0800007013.hg.1	CHMP7	charged multivesicular body protein 7	-1.82	7.48	8.34	0.35	0.11	3.60E-03	2.80E-02	Multiple_Complex
TC1400010576.hg.1	PABPN1	poly(A) binding protein, nuclear 1	-1.82	13.87	14.74	0.11	0.01	1.90E-03	1.90E-02	Multiple_Complex
TC0200016529.hg.1	ARHGEF4	Rho guanine nucleotide exchange factor 4	-1.82	6.34	7.21	0.44	0.53	1.81E-02	7.97E-02	Multiple_Complex
TC1600011496.hg.1	GPRC5B	G protein-coupled receptor, class C, group 5, member B	-1.82	6	6.87	0.32	0.24	1.11E-02	5.74E-02	Multiple_Complex
TC0900009260.hg.1	MAN1B1	mannosidase, alpha, class 1B, member 1	-1.83	6.39	7.26	0.95	0.05	3.72E-02	1.29E-01	Multiple_Complex
TC1200006700.hg.1	FOXJ2	forkhead box J2	-1.83	6.75	7.62	0.59	0.27	1.64E-02	7.45E-02	Multiple_Complex
TC1700012371.hg.1	ZNF286B; FOXO3B	zinc finger protein 286B; forkhead box O3B pseudogene	-1.83	6.1	6.97	0.43	0.18	1.69E-02	7.61E-02	Multiple_Complex
TC1300006633.hg.1	PABPC3	poly(A) binding protein, cytoplasmic 3	-1.83	8.74	9.61	0.36	0.2	7.30E-03	4.32E-02	Coding
TC1100012535.hg.1	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	-1.83	8.88	9.75	0.04	0.05	3.60E-03	2.77E-02	Multiple_Complex
TC2000007246.hg.1	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	-1.83	5.35	6.22	0.44	0.41	1.47E-02	6.95E-02	Multiple_Complex
TC0200011107.hg.1	EFHD1	EF-hand domain family member D1	-1.83	7.19	8.06	0.25	0.35	6.20E-03	3.90E-02	Multiple_Complex
TC1200006627.hg.1	NCAPD2	non-SMC condensin I complex subunit D2	-1.83	7.59	8.46	0.21	0.17	5.20E-03	3.49E-02	Multiple_Complex
TC0100010078.hg.1	IL6R	interleukin 6 receptor	-1.83	6.94	7.81	0.32	0.31	1.08E-02	5.64E-02	Multiple_Complex
TC2200006637.hg.1	DGCR8	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_022720	-1.83	7.4	8.27	0.41	0.03	7.50E-03	4.43E-02	NonCoding
TC0600014111.hg.1	SYNGAP1; MIR5004	synaptic Ras GTPase activating protein 1; microRNA 5004	-1.83	9.18	10.04	0.31	0.16	7.20E-03	4.30E-02	Multiple_Complex
TC0700012996.hg.1	ZNF746	zinc finger protein 746	-1.83	7.22	8.09	0.17	0.05	2.50E-03	2.26E-02	Multiple_Complex

TC1100013047.hg.1	SF3B2	splicing factor 3b subunit 2	-1.83	11.28	12.15	0.3	0.31	4.60E-03	3.25E-02	Multiple_Complex
TC1200010693.hg.1	TFCP2	transcription factor CP2	-1.83	7.66	8.53	0.45	0.24	1.07E-02	5.60E-02	Multiple_Complex
TC1400010317.hg.1	CKB	creatine kinase, brain	-1.83	8.67	9.54	0.27	0.14	4.00E-03	2.99E-02	Multiple_Complex
TC1900008927.hg.1	EPN1	epsin 1	-1.83	9.52	10.39	0.11	0.33	5.80E-03	3.73E-02	Multiple_Complex
TC0800009247.hg.1	HSF1	heat shock transcription factor 1	-1.83	5.74	6.61	0.59	0.03	1.53E-02	7.10E-02	Multiple_Complex
TC1600011517.hg.1	DOC2A	double C2-like domains, alpha	-1.83	4.73	5.6	0.39	0.28	1.22E-02	6.09E-02	Multiple_Complex
TC1900011736.hg.1	EGLN2	egl-9 family hypoxia-inducible factor 2	-1.83	9.62	10.49	0.76	0.21	1.97E-02	8.42E-02	Multiple_Complex
TC1100009242.hg.1	ABCG4	ATP binding cassette subfamily G member 4	-1.83	5.41	6.28	0.06	0.41	7.70E-03	4.51E-02	Multiple_Complex
TC1000011652.hg.1	FBXW4	F-box and WD repeat domain containing 4	-1.83	9	9.87	0.4	0.27	1.00E-02	5.35E-02	Multiple_Complex
TC0800006760.hg.1	FDFT1	farnesyl-diphosphate farnesyltransferase 1	-1.83	12.01	12.88	0.1	0.13	1.80E-03	1.85E-02	Multiple_Complex
TC1700012199.hg.1	PIGL	phosphatidylinositol glycan anchor biosynthesis class L	-1.83	10.05	10.92	0.1	0.05	3.00E-03	2.48E-02	NonCoding
TC1600007362.hg.1	ATXN2L	ataxin 2-like	-1.83	12.18	13.05	0.37	0.05	3.50E-03	2.72E-02	Multiple_Complex
TC1200006450.hg.1	WNK1	WNK lysine deficient protein kinase 1	-1.83	10.15	11.02	0.65	0.17	1.29E-02	6.36E-02	Multiple_Complex
TC0100010218.hg.1	KIRREL	kin of IRRE like (Drosophila)	-1.83	5	5.87	0.26	0.02	5.20E-03	3.48E-02	Multiple_Complex
TC1700009651.hg.1	TP53	tumor protein p53	-1.83	10.32	11.19	0.13	0.59	9.60E-03	5.21E-02	Multiple_Complex
TC1200008666.hg.1	HSP90B1; MIR3652	heat shock protein 90kDa beta (Grp94), member 1; microRNA 3652	-1.83	14.7	15.57	0.05	0.08	1.60E-03	1.74E-02	Multiple_Complex
TC0200011548.hg.1	TSSC1	tumor suppressing subtransferable candidate 1	-1.83	10.09	10.96	0.47	0.33	1.27E-02	6.28E-02	Multiple_Complex
TC0100013409.hg.1	GPATCH3	G-patch domain containing 3	-1.83	6.01	6.89	0.5	0.28	8.40E-03	4.79E-02	Multiple_Complex
TC0100013634.hg.1	TMEM54	transmembrane protein 54	-1.83	11.74	12.61	0.06	0.21	3.50E-03	2.74E-02	Multiple_Complex
TC1600008972.hg.1	WDR24	WD repeat domain 24	-1.83	6.8	7.67	0.12	0.05	2.60E-03	2.31E-02	Multiple_Complex

TC0100012693.hg.1	DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.83	9.5	10.37	0.35	0.06	4.80E-03	3.29E-02	Multiple_Complex
TC1900012005.hg.1	PNKP	polynucleotide kinase 3-phosphatase	-1.83	9.08	9.96	0.1	0.39	1.04E-02	5.47E-02	Multiple_Complex
TC0700010075.hg.1	GNA12	guanine nucleotide binding protein (G protein) alpha 12	-1.83	9.42	10.3	0.54	0.69	2.70E-02	1.04E-01	Multiple_Complex
TC0100007555.hg.1	MED18	mediator complex subunit 18	-1.83	6.23	7.1	0.32	0.07	3.70E-03	2.84E-02	Multiple_Complex
TC0300014042.hg.1	RAB43	RAB43, member RAS oncogene family	-1.84	7.12	8	0.44	0.34	1.60E-02	7.33E-02	Coding
TC0900009339.hg.1	WASH1	WAS protein family homolog 1	-1.84	10.82	11.69	0.06	0	1.70E-03	1.80E-02	Multiple_Complex
TC0600009362.hg.1	HEY2	hes-related family bHLH transcription factor with YRPW motif 2	-1.84	9.2	10.07	0.05	0.06	3.00E-03	2.47E-02	Multiple_Complex
TC2200008956.hg.1	PHF21B	PHD finger protein 21B	-1.84	4.91	5.79	0.03	0.26	3.30E-03	2.64E-02	Multiple_Complex
TC1000009217.hg.1	FAM175B	family with sequence similarity 175, member B	-1.84	11.12	12	0.21	0.22	2.60E-03	2.30E-02	Multiple_Complex
TC1900007150.hg.1	CC2D1A	coiled-coil and C2 domain containing 1A	-1.84	7.83	8.71	0.06	0.03	2.10E-03	2.00E-02	Multiple_Complex
TC0100018389.hg.1	CDK11A	cyclin-dependent kinase 11A	-1.84	10.77	11.64	0.29	0.13	5.70E-03	3.67E-02	Multiple_Complex
TC0100006771.hg.1	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	-1.84	4.14	5.02	0.33	0.14	3.50E-03	2.72E-02	Multiple_Complex
TC0X00010357.hg.1	GLA	galactosidase, alpha	-1.84	10.15	11.03	0.12	0.26	6.30E-03	3.93E-02	Multiple_Complex
TC0100012760.hg.1	RERE	arginine-glutamic acid dipeptide (RE) repeats	-1.84	8.97	9.84	0.13	0.05	1.60E-03	1.73E-02	Multiple_Complex
TC1000008954.hg.1	CASP7	caspase 7	-1.84	6.17	7.04	0.03	0.23	2.60E-03	2.30E-02	Multiple_Complex
TC1900006764.hg.1	SAFB	scaffold attachment factor B	-1.84	8.34	9.22	0.17	0.28	3.00E-03	2.50E-02	Multiple_Complex
TC0900009051.hg.1	GTF3C5	general transcription factor IIIC subunit 5	-1.84	8.36	9.24	0.13	0.22	2.60E-03	2.28E-02	Multiple_Complex
TC2100007327.hg.1	RRP1	ribosomal RNA processing 1	-1.84	9.09	9.97	0.17	0.08	1.90E-03	1.90E-02	Multiple_Complex
TC0300012315.hg.1	TPRA1	transmembrane protein, adipocyte asscociated 1	-1.84	7.6	8.48	0.13	0.38	6.80E-03	4.13E-02	Multiple_Complex
TC0400008680.hg.1	JADE1	jade family PHD finger 1	-1.84	4.25	5.13	0.3	0.36	1.25E-02	6.21E-02	Multiple_Complex

TC1100006796.hg.1	AKIP1	A kinase (PRKA) interacting protein 1	-1.84	7.43	8.31	0.42	0.28	5.90E-03	3.79E-02	Multiple_Complex
TC0900012119.hg.1	GALT	galactose-1-phosphate uridylyltransferase	-1.84	8.16	9.04	0.19	0.44	4.76E-02	1.52E-01	Multiple_Complex
TC2100007852.hg.1	RWDD2B	RWD domain containing 2B	-1.84	10.03	10.91	0.46	0.02	8.00E-03	4.61E-02	Multiple_Complex
TC0200007048.hg.1	MAPRE3	microtubule-associated protein, RP/EB family, member 3	-1.84	8.04	8.92	0.03	0.01	3.00E-03	2.50E-02	Multiple_Complex
TC1200006643.hg.1	PTMS	parathymosin	-1.84	10.88	11.75	0.06	0.08	2.20E-03	2.07E-02	Multiple_Complex
TC0300013380.hg.1	ALG3	ALG3, alpha-1,3- mannosyltransferase	-1.84	10.64	11.52	0.24	0.16	4.60E-03	3.21E-02	Multiple_Complex
TC0X00007222.hg.1	PLP2	proteolipid protein 2 (colonic epithelium-enriched)	-1.84	6.07	6.95	0.07	0.27	2.80E-03	2.41E-02	Multiple_Complex
TC1200010865.hg.1	ITGA7	integrin alpha 7	-1.84	6.91	7.79	0.16	0.26	3.50E-03	2.74E-02	Multiple_Complex
TC0600007774.hg.1	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	-1.84	10.65	11.53	0.35	0.16	6.90E-03	4.20E-02	Multiple_Complex
TC1900007864.hg.1	TMEM147	transmembrane protein 147	-1.84	12.5	13.38	0.44	0.04	6.30E-03	3.95E-02	Multiple_Complex
TC0100012062.hg.1	TBCE	tubulin folding cofactor E	-1.84	9.53	10.41	0.13	0.16	2.80E-03	2.37E-02	Multiple_Complex
TC0700013231.hg.1	MNX1	motor neuron and pancreas homeobox 1	-1.84	5.77	6.65	0.39	0.13	4.10E-03	2.99E-02	Multiple_Complex
TC1500010784.hg.1	NGRN; TTLL13P	neugrin, neurite outgrowth associated; tubulin tyrosine ligase-like family member 13, pseudogene	-1.84	10.47	11.36	0.5	0.13	7.60E-03	4.46E-02	Multiple_Complex
TC0900011673.hg.1	CRAT	carnitine O-acetyltransferase	-1.84	7.62	8.5	0.02	0.16	2.70E-03	2.32E-02	Multiple_Complex
TC0X00009581.hg.1	ELK1	ELK1, member of ETS oncogene family	-1.84	9.02	9.9	0.04	0.02	1.60E-03	1.77E-02	Multiple_Complex
TC1700012279.hg.1	HOXB-AS3	HOXB cluster antisense RNA 3	-1.84	11.51	12.39	0.05	0.23	8.80E-03	4.90E-02	Multiple_Complex
TC0100012497.hg.1	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	-1.84	13.1	13.99	0.28	0.1	2.50E-03	2.25E-02	Multiple_Complex
TC2200009333.hg.1	AP1B1	adaptor-related protein complex 1, beta 1 subunit	-1.84	11.93	12.81	0.23	0.09	2.00E-03	1.96E-02	Multiple_Complex
TC1100007430.hg.1	GYLTL1B	glycosyltransferase-like 1B	-1.84	11.02	11.91	0.47	0.36	8.50E-03	4.83E-02	Multiple_Complex

TC0700011924.hg.1	TMEM130	transmembrane protein 130	-1.84	6.05	6.93	0.1	0.55	1.20E-02	6.04E-02	Multiple_Complex
TC1100011187.hg.1	MEN1	multiple endocrine neoplasia I	-1.84	9.01	9.89	0.18	0.1	1.90E-03	1.90E-02	Multiple_Complex
TC1200008726.hg.1	TCP11L2	t-complex 11, testis-specific-like 2	-1.84	7.87	8.75	0.42	0.46	1.12E-02	5.78E-02	Multiple_Complex
TC1700012304.hg.1	COG1	component of oligomeric golgi complex 1	-1.85	10.29	11.17	0.16	0.25	3.00E-03	2.50E-02	Multiple_Complex
TC1000011567.hg.1	CRTAC1	cartilage acidic protein 1	-1.85	4.66	5.54	0.66	0.03	1.72E-02	7.71E-02	Multiple_Complex
TC1900011775.hg.1	GRWD1	glutamate-rich WD repeat containing 1	-1.85	6.86	7.75	0.09	0.42	6.50E-03	4.00E-02	Multiple_Complex
TC0200013746.hg.1	TGFBRAP1	transforming growth factor beta receptor associated protein 1	-1.85	8.63	9.51	0.31	0.29	5.30E-03	3.53E-02	Multiple_Complex
TC0200010264.hg.1	MFSD6	major facilitator superfamily domain containing 6	-1.85	9.46	10.34	0.18	0.13	1.14E-02	5.85E-02	Multiple_Complex
TC1900010941.hg.1	ERCC1	excision repair cross-complementation group 1	-1.85	9.01	9.89	0.15	0.03	3.30E-03	2.65E-02	Multiple_Complex
TC0300014043.hg.1	ISY1	ISY1 splicing factor homolog	-1.85	8.83	9.72	0.25	0.21	3.60E-03	2.76E-02	Multiple_Complex
TC2100007803.hg.1	APP	amyloid beta (A4) precursor protein	-1.85	13.15	14.04	0.09	0.13	1.70E-03	1.83E-02	Multiple_Complex
TC0800009961.hg.1	CLU; MIR6843	clusterin; microRNA 6843	-1.85	8.11	8.99	0.16	0.22	2.50E-03	2.23E-02	Multiple_Complex
TC0100015471.hg.1	ZNF697	zinc finger protein 697	-1.85	6.24	7.13	0.31	0.05	5.50E-03	3.60E-02	Multiple_Complex
TC0100009324.hg.1	FAM102B	family with sequence similarity 102, member B	-1.85	8.91	9.8	0.45	0.32	6.90E-03	4.18E-02	Multiple_Complex
TC1500007202.hg.1	USP8	ubiquitin specific peptidase 8	-1.85	7.87	8.75	0.18	0.06	1.80E-03	1.85E-02	Multiple_Complex
TC0700008517.hg.1	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	-1.85	10.34	11.23	0.16	0.11	2.30E-03	2.12E-02	Multiple_Complex
TC0100016887.hg.1	ZNF281	zinc finger protein 281	-1.85	9.49	10.37	0.3	0.34	4.40E-03	3.16E-02	Multiple_Complex
TC1100012510.hg.1	HYOU1	hypoxia up-regulated 1	-1.85	14.13	15.02	0.15	0.01	1.70E-03	1.81E-02	Multiple_Complex
TC1700012053.hg.1	FAAP100	Fanconi anemia core complex associated protein 100	-1.85	5.73	6.62	0.48	0.28	1.74E-02	7.76E-02	Multiple_Complex
TC1700008014.hg.1	ADAM11	ADAM metallopeptidase domain 11	-1.85	3.77	4.66	0.34	0.33	5.10E-03	3.44E-02	Multiple_Complex

TC1100008392.hg.1	PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	-1.85	9.76	10.65	0.15	0.47	1.73E-02	7.74E-02	Multiple_Complex
TC0300009337.hg.1	SMC4	structural maintenance of chromosomes 4	-1.85	11.58	12.47	0.07	0.13	2.10E-03	2.01E-02	Multiple_Complex
TC0100009344.hg.1	SARS	seryl-tRNA synthetase	-1.85	12.7	13.59	0.35	0.03	3.70E-03	2.81E-02	Multiple_Complex
TC2000009925.hg.1	SYS1-DBNDD2	SYS1-DBNDD2 readthrough (NMD candidate)	-1.85	6.96	7.85	0.1	0.28	2.40E-03	2.16E-02	Multiple_Complex
TC0300008381.hg.1	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	-1.85	7.4	8.28	0.02	0.16	4.40E-03	3.15E-02	Multiple_Complex
TC1600011424.hg.1	DDX19B	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19B	-1.85	10.15	11.03	0.16	0.02	2.10E-03	2.03E-02	Multiple_Complex
TC1700007381.hg.1	SUPT6H	SPT6 homolog, histone chaperone	-1.85	9.36	10.25	0.11	0.05	2.90E-03	2.45E-02	Multiple_Complex
TC0500008086.hg.1	NR2F1	nuclear receptor subfamily 2, group F, member 1	-1.85	8.42	9.31	0.02	0.09	3.00E-03	2.48E-02	Multiple_Complex
TC0100015273.hg.1	WDR77	WD repeat domain 77	-1.85	10.63	11.52	0.08	0.13	3.20E-03	2.59E-02	Multiple_Complex
TC0X00010851.hg.1	GPC3	glypican 3	-1.85	9.04	9.92	0.26	0.1	1.06E-02	5.56E-02	Multiple_Complex
TC1100009700.hg.1	PDDC1	Parkinson disease 7 domain containing 1	-1.85	8.02	8.91	0.34	0.29	1.25E-02	6.22E-02	Multiple_Complex
TC1900006864.hg.1	MAP2K7	mitogen-activated protein kinase kinase 7	-1.85	6.55	7.44	0.33	0.62	1.25E-02	6.21E-02	Multiple_Complex
TC1600011387.hg.1	STX4	syntaxin 4	-1.85	7.33	8.22	0.04	0.39	7.20E-03	4.29E-02	Multiple_Complex
TC1900008564.hg.1	ATF5; MIR4751	activating transcription factor 5; microRNA 4751	-1.85	5.07	5.96	0.15	0.53	9.00E-03	4.97E-02	Multiple_Complex
TC0100018221.hg.1	C1orf50	chromosome 1 open reading frame 50	-1.85	8.25	9.14	0.22	0.03	6.00E-03	3.80E-02	Multiple_Complex
TC0600014095.hg.1	RPP21	ribonuclease P/MRP 21kDa subunit	-1.85	9.32	10.21	0.4	0.29	1.95E-02	8.36E-02	Multiple_Complex
TC1200009196.hg.1	MLXIP	MLX interacting protein	-1.85	5.24	6.13	0.15	0.5	9.40E-03	5.14E-02	Multiple_Complex
TC0900012179.hg.1	SPTAN1	spectrin, alpha, non-erythrocytic 1	-1.85	8.43	9.32	0.67	0.4	1.84E-02	8.05E-02	Multiple_Complex
TC1200006787.hg.1	GABARAPL1	GABA(A) receptor-associated protein like 1	-1.85	11.16	12.05	0.32	0.08	3.00E-03	2.49E-02	Multiple_Complex
TC1800006731.hg.1	TUBB6	tubulin, beta 6 class V	-1.85	7.89	8.78	0.45	0.12	5.70E-03	3.69E-02	Multiple_Complex
TC1700011305.hg.1	HEATR6	HEAT repeat containing 6	-1.85	7.78	8.67	0.69	0.14	1.30E-02	6.38E-02	Multiple_Complex

TC0200008084.hg.1	TTC31	tetratricopeptide repeat domain 31	-1.85	5.39	6.28	0.59	0.07	1.89E-02	8.19E-02	Multiple_Complex
TC1700007360.hg.1	TMEM97	transmembrane protein 97	-1.85	10.1	10.99	0.33	0.35	4.80E-03	3.32E-02	Coding
TC1600009412.hg.1	TXNDC11	thioredoxin domain containing 11	-1.85	8.15	9.04	0.92	0.07	4.06E-02	1.36E-01	Multiple_Complex
TC1200007209.hg.1	DDX11	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_030653	-1.85	8.32	9.21	0.4	0.16	1.13E-02	5.79E-02	NonCoding
TC0200007702.hg.1	PAPOLG	poly(A) polymerase gamma	-1.85	10.29	11.18	0.23	0.08	1.80E-03	1.89E-02	Multiple_Complex
TC1200008835.hg.1	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.85	9.88	10.77	0.26	0.03	2.00E-03	2.00E-02	Multiple_Complex
TC0700008568.hg.1	SRRT	serrate, RNA effector molecule	-1.85	10.48	11.37	0.36	0.11	3.60E-03	2.79E-02	Multiple_Complex
TC0500007758.hg.1	FCHO2	FCH domain only 2	-1.85	6.07	6.96	0.6	0.11	9.20E-03	5.05E-02	Multiple_Complex
TC1700008897.hg.1	MRPS7	mitochondrial ribosomal protein S7	-1.85	12.4	13.29	0.41	0.02	4.70E-03	3.29E-02	Multiple_Complex
TC0300011203.hg.1	DCP1A	decapping mRNA 1A	-1.86	6.42	7.31	0.52	0.51	2.29E-02	9.35E-02	Multiple_Complex
TC0100008383.hg.1	MRPL37	mitochondrial ribosomal protein L37	-1.86	12.37	13.26	0.18	0.02	2.60E-03	2.29E-02	Multiple_Complex
TC0200010636.hg.1	MAP2	microtubule associated protein 2	-1.86	8.16	9.05	0.06	0.06	1.70E-03	1.81E-02	Multiple_Complex
TC0700012695.hg.1	C7orf49	chromosome 7 open reading frame 49	-1.86	7.07	7.96	0.01	0.19	2.10E-03	2.02E-02	Multiple_Complex
TC1500007914.hg.1	TMEM266	transmembrane protein 266	-1.86	7.4	8.29	0.33	0.51	9.10E-03	5.02E-02	Multiple_Complex
TC0100014457.hg.1	JAK1	Janus kinase 1	-1.86	11.09	11.98	0.35	0.2	3.70E-03	2.84E-02	Multiple_Complex
TC0100015645.hg.1	NBPF11	neuroblastoma breakpoint family, member 11	-1.86	8.93	9.82	0.23	0.09	8.40E-03	4.81E-02	Multiple_Complex
TC0400009258.hg.1	PALLD	palladin, cytoskeletal associated protein	-1.86	10.83	11.72	0.18	0.12	1.90E-03	1.93E-02	Multiple_Complex
TC1700007779.hg.1	MSL1	male-specific lethal 1 homolog (Drosophila)	-1.86	7.25	8.14	0.07	0.28	3.60E-03	2.79E-02	Multiple_Complex
TC0500007114.hg.1	RAI14	retinoic acid induced 14	-1.86	11.63	12.52	0.03	0.03	1.20E-03	1.50E-02	Multiple_Complex
TC1200012202.hg.1	ANAPC5	anaphase promoting complex subunit 5	-1.86	10.76	11.65	0.12	0.2	2.00E-03	1.99E-02	Multiple_Complex

TC1500010072.hg.1	SIN3A	SIN3 transcription regulator family member A	-1.86	11.63	12.52	0	0.13	2.10E-03	2.02E-02	Multiple_Complex
TC1700009040.hg.1	SYNGR2	synaptogyrin 2	-1.86	10.66	11.56	0.3	0.23	3.40E-03	2.68E-02	Multiple_Complex
TC1900011845.hg.1	MFSD12	major facilitator superfamily domain containing 12	-1.86	5.72	6.62	0.67	0.55	3.19E-02	1.16E-01	Multiple_Complex
TC0800008626.hg.1	UTP23	UTP23, small subunit (SSU) processome component, homolog (yeast)	-1.86	9.55	10.44	0.03	0.37	3.30E-03	2.64E-02	Multiple_Complex
TC1600008144.hg.1	C16orf70	chromosome 16 open reading frame 70	-1.86	8.31	9.2	0.35	0.02	3.00E-03	2.50E-02	Multiple_Complex
TC1500007986.hg.1	MORF4L1	mortality factor 4 like 1	-1.86	11.99	12.89	0.25	0.18	2.60E-03	2.28E-02	Multiple_Complex
TC1600010855.hg.1	GLG1	golgi glycoprotein 1	-1.86	9.74	10.63	0.11	0.22	2.70E-03	2.33E-02	Multiple_Complex
TC0900009882.hg.1	DCAF12	DDB1 and CUL4 associated factor 12	-1.86	11.43	12.32	0.23	0.22	3.20E-03	2.56E-02	Multiple_Complex
TC0400008053.hg.1	AFF1	AF4/FMR2 family, member 1	-1.86	8.67	9.57	0.1	0.02	2.90E-03	2.42E-02	Multiple_Complex
TC0300013789.hg.1	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	-1.86	6.02	6.92	0.02	0.3	7.60E-03	4.46E-02	Multiple_Complex
TC1900008254.hg.1	ZNF234	zinc finger protein 234	-1.86	5.45	6.35	0.38	0.19	6.50E-03	4.00E-02	Multiple_Complex
TC1100010688.hg.1	PHF21A	PHD finger protein 21A	-1.86	11.02	11.91	0	0.13	2.50E-03	2.24E-02	Multiple_Complex
TC0800011634.hg.1	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	-1.86	5.55	6.44	0.5	0.35	9.80E-03	5.26E-02	Multiple_Complex
TC0600011232.hg.1	HIST1H1B	histone cluster 1, H1b	-1.86	6.97	7.86	0.07	1.1	4.86E-02	1.54E-01	Multiple_Complex
TC1900008013.hg.1	PSMD8	proteasome 26S subunit, non-ATPase 8	-1.86	13.19	14.09	0.23	0.18	2.10E-03	2.00E-02	Multiple_Complex
TC1200011400.hg.1	CCDC59	coiled-coil domain containing 59	-1.86	12.98	13.88	0.03	0.1	1.90E-03	1.89E-02	Multiple_Complex
TC1500008703.hg.1	CYFIP1	cytoplasmic FMR1 interacting protein 1	-1.86	8.29	9.19	0.29	0.34	7.50E-03	4.43E-02	Multiple_Complex
TC0900009301.hg.1	MRPL41	mitochondrial ribosomal protein L41	-1.86	11.95	12.85	0.06	0.07	1.30E-03	1.57E-02	Multiple_Complex
TC1700009451.hg.1	CLUH	clustered mitochondria (cluA/CLU1) homolog	-1.86	7.56	8.46	0.61	0.23	1.07E-02	5.58E-02	Multiple_Complex

TC0400011600.hg.1	PITX2	paired-like homeodomain 2	-1.86	7.97	8.87	0.03	0.15	1.80E-03	1.87E-02	Multiple_Complex
TC1900007320.hg.1	DDA1	DET1 and DDB1 associated 1	-1.86	10.03	10.92	0.07	0.45	5.10E-03	3.45E-02	Multiple_Complex
TC0900011815.hg.1	AK8	adenylate kinase 8	-1.87	7.59	8.49	0.09	0.77	3.14E-02	1.15E-01	Multiple_Complex
TC1100009237.hg.1	VPS11	vacuolar protein sorting 11 homolog (S. cerevisiae)	-1.87	7.14	8.04	0.22	0.1	3.50E-03	2.72E-02	Multiple_Complex
TC1600008938.hg.1	AXIN1	axin 1	-1.87	8.5	9.4	0.45	0.04	5.80E-03	3.72E-02	Multiple_Complex
TC2000007666.hg.1	RNF114	ring finger protein 114	-1.87	10.07	10.97	0.24	0.04	2.30E-03	2.11E-02	Multiple_Complex
TC0900007165.hg.1	TRMT10B	tRNA methyltransferase 10B	-1.87	7.75	8.65	0	0.03	6.70E-03	4.11E-02	Multiple_Complex
TC0200016706.hg.1	MRPS5	mitochondrial ribosomal protein S5	-1.87	11.41	12.31	0.27	0.01	2.30E-03	2.15E-02	Multiple_Complex
TC2000007476.hg.1	STK4	serine/threonine kinase 4	-1.87	9.09	9.99	0.49	0.44	1.03E-02	5.44E-02	Multiple_Complex
TC2200007085.hg.1	RNF185	ring finger protein 185	-1.87	9.16	10.06	0.11	0.21	2.30E-03	2.12E-02	Multiple_Complex
TC1000008651.hg.1	HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	-1.87	8.26	9.16	0.28	0.13	7.60E-03	4.45E-02	Multiple_Complex
TSUnmapped00000585.hg.1	LRIG1		-1.87	6.61	7.51	0.08	0.13	6.40E-03	3.96E-02	NonCoding
TC2000010026.hg.1	TMEM189	transmembrane protein 189	-1.87	8.5	9.4	0.18	0.22	3.10E-03	2.52E-02	Multiple_Complex
TSUnmapped00000486.hg.1	MLXIP	MLX interacting protein	-1.87	6.67	7.57	0.07	0.14	2.40E-03	2.19E-02	Coding
TC0900011626.hg.1	CIZ1	CDKN1A interacting zinc finger protein 1	-1.87	12.15	13.05	0.04	0.15	1.70E-03	1.79E-02	Multiple_Complex
TC2200009271.hg.1	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	-1.87	10.53	11.43	0.27	0.1	2.30E-03	2.13E-02	Multiple_Complex
TC1100011157.hg.1	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	-1.87	12.79	13.69	0	0.04	1.30E-03	1.57E-02	Multiple_Complex
TC1100009026.hg.1	SIK2	salt-inducible kinase 2	-1.87	8.08	8.98	0.2	0.59	1.03E-02	5.46E-02	Multiple_Complex
TC1400010767.hg.1	ZFYVE26	zinc finger, FYVE domain containing 26	-1.87	7.2	8.1	0.05	0.06	4.90E-03	3.34E-02	Multiple_Complex
TC0500008917.hg.1	KIAA0141	KIAA0141	-1.87	6.72	7.62	0.39	0.71	1.80E-02	7.94E-02	Multiple_Complex

TC1100006888.hg.1	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	-1.87	9.68	10.58	0.08	0.26	2.60E-03	2.28E-02	Multiple_Complex
TC0X00009386.hg.1	SRPX	sushi-repeat containing protein, X-linked	-1.87	8.12	9.02	0.39	0.23	1.67E-02	7.54E-02	Multiple_Complex
TC1600007887.hg.1	RBL2	retinoblastoma-like 2	-1.87	7.82	8.72	0.17	0.1	2.70E-03	2.33E-02	Multiple_Complex
TC0100016035.hg.1	ETV3	ets variant 3	-1.87	10.48	11.38	0.02	0.2	1.70E-03	1.77E-02	Multiple_Complex
TC1100008091.hg.1	CCS	copper chaperone for superoxide dismutase	-1.87	5.77	6.68	0.17	0.1	6.80E-03	4.13E-02	Multiple_Complex
TC1100010712.hg.1	ARHGAP1	Rho GTPase activating protein 1	-1.87	9.92	10.82	0.24	0.16	3.00E-03	2.48E-02	Multiple_Complex
TC0100010872.hg.1	SMG7	SMG7 nonsense mediated mRNA decay factor	-1.87	7.67	8.58	0.11	0.06	1.60E-03	1.77E-02	Multiple_Complex
TC1500010658.hg.1	VIMP	VCP-interacting membrane selenoprotein	-1.87	8.18	9.08	0.2	0.11	2.10E-03	2.00E-02	Multiple_Complex
TC1200006520.hg.1	TSPAN9	tetraspanin 9	-1.87	6.47	7.37	0.49	0.56	3.56E-02	1.25E-01	Multiple_Complex
TC0X00007557.hg.1	MED12	mediator complex subunit 12	-1.87	9.57	10.48	0.3	0.26	3.60E-03	2.76E-02	Multiple_Complex
TC0X00007522.hg.1	FAM155B	family with sequence similarity 155, member B	-1.87	8.38	9.29	0.6	0.17	4.26E-02	1.41E-01	Coding
TC2000008268.hg.1	SLC23A2	solute carrier family 23 (ascorbic acid transporter), member 2	-1.87	9.26	10.16	0.35	0.02	3.40E-03	2.70E-02	Multiple_Complex
TC0900009953.hg.1	MSMP	microseminoprotein, prostate associated	-1.87	8.54	9.45	0.06	0.3	2.10E-03	2.01E-02	Multiple_Complex
TC0300011089.hg.1	MON1A	MON1 secretory trafficking family member A	-1.87	5.5	6.41	0.06	0.21	1.70E-03	1.78E-02	Multiple_Complex
TC0100016664.hg.1	COLGALT2	collagen beta(1-O)galactosyltransferase 2	-1.88	5.94	6.85	0.37	0.19	1.34E-02	6.49E-02	Multiple_Complex
TC0600008087.hg.1	ABCC10	ATP binding cassette subfamily C member 10	-1.88	6.96	7.87	0.3	0.15	5.30E-03	3.54E-02	Multiple_Complex
TC1700009150.hg.1	BAIAP2	BAI1-associated protein 2	-1.88	6.16	7.06	0.6	0.11	1.13E-02	5.82E-02	Multiple_Complex

TC0700013424.hg.1	GS1-259H13.2; TCONS_l2_00026125; TCONS_l2_00026126; ZNF655	transmembrane protein 225-like; Jeck2013 ALT_ACCEPTOR, ALT_DONOR, ncRNA, OVCODE, OVEXON, upstream_start best transcript TCONS_l2_00026125; Salzman2013 ANNOTATED, INTERNAL, ncRNA, OVCODE, OVEXON best transcript TCONS_l2_00026126; novel transcript; Transcript Identified by AceView, Entrez Gene ID(s) 79027	-1.88	7.87	8.78	0.31	0.37	4.50E-03	3.16E-02	Multiple_Complex
TC0700012760.hg.1	ZC3HAV1L	zinc finger CCCH-type, antiviral 1-like	-1.88	6.94	7.85	0.15	0.46	1.03E-02	5.46E-02	Multiple_Complex
TC0600011471.hg.1	DXO	decapping exoribonuclease	-1.88	7.73	8.64	0.31	0.37	5.70E-03	3.71E-02	Multiple_Complex
TC1400006739.hg.1	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	-1.88	7.98	8.89	0.05	0.13	1.50E-02	7.02E-02	Multiple_Complex
TC1900006480.hg.1	PALM	paralemmin	-1.88	5.39	6.29	0.22	0.26	2.50E-03	2.22E-02	Multiple_Complex
TC0100010661.hg.1	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	-1.88	11.82	12.73	0.02	0.09	1.70E-03	1.78E-02	Multiple_Complex
TC1100007287.hg.1	TRIM44	tripartite motif containing 44	-1.88	10.24	11.14	0.06	0.02	3.50E-03	2.72E-02	Multiple_Complex
TC0100007574.hg.1	EPB41	erythrocyte membrane protein band 4.1	-1.88	13.07	13.98	0.11	0.05	1.40E-03	1.63E-02	Multiple_Complex
TC0700011550.hg.1	POM121C	POM121 transmembrane nucleoporin C	-1.88	14.05	14.96	0.05	0.12	1.40E-03	1.60E-02	Multiple_Complex
TC1400010632.hg.1	GPATCH2L	G-patch domain containing 2 like	-1.88	10.2	11.11	0.07	0.04	1.50E-03	1.66E-02	Multiple_Complex
TC1400010039.hg.1	DDX24	DEAD (Asp-Glu-Ala-Asp) box helicase 24	-1.88	13.95	14.86	0.04	0.09	1.30E-03	1.56E-02	Multiple_Complex
TC1500009926.hg.1	LARP6	La ribonucleoprotein domain family, member 6	-1.88	9.23	10.14	0.39	0.29	7.00E-03	4.21E-02	Multiple_Complex
TC1600011421.hg.1	VPS4A	vacuolar protein sorting 4 homolog A (S. cerevisiae)	-1.88	9.64	10.55	0.1	0.14	1.50E-03	1.65E-02	Multiple_Complex
TC0300011834.hg.1	FILIP1L	filamin A interacting protein 1-like	-1.88	7.35	8.26	0.21	0.29	1.20E-02	6.04E-02	Multiple_Complex
TC1900011814.hg.1	ZNF17	zinc finger protein 17	-1.88	8.87	9.78	0.7	0.22	1.74E-02	7.76E-02	Multiple_Complex

TC0X00007274.hg.1	MAGED4B; MAGED4; SNORA11D	melanoma antigen family D4B; melanoma antigen family D4; small nucleolar RNA, H/ACA box 11D	-1.88	7.59	8.5	0.1	0.06	1.30E-03	1.54E-02	Multiple_Complex
TC1900011684.hg.1	BABAM1	BRISC and BRCA1 A complex member 1	-1.88	10.52	11.43	0.36	0.02	2.50E-03	2.26E-02	Multiple_Complex
TC0100012006.hg.1	KCNK1	potassium channel, two pore domain subfamily K, member 1	-1.88	5.64	6.55	0.54	0.16	1.04E-02	5.47E-02	Multiple_Complex
TC0500012818.hg.1	STK10	serine/threonine kinase 10	-1.88	8.64	9.55	0.83	0.18	1.96E-02	8.40E-02	Multiple_Complex
TC0100017079.hg.1	SLC41A1	solute carrier family 41 (magnesium transporter), member 1	-1.88	11.68	12.59	0.03	0.08	1.40E-03	1.62E-02	Multiple_Complex
TC1600010596.hg.1	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	-1.88	12.95	13.86	0.15	0.03	1.50E-03	1.69E-02	Multiple_Complex
TC0100009364.hg.1	CSF1	colony stimulating factor 1 (macrophage)	-1.88	8.21	9.12	0.02	0.17	1.50E-03	1.65E-02	Multiple_Complex
TC0600011253.hg.1	ZSCAN12	zinc finger and SCAN domain containing 12	-1.88	4.91	5.83	0.12	0.16	1.30E-03	1.59E-02	Multiple_Complex
TC2200008186.hg.1	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	-1.88	8.79	9.7	0.21	0.37	3.70E-03	2.82E-02	Multiple_Complex
TC0100011873.hg.1	RNF187	ring finger protein 187	-1.88	12.78	13.69	0.01	0.18	1.40E-03	1.63E-02	Multiple_Complex
TC1600010262.hg.1	BRD7	bromodomain containing 7	-1.88	10.71	11.62	0.18	0.03	2.60E-03	2.30E-02	Multiple_Complex
TC1600009331.hg.1	C16orf72	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_014117	-1.88	8.49	9.4	0.32	0.21	8.10E-03	4.65E-02	NonCoding
TC0100009641.hg.1	NBPF8	neuroblastoma breakpoint family, member 8	-1.88	7.13	8.04	0.19	0.66	1.40E-02	6.70E-02	Multiple_Complex
TC1700009949.hg.1	SREBF1	sterol regulatory element binding transcription factor 1	-1.88	9.27	10.19	0.16	0	2.30E-03	2.14E-02	Multiple_Complex
TC0300007123.hg.1	ZNF620	zinc finger protein 620	-1.88	8.12	9.03	0.23	0	2.87E-02	1.09E-01	Coding
TC0500010085.hg.1	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	-1.89	8.06	8.98	0.11	0.04	1.90E-03	1.90E-02	Multiple_Complex
TC2200007477.hg.1	ACO2	aconitase 2, mitochondrial	-1.89	8.57	9.48	0.19	0.02	2.80E-03	2.38E-02	Multiple_Complex
TC0500009059.hg.1	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	-1.89	11.48	12.4	0.2	0.33	2.70E-03	2.34E-02	Multiple_Complex

TC0600011134.hg.1	HIST1H4D	histone cluster 1, H4d	-1.89	10.56	11.48	0.3	0.06	3.50E-03	2.74E-02	Coding
TC0100014201.hg.1	CC2D1B	coiled-coil and C2 domain containing 1B	-1.89	4.51	5.42	0.06	0.22	1.60E-03	1.76E-02	Multiple_Complex
TC2200009284.hg.1	ARHGAP8	Rho GTPase activating protein 8	-1.89	9.6	10.51	0.55	0.7	2.50E-02	9.91E-02	Multiple_Complex
TC0X00007134.hg.1	USP11	ubiquitin specific peptidase 11	-1.89	12.82	13.73	0.06	0.09	1.20E-03	1.50E-02	Multiple_Complex
TC1600006436.hg.1	SNRNP25	small nuclear ribonucleoprotein, U11/U12 25kDa subunit	-1.89	9.54	10.45	0.32	0.14	5.60E-03	3.63E-02	Multiple_Complex
TC0700008762.hg.1	CBLL1	Cbl proto-oncogene-like 1, E3 ubiquitin protein ligase	-1.89	10.02	10.93	0.18	0.14	2.50E-03	2.23E-02	Multiple_Complex
TC1900008832.hg.1	PRPF31	pre-mRNA processing factor 31	-1.89	11.81	12.73	0.34	0.04	2.80E-03	2.40E-02	Multiple_Complex
TC1900011940.hg.1	ECH1	enoyl-CoA hydratase 1, peroxisomal	-1.89	9.71	10.62	0.19	0.12	1.40E-03	1.64E-02	Multiple_Complex
TC1700008032.hg.1	ACBD4	acyl-CoA binding domain containing 4	-1.89	7.35	8.27	0.38	0.13	2.24E-02	9.18E-02	Multiple_Complex
TC1700010910.hg.1	KANSL1	KAT8 regulatory NSL complex subunit 1	-1.89	10.1	11.01	0.08	0.27	8.50E-03	4.81E-02	Multiple_Complex
TC1900006646.hg.1	GIPC3	GIPC PDZ domain containing family, member 3	-1.89	6.63	7.55	0.15	0.21	4.10E-03	3.00E-02	Multiple_Complex
TC2200007360.hg.1	CBY1	chibby homolog 1 (Drosophila)	-1.89	9.2	10.12	0.45	0.25	1.34E-02	6.51E-02	Multiple_Complex
TC2100006951.hg.1	OLIG1	oligodendrocyte transcription factor 1	-1.89	6.61	7.52	0.15	0.68	1.43E-02	6.80E-02	Multiple_Complex
TC0200007609.hg.1	SPTBN1	spectrin, beta, non-erythrocytic 1	-1.89	12.17	13.09	0.31	0.01	2.30E-03	2.11E-02	Multiple_Complex
TC1600010734.hg.1	NOB1	NIN1/RPN12 binding protein 1 homolog	-1.89	11.54	12.46	0.04	0.32	2.50E-03	2.23E-02	Multiple_Complex
TC0600008027.hg.1	BYSL	bystin-like	-1.89	8.35	9.27	0.5	0.03	6.40E-03	3.97E-02	Multiple_Complex
TC1100009043.hg.1	DIXDC1	DIX domain containing 1	-1.89	6.11	7.03	0.18	0.46	1.73E-02	7.74E-02	Multiple_Complex
TC0X00009942.hg.1	PJA1	praja ring finger 1, E3 ubiquitin protein ligase	-1.89	8.3	9.22	0.31	0.03	5.10E-03	3.43E-02	Multiple_Complex
TC1500007695.hg.1	PAQR5	progestin and adipoQ receptor family member V	-1.89	5.32	6.24	0.21	0.6	1.24E-02	6.19E-02	Multiple_Complex
TC0100012473.hg.1	CCNL2	cyclin L2	-1.89	7.1	8.02	0.43	0.06	4.00E-03	2.95E-02	Multiple_Complex
TC1200012801.hg.1	CS	citrate synthase	-1.89	13.68	14.6	0.02	0.04	1.00E-03	1.39E-02	Multiple_Complex

