Fichiers complémentaires

Table S1. Upregulated and downregulated genes between control and treated HeLa cells identified from microarray analysis.

ID	Gene Symbol	Description	Fold Change	HELA: Controle Avg (log2)	HELA: Peptide Avg (log2)	HELA: Controle Standard Deviation	HELA: Peptide Standard Deviation	P-val	FDR P-val	Group
TC0200014672.hg.1	NR4A2	nuclear receptor subfamily 4, group A, member 2	7.5	12.91	10.01	0.08	0.51	1.83E-06	7.40E-03	Multiple_Complex
TC0600006925.hg.1	GCNT6	glucosaminyl (N-acetyl) transferase 6 [Source:HGNC Symbol;Acc:HGNC:21623]	5.79	6.97	4.44	0.05	0.12	7.96E-07	5.20E-03	Pseudogene
TC1900008496.hg.1	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	5.75	12.55	10.02	0.02	0.21	5.60E-07	5.20E-03	Multiple_Complex
TC1400008940.hg.1	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	5	11.55	9.23	0.2	0.16	2.06E-06	7.40E-03	Multiple_Complex
TC0500012017.hg.1	IRF1	interferon regulatory factor 1	4.9	8.56	6.27	0.11	0.74	1.93E-05	2.00E-02	Multiple_Complex
TC1700006772.hg.1	KDM6B	lysine (K)-specific demethylase 6B	4.75	10.26	8.01	0.03	0.23	9.69E-07	5.20E-03	Multiple_Complex
TC0600009597.hg.1	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	4.71	14.39	12.16	0.04	0.1	5.73E-07	5.20E-03	Multiple_Complex
TC0300006483.hg.1	BHLHE40	basic helix-loop-helix family, member e40	4.27	13.34	11.25	0	0.32	4.12E-06	1.26E-02	Multiple_Complex
TC0200007096.hg.1	FOSL2	FOS-like antigen 2	4.11	10.67	8.63	0.42	0.16	3.11E-05	2.37E-02	Multiple_Complex
TC0600011133.hg.1	HIST1H2BE	Memczak2013 ANTISENSE, CDS, coding, upstream_start, UTR3, UTR5 best transcript NM_003523	3.95	5.99	4.01	0.06	0.22	1.30E-05	1.99E-02	NonCoding
TC1900007012.hg.1	LDLR; MIR6886	low density lipoprotein receptor; microRNA 6886	3.86	11.52	9.57	0.01	0.22	5.65E-05	3.26E-02	Multiple_Complex
TC1200007653.hg.1	NR4A1	nuclear receptor subfamily 4, group A, member 1	3.74	13.76	11.86	0.04	0.33	6.64E-05	3.48E-02	Multiple_Complex
TC1200008667.hg.1	HSP90B1	Transcript Identified by AceView, Entrez Gene ID(s) 7184	3.72	7.52	5.62	0.3	0.65	3.00E-04	7.01E-02	Unassigned

TC1000011749.hg.1	ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	3.71	8.77	6.88	0.01	0.26	8.79E-06	1.91E-02	Multiple_Complex
TC0600014194.hg.1	TIAM2	T-cell lymphoma invasion and metastasis 2	3.7	6.84	4.96	0.52	0.3	3.21E-05	2.37E-02	Multiple_Complex
TC0300006580.hg.1	IRAK2	interleukin 1 receptor associated kinase 2	3.61	10.63	8.78	0.3	0.08	1.76E-05	1.99E-02	Multiple_Complex
TC1000008891.hg.1	DUSP5	dual specificity phosphatase 5	3.58	11.29	9.45	0.32	0.09	7.57E-06	1.91E-02	Multiple_Complex
TC0600011372.hg.1	PPP1R10	protein phosphatase 1, regulatory subunit 10	3.56	13.54	11.71	0.21	0.11	1.96E-05	2.00E-02	Multiple_Complex
TC0100017420.hg.1	DUSP10	dual specificity phosphatase 10	3.51	7.81	6	0.21	0.34	8.82E-05	4.11E-02	Multiple_Complex
TC0600013409.hg.1	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	3.51	9.59	7.78	0.26	0.09	1.00E-04	4.43E-02	Multiple_Complex
TC1700006857.hg.1	USP43	ubiquitin specific peptidase 43	3.5	7.94	6.13	0.65	0.05	4.00E-04	7.51E-02	Multiple_Complex
TC0300010770.hg.1	CSRNP1	cysteine-serine-rich nuclear protein 1	3.44	8.59	6.8	0.38	0.13	2.58E-05	2.13E-02	Multiple_Complex
TC0800011334.hg.1	KLF10	Kruppel-like factor 10	3.43	12.41	10.63	0.18	0.36	1.59E-05	1.99E-02	Multiple_Complex
TC0300009916.hg.1	HES1	hes family bHLH transcription factor 1	3.43	10.16	8.38	0.03	0.4	2.00E-04	5.95E-02	Multiple_Complex
TC0200012977.hg.1	MXD1	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001202514	3.43	7.56	5.79	0.04	0.1	1.45E-05	1.99E-02	NonCoding
TC1900008326.hg.1	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	3.42	9.41	7.63	0.23	0.15	2.00E-04	5.91E-02	Multiple_Complex
TC2100007821.hg.1	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif 1	3.26	8.91	7.2	0.11	0.79	4.00E-04	7.58E-02	Multiple_Complex
TC1100008819.hg.1	KDM4D	lysine (K)-specific demethylase 4D	3.23	6.39	4.7	0.26	1.02	6.50E-03	2.33E-01	Coding
TSUnmapped00000409.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	3.21	9.29	7.61	0.06	0.25	3.76E-05	2.64E-02	NonCoding
TC0600007395.hg.1	ZNF165	zinc finger protein 165	3.14	10.65	9	0.14	0.11	1.38E-05	1.99E-02	Coding
TC1900007679.hg.1	PLEKHF1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	3.14	7.76	6.11	0	0.23	4.56E-05	2.79E-02	Coding

TC1000009612.hg.1	KLF6	Kruppel-like factor 6	3.12	14	12.36	0.13	0.18	2.54E-05	2.13E-02	Multiple_Complex
TC2200008346.hg.1	MN1	meningioma (disrupted in balanced translocation) 1	3.1	8.93	7.3	0.54	0.19	4.00E-04	7.58E-02	Multiple_Complex
TC1600011365.hg.1	NPIPB9	nuclear pore complex interacting protein family, member B9	3.05	11.38	9.77	0.16	0.44	2.00E-04	6.03E-02	Coding
TC0600008109.hg.1	VEGFA	vascular endothelial growth factor A	3.02	13.44	11.84	0.03	0.02	1.61E-05	1.99E-02	Multiple_Complex
TC0600007675.hg.1	BRD2	bromodomain containing 2	3.01	13.83	12.24	0.12	0.24	3.06E-05	2.37E-02	Multiple_Complex
TC1900009287.hg.1	SMIM24	small integral membrane protein 24	3	7.11	5.53	0.25	0.38	3.00E-04	6.03E-02	Multiple_Complex
TSUnmapped00000067.hg.1	HYOU1	hypoxia up-regulated 1	2.96	7.59	6.03	0.24	0.56	7.00E-04	1.01E-01	NonCoding
TC1900008057.hg.1	ZFP36	ZFP36 ring finger protein	2.94	6.8	5.24	0.01	0.57	3.00E-04	7.01E-02	Coding
TC1900008300.hg.1	RELB	v-rel avian reticuloendotheliosis viral oncogene homolog B	2.89	9.78	8.25	0.12	0	5.92E-05	3.26E-02	Multiple_Complex
TC1000012497.hg.1	BORCS7-ASMT	BORCS7-ASMT readthrough (NMD candidate)	2.89	5.27	3.74	0.08	0.51	1.00E-04	5.15E-02	Multiple_Complex
TC0700006520.hg.1	MAFK	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K	2.89	8.23	6.7	0.11	0.06	1.30E-03	1.22E-01	Multiple_Complex
TC0400008429.hg.1	ALPK1	alpha kinase 1	2.88	5.45	3.93	0.71	0.65	2.50E-03	1.61E-01	Multiple_Complex
TC0600007847.hg.1	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2.87	9.38	7.86	0	0.03	1.00E-04	5.15E-02	Multiple_Complex
TC1200009980.hg.1	GPRC5D	G protein-coupled receptor, class C, group 5, member D	2.85	6.55	5.04	0.34	0.28	1.00E-04	4.43E-02	Coding
TC0600006918.hg.1	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	2.83	10.24	8.73	0.04	0.26	3.00E-04	7.50E-02	Multiple_Complex
TC1700010604.hg.1	NR1D1	nuclear receptor subfamily 1, group D, member 1	2.83	7.76	6.26	0.15	0.1	2.00E-04	5.24E-02	Multiple_Complex
TC1100010472.hg.1	CCDC73	coiled-coil domain containing 73	2.83	6.59	5.1	0.25	0.36	2.00E-04	5.95E-02	Multiple_Complex
TC0700013567.hg.1	LINC00174	long intergenic non-protein coding RNA 174	2.83	4.86	3.36	0.2	0.07	1.30E-03	1.24E-01	NonCoding
TC0200016471.hg.1	MXD1	MAX dimerization protein 1	2.81	10.17	8.67	0.06	0.03	2.35E-05	2.10E-02	Multiple_Complex