TC0200016369.hg.1	DTYMK	deoxythymidylate kinase	-1.89	10.36	11.28	0.37	0.21	3.30E-03	2.65E-02	Multiple_Complex
TC1600007425.hg.1	KIF22	kinesin family member 22	-1.89	7.38	8.3	0.32	0.26	3.10E-03	2.51E-02	Multiple_Complex
TC1600008166.hg.1	CTCF	CCCTC-binding factor (zinc finger protein)	-1.89	8.87	9.78	0.39	0	3.10E-03	2.53E-02	Multiple_Complex
TC1700006547.hg.1	SGSM2	small G protein signaling modulator 2	-1.89	8.81	9.73	0.26	0.18	7.40E-03	4.36E-02	Multiple_Complex
TC1100013057.hg.1	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	-1.89	6.84	7.76	0.06	0.02	2.30E-03	2.13E-02	Multiple_Complex
TC2000006561.hg.1	MAVS	mitochondrial antiviral signaling protein	-1.89	6.48	7.4	0.08	0.59	8.70E-03	4.89E-02	Multiple_Complex
TC1600008657.hg.1	USP10	ubiquitin specific peptidase 10	-1.89	12.12	13.04	0.33	0.16	2.80E-03	2.38E-02	Multiple_Complex
TC2200009246.hg.1	ZNRF3	zinc and ring finger 3	-1.89	7.75	8.67	0.34	0.31	6.60E-03	4.04E-02	Multiple_Complex
TC0X00008833.hg.1	FAM50A	family with sequence similarity 50, member A	-1.89	8.33	9.25	0.71	0.24	1.37E-02	6.62E-02	Multiple_Complex
TC1900006835.hg.1	ZNF557	zinc finger protein 557	-1.89	7.3	8.22	0.23	0.29	4.30E-03	3.09E-02	Multiple_Complex
TC1400010071.hg.1	CLMN	calmin (calponin-like, transmembrane)	-1.89	8.92	9.84	0.49	0.03	6.80E-03	4.12E-02	Multiple_Complex
TC0400009790.hg.1	MFSD10	major facilitator superfamily domain containing 10	-1.89	10.05	10.98	0.34	0.33	5.10E-03	3.44E-02	Multiple_Complex
TC1700008690.hg.1	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.89	6.67	7.59	0.05	0.04	1.10E-03	1.45E-02	Multiple_Complex
TC1000008727.hg.1	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	-1.89	5.75	6.67	0.19	0.29	9.10E-03	5.01E-02	Multiple_Complex
TC2200009021.hg.1	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1	-1.89	4.81	5.73	0.02	0.23	3.70E-03	2.81E-02	Multiple_Complex
TC0100007716.hg.1	ZNF362	zinc finger protein 362	-1.9	7.3	8.22	0.34	0.07	1.25E-02	6.21E-02	Multiple_Complex
TC0100008034.hg.1	ZNF691	zinc finger protein 691	-1.9	6.3	7.23	0.44	0.56	1.56E-02	7.19E-02	Multiple_Complex
TC1100011090.hg.1	EML3	echinoderm microtubule associated protein like 3	-1.9	8.89	9.81	0.3	0.6	1.07E-02	5.61E-02	Multiple_Complex
TC0100012523.hg.1	MORN1	MORN repeat containing 1	-1.9	5.89	6.81	0.28	0.22	5.40E-03	3.54E-02	Multiple_Complex

TC1500009109.hg.1	C15orf57; MRPL42P5	chromosome 15 open reading frame 57; mitochondrial ribosomal protein L42 pseudogene 5	-1.9	8.01	8.93	0.05	0.02	3.10E-03	2.53E-02	Multiple_Complex
TC1200010809.hg.1	ATF7; NPFF	activating transcription factor 7; neuropeptide FF-amide peptide precursor	-1.9	10.14	11.06	0.21	0.27	2.90E-03	2.42E-02	Multiple_Complex
TC2100008390.hg.1	PTTG1IP	pituitary tumor-transforming 1 interacting protein	-1.9	7.11	8.04	0.3	0.42	5.60E-03	3.67E-02	Multiple_Complex
TC0100013123.hg.1	UBR4	ubiquitin protein ligase E3 component n-recognin 4	-1.9	13.72	14.64	0.16	0.02	1.80E-03	1.85E-02	Multiple_Complex
TC1100011285.hg.1	B4GAT1	beta-1,4-glucuronyltransferase 1	-1.9	10.19	11.12	0.11	0.08	1.10E-03	1.46E-02	Multiple_Complex
TC1600010633.hg.1	ATP6V0D1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	-1.9	9.99	10.91	0.2	0.35	3.70E-03	2.80E-02	Multiple_Complex
TC1100010268.hg.1	TSG101	tumor susceptibility 101	-1.9	11.42	12.34	0.08	0.01	1.40E-03	1.61E-02	Multiple_Complex
TC0700011865.hg.1	DLX5	distal-less homeobox 5	-1.9	3.76	4.68	0.68	0.77	3.85E-02	1.31E-01	Multiple_Complex
TC1500007856.hg.1	CSK	c-src tyrosine kinase	-1.9	6.52	7.44	0.24	0.18	2.20E-03	2.10E-02	Multiple_Complex
TC0100006994.hg.1	PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) member 2	-1.9	8.72	9.65	0.35	0.09	5.60E-03	3.64E-02	Multiple_Complex
TC0600013206.hg.1	SLC18B1	solute carrier family 18, subfamily B, member 1	-1.9	7.71	8.64	0.41	0.1	4.00E-03	2.99E-02	Multiple_Complex
TC0700012883.hg.1	FAM131B	family with sequence similarity 131, member B	-1.9	5.32	6.24	0.54	0	6.00E-03	3.80E-02	Multiple_Complex
TC1900011004.hg.1	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	-1.9	12	12.93	0.19	0.21	3.30E-03	2.63E-02	Multiple_Complex
TC1700010501.hg.1	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	-1.9	11.08	12.01	0.03	0.22	1.50E-03	1.69E-02	Multiple_Complex
TC2000008055.hg.1	ARFGAP1; MIR4326	ADP-ribosylation factor GTPase activating protein 1; microRNA 4326	-1.9	9.56	10.49	0.59	0.12	1.20E-02	6.04E-02	Multiple_Complex
TC1600007366.hg.1	SH2B1	SH2B adaptor protein 1	-1.9	8.05	8.98	0.16	0.22	1.90E-03	1.92E-02	Multiple_Complex
TC0900009892.hg.1	KIF24	kinesin family member 24	-1.9	7.12	8.04	0.4	0.04	4.50E-03	3.18E-02	Multiple_Complex

TC1300008388.hg.1	MTMR6	Transcript Identified by AceView, Entrez Gene ID(s) 9107	-1.9	4.74	5.66	0.04	0.37	9.80E-03	5.29E-02	Unassigned
TC1500006994.hg.1	CHP1	calcineurin-like EF-hand protein 1	-1.9	11.06	11.98	0.02	0.03	4.30E-03	3.10E-02	Multiple_Complex
TC0700008090.hg.1	HSPB1	heat shock 27kDa protein 1	-1.9	13.01	13.94	0.13	0.02	1.40E-03	1.60E-02	Multiple_Complex
TC0200015779.hg.1	DNPEP	aspartyl aminopeptidase	-1.9	5.2	6.12	0.06	0.42	3.10E-03	2.55E-02	Multiple_Complex
TC1600007723.hg.1	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	-1.9	8.1	9.03	0.51	0.3	6.80E-03	4.14E-02	Multiple_Complex
TC1100009824.hg.1	CARS	cysteinyl-tRNA synthetase	-1.9	7.2	8.13	0.2	0.48	5.30E-03	3.50E-02	Multiple_Complex
TC1200007630.hg.1	LETMD1	LETM1 domain containing 1	-1.9	9.82	10.74	0.06	0.25	1.50E-03	1.70E-02	Multiple_Complex
TC1900006821.hg.1	VAV1	vav 1 guanine nucleotide exchange factor	-1.9	5.58	6.51	0.58	0.19	1.16E-02	5.89E-02	Multiple_Complex
TC0100018299.hg.1	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	-1.9	7.5	8.43	0.14	0.08	2.50E-03	2.23E-02	Multiple_Complex
TC0700008561.hg.1	POP7	POP7 homolog, ribonuclease P/MRP subunit	-1.9	9.72	10.65	0.46	0.06	4.30E-03	3.10E-02	Multiple_Complex
TC1900011721.hg.1	HKR1	HKR1, GLI-Kruppel zinc finger family member	-1.9	6.79	7.72	0.2	0.45	7.80E-03	4.53E-02	NonCoding
TC1700007942.hg.1	NBR1	neighbor of BRCA1 gene 1	-1.9	7.75	8.67	0.57	0.11	1.27E-02	6.27E-02	Multiple_Complex
TC0200016115.hg.1	ARL4C	ADP-ribosylation factor like GTPase 4C	-1.9	7.15	8.08	0.04	0.23	5.20E-03	3.49E-02	Multiple_Complex
TC0100018417.hg.1	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	-1.9	6.43	7.36	0.24	0.4	5.50E-03	3.61E-02	Multiple_Complex
TC0600011583.hg.1	C6orf1	chromosome 6 open reading frame 1	-1.91	8.82	9.75	0.44	0.53	1.25E-02	6.22E-02	Multiple_Complex
TSUnmapped00000777.hg.1	HYOU1	hypoxia up-regulated 1	-1.91	12.14	13.07	0.25	0.08	1.90E-03	1.89E-02	Coding
TC1600008178.hg.1	PSKH1	protein serine kinase H1	-1.91	5.24	6.17	0.35	0.01	2.70E-03	2.32E-02	Multiple_Complex
TC2100008087.hg.1	HLCS	holocarboxylase synthetase (biotin-(proprionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)	-1.91	7.56	8.49	0.17	0.1	1.80E-03	1.85E-02	Multiple_Complex

TC0100011417.hg.1	CR1L	complement component (3b/4b) receptor 1-like	-1.91	4.49	5.42	0.43	0.03	7.40E-03	4.39E-02	Multiple_Complex
TC1600006533.hg.1	UBE2I	ubiquitin conjugating enzyme E2I	-1.91	10.08	11.01	0.1	0.2	1.70E-03	1.77E-02	Multiple_Complex
TC0700008004.hg.1	GTF2IRD1	GTF2I repeat domain containing 1	-1.91	7.3	8.23	0.39	0.25	4.20E-03	3.05E-02	Multiple_Complex
TC1900010076.hg.1	ATP13A1	ATPase type 13A1	-1.91	10.48	11.41	0.24	0.23	2.60E-03	2.30E-02	Multiple_Complex
TC0100007477.hg.1	ARID1A	AT rich interactive domain 1A (SWI-like)	-1.91	8.03	8.96	0.26	0.25	2.50E-03	2.23E-02	Multiple_Complex
TC1900008053.hg.1	SAMD4B	sterile alpha motif domain containing 4B	-1.91	11.88	12.81	0	0.06	1.70E-03	1.77E-02	Multiple_Complex
TC0100006840.hg.1	TARDBP	TAR DNA binding protein	-1.91	11.53	12.46	0.34	0.24	3.10E-03	2.51E-02	Multiple_Complex
TSUnmapped00000380.hg.1	FBL	fibrillarin	-1.91	13.08	14.01	0.08	0.35	5.20E-03	3.46E-02	Coding
TC1500008309.hg.1	ZNF774	zinc finger protein 774	-1.91	7.41	8.34	0.33	0.09	2.10E-03	2.02E-02	Multiple_Complex
TC0900008949.hg.1	NCS1	neuronal calcium sensor 1	-1.91	9.49	10.42	0.26	0.36	3.90E-03	2.92E-02	Multiple_Complex
TC1600008275.hg.1	SF3B3	splicing factor 3b subunit 3	-1.91	10.46	11.39	0.19	0.15	1.90E-03	1.89E-02	Multiple_Complex
TC1700012470.hg.1	H3F3B	H3 histone, family 3B (H3.3B)	-1.91	12.62	13.55	0.47	0.04	4.60E-03	3.21E-02	Multiple_Complex
TC1100007688.hg.1	ZDHHC5	zinc finger, DHHC-type containing 5	-1.91	9.92	10.85	0.19	0.23	2.00E-03	1.96E-02	Multiple_Complex
TC1200012862.hg.1	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	-1.91	9.47	10.4	0.4	0.13	3.80E-03	2.89E-02	Multiple_Complex
TC2200008300.hg.1	TFIP11	tuftelin interacting protein 11	-1.91	6.05	6.98	0.69	0.29	1.34E-02	6.51E-02	Multiple_Complex
TC0300010357.hg.1	CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	-1.91	10.03	10.96	0.09	0.05	3.00E-03	2.50E-02	Multiple_Complex
TC1600008971.hg.1	JMJD8	jumonji domain containing 8	-1.91	11.06	11.99	0.08	0.01	1.00E-03	1.40E-02	Multiple_Complex
TC0900011072.hg.1	ABCA1	ATP binding cassette subfamily A member 1	-1.91	7.67	8.6	0.01	0.11	9.70E-03	5.24E-02	Multiple_Complex
TC1100007819.hg.1	MYRF	myelin regulatory factor	-1.91	6.58	7.52	0.9	0.3	3.63E-02	1.26E-01	Multiple_Complex
TC1900009396.hg.1	LONP1	lon peptidase 1, mitochondrial	-1.91	8.74	9.67	0.19	0.28	2.10E-03	2.00E-02	Multiple_Complex
TC0500008308.hg.1	WDR36	WD repeat domain 36	-1.91	8.26	9.19	0.13	0.09	3.00E-03	2.49E-02	Multiple_Complex

TC1200010705.hg.1	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6	-1.91	8.19	9.13	0.55	0.32	7.40E-03	4.38E-02	Multiple_Complex
TC1200012646.hg.1	ESYT1	extended synaptotagmin-like protein 1	-1.91	8.3	9.24	0.49	0.32	6.40E-03	3.96E-02	Multiple_Complex
TC0700008560.hg.1	GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2	-1.91	10.04	10.98	0.1	0.24	1.50E-03	1.67E-02	Multiple_Complex
TC1300006919.hg.1	FREM2	FRAS1 related extracellular matrix protein 2	-1.91	7.93	8.87	0.26	0.58	1.15E-02	5.87E-02	Multiple_Complex
TC1500010888.hg.1	PARP6	poly(ADP-ribose) polymerase family member 6	-1.91	11.65	12.59	0.37	0.18	3.80E-03	2.86E-02	Multiple_Complex
TC1900010511.hg.1	POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	-1.91	10.14	11.07	0.28	0.08	2.00E-03	1.99E-02	Multiple_Complex
TC0500012163.hg.1	CDC23	cell division cycle 23	-1.92	8	8.94	0.62	0.78	3.59E-02	1.25E-01	Multiple_Complex
TC1900008989.hg.1	ZNF460	zinc finger protein 460	-1.92	10.62	11.56	0.06	0.2	1.10E-03	1.47E-02	Multiple_Complex
TC0X00008712.hg.1	MAMLD1	mastermind-like domain containing 1	-1.92	5.43	6.37	0.7	0.11	1.61E-02	7.36E-02	Multiple_Complex
TC2200007486.hg.1	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	-1.92	11.49	12.43	0.17	0.04	1.30E-03	1.59E-02	Multiple_Complex
TC1200007989.hg.1	TMEM5	transmembrane protein 5	-1.92	9.53	10.47	0.33	0.28	4.40E-03	3.15E-02	Multiple_Complex
TC1400009151.hg.1	TRIM9	tripartite motif containing 9	-1.92	6.78	7.72	0.71	0.75	3.31E-02	1.19E-01	Multiple_Complex
TC0800011479.hg.1	SYBU	syntabulin (syntaxin-interacting)	-1.92	5.36	6.3	0.21	0.41	7.10E-03	4.27E-02	Multiple_Complex
TC2000007915.hg.1	GNAS	GNAS complex locus	-1.92	12.3	13.24	0.05	0.22	1.80E-03	1.88E-02	Multiple_Complex
TC1900008059.hg.1	SUPT5H	SPT5 homolog, DSIF elongation factor subunit	-1.92	10.96	11.9	0.09	0.1	1.00E-03	1.39E-02	Multiple_Complex
TC2200009365.hg.1	CHKB	choline kinase beta	-1.92	7.37	8.31	0.22	0.7	1.64E-02	7.45E-02	Multiple_Complex
TC1900011682.hg.1	RAB8A	RAB8A, member RAS oncogene family	-1.92	10.22	11.17	0.15	0.11	1.50E-03	1.70E-02	Multiple_Complex
TC0100013548.hg.1	PUM1	pumilio RNA binding family member 1	-1.92	11.44	12.38	0.35	0.07	2.20E-03	2.08E-02	Multiple_Complex
TC1200009722.hg.1	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	-1.92	8.51	9.46	0.36	0.1	6.70E-03	4.08E-02	Multiple_Complex

TC0700010918.hg.1	NUDCD3	NudC domain containing 3	-1.92	9.32	10.27	0.17	0.34	4.90E-03	3.34E-02	Multiple_Complex
TC0900009909.hg.1	DCTN3	dynactin 3 (p22)	-1.92	14.14	15.08	0.26	0.15	2.70E-03	2.31E-02	Multiple_Complex
TC0900008337.hg.1	ZNF462	zinc finger protein 462	-1.92	6.01	6.95	0.2	0.14	1.40E-03	1.63E-02	Multiple_Complex
TC1600007191.hg.1	EEF2K	eukaryotic elongation factor 2 kinase	-1.92	6.66	7.6	0.14	0.1	1.80E-03	1.85E-02	Multiple_Complex
TC1900008992.hg.1	ZNF543	zinc finger protein 543	-1.92	8.62	9.57	0.38	0.15	3.00E-03	2.50E-02	Multiple_Complex
TC0700010910.hg.1	POLD2	polymerase (DNA directed), delta 2, accessory subunit	-1.92	10.27	11.21	0.09	0.42	2.80E-03	2.38E-02	Multiple_Complex
TC2000008473.hg.1	KIF16B	kinesin family member 16B	-1.92	6.3	7.24	0.87	0.04	3.94E-02	1.34E-01	Multiple_Complex
TSUnmapped00000608.hg.1	ZNF35	zinc finger protein 35	-1.92	5.48	6.43	0.3	0.37	3.80E-03	2.89E-02	Coding
TC2000007537.hg.1	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	-1.93	4.09	5.03	0.22	0.21	2.70E-03	2.36E-02	Multiple_Complex
TC0100010526.hg.1	TBX19	T-box 19	-1.93	5.53	6.47	0.59	0.01	1.12E-02	5.76E-02	Multiple_Complex
TC0300013854.hg.1	NXPE3	neurexophilin and PC-esterase domain family, member 3	-1.93	5.83	6.77	0.54	0.14	5.30E-03	3.51E-02	Multiple_Complex
TC0500009591.hg.1	FAF2	Fas associated factor family member 2	-1.93	13.27	14.22	0.13	0.02	1.00E-03	1.39E-02	Multiple_Complex
TC0X00007923.hg.1	CSTF2	cleavage stimulation factor, 3 pre-RNA, subunit 2	-1.93	7.66	8.61	0.33	0.07	1.90E-03	1.90E-02	Multiple_Complex
TC2000010027.hg.1	TMEM189-UBE2V1	TMEM189-UBE2V1 readthrough	-1.93	10.93	11.88	0.06	0.06	1.60E-03	1.72E-02	Multiple_Complex
TC0700013380.hg.1	ASL	argininosuccinate lyase	-1.93	6.29	7.24	0.57	0.08	1.87E-02	8.16E-02	Multiple_Complex
TC0500009211.hg.1	CYFIP2	cytoplasmic FMR1 interacting protein 2	-1.93	5.63	6.58	0.13	0.33	2.20E-03	2.06E-02	Multiple_Complex
TC2200007195.hg.1	HMGXB4	HMG box domain containing 4	-1.93	7.15	8.09	0.68	0.6	1.95E-02	8.37E-02	Multiple_Complex
TC1200012143.hg.1	CIT; MIR1178	citron rho-interacting serine/threonine kinase; microRNA 1178	-1.93	7.9	8.85	0.18	0.35	3.00E-03	2.49E-02	Multiple_Complex
TC1000006863.hg.1	RPP38	ribonuclease P/MRP 38kDa subunit	-1.93	9.82	10.76	0.01	0.47	3.50E-03	2.75E-02	Multiple_Complex
TC2000007089.hg.1	TPX2	TPX2, microtubule-associated	-1.93	12.13	13.08	0.17	0.06	1.00E-03	1.40E-02	Multiple_Complex

TC0100007638.hg.1	SERINC2	serine incorporator 2	-1.93	11.05	12	0.08	0.14	1.00E-03	1.40E-02	Multiple_Complex
TC0200016494.hg.1	CNNM4	cyclin and CBS domain divalent metal cation transport mediator 4	-1.93	9.16	10.11	0.13	0.13	3.80E-03	2.89E-02	Multiple_Complex
TC1400007732.hg.1	VASH1	vasohibin 1	-1.93	6.83	7.78	0.09	0.13	3.50E-03	2.73E-02	Multiple_Complex
TC0600014287.hg.1	MOCS1	molybdenum cofactor synthesis 1	-1.93	4.97	5.92	0.37	0.29	4.50E-03	3.20E-02	Multiple_Complex
TC2200007963.hg.1	DGCR2; DGCR11	DiGeorge syndrome critical region gene 2; DiGeorge syndrome critical region gene 11 (non-protein coding)	-1.93	7.97	8.92	0.47	0.28	5.30E-03	3.51E-02	Multiple_Complex
TC0100007958.hg.1	ZFP69B	ZFP69 zinc finger protein B	-1.93	5.88	6.83	0.88	0.09	2.58E-02	1.01E-01	Multiple_Complex
TC0600011809.hg.1	CCND3	cyclin D3	-1.93	10.92	11.87	0.11	0.11	1.70E-03	1.80E-02	Multiple_Complex
TC0700010035.hg.1	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	-1.93	7.63	8.59	0.26	0.12	1.50E-03	1.67E-02	Multiple_Complex
TC2000007243.hg.1	AAR2	AAR2 splicing factor homolog	-1.93	10.12	11.08	0.14	0.11	9.30E-03	5.08E-02	Multiple_Complex
TC1500008360.hg.1	SLCO3A1	solute carrier organic anion transporter family, member 3A1	-1.93	5.77	6.72	0.07	0.13	3.40E-03	2.68E-02	Multiple_Complex
TC2000008946.hg.1	GGT7	gamma-glutamyltransferase 7	-1.93	5.78	6.74	0.06	0.18	1.30E-03	1.59E-02	Multiple_Complex
TC1700010540.hg.1	PCGF2	polycomb group ring finger 2	-1.94	6.76	7.71	0.08	0.29	1.90E-03	1.93E-02	Coding
TC0100010806.hg.1	XPR1	xenotropic and polytropic retrovirus receptor 1	-1.94	9.7	10.66	0.55	0.14	6.50E-03	4.02E-02	Multiple_Complex
TC1900007396.hg.1	KXD1	KxDL motif containing 1	-1.94	12.96	13.91	0.3	0.03	1.90E-03	1.90E-02	Multiple_Complex
TC1600010651.hg.1	RANBP10	RAN binding protein 10	-1.94	9.2	10.15	0.08	0.06	1.32E-02	6.43E-02	Multiple_Complex
TC0100014048.hg.1	POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)	-1.94	9.39	10.35	0.17	0.36	2.80E-03	2.39E-02	Multiple_Complex
TC2000007507.hg.1	ZSWIM1	zinc finger, SWIM-type containing 1	-1.94	7.8	8.75	0.38	0.36	5.60E-03	3.66E-02	Multiple_Complex
TC0200008502.hg.1	NCAPH	non-SMC condensin I complex subunit H	-1.94	8.63	9.58	0.07	0.23	1.40E-03	1.64E-02	Multiple_Complex

TC0600014086.hg.1	ZNF391	zinc finger protein 391	-1.94	9.59	10.54	0.09	0.06	3.10E-03	2.55E-02	Multiple_Complex
TC0100011963.hg.1	SPRTN	SprT-like N-terminal domain	-1.94	9.92	10.87	0.12	0.36	3.40E-03	2.66E-02	Multiple_Complex
TC1900008432.hg.1	EHD2	EH domain containing 2	-1.94	8.66	9.61	0.47	0.29	4.70E-03	3.25E-02	Multiple_Complex
TC1900008042.hg.1	PAK4	p21 protein (Cdc42/Rac)-activated kinase 4	-1.94	7.99	8.94	0.07	0.05	3.80E-03	2.85E-02	Multiple_Complex
TC1200012723.hg.1	ZNF664	zinc finger protein 664	-1.94	6.01	6.96	0.32	0.17	7.40E-03	4.36E-02	Multiple_Complex
TC0700010185.hg.1	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	-1.94	13.76	14.71	0.01	0.08	8.00E-04	1.23E-02	Multiple_Complex
TC0700009886.hg.1	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	-1.94	7.5	8.46	0.27	0.19	2.10E-03	2.01E-02	Multiple_Complex
TC0500008863.hg.1	IK; MIR3655	IK cytokine, down-regulator of HLA II; microRNA 3655	-1.94	9.58	10.54	0.5	0.03	6.00E-03	3.80E-02	Multiple_Complex
TC1800006448.hg.1	TYMS	thymidylate synthetase	-1.94	11.61	12.57	0.14	0.32	2.60E-03	2.28E-02	Multiple_Complex
TC1500009457.hg.1	MYO5A	myosin VA	-1.94	5.81	6.77	0.37	0.11	3.00E-03	2.50E-02	Multiple_Complex
TC1200008931.hg.1	RITA1	RBPJ interacting and tubulin associated 1	-1.94	11.29	12.25	0.26	0.28	2.70E-03	2.36E-02	Coding
TC1900010045.hg.1	BORCS8; MEF2B; MEF2BNB-MEF2B	BLOC-1 related complex subunit 8; myocyte enhancer factor 2B; MEF2BNB-MEF2B readthrough	-1.94	8.52	9.48	0.21	0.26	2.40E-03	2.16E-02	Multiple_Complex
TC2200007811.hg.1	NCAPH2	non-SMC condensin II complex subunit H2	-1.94	6.81	7.77	0.13	0.13	2.00E-03	1.98E-02	Multiple_Complex
TC0200009299.hg.1	IMP4	IMP4 homolog, U3 small nucleolar ribonucleoprotein	-1.94	5.44	6.4	0.31	0.15	4.60E-03	3.23E-02	Multiple_Complex
TC1300008272.hg.1	LATS2	large tumor suppressor kinase 2	-1.94	6.77	7.73	0.61	0.95	3.76E-02	1.30E-01	Multiple_Complex
TC0200008065.hg.1	TET3	tet methylcytosine dioxygenase 3	-1.94	4.84	5.8	0.54	0.05	6.50E-03	4.03E-02	Multiple_Complex
TC0300008477.hg.1	TIMMDC1	translocase of inner mitochondrial membrane domain containing 1	-1.94	10.78	11.74	0.32	0	1.60E-03	1.74E-02	Multiple_Complex
TC0200016681.hg.1	WDR92	WD repeat domain 92	-1.94	6.74	7.7	0.11	0.21	1.30E-03	1.54E-02	Multiple_Complex
TC0100008079.hg.1	IPO13	importin 13	-1.94	8.64	9.6	0.41	0.11	2.70E-03	2.32E-02	Multiple_Complex

TC1700008232.hg.1	PDK2	pyruvate dehydrogenase kinase, isozyme 2	-1.94	7.92	8.88	0.11	0.59	6.90E-03	4.17E-02	Multiple_Complex
TC2200009347.hg.1	ANKRD54; MIR658	ankyrin repeat domain 54; microRNA 658	-1.94	6.28	7.24	0.04	0.04	1.37E-02	6.62E-02	Multiple_Complex
TC0300010664.hg.1	GLB1; TMPPE	galactosidase beta 1; transmembrane protein with metallophosphoesterase domain	-1.94	10.47	11.43	0.23	0.01	1.20E-03	1.50E-02	Multiple_Complex
TC1800007316.hg.1	SKA1	spindle and kinetochore associated complex subunit 1	-1.94	7.19	8.15	0.62	0.19	9.70E-03	5.22E-02	Multiple_Complex
TC1000008712.hg.1	PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	-1.94	8.75	9.7	0.16	0	2.20E-03	2.09E-02	Multiple_Complex
TC0600013574.hg.1	RMND1	required for meiotic nuclear division 1 homolog	-1.94	8.81	9.77	0.11	0.09	1.10E-03	1.48E-02	Multiple_Complex
TC0900011980.hg.1	SEC16A	SEC16 homolog A, endoplasmic reticulum export factor	-1.95	6.47	7.43	0.31	0.03	2.60E-03	2.28E-02	Multiple_Complex
TC1200010653.hg.1	CERS5	ceramide synthase 5	-1.95	10.88	11.84	0.04	0.34	2.70E-03	2.34E-02	Multiple_Complex
TC0900009268.hg.1	NDOR1	NADPH dependent diflavin oxidoreductase 1	-1.95	7.57	8.53	0.92	0.2	2.40E-02	9.65E-02	Multiple_Complex
TSUnmapped00000106.hg.1	LRP6	LDL receptor related protein 6	-1.95	8.28	9.24	0.16	0.01	9.00E-04	1.31E-02	NonCoding
TC0900007117.hg.1	CLTA	clathrin, light chain A	-1.95	12.92	13.88	0.11	0.15	9.00E-04	1.32E-02	Multiple_Complex
TC0500006730.hg.1	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	-1.95	14.25	15.21	0.45	0.04	2.50E-03	2.26E-02	Multiple_Complex
TC0800006978.hg.1	POLR3D	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	-1.95	6.65	7.61	0.25	0.09	2.60E-03	2.30E-02	Multiple_Complex
TC1800008779.hg.1	NARS	asparaginyl-tRNA synthetase	-1.95	7.32	8.28	0.49	0.08	8.60E-03	4.86E-02	Multiple_Complex
TC1100008270.hg.1	CTTN	cortactin	-1.95	8	8.97	0.05	0.21	1.40E-03	1.64E-02	Multiple_Complex
TC0700013460.hg.1	METTL2B	methyltransferase like 2B	-1.95	11.19	12.16	0.56	0.19	4.90E-03	3.36E-02	Multiple_Complex
TC0X00006483.hg.1	GYG2	glycogenin 2	-1.95	5.77	6.73	0.1	0.09	1.90E-03	1.89E-02	Multiple_Complex
TC1400009649.hg.1	NUMB	numb homolog (Drosophila)	-1.95	11.13	12.09	0.03	0.15	8.00E-04	1.27E-02	Multiple_Complex

TC0X00008759.hg.1	NSDHL	NAD(P) dependent steroid dehydrogenase-like	-1.95	9.81	10.77	0.21	0.18	1.90E-03	1.90E-02	Multiple_Complex
TC1600008963.hg.1	C16orf13	chromosome 16 open reading frame 13	-1.95	11.37	12.34	0.32	0.23	2.70E-03	2.36E-02	Multiple_Complex
TC0X00007148.hg.1	ARAF	A-Raf proto-oncogene, serine/threonine kinase	-1.95	10.93	11.89	0.06	0.12	1.30E-03	1.55E-02	Multiple_Complex
TC0800012305.hg.1	MTFR1	mitochondrial fission regulator 1	-1.95	10.27	11.23	0.58	0.11	5.50E-03	3.59E-02	Multiple_Complex
TC1700010221.hg.1	DHRS13	dehydrogenase/reductase (SDR family) member 13	-1.95	5.72	6.69	0.75	0.47	2.56E-02	1.01E-01	Multiple_Complex
TC0100008347.hg.1	CPT2	carnitine palmitoyltransferase 2	-1.95	5.94	6.9	0.18	0.17	5.80E-03	3.74E-02	Multiple_Complex
TC1100009618.hg.1	GLB1L2	galactosidase beta 1 like 2	-1.95	8.39	9.35	0.09	0.07	3.40E-03	2.66E-02	Multiple_Complex
TC1300008080.hg.1	TUBGCP3	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_006322	-1.95	7.41	8.38	0.29	0.27	6.70E-03	4.09E-02	NonCoding
TC0100006806.hg.1	UBE4B	ubiquitination factor E4B	-1.95	8.36	9.32	0.31	0.11	2.20E-03	2.08E-02	Multiple_Complex
TC1200007892.hg.1	ARHGEF25	Rho guanine nucleotide exchange factor 25	-1.95	8.75	9.71	0.92	0.08	2.18E-02	9.00E-02	Multiple_Complex
TC0600011127.hg.1	HIST1H1C	histone cluster 1, H1c	-1.95	10.29	11.26	0.42	0.28	3.30E-03	2.62E-02	Multiple_Complex
TC0200007054.hg.1	ABHD1	abhydrolase domain containing 1	-1.95	4.6	5.56	0.08	0.18	1.97E-02	8.41E-02	Multiple_Complex
TC1600011428.hg.1	TERF2IP	telomeric repeat binding factor 2, interacting protein	-1.96	10.81	11.78	0.1	0.02	8.00E-04	1.25E-02	Coding
TC1700007102.hg.1	ALKBH5	alkB homolog 5, RNA demethylase	-1.96	10.03	11	0.52	0.12	3.80E-03	2.88E-02	Multiple_Complex
TC2200007776.hg.1	ZBED4	zinc finger, BED-type containing 4	-1.96	6.71	7.67	0.13	0.13	1.90E-03	1.89E-02	Coding
TC1700010811.hg.1	HDAC5	histone deacetylase 5	-1.96	8.32	9.29	0.22	0.32	2.10E-03	2.04E-02	Multiple_Complex
TC0X00011209.hg.1	FAM3A	family with sequence similarity 3, member A	-1.96	8.06	9.03	0.17	0.28	4.30E-03	3.12E-02	Multiple_Complex
TSUnmapped00000502.hg.1	MLXIP	MLX interacting protein	-1.96	8.95	9.92	0.04	0.35	4.60E-03	3.23E-02	NonCoding
TC1700007982.hg.1	C17orf53	chromosome 17 open reading frame 53	-1.96	10.9	11.87	0.6	0.19	5.60E-03	3.66E-02	Multiple_Complex
TC1100008012.hg.1	DPF2	D4, zinc and double PHD fingers family 2	-1.96	12.69	13.66	0.27	0.17	2.00E-03	1.96E-02	Multiple_Complex

TSUnmapped00000336.hg.1	RCC2	regulator of chromosome condensation 2	-1.96	9.67	10.64	0.18	0.03	9.00E-04	1.34E-02	Coding
TC0X00011277.hg.1	CA5B	carbonic anhydrase VB, mitochondrial	-1.96	10.97	11.94	0.48	0.03	5.90E-03	3.77E-02	Multiple_Complex
TC1300008359.hg.1	PARP4	poly(ADP-ribose) polymerase family member 4	-1.96	6.52	7.49	0.07	0.24	2.20E-03	2.09E-02	Multiple_Complex
TC1100011643.hg.1	ARRB1	arrestin, beta 1	-1.96	8.08	9.05	0.03	0.15	1.50E-03	1.70E-02	Multiple_Complex
TC1800009280.hg.1	HDHD2	haloacid dehalogenase-like hydrolase domain containing 2	-1.96	5.07	6.04	0.36	0.44	5.00E-03	3.40E-02	Multiple_Complex
TC1700008372.hg.1	SCPEP1	serine carboxypeptidase 1	-1.96	8.57	9.54	0.24	0.03	1.90E-03	1.91E-02	Multiple_Complex
TC0100007556.hg.1	PHACTR4	phosphatase and actin regulator 4	-1.96	10.54	11.51	0.22	0.16	1.40E-03	1.62E-02	Multiple_Complex
TC0400009038.hg.1	KIAA0922	KIAA0922	-1.96	7.64	8.61	0.04	0.12	1.40E-03	1.60E-02	Multiple_Complex
TC0700013391.hg.1	NSUN5P1	NOP2/Sun domain family, member 5 pseudogene 1	-1.96	6.66	7.63	0.42	0.04	5.60E-03	3.64E-02	Multiple_Complex
TC0200010788.hg.1	ARPC2	actin related protein 2/3 complex subunit 2	-1.96	11.11	12.08	0.69	0.1	1.03E-02	5.44E-02	Multiple_Complex
TC0300013864.hg.1	PDIA5; MIR7110	protein disulfide isomerase family A, member 5; microRNA 7110	-1.96	8.86	9.83	0.3	0.17	2.10E-03	2.00E-02	Multiple_Complex
TC1900009001.hg.1	ZIK1	zinc finger protein interacting with K protein 1	-1.96	4.44	5.41	0.29	0.05	8.80E-03	4.93E-02	Multiple_Complex
TC1700007519.hg.1	PSMD11	proteasome 26S subunit, non-ATPase 11	-1.96	8.99	9.97	0.35	0.18	3.10E-03	2.53E-02	Multiple_Complex
TC1200007861.hg.1	LRP1	LDL receptor related protein 1	-1.96	8.63	9.61	0.33	0.04	1.60E-03	1.76E-02	Multiple_Complex
TC0800007414.hg.1	GOLGA7	golgin A7	-1.96	12.02	12.99	0.07	0.02	1.90E-03	1.92E-02	Multiple_Complex
TC0300007409.hg.1	SLC38A3	solute carrier family 38, member 3	-1.96	5.89	6.86	0.14	0.17	1.30E-03	1.59E-02	Multiple_Complex
TC2200008134.hg.1	ZNF280B	zinc finger protein 280B	-1.96	10.63	11.6	0.07	0.13	1.20E-03	1.48E-02	Multiple_Complex
TC1200012835.hg.1	NT5DC3	5-nucleotidase domain containing 3	-1.96	8.81	9.79	0.21	0	2.50E-03	2.21E-02	Multiple_Complex
TC0100017446.hg.1	SUSD4	sushi domain containing 4	-1.96	9.59	10.57	0.04	0.01	4.05E-02	1.36E-01	Multiple_Complex
TC0700009079.hg.1	TSPAN33	tetraspanin 33	-1.96	8.49	9.46	0.06	0.36	3.00E-03	2.48E-02	Multiple_Complex

TC0900008899.hg.1	DOLPP1	dolichyldiphosphatase 1	-1.96	7.89	8.86	0.2	0.35	5.00E-03	3.41E-02	Multiple_Complex
TC1100013032.hg.1	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	-1.96	9.77	10.74	0.11	0.25	3.00E-03	2.48E-02	Multiple_Complex
TC1600011045.hg.1	MBTPS1	membrane bound transcription factor peptidase, site 1	-1.96	10.78	11.75	0.07	0.18	1.90E-03	1.89E-02	Multiple_Complex
TC2200008856.hg.1	NAGA	N-acetylgalactosaminidase, alpha-	-1.97	5.82	6.8	0.11	0.68	8.20E-03	4.70E-02	Multiple_Complex
TC0900009276.hg.1	NELFB	negative elongation factor complex member B	-1.97	9.01	9.99	0.07	0.03	7.00E-04	1.21E-02	Multiple_Complex
TC1900011941.hg.1	HNRNPL	heterogeneous nuclear ribonucleoprotein L	-1.97	13.15	14.13	0.12	0.1	8.00E-04	1.28E-02	Multiple_Complex
TC2200008036.hg.1	USP41	ubiquitin specific peptidase 41	-1.97	11.91	12.89	0.58	0.15	7.80E-03	4.54E-02	Multiple_Complex
TC0900010588.hg.1	HNRNPK; MIR7-1	heterogeneous nuclear ribonucleoprotein K; microRNA 7-1	-1.97	13.25	14.23	0.25	0.08	1.30E-03	1.57E-02	Multiple_Complex
TC0500010394.hg.1	DROSHA	drosha, ribonuclease type III	-1.97	9.36	10.33	0.25	0.16	1.30E-03	1.55E-02	Multiple_Complex
TC1700009809.hg.1	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	-1.97	6.29	7.27	0.18	0.27	2.90E-03	2.44E-02	Coding
TC1200010833.hg.1	CBX5; MIR3198-2	chromobox homolog 5; microRNA 3198-2	-1.97	13.7	14.68	0.09	0.09	9.00E-04	1.33E-02	Multiple_Complex
TC1100013173.hg.1	C11orf98; LBHD1	chromosome 11 open reading frame 98; LBH domain containing 1	-1.97	12.89	13.87	0.07	0.16	8.00E-04	1.25E-02	Multiple_Complex
TC0200015720.hg.1	AAMP	angio-associated migratory cell protein	-1.97	7.45	8.43	0.25	0.09	3.50E-03	2.73E-02	Multiple_Complex
TC1700010076.hg.1	USP22	ubiquitin specific peptidase 22	-1.97	13.04	14.02	0.22	0.24	1.60E-03	1.75E-02	Multiple_Complex
TC1900006528.hg.1	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	-1.97	7.38	8.36	0.48	0.72	1.81E-02	7.97E-02	Multiple_Complex
TC1900009740.hg.1	DHPS	deoxyhypusine synthase	-1.97	10.55	11.53	0.4	0.03	3.30E-03	2.65E-02	Multiple_Complex
TC2200007952.hg.1	CLTCL1	clathrin, heavy chain-like 1	-1.97	7.7	8.68	0.63	0.08	9.90E-03	5.31E-02	Multiple_Complex
TC1200010577.hg.1	ZNF641	zinc finger protein 641	-1.97	5.16	6.14	0.1	0.03	2.30E-03	2.12E-02	Multiple_Complex
TC1600010628.hg.1	ZDHHC1	zinc finger, DHHC-type containing 1	-1.97	4.56	5.54	0.44	0.57	1.32E-02	6.44E-02	Multiple_Complex

TC1600010765.hg.1	COG4	component of oligomeric golgi complex 4	-1.97	5.55	6.53	0.46	0.48	6.60E-03	4.04E-02	Multiple_Complex
TC0300013949.hg.1	SATB1	SATB homeobox 1	-1.97	9.5	10.48	0.09	0.07	1.10E-03	1.48E-02	Multiple_Complex
TC0100018502.hg.1	GBA	glucosidase, beta, acid	-1.97	8.9	9.88	0.68	0.33	1.11E-02	5.73E-02	Multiple_Complex
TC0900006937.hg.1	ACO1	aconitase 1, soluble	-1.97	9.05	10.03	0.15	0.11	1.10E-03	1.43E-02	Multiple_Complex
TC0800008674.hg.1	DEPTOR	DEP domain containing MTOR-interacting protein	-1.97	3.97	4.95	0.21	0.39	6.20E-03	3.89E-02	Multiple_Complex
TC1700006775.hg.1	CHD3	chromodomain helicase DNA binding protein 3	-1.97	8.9	9.88	0.11	0.03	8.00E-04	1.28E-02	Multiple_Complex
TC0800009301.hg.1	C8orf33	chromosome 8 open reading frame 33	-1.97	11.52	12.5	0.24	0.22	1.90E-03	1.90E-02	Multiple_Complex
TC0100013760.hg.1	SF3A3	splicing factor 3a subunit 3	-1.97	10.75	11.74	0.39	0.07	2.20E-03	2.10E-02	Multiple_Complex
TC0700013509.hg.1	DAGLB	diacylglycerol lipase, beta	-1.98	10.19	11.17	0.22	0.03	1.30E-03	1.57E-02	Multiple_Complex
TC1000007954.hg.1	SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter), member 3	-1.98	4.85	5.83	0.46	0.13	9.90E-03	5.31E-02	Multiple_Complex
TC1900011033.hg.1	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	-1.98	9.35	10.33	0.13	0.2	9.00E-04	1.34E-02	Multiple_Complex
TC2200009186.hg.1	PEX26	peroxisomal biogenesis factor 26	-1.98	8.18	9.16	0.6	0.05	4.60E-03	3.24E-02	Multiple_Complex
TC1900009670.hg.1	DOCK6	dedicator of cytokinesis 6	-1.98	7.59	8.58	0.08	0.36	3.10E-03	2.52E-02	Multiple_Complex
TC2200007324.hg.1	MICALL1	MICAL-like 1	-1.98	6.81	7.79	0.37	0.2	5.00E-03	3.38E-02	Multiple_Complex
TC0100015916.hg.1	IL6R	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_000565	-1.98	6.72	7.7	1.18	0.03	4.82E-02	1.53E-01	NonCoding
TC0500007682.hg.1	GTF2H2C_2; GTF2H2C; GTF2H2B	GTF2H2 family member C, copy 2; GTF2H2 family member C; general transcription factor IIH subunit 2B (pseudogene)	-1.98	10.99	11.97	0.29	0.14	1.80E-03	1.85E-02	Multiple_Complex
TC1000012490.hg.1	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	-1.98	7.42	8.41	0.09	0.06	1.00E-03	1.39E-02	Multiple_Complex
TC0900012135.hg.1	ANKRD20A4	ankyrin repeat domain 20 family, member A4	-1.98	6.05	7.04	0.17	0.24	1.30E-03	1.59E-02	Multiple_Complex
TC2200006607.hg.1	CDC45	cell division cycle 45	-1.98	9.92	10.91	0.53	0.07	1.00E-02	5.34E-02	Multiple_Complex

TC0100016649.hg.1	NMNAT2	nicotinamide nucleotide adenylyltransferase 2	-1.98	6.12	7.1	0.07	0.32	1.40E-03	1.64E-02	Multiple_Complex
TC0200014288.hg.1	FAM168B	family with sequence similarity 168, member B	-1.98	8.86	9.84	0.39	0.16	3.20E-03	2.58E-02	Multiple_Complex
TC0100008375.hg.1	TCEANC2; MIR4781	transcription elongation factor A (SII) N-terminal and central domain containing 2; microRNA 4781	-1.98	8.61	9.59	0.15	0.02	1.30E-03	1.55E-02	Multiple_Complex
TC0100018443.hg.1	PLPP3	phospholipid phosphatase 3	-1.98	7.69	8.67	0.68	0.2	1.00E-02	5.34E-02	Multiple_Complex
TC0100011566.hg.1	PROX1	prospero homeobox 1	-1.98	5.48	6.47	0.48	0.13	3.10E-03	2.54E-02	Multiple_Complex
TC1600006488.hg.1	STUB1	STIP1 homology and U-box containing protein 1, E3 ubiquitin protein ligase	-1.98	9.86	10.85	0.1	0.04	7.00E-04	1.17E-02	Multiple_Complex
TC0100007668.hg.1	TXLNA	taxilin alpha	-1.98	8.24	9.23	0.21	0.29	1.90E-03	1.89E-02	Multiple_Complex
TC0700013290.hg.1	NCAPG2	non-SMC condensin II complex subunit G2	-1.98	7.66	8.65	0.41	0.22	3.10E-03	2.51E-02	Multiple_Complex
TC1900006628.hg.1	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	-1.98	8.94	9.93	0.79	0.18	1.44E-02	6.84E-02	Multiple_Complex
TC0900008150.hg.1	TMOD1	tropomodulin 1	-1.98	8.16	9.14	0.25	0.04	2.10E-03	2.00E-02	Multiple_Complex
TC0200012299.hg.1	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	-1.98	9.41	10.39	0.51	0.11	7.20E-03	4.30E-02	Multiple_Complex
TC1100009709.hg.1	CHID1	chitinase domain containing 1	-1.98	5.72	6.71	0.17	0.28	1.70E-03	1.83E-02	Multiple_Complex
TC0700008552.hg.1	AGFG2	ArfGAP with FG repeats 2	-1.98	7.13	8.12	0.78	0.49	1.79E-02	7.92E-02	Multiple_Complex
TC0400009704.hg.1	CPLX1	complexin 1	-1.98	4.99	5.98	0.09	0	7.00E-04	1.17E-02	Multiple_Complex
TC0200010577.hg.1	ADAM23	ADAM metallopeptidase domain 23	-1.98	6.66	7.65	0.54	0.21	6.00E-03	3.83E-02	Multiple_Complex
TC0400006639.hg.1	NSG1; D4S234E	neuron specific gene family member 1; Neuron-specific protein family member 1 [Source:UniProtKB/Swiss-Prot;Acc:P42857]	-1.98	7.22	8.21	0.15	0.08	1.00E-02	5.34E-02	Multiple_Complex
TC0300012145.hg.1	FSTL1; MIR198	follistatin like 1; microRNA 198	-1.98	9.54	10.53	0.09	0.09	7.10E-03	4.24E-02	Multiple_Complex
TC0300007065.hg.1	DLEC1	deleted in lung and esophageal cancer 1	-1.98	5.35	6.34	0.17	0.56	4.30E-03	3.12E-02	Multiple_Complex

TC0700008072.hg.1	RHBDD2	rhomboid domain containing 2	-1.98	10.07	11.06	0.17	0.44	2.60E-03	2.27E-02	Multiple_Complex
TC1700007899.hg.1	MLX	MLX, MAX dimerization protein	-1.99	9.23	10.22	0.91	0.38	2.34E-02	9.47E-02	Multiple_Complex
TC1400008590.hg.1	OSGEP	O-sialoglycoprotein endopeptidase	-1.99	9.08	10.07	0.04	0.35	1.50E-03	1.68E-02	Multiple_Complex
TC0500009587.hg.1	HIGD2A	HIG1 hypoxia inducible domain family, member 2A	-1.99	8.34	9.33	0.37	0.69	1.32E-02	6.44E-02	Multiple_Complex
TC1900011641.hg.1	OAZ1	ornithine decarboxylase antizyme 1	-1.99	13.81	14.8	0.33	0.04	1.40E-03	1.61E-02	Multiple_Complex
TC1200009177.hg.1	TMEM120B	transmembrane protein 120B	-1.99	6.28	7.27	0.24	0.18	2.80E-03	2.37E-02	Multiple_Complex
TC0100010152.hg.1	LMNA	lamin A/C	-1.99	7.62	8.61	0.45	0.17	1.19E-02	6.00E-02	Multiple_Complex
TC0100014274.hg.1	PARS2	prolyl-tRNA synthetase 2, mitochondrial (putative)	-1.99	8.08	9.07	0.03	0.27	2.90E-03	2.45E-02	Coding
TC0900009932.hg.1	STOML2	stomatin (EPB72)-like 2	-1.99	13.45	14.44	0.05	0.06	7.00E-04	1.17E-02	Multiple_Complex
TC1400010012.hg.1	LGMN	legumain	-1.99	11.55	12.54	0.19	0	3.00E-03	2.50E-02	Multiple_Complex
TC1200006555.hg.1	CCND2	cyclin D2	-1.99	13.16	14.15	0.09	0.06	2.10E-03	2.04E-02	Multiple_Complex
TC1400008214.hg.1	WDR25	WD repeat domain 25	-1.99	6	7	0.7	0.22	1.36E-02	6.57E-02	Multiple_Complex
TC0600010002.hg.1	SYNJ2	synaptojanin 2	-1.99	5.87	6.86	0.44	0.17	1.21E-02	6.09E-02	Multiple_Complex
TC2000008023.hg.1	SLCO4A1	solute carrier organic anion transporter family, member 4A1	-1.99	4.59	5.58	0.74	0.11	2.35E-02	9.50E-02	Multiple_Complex
TC2200008181.hg.1	ZNF70	zinc finger protein 70	-1.99	8.61	9.61	0.02	0.11	2.30E-03	2.13E-02	Multiple_Complex
TC1800006506.hg.1	MYL12A	myosin light chain 12A	-1.99	12.12	13.12	0.3	0.3	3.10E-03	2.54E-02	Multiple_Complex
TC1600011521.hg.1	ZNF768	zinc finger protein 768	-1.99	9.89	10.88	0.2	0.06	3.40E-03	2.68E-02	Coding
TC0200009616.hg.1	KIF5C	kinesin family member 5C	-1.99	10.33	11.32	0.43	0.26	4.30E-03	3.12E-02	Multiple_Complex
TC1300008144.hg.1	TFDP1	transcription factor Dp-1	-1.99	10.05	11.05	0.38	0.05	2.00E-03	1.95E-02	Multiple_Complex
TC1200006737.hg.1	PHC1	polyhomeotic homolog 1 (Drosophila)	-1.99	9.18	10.18	0.21	0.06	3.30E-03	2.63E-02	Multiple_Complex
TC0100006483.hg.1	ISG15	ISG15 ubiquitin-like modifier	-1.99	7.68	8.67	0.06	0.23	1.20E-03	1.49E-02	Multiple_Complex

TC0X00010989.hg.1	LDOC1	leucine zipper, down-regulated in cancer 1	-1.99	8.83	9.82	0.07	0.36	2.10E-03	2.01E-02	Multiple_Complex
TC1100012520.hg.1	MCAM; MIR6756	melanoma cell adhesion molecule; microRNA 6756	-1.99	5.41	6.41	0.5	0.13	3.40E-03	2.69E-02	Multiple_Complex
TC1600008034.hg.1	NDRG4	NDRG family member 4	-1.99	8.23	9.23	0.45	0.28	1.15E-02	5.88E-02	Multiple_Complex
TC1400008637.hg.1	SALL2	spalt-like transcription factor 2	-1.99	7.12	8.11	0.27	0.09	1.70E-03	1.78E-02	Multiple_Complex
TC1900008036.hg.1	MRPS12	mitochondrial ribosomal protein S12	-1.99	6.37	7.36	0.33	0.71	1.32E-02	6.44E-02	Multiple_Complex
TC0500013089.hg.1	GFPT2	glutamine-fructose-6-phosphate transaminase 2	-1.99	7.83	8.82	0.21	0.58	7.20E-03	4.30E-02	Multiple_Complex
TC0900008742.hg.1	ARPC5L	actin related protein 2/3 complex subunit 5-like	-1.99	7.75	8.74	0.13	0.05	8.00E-04	1.25E-02	Multiple_Complex
TC1600011315.hg.1	FAM234A; ARHGDIG	family with sequence similarity 234, member A; Rho GDP dissociation inhibitor (GDI) gamma	-1.99	12.06	13.06	0.14	0.06	2.10E-03	2.01E-02	Multiple_Complex
TC1200012730.hg.1	PXMP2	peroxisomal membrane protein 2	-1.99	9.2	10.2	0.14	0.12	8.00E-04	1.23E-02	Multiple_Complex
TC0500009629.hg.1	TMED9	transmembrane p24 trafficking protein 9	-1.99	11.51	12.51	0.03	0.05	7.00E-04	1.17E-02	Multiple_Complex
TSUnmapped00000300.hg.1	HYOU1	hypoxia up-regulated 1	-1.99	12.65	13.65	0.28	0.05	1.20E-03	1.49E-02	Coding
TC0500013429.hg.1	RNF130	ring finger protein 130	-1.99	11.63	12.63	0.1	0.2	8.00E-04	1.24E-02	Multiple_Complex
TC1600006574.hg.1	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	-1.99	13.2	14.19	0.26	0.2	1.30E-03	1.57E-02	Multiple_Complex
TC0400012891.hg.1	NELFA; MIR943	negative elongation factor complex member A; microRNA 943	-1.99	13.01	14.01	0.1	0.29	1.10E-03	1.44E-02	Multiple_Complex
TC0200015608.hg.1	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	-1.99	7.19	8.19	0.69	0.24	9.80E-03	5.28E-02	Multiple_Complex
TC0300006552.hg.1	MTMR14	myotubularin related protein 14	-2	11.48	12.47	0	0.05	1.10E-03	1.44E-02	Multiple_Complex
TC0300006579.hg.1	VHL	von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase	-2	8.1	9.09	0.06	0.12	1.60E-03	1.73E-02	Multiple_Complex
TC0600007480.hg.1	HLA-F	major histocompatibility complex, class I, F	-2	10.85	11.84	0.43	0.25	3.20E-03	2.55E-02	Multiple_Complex

TC1700007599.hg.1	AP2B1	adaptor-related protein complex 2, beta 1 subunit	-2	10.05	11.05	0.04	0.01	1.10E-03	1.47E-02	Multiple_Complex
TC1600011577.hg.1	C16orf95	chromosome 16 open reading frame 95	-2	9.16	10.15	0.59	0.66	2.08E-02	8.74E-02	Multiple_Complex
TC1200006640.hg.1	COPS7A	COP9 signalosome subunit 7A	-2	7.2	8.2	0.52	0.17	5.80E-03	3.73E-02	Multiple_Complex
TC0100017018.hg.1	ETNK2	ethanolamine kinase 2	-2	11.27	12.27	0.67	0.05	1.48E-02	6.96E-02	Multiple_Complex
TSUnmapped00000138.hg.1	HYOU1	hypoxia up-regulated 1	-2	11.67	12.67	0.33	0.07	1.60E-03	1.74E-02	Coding
TC0200008655.hg.1	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	-2	7	7.99	0.43	0.31	9.80E-03	5.27E-02	Multiple_Complex
TC0200016610.hg.1	CAPN10	calpain 10	-2	7.13	8.13	0.19	0.13	1.20E-03	1.50E-02	Multiple_Complex
TC1900010050.hg.1	SUGP1	SURP and G-patch domain containing 1	-2	9.98	10.98	0.03	0.03	6.00E-04	1.13E-02	Multiple_Complex
TC0100007160.hg.1	MRTO4	MRT4 homolog, ribosome maturation factor	-2	6.39	7.38	0.12	0.49	4.60E-03	3.23E-02	Multiple_Complex
TC0300010240.hg.1	SEC13	SEC13 homolog, nuclear pore and COPII coat complex component	-2	9.28	10.28	0.06	0.31	1.09E-02	5.69E-02	Multiple_Complex
TC1900008103.hg.1	PLD3	phospholipase D family, member 3	-2	11.28	12.28	0.04	0.16	7.00E-04	1.16E-02	Multiple_Complex
TC0600007847.hg.1	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	-2	7.46	8.46	0.28	0.46	3.00E-03	2.50E-02	Multiple_Complex
TC2200009366.hg.1	CHKB-CPT1B	CHKB-CPT1B readthrough (NMD candidate)	-2	5.92	6.92	0.62	0.07	5.40E-03	3.56E-02	Multiple_Complex
TC0700013413.hg.1	TRRAP	transformation/transcription domain-associated protein	-2	9.8	10.8	0.24	0.05	1.60E-03	1.74E-02	Multiple_Complex
TC1900012016.hg.1	ETFB	electron-transfer-flavoprotein, beta polypeptide	-2	12.42	13.42	0.15	0.13	1.00E-03	1.40E-02	Multiple_Complex
TC0900008483.hg.1	SLC31A1	solute carrier family 31 (copper transporter), member 1	-2	12.5	13.5	0.1	0	7.00E-04	1.18E-02	Multiple_Complex
TC1300008918.hg.1	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	-2	7.57	8.57	0.46	0.24	5.90E-03	3.79E-02	Multiple_Complex
TC1700009541.hg.1	CAMTA2	calmodulin binding transcription activator 2	-2	9.3	10.3	0.33	0.45	5.30E-03	3.52E-02	Multiple_Complex

TC0200016366.hg.1	THAP4	THAP domain containing 4	-2	10.56	11.57	0.1	0.11	7.00E-04	1.19E-02	Multiple_Complex
TC1200009160.hg.1	P2RX4	purinergic receptor P2X, ligand gated ion channel, 4	-2	6.14	7.14	0.28	0.25	3.40E-03	2.66E-02	Multiple_Complex
TC1200012145.hg.1	RAB35	RAB35, member RAS oncogene family	-2	5.87	6.87	0.03	0.34	2.60E-03	2.30E-02	Multiple_Complex
TC0600014320.hg.1	TBX18	T-box 18	-2	5.56	6.56	0.06	0.44	2.00E-03	1.98E-02	Multiple_Complex
TC1000011683.hg.1	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	-2	12.77	13.77	0.21	0.05	8.00E-04	1.25E-02	Multiple_Complex
TC1100013190.hg.1	CFL1	cofilin 1 (non-muscle)	-2	13.87	14.88	0.12	0.04	7.00E-04	1.17E-02	Multiple_Complex
TC1900008420.hg.1	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-2	5.66	6.66	0.28	0.38	3.90E-03	2.94E-02	Multiple_Complex
TC0700011495.hg.1	TBL2	transducin (beta)-like 2	-2	10.45	11.45	0.16	0.13	3.50E-03	2.74E-02	Multiple_Complex
TC1700008095.hg.1	LRRC37A	leucine rich repeat containing 37A	-2	10.86	11.86	0.48	0.2	6.20E-03	3.89E-02	Multiple_Complex
TC1000011501.hg.1	TCTN3	tectonic family member 3	-2	11.37	12.37	0.08	0.09	9.00E-04	1.32E-02	Multiple_Complex
TC0X00007129.hg.1	UBA1	ubiquitin-like modifier activating enzyme 1	-2.01	9.41	10.41	0.21	0.04	8.00E-04	1.26E-02	Multiple_Complex
TC1700007080.hg.1	RAI1	retinoic acid induced 1	-2.01	6.34	7.35	1.14	0.04	3.32E-02	1.20E-01	Multiple_Complex
TC1500009753.hg.1	OAZ2	ornithine decarboxylase antizyme 2	-2.01	8.52	9.53	0.14	0.02	1.10E-03	1.45E-02	Multiple_Complex
TSUnmapped00000038.hg.1	ZNF780A	zinc finger protein 780A	-2.01	5.43	6.44	0.09	0.3	1.60E-03	1.73E-02	Coding
TC1200007891.hg.1	DTX3	deltex 3, E3 ubiquitin ligase	-2.01	6.64	7.64	0.13	0.19	1.12E-02	5.77E-02	Multiple_Complex
TC0700009236.hg.1	CALD1	caldesmon 1	-2.01	7.63	8.63	0.18	0.25	1.10E-03	1.45E-02	Multiple_Complex
TC0600007832.hg.1	BRPF3	bromodomain and PHD finger containing 3	-2.01	7.39	8.39	0.28	0.06	9.00E-04	1.34E-02	Multiple_Complex
TC0600010343.hg.1	TBP	TATA box binding protein	-2.01	10.16	11.16	0.12	0.09	6.00E-04	1.13E-02	Multiple_Complex
TC0200016772.hg.1	NHEJ1	nonhomologous end-joining factor 1	-2.01	8.75	9.76	0.17	0.16	1.10E-03	1.48E-02	Multiple_Complex
TC1600009951.hg.1	TBX6	T-box 6	-2.01	4.87	5.88	0.17	0.05	1.20E-03	1.52E-02	Multiple_Complex

TC0900009931.hg.1	PIGO	phosphatidylinositol glycan anchor biosynthesis class O	-2.01	7.64	8.65	0.18	0.27	1.20E-03	1.50E-02	Multiple_Complex
TC1500006956.hg.1	BAHD1	bromo adjacent homology domain containing 1	-2.01	7.29	8.29	0.08	0.07	2.60E-03	2.29E-02	Multiple_Complex
TC2000009956.hg.1	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-2.01	9.96	10.97	0.25	0.27	1.50E-03	1.70E-02	Multiple_Complex
TC0100009366.hg.1	STRIP1	striatin interacting protein 1	-2.01	9.32	10.33	0.38	0.17	2.20E-03	2.06E-02	Multiple_Complex
TC1900006605.hg.1	ZNF57	zinc finger protein 57	-2.01	10.77	11.78	0.3	0.29	3.90E-03	2.94E-02	Coding
TC0X00008027.hg.1	ZCCHC18	zinc finger, CCHC domain containing 18	-2.01	5.16	6.17	0.37	0.22	2.30E-03	2.11E-02	Multiple_Complex
TC1900007176.hg.1	PKN1	protein kinase N1	-2.01	9.28	10.29	0.61	0.14	4.40E-03	3.15E-02	Multiple_Complex
TC2200009272.hg.1	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D	-2.01	5.41	6.42	0.67	0	2.56E-02	1.01E-01	Coding
TC1500010923.hg.1	DET1	de-etiolated homolog 1 (Arabidopsis)	-2.01	6.36	7.37	0.1	0.17	1.40E-03	1.65E-02	Multiple_Complex
TC0X00010837.hg.1	MBNL3	muscleblind-like splicing regulator 3	-2.01	8.48	9.49	0.44	0.11	2.00E-03	1.95E-02	Multiple_Complex
TC0700010934.hg.1	H2AFV	H2A histone family, member V	-2.01	12.44	13.45	0.26	0.02	9.00E-04	1.31E-02	Multiple_Complex
TC0100010185.hg.1	APOA1BP	apolipoprotein A-I binding protein	-2.01	12.21	13.22	0.02	0.01	7.00E-04	1.21E-02	Multiple_Complex
TC2100007451.hg.1	COL6A2	collagen, type VI, alpha 2	-2.01	4.73	5.74	0.2	0.34	3.50E-03	2.74E-02	Multiple_Complex
TC0100017844.hg.1	NID1	nidogen 1	-2.01	10.47	11.48	0.08	0.09	2.60E-03	2.29E-02	Multiple_Complex
TC2000006518.hg.1	NOP56; SNORD57; SNORD56; SNORA51; SNORD110; SNORD86; MIR1292	NOP56 ribonucleoprotein; small nucleolar RNA, C/D box 57; small nucleolar RNA, C/D box 56; small nucleolar RNA, H/ACA box 51; small nucleolar RNA, C/D box 110; small nucleolar RNA, C/D box 86; microRNA 1292	-2.01	12.4	13.41	0.2	0.42	2.20E-03	2.08E-02	Multiple_Complex
TC0600012960.hg.1	TSPYL1	TSPY-like 1	-2.01	9.09	10.1	0.18	0.36	1.60E-03	1.76E-02	Coding
TC0X00007053.hg.1	MAOA	monoamine oxidase A	-2.01	6.08	7.09	0.15	0.36	3.00E-03	2.49E-02	Multiple_Complex

TC0700006583.hg.1	SDK1	sidekick cell adhesion molecule 1	-2.01	5.41	6.42	0.48	0.68	1.08E-02	5.63E-02	Multiple_Complex
TC0200013109.hg.1	PCGF1	polycomb group ring finger 1	-2.01	10.73	11.74	0.23	0.09	3.10E-03	2.54E-02	Multiple_Complex
TC1400006741.hg.1	NYNRIN	NYN domain and retroviral integrase containing	-2.01	6.16	7.17	0.44	0.65	1.01E-02	5.38E-02	Multiple_Complex
TC0400010904.hg.1	YTHDC1	YTH domain containing 1	-2.02	7.25	8.26	0.15	0.16	9.00E-04	1.31E-02	Multiple_Complex
TC1100006966.hg.1	NCR3LG1	natural killer cell cytotoxicity receptor 3 ligand 1	-2.02	11.43	12.45	0.41	0.09	2.40E-03	2.17E-02	Multiple_Complex
TC1100007995.hg.1	CDCA5	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, UTR3 best transcript NM_080668	-2.02	7.55	8.56	0.31	0.6	1.43E-02	6.83E-02	NonCoding
TC1700009801.hg.1	ELAC2	elaC ribonuclease Z 2	-2.02	8.34	9.35	0.25	0.09	1.50E-03	1.66E-02	Multiple_Complex
TC1200009748.hg.1	ZNF384	zinc finger protein 384	-2.02	7.97	8.98	0.15	0.16	1.50E-03	1.67E-02	Multiple_Complex
TC1700007897.hg.1	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	-2.02	6.12	7.14	0.23	0.07	4.00E-03	2.96E-02	Multiple_Complex
TC1500007860.hg.1	MPI	mannose phosphate isomerase	-2.02	10.53	11.54	0.16	0.2	1.00E-03	1.40E-02	Multiple_Complex
TC1100011280.hg.1	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	-2.02	9.35	10.36	0.21	0.08	7.00E-04	1.21E-02	Multiple_Complex
TC1900011854.hg.1	ELAVL1	ELAV like RNA binding protein 1	-2.02	14.62	15.63	0.2	0.17	9.00E-04	1.33E-02	Multiple_Complex
TC1600011316.hg.1	ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma	-2.02	7.18	8.19	0.84	0.22	1.56E-02	7.19E-02	Multiple_Complex
TC0300008355.hg.1	BOC	BOC cell adhesion associated, oncogene regulated	-2.02	5.76	6.78	0.2	0.53	3.50E-03	2.73E-02	Multiple_Complex
TC0600010688.hg.1	LYRM4	LYR motif containing 4	-2.02	5.16	6.18	0.15	0.49	4.90E-03	3.34E-02	Multiple_Complex
TC1600009737.hg.1	GGA2	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	-2.02	11.03	12.04	0.17	0.09	7.00E-04	1.19E-02	Multiple_Complex
TC0300013829.hg.1	RBM5	RNA binding motif protein 5	-2.02	12.98	13.99	0.16	0.08	1.10E-03	1.43E-02	Multiple_Complex
TC1700011744.hg.1	MIF4GD	MIF4G domain containing	-2.02	6.4	7.41	0.21	0.36	2.10E-03	2.00E-02	Multiple_Complex
TC0500012059.hg.1	VDAC1	voltage-dependent anion channel 1	-2.02	7.69	8.7	0.41	0.11	1.80E-03	1.89E-02	Multiple_Complex

TC1100009233.hg.1	CCDC84	coiled-coil domain containing 84	-2.02	5.88	6.89	0.59	0.31	1.55E-02	7.18E-02	Multiple_Complex
TC0100013696.hg.1	PSMB2	proteasome subunit beta 2	-2.02	13.03	14.05	0.02	0.04	5.00E-04	1.05E-02	Multiple_Complex
TC0100016018.hg.1	CRABP2	cellular retinoic acid binding protein 2	-2.02	11.9	12.92	0.55	0.11	5.20E-03	3.46E-02	Coding
TC0500013377.hg.1	HARS	histidyl-tRNA synthetase	-2.02	9.25	10.27	0.38	0.12	1.70E-03	1.83E-02	Multiple_Complex
TC1600008984.hg.1	RPUSD1	RNA pseudouridylate synthase domain containing 1	-2.02	6.78	7.8	0.46	0.11	7.00E-03	4.21E-02	Multiple_Complex
TC1500007004.hg.1	RTF1	RTF1 homolog, Paf1/RNA polymerase II complex component	-2.02	8.92	9.93	0.47	0.27	3.00E-03	2.48E-02	Multiple_Complex
TC0100010133.hg.1	MSTO1; MSTO2P	misato 1, mitochondrial distribution and morphology regulator; misato family member 2, pseudogene	-2.02	11.33	12.35	0.18	0.11	1.00E-03	1.38E-02	Multiple_Complex
TSUnmapped00000485.hg.1	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	-2.02	8.91	9.93	0.32	0.17	2.80E-03	2.41E-02	Coding
TC2200009336.hg.1	NIPSNAP1	nipsnap homolog 1 (C. elegans)	-2.02	8.2	9.22	0.23	0.31	2.10E-03	2.02E-02	Multiple_Complex
TC0600007789.hg.1	ZNF76	zinc finger protein 76	-2.02	7.72	8.74	0.68	0.15	9.30E-03	5.09E-02	Multiple_Complex
TC1100008008.hg.1	POLA2	polymerase (DNA directed), alpha 2, accessory subunit	-2.02	9.86	10.88	0.23	0.06	2.00E-03	1.96E-02	Multiple_Complex
TC1200010971.hg.1	DCTN2	dynactin 2 (p50)	-2.03	10.6	11.62	0.18	0.05	1.20E-03	1.49E-02	Multiple_Complex
TC1900011475.hg.1	ISOC2	isochorismatase domain containing 2	-2.03	7.4	8.42	0.01	0.53	3.40E-03	2.68E-02	Multiple_Complex
TC1700007204.hg.1	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	-2.03	9.55	10.57	0.17	0.13	6.00E-04	1.16E-02	Multiple_Complex
TC0700007633.hg.1	SUMF2	sulfatase modifying factor 2	-2.03	11.37	12.39	0.08	0.33	1.20E-03	1.53E-02	Multiple_Complex
TC1500008167.hg.1	ZNF592	zinc finger protein 592	-2.03	8.78	9.8	0.28	0.08	8.00E-04	1.28E-02	Multiple_Complex
TC0100013744.hg.1	MEAF6	MYST/Esa1-associated factor 6	-2.03	10.5	11.52	0.19	0.09	7.00E-04	1.16E-02	Multiple_Complex
TC1900011829.hg.1	ZNF324	zinc finger protein 324	-2.03	4.62	5.64	0.34	0.76	1.24E-02	6.19E-02	Multiple_Complex

TC0700009692.hg.1	SLC4A2	solute carrier family 4 (anion exchanger), member 2	-2.03	8.55	9.57	0.05	0.07	5.00E-04	1.07E-02	Multiple_Complex
TC2200007404.hg.1	MIEF1	mitochondrial elongation factor 1	-2.03	6.46	7.48	0.1	0.07	3.00E-03	2.47E-02	Multiple_Complex
TC0600014107.hg.1	STK19	serine/threonine kinase 19	-2.03	6.04	7.06	0.23	0.03	1.47E-02	6.92E-02	Multiple_Complex
TC1600011220.hg.1	CYBA	cytochrome b-245, alpha polypeptide	-2.03	9.04	10.06	0.28	0.05	2.10E-03	2.00E-02	Multiple_Complex
TC0100009950.hg.1	ZNF687	zinc finger protein 687	-2.03	9.32	10.34	0.04	0.15	5.00E-04	1.06E-02	Multiple_Complex
TC1900011766.hg.1	MARK4	MAP/microtubule affinity-regulating kinase 4	-2.03	11.61	12.63	0	0.11	6.00E-04	1.08E-02	Multiple_Complex
TC0100007909.hg.1	BMP8A	bone morphogenetic protein 8a	-2.03	5.76	6.78	0.25	0.58	4.20E-03	3.05E-02	Coding
TC0700011554.hg.1	PMS2P3	PMS1 homolog 2, mismatch repair system component pseudogene 3	-2.03	12.13	13.16	0.05	0.18	1.50E-03	1.66E-02	Multiple_Complex
TC0400009132.hg.1	ETFDH	electron-transferring-flavoprotein dehydrogenase	-2.03	5.67	6.69	0.06	0.4	3.50E-03	2.73E-02	Multiple_Complex
TC0400009953.hg.1	AFAP1	actin filament associated protein 1	-2.03	5.17	6.2	0.46	0.37	4.50E-03	3.16E-02	Multiple_Complex
TC1700009221.hg.1	GPS1	G protein pathway suppressor 1	-2.03	10.24	11.27	0.27	0.09	9.00E-04	1.32E-02	Multiple_Complex
TC1900007025.hg.1	PLPPR2	phospholipid phosphatase related 2	-2.03	8.12	9.15	0.1	0.33	1.20E-03	1.52E-02	Multiple_Complex
TC1400010764.hg.1	VTI1B	vesicle transport through interaction with t-SNAREs 1B	-2.03	11.81	12.83	0.48	0.12	2.50E-03	2.21E-02	Multiple_Complex
TC0800011669.hg.1	DERL1	derlin 1	-2.04	11.4	12.43	0.23	0.03	1.00E-03	1.36E-02	Multiple_Complex
TC0600012038.hg.1	MCM3	minichromosome maintenance complex component 3	-2.04	10.52	11.55	0.33	0.04	1.10E-03	1.47E-02	Multiple_Complex
TC1500007545.hg.1	SNX1	sorting nexin 1	-2.04	8.59	9.62	0.26	0.09	8.00E-04	1.27E-02	Multiple_Complex
TC0700013050.hg.1	KCNH2	potassium channel, voltage gated eag related subfamily H, member 2	-2.04	5.78	6.81	0.19	0.56	6.90E-03	4.20E-02	Multiple_Complex
TSUnmapped00000293.hg.1	RCC2	regulator of chromosome condensation 2	-2.04	11.6	12.63	0.57	0.16	3.60E-03	2.77E-02	NonCoding

TC0700011344.hg.1	GUSB	glucuronidase, beta	-2.04	9.48	10.5	0.36	0.02	1.30E-03	1.57E-02	Multiple_Complex
TC2000006520.hg.1	EBF4	early B-cell factor 4	-2.04	7.01	8.03	0.06	0.88	1.73E-02	7.74E-02	Multiple_Complex
TC1700012474.hg.1	EXOC7; MIR6868	exocyst complex component 7; microRNA 6868	-2.04	8.56	9.59	0.45	0.25	3.30E-03	2.65E-02	Multiple_Complex
TSUnmapped00000558.hg.1	HYOU1	hypoxia up-regulated 1	-2.04	12.28	13.3	0.02	0.08	5.00E-04	1.04E-02	NonCoding
TC1900007329.hg.1	PGLS	6-phosphogluconolactonase	-2.04	5.97	7	0.04	0.36	1.60E-03	1.71E-02	Multiple_Complex
TSUnmapped00000313.hg.1	CCDC84	coiled-coil domain containing 84	-2.04	7.8	8.83	0.59	0.06	6.90E-03	4.17E-02	NonCoding
TC0300007437.hg.1	MANF	mesencephalic astrocyte-derived neurotrophic factor	-2.04	12.43	13.46	0.23	0.15	9.00E-04	1.31E-02	Multiple_Complex
TC0600007307.hg.1	BTN2A1	butyrophilin, subfamily 2, member A1	-2.04	7.75	8.78	0.5	0.15	3.60E-03	2.77E-02	Multiple_Complex
TC1100013184.hg.1	CDCA5	cell division cycle associated 5	-2.04	10.87	11.9	0.43	0.03	2.00E-03	1.95E-02	Multiple_Complex
TC0200008501.hg.1	ITPRIPL1	inositol 1,4,5-trisphosphate receptor interacting protein-like 1	-2.04	6.57	7.6	0.16	0.21	9.00E-04	1.34E-02	Coding
TC0700012680.hg.1	SLC35B4	solute carrier family 35 (UDP-xylose/UDP-N-acetylglucosamine transporter), member B4	-2.04	7.38	8.41	0.05	0.07	5.00E-04	1.00E-02	Multiple_Complex
TC0300007077.hg.1	ACVR2B	activin A receptor type IIB	-2.04	6.52	7.55	0.2	0.24	9.00E-04	1.31E-02	Multiple_Complex
TC0400006578.hg.1	SH3BP2	SH3-domain binding protein 2	-2.04	6.04	7.07	0.58	0.42	1.88E-02	8.16E-02	Multiple_Complex
TC0300014021.hg.1	CPOX	coproporphyrinogen oxidase	-2.04	7.64	8.67	0.75	0.25	1.14E-02	5.85E-02	Multiple_Complex
TC1900009198.hg.1	BTBD2	BTB (POZ) domain containing 2	-2.04	8.73	9.76	0.44	0.01	1.70E-03	1.77E-02	Multiple_Complex
TC1100013140.hg.1	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	-2.05	12.58	13.61	0.16	0.2	8.00E-04	1.24E-02	Multiple_Complex
TC1100011126.hg.1	PLA2G16	phospholipase A2, group XVI	-2.05	9.52	10.56	0.4	0.34	5.20E-03	3.46E-02	Multiple_Complex
TC1900006502.hg.1	WDR18	WD repeat domain 18	-2.05	7.58	8.61	0.63	0.54	1.16E-02	5.90E-02	Multiple_Complex

TC0400006703.hg.1	KIAA0232	KIAA0232	-2.05	7.77	8.8	0.24	0.69	7.10E-03	4.24E-02	Multiple_Complex
TC1900007398.hg.1	C19orf60	chromosome 19 open reading frame 60	-2.05	9.48	10.52	0.51	0.05	3.00E-03	2.48E-02	Multiple_Complex
TC0600011483.hg.1	PBX2	pre-B-cell leukemia homeobox 2	-2.05	10.35	11.38	0.39	0.03	3.20E-03	2.59E-02	Multiple_Complex
TC0300007606.hg.1	ABHD6	abhydrolase domain containing 6	-2.05	8.28	9.32	0.3	0.31	1.50E-03	1.65E-02	Multiple_Complex
TC0900008945.hg.1	GPR107	G protein-coupled receptor 107	-2.05	10.2	11.24	0.39	0.07	2.50E-03	2.24E-02	Multiple_Complex
TC0600011880.hg.1	GTPBP2	GTP binding protein 2	-2.05	12.45	13.49	0.12	0.03	8.00E-04	1.28E-02	Multiple_Complex
TC1700008028.hg.1	NMT1	N-myristoyltransferase 1	-2.05	10.08	11.11	0.04	0.29	1.10E-03	1.44E-02	Multiple_Complex
TC1100010718.hg.1	LRP4	LDL receptor related protein 4	-2.05	6.66	7.7	0.08	0.29	1.40E-03	1.64E-02	Multiple_Complex
TC0300012935.hg.1	SHOX2	short stature homeobox 2	-2.05	7.1	8.13	0.43	0.38	3.80E-03	2.88E-02	Multiple_Complex
TC0100018486.hg.1	CDC42SE1	CDC42 small effector 1	-2.05	9.3	10.34	0.14	0.08	5.00E-04	1.02E-02	Multiple_Complex
TC1700009971.hg.1	TOP3A	topoisomerase (DNA) III alpha	-2.05	7.05	8.09	0.49	0.09	3.80E-03	2.87E-02	Multiple_Complex
TC0900009952.hg.1	GBA2	glucosidase, beta (bile acid) 2	-2.05	7.83	8.87	0.32	0	9.30E-03	5.11E-02	Multiple_Complex
TC0200013700.hg.1	MFSD9	major facilitator superfamily domain containing 9	-2.05	8.75	9.79	0	0.2	1.20E-03	1.51E-02	Multiple_Complex
TC0100007786.hg.1	AGO1	argonaute RISC catalytic component 1	-2.05	10.7	11.74	0.15	0.18	1.00E-03	1.40E-02	Multiple_Complex
TC1100009207.hg.1	KMT2A	lysine (K)-specific methyltransferase 2A	-2.05	10.03	11.07	0.09	0.13	6.00E-04	1.10E-02	Multiple_Complex
TC1000007852.hg.1	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	-2.05	12.18	13.22	0.13	0.27	8.00E-04	1.28E-02	Multiple_Complex
TC1500008154.hg.1	ZSCAN2	zinc finger and SCAN domain containing 2	-2.05	6.79	7.82	0.12	0.35	1.40E-03	1.60E-02	Multiple_Complex
TC0600007771.hg.1	UHRF1BP1	UHRF1 binding protein 1	-2.05	8.3	9.34	0.33	0.48	3.00E-03	2.50E-02	Multiple_Complex
TC0X00009867.hg.1	SPIN4	spindlin family, member 4	-2.05	6.48	7.52	0.26	0.17	1.60E-03	1.76E-02	Coding
TC1700009113.hg.1	GAA	glucosidase, alpha; acid	-2.05	8.88	9.92	0.41	0.19	1.80E-03	1.85E-02	Multiple_Complex
TC0100007458.hg.1	DHDDS	dehydrodolichyl diphosphate synthase subunit	-2.05	7.61	8.64	0.21	0.22	9.00E-04	1.29E-02	Multiple_Complex

TC2000008345.hg.1	TMX4	thioredoxin-related transmembrane protein 4	-2.05	6.01	7.04	0.28	0.02	1.20E-03	1.51E-02	Multiple_Complex
TC1900012056.hg.1	ZNF772	zinc finger protein 772	-2.05	5.37	6.41	0.07	0.21	9.00E-04	1.32E-02	Multiple_Complex
TC1200011770.hg.1	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	-2.05	7.28	8.32	0.13	0.12	6.00E-04	1.12E-02	Multiple_Complex
TC1900008558.hg.1	MED25; MIR6800	mediator complex subunit 25; microRNA 6800	-2.05	6.84	7.88	0.12	0.6	4.40E-03	3.13E-02	Multiple_Complex
TC0900010969.hg.1	CORO2A	coronin, actin binding protein, 2A	-2.05	7.37	8.41	0.33	0.05	9.00E-04	1.31E-02	Multiple_Complex
TSUnmapped00000322.hg.1	HYOU1	hypoxia up-regulated 1	-2.05	9.5	10.53	0.54	0.01	2.80E-03	2.38E-02	Coding
TC1900009757.hg.1	FARSA	phenylalanyl-tRNA synthetase alpha subunit	-2.05	11.56	12.6	0.48	0.09	2.10E-03	2.02E-02	Multiple_Complex
TC0X00008860.hg.1	F8A2; F8A3; F8A1	coagulation factor VIII-associated 2; coagulation factor VIII-associated 3; coagulation factor VIII-associated 1	-2.06	7.74	8.78	0.4	0.13	1.60E-03	1.73E-02	Coding
TC0100008757.hg.1	LHX8	LIM homeobox 8	-2.06	6.95	7.99	0.67	0.14	7.10E-03	4.27E-02	Multiple_Complex
TC1900006976.hg.1	MRPL4	mitochondrial ribosomal protein L4	-2.06	8.29	9.32	0.35	0.34	4.50E-03	3.19E-02	Multiple_Complex
TC1700009538.hg.1	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	-2.06	10.22	11.26	0.02	0.19	5.00E-04	1.04E-02	Multiple_Complex
TC0600014261.hg.1	DDX39B; SNORD84	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B; small nucleolar RNA, C/D box 84	-2.06	10.73	11.77	0.11	0.14	6.00E-04	1.08E-02	Multiple_Complex
TC2200008055.hg.1	PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	-2.06	11.1	12.14	0.43	0.11	2.00E-03	1.98E-02	Multiple_Complex
TC1900007267.hg.1	AP1M1	adaptor-related protein complex 1, mu 1 subunit	-2.06	10.35	11.39	0.21	0.03	6.00E-04	1.07E-02	Multiple_Complex
TC0600008035.hg.1	TAF8	TATA box binding protein associated factor 8	-2.06	11.52	12.56	0.23	0.13	1.20E-03	1.52E-02	Multiple_Complex
TC0100013692.hg.1	KIAA0319L	KIAA0319-like	-2.06	11.24	12.28	0.06	0.07	2.10E-03	2.00E-02	Multiple_Complex
TC0600007610.hg.1	MSH5; MSH5-SAPCD1; SAPCD1	mutS homolog 5; MSH5-SAPCD1 readthrough (NMD candidate); suppressor APC domain containing 1	-2.06	8.92	9.96	0.13	0.2	6.00E-04	1.13E-02	Multiple_Complex
TC1100008208.hg.1	IGHMBP2	immunoglobulin mu binding protein 2	-2.06	8.45	9.49	0.3	0.21	1.80E-03	1.88E-02	Multiple_Complex

TC1700008917.hg.1	SAP30BP	SAP30 binding protein	-2.06	11.84	12.88	0.14	0.05	1.20E-03	1.49E-02	Multiple_Complex
TC1400009337.hg.1	DHRS7	dehydrogenase/reductase (SDR family) member 7	-2.06	10.99	12.03	0.29	0.1	1.30E-03	1.57E-02	Multiple_Complex
TC0700013396.hg.1	CLDN12	claudin 12	-2.06	6.95	7.99	0.35	0.37	2.50E-03	2.23E-02	Multiple_Complex
TC0500011277.hg.1	ANKRD34B	ankyrin repeat domain 34B	-2.06	4.5	5.54	0.06	0.05	3.00E-03	2.49E-02	Coding
TC1200011846.hg.1	CORO1C	coronin, actin binding protein, 1C	-2.06	10.56	11.6	0	0.21	9.00E-04	1.32E-02	Multiple_Complex
TC1700008531.hg.1	METTL2A	methyltransferase like 2A	-2.06	10.46	11.5	0.22	0.1	8.00E-04	1.25E-02	Multiple_Complex
TC1100008514.hg.1	TSKU	tsukushi, small leucine rich proteoglycan	-2.06	6.81	7.86	0.72	0.18	6.20E-03	3.91E-02	Multiple_Complex
TC1300008181.hg.1	CHAMP1	chromosome alignment maintaining phosphoprotein 1	-2.06	8.82	9.86	0.39	0.03	2.00E-03	1.95E-02	Multiple_Complex
TC2200008447.hg.1	PES1	pescadillo ribosomal biogenesis factor 1	-2.06	9.04	10.08	0.28	0.06	8.00E-04	1.23E-02	Multiple_Complex
TC1100006731.hg.1	ILK	integrin linked kinase	-2.06	9.16	10.21	0.02	0.04	7.00E-04	1.19E-02	Multiple_Complex
TC1100006500.hg.1	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	-2.06	12.35	13.39	0.16	0.1	7.00E-04	1.22E-02	Multiple_Complex
TC0100008094.hg.1	RNF220	ring finger protein 220	-2.07	11.05	12.1	0.06	0.29	9.00E-04	1.33E-02	Multiple_Complex
TC0100013998.hg.1	HECTD3	HECT domain containing E3 ubiquitin protein ligase 3	-2.07	8.02	9.07	0.21	0.19	1.00E-03	1.36E-02	Multiple_Complex
TC1500009218.hg.1	ZSCAN29	zinc finger and SCAN domain containing 29	-2.07	7.4	8.45	0.18	0.03	9.00E-04	1.34E-02	Multiple_Complex
TC1100009171.hg.1	RNF214	ring finger protein 214	-2.07	7.48	8.53	0.33	0.1	9.00E-04	1.33E-02	Multiple_Complex
TC2000008951.hg.1	GSS	glutathione synthetase	-2.07	7.9	8.95	0.33	0.12	1.40E-03	1.62E-02	Multiple_Complex
TC0300013763.hg.1	RUBCN; MIR922	RUN domain and cysteine-rich domain containing, Beclin 1-interacting protein; microRNA 922	-2.07	8.1	9.15	0.69	0.22	1.16E-02	5.89E-02	Multiple_Complex
TC0900012021.hg.1	FBXW5	F-box and WD repeat domain containing 5	-2.07	7.54	8.59	0.41	0.23	1.90E-03	1.89E-02	Multiple_Complex
TC1000008574.hg.1	PGAM1	phosphoglycerate mutase 1 (brain)	-2.07	12.86	13.91	0.3	0.13	1.10E-03	1.48E-02	Multiple_Complex
TC1600006561.hg.1	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	-2.07	8.74	9.78	0.61	0.33	8.10E-03	4.67E-02	Multiple_Complex

TC0700012584.hg.1	UBE2H	ubiquitin conjugating enzyme E2H	-2.07	9.84	10.89	0.15	0.09	6.00E-04	1.09E-02	Multiple_Complex
TC0400012757.hg.1	RNF4	ring finger protein 4	-2.07	9.79	10.84	0.15	0.06	5.00E-04	1.02E-02	Multiple_Complex
TC0200009344.hg.1	CCDC74A	coiled-coil domain containing 74A	-2.07	7.94	8.99	0.07	0.1	1.20E-03	1.52E-02	Multiple_Complex
TC1400008694.hg.1	ACIN1	apoptotic chromatin condensation inducer 1	-2.07	8.78	9.83	0.53	0.17	2.50E-03	2.25E-02	Multiple_Complex
TC0700013620.hg.1	IMPDH1	IMP (inosine 5-monophosphate) dehydrogenase 1	-2.07	7.95	9	0.26	0.2	2.20E-03	2.05E-02	Multiple_Complex
TC1700006804.hg.1	PFAS	phosphoribosylformylglycinamidine synthase	-2.07	9.69	10.74	0.36	0.08	1.00E-03	1.40E-02	Multiple_Complex
TC0600011843.hg.1	TBCC	tubulin folding cofactor C	-2.07	7.08	8.13	0.04	0.34	8.00E-04	1.28E-02	Coding
TC1100012708.hg.1	FEZ1	fasciculation and elongation protein zeta 1	-2.07	8.45	9.5	0.89	0.18	1.18E-02	5.98E-02	Multiple_Complex
TC1900009608.hg.1	EIF3G	eukaryotic translation initiation factor 3, subunit G	-2.07	12.14	13.19	0.42	0.2	1.80E-03	1.86E-02	Multiple_Complex
TC1800007066.hg.1	MAPRE2	microtubule-associated protein, RP/EB family, member 2	-2.07	8.77	9.82	0.04	0.04	7.00E-04	1.17E-02	Multiple_Complex
TC0X00008381.hg.1	OCRL	oculocerebrorenal syndrome of Lowe	-2.07	10.2	11.25	0.05	0.25	8.00E-04	1.24E-02	Multiple_Complex
TC0800012126.hg.1	TOP1MT	topoisomerase (DNA) I, mitochondrial	-2.07	8.24	9.29	0.03	0.1	5.00E-04	1.07E-02	Multiple_Complex
TC0100007659.hg.1	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	-2.07	11.75	12.8	0	0.04	5.00E-04	1.07E-02	Multiple_Complex
TC1900011817.hg.1	ZNF773	zinc finger protein 773	-2.07	5.9	6.96	0.38	0.39	2.80E-03	2.41E-02	Multiple_Complex
TC1100013031.hg.1	NUDT22	nudix hydrolase 22	-2.08	6.96	8.02	0.67	0.23	5.90E-03	3.79E-02	Multiple_Complex
TC1900009808.hg.1	ADGRL1	adhesion G protein-coupled receptor L1	-2.08	7.77	8.83	0.13	0	1.70E-03	1.81E-02	Multiple_Complex
TC0300007356.hg.1	ARIH2	ariadne RBR E3 ubiquitin protein ligase 2	-2.08	7.93	8.98	0.21	0.03	1.80E-03	1.87E-02	Multiple_Complex
TC0100007569.hg.1	GMEB1	glucocorticoid modulatory element binding protein 1	-2.08	8.89	9.95	0.3	0.19	1.30E-03	1.58E-02	Multiple_Complex
TC0X00007363.hg.1	MAGED2	MAGE family member D2	-2.08	9.31	10.36	0.66	0.07	5.30E-03	3.52E-02	Multiple_Complex
TC0500009622.hg.1	GRK6	G protein-coupled receptor kinase 6	-2.08	7.6	8.65	0.13	0.31	1.00E-03	1.36E-02	Multiple_Complex