TC0200016452.hg.1	REL	v-rel avian reticuloendotheliosis viral oncogene homolog	2.8	12.66	11.17	0.17	0.11	3.90E-05	2.64E-02	Multiple_Complex
TC0400011043.hg.1	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	2.77	9.21	7.74	0.24	0.11	6.84E-05	3.49E-02	Multiple_Complex
TSUnmapped00000328.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	2.76	7.94	6.48	0.11	0.08	4.00E-04	7.58E-02	NonCoding
TC0100010111.hg.1	EFNA1	ephrin-A1	2.75	12.97	11.51	0.06	0.02	2.00E-04	5.31E-02	Multiple_Complex
TC1600008407.hg.1	NPIPB15	nuclear pore complex interacting protein family, member B15	2.75	11.14	9.68	0.26	0.33	2.00E-04	5.95E-02	Multiple_Complex
TC1800007411.hg.1	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	2.75	11.68	10.22	0.16	0.21	2.00E-04	5.95E-02	Multiple_Complex
TC1600009855.hg.1	NPIPB6	nuclear pore complex interacting protein family, member B6	2.7	12.03	10.59	0.02	0.26	2.00E-04	5.95E-02	Coding
TC1100008665.hg.1	CCDC81	coiled-coil domain containing 81	2.68	6.78	5.36	0.01	0.09	9.36E-05	4.27E-02	Multiple_Complex
TC0600007862.hg.1	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	2.64	8.89	7.49	0.19	0.09	4.00E-04	7.58E-02	Multiple_Complex
TC1900008279.hg.1	BCL3; MIR8085	B-cell CLL/lymphoma 3; microRNA 8085	2.63	6.67	5.27	0.17	0.21	2.00E-04	5.95E-02	Multiple_Complex
TC1600008128.hg.1	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	2.63	5.81	4.41	0.05	0.46	1.00E-03	1.13E-01	Multiple_Complex
TC0600008972.hg.1	PRDM1	PR domain containing 1, with ZNF domain	2.61	10.88	9.5	0.27	0.13	7.63E-05	3.72E-02	Multiple_Complex
TC0600011690.hg.1	TMEM217	transmembrane protein 217	2.6	6.93	5.56	0.05	0.44	2.00E-04	5.95E-02	Multiple_Complex
TC0700013442.hg.1	LSMEM1	leucine-rich single-pass membrane protein 1	2.59	10.53	9.16	0.49	0.18	3.00E-04	7.06E-02	Multiple_Complex
TC0100009364.hg.1	CSF1	colony stimulating factor 1 (macrophage)	2.59	12.36	10.99	0.14	0.02	5.83E-05	3.26E-02	Multiple_Complex
TC0100011533.hg.1	ATF3	activating transcription factor 3	2.59	13.56	12.19	0.12	0.09	5.19E-05	3.09E-02	Multiple_Complex
TC1300008091.hg.1	ATP11A	Transcript Identified by AceView, Entrez Gene ID(s) 23250	2.58	5.58	4.22	0.94	0.85	1.08E-02	2.74E-01	Unassigned
TC1900008860.hg.1	LENG8	leukocyte receptor cluster (LRC) member 8	2.57	12.06	10.69	0.14	0.35	1.00E-04	5.15E-02	Multiple_Complex

TC0100018323.hg.1	IER5	immediate early response 5	2.57	8.25	6.89	0.48	0.28	2.00E-03	1.48E-01	Coding
TC1700012295.hg.1	ARSG	arylsulfatase G	2.56	11.54	10.18	0.12	0.01	1.00E-04	5.13E-02	Multiple_Complex
TC1600007982.hg.1	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	2.56	12.09	10.73	0.18	0.08	6.54E-05	3.48E-02	Multiple_Complex
TC1600007353.hg.1	NPIPB8	nuclear pore complex interacting protein family, member B8	2.56	12.61	11.26	0.1	0.15	4.00E-04	7.51E-02	Coding
TC1900009134.hg.1	SBNO2	strawberry notch homolog 2 (Drosophila)	2.55	8.8	7.45	0.02	0.08	2.00E-04	5.24E-02	Multiple_Complex
TC1000012496.hg.1	AS3MT	arsenite methyltransferase	2.54	6.09	4.74	0.08	0.69	9.00E-04	1.11E-01	Multiple_Complex
TC1100006831.hg.1	ADM	adrenomedullin	2.53	8.83	7.49	0.34	0.13	2.00E-04	5.95E-02	Coding
TC1100011259.hg.1	FOSL1	FOS-like antigen 1	2.52	10.25	8.92	0.55	0.61	3.70E-03	1.90E-01	Multiple_Complex
TC1200010839.hg.1	ITGA5	integrin alpha 5	2.51	9.26	7.94	0.03	0.02	2.00E-04	5.95E-02	Multiple_Complex
TC0100011378.hg.1	RASSF5	Ras association (RalGDS/AF-6) domain family member 5	2.51	10.81	9.48	0.07	0.18	1.20E-03	1.18E-01	Multiple_Complex
TC1700010879.hg.1	MAP3K14	mitogen-activated protein kinase kinase kinase 14	2.51	8.34	7.02	0.38	0.05	2.00E-04	5.91E-02	Multiple_Complex
TC0900010388.hg.1	TMEM2	Transcript Identified by AceView, Entrez Gene ID(s) 23670	2.48	5.23	3.92	0.39	0.35	1.00E-03	1.13E-01	Unassigned
TC1400008382.hg.1	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	2.47	8.91	7.6	0.18	0.64	1.00E-03	1.14E-01	Multiple_Complex
TC1600009916.hg.1	NPIPB11	nuclear pore complex interacting protein family, member B11	2.46	12.23	10.93	0.09	0.18	1.00E-04	5.15E-02	Coding
TC1200007210.hg.1	DDX11	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_030653	2.46	7.58	6.28	0.67	0.27	2.69E-02	3.58E-01	NonCoding
TC1200012258.hg.1	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	2.45	9.91	8.62	0.07	0.29	2.00E-04	5.95E-02	Multiple_Complex
TC1900008824.hg.1	MYADM	myeloid-associated differentiation marker	2.44	10.87	9.59	0	0.14	5.00E-04	8.36E-02	Multiple_Complex
TC0400012078.hg.1	NR3C2	nuclear receptor subfamily 3, group C, member 2	2.43	4.83	3.54	0.03	0.91	5.10E-03	2.13E-01	Multiple_Complex