TSUnmapped00000068.hg.1	ZNF780A	zinc finger protein 780A	-2.08	5.4	6.45	0.36	0.12	1.54E-02	7.13E-02	Coding
TC0100012889.hg.1	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	-2.08	9.91	10.96	0.32	0.02	8.00E-04	1.25E-02	Multiple_Complex
TC0700013419.hg.1	ARPC1A	actin related protein 2/3 complex subunit 1A	-2.08	11.57	12.62	0.4	0.02	1.10E-03	1.47E-02	Multiple_Complex
TC1500008442.hg.1	NR2F2	nuclear receptor subfamily 2, group F, member 2	-2.08	10.19	11.24	0.08	0.14	7.00E-04	1.21E-02	Multiple_Complex
TC1100008120.hg.1	KDM2A	lysine (K)-specific demethylase 2A	-2.08	8.28	9.33	0.42	0.09	1.30E-03	1.57E-02	Multiple_Complex
TC1600008709.hg.1	COX4I1	cytochrome c oxidase subunit IV isoform 1	-2.08	11.72	12.78	0.81	0.06	8.60E-03	4.85E-02	Multiple_Complex
TC2200008799.hg.1	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	-2.08	10.86	11.91	0.14	0.11	8.00E-04	1.27E-02	Multiple_Complex
TC1700010191.hg.1	POLDIP2	polymerase (DNA-directed), delta interacting protein 2	-2.08	10	11.05	0.39	0.1	1.20E-03	1.50E-02	Multiple_Complex
TC1100011735.hg.1	INTS4	integrator complex subunit 4	-2.08	6.52	7.57	0.36	0.44	4.30E-03	3.12E-02	Multiple_Complex
TC0X00008526.hg.1	FHL1	four and a half LIM domains 1	-2.08	5.72	6.77	0.11	0.3	1.00E-03	1.36E-02	Multiple_Complex
TSUnmapped00000591.hg.1	HHAT	hedgehog acyltransferase	-2.08	6.05	7.11	0.5	0.38	4.00E-03	2.99E-02	Coding
TC1700012089.hg.1	DCXR	dicarbonyl/L-xylulose reductase	-2.08	11.92	12.98	0.37	0.3	2.40E-03	2.20E-02	Multiple_Complex
TC0600007836.hg.1	KCTD20	potassium channel tetramerization domain containing 20	-2.08	8.64	9.7	0.03	0.11	5.00E-04	1.00E-02	Multiple_Complex
TC0100007162.hg.1	PQLC2	PQ loop repeat containing 2	-2.08	9.34	10.4	0.05	0.38	2.90E-03	2.44E-02	Multiple_Complex
TC0700009977.hg.1	PDGFA	platelet-derived growth factor alpha polypeptide	-2.08	5.37	6.43	0.07	0.42	4.10E-03	3.03E-02	Multiple_Complex
TC2200008886.hg.1	CYB5R3	cytochrome b5 reductase 3	-2.08	7.95	9.01	0.35	0.13	9.00E-04	1.33E-02	Multiple_Complex
TC1700011773.hg.1	WBP2	WW domain binding protein 2	-2.08	9.1	10.16	0.17	0.29	1.10E-03	1.45E-02	Multiple_Complex
TC2200009267.hg.1	GTPBP1	GTP binding protein 1	-2.08	7.09	8.14	0.16	0.4	5.10E-03	3.45E-02	Coding
TC1800007963.hg.1	EPB41L3	erythrocyte membrane protein band 4.1-like 3	-2.08	9.64	10.7	0.14	0.14	1.70E-03	1.79E-02	Multiple_Complex

TC0800007316.hg.1	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	-2.08	10.56	11.62	0.19	0	6.00E-04	1.13E-02	Multiple_Complex
TC0300010427.hg.1	RFTN1	raftlin, lipid raft linker 1	-2.08	6.32	7.38	1.02	0.61	2.96E-02	1.11E-01	Multiple_Complex
TC0X00006764.hg.1	MBTPS2; YY2	membrane bound transcription factor peptidase, site 2; YY2 transcription factor	-2.09	11.05	12.11	0.1	0	7.00E-04	1.18E-02	Multiple_Complex
TC1000009589.hg.1	PITRM1	pitrilysin metallopeptidase 1	-2.09	8.87	9.93	0.75	0.02	1.11E-02	5.73E-02	Multiple_Complex
TC1000012090.hg.1	IKZF5	IKAROS family zinc finger 5	-2.09	9.69	10.75	0	0.11	7.00E-04	1.16E-02	Multiple_Complex
TC2000008213.hg.1	DDRGK1	DDRGK domain containing 1	-2.09	12.29	13.35	0.29	0.01	8.00E-04	1.27E-02	Multiple_Complex
TC1600011556.hg.1	PDF; COG8; TMED6	peptide deformylase (mitochondrial); component of oligomeric golgi complex 8; transmembrane p24 trafficking protein 6	-2.09	8.1	9.16	0.35	0.38	2.20E-03	2.10E-02	Multiple_Complex
TC0100013072.hg.1	ATP13A2	ATPase type 13A2	-2.09	7.09	8.15	1.05	0.1	2.27E-02	9.27E-02	Multiple_Complex
TC1700007361.hg.1	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-2.09	8.78	9.84	0.28	0.26	1.20E-03	1.50E-02	Multiple_Complex
TC1700007866.hg.1	NKIRAS2	NFKB inhibitor interacting Ras-like 2	-2.09	12	13.06	0.02	0.03	8.00E-04	1.23E-02	Multiple_Complex
TC2000008678.hg.1	CST3	cystatin C	-2.09	10.15	11.22	0.47	0.19	4.10E-03	3.01E-02	Multiple_Complex
TC1700007929.hg.1	RUNDC1	RUN domain containing 1	-2.09	8.37	9.43	0.88	0.2	1.39E-02	6.67E-02	Multiple_Complex
TC1900011636.hg.1	UBE2M	ubiquitin-conjugating enzyme E2M	-2.09	13.44	14.5	0.13	0.09	4.00E-04	9.80E-03	Multiple_Complex
TC1500010720.hg.1	IVD	isovaleryl-CoA dehydrogenase	-2.09	6.49	7.55	0.49	0.7	1.33E-02	6.46E-02	Multiple_Complex
TC2000009953.hg.1	OSBPL2	oxysterol binding protein-like 2	-2.09	12.63	13.69	0.02	0.16	1.30E-03	1.58E-02	Multiple_Complex
TC0100017078.hg.1	RAB29	RAB29, member RAS oncogene family	-2.09	6.66	7.72	0.1	0.13	7.00E-04	1.19E-02	Multiple_Complex
TC0200016074.hg.1	NGEF	neuronal guanine nucleotide exchange factor	-2.09	5.59	6.65	0.05	0.39	4.90E-03	3.36E-02	Multiple_Complex
TC0600013727.hg.1	EZR	ezrin	-2.09	10.62	11.69	0.45	0.07	1.40E-03	1.63E-02	Multiple_Complex

TC0200007854.hg.1	MEIS1	Meis homeobox 1	-2.09	7.94	9.01	0.3	0.17	1.20E-03	1.49E-02	Multiple_Complex
TC0300011077.hg.1	IP6K1	inositol hexakisphosphate kinase 1	-2.09	9.72	10.78	0.68	0.13	4.20E-03	3.06E-02	Multiple_Complex
TC0200010807.hg.1	TTLL4	tubulin tyrosine ligase-like family member 4	-2.09	9.11	10.17	0.06	0.21	1.30E-03	1.56E-02	Multiple_Complex
TC0700010728.hg.1	HERPUD2	HERPUD family member 2	-2.09	8.63	9.69	0.62	0.31	5.40E-03	3.57E-02	Multiple_Complex
TC1200010857.hg.1	PHC1	Homo sapiens polyhomeotic homolog 1 (Drosophila), mRNA (cDNA clone MGC:87926 IMAGE:5788132), complete cds.; Homo sapiens polyhomeotic homolog 1 (Drosophila), mRNA (cDNA clone MGC:189745 IMAGE:9057069), complete cds.	-2.09	9.43	10.5	0.34	0	1.40E-03	1.61E-02	Multiple_Complex
TC0X00011102.hg.1	CD99L2	CD99 molecule-like 2	-2.09	8.78	9.85	0.08	0.06	8.50E-03	4.83E-02	Multiple_Complex
TC1600009731.hg.1	COG7	component of oligomeric golgi complex 7	-2.1	8.62	9.69	0.4	0.04	1.40E-03	1.63E-02	Multiple_Complex
TC1100009419.hg.1	EI24	etoposide induced 2.4	-2.1	10.6	11.67	0.26	0.06	6.00E-04	1.13E-02	Multiple_Complex
TC1100012358.hg.1	USP28	ubiquitin specific peptidase 28	-2.1	6.05	7.11	0.46	0.33	3.50E-03	2.73E-02	Multiple_Complex
TC0X00007368.hg.1	TRO	trophinin	-2.1	6.49	7.56	0.39	0.24	3.50E-03	2.72E-02	Multiple_Complex
TC2200009244.hg.1	CCDC117	coiled-coil domain containing 117	-2.1	9.4	10.47	0.25	0.14	1.20E-03	1.53E-02	Multiple_Complex
TC1700006767.hg.1	WRAP53	WD repeat containing, antisense to TP53	-2.1	8.64	9.7	0.18	0.11	7.00E-04	1.17E-02	Multiple_Complex
TC0100013602.hg.1	TMEM234	transmembrane protein 234	-2.1	8.48	9.55	0.51	0.1	2.10E-03	2.03E-02	Multiple_Complex
TC1900008505.hg.1	BAX	BCL2-associated X protein	-2.1	9.59	10.66	0.25	0.04	5.00E-04	1.04E-02	Multiple_Complex
TC0200011362.hg.1	RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	-2.1	6.39	7.46	0.03	0.1	1.90E-03	1.92E-02	Multiple_Complex
TC1800008584.hg.1	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	-2.1	7.2	8.27	0.16	0.11	3.00E-03	2.50E-02	Multiple_Complex

TC1900007208.hg.1	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	-2.1	7.02	8.09	0.68	0.27	7.20E-03	4.30E-02	Multiple_Complex
TC0900007807.hg.1	DAPK1	death-associated protein kinase 1	-2.1	8.36	9.43	0.36	0.37	2.00E-03	1.97E-02	Multiple_Complex
TC0X00008070.hg.1	FRMPD3	FERM and PDZ domain containing 3	-2.1	7.91	8.98	0.38	0.09	1.40E-03	1.64E-02	Multiple_Complex
TC0300014047.hg.1	ISY1-RAB43	ISY1-RAB43 readthrough	-2.1	7.63	8.7	0.19	0.16	2.60E-03	2.30E-02	Coding
TC1000007761.hg.1	ARID5B	AT rich interactive domain 5B (MRF1-like)	-2.1	7.46	8.53	0.29	0.02	7.00E-04	1.17E-02	Multiple_Complex
TC0600014257.hg.1	HLA-C	major histocompatibility complex, class I, C	-2.1	11.29	12.37	0.36	0.18	1.90E-03	1.92E-02	Multiple_Complex
TC0X00008828.hg.1	EMD	emerin	-2.1	10.35	11.42	0.48	0	2.30E-03	2.14E-02	Multiple_Complex
TC0700013060.hg.1	TMUB1	transmembrane and ubiquitin-like domain containing 1	-2.1	10.15	11.23	0.11	0.39	1.30E-03	1.55E-02	Multiple_Complex
TC1000011135.hg.1	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	-2.1	9.46	10.54	0.05	0.24	1.00E-03	1.36E-02	Multiple_Complex
TC1100009212.hg.1	PHLDB1; MIR6716	pleckstrin homology-like domain, family B, member 1; microRNA 6716	-2.1	5.09	6.16	0.44	0.36	2.60E-03	2.28E-02	Multiple_Complex
TC0700010854.hg.1	INHBA	inhibin beta A	-2.1	10.98	12.06	0.75	0.03	5.60E-03	3.65E-02	Multiple_Complex
TC1200007560.hg.1	DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	-2.1	6.86	7.94	0.05	0.18	5.00E-04	1.04E-02	Multiple_Complex
TC2200009259.hg.1	SMTN	smoothelin	-2.1	10.35	11.43	0.34	0.17	1.10E-03	1.46E-02	Multiple_Complex
TC0700012701.hg.1	CNOT4	CCR4-NOT transcription complex subunit 4	-2.11	8.14	9.22	0.2	0.01	4.00E-04	9.90E-03	Multiple_Complex
TC1100006722.hg.1	CCKBR	cholecystokinin B receptor	-2.11	6.36	7.43	0.22	0.26	1.10E-03	1.46E-02	Multiple_Complex
TC1900007436.hg.1	GATAD2A; MIR640	GATA zinc finger domain containing 2A; microRNA 640	-2.11	11.43	12.5	0.35	0.12	1.10E-03	1.48E-02	Multiple_Complex
TC0600008127.hg.1	SLC29A1	solute carrier family 29 (equilibrative nucleoside transporter), member 1	-2.11	8.02	9.09	0.02	0.03	4.00E-04	9.60E-03	Multiple_Complex
TC2200008136.hg.1	PRAME	preferentially expressed antigen in melanoma	-2.11	7.33	8.4	0.27	0.24	3.80E-03	2.89E-02	Multiple_Complex
TC1900011786.hg.1	NR1H2	nuclear receptor subfamily 1, group H, member 2	-2.11	6.07	7.15	0.33	0.03	9.00E-04	1.29E-02	Multiple_Complex

TC0100011129.hg.1	NR5A2	nuclear receptor subfamily 5, group A, member 2	-2.11	4.96	6.03	0.66	1	2.82E-02	1.07E-01	Multiple_Complex
TC1700010693.hg.1	ACLY	ATP citrate lyase	-2.11	12.68	13.76	0.11	0.12	5.00E-04	1.05E-02	Multiple_Complex
TC0100017568.hg.1	JMJD4	jumonji domain containing 4	-2.11	7.31	8.39	0.01	0.17	9.00E-04	1.32E-02	Multiple_Complex
TC0200016643.hg.1	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	-2.11	7.34	8.42	0.34	0.41	6.60E-03	4.05E-02	Multiple_Complex
TC1500010422.hg.1	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-2.11	10.61	11.69	0.25	0.23	1.80E-03	1.88E-02	Multiple_Complex
TC2000008200.hg.1	PCED1A	PC-esterase domain containing 1A	-2.11	11.33	12.41	0.32	0.09	1.00E-03	1.39E-02	Multiple_Complex
TC0100012496.hg.1	NADK	NAD kinase	-2.11	9.56	10.64	0.08	0.11	4.00E-04	9.10E-03	Multiple_Complex
TC1700010762.hg.1	VAT1	vesicle amine transport 1	-2.11	10.15	11.23	0.32	0.36	1.60E-03	1.72E-02	Multiple_Complex
TC0X00011404.hg.1	IDS	iduronate 2-sulfatase	-2.11	10.17	11.25	0.15	0.16	1.60E-03	1.72E-02	Multiple_Complex
TC0100007295.hg.1	EPHB2	EPH receptor B2	-2.11	6.94	8.02	0.09	0.07	3.00E-04	8.90E-03	Multiple_Complex
TC1100008342.hg.1	INPPL1	inositol polyphosphate phosphatase-like 1	-2.11	8.82	9.9	0.48	0.29	2.40E-03	2.18E-02	Multiple_Complex
TC1200012861.hg.1	DIABLO	diablo, IAP-binding mitochondrial protein	-2.11	10.11	11.19	0.34	0.42	3.70E-03	2.85E-02	Multiple_Complex
TC1700010202.hg.1	KIAA0100	KIAA0100	-2.11	10.94	12.02	0.35	0.21	1.60E-03	1.71E-02	Multiple_Complex
TC0100013545.hg.1	SDC3	syndecan 3	-2.11	8.42	9.5	0.21	0.5	2.40E-03	2.20E-02	Multiple_Complex
TC0700008094.hg.1	ZP3	zona pellucida glycoprotein 3 (sperm receptor)	-2.11	8.02	9.1	0.29	0.09	7.00E-04	1.16E-02	Multiple_Complex
TC1200010650.hg.1	RACGAP1	Rac GTPase activating protein 1	-2.11	10.9	11.98	0.39	0.22	1.10E-03	1.46E-02	Multiple_Complex
TC0900011163.hg.1	PTPN3	protein tyrosine phosphatase, non-receptor type 3	-2.11	7.08	8.16	0.17	0.28	1.60E-03	1.74E-02	Multiple_Complex
TC1200012864.hg.1	CCDC92	coiled-coil domain containing 92	-2.12	6.31	7.39	0.52	0.23	1.10E-02	5.70E-02	Multiple_Complex
TC1900009433.hg.1	TUBB4A	tubulin, beta 4A class IVa	-2.12	10.99	12.08	0.01	0.47	1.60E-03	1.76E-02	Coding
TC1900011851.hg.1	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	-2.12	12.32	13.4	0.47	0.16	1.60E-03	1.74E-02	Multiple_Complex

TC1100010893.hg.1	SLC43A1	solute carrier family 43 (amino acid system L transporter), member 1	-2.12	5.2	6.28	0.01	0.01	6.20E-03	3.88E-02	Multiple_Complex
TC1900008399.hg.1	ARHGAP35	Rho GTPase activating protein 35	-2.12	8.53	9.61	0.23	0.28	8.00E-04	1.27E-02	Multiple_Complex
TC0100013983.hg.1	TMEM53	transmembrane protein 53	-2.12	5.84	6.92	0.13	0.05	1.10E-03	1.48E-02	Multiple_Complex
TC0X00007149.hg.1	TIMP1	TIMP metallopeptidase inhibitor 1	-2.12	10.69	11.77	0.65	0.12	3.70E-03	2.82E-02	Multiple_Complex
TC1100011050.hg.1	FADS1; MIR1908	fatty acid desaturase 1; microRNA 1908	-2.12	10.05	11.13	0.27	0.27	1.30E-03	1.56E-02	Multiple_Complex
TC0100012849.hg.1	CASZ1	castor zinc finger 1	-2.12	5.77	6.86	0.05	0.22	1.50E-03	1.67E-02	Multiple_Complex
TC0200012074.hg.1	EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	-2.12	8.48	9.56	0.06	0.13	4.00E-04	9.70E-03	Multiple_Complex
TC0500011648.hg.1	EFNA5	ephrin-A5	-2.12	9.51	10.59	0.52	0.2	2.30E-03	2.12E-02	Multiple_Complex
TC0200010805.hg.1	BCS1L	BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone	-2.12	8.93	10.01	0.22	0.39	1.40E-03	1.61E-02	Multiple_Complex
TC1700012076.hg.1	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	-2.12	13.08	14.17	0.13	0.13	4.00E-04	9.70E-03	Multiple_Complex
TC1200009457.hg.1	ULK1	unc-51 like autophagy activating kinase 1	-2.12	7.62	8.71	0.44	0.35	2.00E-03	1.95E-02	Multiple_Complex
TC0500009652.hg.1	HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B	-2.12	13.23	14.32	0.4	0.05	9.00E-04	1.34E-02	Multiple_Complex
TC1200010926.hg.1	BAZ2A	bromodomain adjacent to zinc finger domain 2A	-2.12	9.28	10.37	0.34	0.18	9.00E-04	1.31E-02	Multiple_Complex
TC1900007313.hg.1	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	-2.12	8.8	9.89	0.42	0.22	4.30E-03	3.10E-02	Multiple_Complex
TC2100007534.hg.1	TEKT4P2	tektin 4 pseudogene 2	-2.12	7.61	8.69	0.31	0.2	1.10E-03	1.45E-02	Multiple_Complex
TC1500007062.hg.1	CKMT1B; CKMT1A	creatine kinase, mitochondrial 1B; creatine kinase, mitochondrial 1A	-2.12	5.13	6.22	0.24	0.86	2.21E-02	9.09E-02	Multiple_Complex
TC0300011173.hg.1	NT5DC2	5-nucleotidase domain containing 2	-2.12	14.4	15.48	0.23	0.09	5.00E-04	1.04E-02	Multiple_Complex
TC2200008459.hg.1	MORC2	MORC family CW-type zinc finger 2	-2.13	8.25	9.34	0.37	0.01	1.40E-03	1.64E-02	Multiple_Complex
TC0900012080.hg.1	ARRDC1-AS1	ARRDC1 antisense RNA 1	-2.13	10.41	11.49	0.22	0.25	1.20E-03	1.52E-02	Multiple_Complex

TC0X00011173.hg.1	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	-2.13	8.89	9.97	0.31	0.63	6.30E-03	3.95E-02	Multiple_Complex
TC1700012092.hg.1	DUS1L	dihydrouridine synthase 1-like	-2.13	8.07	9.16	0.2	0.43	1.80E-03	1.88E-02	Multiple_Complex
TC1100013036.hg.1	PPP2R5B	protein phosphatase 2, regulatory subunit B, beta	-2.13	8.19	9.28	0.27	0.04	1.40E-03	1.64E-02	Multiple_Complex
TC0700011563.hg.1	STYXL1	serine/threonine/tyrosine interacting-like 1	-2.13	10.72	11.81	0.04	0.01	4.00E-04	9.50E-03	Multiple_Complex
TC2000007488.hg.1	PIGT	phosphatidylinositol glycan anchor biosynthesis class T	-2.13	10.41	11.49	0.19	0.02	1.10E-03	1.42E-02	Multiple_Complex
TC1900007384.hg.1	GDF15	growth differentiation factor 15	-2.13	7.21	8.3	0.03	0.23	1.30E-03	1.59E-02	Multiple_Complex
TC0900011992.hg.1	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2	-2.13	6.87	7.96	0.18	0	5.00E-04	1.07E-02	Multiple_Complex
TC1200012533.hg.1	POLE	polymerase (DNA directed), epsilon, catalytic subunit	-2.13	6.62	7.71	0.05	0.13	6.00E-04	1.10E-02	Multiple_Complex
TC0600008064.hg.1	PPP2R5D	protein phosphatase 2, regulatory subunit B, delta	-2.13	8.85	9.94	0.03	0.26	1.70E-03	1.77E-02	Multiple_Complex
TC0100014349.hg.1	JUN	jun proto-oncogene	-2.13	12.14	13.23	0.62	0.23	3.20E-03	2.60E-02	Multiple_Complex
TC0300011247.hg.1	WNT5A	wingless-type MMTV integration site family, member 5A	-2.13	6.43	7.52	0.37	0.12	1.50E-03	1.67E-02	Multiple_Complex
TC2000009944.hg.1	RTFDC1	replication termination factor 2 domain containing 1	-2.13	10.6	11.69	0.19	0.13	7.00E-04	1.17E-02	Multiple_Complex
TC1900008146.hg.1	CCDC97	coiled-coil domain containing 97	-2.13	9.74	10.83	0.22	0.12	8.00E-04	1.25E-02	Coding
TC1600006760.hg.1	UBN1	ubinuclein 1	-2.13	10.1	11.19	0.28	0.03	1.20E-03	1.52E-02	Multiple_Complex
TC2100006909.hg.1	HUNK	hormonally up-regulated Neu-associated kinase	-2.13	5.92	7.01	0.23	0.37	8.50E-03	4.82E-02	Multiple_Complex
TC1200010977.hg.1	CDK4	cyclin-dependent kinase 4	-2.13	13.32	14.41	0.1	0.09	3.00E-04	8.20E-03	Multiple_Complex
TC2200007505.hg.1	03-Sep	septin 3	-2.13	9.78	10.87	0.39	0.19	1.10E-03	1.43E-02	Multiple_Complex
TC0100010123.hg.1	FDPS	farnesyl diphosphate synthase	-2.13	10.21	11.3	0.42	0.17	1.40E-03	1.64E-02	Multiple_Complex
TC1500007554.hg.1	ZNF609	zinc finger protein 609	-2.13	8.08	9.17	0.39	0.12	1.00E-03	1.40E-02	Multiple_Complex
TC2200006678.hg.1	SNAP29	synaptosome associated protein 29kDa	-2.13	10.19	11.29	0.09	0.24	5.00E-04	1.02E-02	Multiple_Complex

TC0300009866.hg.1	CCDC50	coiled-coil domain containing 50	-2.13	7.33	8.42	0.31	0.13	8.00E-04	1.25E-02	Multiple_Complex
TC1100013138.hg.1	RRP8	ribosomal RNA processing 8, methyltransferase, homolog (yeast)	-2.13	8.81	9.9	0.31	0.01	7.00E-04	1.22E-02	Multiple_Complex
TC0900009209.hg.1	PMPCA	peptidase (mitochondrial processing) alpha	-2.13	7.58	8.68	0.31	0.1	7.00E-04	1.20E-02	Multiple_Complex
TC0100012593.hg.1	WRAP73	WD repeat containing, antisense to TP73	-2.13	5.5	6.59	0.89	0.56	1.76E-02	7.81E-02	Multiple_Complex
TC1000010930.hg.1	PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	-2.13	10.01	11.1	0.03	0.16	4.00E-04	9.30E-03	Multiple_Complex
TC0100013229.hg.1	HSPG2	heparan sulfate proteoglycan 2	-2.14	6.12	7.21	0.25	0.07	9.00E-04	1.30E-02	Multiple_Complex
TC1700009378.hg.1	PITPNA	phosphatidylinositol transfer protein, alpha	-2.14	9.23	10.32	0.03	0.04	3.00E-04	8.00E-03	Multiple_Complex
TC0300009247.hg.1	ARHGEF26	Rho guanine nucleotide exchange factor 26	-2.14	6.09	7.19	0.29	0.19	9.00E-04	1.34E-02	Multiple_Complex
TC1500010854.hg.1	GPR176	G protein-coupled receptor 176	-2.14	6.63	7.73	0.62	0.09	2.90E-03	2.41E-02	Multiple_Complex
TC2100007263.hg.1	PDE9A	phosphodiesterase 9A	-2.14	8.7	9.79	0.07	0.24	9.00E-04	1.32E-02	Multiple_Complex
TC1100008505.hg.1	EMSY	EMSY BRCA2-interacting transcriptional repressor	-2.14	10.14	11.23	0.47	0.09	1.20E-03	1.50E-02	Multiple_Complex
TC0300014093.hg.1	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	-2.14	8.36	9.46	0.01	0.39	2.50E-03	2.21E-02	Multiple_Complex
TC1900011031.hg.1	KPTN	kaptin (actin binding protein)	-2.14	5.44	6.54	0.08	0.11	2.12E-02	8.82E-02	Multiple_Complex
TC2000008860.hg.1	COMMD7	COMM domain containing 7	-2.14	9.27	10.36	0.3	0	1.00E-03	1.40E-02	Multiple_Complex
TC0300006555.hg.1	BRPF1	bromodomain and PHD finger containing 1	-2.14	6.35	7.45	0.75	0.28	8.80E-03	4.93E-02	Multiple_Complex
TC1600009040.hg.1	C16orf91	chromosome 16 open reading frame 91	-2.14	9.23	10.33	0.21	0.59	2.50E-03	2.25E-02	Multiple_Complex
TC0700010020.hg.1	PSMG3	proteasome (prosome, macropain) assembly chaperone 3	-2.14	11.98	13.08	0.08	0.07	3.00E-04	8.10E-03	Multiple_Complex
TC0300012323.hg.1	MGLL	monoglyceride lipase	-2.14	4.74	5.83	0.23	0.07	7.00E-04	1.17E-02	Multiple_Complex
TC1900008498.hg.1	NUCB1	nucleobindin 1	-2.14	7.63	8.73	0.11	0.03	4.00E-04	9.10E-03	Multiple_Complex

TC0900009290.hg.1	NOXA1	NADPH oxidase activator 1	-2.14	5.94	7.04	0.39	0.33	2.90E-03	2.45E-02	Coding
TC0900012066.hg.1	NSMF; MIR7114	NMDA receptor synaptonuclear signaling and neuronal migration factor; microRNA 7114	-2.14	8.39	9.49	0.23	0.7	5.30E-03	3.52E-02	Multiple_Complex
TC0600014273.hg.1	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	-2.14	6.14	7.24	0.54	0.1	6.70E-03	4.12E-02	Multiple_Complex
TC1100012834.hg.1	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif 8	-2.14	5.15	6.25	0.41	0.17	1.40E-03	1.64E-02	Multiple_Complex
TC2200008710.hg.1	JOSD1	Josephin domain containing 1	-2.14	11.83	12.93	0.19	0.17	4.00E-04	9.90E-03	Multiple_Complex
TC1100011092.hg.1	GANAB	glucosidase, alpha; neutral AB	-2.14	12.73	13.83	0.15	0.01	6.00E-04	1.07E-02	Multiple_Complex
TSUnmapped00000169.hg.1	TCF20	transcription factor 20 (AR1)	-2.14	7.96	9.06	0.79	0.11	6.40E-03	3.96E-02	Coding
TSUnmapped00000402.hg.1	TCF20	transcription factor 20 (AR1)	-2.14	7.96	9.06	0.79	0.11	6.40E-03	3.96E-02	Coding
TC1600009420.hg.1	RSL1D1	ribosomal L1 domain containing 1	-2.15	11.48	12.58	0.34	0.16	8.00E-04	1.27E-02	Multiple_Complex
TC1000011923.hg.1	GFRA1	GDNF family receptor alpha 1	-2.15	7.42	8.52	0.12	0.14	4.00E-04	9.50E-03	Multiple_Complex
TSUnmapped00000236.hg.1	TCF20	transcription factor 20 (AR1)	-2.15	7.79	8.89	0.78	0.1	5.70E-03	3.70E-02	Coding
TSUnmapped00000511.hg.1	TCF20	transcription factor 20 (AR1)	-2.15	7.79	8.89	0.78	0.1	5.70E-03	3.70E-02	Coding
TC0200015739.hg.1	ZNF142	zinc finger protein 142	-2.15	9.2	10.31	0.04	0.22	4.00E-04	9.00E-03	Multiple_Complex
TC0700007857.hg.1	TMEM248	transmembrane protein 248	-2.15	8.9	10	0.39	0.2	1.50E-03	1.68E-02	Multiple_Complex
TC0100017586.hg.1	C1orf35	chromosome 1 open reading frame 35	-2.15	8.75	9.85	0.05	0.11	7.00E-04	1.21E-02	Multiple_Complex
TC1900008019.hg.1	EIF3K	eukaryotic translation initiation factor 3, subunit K	-2.15	14.18	15.29	0.16	0.1	4.00E-04	9.80E-03	Multiple_Complex
TC1600007113.hg.1	C16orf62	chromosome 16 open reading frame 62	-2.15	9.17	10.27	0.41	0.07	3.10E-03	2.53E-02	Multiple_Complex
TC1800007620.hg.1	SOCS6	suppressor of cytokine signaling 6	-2.15	4.66	5.76	0.2	0.28	8.00E-04	1.23E-02	Multiple_Complex

TC1700010851.hg.1	KIF18B	kinesin family member 18B	-2.15	8.98	10.09	0.84	0.3	8.70E-03	4.89E-02	Multiple_Complex
TC0500009580.hg.1	SIMC1	SUMO-interacting motifs containing 1	-2.15	9.46	10.56	0.29	0.11	1.81E-02	7.98E-02	Multiple_Complex
TC2100008508.hg.1	CHAF1B	chromatin assembly factor 1, subunit B (p60)	-2.15	11.28	12.38	0.27	0.03	5.00E-04	1.07E-02	Multiple_Complex
TC0500009599.hg.1	TSPAN17	tetraspanin 17	-2.15	5.47	6.58	0.47	0.15	2.40E-03	2.20E-02	Multiple_Complex
TC0100007512.hg.1	GPR3	G protein-coupled receptor 3	-2.15	5.74	6.84	0.92	0.23	1.16E-02	5.92E-02	Coding
TC0100014889.hg.1	BARHL2	BarH-like homeobox 2	-2.15	7.69	8.79	0.04	0.16	1.40E-03	1.64E-02	Coding
TC1400009732.hg.1	C14orf1	chromosome 14 open reading frame 1	-2.15	12.34	13.44	0.02	0.1	4.00E-04	9.20E-03	Multiple_Complex
TC0100015890.hg.1	DENND4B	DENN/MADD domain containing 4B	-2.15	6.8	7.91	0.54	0.98	1.88E-02	8.17E-02	Multiple_Complex
TC0300009701.hg.1	PSMD2	proteasome 26S subunit, non-ATPase 2	-2.15	8.29	9.39	0.54	0.01	5.20E-03	3.48E-02	Multiple_Complex
TC0700011982.hg.1	GATS	GATS, stromal antigen 3 opposite strand	-2.15	6.82	7.93	0.23	0.47	2.10E-03	2.00E-02	Multiple_Complex
TC2200006862.hg.1	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-2.15	8.07	9.17	0.24	0.13	1.70E-03	1.80E-02	Multiple_Complex
TC1000008048.hg.1	ZSWIM8	zinc finger, SWIM-type containing 8	-2.15	8.97	10.07	0.54	0.28	2.90E-03	2.45E-02	Multiple_Complex
TC0900011846.hg.1	REXO4	REX4 homolog, 3-5 exonuclease	-2.15	8.57	9.68	0.16	0.22	5.00E-04	1.00E-02	Multiple_Complex
TC0500007676.hg.1	MARVELD2	MARVEL domain containing 2	-2.15	10.33	11.43	0.17	0.05	3.00E-04	8.40E-03	Multiple_Complex
TC1700010571.hg.1	MED1	mediator complex subunit 1	-2.15	11.07	12.18	0.25	0.1	5.00E-04	1.01E-02	Multiple_Complex
TC1700010101.hg.1	C17orf51	chromosome 17 open reading frame 51	-2.15	7.39	8.5	0.1	0.33	1.70E-03	1.79E-02	Multiple_Complex
TC1700010436.hg.1	PEX12	peroxisomal biogenesis factor 12	-2.16	7.45	8.56	0.16	0.1	3.00E-04	8.30E-03	Coding
TC0700011476.hg.1	NSUN5P2; NSUN5P1	NOP2/Sun domain family, member 5 pseudogene 2; NOP2/Sun domain family, member 5 pseudogene 1	-2.16	10.28	11.38	0.05	0.2	4.00E-04	9.30E-03	Multiple_Complex
TC1000011592.hg.1	COX15	cytochrome c oxidase assembly homolog 15 (yeast)	-2.16	9.74	10.85	0.4	0.2	1.30E-03	1.57E-02	Multiple_Complex

TC1700012352.hg.1	TRAPPC1	trafficking protein particle complex 1	-2.16	11.07	12.18	0.04	0.07	3.00E-04	8.00E-03	Multiple_Complex
TC1100007826.hg.1	BEST1	bestrophin 1	-2.16	6.89	7.99	0.47	0.11	1.60E-03	1.73E-02	Multiple_Complex
TC0700012734.hg.1	CREB3L2	cAMP responsive element binding protein 3-like 2	-2.16	8.68	9.78	0.05	0.1	3.00E-04	8.00E-03	Multiple_Complex
TC1700010497.hg.1	SYNRG	synergin, gamma	-2.16	9.12	10.23	0.57	0.15	2.40E-03	2.16E-02	Multiple_Complex
TC0100015957.hg.1	ASH1L; MIR555	ash1 (absent, small, or homeotic)-like (Drosophila); microRNA 555	-2.16	10.3	11.41	0.38	0.26	1.50E-03	1.66E-02	Multiple_Complex
TC0100015793.hg.1	POGZ	Transcript Identified by AceView, Entrez Gene ID(s) 23126	-2.16	4.66	5.78	0.13	0.8	9.90E-03	5.32E-02	Unassigned
TC1200012711.hg.1	LINC00173	long intergenic non-protein coding RNA 173	-2.16	7	8.11	0.05	0.48	2.90E-03	2.45E-02	NonCoding
TC0900011829.hg.1	RALGDS	ral guanine nucleotide dissociation stimulator	-2.16	5.65	6.77	0.12	0.23	9.00E-04	1.29E-02	Multiple_Complex
TC1400008478.hg.1	PACS2	phosphofurin acidic cluster sorting protein 2	-2.16	7.07	8.19	0.05	0.05	4.00E-04	9.70E-03	Multiple_Complex
TC2200009275.hg.1	ADSL	adenylosuccinate lyase	-2.16	8.93	10.04	0.79	0.15	7.30E-03	4.32E-02	Multiple_Complex
TC0100013854.hg.1	SCMH1	sex comb on midleg homolog 1 (Drosophila)	-2.16	9.39	10.5	0.1	0.02	4.00E-04	9.90E-03	Multiple_Complex
TC0800009113.hg.1	PTP4A3	protein tyrosine phosphatase type IVA, member 3	-2.16	9.02	10.13	0.09	0.13	3.00E-04	8.00E-03	Multiple_Complex
TC1300008487.hg.1	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-2.16	11.49	12.6	0.06	0.16	3.00E-04	8.00E-03	Multiple_Complex
TC0100009339.hg.1	TMEM167B	transmembrane protein 167B	-2.16	10.1	11.21	0.31	0.18	8.00E-04	1.23E-02	Multiple_Complex
TC1200009753.hg.1	MLF2	myeloid leukemia factor 2	-2.16	11.01	12.12	0.07	0.01	3.00E-04	8.00E-03	Multiple_Complex
TC1700011892.hg.1	TK1	thymidine kinase 1, soluble	-2.17	6.15	7.27	0.22	0.07	1.00E-03	1.40E-02	Multiple_Complex
TC0300012728.hg.1	PLSCR1	phospholipid scramblase 1	-2.17	7.17	8.29	0.39	0.13	1.00E-03	1.40E-02	Multiple_Complex
TC1200009183.hg.1	SETD1B	SET domain containing 1B	-2.17	6.57	7.69	0.13	0.14	6.00E-04	1.08E-02	Multiple_Complex
TC1700011652.hg.1	FAM104A	family with sequence similarity 104, member A	-2.17	6.52	7.63	0.3	0.5	4.90E-03	3.34E-02	Multiple_Complex

TC0100008082.hg.1	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	-2.17	8.03	9.15	0.99	0.3	1.41E-02	6.75E-02	Multiple_Complex
TC0200010852.hg.1	GMPPA	GDP-mannose pyrophosphorylase A	-2.17	9.13	10.25	0.28	0.14	6.00E-04	1.13E-02	Multiple_Complex
TC1100011545.hg.1	ANAPC15	anaphase promoting complex subunit 15	-2.17	9.64	10.75	0.06	0.24	4.00E-04	9.10E-03	Multiple_Complex
TC1700011424.hg.1	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	-2.17	11.41	12.53	0.48	0.14	1.50E-03	1.65E-02	Multiple_Complex
TC0100015918.hg.1	UBE2Q1	ubiquitin-conjugating enzyme E2Q family member 1	-2.17	11.49	12.61	0.39	0.14	8.00E-04	1.25E-02	Multiple_Complex
TC0400012905.hg.1	QDPR	quinoid dihydropteridine reductase	-2.17	8.6	9.72	0.46	0.11	1.10E-03	1.47E-02	Multiple_Complex
TC2000008960.hg.1	EDEM2	ER degradation enhancer, mannosidase alpha-like 2	-2.17	7.82	8.94	0.23	0.12	4.00E-04	9.30E-03	Multiple_Complex
TC0300007610.hg.1	PXK	PX domain containing serine/threonine kinase	-2.17	10.59	11.7	0.47	0.1	3.20E-03	2.59E-02	Multiple_Complex
TC0200010796.hg.1	CTDSP1	CTD small phosphatase 1	-2.17	6.23	7.35	0.32	0.27	1.20E-03	1.50E-02	Multiple_Complex
TC1600009202.hg.1	CREBBP	CREB binding protein	-2.17	12.28	13.4	0.05	0.16	6.00E-04	1.16E-02	Multiple_Complex
TC1000008942.hg.1	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	-2.17	6.12	7.24	0.24	0.06	4.00E-04	9.90E-03	Multiple_Complex
TC1200007864.hg.1	NXPH4	neurexophilin 4	-2.17	5.28	6.4	0.08	0.16	2.10E-03	2.04E-02	Multiple_Complex
TC0900011610.hg.1	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	-2.17	6.3	7.41	0.13	0.19	1.00E-03	1.40E-02	Multiple_Complex
TC0100018390.hg.1	SLC35E2	solute carrier family 35, member E2	-2.17	9.66	10.78	0.4	0.26	2.80E-03	2.41E-02	Multiple_Complex
TC1100012389.hg.1	CADM1	cell adhesion molecule 1	-2.17	8.55	9.67	0.62	0.25	2.05E-02	8.64E-02	Multiple_Complex
TC2200008832.hg.1	DESI1	desumoylating isopeptidase 1	-2.17	11.65	12.77	0.63	0.26	3.60E-03	2.79E-02	Multiple_Complex
TC2000009903.hg.1	HM13; MCTS2P	histocompatibility (minor) 13; malignant T-cell amplified sequence 2, pseudogene	-2.17	12.64	13.76	0.2	0	4.00E-04	9.50E-03	Multiple_Complex

TC0100013629.hg.1	YARS	tyrosyl-tRNA synthetase	-2.17	12.39	13.51	0.12	0.28	5.00E-04	1.03E-02	Multiple_Complex
TC0300008702.hg.1	MCM2	minichromosome maintenance complex component 2	-2.17	10.48	11.6	0.37	0.04	1.20E-03	1.50E-02	Multiple_Complex
TC0600009140.hg.1	GTF3C6	general transcription factor IIIC subunit 6	-2.18	10.64	11.76	0.18	0.05	3.00E-04	8.80E-03	Multiple_Complex
TC0200011386.hg.1	PPP1R7	protein phosphatase 1, regulatory subunit 7	-2.18	10.48	11.6	0.28	0.1	1.20E-03	1.50E-02	Multiple_Complex
TC1900007181.hg.1	TECR; MIR639	trans-2,3-enoyl-CoA reductase; microRNA 639	-2.18	12.23	13.35	0.17	0.12	5.00E-04	1.00E-02	Multiple_Complex
TC1900008384.hg.1	CALM3	calmodulin 3 (phosphorylase kinase, delta)	-2.18	11.6	12.72	0.07	0	4.00E-04	9.30E-03	Multiple_Complex
TC1600008149.hg.1	E2F4	E2F transcription factor 4, p107/p130-binding	-2.18	8.25	9.37	0.54	0.19	2.30E-03	2.12E-02	Multiple_Complex
TC0700012712.hg.1	LUZP6; MTPN	leucine zipper protein 6; myotrophin	-2.18	11.26	12.38	0.01	0.02	2.00E-04	7.10E-03	Multiple_Complex
TC0100011692.hg.1	MIA3	melanoma inhibitory activity family, member 3	-2.18	11.86	12.99	0.18	0.07	4.00E-04	9.10E-03	Multiple_Complex
TC1700009686.hg.1	SLC25A35	solute carrier family 25, member 35	-2.18	6.54	7.67	0.13	0.35	2.30E-03	2.15E-02	Multiple_Complex
TC1000010990.hg.1	DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12	-2.18	8.52	9.64	0.13	0.19	6.00E-04	1.07E-02	Multiple_Complex
TC2200009351.hg.1	CSNK1E	casein kinase 1, epsilon	-2.18	13.82	14.94	0.35	0.06	6.00E-04	1.08E-02	Coding
TC0500012236.hg.1	PFDN1	prefoldin subunit 1	-2.18	8.67	9.8	0.21	0.05	4.00E-04	9.60E-03	Multiple_Complex
TC0900008953.hg.1	ASS1	argininosuccinate synthase 1	-2.18	12.44	13.56	0.21	0.01	4.00E-04	9.30E-03	Multiple_Complex
TC1200010946.hg.1	NEMP1	nuclear envelope integral membrane protein 1	-2.18	11.93	13.06	0.11	0.24	7.00E-04	1.17E-02	Multiple_Complex
TC1200009071.hg.1	PEBP1	phosphatidylethanolamine binding protein 1	-2.18	9.68	10.8	0.43	0.06	8.00E-04	1.27E-02	Multiple_Complex
TSUnmapped00000327.hg.1	HYOU1	hypoxia up-regulated 1	-2.18	10.79	11.91	0.51	0.22	1.60E-03	1.76E-02	Coding
TC0600014275.hg.1	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	-2.18	5.89	7.02	0.64	0.17	3.60E-03	2.77E-02	Multiple_Complex
TC1000008668.hg.1	SFXN3	sideroflexin 3	-2.18	7.63	8.76	0.02	0.35	1.70E-03	1.82E-02	Multiple_Complex
TC2100008538.hg.1	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	-2.18	5.88	7.01	0.11	0.1	6.00E-04	1.13E-02	Multiple_Complex

TC1200010686.hg.1	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 2	-2.18	5.85	6.98	0.33	0.37	2.50E-03	2.22E-02	Multiple_Complex
TC1700008019.hg.1	CCDC103	coiled-coil domain containing 103	-2.18	5.58	6.7	0.4	0.31	1.70E-03	1.80E-02	Coding
TC1900007988.hg.1	SIPA1L3	signal-induced proliferation-associated 1 like 3	-2.19	8.58	9.71	0.04	0.09	2.00E-04	7.40E-03	Multiple_Complex
TC1900011787.hg.1	POLD1	polymerase (DNA directed), delta 1, catalytic subunit	-2.19	9.9	11.03	0.39	0.48	4.70E-03	3.26E-02	Multiple_Complex
TC0700010046.hg.1	FTSJ2	FtsJ RNA methyltransferase homolog 2 (E. coli)	-2.19	6.83	7.96	0.43	0.48	2.60E-03	2.29E-02	Multiple_Complex
TC0700012761.hg.1	ZC3HAV1	zinc finger CCCH-type, antiviral 1	-2.19	7.52	8.65	0.05	0.19	7.00E-04	1.16E-02	Multiple_Complex
TC0200016360.hg.1	STK25	serine/threonine kinase 25	-2.19	10.59	11.72	0.09	0.08	6.00E-04	1.15E-02	Multiple_Complex
TC1200012790.hg.1	KMT2D	lysine (K)-specific methyltransferase 2D	-2.19	8.37	9.5	0.08	0.22	3.00E-04	8.30E-03	Multiple_Complex
TC1900007115.hg.1	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	-2.19	7.4	8.53	0.23	0.08	5.00E-04	1.04E-02	Multiple_Complex
TC1700010230.hg.1	TIAF1; MYO18A	TGFB1-induced anti-apoptotic factor 1; myosin XVIIIA	-2.19	6.4	7.53	0.41	0.47	2.80E-03	2.39E-02	Multiple_Complex
TC1900007108.hg.1	CALR	calreticulin	-2.19	12.76	13.89	0.08	0.25	4.00E-04	9.50E-03	Multiple_Complex
TC1400006551.hg.1	ARHGEF40	Rho guanine nucleotide exchange factor (GEF) 40	-2.19	7.01	8.15	0.3	0.27	9.00E-04	1.34E-02	Multiple_Complex
TC0600014198.hg.1	TULP4	tubby like protein 4	-2.19	10.44	11.58	0.31	0.18	7.00E-04	1.21E-02	Multiple_Complex
TC1700007105.hg.1	LLGL1	lethal giant larvae homolog 1 (Drosophila)	-2.19	8.88	10.01	0.25	0.38	4.10E-03	3.01E-02	Multiple_Complex
TC0100015991.hg.1	SMG5	SMG5 nonsense mediated mRNA decay factor	-2.19	8.32	9.45	0.06	0.4	8.00E-04	1.23E-02	Multiple_Complex
TC1100007906.hg.1	RTN3	reticulon 3	-2.19	14.15	15.28	0.34	0.05	8.00E-04	1.26E-02	Multiple_Complex
TC0700012836.hg.1	KIAA1147	KIAA1147	-2.2	8.1	9.24	0.14	0.06	1.00E-03	1.36E-02	Multiple_Complex
TC1600011115.hg.1	EMC8	ER membrane protein complex subunit 8	-2.2	8.98	10.11	0.9	0.3	1.07E-02	5.59E-02	Multiple_Complex
TC1500009736.hg.1	PPIB	peptidylprolyl isomerase B (cyclophilin B)	-2.2	10.01	11.14	0.11	0.18	3.00E-04	8.00E-03	Multiple_Complex