TC1800006655.hg.1	TXNDC2	thioredoxin domain containing 2 (spermatozoa)	2.43	7.57	6.29	0.24	0.46	2.10E-03	1.49E-01	Multiple_Complex
TC0700008004.hg.1	GTF2IRD1	GTF2I repeat domain containing 1	2.42	8.94	7.66	0.14	0.16	5.00E-04	8.29E-02	Multiple_Complex
TC0200014414.hg.1	CXCR4	chemokine (C-X-C motif) receptor 4	2.42	14.39	13.11	0.09	0.12	3.00E-04	7.01E-02	Multiple_Complex
TC0600014074.hg.1	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	2.42	11.09	9.81	0.02	0.14	2.00E-04	5.95E-02	Multiple_Complex
TC0100012734.hg.1	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	2.41	9.63	8.36	0.09	0.44	7.00E-04	1.02E-01	Coding
TC1700010738.hg.1	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit	2.4	10.1	8.84	0.06	0.19	1.00E-04	5.15E-02	Multiple_Complex
TC0100013028.hg.1	EPHA2	EPH receptor A2	2.39	10.32	9.07	0.02	0.06	7.00E-04	1.02E-01	Multiple_Complex
TC0300012918.hg.1	CCNL1	cyclin L1	2.39	12.25	11	0.12	0.2	7.00E-04	1.02E-01	Multiple_Complex
TC0800010382.hg.1	SNAI2	snail family zinc finger 2	2.39	11.99	10.74	0.38	0.16	7.00E-04	1.02E-01	Coding
TC1700011436.hg.1	ERN1	endoplasmic reticulum to nucleus signaling 1	2.38	9.15	7.89	0.32	0.03	2.00E-04	5.95E-02	Multiple_Complex
TC1900007173.hg.1	ADGRE5	adhesion G protein-coupled receptor E5	2.37	8.8	7.56	0.34	0.23	4.00E-04	7.50E-02	Multiple_Complex
TC0100016000.hg.1	MEF2D	myocyte enhancer factor 2D	2.36	10.09	8.85	0.05	0.11	8.00E-04	1.06E-01	Multiple_Complex
TC0300014073.hg.1	PLCH1	phospholipase C, eta 1	2.35	5.71	4.48	0.22	0.12	4.00E-04	7.58E-02	Multiple_Complex
TC0300012900.hg.1	TIPARP	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001184717	2.34	12.92	11.69	0.22	0.02	2.00E-04	5.95E-02	NonCoding
TC0900008545.hg.1	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	2.34	9.06	7.83	0.21	0.18	3.30E-03	1.80E-01	Multiple_Complex
TC1900006977.hg.1	ICAM1	intercellular adhesion molecule 1	2.33	11.11	9.89	0.16	0.07	2.00E-03	1.48E-01	Multiple_Complex
TC0300009289.hg.1	LEKR1	leucine, glutamate and lysine rich 1	2.33	5.62	4.4	0.29	0.36	9.00E-04	1.11E-01	Multiple_Complex
TC0500013280.hg.1	ZDHHC11B	zinc finger, DHHC-type containing 11B	2.33	9.68	8.46	0.34	0.06	1.30E-03	1.22E-01	Multiple_Complex

TC0700008582.hg.1	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	2.33	8.72	7.51	0.33	0.28	2.00E-03	1.47E-01	Multiple_Complex
TC1400009524.hg.1	ZFP36L1	ZFP36 ring finger protein-like 1	2.32	11.38	10.17	0.12	0.25	4.00E-04	7.58E-02	Coding
TC2200008734.hg.1	CBX7	chromobox homolog 7	2.32	6.42	5.21	0.04	0.01	6.00E-04	9.67E-02	Multiple_Complex
TC0100007295.hg.1	EPHB2	EPH receptor B2	2.31	6.46	5.25	0.04	0.11	1.00E-04	5.15E-02	Multiple_Complex
TC0100015271.hg.1	OVGP1	oviductal glycoprotein 1	2.31	5.8	4.59	0.47	0.49	2.70E-03	1.66E-01	Multiple_Complex
TC1200009891.hg.1	CLEC7A	C-type lectin domain family 7, member A	2.31	8.37	7.16	0.38	0.05	1.00E-03	1.13E-01	Multiple_Complex
TC1400010261.hg.1	MOK	MOK protein kinase	2.3	8.87	7.67	0.11	0.11	5.00E-04	8.89E-02	Multiple_Complex
TC0200014192.hg.1	SAP130	Sin3A associated protein 130kDa	2.29	11.22	10.02	0.1	0.24	5.00E-04	8.89E-02	Multiple_Complex
TC0800009094.hg.1	DENND3	DENN/MADD domain containing 3	2.29	7.99	6.79	0.32	0.07	6.00E-04	9.37E-02	Multiple_Complex
TC0100017064.hg.1	NUAK2	NUAK family, SNF1-like kinase, 2	2.29	6.58	5.39	0.27	0.06	6.00E-04	9.37E-02	Multiple_Complex
TC1100010505.hg.1	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	2.29	8.45	7.26	0.1	0.62	2.50E-03	1.61E-01	Multiple_Complex
TC0500010869.hg.1	ELOVL7	ELOVL fatty acid elongase 7	2.28	5.6	4.41	0.31	0.08	1.50E-03	1.31E-01	Multiple_Complex
TC0700011842.hg.1	PDK4	pyruvate dehydrogenase kinase, isozyme 4	2.28	11.14	9.95	0.07	0.34	1.10E-03	1.16E-01	Multiple_Complex
TSUnmapped00000141.hg.1	HMBS	hydroxymethylbilane synthase	2.28	7.26	6.07	0.06	0.25	1.10E-03	1.15E-01	NonCoding
TC0100010078.hg.1	IL6R	interleukin 6 receptor	2.27	7.09	5.91	0.3	0.35	1.60E-03	1.36E-01	Multiple_Complex
TC0300007256.hg.1	CCR2	chemokine (C-C motif) receptor 2	2.27	7.51	6.33	0.2	0.14	4.00E-04	7.58E-02	Multiple_Complex
TC0300008999.hg.1	ZBTB38	zinc finger and BTB domain containing 38	2.26	13.06	11.88	0.3	0.22	3.00E-02	3.66E-01	Multiple_Complex
TC0300013855.hg.1	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	2.26	11.44	10.26	0.29	0.15	7.00E-04	1.00E-01	Multiple_Complex
TC0700011477.hg.1	TRIM74	tripartite motif containing 74	2.26	6.45	5.27	0.23	0.09	1.10E-03	1.18E-01	Coding

TC1400008637.hg.1	SALL2	spalt-like transcription factor 2	2.25	6.41	5.24	0	0.29	5.00E-04	8.69E-02	Multiple_Complex
TC0500013298.hg.1	C1QTNF3	C1q and tumor necrosis factor related protein 3	2.25	6.89	5.72	0.02	0.56	1.50E-03	1.31E-01	Multiple_Complex
TC1800006905.hg.1	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	2.25	9.07	7.9	0.07	0.11	8.00E-04	1.04E-01	Multiple_Complex
TC1700009498.hg.1	ATP2A3	ATPase, Ca++ transporting, ubiquitous	2.24	8.04	6.87	0.31	0.08	2.00E-03	1.48E-01	Multiple_Complex
TC0300013973.hg.1	CELSR3; MIR4793	cadherin, EGF LAG seven-pass G-type receptor 3; microRNA 4793	2.24	6.4	5.24	0.02	0.9	1.86E-02	3.25E-01	Multiple_Complex
TC1500006981.hg.1	DLL4	delta-like 4 (Drosophila)	2.24	7.82	6.66	0.33	0.12	1.50E-03	1.33E-01	Multiple_Complex
TC0600014153.hg.1	CFAP206	cilia and flagella associated protein 206	2.24	6.1	4.94	0.05	0.21	1.20E-03	1.18E-01	Multiple_Complex
TC0900009127.hg.1	COL5A1	collagen, type V, alpha 1	2.24	9.99	8.83	0.03	0.11	1.21E-02	2.84E-01	Multiple_Complex
TC0400008053.hg.1	AFF1	AF4/FMR2 family, member 1	2.23	12.64	11.48	0.3	0.18	5.00E-04	8.29E-02	Multiple_Complex
TC1700009079.hg.1	C1QTNF1	C1q and tumor necrosis factor related protein 1	2.22	6.69	5.54	0.04	0.39	5.60E-03	2.19E-01	Multiple_Complex
TC1600011186.hg.1	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	2.22	13.9	12.75	0.03	0.03	2.00E-04	5.95E-02	Multiple_Complex
TC1200008726.hg.1	TCP11L2	t-complex 11, testis-specific-like 2	2.22	7.67	6.52	0.17	0.19	2.30E-03	1.55E-01	Multiple_Complex
TSUnmapped00000500.hg.1	HYOU1	hypoxia up-regulated 1	2.22	6.82	5.67	0.18	0.49	1.60E-03	1.35E-01	NonCoding
TC0900008219.hg.1	NR4A3	nuclear receptor subfamily 4, group A, member 3	2.22	11.64	10.49	0.02	0.09	4.00E-04	7.51E-02	Multiple_Complex
TC0200006679.hg.1	C2orf48	chromosome 2 open reading frame 48	2.21	7.57	6.42	0.43	0.36	3.50E-03	1.85E-01	Multiple_Complex
TC0100006874.hg.1	PLOD1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	2.21	13.09	11.95	0.12	0.37	2.20E-03	1.54E-01	Multiple_Complex
TC1900008755.hg.1	ZNF331	zinc finger protein 331	2.2	10.93	9.79	0.11	0.27	5.00E-04	8.29E-02	Multiple_Complex
TC1600009524.hg.1	NPIPA5	nuclear pore complex interacting protein family, member A5	2.2	11.23	10.09	0.13	0.07	1.00E-03	1.13E-01	Coding

TC1200009198.hg.1	LRRC43	leucine rich repeat containing 43	2.2	5.96	4.82	0.25	0.49	1.40E-03	1.31E-01	Multiple_Complex
TC0300011485.hg.1	FOXP1	forkhead box P1	2.2	8.15	7.01	0	0.29	5.00E-04	8.29E-02	Multiple_Complex
TC0600007711.hg.1	ITPR3	inositol 1,4,5-trisphosphate receptor, type 3	2.2	9.07	7.93	0.18	0.99	3.84E-02	3.94E-01	Multiple_Complex
TC1900006588.hg.1	GADD45B	growth arrest and DNA-damage-inducible, beta	2.19	11.09	9.96	0.24	0.14	8.00E-04	1.03E-01	Multiple_Complex
TC1600007985.hg.1	CETP	cholesteryl ester transfer protein, plasma	2.19	5.46	4.33	0.32	0.02	7.00E-04	1.02E-01	Multiple_Complex
TC0600009843.hg.1	PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	2.19	8.9	7.77	0.07	0.12	4.00E-04	7.58E-02	Multiple_Complex
TC0900012055.hg.1	EXD3	exonuclease 3-5 domain containing 3	2.19	7.59	6.46	0.8	0.19	9.40E-03	2.62E-01	Multiple_Complex
TC0X00007292.hg.1	SSX8	synovial sarcoma, X breakpoint 8	2.18	4.64	3.52	0.1	0	3.00E-04	7.50E-02	Multiple_Complex
TC0200007722.hg.1	USP34	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_014709	2.18	8.95	7.82	0.28	0.41	2.50E-03	1.61E-01	NonCoding
TC0100018553.hg.1	PLEKHA6	pleckstrin homology domain containing, family A member 6	2.18	8.67	7.55	0.15	0.7	3.50E-03	1.84E-01	Multiple_Complex
TC2000008023.hg.1	SLCO4A1	solute carrier organic anion transporter family, member 4A1	2.17	7.74	6.62	0.17	0.69	1.29E-02	2.87E-01	Multiple_Complex
TC2000007488.hg.1	PIGT	phosphatidylinositol glycan anchor biosynthesis class T	2.17	11.49	10.37	0.25	0.32	9.00E-04	1.09E-01	Multiple_Complex
TC0200006674.hg.1	KLF11	Kruppel-like factor 11	2.17	11.67	10.55	0.24	0.04	3.00E-04	7.50E-02	Multiple_Complex
TC1900007384.hg.1	GDF15	growth differentiation factor 15	2.17	8.82	7.71	0.43	0.01	1.10E-03	1.17E-01	Multiple_Complex
TC0500009673.hg.1	ZNF454	zinc finger protein 454	2.16	5.48	4.37	0.37	0.33	1.20E-03	1.22E-01	Multiple_Complex
TC0400009001.hg.1	FAM160A1	family with sequence similarity 160, member A1	2.16	9.19	8.08	0.12	0.22	8.40E-03	2.52E-01	Multiple_Complex
TC1200008803.hg.1	MVK	mevalonate kinase	2.15	9.48	8.38	0.12	0.09	6.00E-04	9.37E-02	Multiple_Complex
TC1600011487.hg.1	NPIPA8	nuclear pore complex interacting protein family, member A8	2.15	11.67	10.56	0.09	0.27	3.40E-03	1.83E-01	Coding

TC1900010016.hg.1	ISYNA1	inositol-3-phosphate synthase 1	2.15	6.99	5.89	0.24	0.98	1.51E-02	3.04E-01	Multiple_Complex
TC0100008503.hg.1	HOOK1	hook microtubule-tethering protein 1	2.15	6.41	5.31	0.93	0.12	1.03E-02	2.69E-01	Multiple_Complex
TC0200008663.hg.1	IL1R2	interleukin 1 receptor, type II	2.15	5.88	4.78	0.19	0.63	1.72E-02	3.15E-01	Multiple_Complex
TC0300006677.hg.1	SLC6A6	solute carrier family 6 (neurotransmitter transporter), member 6	2.15	11.26	10.16	0.01	0.09	3.00E-04	6.05E-02	Multiple_Complex
TC0600008757.hg.1	PNRC1	proline-rich nuclear receptor coactivator 1	2.15	10.31	9.21	0.25	0.3	2.00E-03	1.48E-01	Multiple_Complex
TC1000007061.hg.1	GPR158	G protein-coupled receptor 158	2.14	8.93	7.83	0.03	0.03	7.00E-04	1.02E-01	Multiple_Complex
TC0600011376.hg.1	PPP1R18	protein phosphatase 1, regulatory subunit 18	2.14	11.74	10.64	0.2	0.16	7.00E-04	1.02E-01	Multiple_Complex
TC0100018166.hg.1	CLCN6	chloride channel, voltage-sensitive 6	2.13	9.21	8.12	0.45	0.15	2.00E-03	1.47E-01	Multiple_Complex
TC0800008801.hg.1	TRIB1	tribbles pseudokinase 1	2.13	11.4	10.31	0.01	0.27	6.00E-04	9.20E-02	Multiple_Complex
TC1900009795.hg.1	RFX1	regulatory factor X, 1 (influences HLA class II expression)	2.13	6.59	5.49	0.12	0.33	7.00E-04	1.00E-01	Multiple_Complex
TC1200012016.hg.1	TBX3	T-box 3	2.13	15.21	14.12	0.24	0.14	6.00E-04	8.97E-02	Multiple_Complex
TC0100008075.hg.1	ST3GAL3; MIR6079	ST3 beta-galactoside alpha-2,3-sialyltransferase 3; microRNA 6079	2.13	7.85	6.76	0.2	0.12	9.50E-03	2.62E-01	Multiple_Complex
TC1400009329.hg.1	RTN1	reticulon 1	2.12	6.07	4.99	0.09	0.3	2.80E-03	1.69E-01	Multiple_Complex
TC1500008995.hg.1	GOLGA8B	golgin A8 family, member B	2.12	9.29	8.2	0.12	0.01	4.00E-04	8.29E-02	Multiple_Complex
TC1100012545.hg.1	TRIM29	tripartite motif containing 29	2.12	11.74	10.66	0.04	0.29	3.20E-03	1.76E-01	Multiple_Complex
TC0400011685.hg.1	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	2.11	5.93	4.85	0.52	0.07	9.90E-03	2.67E-01	Multiple_Complex
TC1700008228.hg.1	ITGA3	integrin alpha 3	2.11	12.07	11	0.27	0.12	1.61E-02	3.08E-01	Multiple_Complex
TC0700013429.hg.1	PILRA	paired immunoglobin-like type 2 receptor alpha	2.11	9.88	8.81	0.4	0.24	6.60E-03	2.34E-01	Multiple_Complex
TC2200009187.hg.1	TUBA8	tubulin, alpha 8	2.11	5.61	4.53	0.07	0.05	1.00E-03	1.13E-01	Multiple_Complex
TC2000009253.hg.1	ZNF335	zinc finger protein 335	2.11	7.13	6.05	0.18	0.19	8.00E-04	1.06E-01	Multiple_Complex