TC0100014365.hg.1	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	-2.2	7.87	9.01	0.05	0.04	8.00E-04	1.25E-02	Multiple_Complex
TC1100006576.hg.1	CD81	CD81 molecule	-2.2	9.12	10.26	0.52	0.17	1.60E-03	1.76E-02	Multiple_Complex
TC0300007432.hg.1	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	-2.2	8.88	10.02	0.67	0.81	1.30E-02	6.37E-02	Multiple_Complex
TC0500012979.hg.1	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	-2.2	11.3	12.44	0.18	0.05	5.00E-04	1.02E-02	Multiple_Complex
TC1200011320.hg.1	BBS10	Bardet-Biedl syndrome 10	-2.2	10.84	11.98	0.53	0.19	1.80E-03	1.85E-02	Coding
TC0600013542.hg.1	ULBP3	UL16 binding protein 3	-2.2	8.02	9.16	0.21	0.13	6.00E-04	1.08E-02	Coding
TC0100009524.hg.1	VANGL1	VANGL planar cell polarity protein 1	-2.2	7.97	9.11	0.6	0.04	2.10E-03	2.01E-02	Multiple_Complex
TC0100013611.hg.1	BSDC1	BSD domain containing 1	-2.2	8.34	9.48	0.2	0.01	8.00E-04	1.25E-02	Multiple_Complex
TC0100012816.hg.1	CLSTN1	calsyntenin 1	-2.2	8.15	9.29	0.14	0.1	9.00E-04	1.33E-02	Multiple_Complex
TC1200009253.hg.1	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	-2.2	11.92	13.06	0.29	0.07	6.00E-04	1.15E-02	Multiple_Complex
TC2000009967.hg.1	NSFL1C	NSFL1 (p97) cofactor (p47)	-2.2	10.8	11.94	0.2	0.16	5.00E-04	1.05E-02	Multiple_Complex
TC1100008819.hg.1	KDM4D	lysine (K)-specific demethylase 4D	-2.2	5.98	7.12	1.06	0.04	4.50E-02	1.46E-01	Coding
TC0900009861.hg.1	NOL6	nucleolar protein 6 (RNA-associated)	-2.2	4.9	6.04	0.75	0.62	1.93E-02	8.32E-02	Multiple_Complex
TC0200011125.hg.1	ATG16L1	autophagy related 16-like 1	-2.2	5.17	6.31	0.13	0.13	8.00E-04	1.24E-02	Multiple_Complex
TC0100015931.hg.1	PMVK	phosphomevalonate kinase	-2.21	6.07	7.21	0.35	0.43	1.40E-03	1.61E-02	Multiple_Complex
TC1800007829.hg.1	HSBP1L1	heat shock factor binding protein 1-like 1	-2.21	8.63	9.78	0.01	0.13	2.00E-04	7.50E-03	Multiple_Complex
TC2200007780.hg.1	CRELD2	cysteine rich with EGF-like domains 2	-2.21	6.64	7.78	0.45	0.19	1.20E-03	1.50E-02	Multiple_Complex
TC0100009902.hg.1	PRPF3	pre-mRNA processing factor 3	-2.21	9.56	10.7	0.03	0.07	3.00E-04	8.00E-03	Multiple_Complex
TC0900011035.hg.1	TMEM246	transmembrane protein 246	-2.21	8.56	9.7	0.29	0.24	1.90E-03	1.93E-02	Multiple_Complex
TC1700007042.hg.1	MPRIP	myosin phosphatase Rho interacting protein	-2.21	12.23	13.38	0.25	0.12	4.00E-04	9.00E-03	Multiple_Complex
TC0300008558.hg.1	DTX3L	deltex 3 like, E3 ubiquitin ligase	-2.21	5.77	6.91	0.79	0.29	6.60E-03	4.06E-02	Multiple_Complex

TC0200011991.hg.1	ADCY3	adenylate cyclase 3	-2.21	6.01	7.15	0.13	0.47	1.10E-03	1.48E-02	Multiple_Complex
TC0X00008831.hg.1	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	-2.21	8.93	10.07	0.2	0.24	7.00E-04	1.18E-02	Multiple_Complex
TC0700007374.hg.1	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	-2.21	6.79	7.94	0.08	0.01	3.00E-04	7.80E-03	Multiple_Complex
TC2200009346.hg.1	C1QTNF6	C1q and tumor necrosis factor related protein 6	-2.21	8.62	9.77	0.12	0.27	1.90E-03	1.92E-02	NonCoding
TC1400007695.hg.1	EIF2B2	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	-2.21	12.25	13.39	0.17	0.04	5.00E-04	1.02E-02	Multiple_Complex
TC2000007438.hg.1	MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	-2.21	10.34	11.49	0.17	0.31	5.00E-04	1.03E-02	Multiple_Complex
TC0300011029.hg.1	UQCRC1	ubiquinol-cytochrome c reductase core protein I	-2.21	10.29	11.44	0.24	0.14	4.00E-04	9.20E-03	Multiple_Complex
TC1600009608.hg.1	NOMO2	NODAL modulator 2	-2.21	13.09	14.24	0.03	0.1	2.00E-04	7.40E-03	Multiple_Complex
TC0X00010799.hg.1	ELF4	E74-like factor 4 (ets domain transcription factor)	-2.21	7.65	8.8	0.04	0.15	4.00E-04	9.20E-03	Multiple_Complex
TC1900011901.hg.1	SLC35E1	solute carrier family 35, member E1	-2.21	8.81	9.96	0.16	0.13	1.00E-03	1.40E-02	Multiple_Complex
TC1600011326.hg.1	HN1L	hematological and neurological expressed 1-like	-2.21	10.44	11.59	0.4	0.26	9.00E-04	1.33E-02	Multiple_Complex
TC0600014094.hg.1	TRIM39	tripartite motif containing 39	-2.22	8.54	9.69	0.62	0.01	5.00E-03	3.39E-02	Coding
TC1100011367.hg.1	UNC93B1	unc-93 homolog B1 (C. elegans)	-2.22	5.99	7.14	0.53	0.74	1.41E-02	6.75E-02	Multiple_Complex
TSUnmapped00000488.hg.1	ZDHHC3	zinc finger, DHHC-type containing 3	-2.22	10.74	11.89	0.15	0.25	4.00E-04	9.50E-03	Coding
TC1700006763.hg.1	ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	-2.22	7.03	8.18	0.52	0.06	1.30E-03	1.57E-02	Multiple_Complex
TC1200012588.hg.1	P3H3	prolyl 3-hydroxylase 3	-2.22	8.85	10	0.71	0.27	3.70E-03	2.85E-02	Multiple_Complex
TC0X00009213.hg.1	MAP7D2	MAP7 domain containing 2	-2.22	7.48	8.63	0.5	0.21	9.40E-03	5.14E-02	Multiple_Complex
TC2000009317.hg.1	SULF2	sulfatase 2	-2.22	8.98	10.13	0.12	0.14	6.00E-04	1.10E-02	Multiple_Complex

TC0900012277.hg.1	AK1	adenylate kinase 1	-2.22	10.05	11.2	0.34	0.09	5.00E-04	1.06E-02	Coding
TC1100013028.hg.1	OTUB1	OTU deubiquitinase, ubiquitin aldehyde binding 1	-2.22	11.87	13.02	0.13	0.05	3.00E-04	8.80E-03	Multiple_Complex
TC1600011555.hg.1	SLC12A4	solute carrier family 12 (potassium/chloride transporter), member 4	-2.22	7.5	8.65	0.42	0.08	1.90E-03	1.91E-02	Multiple_Complex
TC1200010927.hg.1	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	-2.22	14.81	15.96	0.03	0.1	2.00E-04	7.20E-03	Multiple_Complex
TC1700012369.hg.1	FLCN	folliculin	-2.22	9.79	10.94	0.16	0.14	7.00E-04	1.16E-02	Multiple_Complex
TC0X00011194.hg.1	FLNA	filamin A, alpha	-2.22	10.29	11.44	0.54	0.33	2.60E-03	2.28E-02	Multiple_Complex
TC1200012149.hg.1	GCN1; MIR4498	GCN1 eIF2 alpha kinase activator homolog; microRNA 4498	-2.22	11.03	12.18	0.09	0.13	4.00E-04	9.30E-03	Multiple_Complex
TC0700010463.hg.1	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	-2.22	8.24	9.39	0.78	0.13	5.20E-03	3.47E-02	Multiple_Complex
TC1900011867.hg.1	TMEM205	transmembrane protein 205	-2.22	12.26	13.41	0.11	0.1	7.00E-04	1.22E-02	Multiple_Complex
TC1900009325.hg.1	MAP2K2	mitogen-activated protein kinase kinase 2	-2.23	13.25	14.4	0.05	0.09	3.00E-04	8.20E-03	Multiple_Complex
TC1900010854.hg.1	ZNF428	zinc finger protein 428	-2.23	7.06	8.21	0.88	0.16	6.60E-03	4.05E-02	Multiple_Complex
TC1100009973.hg.1	ARFIP2	ADP-ribosylation factor interacting protein 2	-2.23	8.09	9.25	0	0.03	4.00E-04	9.20E-03	Multiple_Complex
TC1900012007.hg.1	NUP62; IL4I1	nucleoporin 62kDa; interleukin 4 induced 1	-2.23	9.35	10.5	0.68	0.04	2.40E-03	2.20E-02	Multiple_Complex
TC0200012073.hg.1	GTF3C2	general transcription factor IIIC subunit 2	-2.23	8.45	9.61	0.22	0.17	3.00E-04	8.80E-03	Multiple_Complex
TC0500008854.hg.1	ANKHD1; EIF4EBP3; ANKHD1-EIF4EBP3	ankyrin repeat and KH domain containing 1; eukaryotic translation initiation factor 4E binding protein 3; ANKHD1-EIF4EBP3 readthrough	-2.23	8.5	9.65	0.33	0.15	1.10E-03	1.46E-02	Multiple_Complex
TC1100013071.hg.1	POLD3	polymerase (DNA-directed), delta 3, accessory subunit	-2.23	10.46	11.62	0.12	0.04	3.00E-04	8.10E-03	Multiple_Complex
TC2000007717.hg.1	MOCS3	molybdenum cofactor synthesis 3	-2.23	6.61	7.77	0.03	0.08	7.00E-04	1.19E-02	Coding
TC0300009890.hg.1	HRASLS	HRAS-like suppressor	-2.23	9.09	10.25	0.22	0.04	5.00E-04	1.04E-02	Coding

TC0200009938.hg.1	GORASP2	golgi reassembly stacking protein 2	-2.23	10.41	11.57	0.12	0.23	8.00E-04	1.27E-02	Multiple_Complex
TC1700008563.hg.1	DCAF7	DDB1 and CUL4 associated factor 7	-2.23	11.24	12.4	0.2	0.01	1.50E-03	1.70E-02	Multiple_Complex
TC1100013022.hg.1	FADS2	fatty acid desaturase 2	-2.23	8.95	10.11	0.32	0.52	1.80E-03	1.86E-02	Multiple_Complex
TC0X00009762.hg.1	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	-2.23	11.02	12.18	0.33	0.11	7.00E-04	1.16E-02	Multiple_Complex
TC1600009035.hg.1	TSR3	TSR3, 20S rRNA accumulation, homolog (S. cerevisiae)	-2.24	7.94	9.1	0.32	0.07	4.00E-04	9.80E-03	Multiple_Complex
TC1900007760.hg.1	FAAP24	Fanconi anemia core complex associated protein 24	-2.24	7.88	9.04	0.17	0.3	7.00E-04	1.17E-02	Multiple_Complex
TC2200008847.hg.1	CENPM	centromere protein M	-2.24	9.15	10.32	0.05	0.25	4.00E-04	9.70E-03	Multiple_Complex
TC0200013079.hg.1	DUSP11	dual specificity phosphatase 11	-2.24	12.19	13.35	0.46	0.02	8.00E-04	1.26E-02	Multiple_Complex
TC1000011669.hg.1	LDB1	LIM domain binding 1	-2.24	10.32	11.48	0.46	0.07	1.00E-03	1.36E-02	Multiple_Complex
TC0200014249.hg.1	CCDC74B	coiled-coil domain containing 74B	-2.24	7.71	8.87	0.5	0	5.10E-03	3.43E-02	Multiple_Complex
TC0700009606.hg.1	ZNF282	zinc finger protein 282	-2.24	8.66	9.82	0.17	0.09	3.00E-04	8.60E-03	Multiple_Complex
TC0100007584.hg.1	PTPRU	protein tyrosine phosphatase, receptor type, U	-2.24	9.49	10.65	0.16	0.25	3.00E-03	2.48E-02	Multiple_Complex
TC2200007932.hg.1	PI4KAP1	phosphatidylinositol 4-kinase, catalytic, alpha pseudogene 1	-2.24	10.43	11.59	0.74	0.32	7.00E-03	4.21E-02	Multiple_Complex
TC1700008102.hg.1	LRRC37A2	leucine rich repeat containing 37, member A2	-2.24	10.19	11.35	0.67	0.08	4.70E-03	3.28E-02	Multiple_Complex
TC0500010932.hg.1	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	-2.24	8.01	9.17	0.76	0.36	1.36E-02	6.57E-02	Multiple_Complex
TC0700006466.hg.1	DNAAF5	dynein, axonemal, assembly factor 5	-2.24	6.63	7.8	1.11	0.18	1.89E-02	8.17E-02	Multiple_Complex
TC1900010037.hg.1	SUGP2	SURP and G-patch domain containing 2	-2.24	8.39	9.56	0.11	0.12	7.00E-04	1.21E-02	Multiple_Complex
TC0900007064.hg.1	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	-2.24	9.28	10.44	0.3	0.04	4.00E-04	9.40E-03	Coding
TC1400010703.hg.1	MTA1	metastasis associated 1	-2.24	10.02	11.18	0.24	0.03	3.00E-04	8.60E-03	Multiple_Complex

TC2000010007.hg.1	RBM12; CPNE1	RNA binding motif protein 12; copine I	-2.24	9.3	10.46	0.53	0.23	3.20E-03	2.59E-02	Multiple_Complex
TC1700009327.hg.1	GEMIN4	gem nuclear organelle associated protein 4	-2.24	6.63	7.79	0.29	0.46	2.20E-03	2.08E-02	Multiple_Complex
TC0X00007353.hg.1	TSR2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	-2.24	7.44	8.6	0.31	0.11	7.00E-04	1.17E-02	Coding
TC0400006538.hg.1	TACC3	transforming, acidic coiled-coil containing protein 3	-2.24	8.37	9.53	0.14	0.27	4.00E-04	9.70E-03	Multiple_Complex
TC0200016686.hg.1	TEX261	testis expressed 261	-2.24	8.69	9.86	0.56	0.31	1.90E-03	1.90E-02	Multiple_Complex
TC0700010561.hg.1	HOXA5	homeobox A5	-2.24	9.33	10.5	0.09	0.08	2.00E-04	7.00E-03	Multiple_Complex
TC1900011067.hg.1	TMEM143	transmembrane protein 143	-2.24	3.39	4.55	0.19	0.36	5.60E-03	3.67E-02	Multiple_Complex
TC0700012812.hg.1	MKRN1	makorin ring finger protein 1	-2.24	8.46	9.63	0.06	0.27	5.00E-04	1.02E-02	Multiple_Complex
TC1500008267.hg.1	TICRR	TOPBP1-interacting checkpoint and replication regulator	-2.24	6.41	7.57	0.23	0.03	1.80E-03	1.83E-02	Multiple_Complex
TC0600011857.hg.1	CUL7	cullin 7	-2.24	8.58	9.74	0.05	0.41	1.60E-03	1.74E-02	Multiple_Complex
TC0500012937.hg.1	NOP16	NOP16 nucleolar protein	-2.24	10.36	11.53	0.39	0.08	5.00E-04	1.07E-02	Multiple_Complex
TC1600009422.hg.1	GSPT1	G1 to S phase transition 1	-2.24	10.3	11.46	0.07	0.25	3.00E-04	8.00E-03	Multiple_Complex
TC0200013517.hg.1	SNRNP200	small nuclear ribonucleoprotein, U5 200kDa subunit	-2.24	13.78	14.94	0.3	0.04	4.00E-04	9.00E-03	Multiple_Complex
TC1600010680.hg.1	SLC7A6OS	solute carrier family 7, member 6 opposite strand	-2.25	7.2	8.36	0.91	0.25	8.50E-03	4.84E-02	Multiple_Complex
TC0500009609.hg.1	FGFR4	fibroblast growth factor receptor 4	-2.25	9.95	11.12	0.02	0.08	5.00E-04	1.06E-02	Multiple_Complex
TC1900008689.hg.1	PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	-2.25	6.77	7.94	0.31	0.07	2.10E-03	2.02E-02	Multiple_Complex
TC1500007851.hg.1	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	-2.25	8.34	9.51	0	0.6	2.20E-03	2.05E-02	Multiple_Complex
TC1900006576.hg.1	DOT1L	DOT1-like histone H3K79 methyltransferase	-2.25	6.86	8.03	0.24	0.28	1.30E-03	1.55E-02	Multiple_Complex
TC0200013750.hg.1	FHL2	four and a half LIM domains 2	-2.25	7.49	8.66	0.8	0.11	4.10E-03	3.02E-02	Multiple_Complex
TC0600009262.hg.1	SLC35F1	solute carrier family 35, member F1	-2.25	10.27	11.44	0.4	0.12	1.00E-03	1.42E-02	Coding

TC1100012509.hg.1	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	-2.25	7.7	8.87	0.05	0.17	2.80E-03	2.37E-02	Multiple_Complex
TC2200008819.hg.1	RANGAP1	Ran GTPase activating protein 1	-2.25	9.62	10.79	0.92	0.41	9.70E-03	5.24E-02	Multiple_Complex
TC0X00007132.hg.1	CDK16	cyclin-dependent kinase 16	-2.25	12.08	13.26	0.27	0.05	7.00E-04	1.16E-02	Multiple_Complex
TC1500010020.hg.1	UBL7	ubiquitin-like 7	-2.25	12.12	13.29	0.43	0.1	7.00E-04	1.22E-02	Multiple_Complex
TC1000010961.hg.1	PSAP	prosaposin	-2.25	12.95	14.12	0.3	0.06	3.00E-04	8.80E-03	Multiple_Complex
TC2200008370.hg.1	XBP1	X-box binding protein 1	-2.25	11.31	12.48	0	0.36	7.00E-04	1.22E-02	Multiple_Complex
TC1400006519.hg.1	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-2.26	9.16	10.34	0.01	0.07	3.00E-04	7.70E-03	Multiple_Complex
TC1100009245.hg.1	CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	-2.26	7.06	8.24	0.24	0.12	3.00E-04	8.00E-03	Multiple_Complex
TC1700009376.hg.1	MYO1C	myosin IC	-2.26	6.91	8.09	0.03	0.06	3.00E-04	8.00E-03	Multiple_Complex
TC1600011386.hg.1	ORAI3	ORAI calcium release-activated calcium modulator 3	-2.26	5.78	6.95	0.53	0.55	6.50E-03	4.02E-02	Multiple_Complex
TC1000012162.hg.1	UROS	uroporphyrinogen III synthase	-2.26	10.16	11.34	0.02	0.04	2.00E-04	6.40E-03	Multiple_Complex
TC1900008415.hg.1	CCDC9	coiled-coil domain containing 9	-2.26	4.51	5.69	0.27	0.06	9.10E-03	5.01E-02	Multiple_Complex
TC1600007973.hg.1	NUP93	nucleoporin 93kDa	-2.26	6	7.18	0.04	0.14	7.00E-04	1.19E-02	Multiple_Complex
TC1600011478.hg.1	TMEM186	transmembrane protein 186	-2.26	6.98	8.16	0.99	0.18	1.60E-02	7.35E-02	Multiple_Complex
TC0100017241.hg.1	TMEM206	transmembrane protein 206	-2.26	7.05	8.23	0.5	0.33	2.40E-03	2.16E-02	Multiple_Complex
TC0300013408.hg.1	EHHADH	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	-2.26	5	6.18	0.34	0.5	1.60E-03	1.74E-02	Multiple_Complex
TC2000009874.hg.1	PSMF1	proteasome inhibitor subunit 1	-2.26	12.54	13.72	0.19	0.02	4.00E-04	9.10E-03	Multiple_Complex
TC0200011130.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	-2.26	7.57	8.75	0.64	0.03	2.50E-03	2.24E-02	Multiple_Complex
TC1600011329.hg.1	TBC1D24	TBC1 domain family, member 24	-2.26	7.81	8.98	0.31	0.05	5.00E-04	1.02E-02	Multiple_Complex
TC1900009805.hg.1	SAMD1	sterile alpha motif domain containing 1	-2.26	8.14	9.32	0.44	0.46	2.00E-03	1.95E-02	Multiple_Complex

TC1900011861.hg.1	S1PR2	sphingosine-1-phosphate receptor 2	-2.26	8.92	10.09	0.11	0.07	3.00E-04	8.00E-03	Multiple_Complex
TC1900008404.hg.1	NPAS1	neuronal PAS domain protein 1	-2.26	5.14	6.32	0.99	0.59	1.51E-02	7.05E-02	Multiple_Complex
TC1700007135.hg.1	TRIM16L	tripartite motif containing 16-like	-2.26	8.04	9.22	0.43	0.43	1.50E-03	1.65E-02	Multiple_Complex
TC0400010167.hg.1	DCAF16	DDB1 and CUL4 associated factor 16	-2.26	11.07	12.25	0.08	0.18	2.00E-04	7.00E-03	Multiple_Complex
TC0400006685.hg.1	WFS1	Wolfram syndrome 1 (wolframin)	-2.26	8.99	10.17	0.48	0.08	8.00E-04	1.23E-02	Multiple_Complex
TC1700011746.hg.1	SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	-2.27	6.99	8.17	0.68	0.21	5.70E-03	3.70E-02	Multiple_Complex
TC0X00009427.hg.1	BCOR	BCL6 corepressor	-2.27	9.79	10.97	0.17	0.06	6.00E-04	1.11E-02	Multiple_Complex
TC0900011634.hg.1	TRUB2	TruB pseudouridine (psi) synthase family member 2	-2.27	7.03	8.22	0.06	0.08	2.00E-04	7.60E-03	Multiple_Complex
TC1400007761.hg.1	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	-2.27	11.96	13.14	0.24	0.3	5.00E-04	1.00E-02	Multiple_Complex
TC1900009048.hg.1	ZNF584	zinc finger protein 584	-2.27	8.59	9.77	0.29	0.16	5.00E-04	1.00E-02	Multiple_Complex
TC0600011945.hg.1	RCAN2	regulator of calcineurin 2	-2.27	7.46	8.64	0.81	0.13	6.50E-03	4.03E-02	Coding
TC0800007809.hg.1	YTHDF3	YTH N(6)-methyladenosine RNA binding protein 3	-2.27	11.21	12.39	0.2	0.14	6.00E-04	1.08E-02	Multiple_Complex
TC1700006524.hg.1	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	-2.27	8.42	9.6	0.78	0.05	3.40E-03	2.70E-02	Multiple_Complex
TC0X00009760.hg.1	SMC1A	structural maintenance of chromosomes 1A	-2.27	11.7	12.88	0.11	0.09	2.00E-04	7.00E-03	Multiple_Complex
TC1000008575.hg.1	ZDHHC16	zinc finger, DHHC-type containing 16	-2.27	10.62	11.8	0.19	0.13	3.00E-04	7.70E-03	Multiple_Complex
TC0600007344.hg.1	PRSS16	protease, serine, 16 (thymus)	-2.27	9.36	10.55	0.65	0.22	3.00E-03	2.49E-02	Multiple_Complex
TC0600011404.hg.1	CCHCR1	coiled-coil alpha-helical rod protein 1	-2.27	4.93	6.12	0.28	0.04	1.80E-03	1.86E-02	Multiple_Complex
TC0100016322.hg.1	GPR161	G protein-coupled receptor 161	-2.27	7.37	8.55	0.5	0.23	1.20E-03	1.51E-02	Multiple_Complex
TC1100013084.hg.1	AMOTL1	angiomotin like 1	-2.27	7.72	8.9	0.06	0.05	3.00E-04	8.30E-03	Multiple_Complex

TC1800007411.hg.1	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	-2.27	8.1	9.28	0.49	0.08	1.00E-03	1.41E-02	Multiple_Complex
TC2200007138.hg.1	FBXO7	F-box protein 7	-2.27	12.1	13.28	0.12	0.1	2.00E-04	7.10E-03	Multiple_Complex
TC1700011561.hg.1	WIPI1	WD repeat domain, phosphoinositide interacting 1	-2.27	7.5	8.68	1.12	0.23	3.10E-02	1.14E-01	Multiple_Complex
TC1700011114.hg.1	ANKRD40	ankyrin repeat domain 40	-2.27	10.59	11.77	0.46	0.02	9.00E-04	1.32E-02	Multiple_Complex
TC1700010563.hg.1	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	-2.27	8.25	9.44	0.14	0.32	5.00E-04	1.03E-02	Multiple_Complex
TC1500006965.hg.1	RAD51	RAD51 recombinase	-2.27	6.77	7.95	0.23	0.13	4.00E-04	9.80E-03	Multiple_Complex
TC2000009965.hg.1	FKBP1A; MIR6869	FK506 binding protein 1A; microRNA 6869	-2.28	11.41	12.6	0.25	0	2.00E-04	7.40E-03	Multiple_Complex
TC2200009303.hg.1	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	-2.28	5.45	6.64	0.31	0.16	1.60E-03	1.73E-02	Coding
TC0500013015.hg.1	PHYKPL	5-phosphohydroxy-L-lysine phospho-lyase	-2.28	11.07	12.26	0.17	0.11	6.00E-04	1.14E-02	Multiple_Complex
TC0100009646.hg.1	NBPF26	neuroblastoma breakpoint family, member 26	-2.28	8.96	10.15	0.41	0.65	3.10E-03	2.51E-02	Coding
TC0700011054.hg.1	GRB10	growth factor receptor bound protein 10	-2.28	8.19	9.38	0.13	0.02	3.00E-04	8.00E-03	Multiple_Complex
TC1500007520.hg.1	APH1B	APH1B gamma secretase subunit	-2.28	7.87	9.06	0.15	0.05	2.00E-04	7.40E-03	Multiple_Complex
TC0600014264.hg.1	DDAH2	dimethylarginine dimethylaminohydrolase 2	-2.28	7.59	8.78	0.45	0.11	7.00E-04	1.17E-02	Multiple_Complex
TC1200009250.hg.1	GTF2H3	general transcription factor IIH subunit 3	-2.28	11.4	12.59	0.24	0	2.00E-04	7.60E-03	Multiple_Complex
TC0500009061.hg.1	PCYOX1L	prenylcysteine oxidase 1 like	-2.28	8.61	9.8	0.02	0.37	1.10E-03	1.43E-02	Multiple_Complex
TC1400010625.hg.1	ZNF410	zinc finger protein 410	-2.28	6.95	8.14	0.68	0.47	1.59E-02	7.31E-02	Multiple_Complex
TC0200016474.hg.1	NAGK	N-acetylglucosamine kinase	-2.28	7.15	8.34	0.49	0.13	4.50E-03	3.20E-02	Multiple_Complex
TC0300007410.hg.1	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	-2.28	8.12	9.3	0.5	0.23	1.00E-03	1.40E-02	Multiple_Complex

TC0100016629.hg.1	RNASEL	ribonuclease L (2,5-oligoisoadenylate synthetase-dependent)	-2.28	5.84	7.03	0.37	0.18	5.40E-03	3.58E-02	Coding
TC1600009953.hg.1	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	-2.28	5.15	6.34	1.1	0.09	1.23E-02	6.14E-02	Multiple_Complex
TC2000006442.hg.1	NRSN2	neurensin 2	-2.28	7.09	8.28	0.42	0.21	9.00E-04	1.32E-02	Multiple_Complex
TC0700012555.hg.1	TNPO3	transportin 3	-2.28	9.39	10.58	0.44	0.01	6.00E-04	1.15E-02	Multiple_Complex
TC1600007096.hg.1	TMC7	transmembrane channel like 7	-2.28	5.56	6.75	0.52	0.28	9.70E-03	5.24E-02	Multiple_Complex
TC0300013827.hg.1	WDR6	WD repeat domain 6	-2.28	5.78	6.97	0.2	0.26	6.00E-04	1.16E-02	Multiple_Complex
TC1900006524.hg.1	CIRBP	cold inducible RNA binding protein	-2.29	11.8	12.99	0.35	0.05	5.00E-04	1.02E-02	Multiple_Complex
TC1700009436.hg.1	MNT	MAX network transcriptional repressor	-2.29	8.71	9.91	0.05	0.2	4.00E-04	9.20E-03	Multiple_Complex
TC0100008057.hg.1	CDC20	cell division cycle 20	-2.29	7.45	8.64	0.02	0.32	5.00E-04	1.06E-02	Multiple_Complex
TC1900009743.hg.1	TNPO2	transportin 2	-2.29	11.13	12.32	0.3	0.21	5.00E-04	1.00E-02	Multiple_Complex
TC2200008487.hg.1	PISD; MIR7109	phosphatidylserine decarboxylase; microRNA 7109	-2.29	6.8	8	0.64	0.2	1.90E-03	1.90E-02	Multiple_Complex
TC0100015680.hg.1	NBPF9	neuroblastoma breakpoint family, member 9	-2.29	7.43	8.62	0.74	0.38	8.30E-03	4.73E-02	Multiple_Complex
TC0X00011159.hg.1	HAUS7; TREX2	HAUS augmin like complex subunit 7; three prime repair exonuclease 2	-2.29	9.54	10.73	0.03	0.19	3.00E-04	7.90E-03	Multiple_Complex
TC1100008398.hg.1	PAAF1	proteasomal ATPase-associated factor 1	-2.29	8.27	9.46	0.22	0.19	1.00E-03	1.40E-02	Multiple_Complex
TC0900010980.hg.1	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	-2.29	5.88	7.07	0.33	0.26	7.00E-04	1.22E-02	Multiple_Complex
TC1900008902.hg.1	BRSK1	BR serine/threonine kinase 1	-2.29	7.79	8.99	0.6	0.02	5.00E-03	3.39E-02	Multiple_Complex
TC1900009217.hg.1	PLEKHJ1; MIR6789	pleckstrin homology domain containing, family J member 1; microRNA 6789	-2.29	6.94	8.14	0.52	0.36	4.80E-03	3.33E-02	Multiple_Complex
TC0200011890.hg.1	LAPTM4A	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_014713	-2.3	4.93	6.13	0.12	0.16	5.00E-04	1.06E-02	NonCoding

TC0500008864.hg.1	WDR55	WD repeat domain 55	-2.3	6.86	8.06	0.1	0.09	1.00E-04	6.20E-03	Multiple_Complex
TC2000009250.hg.1	PLTP	phospholipid transfer protein	-2.3	7.71	8.91	0.22	0.45	9.00E-04	1.29E-02	Multiple_Complex
TC1200012657.hg.1	CAND1	cullin-associated and neddylation-dissociated 1	-2.3	7.25	8.45	0.04	0.26	7.00E-04	1.18E-02	Multiple_Complex
TC0600011248.hg.1	ZKSCAN4	zinc finger with KRAB and SCAN domains 4	-2.3	4.59	5.79	0.23	0.65	4.80E-03	3.30E-02	Multiple_Complex
TC1700009974.hg.1	SHMT1; MIR6778	serine hydroxymethyltransferase 1 (soluble); microRNA 6778	-2.3	7.6	8.8	0.24	0.43	8.00E-04	1.24E-02	Multiple_Complex
TC1000011579.hg.1	HPS1; MIR4685	Hermansky-Pudlak syndrome 1; microRNA 4685	-2.3	6.2	7.4	0.17	0.05	2.00E-04	7.10E-03	Multiple_Complex
TC0600014235.hg.1	BLOC1S5-TXNDC5	BLOC1S5-TXNDC5 readthrough (NMD candidate)	-2.3	8.62	9.82	0.03	0.22	4.00E-04	9.10E-03	Multiple_Complex
TC1100008049.hg.1	BANF1	barrier to autointegration factor 1	-2.3	12.85	14.05	0.04	0.03	1.00E-04	5.90E-03	Multiple_Complex
TC1700009498.hg.1	ATP2A3	ATPase, Ca++ transporting, ubiquitous	-2.3	7.31	8.52	0.37	0.44	1.60E-03	1.74E-02	Multiple_Complex
TC0100015952.hg.1	CLK2	CDC like kinase 2	-2.3	7.51	8.72	0.38	0.51	2.00E-03	1.95E-02	Multiple_Complex
TC0700013381.hg.1	CRCP	CGRP receptor component	-2.3	9.71	10.91	0.22	0.26	4.00E-04	9.10E-03	Multiple_Complex
TC0X00007267.hg.1	MAGED1	MAGE family member D1	-2.3	8.76	9.97	0.47	0.38	1.20E-03	1.52E-02	Multiple_Complex
TC0300011052.hg.1	LAMB2	laminin, beta 2 (laminin S)	-2.31	8.83	10.03	0.34	0.43	1.20E-03	1.51E-02	Multiple_Complex
TC1600007026.hg.1	NOMO3; NOMO2	NODAL modulator 3; NODAL modulator 2	-2.31	13.43	14.63	0.01	0.13	2.00E-04	6.70E-03	Multiple_Complex
TC1100009940.hg.1	TRIM5	tripartite motif containing 5	-2.31	4.39	5.6	0.02	0.4	3.60E-03	2.79E-02	Multiple_Complex
TC1900010696.hg.1	AKT2	v-akt murine thymoma viral oncogene homolog 2	-2.31	8.25	9.45	0.53	0.23	1.10E-03	1.48E-02	Multiple_Complex
TC1000007925.hg.1	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	-2.31	10.55	11.75	0.01	0.15	5.00E-04	1.05E-02	Multiple_Complex
TC0700009493.hg.1	ZYX	zyxin	-2.31	7.52	8.73	0.36	0.36	2.50E-03	2.24E-02	Multiple_Complex
TC1100012445.hg.1	BACE1	beta-site APP-cleaving enzyme 1	-2.31	8.44	9.65	0.49	0.12	2.90E-03	2.43E-02	Multiple_Complex

TC1600011409.hg.1	PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2	-2.31	7.78	8.99	0.32	0.08	3.00E-04	8.60E-03	Multiple_Complex
TC0100007858.hg.1	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein (yeast)	-2.31	10.01	11.22	0.71	0.04	2.00E-03	1.96E-02	Multiple_Complex
TC2200008906.hg.1	TTLL12	tubulin tyrosine ligase-like family member 12	-2.31	10.91	12.12	0.33	0.44	9.00E-04	1.34E-02	Multiple_Complex
TC2200007318.hg.1	H1F0	H1 histone family, member 0	-2.31	11.52	12.73	0.09	0.11	3.00E-04	8.50E-03	Multiple_Complex
TC0700008328.hg.1	RBM48	RNA binding motif protein 48	-2.31	7.3	8.51	0.45	0.09	4.90E-03	3.36E-02	Coding
TC0100013578.hg.1	ADGRB2	adhesion G protein-coupled receptor B2	-2.31	4.82	6.03	0.5	0.29	1.20E-03	1.52E-02	Multiple_Complex
TC0900008750.hg.1	GAPVD1	GTPase activating protein and VPS9 domains 1	-2.31	9.47	10.68	0.11	0.23	2.00E-04	7.00E-03	Multiple_Complex
TC0100016162.hg.1	B4GALT3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	-2.32	6.18	7.39	0.24	0.1	4.00E-04	9.10E-03	Multiple_Complex
TC1900008555.hg.1	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	-2.32	6.66	7.87	0.12	0.23	3.00E-04	8.00E-03	Multiple_Complex
TC1200008942.hg.1	PLBD2	phospholipase B domain containing 2	-2.32	7.91	9.12	0.38	0.09	7.00E-04	1.18E-02	Multiple_Complex
TC1200011936.hg.1	ATXN2	ataxin 2	-2.32	9.95	11.16	0.14	0.21	3.00E-04	8.00E-03	Multiple_Complex
TC1700009319.hg.1	VPS53; RPS4XP17	vacuolar protein sorting 53 homolog (S. cerevisiae); ribosomal protein S4X pseudogene 17	-2.32	7.95	9.16	0.75	0.21	5.80E-03	3.73E-02	Multiple_Complex
TC1100011128.hg.1	ATL3	atlastin GTPase 3	-2.32	5.52	6.73	0.39	0.35	1.20E-03	1.50E-02	Multiple_Complex
TC1700010997.hg.1	HOXB9	homeobox B9	-2.32	8.91	10.12	0.81	0	6.40E-03	3.96E-02	Multiple_Complex
TC0700012995.hg.1	ZNF777	zinc finger protein 777	-2.32	7.41	8.62	0.48	0.06	6.80E-03	4.15E-02	Coding
TC1900009240.hg.1	GNG7	guanine nucleotide binding protein (G protein), gamma 7	-2.32	11.57	12.79	0.23	0.19	7.00E-04	1.16E-02	Coding
TC0X00007561.hg.1	NONO	non-POU domain containing, octamer-binding	-2.32	11.9	13.11	0.24	0.05	2.00E-04	7.10E-03	Multiple_Complex
TC1600006822.hg.1	METTL22	methyltransferase like 22	-2.32	9.82	11.04	0.43	0.09	1.20E-03	1.52E-02	Multiple_Complex

TC0100015756.hg.1	ARNT	aryl hydrocarbon receptor nuclear translocator	-2.32	8.35	9.56	0.57	0.09	1.20E-03	1.51E-02	Multiple_Complex
TC1000011485.hg.1	PDLIM1	PDZ and LIM domain 1	-2.32	9.42	10.63	0.52	0.38	1.40E-03	1.62E-02	Multiple_Complex
TC1100010897.hg.1	UBE2L6	ubiquitin-conjugating enzyme E2L 6	-2.32	5.83	7.05	0.6	0.8	8.70E-03	4.89E-02	Multiple_Complex
TC0200011731.hg.1	PDIA6	protein disulfide isomerase family A, member 6	-2.32	12.76	13.98	0.03	0.05	1.00E-04	6.30E-03	Multiple_Complex
TC0700011510.hg.1	RFC2	replication factor C subunit 2	-2.33	11.46	12.68	0.41	0.06	8.00E-04	1.27E-02	Multiple_Complex
TC1700007976.hg.1	G6PC3	glucose 6 phosphatase, catalytic, 3	-2.33	10.84	12.06	0.2	0.14	2.00E-04	6.90E-03	Multiple_Complex
TC1100007390.hg.1	EXT2	exostosin glycosyltransferase 2	-2.33	9.74	10.96	0.12	0.11	1.00E-04	6.10E-03	Multiple_Complex
TC0100014050.hg.1	LRRC41	leucine rich repeat containing 41	-2.33	9.7	10.92	0.05	0.33	3.00E-04	8.30E-03	Multiple_Complex
TC1700006768.hg.1	EFNB3	ephrin-B3	-2.33	4.73	5.95	0.19	0.3	8.00E-04	1.26E-02	Coding
TC1700006772.hg.1	KDM6B	lysine (K)-specific demethylase 6B	-2.33	8.39	9.61	0.21	0.01	2.00E-04	7.40E-03	Multiple_Complex
TC1900006622.hg.1	NCLN	nicalin	-2.33	6.93	8.15	0.48	0.4	1.30E-03	1.56E-02	Multiple_Complex
TC0100012788.hg.1	GPR157	G protein-coupled receptor 157	-2.33	5.69	6.91	0.11	0.23	1.10E-03	1.47E-02	Multiple_Complex
TC2200008356.hg.1	TTC28	tetratricopeptide repeat domain 28	-2.33	9.8	11.02	0.04	0.18	8.00E-04	1.27E-02	Multiple_Complex
TC1600009883.hg.1	TUFM; MIR4721	Tu translation elongation factor, mitochondrial; microRNA 4721	-2.33	12.27	13.49	0.1	0.04	4.00E-04	9.10E-03	Multiple_Complex
TC0200012072.hg.1	MPV17	MpV17 mitochondrial inner membrane protein	-2.33	11.61	12.83	0.31	0.06	4.00E-04	9.00E-03	Multiple_Complex
TC1100008175.hg.1	NDUFS8; MIR4691; MIR7113	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase); microRNA 4691; microRNA 7113	-2.33	7.96	9.18	0.53	0.11	1.10E-03	1.44E-02	Multiple_Complex
TC1700007641.hg.1	DHRS11	dehydrogenase/reductase (SDR family) member 11	-2.33	6.82	8.04	0.28	0.1	9.00E-04	1.32E-02	Multiple_Complex
TC1200009445.hg.1	SFSWAP	splicing factor, suppressor of white-apricot family	-2.33	12	13.22	0.34	0.08	3.00E-04	8.30E-03	Multiple_Complex
TC1600006979.hg.1	MKL2; TVP23CP2	MKL/myocardin-like 2; TVP23C pseudogene 2	-2.33	8.39	9.62	0.22	0.04	4.00E-04	9.10E-03	Multiple_Complex
TC1600011325.hg.1	CRAMP1	cramped chromatin regulator homolog 1	-2.34	6.61	7.84	0.03	0.09	3.00E-04	8.30E-03	Multiple_Complex

TC0100016022.hg.1	HDGF	hepatoma-derived growth factor	-2.34	8.55	9.78	0.82	0.3	4.10E-03	3.02E-02	Multiple_Complex
TC1600009944.hg.1	KCTD13	potassium channel tetramerization domain containing 13	-2.34	9.74	10.96	0.24	0.08	6.80E-03	4.16E-02	Multiple_Complex
TC0500009606.hg.1	ZNF346	zinc finger protein 346	-2.34	8.91	10.14	0.09	0.09	2.00E-04	7.10E-03	Multiple_Complex
TC0900010946.hg.1	TSTD2	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	-2.34	7.2	8.43	0.01	0.19	3.00E-04	8.00E-03	Multiple_Complex
TC1900009425.hg.1	GTF2F1	general transcription factor IIF subunit 1	-2.34	9.23	10.45	0.41	0.12	4.00E-04	9.60E-03	Multiple_Complex
TC2000008894.hg.1	E2F1	E2F transcription factor 1	-2.34	6.85	8.07	0.61	0.68	9.10E-03	5.00E-02	Multiple_Complex
TC1000011585.hg.1	GOT1	glutamic-oxaloacetic transaminase 1, soluble	-2.34	12.23	13.46	0.15	0.05	2.00E-04	7.20E-03	Multiple_Complex
TC0100007678.hg.1	HDAC1	histone deacetylase 1	-2.34	10.89	12.12	0.4	0.05	5.00E-04	1.03E-02	Multiple_Complex
TC1300008660.hg.1	PROSER1	proline and serine rich 1	-2.34	11.15	12.38	0.69	0.29	2.90E-03	2.44E-02	Multiple_Complex
TC0900009912.hg.1	SIGMAR1	sigma non-opioid intracellular receptor 1	-2.34	10.86	12.09	0.21	0.25	7.00E-04	1.19E-02	Multiple_Complex
TC0X00007119.hg.1	JADE3	jade family PHD finger 3	-2.34	7	8.23	0.72	0.11	2.10E-03	2.04E-02	Multiple_Complex
TC1900006992.hg.1	ILF3	interleukin enhancer binding factor 3	-2.34	10.23	11.46	0.84	0.26	5.70E-03	3.68E-02	Multiple_Complex
TC2200006521.hg.1	BCL2L13	BCL2-like 13 (apoptosis facilitator)	-2.34	7.68	8.91	1.06	0.14	1.18E-02	5.97E-02	Multiple_Complex
TC1700012342.hg.1	DHX33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	-2.35	8.1	9.33	0.44	0.1	5.00E-04	1.07E-02	Multiple_Complex
TC1600010450.hg.1	CIAPIN1	cytokine induced apoptosis inhibitor 1	-2.35	7.03	8.26	1.3	0.35	2.65E-02	1.03E-01	Multiple_Complex
TC0100009937.hg.1	C1orf56	chromosome 1 open reading frame 56	-2.35	7.75	8.98	0.13	0.01	1.00E-04	6.10E-03	Multiple_Complex
TC0500012282.hg.1	HDAC3	histone deacetylase 3	-2.35	7.9	9.13	0.32	0.05	1.90E-03	1.89E-02	Multiple_Complex
TC0300006561.hg.1	JAGN1	jagunal homolog 1	-2.35	8.03	9.26	0.2	0.42	1.10E-03	1.48E-02	Multiple_Complex
TC1700009189.hg.1	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	-2.35	9.43	10.66	0.84	0.09	3.40E-03	2.71E-02	Multiple_Complex