TC0600014256.hg.1	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	2.1	7.5	6.43	0.43	0.16	2.05E-02	3.32E-01	Multiple_Complex
TC1700007982.hg.1	C17orf53	chromosome 17 open reading frame 53	2.1	12.52	11.45	0	0.01	3.00E-03	1.73E-01	Multiple_Complex
TC1600011353.hg.1	NPIPA3	nuclear pore complex interacting protein family, member A3	2.1	10.41	9.34	0.04	0.1	1.70E-03	1.40E-01	Multiple_Complex
TC1500009130.hg.1	RHOV	ras homolog family member V	2.09	8.99	7.93	0.04	0.44	1.15E-02	2.81E-01	Multiple_Complex
TC0300008705.hg.1	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	2.08	7.07	6.02	0.01	0.27	2.60E-03	1.64E-01	Multiple_Complex
TC1700009566.hg.1	NLRP1	NLR family, pyrin domain containing 1	2.08	7.07	6.02	0.38	0.99	2.75E-02	3.59E-01	Multiple_Complex
TC1100011310.hg.1	PC	pyruvate carboxylase	2.07	7.35	6.3	0.1	0.42	1.30E-03	1.26E-01	Multiple_Complex
TC0800007382.hg.1	IDO1	indoleamine 2,3-dioxygenase 1	2.07	4.83	3.78	0.75	0.33	2.02E-02	3.31E-01	Multiple_Complex
TC0100010152.hg.1	LMNA	lamin A/C	2.07	12.06	11.01	0.68	0.06	8.80E-03	2.57E-01	Multiple_Complex
TC1100007818.hg.1	DAGLA	diacylglycerol lipase, alpha	2.06	6.21	5.17	0.43	0.25	2.10E-03	1.49E-01	Multiple_Complex
TC0700012165.hg.1	ATXN7L1	ataxin 7-like 1	2.06	5.9	4.86	0.03	0.12	3.30E-03	1.80E-01	Multiple_Complex
TC1600006587.hg.1	TSC2	tuberous sclerosis 2	2.06	7.73	6.69	0.36	0.37	1.79E-02	3.21E-01	Multiple_Complex
TC1400008214.hg.1	WDR25	WD repeat domain 25	2.06	9.68	8.64	0.15	0.45	1.06E-02	2.71E-01	Multiple_Complex
TC1500007851.hg.1	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	2.05	6.75	5.71	0.19	0.25	4.60E-03	2.06E-01	Multiple_Complex
TC0100008664.hg.1	GADD45A	growth arrest and DNA-damage-inducible, alpha	2.05	9.67	8.63	0.07	0.46	5.70E-03	2.21E-01	Multiple_Complex
TC2000009588.hg.1	MTRNR2L3	MT-RNR2-like 3	2.05	9.28	8.24	0.2	0.11	6.10E-03	2.27E-01	Coding
TC0700009647.hg.1	ZNF862	zinc finger protein 862	2.05	6.59	5.55	0.05	0.19	1.10E-03	1.15E-01	Multiple_Complex
TC0500009488.hg.1	CREBRF	CREB3 regulatory factor	2.05	8.1	7.07	0.11	0.11	3.70E-03	1.88E-01	Multiple_Complex
TC1100012000.hg.1	GPR83	G protein-coupled receptor 83	2.05	4.61	3.58	0.11	0.18	1.90E-03	1.46E-01	Multiple_Complex
TC1400007548.hg.1	GALNT16	polypeptide N-acetylgalactosaminyltransferase 16	2.05	6.62	5.59	0.37	0.45	6.20E-03	2.28E-01	Multiple_Complex
TC1700008263.hg.1	ABCC3	ATP binding cassette subfamily C member 3	2.05	9.6	8.56	0.12	0.07	4.30E-03	2.04E-01	Multiple_Complex

TC1600006685.hg.1	ZNF75A	zinc finger protein 75a	2.05	7.08	6.05	0.2	0.26	9.00E-04	1.11E-01	Multiple_Complex
TC0300010329.hg.1	NUP210	nucleoporin 210kDa	2.04	11.6	10.57	0.12	0.16	1.04E-02	2.69E-01	Multiple_Complex
TC0200007132.hg.1	YPEL5	yippee like 5	2.04	11.24	10.21	0.16	0.55	4.40E-03	2.04E-01	Multiple_Complex
TC0X00010670.hg.1	TMEM255A	transmembrane protein 255A	2.04	6.25	5.22	0.35	0.09	1.34E-02	2.89E-01	Multiple_Complex
TC1000011726.hg.1	SH3PXD2A	SH3 and PX domains 2A	2.04	9.24	8.21	0.18	0.01	2.60E-03	1.64E-01	Multiple_Complex
TC1900009188.hg.1	REXO1; MIR1909	REX1, RNA exonuclease 1 homolog; microRNA 1909	2.04	9.09	8.06	0.11	0.03	6.00E-04	9.37E-02	Multiple_Complex
TC0900010582.hg.1	KIF27	kinesin family member 27	2.03	6.93	5.9	0.29	0.36	2.10E-03	1.51E-01	Multiple_Complex
TC0900010769.hg.1	NFIL3	nuclear factor, interleukin 3 regulated	2.03	13.15	12.13	0.05	0.03	5.00E-04	8.29E-02	Coding
TC1500010733.hg.1	C15orf48; MIR147B	chromosome 15 open reading frame 48; microRNA 147b	2.03	4.95	3.93	0.56	0.53	8.50E-03	2.54E-01	Multiple_Complex
TC0100016072.hg.1	OR6P1	olfactory receptor, family 6, subfamily P, member 1	2.03	5.09	4.07	0.16	0.57	7.70E-03	2.48E-01	Coding
TC1800007508.hg.1	TNFRSF11A	Transcript Identified by AceView, Entrez Gene ID(s) 8792	2.03	5.88	4.86	0.08	0.31	1.40E-03	1.31E-01	Unassigned
TC1200012248.hg.1	HCAR3	hydroxycarboxylic acid receptor 3	2.03	4.87	3.85	0.33	0.26	7.50E-03	2.46E-01	Coding
TC0300009282.hg.1	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	2.03	11.47	10.45	0.28	0.04	9.00E-04	1.09E-01	Multiple_Complex
TC1600006633.hg.1	SRRM2	serine/arginine repetitive matrix 2	2.02	13.42	12.4	0.16	0.32	1.70E-02	3.14E-01	Multiple_Complex
TC2100008562.hg.1	RUNX1	runt-related transcription factor 1	2.02	11.58	10.56	0.01	0.21	1.20E-03	1.19E-01	Multiple_Complex
TC1500008988.hg.1	GOLGA8A; GOLGA8B	golgin A8 family, member A; golgin A8 family, member B	2.02	9.18	8.17	0.02	0.04	5.00E-04	8.35E-02	Multiple_Complex
TC1500010407.hg.1	ANPEP	alanyl (membrane) aminopeptidase	2.02	6.67	5.65	0.49	0.25	1.67E-02	3.12E-01	Multiple_Complex
TC0100012760.hg.1	RERE	arginine-glutamic acid dipeptide (RE) repeats	2.02	10.46	9.44	0.04	0.03	5.00E-04	8.89E-02	Multiple_Complex
TC1300009765.hg.1	IRS2	insulin receptor substrate 2	2.02	9.39	8.38	0.37	0.51	8.20E-03	2.50E-01	Multiple_Complex
TC1600009165.hg.1	MMP25-AS1	MMP25 antisense RNA 1	2.01	5.56	4.55	0.44	0.13	3.96E-02	3.96E-01	NonCoding
TC1700010686.hg.1	JUP	junction plakoglobin	2.01	11.91	10.9	0.28	0.03	1.50E-03	1.33E-01	Multiple_Complex

TC1700008033.hg.1	HEXIM1	hexamethylene bis-acetamide inducible 1	2.01	10.55	9.54	0.22	0.09	1.30E-03	1.22E-01	Coding
TC0100014910.hg.1	TGFBR3	transforming growth factor beta receptor III	2.01	11.67	10.67	0.15	0.05	3.70E-03	1.90E-01	Multiple_Complex
TC1000006912.hg.1	MRC1	mannose receptor, C type 1	2.01	6.26	5.25	0.09	0.43	3.50E-03	1.84E-01	Coding
TC1900008828.hg.1	CACNG6	calcium channel, voltage-dependent, gamma subunit 6	2.01	5.93	4.92	0.71	0.41	1.62E-02	3.09E-01	Multiple_Complex
TC0600010707.hg.1	NRN1	neuritin 1	2.01	4.72	3.72	1.09	0.02	4.19E-02	4.02E-01	Multiple_Complex
TC0100010543.hg.1	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	2	11.68	10.68	0.04	0.24	1.53E-02	3.04E-01	Multiple_Complex
TC1200008933.hg.1	TPCN1	two pore segment channel 1	2	9.21	8.21	0.08	0.85	1.84E-02	3.24E-01	Multiple_Complex
TC0100014459.hg.1	LINC01359	long intergenic non-protein coding RNA 1359	2	7.16	6.16	0.11	0.86	1.90E-02	3.26E-01	NonCoding
TC1600011354.hg.1	NPIPA2	nuclear pore complex interacting protein family, member A2	2	10.38	9.38	0.1	0.05	2.80E-03	1.69E-01	Coding
TC0300013025.hg.1	BCHE	butyrylcholinesterase	2	5.32	4.33	0.37	0.21	3.00E-03	1.72E-01	Coding
TC1200006788.hg.1	KLRD1	killer cell lectin-like receptor subfamily D, member 1	2	4.68	3.68	0.68	0.24	1.50E-02	3.04E-01	Multiple_Complex
TC0500007641.hg.1	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	1.99	5.46	4.47	0.68	0.62	2.10E-02	3.34E-01	Multiple_Complex
TC2100007394.hg.1	ITGB2	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001127491	1.99	6.29	5.29	0.64	0.07	1.33E-02	2.89E-01	NonCoding
TC2100008297.hg.1	SIK1	salt-inducible kinase 1	1.99	11.53	10.54	0.03	0.01	4.82E-02	4.21E-01	Multiple_Complex
TC1900012010.hg.1	SHANK1	SH3 and multiple ankyrin repeat domains 1	1.99	6.85	5.85	0.27	0.4	5.10E-03	2.13E-01	Multiple_Complex
TC0200015424.hg.1	ALS2CR12	amyotrophic lateral sclerosis 2 chromosome region candidate 12	1.99	5.41	4.42	0.27	0.06	1.60E-03	1.35E-01	Multiple_Complex
TC1100006756.hg.1	SYT9	synaptotagmin IX	1.98	5.36	4.37	0.44	0.41	7.00E-03	2.40E-01	Multiple_Complex
TC0300007383.hg.1	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	1.98	11.49	10.51	0.13	0.33	1.70E-03	1.40E-01	Multiple_Complex

TC0900011209.hg.1	C9orf84	chromosome 9 open reading frame 84	1.98	6.41	5.42	0.05	0.38	2.00E-03	1.47E-01	Multiple_Complex
TC0100014769.hg.1	MCOLN3	mucolipin 3	1.98	5.86	4.87	0.08	0.2	1.10E-03	1.16E-01	Multiple_Complex
TC1700006524.hg.1	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	1.98	6.53	5.55	0.05	0.07	1.00E-02	2.68E-01	Multiple_Complex
TC0500013300.hg.1	C9	complement component 9	1.98	5.29	4.31	0.65	0.61	2.00E-02	3.29E-01	Multiple_Complex
TC0500012497.hg.1	TNIP1	TNFAIP3 interacting protein 1	1.98	10.29	9.31	0.03	0.17	7.00E-04	1.02E-01	Multiple_Complex
TC0800012176.hg.1	PLEC	plectin	1.98	10.24	9.26	0.39	0.05	4.30E-03	2.03E-01	Multiple_Complex
TC1000010172.hg.1	SVIL	supervillin	1.98	7.11	6.12	0.18	0.23	1.30E-03	1.26E-01	Multiple_Complex
TC0700012911.hg.1	CTAGE8	CTAGE family, member 8	1.97	6.18	5.2	0.47	0.03	3.00E-03	1.72E-01	Coding
TC0500006493.hg.1	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	1.97	7.08	6.1	0.02	0.09	1.60E-03	1.35E-01	Coding
TC0200011093.hg.1	ALPP	alkaline phosphatase, placental	1.97	11.81	10.83	0.3	0.48	4.90E-03	2.13E-01	Multiple_Complex
TC0600010777.hg.1	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	1.97	10.28	9.3	0.06	0.12	2.80E-03	1.68E-01	Multiple_Complex
TC0100014349.hg.1	JUN	jun proto-oncogene	1.97	9.15	8.18	0.08	0.05	6.40E-03	2.31E-01	Multiple_Complex
TC0500010635.hg.1	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	1.97	10.85	9.87	0.03	0.07	2.10E-03	1.49E-01	Multiple_Complex
TC1000012567.hg.1	AGAP5	ArfGAP with GTPase domain, ankyrin repeat and PH domain 5	1.96	11.58	10.61	0.13	0.11	9.00E-04	1.09E-01	Multiple_Complex
TC1000011696.hg.1	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	1.96	5.49	4.52	0.67	0.46	1.39E-02	2.93E-01	Multiple_Complex
TC1600011355.hg.1	NPIPA1	nuclear pore complex interacting protein family, member A1	1.96	10	9.03	0.01	0.12	2.40E-03	1.61E-01	Multiple_Complex
TC1700008016.hg.1	HIGD1B	HIG1 hypoxia inducible domain family, member 1B	1.96	6.24	5.27	0.01	0.09	4.90E-03	2.13E-01	Multiple_Complex
TC0200014170.hg.1	MAP3K2	mitogen-activated protein kinase kinase kinase 2	1.96	9.5	8.53	0.21	0.04	3.00E-03	1.72E-01	Multiple_Complex

TC1900010580.hg.1	ZNF573	Transcript Identified by AceView, Entrez Gene ID(s) 126231	1.96	6.35	5.38	0.38	0.46	5.90E-03	2.25E-01	Unassigned
TC1600009446.hg.1	CPPED1	calcineurin-like phosphoesterase domain containing 1	1.95	6.99	6.02	0.43	0.28	2.27E-02	3.40E-01	Multiple_Complex
TC0100014013.hg.1	CCDC163P	coiled-coil domain containing 163, pseudogene	1.95	6.29	5.33	0.02	0.54	5.30E-03	2.15E-01	Multiple_Complex
TC1700012379.hg.1	VTN	vitronectin	1.95	10.38	9.42	0.33	0.11	7.80E-03	2.48E-01	Multiple_Complex
TC0800011579.hg.1	EXT1	exostosin glycosyltransferase 1	1.95	9.44	8.48	0.25	0.27	7.70E-03	2.48E-01	Multiple_Complex
TC0200015476.hg.1	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1.94	11.81	10.85	0.19	0.26	1.70E-03	1.40E-01	Multiple_Complex
TC0100013339.hg.1	RUNX3	runt-related transcription factor 3	1.94	8.29	7.34	0.23	0	1.40E-03	1.26E-01	Multiple_Complex
TC0200011130.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	1.94	10.5	9.55	0.04	0.33	8.80E-03	2.57E-01	Multiple_Complex
TC1600009042.hg.1	CLCN7	chloride channel, voltage-sensitive 7	1.94	7.83	6.87	0.15	0.31	3.20E-03	1.79E-01	Multiple_Complex
TC2200007620.hg.1	FBLN1	fibulin 1	1.94	6	5.05	0.81	0.28	1.80E-02	3.23E-01	Multiple_Complex
TC1600011351.hg.1	CARHSP1	Jeck2013 ANTISENSE, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_001042476	1.94	8.67	7.71	0.2	0.27	2.90E-03	1.71E-01	NonCoding
TC1300009809.hg.1	LINC00346	long intergenic non-protein coding RNA 346	1.94	6.44	5.49	0.39	0.03	2.90E-03	1.69E-01	Multiple_Complex
TC1200007421.hg.1	ANO6	Transcript Identified by AceView, Entrez Gene ID(s) 196527	1.94	5.32	4.37	0.02	0.28	2.57E-02	3.51E-01	Unassigned
TC1900010076.hg.1	ATP13A1	ATPase type 13A1	1.93	11.98	11.03	0.13	0.21	2.30E-03	1.59E-01	Multiple_Complex
TC0100015350.hg.1	AMPD1	adenosine monophosphate deaminase 1	1.93	5.32	4.37	0.23	0.2	2.40E-03	1.61E-01	Multiple_Complex
TC2000009218.hg.1	SDC4	syndecan 4	1.93	10.18	9.23	0.11	0.19	1.50E-03	1.31E-01	Multiple_Complex
TC0900010910.hg.1	SLC35D2	solute carrier family 35 (UDP-GlcNAc/UDP-glucose transporter), member D2	1.93	6.77	5.83	0.1	0.18	3.70E-03	1.88E-01	Multiple_Complex
TC0600012064.hg.1	GCM1	glial cells missing homolog 1 (Drosophila)	1.93	7.37	6.42	0.09	0.56	7.60E-03	2.48E-01	Coding