TC1600009779.hg.1	ARHGAP17	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001006634	-2.35	4.67	5.9	0.35	0.03	1.80E-03	1.86E-02	NonCoding
TC1100011829.hg.1	CREBZF	CREB/ATF bZIP transcription factor	-2.35	8.88	10.11	0.07	0.17	2.00E-04	7.20E-03	Multiple_Complex
TC0600008071.hg.1	PTK7	protein tyrosine kinase 7 (inactive)	-2.36	6.76	8	0.12	0.12	2.00E-04	7.20E-03	Multiple_Complex
TC1600011186.hg.1	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	-2.36	10.74	11.98	0.13	0.02	1.00E-04	5.80E-03	Multiple_Complex
TC0100011812.hg.1	ADCK3	aarF domain containing kinase 3	-2.36	6	7.24	0.08	0.2	9.00E-04	1.34E-02	Multiple_Complex
TC0100018298.hg.1	INTS3	integrator complex subunit 3	-2.36	10.17	11.41	0.45	0.08	6.00E-04	1.08E-02	Multiple_Complex
TC0800007086.hg.1	DPYSL2	dihydropyrimidinase-like 2	-2.36	8.14	9.37	0.76	0.09	2.30E-03	2.12E-02	Multiple_Complex
TC0900011597.hg.1	SH2D3C	SH2 domain containing 3C	-2.36	6.33	7.57	0.16	0.08	3.00E-04	8.30E-03	Multiple_Complex
TC0900011659.hg.1	C9orf114	chromosome 9 open reading frame 114	-2.36	6.02	7.26	0.36	0.67	7.50E-03	4.40E-02	Multiple_Complex
TC1900006470.hg.1	BSG	basigin (Ok blood group)	-2.36	13.81	15.05	0.07	0.01	2.00E-04	6.90E-03	Multiple_Complex
TC1700008151.hg.1	NFE2L1	nuclear factor, erythroid 2-like 1	-2.36	12.55	13.79	0.47	0.05	5.00E-04	1.04E-02	Multiple_Complex
TC0400012378.hg.1	SH3RF1	SH3 domain containing ring finger 1	-2.36	8.33	9.57	0.36	0.07	4.00E-04	9.40E-03	Multiple_Complex
TC0600014262.hg.1	ABHD16A	abhydrolase domain containing 16A	-2.36	8.31	9.55	0.21	0.02	8.00E-04	1.27E-02	Multiple_Complex
TC1700007890.hg.1	ATP6V0A1; MIR5010	ATPase, H+ transporting, lysosomal V0 subunit a1; microRNA 5010	-2.36	12.1	13.34	0.53	0.06	9.00E-04	1.32E-02	Multiple_Complex
TC0300014041.hg.1	RUVBL1	RuvB-like AAA ATPase 1	-2.36	11.04	12.28	0.4	0.1	4.00E-04	9.80E-03	Multiple_Complex
TC1600011330.hg.1	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	-2.36	11.91	13.15	0.18	0.27	4.00E-04	9.00E-03	Multiple_Complex
TC1100007935.hg.1	STIP1	stress-induced phosphoprotein 1	-2.36	11.47	12.71	0.3	0.17	3.00E-04	8.00E-03	Multiple_Complex
TC0800012223.hg.1	RECQL4	RecQ helicase-like 4	-2.36	7.09	8.33	0.15	0.02	2.00E-04	7.10E-03	Multiple_Complex

TC1600009247.hg.1	GLYR1	glyoxylate reductase 1 homolog (Arabidopsis)	-2.36	8.91	10.15	0.76	0.08	2.40E-03	2.19E-02	Multiple_Complex
TC1600007485.hg.1	FBRS	fibrosin	-2.36	5.66	6.9	0.14	0.03	1.00E-04	5.80E-03	Multiple_Complex
TC1900009859.hg.1	BRD4	bromodomain containing 4	-2.37	11.06	12.3	0.57	0.1	1.20E-03	1.50E-02	Multiple_Complex
TC1700009954.hg.1	TOM1L2	target of myb1 like 2 membrane trafficking protein	-2.37	8.13	9.37	0.28	0.19	3.00E-04	8.80E-03	Multiple_Complex
TC1100008136.hg.1	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-2.37	9.32	10.57	0.79	0.6	6.50E-03	4.00E-02	Multiple_Complex
TC1900011909.hg.1	COPE	coatomer protein complex subunit epsilon	-2.37	11	12.24	0.41	0.19	5.00E-04	9.90E-03	Multiple_Complex
TC1400010765.hg.1	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	-2.37	9.11	10.35	0.12	0.12	2.00E-04	7.10E-03	Multiple_Complex
TC0100011203.hg.1	RNPEP	arginyl aminopeptidase (aminopeptidase B)	-2.37	7.73	8.97	0.49	0.11	6.40E-03	3.97E-02	Multiple_Complex
TC0100014788.hg.1	ZNHIT6	zinc finger, HIT-type containing 6	-2.37	8.35	9.6	0.21	0.14	2.00E-04	6.70E-03	Multiple_Complex
TC0200007050.hg.1	AGBL5	ATP/GTP binding protein-like 5	-2.37	10.49	11.74	0.02	0.03	9.96E-05	5.80E-03	Multiple_Complex
TC0400012972.hg.1	RNF150	ring finger protein 150	-2.37	6.38	7.62	0.82	0.14	3.30E-03	2.61E-02	Multiple_Complex
TC1900007355.hg.1	CCDC124	coiled-coil domain containing 124	-2.37	10.18	11.42	0.68	0.17	1.70E-03	1.78E-02	Multiple_Complex
TC1700007658.hg.1	AATF	apoptosis antagonizing transcription factor	-2.37	10.02	11.27	0.53	0.05	7.00E-04	1.17E-02	Multiple_Complex
TC0700008081.hg.1	MDH2	malate dehydrogenase 2	-2.37	12.3	13.55	0	0.32	2.00E-04	7.30E-03	Multiple_Complex
TC0900011955.hg.1	CAMSAP1	calmodulin regulated spectrin-associated protein 1	-2.37	7.21	8.46	0.56	0.04	6.60E-03	4.04E-02	Multiple_Complex
TC0100016159.hg.1	DEDD	death effector domain containing	-2.38	7.91	9.16	0.33	0.39	7.00E-04	1.22E-02	Multiple_Complex
TC2000009579.hg.1	BMP7	bone morphogenetic protein 7	-2.38	6.72	7.97	0.06	0.75	2.60E-03	2.29E-02	Multiple_Complex
TC0900012151.hg.1	ANKRD19P	ankyrin repeat domain 19, pseudogene	-2.38	7.73	8.98	0.78	0.33	4.00E-03	2.98E-02	Multiple_Complex
TC1400009629.hg.1	ZFYVE1	zinc finger, FYVE domain containing 1	-2.38	6.64	7.89	0.04	0.23	6.00E-04	1.08E-02	Multiple_Complex
TC0700011968.hg.1	ZNF3	zinc finger protein 3	-2.38	7.65	8.9	0.07	0.38	1.07E-02	5.58E-02	Multiple_Complex

TC2200006540.hg.1	USP18	ubiquitin specific peptidase 18	-2.38	9.13	10.38	0.04	0.38	7.00E-04	1.17E-02	Multiple_Complex
TC2100008467.hg.1	C21orf58	chromosome 21 open reading frame 58	-2.38	6.14	7.39	0.15	0.3	2.20E-03	2.09E-02	Multiple_Complex
TC1900009176.hg.1	TCF3	transcription factor 3	-2.38	9.49	10.74	0.51	0.51	3.30E-03	2.65E-02	Multiple_Complex
TC0600008006.hg.1	FOXP4; MIR4641	forkhead box P4; microRNA 4641	-2.38	7.62	8.86	0.92	0.6	1.09E-02	5.67E-02	Multiple_Complex
TC0300007236.hg.1	LARS2	leucyl-tRNA synthetase 2, mitochondrial	-2.38	5.06	6.31	0.06	0.56	8.00E-04	1.28E-02	Multiple_Complex
TC1700008895.hg.1	NUP85	nucleoporin 85kDa	-2.38	10.04	11.29	0.02	0.13	1.00E-04	6.20E-03	Multiple_Complex
TC0600008073.hg.1	SRF	serum response factor	-2.38	7.76	9.01	0.42	0.19	7.00E-04	1.18E-02	Multiple_Complex
TC1600008505.hg.1	WWOX	WW domain containing oxidoreductase	-2.38	11.04	12.29	0.32	0.21	2.80E-03	2.39E-02	Multiple_Complex
TC1700007565.hg.1	TMEM132E	transmembrane protein 132E	-2.38	6.02	7.27	0.32	0.48	4.20E-03	3.05E-02	Multiple_Complex
TC0200014190.hg.1	AMMECR1L	AMMECR1 like	-2.38	9.3	10.55	0.03	0.06	4.00E-04	9.80E-03	Multiple_Complex
TC1100009024.hg.1	LAYN	layilin	-2.38	5.16	6.41	0.04	0.09	2.00E-04	7.20E-03	Multiple_Complex
TC1300006658.hg.1	WASF3	WAS protein family, member 3	-2.38	8.13	9.39	0.12	0.19	9.00E-04	1.29E-02	Multiple_Complex
TC1900007754.hg.1	NUDT19	nudix hydrolase 19	-2.38	6.53	7.79	0.15	0	1.70E-03	1.78E-02	Multiple_Complex
TC0100010104.hg.1	ZBTB7B	zinc finger and BTB domain containing 7B	-2.38	7.01	8.26	0.34	0.43	1.50E-03	1.70E-02	Multiple_Complex
TC1600008585.hg.1	CMIP	c-Maf inducing protein	-2.39	10.15	11.4	0.12	0.26	2.00E-04	7.40E-03	Multiple_Complex
TC1900007399.hg.1	TMEM59L	transmembrane protein 59-like	-2.39	8.09	9.35	0.39	0.34	6.00E-04	1.13E-02	Multiple_Complex
TC1500006930.hg.1	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	-2.39	9.53	10.78	0.21	0.23	3.00E-04	8.00E-03	Multiple_Complex
TC2200008489.hg.1	PRR14L	proline rich 14-like	-2.39	9.62	10.87	0.31	0.03	3.00E-04	8.50E-03	Multiple_Complex
TC2100007491.hg.1	CBS	cystathionine-beta-synthase	-2.39	9.19	10.45	0.1	0	9.82E-05	5.80E-03	Multiple_Complex
TC1200009467.hg.1	NOC4L	nucleolar complex associated 4 homolog	-2.39	8.12	9.37	0.33	0.62	1.50E-03	1.69E-02	Multiple_Complex
TC1500010047.hg.1	SCAMP2	secretory carrier membrane protein 2	-2.39	5.19	6.44	0.81	0.1	3.10E-03	2.55E-02	Multiple_Complex

TC0X00008826.hg.1	FLNA	Jeck2013 ANTISENSE, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_001110556	-2.39	5.33	6.59	0.27	0	2.00E-03	1.99E-02	NonCoding
TC1200009300.hg.1	BRI3BP	BRI3 binding protein	-2.39	10.26	11.52	0.51	0.01	5.00E-04	1.07E-02	Multiple_Complex
TC1700008180.hg.1	UBE2Z	ubiquitin-conjugating enzyme E2Z	-2.39	11	12.26	0.11	0.08	3.00E-04	8.00E-03	Multiple_Complex
TC1700010700.hg.1	DNAJC7	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic, OVERLAPTX, OVEXON best transcript NM_003315	-2.39	5.82	7.08	0.53	0.19	7.00E-04	1.17E-02	NonCoding
TC0200013104.hg.1	MOGS	mannosyl-oligosaccharide glucosidase	-2.39	8.37	9.63	0.47	0.08	1.10E-03	1.42E-02	Multiple_Complex
TC2000007695.hg.1	PTPN1	protein tyrosine phosphatase, non-receptor type 1	-2.4	11.38	12.64	0.26	0.17	2.00E-04	7.30E-03	Multiple_Complex
TC1200011140.hg.1	GRIP1	glutamate receptor interacting protein 1	-2.4	7.47	8.73	0.15	0.11	3.00E-04	8.10E-03	Multiple_Complex
TC1200010806.hg.1	MAP3K12	mitogen-activated protein kinase kinase kinase 12	-2.4	7.23	8.49	0.22	0.59	4.20E-03	3.08E-02	Multiple_Complex
TC0300008735.hg.1	RAB7A	RAB7A, member RAS oncogene family	-2.4	13.09	14.35	0.07	0.04	1.00E-04	6.10E-03	Multiple_Complex
TC1600006597.hg.1	MLST8	MTOR associated protein, LST8 homolog	-2.4	7.84	9.11	0.21	0.19	2.00E-04	6.40E-03	Multiple_Complex
TC0900008902.hg.1	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	-2.4	7.82	9.08	0.08	0.19	1.00E-04	6.10E-03	Multiple_Complex
TC1600010439.hg.1	FAM192A	family with sequence similarity 192, member A	-2.4	8.94	10.2	0.38	0.28	5.00E-04	1.00E-02	Multiple_Complex
TC0600014362.hg.1	TFB1M	transcription factor B1, mitochondrial	-2.4	8.08	9.35	0.1	0	2.00E-04	7.20E-03	Multiple_Complex
TC0600011635.hg.1	FKBP5	FK506 binding protein 5	-2.4	8.86	10.13	0.3	0.2	4.00E-04	9.60E-03	Multiple_Complex
TC1500006748.hg.1	FAN1	FANCD2/FANCI-associated nuclease 1	-2.4	8.18	9.44	0.25	0.44	5.00E-04	1.04E-02	Multiple_Complex
TC1500007072.hg.1	PDIA3	protein disulfide isomerase family A member 3	-2.4	8.37	9.64	0.15	0.05	1.00E-04	5.80E-03	Multiple_Complex
TC0600006659.hg.1	BPHL	biphenyl hydrolase-like (serine hydrolase)	-2.4	7.87	9.13	0.4	0.29	5.30E-03	3.54E-02	Multiple_Complex
TC0X00008836.hg.1	PLXNA3	plexin A3	-2.4	6.25	7.52	0.4	0.57	4.20E-03	3.04E-02	Multiple_Complex

TC0400011180.hg.1	SCD5	stearoyl-CoA desaturase 5	-2.4	5.02	6.29	0.6	0.69	6.10E-03	3.86E-02	Coding
TC2200009350.hg.1	CSNK1E	casein kinase 1, epsilon	-2.4	14.27	15.54	0.37	0.04	3.00E-04	8.00E-03	Multiple_Complex
TC2000007283.hg.1	SRC	SRC proto-oncogene, non-receptor tyrosine kinase	-2.4	6.11	7.38	0.66	0.07	5.10E-03	3.44E-02	Multiple_Complex
TC1000006639.hg.1	FBXO18	F-box protein, helicase, 18	-2.4	9.42	10.68	1.03	0.3	8.00E-03	4.64E-02	Multiple_Complex
TC1900006989.hg.1	ATG4D	autophagy related 4D, cysteine peptidase	-2.41	8.54	9.81	0.29	0.07	7.00E-04	1.21E-02	Multiple_Complex
TC1900009791.hg.1	C19orf57	chromosome 19 open reading frame 57	-2.41	5.16	6.43	0.19	0.21	2.00E-04	7.20E-03	Multiple_Complex
TC1900007908.hg.1	CAPNS1	calpain, small subunit 1	-2.41	11.44	12.71	0.15	0.09	1.00E-04	5.80E-03	Multiple_Complex
TC1700012198.hg.1	PIGL	phosphatidylinositol glycan anchor biosynthesis class L	-2.41	10.14	11.41	0.19	0.02	2.00E-04	7.30E-03	Multiple_Complex
TC1500010151.hg.1	CHRNA3	cholinergic receptor, nicotinic alpha 3	-2.41	5.59	6.86	0.14	0.02	1.20E-03	1.50E-02	Multiple_Complex
TC1100008236.hg.1	CCND1	cyclin D1	-2.41	6.66	7.93	1	0.27	7.10E-03	4.27E-02	Multiple_Complex
TC2200008594.hg.1	MYH9	myosin, heavy chain 9, non-muscle	-2.41	9.95	11.22	0.15	0.15	2.00E-04	6.70E-03	Multiple_Complex
TC1200010839.hg.1	ITGA5	integrin alpha 5	-2.42	7.04	8.31	0.34	0.28	3.00E-04	8.60E-03	Multiple_Complex
TC1100008147.hg.1	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	-2.42	9.66	10.93	0.44	0.11	7.00E-04	1.16E-02	Multiple_Complex
TC0100018435.hg.1	EBNA1BP2; MIR6733	EBNA1 binding protein 2; microRNA 6733	-2.42	9.19	10.46	0.1	0.31	3.00E-04	8.30E-03	Multiple_Complex
TC1900011113.hg.1	GYS1	glycogen synthase 1 (muscle)	-2.42	9.71	10.99	0.22	0.07	2.00E-04	6.70E-03	Multiple_Complex
TC1100006516.hg.1	BRSK2	BR serine/threonine kinase 2	-2.42	7.66	8.94	0.13	0.01	1.10E-03	1.47E-02	Multiple_Complex
TC1400008749.hg.1	RABGGTA	Rab geranylgeranyltransferase, alpha subunit	-2.42	7.96	9.23	0.69	0.1	1.30E-03	1.57E-02	Multiple_Complex
TC0200010545.hg.1	NRP2	neuropilin 2	-2.42	7.58	8.85	0.01	0.13	1.30E-03	1.55E-02	Multiple_Complex
TC0300010999.hg.1	MAP4	microtubule associated protein 4	-2.42	11.72	12.99	0.4	0.13	4.00E-04	9.80E-03	Multiple_Complex
TC1900008172.hg.1	ZNF574	zinc finger protein 574	-2.42	6.45	7.73	0.55	0.37	2.30E-03	2.14E-02	Coding

TC0200012161.hg.1	GALNT14	polypeptide N-acetylgalactosaminyltransferase 14	-2.42	6.57	7.85	0.33	0.01	2.00E-04	7.40E-03	Multiple_Complex
TC2000007633.hg.1	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	-2.42	10.24	11.52	0	0.19	1.00E-04	6.10E-03	Multiple_Complex
TC1900008020.hg.1	ACTN4	actinin, alpha 4	-2.43	10.78	12.06	0.75	0.31	2.70E-03	2.32E-02	Multiple_Complex
TC0100018207.hg.1	TSSK3	testis-specific serine kinase 3	-2.43	6.7	7.98	0.53	0.15	6.30E-03	3.92E-02	Coding
TC0100018388.hg.1	SLC35E2B	solute carrier family 35, member E2B	-2.43	9.13	10.41	0.27	0.41	1.90E-03	1.93E-02	Multiple_Complex
TC1000007913.hg.1	H2AFY2	H2A histone family, member Y2	-2.43	10.12	11.4	0.64	0.03	1.20E-03	1.51E-02	Coding
TC0700012016.hg.1	EPHB4	EPH receptor B4	-2.43	6.26	7.54	0.02	0.31	3.00E-04	8.00E-03	Multiple_Complex
TC1900011733.hg.1	RAB4B; MIA-RAB4B; RAB4B-EGLN2	RAB4B, member RAS oncogene family; MIA-RAB4B readthrough (NMD candidate); RAB4B-EGLN2 readthrough (NMD candidate)	-2.43	6.1	7.38	0.09	0.21	1.00E-04	5.90E-03	Multiple_Complex
TC1200008790.hg.1	USP30	ubiquitin specific peptidase 30	-2.43	10.86	12.14	0.19	0.13	3.00E-04	7.70E-03	Multiple_Complex
TC0300006544.hg.1	SETD5	SET domain containing 5	-2.43	10.35	11.63	0.61	0.18	1.20E-03	1.51E-02	Multiple_Complex
TC0500008855.hg.1	SLC35A4	solute carrier family 35, member A4	-2.43	8.04	9.33	0.34	0.09	3.00E-04	8.20E-03	Multiple_Complex
TC0300011403.hg.1	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-2.43	7.67	8.95	0.3	0.08	3.00E-04	8.00E-03	Multiple_Complex
TC0800012165.hg.1	SCRIB; MIR937	scribbled planar cell polarity protein; microRNA 937	-2.44	6.43	7.71	0.07	0.05	9.82E-05	5.80E-03	Multiple_Complex
TC0X00009890.hg.1	ZC4H2	zinc finger, C4H2 domain containing	-2.44	11.46	12.75	0.26	0.2	6.00E-04	1.16E-02	Multiple_Complex
TC2100008461.hg.1	SPATC1L	spermatogenesis and centriole associated 1-like	-2.44	5.83	7.12	0.41	0.08	3.00E-04	8.00E-03	Coding
TC0700006549.hg.1	EIF3B	eukaryotic translation initiation factor 3, subunit B	-2.44	8.2	9.49	0.72	0.22	2.00E-03	1.98E-02	Multiple_Complex
TC2200007523.hg.1	SERHL	serine hydrolase-like (pseudogene)	-2.44	6.32	7.61	0.71	0.2	1.60E-03	1.76E-02	Multiple_Complex
TC1100013202.hg.1	ORAOV1	oral cancer overexpressed 1	-2.44	4.87	6.16	0.32	0.19	1.40E-03	1.60E-02	Multiple_Complex

TC1500007833.hg.1	PML	promyelocytic leukemia	-2.44	4.83	6.12	0.75	0.25	3.60E-03	2.78E-02	Multiple_Complex
TC1200007208.hg.1	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11	-2.44	9.57	10.85	0.23	0.32	8.00E-04	1.28E-02	Multiple_Complex
TC0X00011184.hg.1	IRAK1; MIR718	interleukin 1 receptor associated kinase 1; microRNA 718	-2.45	8.87	10.16	0.09	0.42	5.00E-04	1.03E-02	Multiple_Complex
TC1100011258.hg.1	FIBP	fibroblast growth factor (acidic) intracellular binding protein	-2.45	6.75	8.05	0.54	0.37	1.00E-03	1.40E-02	Multiple_Complex
TC0100010161.hg.1	PMF1; PMF1-BGLAP; BGLAP	polyamine-modulated factor 1; PMF1-BGLAP readthrough; bone gamma-carboxyglutamate (gla) protein	-2.45	9.32	10.61	0.11	0.01	2.00E-04	6.60E-03	Multiple_Complex
TC0600009094.hg.1	SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	-2.45	6.55	7.85	0.96	0.15	5.40E-03	3.59E-02	Multiple_Complex
TC0100006989.hg.1	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	-2.45	9.35	10.64	0.33	0.24	5.00E-04	1.02E-02	Multiple_Complex
TC1700009528.hg.1	CXCL16	chemokine (C-X-C motif) ligand 16	-2.45	9.41	10.7	0.17	0.12	3.00E-04	7.70E-03	Multiple_Complex
TC1200012808.hg.1	R3HDM2	R3H domain containing 2	-2.45	10.31	11.6	0.42	0.29	1.10E-03	1.48E-02	Multiple_Complex
TC1300009004.hg.1	ATP7B	ATPase, Cu++ transporting, beta polypeptide	-2.45	6.37	7.66	0.07	0.01	3.00E-04	7.70E-03	Multiple_Complex
TC0100012687.hg.1	NOL9	nucleolar protein 9	-2.45	8.72	10.02	0.02	0.17	2.00E-04	7.60E-03	Multiple_Complex
TC0100013747.hg.1	SNIP1	Smad nuclear interacting protein 1	-2.45	7.89	9.18	0.33	0.12	2.00E-04	6.90E-03	Multiple_Complex
TC2000009914.hg.1	TGIF2	TGFB-induced factor homeobox 2	-2.45	8.11	9.41	0.54	0.07	8.00E-04	1.23E-02	Multiple_Complex
TC2000009923.hg.1	SYS1	Sys1 golgi trafficking protein	-2.46	7.66	8.96	0.31	0.49	8.00E-04	1.23E-02	Multiple_Complex
TC1200010984.hg.1	CTDSP2	CTD small phosphatase 2	-2.46	7.21	8.5	0.22	0	1.00E-04	5.80E-03	Multiple_Complex
TC0200010897.hg.1	SGPP2	sphingosine-1-phosphate phosphatase 2	-2.46	9.08	10.38	0.18	0.37	1.20E-03	1.51E-02	Multiple_Complex
TC0100015761.hg.1	CERS2	ceramide synthase 2	-2.46	10.12	11.41	0.33	0.05	2.00E-04	7.20E-03	Multiple_Complex
TC0100007968.hg.1	NFYC	nuclear transcription factor Y subunit gamma	-2.46	7.96	9.25	0.45	0.26	5.00E-04	1.02E-02	Multiple_Complex

TC1700012262.hg.1	PSME3	proteasome activator subunit 3	-2.46	9.18	10.48	0.25	0.01	2.00E-04	6.70E-03	Multiple_Complex
TC1200009742.hg.1	CHD4	chromodomain helicase DNA binding protein 4	-2.46	6.66	7.96	0.62	0.11	8.00E-04	1.28E-02	Multiple_Complex
TC0700010925.hg.1	DDX56	DEAD (Asp-Glu-Ala-Asp) box helicase 56	-2.46	9.42	10.72	0.44	0.3	5.00E-04	1.04E-02	Multiple_Complex
TC0900011709.hg.1	TOR1A	torsin family 1, member A (torsin A)	-2.46	8.98	10.28	0.08	0.02	2.00E-04	7.10E-03	Multiple_Complex
TC0600007402.hg.1	ZKSCAN8	zinc finger with KRAB and SCAN domains 8	-2.46	11.22	12.53	0.08	0.03	9.15E-05	5.70E-03	Multiple_Complex
TC0300011167.hg.1	BAP1	BRCA1 associated protein 1	-2.46	8.21	9.51	0.56	0.12	7.00E-04	1.19E-02	Multiple_Complex
TC1600006633.hg.1	SRRM2	serine/arginine repetitive matrix 2	-2.46	12.47	13.77	0.9	0.01	4.30E-03	3.10E-02	Multiple_Complex
TC2200008482.hg.1	EIF4ENIF1	eukaryotic translation initiation factor 4E nuclear import factor 1	-2.46	8.04	9.34	0.68	0.22	1.90E-03	1.89E-02	Multiple_Complex
TC2200007790.hg.1	TRABD	TraB domain containing	-2.46	7.95	9.25	0.26	0.06	1.00E-04	6.10E-03	Multiple_Complex
TC1000009844.hg.1	SEPHS1	selenophosphate synthetase 1	-2.47	8.79	10.09	0.48	0.06	5.00E-04	1.03E-02	Multiple_Complex
TC1700009640.hg.1	ZBTB4	zinc finger and BTB domain containing 4	-2.47	6.05	7.35	0.02	0.17	2.00E-04	6.40E-03	Multiple_Complex
TC2000008721.hg.1	APMAP	adipocyte plasma membrane associated protein	-2.47	8.84	10.14	0.31	0.29	4.00E-04	9.30E-03	Multiple_Complex
TC1500008485.hg.1	IGF1R	insulin-like growth factor 1 receptor	-2.47	9.88	11.18	0.2	0.14	1.00E-04	5.80E-03	Multiple_Complex
TSUnmapped00000801.hg.1	VPS11	VPS11, CORVET/HOPS core subunit [Source:HGNC Symbol;Acc:HGNC:14583]	-2.47	8.67	9.98	0.13	0.05	2.00E-04	6.40E-03	Coding
TC0700012122.hg.1	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	-2.47	8.37	9.67	0.14	0.14	1.00E-04	5.80E-03	Multiple_Complex
TC0900008927.hg.1	NTMT1	N-terminal Xaa-Pro-Lys N-methyltransferase 1	-2.47	11.07	12.37	0.63	0.05	1.00E-03	1.36E-02	Multiple_Complex
TC0100007489.hg.1	NUDC	nudC nuclear distribution protein	-2.47	9.09	10.4	0.77	0.28	2.70E-03	2.34E-02	Multiple_Complex
TC1400009701.hg.1	AREL1	apoptosis resistant E3 ubiquitin protein ligase 1	-2.47	9.54	10.85	0.78	0.18	2.10E-03	2.05E-02	Multiple_Complex
TC0100016129.hg.1	COPA	coatomer protein complex subunit alpha	-2.48	9.47	10.78	0.39	0.34	6.00E-04	1.07E-02	Multiple_Complex
TC0700008003.hg.1	CLIP2	CAP-GLY domain containing linker protein 2	-2.48	5.5	6.8	0.06	0.28	7.00E-04	1.17E-02	Multiple_Complex

TC0100017505.hg.1	SDE2	SDE2 telomere maintenance homolog (S. pombe)	-2.48	9.26	10.57	0.2	0.05	2.00E-04	7.10E-03	Multiple_Complex
TC1100009521.hg.1	APLP2	amyloid beta (A4) precursor-like protein 2	-2.48	10.5	11.81	0.1	0.02	2.00E-04	6.40E-03	Multiple_Complex
TC0200008351.hg.1	RPIA	ribose 5-phosphate isomerase A	-2.48	5.21	6.52	0.45	0.32	1.20E-03	1.51E-02	Multiple_Complex
TC0100013497.hg.1	SRSF4	serine/arginine-rich splicing factor 4	-2.48	10.48	11.79	0.28	0.1	1.00E-04	6.30E-03	Multiple_Complex
TC0400011744.hg.1	ANXA5	annexin A5	-2.48	10.06	11.37	0.03	0.31	3.00E-04	7.90E-03	Multiple_Complex
TC0400008947.hg.1	TMEM184C	transmembrane protein 184C	-2.48	9.77	11.09	0.66	0.07	1.00E-03	1.41E-02	Multiple_Complex
TC1100009203.hg.1	UBE4A	ubiquitination factor E4A	-2.48	10.78	12.09	0.24	0.05	2.00E-04	6.60E-03	Multiple_Complex
TC0200012713.hg.1	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-2.48	8.29	9.61	0.29	0.14	5.70E-03	3.69E-02	Multiple_Complex
TC1200010633.hg.1	MCRS1	microspherule protein 1	-2.49	9.85	11.16	0.61	0.1	9.00E-04	1.34E-02	Multiple_Complex
TC0X00011168.hg.1	BCAP31	B-cell receptor-associated protein 31	-2.49	11.68	12.99	0.06	0.12	2.00E-04	6.40E-03	Multiple_Complex
TC1900011957.hg.1	GSK3A	glycogen synthase kinase 3 alpha	-2.49	10.32	11.63	0.13	0.12	1.00E-04	6.30E-03	Multiple_Complex
TC1000007959.hg.1	CDH23	cadherin-related 23	-2.49	7.12	8.44	0.37	0.09	9.00E-04	1.32E-02	Multiple_Complex
TC1900011821.hg.1	ZNF776	zinc finger protein 776	-2.49	7.24	8.55	0.24	0.08	7.00E-04	1.16E-02	Multiple_Complex
TC1100012514.hg.1	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	-2.49	9.12	10.44	0.15	0.15	2.00E-04	6.50E-03	Multiple_Complex
TC0200016093.hg.1	USP40	ubiquitin specific peptidase 40	-2.49	6.68	7.99	0.28	0.05	2.00E-04	6.50E-03	Multiple_Complex
TC0300011109.hg.1	TMEM115	transmembrane protein 115	-2.49	10.3	11.62	0.25	0.08	1.00E-04	5.80E-03	Multiple_Complex
TC0300007596.hg.1	FLNB	filamin B, beta	-2.49	7.28	8.6	0.07	0.43	3.00E-04	8.80E-03	Multiple_Complex
TC1900007110.hg.1	RAD23A	RAD23 homolog A, nucleotide excision repair protein	-2.49	13.29	14.61	0.36	0.07	2.00E-04	6.90E-03	Multiple_Complex
TC0700007426.hg.1	ADCY1	adenylate cyclase 1 (brain)	-2.49	7.47	8.78	0.12	0.38	6.00E-04	1.12E-02	Multiple_Complex
TC0300013975.hg.1	IP6K2	inositol hexakisphosphate kinase 2	-2.49	7.71	9.03	0.58	0.38	1.00E-03	1.40E-02	Multiple_Complex

TC1200006905.hg.1	FAM234B	family with sequence similarity 234, member B	-2.5	8.22	9.54	0.6	0.04	1.20E-03	1.49E-02	Multiple_Complex
TC0900009949.hg.1	TPM2	tropomyosin 2 (beta)	-2.5	6.94	8.26	0.23	0.48	5.00E-04	1.03E-02	Multiple_Complex
TC1500007814.hg.1	NEO1	neogenin 1	-2.5	6.6	7.92	0.57	0.13	1.00E-03	1.40E-02	Multiple_Complex
TC0900010789.hg.1	IARS	isoleucyl-tRNA synthetase	-2.5	11.79	13.11	0.3	0.23	2.00E-04	6.80E-03	Multiple_Complex
TC1100011030.hg.1	DDB1	damage-specific DNA binding protein 1	-2.5	12.21	13.54	0.01	0.04	7.52E-05	5.50E-03	Multiple_Complex
TC2200009279.hg.1	SMDT1	single-pass membrane protein with aspartate-rich tail 1	-2.5	11.33	12.65	0.01	0.3	1.00E-04	6.30E-03	Multiple_Complex
TC1100008469.hg.1	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	-2.51	8.48	9.81	0.24	0.49	5.00E-04	1.03E-02	Multiple_Complex
TC1000011555.hg.1	MORN4	MORN repeat containing 4	-2.51	7.85	9.18	0.21	0.08	2.00E-04	7.40E-03	Multiple_Complex
TC1100007940.hg.1	VEGFB	vascular endothelial growth factor B	-2.51	8.85	10.18	0.55	0.04	6.00E-04	1.08E-02	Multiple_Complex
TC1500007829.hg.1	LOXL1	lysyl oxidase-like 1	-2.51	6.43	7.76	0.45	0.07	1.30E-03	1.55E-02	Multiple_Complex
TC1000008585.hg.1	MARVELD1	MARVEL domain containing 1	-2.51	6.69	8.01	0.11	0.15	3.00E-04	8.00E-03	Multiple_Complex
TC0100009365.hg.1	AHCYL1	adenosylhomocysteinase like 1	-2.51	12.18	13.51	0.06	0.11	1.00E-04	5.80E-03	Multiple_Complex
TC1600011342.hg.1	NAA60	N(alpha)-acetyltransferase 60, NatF catalytic subunit	-2.51	9.67	11	0.21	0.22	2.00E-04	6.60E-03	Multiple_Complex
TC1400010289.hg.1	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	-2.51	9.89	11.22	0.24	0	1.00E-04	5.80E-03	Multiple_Complex
TC0300008766.hg.1	COPG1	coatomer protein complex subunit gamma 1	-2.51	10.18	11.51	0.35	0.11	2.00E-04	7.10E-03	Multiple_Complex
TC1100009450.hg.1	DCPS	decapping enzyme, scavenger	-2.51	7.2	8.53	0.24	0.5	7.00E-04	1.17E-02	Multiple_Complex
TC1700008635.hg.1	RGS9	regulator of G-protein signaling 9	-2.51	5.12	6.45	0.25	0.04	9.00E-04	1.34E-02	Multiple_Complex
TC0200006725.hg.1	GREB1	growth regulation by estrogen in breast cancer 1	-2.51	5.7	7.03	0.29	0.44	5.00E-04	1.02E-02	Multiple_Complex
TC1100009248.hg.1	RNF26	ring finger protein 26	-2.52	8.57	9.9	0.04	0.11	2.00E-04	6.50E-03	Coding
TC1900011739.hg.1	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	-2.52	8.74	10.07	0.29	0.07	1.00E-04	6.30E-03	Multiple_Complex

TC1600011228.hg.1	PIEZO1	piezo-type mechanosensitive ion channel component 1	-2.52	7.45	8.78	0.23	0.13	2.00E-04	6.70E-03	Multiple_Complex
TC1700010731.hg.1	PSMC3IP	PSMC3 interacting protein	-2.52	8.95	10.29	0.04	0.1	7.92E-05	5.50E-03	Multiple_Complex
TC0800009955.hg.1	TRIM35	tripartite motif containing 35	-2.52	6.14	7.48	0.04	0.43	3.00E-04	8.90E-03	Multiple_Complex
TC1700010703.hg.1	NKIRAS2	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_001001349	-2.52	11.03	12.36	0.36	0.22	6.00E-04	1.11E-02	NonCoding
TC0800010918.hg.1	ZNF704	zinc finger protein 704	-2.52	6.43	7.77	0.26	0.09	3.00E-04	7.90E-03	Multiple_Complex
TC2200007401.hg.1	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	-2.52	5.08	6.42	0.13	0.35	2.00E-04	6.70E-03	Multiple_Complex
TC2000008104.hg.1	PRPF6	pre-mRNA processing factor 6	-2.52	7.09	8.43	0.4	0.11	7.00E-04	1.21E-02	Multiple_Complex
TC0100007505.hg.1	WDTC1	WD and tetratricopeptide repeats 1	-2.52	9.68	11.01	0.01	0.18	4.00E-04	8.90E-03	Multiple_Complex
TC1200007842.hg.1	SPRYD4	SPRY domain containing 4	-2.52	8.33	9.66	0.18	0.04	8.65E-05	5.70E-03	Coding
TC1100011602.hg.1	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	-2.53	8.64	9.98	0.03	0.02	9.25E-05	5.70E-03	Multiple_Complex
TC2200006614.hg.1	GP1BB; SEPT5	glycoprotein Ib (platelet), beta polypeptide; septin 5	-2.53	6.97	8.31	0.45	0.45	1.50E-03	1.65E-02	Multiple_Complex
TC1700006592.hg.1	GSG2	germ cell associated 2 (haspin)	-2.53	6.89	8.23	0.33	0.09	2.00E-04	7.30E-03	Coding
TC0X00007127.hg.1	RBM10	RNA binding motif protein 10	-2.53	7.43	8.77	0.71	0.25	2.60E-03	2.29E-02	Multiple_Complex
TC1700011756.hg.1	CASKIN2	CASK interacting protein 2	-2.53	7.55	8.89	0.79	0.1	2.10E-03	2.00E-02	Multiple_Complex
TC0800007459.hg.1	POMK	protein-O-mannose kinase	-2.53	10.48	11.82	0.38	0.08	2.00E-04	7.30E-03	Multiple_Complex
TC1700006480.hg.1	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	-2.53	8.52	9.86	0.12	0.57	7.00E-04	1.20E-02	Multiple_Complex
TC1900008547.hg.1	PRR12	proline rich 12	-2.53	7.24	8.58	0.36	0.22	5.00E-04	1.03E-02	Multiple_Complex
TC0900010019.hg.1	ZBTB5	zinc finger and BTB domain containing 5	-2.54	5.62	6.97	0.29	0.4	3.00E-04	8.10E-03	Coding
TC0100009580.hg.1	WDR3	WD repeat domain 3	-2.54	7.4	8.75	0.19	0.28	3.00E-04	7.90E-03	Multiple_Complex

TC1600009642.hg.1	GDE1	glycerophosphodiester phosphodiesterase 1	-2.54	8.76	10.11	0.02	0.05	1.00E-04	5.80E-03	Multiple_Complex
TC0100008073.hg.1	KDM4A	lysine (K)-specific demethylase 4A	-2.54	5.18	6.52	0.27	0.72	3.00E-03	2.48E-02	Multiple_Complex
TC0X00007999.hg.1	BEX4	brain expressed X-linked 4	-2.54	10.11	11.45	0.26	0.28	4.10E-03	3.00E-02	Multiple_Complex
TC0100006931.hg.1	PDPN	podoplanin	-2.55	6.18	7.53	0.25	0.18	1.90E-03	1.90E-02	Multiple_Complex
TC0300013793.hg.1	TMEM43	transmembrane protein 43	-2.55	9.56	10.91	0.71	0.07	2.70E-03	2.33E-02	Multiple_Complex
TC1200012254.hg.1	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	-2.55	6.9	8.25	0.44	0.48	1.20E-03	1.52E-02	Multiple_Complex
TC1700010802.hg.1	MPP2	membrane protein, palmitoylated 2	-2.55	4.69	6.04	0.9	0.09	9.10E-03	5.03E-02	Multiple_Complex
TC0300007579.hg.1	PDE12	phosphodiesterase 12	-2.55	8.56	9.91	0.33	0.03	1.00E-04	5.80E-03	Coding
TC2000009268.hg.1	ELMO2	engulfment and cell motility 2	-2.55	8.63	9.98	0.73	0.37	3.80E-03	2.86E-02	Multiple_Complex
TC1100013054.hg.1	RAD9A	RAD9 checkpoint clamp component A	-2.55	6.08	7.43	0.51	0.14	5.00E-04	1.02E-02	Multiple_Complex
TC1700011055.hg.1	SPOP	speckle-type POZ protein	-2.55	7.24	8.59	0.28	0.01	9.13E-05	5.70E-03	Multiple_Complex
TC0600012958.hg.1	TSPYL4	TSPY-like 4	-2.55	7.23	8.58	0.25	0.02	2.00E-04	6.50E-03	Multiple_Complex
TC1200006896.hg.1	GPRC5A; MIR614	G protein-coupled receptor, class C, group 5, member A; microRNA 614	-2.55	8.75	10.1	0.05	0.23	7.17E-05	5.40E-03	Multiple_Complex
TC1700011084.hg.1	PPP1R9B	protein phosphatase 1, regulatory subunit 9B	-2.55	5.75	7.1	0.7	0.49	4.30E-03	3.12E-02	Multiple_Complex
TC2000010022.hg.1	ZNFX1	zinc finger, NFX1-type containing 1	-2.56	6.21	7.56	0.69	0.08	1.10E-03	1.45E-02	Multiple_Complex
TC1200011870.hg.1	KCTD10	potassium channel tetramerization domain containing 10	-2.56	7.17	8.53	0.25	0.04	7.60E-05	5.50E-03	Multiple_Complex
TC0400009518.hg.1	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	-2.56	9.19	10.55	0.08	0.11	7.21E-05	5.40E-03	Multiple_Complex
TC1900010782.hg.1	ATP1A3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-2.56	6.92	8.28	0.96	0.18	3.70E-03	2.82E-02	Multiple_Complex

TC0300010862.hg.1	POMGNT2	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)	-2.56	8.63	9.98	0.64	0.01	8.00E-04	1.27E-02	Multiple_Complex
TC0100016678.hg.1	FAM129A	family with sequence similarity 129, member A	-2.56	6.88	8.23	0.49	0.16	5.00E-04	1.03E-02	Multiple_Complex
TC1900008297.hg.1	CLPTM1	cleft lip and palate associated transmembrane protein 1	-2.56	7.81	9.16	0	0.28	1.00E-04	6.30E-03	Multiple_Complex
TC1900008343.hg.1	QPCTL	glutaminyl-peptide cyclotransferase-like	-2.56	5.81	7.17	0.34	0.43	4.00E-04	9.10E-03	Multiple_Complex
TC2200006643.hg.1	ZDHHC8	zinc finger, DHHC-type containing 8	-2.56	9.78	11.14	0.39	0.18	8.00E-04	1.23E-02	Multiple_Complex
TC1700006654.hg.1	RNF167	ring finger protein 167	-2.56	7.35	8.71	0.76	0.14	1.70E-03	1.83E-02	Multiple_Complex
TC1600007944.hg.1	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	-2.57	7.86	9.22	0.12	0.37	2.00E-04	7.40E-03	Multiple_Complex
TC0800006680.hg.1	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-2.57	7.46	8.82	0.4	0.1	4.00E-04	9.50E-03	Multiple_Complex
TC1700009551.hg.1	ZNF232	zinc finger protein 232	-2.57	8.18	9.54	0.45	0.61	2.30E-03	2.12E-02	Multiple_Complex
TC1600006644.hg.1	FLYWCH1	FLYWCH-type zinc finger 1	-2.57	8.07	9.44	0.7	0.16	1.80E-03	1.86E-02	Multiple_Complex
TC2200007309.hg.1	SH3BP1; PDXP	SH3-domain binding protein 1; pyridoxal (pyridoxine, vitamin B6) phosphatase	-2.57	8.34	9.7	0.1	0.34	6.00E-04	1.08E-02	Multiple_Complex
TC1700006808.hg.1	RANGRF	RAN guanine nucleotide release factor	-2.57	8.82	10.19	0.6	0.02	5.00E-04	1.06E-02	Multiple_Complex
TC0700013327.hg.1	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	-2.57	6.83	8.2	0.87	0.26	2.40E-03	2.20E-02	Coding
TC0600006869.hg.1	DSP	desmoplakin	-2.58	7.81	9.17	0.7	0.28	1.10E-03	1.48E-02	Multiple_Complex
TC0700007098.hg.1	GARS	glycyl-tRNA synthetase	-2.58	13.64	15	0.14	0.05	7.14E-05	5.40E-03	Multiple_Complex
TC0100016000.hg.1	MEF2D	myocyte enhancer factor 2D	-2.58	6.69	8.06	0.52	0.22	4.00E-04	9.30E-03	Multiple_Complex
TC0100017528.hg.1	PARP1	poly(ADP-ribose) polymerase 1	-2.58	11.25	12.61	0.33	0.08	1.00E-04	6.30E-03	Multiple_Complex
TC1700007399.hg.1	ERAL1	Era-like 12S mitochondrial rRNA chaperone 1	-2.58	9.65	11.02	0.11	0.07	6.12E-05	5.20E-03	Multiple_Complex

TC1700007097.hg.1	GID4	GID complex subunit 4 homolog	-2.58	9.59	10.95	0.37	0.05	1.00E-04	5.90E-03	Multiple_Complex
TC0800007004.hg.1	RHOBTB2	Rho-related BTB domain containing 2	-2.58	7.51	8.88	0.16	0.24	1.00E-04	5.80E-03	Multiple_Complex
TC0200014785.hg.1	FIGN	fidgetin	-2.58	6.66	8.02	0.64	0.26	1.70E-03	1.78E-02	Multiple_Complex
TC1000006816.hg.1	OPTN	optineurin	-2.58	7.71	9.08	0.03	0.09	4.45E-05	4.90E-03	Multiple_Complex
TC0500013204.hg.1	CAST	calpastatin	-2.58	11.26	12.63	0.21	0.2	9.34E-05	5.70E-03	Multiple_Complex
TC0200012075.hg.1	ZNF513	zinc finger protein 513	-2.59	6.41	7.78	0.66	0.56	2.00E-03	1.96E-02	Multiple_Complex
TC0200013535.hg.1	LMAN2L	lectin, mannose-binding 2-like	-2.59	7.44	8.81	0.07	0.14	1.00E-04	5.80E-03	Multiple_Complex
TC0800007027.hg.1	SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	-2.59	6.02	7.39	0.75	0.47	2.10E-03	2.00E-02	Multiple_Complex
TC0200016416.hg.1	SLC35F6	solute carrier family 35, member F6	-2.59	8.05	9.42	0.38	0.1	2.00E-04	6.70E-03	Multiple_Complex
TC2100008385.hg.1	SUMO3	small ubiquitin-like modifier 3	-2.59	10.88	12.26	0.24	0.24	1.00E-04	5.80E-03	Multiple_Complex
TC0900008881.hg.1	PKN3	protein kinase N3	-2.59	7.99	9.36	0.11	0.24	7.59E-05	5.50E-03	Multiple_Complex
TC0X00007196.hg.1	WDR13	WD repeat domain 13	-2.59	6.9	8.27	0.39	0.22	3.00E-04	8.90E-03	Multiple_Complex
TC1900006956.hg.1	PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	-2.59	8.64	10.01	0.3	0.07	7.00E-04	1.16E-02	Multiple_Complex
TC2200008966.hg.1	KIAA0930	KIAA0930	-2.59	8.83	10.2	0.26	0.29	2.00E-04	6.90E-03	Multiple_Complex
TC1900011806.hg.1	ZNF582-AS1	ZNF582 antisense RNA 1 (head to head)	-2.59	7.93	9.3	0.17	0.21	1.00E-03	1.40E-02	NonCoding
TC1600010647.hg.1	ACD	adrenocortical dysplasia homolog (mouse)	-2.59	7.96	9.34	0.33	0.03	4.00E-04	9.40E-03	Multiple_Complex
TC1600007511.hg.1	ZNF646	zinc finger protein 646	-2.6	6.94	8.32	0.63	0.52	2.60E-03	2.31E-02	Coding
TC1800007071.hg.1	ZNF397	zinc finger protein 397	-2.6	7.02	8.39	0.04	0.23	1.00E-04	6.10E-03	Multiple_Complex
TC1100008123.hg.1	ADRBK1	adrenergic, beta, receptor kinase 1	-2.6	6.34	7.72	0.83	0.58	5.10E-03	3.42E-02	Multiple_Complex
TC0300006520.hg.1	LMCD1; LINC00312	LIM and cysteine-rich domains 1; long intergenic non-protein coding RNA 312	-2.6	6.07	7.44	0.35	0.35	8.00E-04	1.26E-02	Multiple_Complex