TC0900009414.hg.1	RFX3	regulatory factor X, 3 (influences HLA class II expression)	1.93	6.46	5.52	0.06	0.17	2.12E-02	3.34E-01	Multiple_Complex
TC1000007990.hg.1	DDIT4	DNA damage inducible transcript 4	1.92	11.78	10.84	0.06	0.34	1.51E-02	3.04E-01	Multiple_Complex
TC0700008031.hg.1	GTF2IRD2B	GTF2I repeat domain containing 2B	1.92	5.01	4.07	0.03	0.15	4.50E-03	2.04E-01	Multiple_Complex
TC0600011121.hg.1	HIST1H1A	histone cluster 1, H1a	1.92	8.37	7.43	0	0.44	3.20E-03	1.78E-01	Coding
TC1500010888.hg.1	PARP6	poly(ADP-ribose) polymerase family member 6	1.92	10.66	9.72	0.12	0.25	3.70E-03	1.90E-01	Multiple_Complex
TC0500013020.hg.1	CLK4	CDC like kinase 4	1.92	12.52	11.58	0.39	0.1	2.80E-03	1.69E-01	Multiple_Complex
TC1300009924.hg.1	GAS6	growth arrest-specific 6	1.92	6.89	5.95	0.08	0.48	4.20E-03	2.03E-01	Multiple_Complex
TC2000008950.hg.1	ACSS2	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001076552	1.92	4.23	3.29	0.18	0.66	1.25E-02	2.86E-01	NonCoding
TC0700012754.hg.1	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	1.92	8.65	7.71	0.1	0.49	9.50E-03	2.62E-01	Multiple_Complex
TC1100010818.hg.1	OR4C46	olfactory receptor, family 4, subfamily C, member 46	1.92	4.58	3.64	0.83	0.05	1.94E-02	3.26E-01	Coding
TC0300009500.hg.1	FNDC3B	fibronectin type III domain containing 3B	1.92	14.64	13.7	0.29	0.12	1.70E-03	1.40E-01	Multiple_Complex
TC1800006852.hg.1	GATA6	GATA binding protein 6	1.91	7.32	6.38	0.14	0.14	1.50E-03	1.31E-01	Coding
TC0900008851.hg.1	DNM1	dynamin 1	1.91	8.95	8.02	0.37	0.21	3.30E-03	1.81E-01	Multiple_Complex
TC0500007623.hg.1	MAST4	microtubule associated serine/threonine kinase family member 4	1.9	9.33	8.4	0.08	0.24	1.90E-03	1.43E-01	Multiple_Complex
TC0100011389.hg.1	IL20	interleukin 20	1.9	8.97	8.04	0.2	1.05	3.66E-02	3.90E-01	Coding
TC2000007760.hg.1	TSHZ2	teashirt zinc finger homeobox 2	1.9	9.65	8.72	0.28	0.15	2.40E-03	1.61E-01	Coding
TC0700008786.hg.1	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	1.9	12.86	11.93	0.03	0.06	7.90E-03	2.48E-01	Multiple_Complex
TC0600008092.hg.1	TJAP1	tight junction associated protein 1 (peripheral)	1.9	9.47	8.54	0.14	0.41	4.10E-03	2.01E-01	Multiple_Complex
TC0500011296.hg.1	ACOT12	acyl-CoA thioesterase 12	1.9	4.56	3.63	0.2	0.67	1.86E-02	3.25E-01	Multiple_Complex
TC1000011130.hg.1	DLG5	discs, large homolog 5 (Drosophila)	1.9	8.69	7.76	0.26	0.02	1.27E-02	2.87E-01	Multiple_Complex

TC2000007102.hg.1	HCK	HCK proto-oncogene, Src family tyrosine kinase	1.9	5.39	4.47	0.18	0.61	1.01E-02	2.68E-01	Multiple_Complex
TC0200009331.hg.1	POTEE	POTE ankyrin domain family, member E	1.9	6.44	5.51	0.07	0.41	1.22E-02	2.84E-01	Coding
TC1700012218.hg.1	SARM1	sterile alpha and TIR motif containing 1	1.9	5.74	4.81	0.04	0.51	7.80E-03	2.48E-01	Multiple_Complex
TC0700011066.hg.1	COBL	cordon-bleu WH2 repeat protein	1.9	12.74	11.82	0.06	0.27	2.10E-03	1.49E-01	Multiple_Complex
TC1900011066.hg.1	CCDC114	coiled-coil domain containing 114	1.9	6.59	5.66	0.22	0.36	6.90E-03	2.39E-01	Multiple_Complex
TC0700012701.hg.1	CNOT4	CCR4-NOT transcription complex subunit 4	1.9	9.7	8.77	0.12	0	1.40E-03	1.26E-01	Multiple_Complex
TC0300012021.hg.1	CFAP44	cilia and flagella associated protein 44	1.9	6	5.08	0.17	0.76	2.40E-02	3.46E-01	Multiple_Complex
TC0100010389.hg.1	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	1.89	9.42	8.51	0.17	0.6	7.40E-03	2.46E-01	Multiple_Complex
TC2000009458.hg.1	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1.89	6.05	5.13	0.16	0.13	8.30E-03	2.50E-01	Multiple_Complex
TC1900008445.hg.1	ZNF114	zinc finger protein 114	1.89	10.33	9.41	0.09	0.13	4.40E-03	2.04E-01	Multiple_Complex
TC0X00008481.hg.1	FAM122C	family with sequence similarity 122C	1.89	9.35	8.43	0.46	0.16	5.80E-03	2.23E-01	Multiple_Complex
TC0100006771.hg.1	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1.88	5.33	4.42	0.01	0.14	2.60E-03	1.64E-01	Multiple_Complex
TC0700011500.hg.1	STX1A	syntaxin 1A (brain)	1.88	7.89	6.98	0.26	0.06	1.27E-02	2.87E-01	Multiple_Complex
TC1700012391.hg.1	MYO19	myosin XIX	1.88	8.31	7.39	0.06	0.31	1.30E-02	2.88E-01	Multiple_Complex
TC1800008235.hg.1	ABHD3	Transcript Identified by AceView, Entrez Gene ID(s) 171586	1.88	8.9	7.99	0.22	0.52	9.10E-03	2.60E-01	Unassigned
TC1600011555.hg.1	SLC12A4	solute carrier family 12 (potassium/chloride transporter), member 4	1.88	8.68	7.77	0.06	0.46	8.10E-03	2.50E-01	Multiple_Complex
TC0300007115.hg.1	EIF1B	eukaryotic translation initiation factor 1B	1.88	9.55	8.64	0.24	0.05	9.80E-03	2.65E-01	Multiple_Complex
TC0300011403.hg.1	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	1.88	5.48	4.58	0.27	0.14	3.50E-03	1.84E-01	Multiple_Complex
TC1900008833.hg.1	CNOT3	CCR4-NOT transcription complex subunit 3	1.87	8.18	7.27	0.05	0.1	1.60E-03	1.35E-01	Multiple_Complex

TC2000009945.hg.1	FAM209A	family with sequence similarity 209, member A	1.87	5.22	4.32	0.26	0.38	9.50E-03	2.62E-01	Coding
TC0200016770.hg.1	MIR6809; TNS1	microRNA 6809; tensin 1	1.87	8.97	8.07	0.36	0.11	4.75E-02	4.21E-01	Multiple_Complex
TC1000007976.hg.1	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	1.87	7.79	6.89	0.24	0.16	3.10E-03	1.73E-01	Multiple_Complex
TC0400008624.hg.1	SPATA5	Transcript Identified by AceView, Entrez Gene ID(s) 166378	1.87	5.98	5.07	0.58	0.08	7.80E-03	2.48E-01	Unassigned
TC1500007633.hg.1	SMAD3	SMAD family member 3	1.87	8.87	7.97	0.14	0.03	4.20E-03	2.01E-01	Multiple_Complex
TC1400007443.hg.1	HSPA2	heat shock 70kDa protein 2	1.87	6.8	5.9	0.36	0.58	1.20E-02	2.83E-01	Multiple_Complex
TC1000007510.hg.1	AGAP9; CTGLF11P	Salzman2013 ANNOTATED, CDS, coding, INTERNAL, OVCODE, OVEXON best transcript NM_001190810; centaurin, gamma-like family, member 11 pseudogene [Source:HGNC Symbol;Acc:HGNC:23660]	1.87	10.49	9.59	0.02	0.15	1.90E-03	1.46E-01	Multiple_Complex
TC0300007437.hg.1	MANF	mesencephalic astrocyte-derived neurotrophic factor	1.87	13.82	12.92	0.16	0.01	2.20E-03	1.54E-01	Multiple_Complex
TC2200007493.hg.1	MEI1	Salzman2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_152513	1.87	15.04	14.14	0.19	0.31	3.80E-03	1.90E-01	NonCoding
TC0500009097.hg.1	SYNPO	synaptopodin	1.87	9.17	8.27	0.42	0.33	9.00E-03	2.59E-01	Multiple_Complex
TC0X00007733.hg.1	FAM46D	family with sequence similarity 46, member D	1.86	4.02	3.12	0.55	0.15	1.93E-02	3.26E-01	Coding
TC0500012818.hg.1	STK10	serine/threonine kinase 10	1.86	11.18	10.29	0.02	0.07	2.10E-02	3.34E-01	Multiple_Complex
TC2200008112.hg.1	TOP3B	topoisomerase (DNA) III beta	1.86	9.97	9.07	0.06	0.28	5.10E-03	2.13E-01	Multiple_Complex
TC0200016274.hg.1	HDAC4	Transcript Identified by AceView, Entrez Gene ID(s) 9759	1.86	6	5.11	0.89	0.51	3.97E-02	3.96E-01	Unassigned
TC1400010722.hg.1	IPO4	importin 4	1.86	7.65	6.75	0.24	0.66	1.30E-02	2.88E-01	Multiple_Complex
TC1400010647.hg.1	BDKRB2	bradykinin receptor B2	1.86	7.05	6.16	0.22	0.4	8.80E-03	2.57E-01	Coding
TC1400010648.hg.1	BDKRB1	bradykinin receptor B1	1.86	6.59	5.69	0.17	0.5	1.06E-02	2.71E-01	Multiple_Complex