TC0100011512.hg.1	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	-2.6	12.92	14.3	0.37	0.13	2.00E-04	7.20E-03	Multiple_Complex
TC1100012519.hg.1	CBL	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_005188	-2.6	5.82	7.2	0.38	0.1	3.00E-04	8.00E-03	NonCoding
TC1200010798.hg.1	AAAS	achalasia, adrenocortical insufficiency, alacrimia	-2.6	13.04	14.42	0.06	0.08	6.08E-05	5.20E-03	Multiple_Complex
TC0700007998.hg.1	EIF4H	eukaryotic translation initiation factor 4H	-2.6	10.91	12.29	0.12	0.07	5.97E-05	5.20E-03	Multiple_Complex
TC1700010732.hg.1	FAM134C	family with sequence similarity 134, member C	-2.61	8.65	10.03	0.07	0.63	6.00E-04	1.09E-02	Multiple_Complex
TC1900006488.hg.1	PTBP1; MIR4745	polypyrimidine tract binding protein 1; microRNA 4745	-2.61	11.69	13.07	0.57	0.21	5.00E-04	1.06E-02	Multiple_Complex
TC0600011808.hg.1	MED20	mediator complex subunit 20	-2.61	7	8.38	0.32	0.2	3.00E-04	7.70E-03	Multiple_Complex
TC0200014382.hg.1	TMEM163	transmembrane protein 163	-2.61	5.91	7.3	0.23	0.25	1.00E-04	5.80E-03	Multiple_Complex
TC0X00009268.hg.1	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	-2.61	6.41	7.79	0.29	0.4	2.70E-03	2.32E-02	Multiple_Complex
TC0400010519.hg.1	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	-2.61	7.91	9.3	0.25	0.13	1.00E-04	5.80E-03	Multiple_Complex
TC0100013925.hg.1	MED8	mediator complex subunit 8	-2.62	9.52	10.9	0.29	0.33	2.00E-04	7.10E-03	Multiple_Complex
TC0X00011315.hg.1	TCEAL3	transcription elongation factor A (SII)-like 3	-2.62	6.19	7.58	0.73	0.36	1.50E-03	1.70E-02	Coding
TC2000008230.hg.1	C20orf27	chromosome 20 open reading frame 27	-2.62	7.8	9.19	0.09	0.36	1.00E-04	5.80E-03	Multiple_Complex
TC1600006485.hg.1	RHOT2	ras homolog family member T2	-2.62	9.21	10.6	0.83	0.15	4.40E-03	3.16E-02	Multiple_Complex
TC0X00009541.hg.1	SLC9A7	solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7	-2.62	5.92	7.31	0.06	0.28	3.50E-03	2.74E-02	Multiple_Complex
TC0400009818.hg.1	LRPAP1	LDL receptor related protein associated protein 1	-2.62	9.57	10.95	0.61	0.15	6.00E-04	1.07E-02	Multiple_Complex
TC1900010720.hg.1	C19orf54	chromosome 19 open reading frame 54	-2.62	5.65	7.04	0.41	0.06	2.00E-04	7.10E-03	Multiple_Complex
TC1100008409.hg.1	PPME1	protein phosphatase methylesterase 1	-2.62	8.55	9.95	1.46	0.22	1.75E-02	7.78E-02	Multiple_Complex

TC1100011331.hg.1	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme	-2.62	10.7	12.09	0.22	0.17	7.00E-05	5.40E-03	Multiple_Complex
TSUnmapped00000725.hg.1	CCDC84	coiled-coil domain containing 84	-2.62	4.55	5.95	0.23	0.44	2.20E-03	2.10E-02	NonCoding
TC1900006616.hg.1	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	-2.63	9.03	10.42	0.73	0	8.00E-04	1.27E-02	Multiple_Complex
TC0600014236.hg.1	TXNDC5	thioredoxin domain containing 5 (endoplasmic reticulum)	-2.63	6.33	7.73	0.27	0.28	2.00E-04	6.70E-03	Multiple_Complex
TC1200009676.hg.1	AKAP3	A kinase (PRKA) anchor protein 3	-2.63	5.69	7.08	0.11	0.07	6.49E-05	5.30E-03	Multiple_Complex
TC0X00009972.hg.1	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	-2.63	9.26	10.65	0.1	0.14	2.00E-04	7.50E-03	Multiple_Complex
TC1700007116.hg.1	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	-2.63	7.1	8.49	0.58	0.19	5.00E-04	1.02E-02	Multiple_Complex
TC1100013226.hg.1	ALG9	ALG9, alpha-1,2-mannosyltransferase	-2.63	8.89	10.28	0.9	0.17	2.50E-03	2.22E-02	Multiple_Complex
TC0200007908.hg.1	ANTXR1	anthrax toxin receptor 1	-2.63	12.26	13.65	0.08	0.15	5.74E-05	5.20E-03	Multiple_Complex
TC1700010717.hg.1	STAT5B	signal transducer and activator of transcription 5B	-2.63	8.78	10.17	0.46	0.09	4.00E-04	9.50E-03	Multiple_Complex
TC0100009241.hg.1	S1PR1	sphingosine-1-phosphate receptor 1	-2.63	6.11	7.51	0.89	0.86	1.08E-02	5.63E-02	Multiple_Complex
TC0700008524.hg.1	CNPY4	canopy FGF signaling regulator 4	-2.63	7	8.4	0.75	0.45	2.40E-03	2.20E-02	Multiple_Complex
TC2000007281.hg.1	MANBAL	mannosidase, beta A, lysosomal-like	-2.64	10.36	11.75	0.29	0.18	1.00E-04	5.80E-03	Multiple_Complex
TC0100010798.hg.1	QSOX1	quiescin Q6 sulfhydryl oxidase 1	-2.64	8.02	9.42	0.07	0.18	1.00E-04	6.10E-03	Multiple_Complex
TC1500007883.hg.1	COMMD4	COMM domain containing 4	-2.64	8.62	10.03	0.73	0.08	1.00E-03	1.37E-02	Multiple_Complex
TC0300013834.hg.1	RAD54L2	RAD54-like 2 (S. cerevisiae)	-2.64	8.48	9.88	0.45	0.07	8.00E-04	1.27E-02	Multiple_Complex
TC1900008303.hg.1	CLASRP	CLK4-associating serine/arginine rich protein	-2.65	7.43	8.83	0.47	0.21	6.00E-04	1.08E-02	Multiple_Complex
TC0600011481.hg.1	AGPAT1; MIR6721	1-acylglycerol-3-phosphate O-acyltransferase 1; microRNA 6721	-2.65	11.25	12.66	0.49	0.12	3.00E-04	8.00E-03	Multiple_Complex

TC2200008903.hg.1	MCAT	malonyl-CoA-acyl carrier protein transacylase	-2.65	9.06	10.47	0.25	0.1	8.09E-05	5.60E-03	Multiple_Complex
TC1100007400.hg.1	TSPAN18	tetraspanin 18	-2.65	8.17	9.58	0.55	0.24	1.20E-03	1.52E-02	Multiple_Complex
TC1400010716.hg.1	HOMEZ	homeobox and leucine zipper encoding	-2.65	8.96	10.37	0.55	0.15	3.00E-04	8.30E-03	Multiple_Complex
TC0100008591.hg.1	PGM1	phosphoglucomutase 1	-2.65	10.98	12.39	0.15	0.09	1.00E-04	5.80E-03	Multiple_Complex
TC0700013488.hg.1	REPIN1	replication initiator 1	-2.65	5.4	6.81	0.46	0.24	1.10E-03	1.48E-02	Multiple_Complex
TC0900008959.hg.1	FUBP3	far upstream element (FUSE) binding protein 3	-2.65	8.89	10.29	0.25	0.08	5.76E-05	5.20E-03	Multiple_Complex
TC1900011209.hg.1	LRRC4B	leucine rich repeat containing 4B	-2.65	6.4	7.81	0.83	0.97	9.60E-03	5.21E-02	Coding
TC1200009964.hg.1	MANSC1	MANSC domain containing 1	-2.66	5.48	6.89	0.7	0.4	1.80E-03	1.87E-02	Coding
TC0400012670.hg.1	FAT1	FAT atypical cadherin 1	-2.66	8.04	9.45	0.79	0.14	1.20E-03	1.53E-02	Multiple_Complex
TC0300010358.hg.1	XPC	xeroderma pigmentosum, complementation group C	-2.66	11.2	12.61	0.08	0.05	4.44E-05	4.90E-03	Multiple_Complex
TC0100016006.hg.1	GPATCH4	G-patch domain containing 4	-2.66	8.03	9.44	0.88	0.17	2.30E-03	2.12E-02	Multiple_Complex
TC0900011382.hg.1	FBXW2	F-box and WD repeat domain containing 2	-2.66	7.28	8.69	0.7	0.31	1.10E-03	1.43E-02	Multiple_Complex
TC2000010034.hg.1	ZNF512B	zinc finger protein 512B	-2.66	8.47	9.88	0.48	0.03	3.00E-04	8.20E-03	Multiple_Complex
TC1900008655.hg.1	ZNF175	zinc finger protein 175	-2.66	7.07	8.48	0.14	0.09	8.46E-05	5.60E-03	Multiple_Complex
TC0200008464.hg.1	KCNIP3	Kv channel interacting protein 3, calsenilin	-2.66	4.95	6.37	0.5	0.36	5.00E-04	1.02E-02	Multiple_Complex
TC1000007891.hg.1	HK1	hexokinase 1	-2.66	3.99	5.4	0.36	0.89	6.00E-03	3.81E-02	Multiple_Complex
TC0200014189.hg.1	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	-2.66	9.66	11.07	0.09	0.33	1.00E-04	5.80E-03	Multiple_Complex
TC2000007386.hg.1	PLCG1; RPL23AP81	phospholipase C, gamma 1; ribosomal protein L23a pseudogene 81	-2.67	6.92	8.34	0.33	0.42	4.00E-04	9.20E-03	Multiple_Complex
TC0700013531.hg.1	HOXA6	homeobox A6	-2.67	6.7	8.12	0	0.19	5.34E-05	5.10E-03	Multiple_Complex
TC2000009196.hg.1	SERINC3	serine incorporator 3	-2.67	10.52	11.94	0.18	0.05	7.83E-05	5.50E-03	Multiple_Complex
TC0X00007188.hg.1	FTSJ1	FtsJ RNA methyltransferase homolog 1 (E. coli)	-2.67	11.46	12.88	0.09	0.24	5.27E-05	5.10E-03	Multiple_Complex

TC0600009534.hg.1	MYB	v-myb avian myeloblastosis viral oncogene homolog	-2.67	7.2	8.62	0.75	0.03	1.10E-03	1.44E-02	Multiple_Complex
TC2000007219.hg.1	ERGIC3	ERGIC and golgi 3	-2.67	9.13	10.55	0.42	0.22	3.00E-04	8.00E-03	Multiple_Complex
TC0200011282.hg.1	TRAF3IP1	TNF receptor-associated factor 3 interacting protein 1	-2.67	6.53	7.95	0.27	0.05	7.45E-05	5.40E-03	Multiple_Complex
TC0600011531.hg.1	VPS52	vacuolar protein sorting 52 homolog (S. cerevisiae)	-2.67	6.55	7.96	0.31	0.39	6.00E-04	1.10E-02	Multiple_Complex
TC0900009905.hg.1	CNTFR	ciliary neurotrophic factor receptor	-2.67	7.98	9.4	0.68	0.19	1.30E-03	1.55E-02	Multiple_Complex
TC0200007047.hg.1	DPYSL5	dihydropyrimidinase-like 5	-2.67	7.07	8.49	0.01	0.39	3.00E-04	8.00E-03	Multiple_Complex
TC0700011508.hg.1	LIMK1	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001204426	-2.68	7.88	9.3	0.39	0.45	5.00E-04	1.07E-02	NonCoding
TC1000012505.hg.1	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	-2.68	7.61	9.03	0.5	0.2	4.60E-03	3.23E-02	Multiple_Complex
TC2000009744.hg.1	LAMA5; MIR4758	laminin, alpha 5; microRNA 4758	-2.68	6.5	7.92	0.88	0.19	3.50E-03	2.73E-02	Multiple_Complex
TC2200008719.hg.1	CBX6	chromobox homolog 6	-2.68	8.38	9.8	0.98	0.29	5.50E-03	3.63E-02	Multiple_Complex
TC1700011017.hg.1	SNF8	SNF8, ESCRT-II complex subunit	-2.68	12.31	13.73	0.07	0.04	3.30E-05	4.50E-03	Multiple_Complex
TC0500008632.hg.1	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5	-2.68	8.81	10.23	0.59	0.07	4.00E-04	8.90E-03	Multiple_Complex
TC1000011736.hg.1	OBFC1	oligonucleotide/oligosaccharide-binding fold containing 1	-2.68	8.51	9.93	0.42	0.17	1.20E-03	1.50E-02	Multiple_Complex
TC2200008099.hg.1	YDJC	YdjC homolog (bacterial)	-2.68	8.62	10.05	0.44	0.1	5.00E-04	1.00E-02	Multiple_Complex
TC1900009752.hg.1	PRDX2	peroxiredoxin 2	-2.68	12.03	13.45	0.69	0.03	8.00E-04	1.26E-02	Multiple_Complex
TC1700006569.hg.1	RAP1GAP2	RAP1 GTPase activating protein 2	-2.68	8.9	10.33	0.75	0.09	2.20E-03	2.09E-02	Multiple_Complex
TC0200006977.hg.1	CENPO	centromere protein O	-2.69	8.89	10.32	0.19	0.21	5.87E-05	5.20E-03	Multiple_Complex
TC0100015783.hg.1	RFX5	regulatory factor X, 5 (influences HLA class II expression)	-2.69	10.55	11.98	0.38	0	2.00E-04	6.60E-03	Multiple_Complex

TC0600014371.hg.1	RNASET2	ribonuclease T2	-2.69	10.77	12.2	0.36	0	8.35E-05	5.60E-03	Multiple_Complex
TC0600011915.hg.1	AARS2	alanyl-tRNA synthetase 2, mitochondrial	-2.69	5.32	6.75	0.12	0.16	4.06E-05	4.80E-03	Multiple_Complex
TC1600008928.hg.1	NPRL3	NPR3-like, GATOR1 complex subunit	-2.69	8.34	9.76	0.26	0.18	1.00E-04	6.10E-03	Multiple_Complex
TC1100011514.hg.1	DHCR7	7-dehydrocholesterol reductase	-2.69	9.78	11.21	0.47	0.24	2.00E-04	7.60E-03	Multiple_Complex
TC1700010849.hg.1	EFTUD2	elongation factor Tu GTP binding domain containing 2	-2.69	10.95	12.37	0.32	0.09	1.00E-04	5.80E-03	Multiple_Complex
TC1600011574.hg.1	GINS2	GINS complex subunit 2 (Psf2 homolog)	-2.69	9.16	10.59	0.41	0.17	2.00E-04	6.70E-03	Multiple_Complex
TC0X00011279.hg.1	TSPAN7	tetraspanin 7	-2.69	10.5	11.93	0.3	0.13	1.00E-04	5.80E-03	Multiple_Complex
TC0100013408.hg.1	GPN2	GPN-loop GTPase 2	-2.69	6.57	8	0.51	0.35	5.00E-04	1.06E-02	Multiple_Complex
TC0700007997.hg.1	LIMK1	LIM domain kinase 1	-2.7	8.67	10.1	0.46	0.12	3.00E-04	8.00E-03	Multiple_Complex
TC0200014160.hg.1	BIN1	bridging integrator 1	-2.7	7.81	9.25	0.38	0.31	4.00E-04	9.00E-03	Multiple_Complex
TC2100008495.hg.1	IL10RB	interleukin 10 receptor, beta	-2.7	7.26	8.69	0.1	0.28	2.00E-04	6.90E-03	Multiple_Complex
TC1600008427.hg.1	ZNRF1	zinc and ring finger 1, E3 ubiquitin protein ligase	-2.7	8.26	9.69	0.66	0.07	7.00E-04	1.16E-02	Multiple_Complex
TC0200008244.hg.1	TGOLN2	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001206844	-2.7	6.11	7.55	0.71	0.51	4.40E-03	3.16E-02	NonCoding
TC0300010209.hg.1	TADA3	transcriptional adaptor 3	-2.7	9.17	10.61	0.49	0.13	3.00E-04	8.00E-03	Multiple_Complex
TC1200012159.hg.1	MSI1	musashi RNA binding protein 1	-2.7	11	12.44	0.5	0.35	5.00E-04	1.00E-02	Multiple_Complex
TC1600009856.hg.1	EIF3C; EIF3CL	eukaryotic translation initiation factor 3, subunit C; eukaryotic translation initiation factor 3, subunit C-like	-2.7	13.19	14.63	0.09	0.14	3.33E-05	4.50E-03	Multiple_Complex
TC1100013042.hg.1	SSSCA1	Sjogren syndrome/scleroderma autoantigen 1	-2.7	5.79	7.22	0.42	0.04	6.00E-04	1.08E-02	Multiple_Complex
TC0100018273.hg.1	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	-2.71	12.5	13.94	0.27	0.09	1.00E-04	5.80E-03	Multiple_Complex

TC2000007012.hg.1	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)	-2.71	5.98	7.42	0.43	0.12	3.00E-04	7.90E-03	Multiple_Complex
TSUnmapped00000732.hg.1	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4 [Source:HGNC Symbol;Acc:HGNC:4061]	-2.71	8.24	9.68	0.31	0.21	1.00E-04	5.80E-03	Coding
TC0600009606.hg.1	ARFGEF3	ARFGEF family member 3	-2.71	7.51	8.94	0.69	0.01	1.80E-03	1.83E-02	Multiple_Complex
TC0200015080.hg.1	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	-2.71	11.38	12.82	0.39	0.05	8.95E-05	5.70E-03	Multiple_Complex
TC1600011385.hg.1	FBXL19	F-box and leucine-rich repeat protein 19	-2.71	6.06	7.49	0.1	0.12	1.00E-04	5.80E-03	Multiple_Complex
TC0700012968.hg.1	PDIA4	protein disulfide isomerase family A, member 4	-2.71	9.93	11.37	0.89	0.01	2.20E-03	2.09E-02	Multiple_Complex
TC0600011375.hg.1	DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	-2.71	6.4	7.84	0.4	0.18	6.00E-04	1.13E-02	Multiple_Complex
TC0500009346.hg.1	WWC1	WW and C2 domain containing 1	-2.71	8.31	9.75	0.08	0.08	7.54E-05	5.50E-03	Multiple_Complex
TC2200006827.hg.1	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	-2.72	10.11	11.55	0.45	0.35	3.60E-03	2.77E-02	Multiple_Complex
TC1400009787.hg.1	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	-2.72	9.41	10.85	0.16	0.14	4.67E-05	5.00E-03	Multiple_Complex
TC1900010334.hg.1	TSHZ3	teashirt zinc finger homeobox 3	-2.72	4.86	6.3	0.72	0.42	1.30E-03	1.57E-02	Multiple_Complex
TC1000011553.hg.1	MMS19	MMS19 homolog, cytosolic iron-sulfur assembly component	-2.72	7.78	9.23	1.09	0	4.60E-03	3.21E-02	Multiple_Complex
TC1900006819.hg.1	TRIP10	thyroid hormone receptor interactor 10	-2.72	8.98	10.42	0.01	0.13	4.95E-05	5.00E-03	Multiple_Complex
TC0200016332.hg.1	KIF1A	kinesin family member 1A	-2.72	8.74	10.18	0.16	0.54	3.00E-04	8.00E-03	Multiple_Complex
TC0400006591.hg.1	HTT	huntingtin	-2.72	10.04	11.49	0	0.08	2.58E-05	4.30E-03	Multiple_Complex
TC0X00009707.hg.1	MAGED4; MAGED4B; SNORA11D; SNORA11E	melanoma antigen family D4; melanoma antigen family D4B; small nucleolar RNA, H/ACA box 11D; small nucleolar RNA, H/ACA box 11E	-2.72	9.2	10.65	0.28	0.19	9.36E-05	5.70E-03	Multiple_Complex

TC2000009204.hg.1	TOMM34	translocase of outer mitochondrial membrane 34	-2.73	10.42	11.87	0	0.13	3.93E-05	4.80E-03	Multiple_Complex
TC2200007398.hg.1	SYNGR1	synaptogyrin 1	-2.73	8.89	10.33	0.55	0.18	6.00E-04	1.13E-02	Multiple_Complex
TC0900008474.hg.1	SNX30	sorting nexin family member 30	-2.73	8.33	9.78	0.14	0.17	1.00E-04	6.20E-03	Multiple_Complex
TC0800012213.hg.1	VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	-2.73	8.11	9.56	0.14	0.08	6.56E-05	5.30E-03	Multiple_Complex
TC2200009152.hg.1	PLXNB2	plexin B2	-2.73	8.33	9.78	0.64	0.15	6.00E-04	1.12E-02	Multiple_Complex
TC1600009943.hg.1	SEZ6L2	seizure related 6 homolog (mouse)-like 2	-2.73	5.08	6.53	0.98	0.22	2.60E-03	2.29E-02	Multiple_Complex
TC1900008967.hg.1	ZNF470	zinc finger protein 470	-2.73	7.59	9.04	0.09	0.11	8.46E-05	5.60E-03	Multiple_Complex
TC0900012181.hg.1	NUP188	nucleoporin 188kDa	-2.73	8.33	9.78	0.08	0.19	6.38E-05	5.30E-03	Multiple_Complex
TC1600011560.hg.1	MTSS1L	metastasis suppressor 1-like	-2.73	9.76	11.21	0.78	0.09	1.10E-03	1.42E-02	Multiple_Complex
TC0700010564.hg.1	HOXA10; HOXA9; MIR196B	homeobox A10; homeobox A9; microRNA 196b	-2.74	8.96	10.41	0.23	0.12	4.00E-04	9.10E-03	Multiple_Complex
TC1400006656.hg.1	OXA1L	oxidase (cytochrome c) assembly 1-like	-2.74	7.66	9.12	0.57	0.59	1.60E-03	1.73E-02	Multiple_Complex
TC1700012184.hg.1	CHRNB1	cholinergic receptor, nicotinic beta 1	-2.74	5.44	6.9	0.68	0.01	6.00E-04	1.15E-02	Multiple_Complex
TC0100010159.hg.1	SLC25A44	solute carrier family 25, member 44	-2.74	8.23	9.68	0.54	0.47	6.00E-04	1.13E-02	Multiple_Complex
TC0600011960.hg.1	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	-2.74	7.73	9.18	0.53	0.06	3.00E-04	8.00E-03	Multiple_Complex
TC0500012567.hg.1	FAXDC2	fatty acid hydroxylase domain containing 2	-2.74	6.94	8.4	0.07	0.33	7.64E-05	5.50E-03	Multiple_Complex
TC1100008029.hg.1	PCNXL3	pecanex-like 3 (Drosophila)	-2.74	6.27	7.73	0.78	0.05	1.70E-03	1.79E-02	Multiple_Complex
TC0200016645.hg.1	ASXL2	additional sex combs like transcriptional regulator 2	-2.74	9.21	10.66	0.35	0.04	6.52E-05	5.30E-03	Multiple_Complex
TC1900011673.hg.1	CCDC130	coiled-coil domain containing 130	-2.74	8.24	9.7	0.97	0.2	3.60E-03	2.79E-02	Multiple_Complex
TC0900011655.hg.1	ZER1	zyg-11 related, cell cycle regulator	-2.75	6.65	8.11	0.07	0.15	9.38E-05	5.70E-03	Multiple_Complex
TC1200007881.hg.1	INHBE	inhibin beta E	-2.75	7.8	9.25	0.93	0.69	9.00E-03	4.99E-02	Multiple_Complex

TC0300007294.hg.1	PTPN23	protein tyrosine phosphatase, non-receptor type 23	-2.75	6.61	8.07	0.03	0.39	2.00E-04	6.60E-03	Multiple_Complex
TC2000007512.hg.1	PCIF1	PDX1 C-terminal inhibiting factor 1	-2.75	7.19	8.65	0.49	0.45	1.00E-03	1.42E-02	Multiple_Complex
TC1000012399.hg.1	ECHS1	enoyl-CoA hydratase, short chain, 1, mitochondrial	-2.75	9	10.46	0.34	0.15	1.00E-04	5.80E-03	Multiple_Complex
TC1200009132.hg.1	RNF10	ring finger protein 10	-2.75	10.56	12.02	0.2	0.17	8.71E-05	5.70E-03	Multiple_Complex
TC0500012980.hg.1	FAM193B	family with sequence similarity 193, member B	-2.75	6.93	8.39	0.25	0.12	1.00E-04	5.80E-03	Multiple_Complex
TSUnmapped00000103.hg.1	MLXIP	MLX interacting protein	-2.75	9.47	10.93	0.28	0.17	2.00E-04	6.50E-03	NonCoding
TC0100018353.hg.1	SNAP47	synaptosome associated protein 47kDa	-2.75	7.25	8.71	0.22	0.24	1.00E-04	5.80E-03	Multiple_Complex
TC0100013432.hg.1	WASF2	WAS protein family, member 2	-2.75	8.66	10.12	0.56	0.03	2.00E-04	7.30E-03	Multiple_Complex
TC0700007367.hg.1	DBNL; MIR6837	drebrin-like; microRNA 6837	-2.76	9.62	11.08	0.7	0.02	6.00E-04	1.15E-02	Multiple_Complex
TC0600011876.hg.1	YIPF3	Yip1 domain family member 3	-2.76	10.82	12.29	0.18	0	8.40E-05	5.60E-03	Multiple_Complex
TC0900007096.hg.1	CREB3	cAMP responsive element binding protein 3	-2.76	9	10.46	0.01	0.4	2.00E-04	6.70E-03	Multiple_Complex
TC0100009877.hg.1	HIST2H3A	histone cluster 2, H3a	-2.76	7.21	8.68	0.33	0.24	1.00E-04	5.80E-03	Coding
TC1600007436.hg.1	TAOK2	TAO kinase 2	-2.76	7.3	8.77	0.05	0.03	2.50E-05	4.30E-03	Multiple_Complex
TC0900007994.hg.1	PHF2	PHD finger protein 2	-2.76	7.77	9.24	0.07	0.38	8.27E-05	5.60E-03	Multiple_Complex
TC1600008239.hg.1	WWP2	WW domain containing E3 ubiquitin protein ligase 2	-2.76	5.74	7.21	0.38	0.09	1.00E-04	5.80E-03	Multiple_Complex
TC0900008811.hg.1	STXBP1	syntaxin binding protein 1	-2.76	10.69	12.16	0.16	0.15	5.84E-05	5.20E-03	Multiple_Complex
TC0900008969.hg.1	ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	-2.76	9.56	11.02	0.02	0.1	2.45E-05	4.30E-03	Multiple_Complex
TC1800006650.hg.1	RAB31	RAB31, member RAS oncogene family	-2.76	9.54	11.01	0.27	0.03	6.62E-05	5.30E-03	Multiple_Complex
TC0700009066.hg.1	FLNC	filamin C, gamma	-2.76	10.93	12.4	0.2	0.08	1.20E-03	1.53E-02	Multiple_Complex
TC0700007986.hg.1	WBSCR22	Williams Beuren syndrome chromosome region 22	-2.77	9.7	11.16	0.38	0.11	8.72E-05	5.70E-03	Multiple_Complex

TC1200011843.hg.1	SART3	squamous cell carcinoma antigen recognized by T-cells 3	-2.77	5.78	7.25	0.48	0.34	5.00E-04	1.07E-02	Multiple_Complex
TC0100015707.hg.1	HIST2H4A; HIST2H4B	histone cluster 2, H4a; histone cluster 2, H4b	-2.77	9.18	10.65	0.42	0.05	3.00E-04	8.30E-03	Multiple_Complex
TC0600014294.hg.1	ZNF318	zinc finger protein 318	-2.77	7.38	8.85	0.33	0.28	1.00E-04	6.20E-03	Multiple_Complex
TC0100016625.hg.1	GLUL	glutamate-ammonia ligase	-2.78	9.87	11.34	0.53	0.01	9.00E-04	1.32E-02	Multiple_Complex
TC1700008984.hg.1	SEC14L1; SCARNA16; SNHG20; MIR6516	SEC14-like lipid binding 1; small Cajal body-specific RNA 16; small nucleolar RNA host gene 20; microRNA 6516	-2.78	8.53	10	0.73	0.34	1.30E-03	1.54E-02	Multiple_Complex
TC0300013981.hg.1	IFRD2	interferon-related developmental regulator 2	-2.78	8.41	9.89	0.56	0.81	2.90E-03	2.42E-02	Multiple_Complex
TC0100016120.hg.1	PIGM	phosphatidylinositol glycan anchor biosynthesis class M	-2.78	9.1	10.57	0.3	0.07	8.13E-05	5.60E-03	Coding
TC2200008434.hg.1	SF3A1	splicing factor 3a, subunit 1, 120kDa	-2.78	11.45	12.92	0.38	0.24	1.00E-04	6.20E-03	Multiple_Complex
TC0300013980.hg.1	GMPPB	GDP-mannose pyrophosphorylase B	-2.78	5.2	6.68	0.77	0.46	1.60E-03	1.76E-02	Multiple_Complex
TC1200007701.hg.1	ZNF740	zinc finger protein 740	-2.78	8.7	10.17	0.48	0	1.00E-04	5.80E-03	Multiple_Complex
TC2000008318.hg.1	FERMT1	fermitin family member 1	-2.78	4.91	6.38	0.08	0.25	6.15E-05	5.20E-03	Multiple_Complex
TC0500009610.hg.1	NSD1	nuclear receptor binding SET domain protein 1	-2.78	8.79	10.26	0.06	0.37	1.00E-04	5.80E-03	Multiple_Complex
TC1900011744.hg.1	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	-2.79	9.43	10.91	0.72	0.09	1.00E-03	1.36E-02	Multiple_Complex
TC2000006833.hg.1	SEC23B	Sec23 homolog B, COPII coat complex component	-2.79	11.12	12.61	0.17	0.04	5.05E-05	5.00E-03	Multiple_Complex
TC1900006520.hg.1	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-2.79	10.91	12.39	0.37	0.06	9.61E-05	5.80E-03	Multiple_Complex
TC2000009973.hg.1	ZNF343	zinc finger protein 343	-2.79	6.13	7.61	0.36	0.02	2.00E-04	6.90E-03	Multiple_Complex
TC2100007318.hg.1	RRP1B	ribosomal RNA processing 1B	-2.8	11.66	13.14	0.23	0.01	3.48E-05	4.60E-03	Multiple_Complex
TC1000007950.hg.1	UNC5B	unc-5 netrin receptor B	-2.8	8.15	9.63	0.42	0.33	6.00E-04	1.13E-02	Multiple_Complex

TC1700011097.hg.1	LRRC59	leucine rich repeat containing 59	-2.8	10.18	11.67	0.4	0.06	8.21E-05	5.60E-03	Multiple_Complex
TC1700010207.hg.1	RAB34	RAB34, member RAS oncogene family	-2.8	8.18	9.66	0.66	0.15	5.00E-04	1.01E-02	Multiple_Complex
TC0100008696.hg.1	HHLA3	HERV-H LTR-associating 3	-2.8	10.1	11.58	0.16	0.08	9.65E-05	5.80E-03	Multiple_Complex
TC2000008845.hg.1	PLAGL2	pleiomorphic adenoma gene-like 2	-2.8	9.34	10.83	0.21	0.14	1.00E-04	5.80E-03	Coding
TC1100007457.hg.1	ATG13	autophagy related 13	-2.8	5.58	7.06	0.26	0.07	9.89E-05	5.80E-03	Multiple_Complex
TC1900007878.hg.1	KMT2B	lysine (K)-specific methyltransferase 2B	-2.8	5.82	7.31	0.3	0.37	3.00E-04	7.80E-03	Multiple_Complex
TC0900010586.hg.1	C9orf64	chromosome 9 open reading frame 64	-2.8	8.37	9.86	0.61	0.65	1.80E-03	1.86E-02	Multiple_Complex
TC0100013837.hg.1	RIMS3	regulating synaptic membrane exocytosis 3	-2.81	7.37	8.86	0.16	0.19	9.24E-05	5.70E-03	Multiple_Complex
TC1900009208.hg.1	AP3D1	adaptor-related protein complex 3, delta 1 subunit	-2.81	9.09	10.58	0.73	0.35	1.00E-03	1.37E-02	Multiple_Complex
TC0X00007200.hg.1	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	-2.81	10.87	12.36	0.27	0.05	4.79E-05	5.00E-03	Multiple_Complex
TC1600010227.hg.1	N4BP1	NEDD4 binding protein 1	-2.81	9.55	11.04	0.43	0.04	1.00E-04	5.90E-03	Multiple_Complex
TC0X00011181.hg.1	HCFC1	host cell factor C1	-2.81	9.19	10.68	0.38	0.09	1.00E-04	5.90E-03	Multiple_Complex
TC0100015781.hg.1	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	-2.82	8.41	9.9	0.34	0.14	7.39E-05	5.40E-03	Multiple_Complex
TC0300010390.hg.1	RBSN	rabenosyn, RAB effector	-2.82	8.44	9.94	0.65	0.03	4.00E-04	9.60E-03	Multiple_Complex
TC1100012633.hg.1	SCN3B	sodium channel, voltage gated, type III beta subunit	-2.82	7.44	8.94	0.27	1.09	7.50E-03	4.40E-02	Multiple_Complex
TC2200009357.hg.1	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	-2.82	8.89	10.39	0.52	0.36	3.00E-04	8.60E-03	Multiple_Complex
TC1600011292.hg.1	FANCA	Fanconi anemia complementation group A	-2.82	7.22	8.72	0.01	0.44	8.91E-05	5.70E-03	Multiple_Complex
TC1200006701.hg.1	NECAP1	NECAP endocytosis associated 1	-2.83	9.6	11.09	0.05	0.09	1.96E-05	4.30E-03	Multiple_Complex
TC1700008186.hg.1	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	-2.83	8.6	10.1	0.81	0.42	1.40E-03	1.61E-02	Multiple_Complex
TC1900008084.hg.1	PSMC4	proteasome 26S subunit, ATPase 4	-2.83	8.98	10.48	0.23	0.04	3.37E-05	4.50E-03	Multiple_Complex
TC1700012434.hg.1	HOXB7	homeobox B7	-2.83	9.03	10.53	0.88	0.07	1.20E-03	1.51E-02	Multiple_Complex

TC1600009200.hg.1	TRAP1	TNF receptor-associated protein 1	-2.83	8.23	9.73	0.3	0.03	5.63E-05	5.20E-03	Multiple_Complex
TC0100007447.hg.1	CEP85	centrosomal protein 85kDa	-2.83	5.02	6.52	0.11	0.35	7.82E-05	5.50E-03	Multiple_Complex
TC0300013520.hg.1	CLDN1	claudin 1	-2.83	9.21	10.72	0.21	0	3.00E-04	8.30E-03	Multiple_Complex
TC1000008643.hg.1	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-2.84	10.95	12.46	0.3	0.2	7.35E-05	5.40E-03	Multiple_Complex
TC0100015819.hg.1	S100A10	S100 calcium binding protein A10	-2.84	9.7	11.2	0.75	0.09	6.00E-04	1.13E-02	Multiple_Complex
TC1900011656.hg.1	STXBP2	syntaxin binding protein 2	-2.84	7.93	9.43	0.27	0.34	2.00E-04	6.70E-03	Multiple_Complex
TC1700009515.hg.1	MYBBP1A	MYB binding protein (P160) 1a	-2.84	7.37	8.87	0.09	0.28	6.53E-05	5.30E-03	Multiple_Complex
TC1100012735.hg.1	SRPR	signal recognition particle receptor (docking protein)	-2.85	11.22	12.73	0.2	0	2.55E-05	4.30E-03	Multiple_Complex
TC1900007098.hg.1	RNASEH2A	ribonuclease H2, subunit A	-2.85	11.01	12.52	0.23	0.11	5.79E-05	5.20E-03	Multiple_Complex
TC1700009318.hg.1	FAM101B	family with sequence similarity 101, member B	-2.85	7.9	9.41	1.64	0.98	3.80E-02	1.31E-01	Multiple_Complex
TC2200009248.hg.1	KREMEN1	kringle containing transmembrane protein 1	-2.85	8.51	10.02	0.4	0.29	1.00E-04	5.80E-03	Multiple_Complex
TC0100009441.hg.1	CTTNBP2NL	CTTNBP2 N-terminal like	-2.85	8.86	10.37	0.09	0.02	2.15E-05	4.30E-03	Multiple_Complex
TC0100008066.hg.1	PTPRF	protein tyrosine phosphatase, receptor type, F	-2.85	6.59	8.1	0.44	0.23	2.00E-04	6.40E-03	Multiple_Complex
TSUnmapped00000351.hg.1	VPS11	VPS11, CORVET/HOPS core subunit [Source:HGNC Symbol;Acc:HGNC:14583]	-2.86	5.06	6.58	0.82	0.03	1.00E-03	1.40E-02	NonCoding
TC1900009133.hg.1	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	-2.86	10.61	12.13	0.71	0.39	7.00E-04	1.17E-02	Multiple_Complex
TC1200012718.hg.1	PSMD9	proteasome 26S subunit, non-ATPase 9	-2.86	10.22	11.73	0.35	0.15	6.70E-05	5.30E-03	Multiple_Complex
TC0300012397.hg.1	PLXND1	plexin D1	-2.86	6.34	7.86	0.77	0.16	1.30E-03	1.55E-02	Multiple_Complex
TC1200009137.hg.1	MLEC	malectin	-2.86	9.8	11.31	0.17	0.07	2.87E-05	4.40E-03	Multiple_Complex
TC0300013973.hg.1	CELSR3; MIR4793	cadherin, EGF LAG seven-pass G-type receptor 3; microRNA 4793	-2.86	6.14	7.65	0.78	0.1	4.30E-03	3.09E-02	Multiple_Complex
TC0200007296.hg.1	GALM	galactose mutarotase (aldose 1-epimerase)	-2.86	8.73	10.25	0.85	0.05	2.40E-03	2.20E-02	Multiple_Complex

TC0300007470.hg.1	PPM1M	protein phosphatase, Mg2+/Mn2+ dependent, 1M	-2.86	8.67	10.19	0.25	0.04	1.00E-04	5.80E-03	Multiple_Complex
TC1600007354.hg.1	EIF3C; EIF3CL	eukaryotic translation initiation factor 3, subunit C; eukaryotic translation initiation factor 3, subunit C-like	-2.86	12.35	13.87	0.21	0.01	3.85E-05	4.80E-03	Multiple_Complex
TC0200007200.hg.1	LTBP1	latent transforming growth factor beta binding protein 1	-2.86	8.61	10.12	0.31	0.07	5.18E-05	5.10E-03	Multiple_Complex
TC1000008744.hg.1	TRIM8	tripartite motif containing 8	-2.87	6.9	8.42	0.4	0.01	6.65E-05	5.30E-03	Multiple_Complex
TC1100008181.hg.1	LRP5	LDL receptor related protein 5	-2.87	10.17	11.69	0.79	0.4	1.00E-03	1.41E-02	Multiple_Complex
TC1900006994.hg.1	DNM2	dynamin 2	-2.87	8.42	9.94	0.77	0.66	2.10E-03	2.01E-02	Multiple_Complex
TC1100007785.hg.1	TMEM109	transmembrane protein 109	-2.87	10.65	12.17	0.2	0.1	2.50E-05	4.30E-03	Multiple_Complex
TSUnmapped00000019.hg.1	DYRK1B	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	-2.88	5.35	6.87	0.09	0.36	6.03E-05	5.20E-03	Coding
TC0100011192.hg.1	IPO9	importin 9	-2.88	13.77	15.3	0.03	0.03	1.70E-05	4.30E-03	Multiple_Complex
TC1700011787.hg.1	RNF157	ring finger protein 157	-2.88	6.48	8.01	0.29	0.8	9.00E-04	1.30E-02	Multiple_Complex
TC0100013134.hg.1	CAPZB	capping protein (actin filament) muscle Z-line, beta	-2.88	10.28	11.81	0.29	0.13	3.91E-05	4.80E-03	Multiple_Complex
TC1200012189.hg.1	C12orf43	chromosome 12 open reading frame 43	-2.88	9.56	11.09	0.33	0.41	3.00E-04	7.70E-03	Multiple_Complex
TC1000008733.hg.1	MFSD13A	major facilitator superfamily domain containing 13A	-2.9	9.33	10.87	0.44	0.34	7.00E-04	1.16E-02	Multiple_Complex
TC1900008575.hg.1	MYH14	myosin, heavy chain 14, non-muscle	-2.9	4.87	6.41	0.06	0.15	1.90E-05	4.30E-03	Multiple_Complex
TC2200007206.hg.1	MCM5	minichromosome maintenance complex component 5	-2.9	9.19	10.73	0.48	0.51	4.00E-04	9.00E-03	Multiple_Complex
TC1000011203.hg.1	ANXA11	annexin A11	-2.9	10.85	12.39	0.18	0.03	4.39E-05	4.90E-03	Multiple_Complex
TC0900011705.hg.1	ASB6	ankyrin repeat and SOCS box containing 6	-2.9	6.73	8.27	0.22	0.53	2.00E-04	6.80E-03	Multiple_Complex

TC0500008890.hg.1	PCDHGC3; PCDHGA12; PCDHGB4; PCDHGA8; PCDHGA1; PCDHGA10; PCDHGA11; PCDHGA2; PCDHGA3; PCDHGA4; PCDHGA5; PCDHGA6; PCDHGA7; PCDHGA9; PCDHGB1; PCDHGB2; PCDHGB3; PCDHGB5; PCDHGB6; PCDHGB7; PCDHGC4; PCDHGC5	protocadherin gamma subfamily C, 3; protocadherin gamma subfamily A, 12; protocadherin gamma subfamily B, 4; protocadherin gamma subfamily A, 8; protocadherin gamma subfamily A, 1; protocadherin gamma subfamily A, 10; protocadherin gamma subfamily A, 11; protocadherin gamma subfamily A, 2; protocadherin gamma subfamily A, 3; protocadherin gamma subfamily A, 4; protocadherin gamma subfamily A, 5; protocadherin gamma subfamily A, 6; protocadherin gamma subfamily A, 7; protocadherin gamma subfamily A, 9; protocadherin gamma subfamily B, 1; protocadherin gamma subfamily B, 2; protocadherin gamma subfamily B, 3; protocadherin gamma subfamily B, 5; protocadherin gamma subfamily B, 6; protocadherin gamma subfamily B, 7; protocadherin gamma subfamily C, 4; protocadherin gamma subfamily C, 5	-2.91	4.66	6.2	0.39	0.12	1.00E-04	6.20E-03	Multiple_Complex
TC0700006567.hg.1	TTYH3	tweety family member 3	-2.91	9.53	11.07	0.69	0.42	6.00E-04	1.13E-02	Multiple_Complex
TC1500009120.hg.1	RMDN3	regulator of microtubule dynamics 3	-2.91	10.32	11.86	0.28	0.12	7.19E-05	5.40E-03	Multiple_Complex

TC1900011872.hg.1	ECSIT	ECSIT signalling integrator	-2.91	8.3	9.84	0.36	0.27	7.36E-05	5.40E-03	Multiple_Complex
TC1900006893.hg.1	RAB11B	RAB11B, member RAS oncogene family	-2.91	5.84	7.38	0.13	0.18	4.74E-05	5.00E-03	Multiple_Complex
TC1900010016.hg.1	ISYNA1	inositol-3-phosphate synthase 1	-2.91	10.69	12.23	0.3	0	2.10E-03	2.02E-02	Multiple_Complex
TC0300010933.hg.1	FYCO1	FYVE and coiled-coil domain containing 1	-2.91	7.65	9.2	0.29	0.08	4.00E-04	9.40E-03	Multiple_Complex
TC1200006648.hg.1	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	-2.91	7.56	9.11	0.2	0.39	9.48E-05	5.70E-03	Multiple_Complex
TC0100009870.hg.1	HIST2H4B; HIST2H4A	histone cluster 2, H4b; histone cluster 2, H4a	-2.92	8.94	10.48	0.17	0.04	5.53E-05	5.20E-03	Coding
TC0200010840.hg.1	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	-2.92	7.09	8.64	0.38	0.31	1.00E-04	5.80E-03	Multiple_Complex
TC1700012126.hg.1	C17orf62	chromosome 17 open reading frame 62	-2.92	8.52	10.07	1.28	0.15	9.80E-03	5.29E-02	Multiple_Complex
TC0300010966.hg.1	CCDC12	coiled-coil domain containing 12	-2.92	8.32	9.87	0.39	0.09	7.07E-05	5.40E-03	Multiple_Complex
TC2000007923.hg.1	NELFCD	negative elongation factor complex member C/D	-2.92	5.34	6.89	0.68	0.05	5.00E-04	1.00E-02	Multiple_Complex
TC0300013022.hg.1	SLITRK3	SLIT and NTRK-like family, member 3	-2.93	4.72	6.27	0.07	0.31	8.00E-04	1.25E-02	Coding
TC0400008331.hg.1	NPNT	nephronectin	-2.93	9.75	11.3	0.26	0.02	1.00E-04	5.80E-03	Multiple_Complex
TC2200007069.hg.1	OSBP2	oxysterol binding protein 2	-2.93	6.85	8.41	0.78	0.71	2.70E-03	2.34E-02	Multiple_Complex
TC2200008112.hg.1	TOP3B	topoisomerase (DNA) III beta	-2.93	10.34	11.9	0.31	0.28	9.34E-05	5.70E-03	Multiple_Complex
TC1000008556.hg.1	LCOR	ligand dependent nuclear receptor corepressor	-2.94	8.31	9.87	0.1	0.49	3.00E-04	8.00E-03	Multiple_Complex
TC0800012378.hg.1	PPP1R16A	protein phosphatase 1, regulatory subunit 16A	-2.94	6.54	8.1	0.2	0.1	3.08E-05	4.40E-03	Multiple_Complex
TC1700009900.hg.1	ZNF287	zinc finger protein 287	-2.94	7.8	9.36	0.7	0.14	2.90E-03	2.44E-02	Multiple_Complex
TC2200008610.hg.1	FOXRED2	FAD-dependent oxidoreductase domain containing 2	-2.94	6.71	8.27	0.67	0.49	7.00E-04	1.17E-02	Multiple_Complex
TC0600011878.hg.1	XPO5	exportin 5	-2.94	10.38	11.94	0.05	0.09	1.48E-05	4.20E-03	Multiple_Complex
TC0600007711.hg.1	ITPR3	inositol 1,4,5-trisphosphate receptor, type 3	-2.95	7.5	9.06	0.98	0.22	8.10E-03	4.65E-02	Multiple_Complex

TC1700010358.hg.1	MYO1D	myosin ID	-2.96	9.21	10.78	0.49	0.04	1.00E-04	5.80E-03	Multiple_Complex
TC1000012391.hg.1	TUBGCP2	tubulin, gamma complex associated protein 2	-2.96	9.31	10.88	0.24	0.22	3.44E-05	4.60E-03	Multiple_Complex
TC1900008112.hg.1	SHKBP1	SH3KBP1 binding protein 1	-2.96	8.1	9.67	0.21	0.2	2.00E-04	7.40E-03	Multiple_Complex
TC1500010764.hg.1	CLK3	CDC like kinase 3	-2.97	8.56	10.13	0.03	0.13	6.70E-05	5.30E-03	Multiple_Complex
TC0X00008832.hg.1	GDI1	GDP dissociation inhibitor 1	-2.97	12.51	14.08	0.08	0.1	1.59E-05	4.20E-03	Multiple_Complex
TC1000008193.hg.1	PPIF	peptidylprolyl isomerase F	-2.97	6.49	8.06	0.24	0.28	4.02E-05	4.80E-03	Multiple_Complex
TC1000007895.hg.1	TSPAN15	tetraspanin 15	-2.98	7.24	8.81	0.34	0.06	4.62E-05	5.00E-03	Multiple_Complex
TC1600009849.hg.1	XPO6	exportin 6	-2.98	8.4	9.97	0.25	0.2	4.98E-05	5.00E-03	Multiple_Complex
TC1900007005.hg.1	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	-2.98	12.11	13.69	0.26	0.05	4.03E-05	4.80E-03	Multiple_Complex
TC0900011533.hg.1	MAPKAP1	mitogen-activated protein kinase associated protein 1	-2.98	8.07	9.65	0.61	0	3.00E-04	8.20E-03	Multiple_Complex
TC1100008065.hg.1	KLC2	kinesin light chain 2	-2.98	7.07	8.65	0.2	0.38	9.67E-05	5.80E-03	Multiple_Complex
TC1200012706.hg.1	ACAD10	acyl-CoA dehydrogenase family, member 10	-2.99	5.8	7.37	0.19	0.17	1.00E-04	5.80E-03	Multiple_Complex
TC0600014101.hg.1	MICA	MHC class I polypeptide-related sequence A	-2.99	7.12	8.7	0.01	0.05	1.35E-05	4.20E-03	Coding
TC0700009696.hg.1	CHPF2; MIR671	chondroitin polymerizing factor 2; microRNA 671	-2.99	10.15	11.73	0.72	0.01	3.00E-04	8.80E-03	Multiple_Complex
TC1500006818.hg.1	EMC4	ER membrane protein complex subunit 4	-2.99	10.63	12.21	0.61	0.04	2.00E-04	7.10E-03	Multiple_Complex
TC1900012050.hg.1	PPP6R1	protein phosphatase 6, regulatory subunit 1	-2.99	9.84	11.42	0.49	0.22	1.00E-04	6.10E-03	Multiple_Complex
TC1400006711.hg.1	DHRS4L1	dehydrogenase/reductase (SDR family) member 4 like 1	-2.99	7.56	9.15	0.82	0.16	5.90E-03	3.75E-02	Multiple_Complex
TC1500010890.hg.1	HEXA	hexosaminidase A (alpha polypeptide)	-2.99	7.46	9.04	0.4	0.19	9.25E-05	5.70E-03	Multiple_Complex
TC0100013924.hg.1	ELOVL1; MIR6734	ELOVL fatty acid elongase 1; microRNA 6734	-3	6.8	8.38	0.46	0.11	2.00E-04	7.10E-03	Multiple_Complex

TC1100011184.hg.1	SF1	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_201998	-3	8.05	9.63	0.28	0.15	2.00E-04	7.40E-03	NonCoding
TC1900011635.hg.1	CHMP2A	charged multivesicular body protein 2A	-3.01	7.58	9.17	0.03	0.06	2.45E-05	4.30E-03	Multiple_Complex
TC0100015701.hg.1	HIST2H3A; HIST2H3C	histone cluster 2, H3a; histone cluster 2, H3c	-3.01	7.32	8.91	0.25	0.26	1.00E-04	5.80E-03	Coding
TC1700007780.hg.1	CASC3; MIR6866	cancer susceptibility candidate 3; microRNA 6866	-3.01	8.17	9.76	0.03	0.08	2.65E-05	4.30E-03	Multiple_Complex
TC1000011904.hg.1	ABLIM1	actin binding LIM protein 1	-3.02	10.83	12.42	0.65	0.05	4.00E-04	9.60E-03	Multiple_Complex
TC1700012276.hg.1	PNPO	pyridoxamine 5-phosphate oxidase	-3.02	7.58	9.17	0.96	0.09	1.20E-03	1.51E-02	Multiple_Complex
TC2000008107.hg.1	TCEA2	transcription elongation factor A (SII), 2	-3.02	8.18	9.77	0.05	0.14	2.09E-05	4.30E-03	Multiple_Complex
TC1700012348.hg.1	NEURL4	neuralized E3 ubiquitin protein ligase 4	-3.02	5.95	7.55	0.9	0.02	8.00E-04	1.25E-02	Multiple_Complex
TC2200009335.hg.1	THOC5	THO complex 5	-3.03	8.35	9.94	0.29	0.08	5.81E-05	5.20E-03	Multiple_Complex
TC1200007595.hg.1	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	-3.03	8.16	9.76	0.17	0.01	3.05E-05	4.40E-03	Multiple_Complex
TC0900009948.hg.1	ARHGEF39	Rho guanine nucleotide exchange factor 39	-3.03	5.34	6.94	0.1	0.08	5.25E-05	5.10E-03	Multiple_Complex
TC0100013503.hg.1	MECR	mitochondrial trans-2-enoyl-CoA reductase	-3.04	6.8	8.41	0.32	0.17	3.01E-05	4.40E-03	Multiple_Complex
TC1600008943.hg.1	TMEM8A	transmembrane protein 8A	-3.04	6.9	8.5	0.18	0.26	4.76E-05	5.00E-03	Multiple_Complex
TC0100008090.hg.1	DMAP1	DNA methyltransferase 1 associated protein 1	-3.04	5.72	7.32	0.7	0.28	7.00E-04	1.17E-02	Multiple_Complex
TC1400007584.hg.1	TTC9	tetratricopeptide repeat domain 9	-3.04	7.92	9.52	0.26	0.16	3.00E-04	8.00E-03	Coding
TC0200016775.hg.1	ATG9A	autophagy related 9A	-3.05	8.66	10.27	0.55	0.09	1.00E-04	5.80E-03	Multiple_Complex
TC0200012863.hg.1	SPRED2	sprouty-related, EVH1 domain containing 2	-3.05	7.24	8.85	0.43	0.32	1.00E-04	5.80E-03	Multiple_Complex
TC2200007607.hg.1	NUP50	nucleoporin 50kDa	-3.05	10.28	11.89	0.49	0.11	1.00E-04	5.80E-03	Multiple_Complex

TC0100007412.hg.1	MAN1C1	mannosidase, alpha, class 1C, member 1	-3.06	6.42	8.03	1.08	0.25	2.00E-03	2.00E-02	Multiple_Complex
TC1900009337.hg.1	SH3GL1	SH3-domain GRB2-like 1	-3.06	7.92	9.53	0.78	0.19	1.30E-03	1.57E-02	Multiple_Complex
TC0400009892.hg.1	CRMP1	collapsin response mediator protein 1	-3.06	8.68	10.29	0.56	0.13	1.20E-03	1.50E-02	Multiple_Complex
TC0700011488.hg.1	NSUN5	NOP2/Sun domain family, member 5	-3.07	9.24	10.86	0.85	0.28	1.80E-03	1.88E-02	Multiple_Complex
TC2200007467.hg.1	ZC3H7B	zinc finger CCCH-type containing 7B	-3.07	6.68	8.3	0.8	0.17	5.00E-04	1.02E-02	Multiple_Complex
TC1200007626.hg.1	METTL7A	methyltransferase like 7A	-3.08	10.39	12.01	0.18	0.06	4.79E-05	5.00E-03	Coding
TC0400009791.hg.1	NOP14	NOP14 nucleolar protein	-3.08	8.5	10.12	0.46	0.3	1.00E-04	5.80E-03	Multiple_Complex
TC0100013713.hg.1	STK40	serine/threonine kinase 40	-3.08	7.18	8.8	0.25	0.13	4.00E-04	9.80E-03	Multiple_Complex
TC1900011764.hg.1	GEMIN7	gem nuclear organelle associated protein 7	-3.08	7.04	8.66	0.4	0.14	9.86E-05	5.80E-03	Multiple_Complex
TC0100008618.hg.1	AK4	adenylate kinase 4	-3.08	7.76	9.38	0	0.21	1.94E-05	4.30E-03	Multiple_Complex
TC0800012211.hg.1	CPSF1; MIR939; MIR1234; MIR6849	cleavage and polyadenylation specific factor 1; microRNA 939; microRNA 1234; microRNA 6849	-3.09	8.4	10.03	0.96	0.05	1.30E-03	1.54E-02	Multiple_Complex
TC0600011884.hg.1	MRPS18A	mitochondrial ribosomal protein S18A	-3.09	12.19	13.81	0.04	0.32	2.79E-05	4.30E-03	Multiple_Complex
TC0900008887.hg.1	TBC1D13	TBC1 domain family, member 13	-3.09	9.1	10.73	1.02	0.26	1.70E-03	1.78E-02	Multiple_Complex
TC1400008341.hg.1	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	-3.09	10.3	11.93	0.65	0.02	2.00E-04	7.10E-03	Multiple_Complex
TC1900007868.hg.1	HAUS5	HAUS augmin like complex subunit 5	-3.09	6.66	8.29	0.16	0.47	2.00E-04	6.90E-03	Multiple_Complex
TC1000009152.hg.1	HTRA1	HtrA serine peptidase 1	-3.09	5.7	7.33	0.18	0.32	1.00E-04	5.80E-03	Multiple_Complex
TC1900011946.hg.1	FBXO27	F-box protein 27	-3.1	8.77	10.4	1.11	0.42	5.60E-03	3.63E-02	Multiple_Complex
TC0500013144.hg.1	CEP72	centrosomal protein 72kDa	-3.1	7.17	8.8	0.18	0.16	2.00E-04	7.10E-03	Multiple_Complex
TC0100011267.hg.1	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-3.1	12.42	14.06	0.69	0.11	4.00E-04	9.20E-03	Multiple_Complex
TC1500007067.hg.1	CKMT1A	creatine kinase, mitochondrial 1A	-3.11	9.23	10.87	0.1	0.4	3.70E-05	4.70E-03	Multiple_Complex

TC0100009944.hg.1	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	-3.11	11.67	13.3	0.9	0.07	8.00E-04	1.25E-02	Multiple_Complex
TC1100007913.hg.1	MARK2	MAP/microtubule affinity-regulating kinase 2	-3.12	6.19	7.83	0.46	0.33	2.00E-04	6.90E-03	Multiple_Complex
TC0500009175.hg.1	LARP1	La ribonucleoprotein domain family, member 1	-3.12	9.52	11.16	0.24	0.16	7.43E-05	5.40E-03	Multiple_Complex
TC0800012478.hg.1	FBXL6	F-box and leucine-rich repeat protein 6	-3.12	7.28	8.92	0.68	0.2	4.00E-04	9.10E-03	Multiple_Complex
TC0600011441.hg.1	BAG6	BCL2 associated athanogene 6	-3.12	11.76	13.4	0.47	0.02	5.55E-05	5.20E-03	Multiple_Complex
TC1700012439.hg.1	RNF43	ring finger protein 43	-3.12	6.27	7.91	0.58	0.08	4.00E-04	9.00E-03	Multiple_Complex
TC0900008574.hg.1	TRIM32	tripartite motif containing 32	-3.12	5.22	6.87	0.65	0.34	6.00E-04	1.11E-02	Coding
TC0500012147.hg.1	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	-3.13	9.84	11.49	0.44	0.39	1.00E-04	5.80E-03	Multiple_Complex
TC1100010887.hg.1	SSRP1	structure specific recognition protein 1	-3.13	10.06	11.7	0.22	0.03	3.50E-05	4.60E-03	Multiple_Complex
TC0100008664.hg.1	GADD45A	growth arrest and DNA-damage-inducible, alpha	-3.13	11.4	13.05	0.01	0.55	2.00E-04	7.20E-03	Multiple_Complex
TC0100016944.hg.1	ARL8A	ADP-ribosylation factor like GTPase 8A	-3.13	7.6	9.25	0.35	0.75	5.00E-04	1.00E-02	Multiple_Complex
TC1200012281.hg.1	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	-3.13	8.53	10.18	0.73	0.07	3.00E-04	7.70E-03	Multiple_Complex
TC0600011535.hg.1	RGL2	ral guanine nucleotide dissociation stimulator-like 2	-3.14	6.47	8.12	0.99	0.2	1.00E-03	1.42E-02	Multiple_Complex
TC0100017171.hg.1	C1orf74	chromosome 1 open reading frame 74	-3.14	5.43	7.08	0.04	0.36	2.90E-05	4.40E-03	Coding
TC0600007599.hg.1	PRRC2A	proline-rich coiled-coil 2A	-3.14	8.77	10.42	0.8	0.06	4.00E-04	9.10E-03	Multiple_Complex
TC0600008066.hg.1	KLHDC3	kelch domain containing 3	-3.14	10.27	11.92	0.38	0.04	3.11E-05	4.40E-03	Multiple_Complex
TC0200007049.hg.1	TMEM214	transmembrane protein 214	-3.14	7.26	8.92	0.61	0.1	2.00E-04	7.20E-03	Multiple_Complex
TC1900009128.hg.1	TMEM259	transmembrane protein 259	-3.14	10.96	12.62	0.51	0.07	7.75E-05	5.50E-03	Multiple_Complex
TC1200010944.hg.1	ZBTB39	zinc finger and BTB domain containing 39	-3.15	8.36	10.01	0.01	0.32	2.22E-05	4.30E-03	Coding
TC2100008285.hg.1	CBS	cystathionine-beta-synthase	-3.15	9.11	10.76	0.21	0.05	1.77E-05	4.30E-03	Multiple_Complex

TC1100008025.hg.1	SCYL1	SCY1-like, kinase-like 1	-3.15	7.39	9.05	0.2	0.09	1.46E-05	4.20E-03	Multiple_Complex
TC1100012984.hg.1	NAT10	N-acetyltransferase 10 (GCN5-related)	-3.15	8.41	10.07	0.31	0.09	2.24E-05	4.30E-03	Multiple_Complex
TC0900007082.hg.1	RUSC2	RUN and SH3 domain containing 2	-3.16	5.36	7.02	0.76	0.33	6.00E-04	1.15E-02	Multiple_Complex
TC1200009590.hg.1	DCP1B	decapping mRNA 1B	-3.16	8.57	10.23	0.34	0.22	4.02E-05	4.80E-03	Multiple_Complex
TC2200006718.hg.1	SDF2L1	stromal cell-derived factor 2-like 1	-3.16	8.56	10.22	0.12	0.33	3.65E-05	4.70E-03	Multiple_Complex
TC1200010902.hg.1	ANKRD52	ankyrin repeat domain 52	-3.16	5.69	7.35	0.29	0.14	2.65E-05	4.30E-03	Multiple_Complex
TC0300007387.hg.1	RNF123	ring finger protein 123	-3.17	7.93	9.59	0.2	0.05	1.50E-05	4.20E-03	Multiple_Complex
TC1900011099.hg.1	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	-3.17	6.22	7.89	0.63	0.64	1.70E-03	1.83E-02	Multiple_Complex
TC1900008543.hg.1	FCGRT	Fc fragment of IgG, receptor, transporter, alpha	-3.17	6.28	7.94	0.08	0.67	3.00E-04	7.90E-03	Multiple_Complex
TC0200013257.hg.1	TGOLN2	trans-golgi network protein 2	-3.17	10.32	11.99	0.28	0.28	3.08E-05	4.40E-03	Multiple_Complex
TC2200008067.hg.1	THAP7	THAP domain containing 7	-3.17	7.89	9.55	0.52	0.67	4.00E-04	9.60E-03	Multiple_Complex
TC1700008254.hg.1	ACSF2	acyl-CoA synthetase family member 2	-3.18	7.61	9.28	0.13	0.35	2.00E-04	6.30E-03	Multiple_Complex
TC1900006466.hg.1	CDC34	cell division cycle 34	-3.18	6.06	7.73	0.97	0.09	8.00E-04	1.25E-02	Multiple_Complex
TC0200013106.hg.1	CCDC142; MRPL53	coiled-coil domain containing 142; mitochondrial ribosomal protein L53	-3.19	4.87	6.54	0.82	0.09	1.50E-03	1.65E-02	Multiple_Complex
TC1800007696.hg.1	TSHZ1	teashirt zinc finger homeobox 1	-3.19	6.23	7.9	0.38	0.16	6.78E-05	5.30E-03	Multiple_Complex
TC1700012054.hg.1	NPLOC4	NPL4 homolog, ubiquitin recognition factor	-3.2	10.74	12.42	0.69	0.05	2.00E-04	6.60E-03	Multiple_Complex
TC1400006691.hg.1	THTPA	thiamine triphosphatase	-3.2	7.27	8.95	0.38	0.38	1.00E-04	5.90E-03	Multiple_Complex
TC1100009969.hg.1	APBB1	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	-3.2	6.88	8.56	0.26	0.92	8.00E-04	1.26E-02	Multiple_Complex
TC1100008002.hg.1	MRPL49	mitochondrial ribosomal protein L49	-3.2	6.79	8.47	0.29	0.52	1.00E-04	5.80E-03	Multiple_Complex
TC1700012433.hg.1	HOXB6	homeobox B6	-3.2	5.32	6.99	0.09	0.7	4.00E-04	9.70E-03	Multiple_Complex

TC1700010199.hg.1	PIGS	phosphatidylinositol glycan anchor biosynthesis class S	-3.2	8.5	10.18	0.55	0.15	8.15E-05	5.60E-03	Multiple_Complex
TC1100009689.hg.1	DEAF1	DEAF1 transcription factor	-3.21	8.5	10.19	1.21	0.25	3.30E-03	2.62E-02	Multiple_Complex
TC0800007431.hg.1	AP3M2	adaptor-related protein complex 3, mu 2 subunit	-3.21	9.71	11.4	0.12	0.01	2.58E-05	4.30E-03	Multiple_Complex
TC0900010614.hg.1	GOLM1	golgi membrane protein 1	-3.21	8.54	10.23	0.6	0.07	9.01E-05	5.70E-03	Multiple_Complex
TC1700012324.hg.1	ABR	active BCR-related	-3.21	7.74	9.43	0.45	0.21	8.07E-05	5.60E-03	Multiple_Complex
TC1200006670.hg.1	CLSTN3	calsyntenin 3	-3.21	8.08	9.76	0.09	0.29	3.00E-04	7.70E-03	Multiple_Complex
TC1700008225.hg.1	DLX4	distal-less homeobox 4	-3.22	4.79	6.48	0.65	0.53	4.00E-04	9.50E-03	Multiple_Complex
TC1600008137.hg.1	CES3; CES2	carboxylesterase 3; carboxylesterase 2	-3.22	8.52	10.21	0.17	0.09	1.16E-05	4.00E-03	Multiple_Complex
TC0100007552.hg.1	SESN2	sestrin 2	-3.22	8.57	10.25	0.27	0.44	5.00E-05	5.00E-03	Multiple_Complex
TC2000009392.hg.1	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	-3.23	6.52	8.21	0.36	0.13	2.69E-05	4.30E-03	Multiple_Complex
TC0100014276.hg.1	DHCR24	24-dehydrocholesterol reductase	-3.23	10.49	12.19	0.19	0.26	2.77E-05	4.30E-03	Multiple_Complex
TC0600014332.hg.1	ZBTB24	zinc finger and BTB domain containing 24	-3.23	7.92	9.61	0.11	0.1	1.07E-05	3.90E-03	Multiple_Complex
TC1900006685.hg.1	FSD1	fibronectin type III and SPRY domain containing 1	-3.23	4.57	6.27	0.1	0.48	4.51E-05	4.90E-03	Multiple_Complex
TC1100010216.hg.1	PLEKHA7	pleckstrin homology domain containing, family A member 7	-3.23	5.71	7.4	0.51	0.14	6.00E-04	1.08E-02	Multiple_Complex
TC1900009627.hg.1	TYK2	tyrosine kinase 2	-3.23	9.46	11.15	0.73	0.23	3.00E-04	8.00E-03	Multiple_Complex
TC0700012636.hg.1	PODXL	podocalyxin-like	-3.23	8.31	10.01	0.62	0.15	2.00E-04	7.10E-03	Multiple_Complex
TC1200008213.hg.1	ATXN7L3B	ataxin 7-like 3B	-3.23	9.42	11.12	0.24	0.1	5.88E-05	5.20E-03	Multiple_Complex
TC1200010921.hg.1	GLS2	glutaminase 2 (liver, mitochondrial)	-3.25	5.81	7.51	0.46	0.26	5.00E-04	1.03E-02	Multiple_Complex
TC0X00011399.hg.1	FAM127B	family with sequence similarity 127, member B	-3.25	8.72	10.42	0.54	0.02	7.31E-05	5.40E-03	Multiple_Complex
TC2200009157.hg.1	SBF1	SET binding factor 1	-3.25	9.44	11.14	0.39	0.4	1.00E-04	5.80E-03	Multiple_Complex

TC0900009127.hg.1	COL5A1	collagen, type V, alpha 1	-3.25	5.17	6.88	0.95	0.47	1.10E-03	1.45E-02	Multiple_Complex
TC0500009088.hg.1	TCOF1	Treacher Collins-Franceschetti syndrome 1	-3.26	9.94	11.64	0.53	0.38	2.00E-04	7.40E-03	Multiple_Complex
TC1300008713.hg.1	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	-3.26	6.85	8.56	0.71	0.03	2.00E-04	7.20E-03	Multiple_Complex
TC2200009273.hg.1	APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	-3.26	8.1	9.81	1.33	0.16	3.90E-03	2.91E-02	Multiple_Complex
TC1100007941.hg.1	FKBP2	FK506 binding protein 2	-3.26	9.2	10.9	0.2	0.44	3.57E-05	4.70E-03	Multiple_Complex
TC0800009237.hg.1	GPAA1	glycosylphosphatidylinositol anchor attachment 1	-3.27	10.09	11.8	0.1	0	6.70E-06	3.40E-03	Multiple_Complex
TC0100018260.hg.1	AMPD2	adenosine monophosphate deaminase 2	-3.27	8.61	10.32	1.23	0	2.90E-03	2.43E-02	Multiple_Complex
TC1700010701.hg.1	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	-3.29	7.33	9.05	0.22	0.16	2.00E-04	6.70E-03	NonCoding
TC1700012315.hg.1	SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	-3.29	7.82	9.53	0.41	0.36	6.46E-05	5.30E-03	Multiple_Complex
TC0X00009650.hg.1	WDR45; PRAF2	WD repeat domain 45; PRA1 domain family, member 2	-3.31	6.75	8.48	0.02	0.44	1.00E-04	5.80E-03	Multiple_Complex
TC0100016973.hg.1	CYB5R1	cytochrome b5 reductase 1	-3.31	8.26	9.99	0.33	0.03	8.43E-05	5.60E-03	Multiple_Complex
TC1900008180.hg.1	ZNF526	zinc finger protein 526	-3.31	5.59	7.32	0.42	0.21	3.24E-05	4.50E-03	Coding
TC0100013087.hg.1	RCC2	regulator of chromosome condensation 2	-3.32	10.15	11.88	0.08	0.31	5.67E-05	5.20E-03	Multiple_Complex
TC2200007307.hg.1	GGA1	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	-3.32	6.65	8.39	0.8	0.54	1.00E-03	1.40E-02	Multiple_Complex
TSUnmapped00000246.hg.1	CCDC84	coiled-coil domain containing 84	-3.32	6.62	8.35	0.06	0.33	2.00E-04	7.20E-03	NonCoding
TC0X00008794.hg.1	SLC6A8	solute carrier family 6 (neurotransmitter transporter), member 8	-3.33	7.77	9.5	0.51	0.09	5.85E-05	5.20E-03	Multiple_Complex
TC1900010043.hg.1	TMEM161A	transmembrane protein 161A	-3.34	6.1	7.84	0.54	0.28	7.45E-05	5.40E-03	Multiple_Complex
TC0100016631.hg.1	RGS16	regulator of G-protein signaling 16	-3.34	8.84	10.58	0.77	0.07	8.00E-04	1.27E-02	Coding

TC1900007297.hg.1	SIN3B	SIN3 transcription regulator family member B	-3.34	4.6	6.34	0.6	0.73	1.70E-03	1.78E-02	Multiple_Complex
TC1200010597.hg.1	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	-3.35	8.12	9.86	0.11	0.18	9.44E-06	3.80E-03	Multiple_Complex
TC1700009394.hg.1	PRPF8	pre-mRNA processing factor 8	-3.35	9.13	10.88	0.22	0.09	2.46E-05	4.30E-03	Multiple_Complex
TC0100006852.hg.1	UBIAD1	UbiA prenyltransferase domain containing 1	-3.36	10.57	12.32	0.2	0.15	7.75E-06	3.50E-03	Multiple_Complex
TC1200007819.hg.1	CDK2	cyclin-dependent kinase 2	-3.36	9.92	11.67	0.76	0.02	2.00E-04	7.50E-03	Multiple_Complex
TC1600006587.hg.1	TSC2	tuberous sclerosis 2	-3.37	7.7	9.46	0.57	0.66	7.00E-04	1.18E-02	Multiple_Complex
TC1000008234.hg.1	FAM213A	family with sequence similarity 213, member A	-3.37	9.93	11.68	0.15	0.05	2.41E-05	4.30E-03	Multiple_Complex
TC1000008271.hg.1	CDHR1	cadherin-related family member 1	-3.37	8.9	10.66	0.91	0.16	1.30E-03	1.57E-02	Multiple_Complex
TC1800007218.hg.1	C18orf25	chromosome 18 open reading frame 25	-3.38	5.66	7.42	0.51	0.21	7.90E-05	5.50E-03	Multiple_Complex
TC0600011536.hg.1	TAPBP	TAP binding protein (tapasin)	-3.39	8.33	10.09	0.76	0.29	3.00E-04	7.90E-03	Multiple_Complex
TC0600014370.hg.1	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	-3.39	5.65	7.41	0.24	0.37	1.00E-04	5.80E-03	Multiple_Complex
TC0900006473.hg.1	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	-3.39	5.44	7.2	0.1	0.11	1.85E-05	4.30E-03	Multiple_Complex
TC1200010641.hg.1	BCDIN3D	BCDIN3 domain containing	-3.39	5.74	7.5	0.07	1.06	1.00E-03	1.41E-02	Multiple_Complex
TC1900011001.hg.1	STRN4	striatin, calmodulin binding protein 4	-3.4	8.43	10.2	0.5	0.07	4.01E-05	4.80E-03	Multiple_Complex
TC0700011973.hg.1	TAF6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	-3.41	9.18	10.95	0.36	0.02	1.56E-05	4.20E-03	Multiple_Complex
TC0300008715.hg.1	EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific	-3.41	6.84	8.61	0.88	0.39	5.00E-04	1.06E-02	Multiple_Complex
TC1400009967.hg.1	TTC7B	tetratricopeptide repeat domain 7B	-3.42	10.66	12.43	0.22	0.09	9.79E-06	3.80E-03	Multiple_Complex
TC2200009266.hg.1	GTPBP1	GTP binding protein 1	-3.43	8.62	10.4	0.46	0.32	4.00E-04	9.10E-03	Multiple_Complex

TC1700009402.hg.1	SMYD4	SET and MYND domain containing 4	-3.43	8.28	10.06	0.25	0.25	3.20E-05	4.50E-03	Multiple_Complex
TC0X00006701.hg.1	TXLNG	taxilin gamma	-3.44	10.58	12.36	0.5	0.01	2.79E-05	4.30E-03	Multiple_Complex
TC1100007247.hg.1	CAPRIN1	cell cycle associated protein 1	-3.45	10.76	12.54	0.19	0.22	1.17E-05	4.00E-03	Multiple_Complex
TC0300009702.hg.1	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	-3.46	11.65	13.44	0.98	0.12	6.00E-04	1.12E-02	Multiple_Complex
TC1400009690.hg.1	ABCD4	ATP binding cassette subfamily D member 4	-3.46	6.68	8.47	0.65	0.09	1.00E-03	1.40E-02	Multiple_Complex
TC1900011944.hg.1	FBXO17	F-box protein 17	-3.47	8.73	10.53	0.26	0.17	1.53E-05	4.20E-03	Multiple_Complex
TC0900010462.hg.1	RFK	riboflavin kinase	-3.47	7.26	9.05	0.68	0.37	3.00E-04	8.00E-03	Multiple_Complex
TC1200010917.hg.1	TIMELESS	timeless circadian clock	-3.47	6.01	7.8	0.16	0.18	1.73E-05	4.30E-03	Multiple_Complex
TC0700009604.hg.1	ZNF398	zinc finger protein 398	-3.48	7.11	8.91	0.2	0.02	2.79E-05	4.30E-03	Multiple_Complex
TC2000007277.hg.1	RPN2	ribophorin II	-3.5	11.7	13.5	0.22	0.1	6.08E-06	3.40E-03	Multiple_Complex
TC0700007132.hg.1	FKBP9	FK506 binding protein 9	-3.5	9.74	11.55	0.67	0.26	1.00E-04	5.80E-03	Multiple_Complex
TC0100009449.hg.1	MOV10	Mov10 RISC complex RNA helicase	-3.51	7.13	8.94	0.18	0.15	6.13E-06	3.40E-03	Multiple_Complex
TC0500013426.hg.1	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	-3.51	9.25	11.06	0.62	0.38	1.00E-04	5.80E-03	Multiple_Complex
TC2100007355.hg.1	PFKL	phosphofructokinase, liver	-3.52	7.71	9.52	0.15	0.5	2.67E-05	4.30E-03	Multiple_Complex
TC2200007027.hg.1	NF2	neurofibromin 2 (merlin)	-3.52	8.27	10.09	0.33	0.63	8.86E-05	5.70E-03	Multiple_Complex
TC1600007235.hg.1	PLK1	polo-like kinase 1	-3.52	10.09	11.91	0.51	0.13	6.86E-05	5.40E-03	Multiple_Complex
TC0100008156.hg.1	NSUN4	NOP2/Sun domain family, member 4	-3.52	7.82	9.63	0.45	0.21	3.65E-05	4.70E-03	Multiple_Complex
TC0900012176.hg.1	URM1	ubiquitin related modifier 1	-3.53	6.87	8.69	0.91	0.11	6.00E-04	1.08E-02	Multiple_Complex
TC0600008531.hg.1	MTO1	mitochondrial tRNA translation optimization 1	-3.53	9.31	11.13	0.62	0.01	7.45E-05	5.40E-03	Multiple_Complex
TC0200015790.hg.1	CHPF	chondroitin polymerizing factor	-3.54	6.76	8.59	0.06	0.18	5.40E-06	3.40E-03	Multiple_Complex
TC1200009621.hg.1	FOXM1	forkhead box M1	-3.55	9.89	11.71	1.19	0.15	1.40E-03	1.61E-02	Multiple_Complex

TC1200009192.hg.1	BCL7A	B-cell CLL/lymphoma 7A	-3.55	8.42	10.25	0.7	0.05	8.83E-05	5.70E-03	Multiple_Complex
TC1900008509.hg.1	RUVBL2	RuvB-like AAA ATPase 2	-3.55	9.4	11.23	0.56	0.64	3.00E-04	7.70E-03	Multiple_Complex
TC1000010273.hg.1	NRP1	neuropilin 1	-3.56	5.44	7.27	0.17	0.4	8.47E-05	5.60E-03	Multiple_Complex
TC0X00007655.hg.1	SLC16A2	solute carrier family 16, member 2 (thyroid hormone transporter)	-3.57	7.19	9.03	0.46	0.27	2.57E-05	4.30E-03	Multiple_Complex
TC1600007014.hg.1	NDE1; MIR484	nudE neurodevelopment protein 1; microRNA 484	-3.61	7.23	9.08	0.4	0.82	5.00E-04	1.00E-02	Multiple_Complex
TC0500010680.hg.1	PARP8	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, intronic best transcript NM_001178056	-3.63	6.33	8.19	0.47	0.04	4.02E-05	4.80E-03	NonCoding
TC1600011416.hg.1	DUS2	dihydrouridine synthase 2	-3.64	8.07	9.93	0.42	0.13	1.84E-05	4.30E-03	Multiple_Complex
TC1200009768.hg.1	LPCAT3	lysophosphatidylcholine acyltransferase 3	-3.65	9.46	11.33	0.06	0.11	1.36E-05	4.20E-03	Multiple_Complex
TC0100006865.hg.1	AGTRAP	angiotensin II receptor-associated protein	-3.65	7	8.87	0.95	0.55	8.00E-04	1.25E-02	Multiple_Complex
TC1700010327.hg.1	COPRS	coordinator of PRMT5, differentiation stimulator	-3.65	7.11	8.97	0.86	0.04	2.00E-04	6.80E-03	Multiple_Complex
TC1700011783.hg.1	SRP68	signal recognition particle 68kDa	-3.67	8.99	10.87	0.7	0.31	2.00E-04	6.70E-03	Multiple_Complex
TC1700006525.hg.1	RPA1	replication protein A1	-3.68	6.99	8.87	1.06	0.45	1.00E-03	1.36E-02	Multiple_Complex
TC1700006729.hg.1	ACADVL	acyl-CoA dehydrogenase, very long chain	-3.7	9.82	11.7	0.98	0.06	4.00E-04	9.10E-03	Multiple_Complex
TC0900012175.hg.1	CDK9	cyclin-dependent kinase 9	-3.7	9.98	11.87	0.05	0.13	2.81E-06	2.80E-03	Multiple_Complex
TC1600007952.hg.1	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	-3.71	11.36	13.25	0.22	0.25	6.45E-06	3.40E-03	Multiple_Complex
TC0100018496.hg.1	PYGO2	pygopus family PHD finger 2	-3.71	8.85	10.74	0.63	0.28	8.35E-05	5.60E-03	Coding
TC0100013949.hg.1	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-3.71	8.39	10.28	0.32	0.05	2.65E-05	4.30E-03	Multiple_Complex
TC2200008477.hg.1	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	-3.72	9.52	11.42	0.81	0.12	2.00E-04	6.40E-03	Multiple_Complex
TC0100018304.hg.1	MTX1	metaxin 1	-3.72	7.96	9.86	0.28	0.26	4.96E-05	5.00E-03	Multiple_Complex

TC0200008468.hg.1	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	-3.74	7.49	9.4	0.69	0.12	8.44E-05	5.60E-03	Multiple_Complex
TC1500006977.hg.1	VPS18	VPS18 CORVET/HOPS core subunit	-3.75	6.19	8.09	0.66	0.46	2.00E-04	6.50E-03	Multiple_Complex
TC1900006565.hg.1	CSNK1G2	casein kinase 1, gamma 2	-3.76	5.77	7.68	1.17	0.49	1.50E-03	1.67E-02	Multiple_Complex
TC2200009196.hg.1	LZTR1	leucine-zipper-like transcription regulator 1	-3.76	6.53	8.44	0.42	0.06	1.04E-05	3.90E-03	Multiple_Complex
TC1400007440.hg.1	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	-3.76	10.81	12.72	0.33	0.08	7.38E-06	3.40E-03	Multiple_Complex
TC1900008141.hg.1	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1	-3.79	7.85	9.77	0.45	0.26	4.63E-05	5.00E-03	Multiple_Complex
TC0100015921.hg.1	ADAR	adenosine deaminase, RNA-specific	-3.79	7.39	9.31	0.8	0.17	1.00E-04	5.80E-03	Multiple_Complex
TC1600007514.hg.1	KAT8	K(lysine) acetyltransferase 8	-3.8	7.15	9.07	0.63	0.13	9.51E-05	5.70E-03	Multiple_Complex
TC0800009830.hg.1	REEP4	receptor accessory protein 4	-3.8	7.11	9.04	0.26	0.19	6.28E-06	3.40E-03	Multiple_Complex
TC0300011054.hg.1	CCDC71	coiled-coil domain containing 71	-3.83	7.15	9.08	0.15	0.32	6.13E-06	3.40E-03	Coding
TC1200012638.hg.1	HOXC9	homeobox C9	-3.83	7.05	8.99	0.05	0.3	5.91E-06	3.40E-03	Multiple_Complex
TC0300007055.hg.1	CTDSPL	CTD small phosphatase like	-3.89	6.68	8.64	0.81	0.18	1.00E-04	5.80E-03	Multiple_Complex
TC0300010329.hg.1	NUP210	nucleoporin 210kDa	-3.92	10.49	12.46	0.81	0.22	1.00E-04	5.80E-03	Multiple_Complex
TC1900007431.hg.1	MAU2	MAU2 sister chromatid cohesion factor	-3.92	8.29	10.27	0.22	0.13	7.09E-06	3.40E-03	Multiple_Complex
TC1500008029.hg.1	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	-3.93	5	6.97	1	0.78	1.10E-03	1.45E-02	Multiple_Complex
TC1200007899.hg.1	09-Mar	membrane associated ring finger 9	-3.96	5.12	7.11	0.59	0.35	6.46E-05	5.30E-03	Multiple_Complex
TC1600009530.hg.1	KIAA0430; MIR6506	KIAA0430; microRNA 6506	-3.98	7.14	9.13	0.88	0.73	1.00E-03	1.40E-02	Multiple_Complex
TC1200007713.hg.1	SP1	Sp1 transcription factor	-3.99	10.37	12.37	0.36	0.19	6.18E-06	3.40E-03	Multiple_Complex

TC1900006691.hg.1	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-4.01	5.08	7.09	1	0.54	1.00E-03	1.40E-02	Multiple_Complex
TC1900012001.hg.1	FUZ	fuzzy planar cell polarity protein	-4.01	6.94	8.94	0.81	0.23	1.00E-04	6.20E-03	Multiple_Complex
TC2200009194.hg.1	MED15	mediator complex subunit 15	-4.04	10.66	12.67	0.71	0.43	1.00E-04	5.80E-03	Multiple_Complex
TC0X00011302.hg.1	MSN	moesin	-4.05	10.97	12.99	0.73	0.13	4.69E-05	5.00E-03	Multiple_Complex
TC0600011465.hg.1	EHMT2	euchromatic histone-lysine N-methyltransferase 2	-4.06	7.39	9.42	0.94	0.55	4.00E-04	9.30E-03	Multiple_Complex
TC0600008120.hg.1	TMEM63B	transmembrane protein 63B	-4.08	7.5	9.53	0.72	0.05	4.32E-05	4.90E-03	Multiple_Complex
TC1900009357.hg.1	MYDGF	myeloid-derived growth factor	-4.09	7.46	9.5	1.11	0.1	6.00E-04	1.08E-02	Multiple_Complex
TC1900011840.hg.1	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	-4.1	8.57	10.6	0.45	0.45	2.18E-05	4.30E-03	Coding
TC0200008080.hg.1	WDR54	WD repeat domain 54	-4.1	6.25	8.29	0.53	0.53	4.69E-05	5.00E-03	Multiple_Complex
TC1700009969.hg.1	FLII	flightless I actin binding protein	-4.11	11.1	13.14	0.05	0.17	4.44E-06	3.40E-03	Multiple_Complex
TC0100015822.hg.1	S100A11	S100 calcium binding protein A11	-4.12	7.86	9.9	0.13	0.06	3.00E-06	2.80E-03	Multiple_Complex
TC0100015598.hg.1	TXNIP	thioredoxin interacting protein	-4.12	7.41	9.45	0.19	0.07	4.46E-06	3.40E-03	Multiple_Complex
TC1900009201.hg.1	MKNK2	MAP kinase interacting serine/threonine kinase 2	-4.12	10.28	12.32	1.71	0.02	4.30E-03	3.12E-02	Multiple_Complex
TC2100007446.hg.1	COL6A1	collagen, type VI, alpha 1	-4.19	8.12	10.19	0.35	0.25	9.69E-06	3.80E-03	Multiple_Complex
TC1900009431.hg.1	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	-4.22	9.41	11.49	0.94	0.48	3.00E-04	8.00E-03	Multiple_Complex
TC1900007125.hg.1	NACC1	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	-4.26	8.15	10.24	0.93	0.04	2.00E-04	6.60E-03	Multiple_Complex
TC0X00009780.hg.1	FGD1	FYVE, RhoGEF and PH domain containing 1	-4.29	8.75	10.85	0.33	0.19	4.46E-06	3.40E-03	Multiple_Complex
TC2200007495.hg.1	SREBF2	sterol regulatory element binding transcription factor 2	-4.3	10.76	12.86	0.56	0.21	2.58E-05	4.30E-03	Multiple_Complex

TC0200007059.hg.1	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	-4.35	8.35	10.47	1.35	0.46	1.40E-03	1.63E-02	Multiple_Complex
TC0100012846.hg.1	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	-4.36	9.5	11.62	0.47	0.05	5.10E-06	3.40E-03	Multiple_Complex
TC1700008228.hg.1	ITGA3	integrin alpha 3	-4.37	5.5	7.63	0.99	0.03	2.00E-04	6.60E-03	Multiple_Complex
TC1700011653.hg.1	SDK2	sidekick cell adhesion molecule 2	-4.42	7.09	9.24	0.79	0.1	4.27E-05	4.90E-03	Multiple_Complex
TC1100009068.hg.1	NCAM1	neural cell adhesion molecule 1	-4.49	9.84	12	0.79	0.22	5.25E-05	5.10E-03	Multiple_Complex
TC0700006629.hg.1	FSCN1	fascin actin-bundling protein 1	-4.5	7.81	9.98	0.7	0.18	3.02E-05	4.40E-03	Multiple_Complex
TC0100018200.hg.1	SEPN1	selenoprotein N, 1	-4.51	8.99	11.16	0.87	0.07	5.65E-05	5.20E-03	Multiple_Complex
TC0700007409.hg.1	CCM2	cerebral cavernous malformation 2	-4.53	8.72	10.89	0.82	0.22	5.94E-05	5.20E-03	Multiple_Complex
TC1700012209.hg.1	SLC47A1	solute carrier family 47 (multidrug and toxin extrusion), member 1	-4.55	10.31	12.5	0.06	0.06	6.90E-06	3.40E-03	Multiple_Complex
TC1900007087.hg.1	WDR83	WD repeat domain 83	-4.59	7.52	9.71	0.47	0.18	2.10E-03	2.00E-02	Multiple_Complex
TC1900008113.hg.1	LTBP4	latent transforming growth factor beta binding protein 4	-4.72	6.06	8.29	0.53	0.29	9.62E-06	3.80E-03	Multiple_Complex
TC0100012869.hg.1	SRM	spermidine synthase	-4.77	7.73	9.99	0.2	0.07	1.31E-05	4.20E-03	Multiple_Complex
TC1700008575.hg.1	PSMC5	proteasome 26S subunit, ATPase 5	-4.77	10.06	12.31	0.02	0.02	1.57E-06	2.80E-03	Multiple_Complex
TC1900008287.hg.1	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	-4.87	6.25	8.53	0.1	0.75	1.92E-05	4.30E-03	Multiple_Complex
TC0700010619.hg.1	SCRN1	secernin 1	-4.89	10.7	12.99	0.55	0.06	1.10E-03	1.43E-02	Multiple_Complex
TC1000011679.hg.1	CUEDC2	CUE domain containing 2	-4.92	9.41	11.71	0.54	0.11	5.09E-06	3.40E-03	Multiple_Complex
TC1200010976.hg.1	AGAP2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	-4.96	8.53	10.84	0.67	0.02	3.37E-05	4.50E-03	Multiple_Complex
TC1200007594.hg.1	ASIC1	acid sensing ion channel 1	-4.99	5.41	7.73	0.78	0.23	5.00E-04	1.03E-02	Multiple_Complex
TC1100006494.hg.1	CD151	CD151 molecule (Raph blood group)	-5.01	7.48	9.8	0.03	0.41	2.98E-06	2.80E-03	Multiple_Complex

TC2000008237.hg.1	MAVS	Jeck2013 ANTISENSE, coding, INTERNAL, OVEXON, UTR3 best transcript NM_020746	-5.5	9.95	12.41	0.16	0.02	4.43E-07	1.90E-03	NonCoding
TC1100006547.hg.1	MRPL23	mitochondrial ribosomal protein L23	-5.67	4.36	6.86	0.33	0.23	2.38E-06	2.80E-03	Multiple_Complex
TC1600006886.hg.1	NUBP1	nucleotide binding protein 1	-5.71	7.95	10.47	0.7	0.36	1.20E-05	4.10E-03	Multiple_Complex
TC1700006646.hg.1	MINK1	misshapen-like kinase 1	-5.76	6.64	9.17	0.77	0.35	1.54E-05	4.20E-03	Multiple_Complex
TC1100013129.hg.1	CTSD	cathepsin D	-5.81	9.33	11.87	1.3	0.33	2.00E-04	7.10E-03	Multiple_Complex
TC1900011841.hg.1	LMNB2; MIR7108	lamin B2; microRNA 7108	-6.23	6.95	9.59	0.81	0.05	1.02E-05	3.90E-03	Multiple_Complex
TC0700010015.hg.1	INTS1	integrator complex subunit 1	-6.59	7.36	10.08	1.17	0.27	6.16E-05	5.20E-03	Multiple_Complex
TC1700012093.hg.1	FASN	fatty acid synthase	-7.24	7.81	10.67	1.12	0.49	4.72E-05	5.00E-03	Multiple_Complex
TC0500012642.hg.1	RNF145	ring finger protein 145	-9.09	7.28	10.47	0.24	0.25	8.98E-08	1.90E-03	Multiple_Complex