TC1900006804.hg.1	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	1.86	10.65	9.76	0.45	0.06	5.70E-03	2.22E-01	Multiple_Complex
TC0200012980.hg.1	ASPRV1; PCBP1-AS1	aspartic peptidase, retroviral-like 1; PCBP1 antisense RNA 1	1.86	8.99	8.09	0.1	0.01	1.70E-03	1.40E-01	Multiple_Complex
TC0200010840.hg.1	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	1.86	9.87	8.98	0.05	0.19	5.90E-03	2.25E-01	Multiple_Complex
TC1000007678.hg.1	MTRNR2L5	MT-RNR2-like 5	1.85	8.02	7.13	0.32	0.75	4.43E-02	4.11E-01	Coding
TC2100007254.hg.1	UBASH3A	ubiquitin associated and SH3 domain containing A	1.85	5.5	4.61	0.93	0.2	4.49E-02	4.14E-01	Multiple_Complex
TC0700013428.hg.1	PILRB; STAG3L5P; PVRIG2P; MIR6840; STAG3L5P-PVRIG2P-PILRB	paired immunoglobin-like type 2 receptor beta; stromal antigen 3-like 5 pseudogene; poliovirus receptor related immunoglobulin domain containing 2, pseudogene; microRNA 6840; STAG3L5P-PVRIG2P-PILRB readthrough	1.85	10.86	9.97	0	0.2	1.40E-02	2.93E-01	Multiple_Complex
TC0400007868.hg.1	PARM1	prostate androgen-regulated mucin-like protein 1	1.85	4.1	3.21	0.23	0.15	2.50E-03	1.61E-01	Multiple_Complex
TC1600008005.hg.1	ADGRG1	adhesion G protein-coupled receptor G1	1.85	6.72	5.83	0.17	0.54	7.40E-03	2.46E-01	Multiple_Complex
TC2100008251.hg.1	TFF1	trefoil factor 1	1.85	10.31	9.42	0.22	0.06	2.20E-03	1.53E-01	Multiple_Complex
TC1600007037.hg.1	NPIPA7	nuclear pore complex interacting protein family, member A7	1.85	12.38	11.5	0.02	0.03	6.70E-03	2.34E-01	Coding
TC0900007082.hg.1	RUSC2	RUN and SH3 domain containing 2	1.85	6.45	5.57	0.3	0.25	2.78E-02	3.59E-01	Multiple_Complex
TC0600011406.hg.1	POU5F1	POU class 5 homeobox 1	1.85	6.05	5.16	0.48	0.33	8.90E-03	2.58E-01	Multiple_Complex
TC1400007259.hg.1	PELI2	pellino E3 ubiquitin protein ligase family member 2	1.85	5.11	4.23	0.34	0.94	4.10E-02	4.00E-01	Multiple_Complex
TC2200009194.hg.1	MED15	mediator complex subunit 15	1.84	11.18	10.3	0.25	0.16	2.51E-02	3.49E-01	Multiple_Complex
TC0100012895.hg.1	MTHFR	methylenetetrahydrofolate reductase (NAD(P)H)	1.84	5.29	4.41	0.02	0.22	5.00E-03	2.13E-01	Multiple_Complex
TC0500008698.hg.1	JADE2	jade family PHD finger 2	1.84	7.78	6.9	0.1	0.41	9.70E-03	2.65E-01	Multiple_Complex

TC0100011451.hg.1	CAMK1G	calcium/calmodulin-dependent protein kinase IG	1.84	5.93	5.05	0.43	0.59	4.21E-02	4.02E-01	Multiple_Complex
TC1100007005.hg.1	LDHC	lactate dehydrogenase C	1.84	7.97	7.09	0.04	0.74	1.52E-02	3.04E-01	Coding
TC1300008084.hg.1	ATP11A	ATPase, class VI, type 11A	1.84	10.34	9.46	0.01	0.08	1.80E-03	1.41E-01	Multiple_Complex
TC1200012841.hg.1	SSH1	slingshot protein phosphatase 1	1.84	7.78	6.9	0.14	0.28	4.40E-03	2.04E-01	Multiple_Complex
TC0300011107.hg.1	ZMYND10	zinc finger, MYND-type containing 10	1.84	8.53	7.65	0.05	0.01	3.00E-03	1.72E-01	Multiple_Complex
TC1700012333.hg.1	TRPV3	transient receptor potential cation channel, subfamily V, member 3	1.84	5.67	4.79	0.07	0.07	1.70E-03	1.40E-01	Multiple_Complex
TC0100018265.hg.1	GSTM5	glutathione S-transferase mu 5	1.84	6.43	5.55	0.12	0.32	4.10E-03	2.01E-01	Multiple_Complex
TC0200013602.hg.1	TSGA10	testis specific 10	1.84	6.88	6.01	0.22	0.34	6.00E-03	2.26E-01	Multiple_Complex
TC1500010042.hg.1	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	1.84	5.73	4.85	0.25	0.26	1.28E-02	2.87E-01	Multiple_Complex
TC1100013040.hg.1	TM7SF2	transmembrane 7 superfamily member 2	1.84	7.87	6.99	0.13	0.11	1.80E-03	1.42E-01	Multiple_Complex
TC0X00007937.hg.1	DRP2	dystrophin related protein 2	1.83	6.43	5.56	0.09	0.38	7.50E-03	2.46E-01	Multiple_Complex
TC0100014889.hg.1	BARHL2	BarH-like homeobox 2	1.83	6.67	5.8	0.02	0.5	6.40E-03	2.31E-01	Coding
TC0900008816.hg.1	CFAP157	cilia and flagella associated protein 157	1.83	5.13	4.26	0.44	0.38	1.91E-02	3.26E-01	Multiple_Complex
TC1900008456.hg.1	ELSPBP1	epididymal sperm binding protein 1	1.83	6.87	6	0.19	0.18	2.90E-03	1.71E-01	Coding
TC1600008889.hg.1	CPNE7	copine VII	1.83	7.57	6.69	0.08	0.96	3.95E-02	3.96E-01	Multiple_Complex
TC1900011891.hg.1	HOOK2	hook microtubule-tethering protein 2	1.83	7.59	6.72	0.12	0	1.46E-02	3.00E-01	Multiple_Complex
TC2000007509.hg.1	CTSA	cathepsin A	1.83	11.08	10.21	0.08	0.27	6.60E-03	2.34E-01	Multiple_Complex
TC0500013282.hg.1	ZDHHC11	zinc finger, DHHC-type containing 11	1.83	8.09	7.22	0.45	0.45	3.27E-02	3.76E-01	Multiple_Complex
TC1000012363.hg.1	NKX6-2	NK6 homeobox 2	1.83	5.2	4.32	0.13	0.06	4.40E-03	2.04E-01	Multiple_Complex
TC0100007800.hg.1	THRAP3	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_005119	1.83	7.14	6.26	0.26	0.03	3.32E-02	3.79E-01	NonCoding

TC0700006890.hg.1	IL6	interleukin 6	1.83	11.91	11.04	0.01	0.14	2.04E-02	3.32E-01	Multiple_Complex
TC1900007031.hg.1	PRKCSH	protein kinase C substrate 80K-H	1.83	13.37	12.5	0.11	0.2	2.50E-03	1.61E-01	Multiple_Complex
TC0400010895.hg.1	TMPRSS11D	transmembrane protease, serine 11D	1.83	5.89	5.02	0.11	0.59	1.30E-02	2.88E-01	Multiple_Complex
TC0100010905.hg.1	SWT1	SWT1 RNA endoribonuclease homolog	1.83	6.67	5.8	0.33	0.02	5.30E-03	2.15E-01	Multiple_Complex
TC0200007102.hg.1	PLB1	phospholipase B1	1.82	6.94	6.07	0.36	0.16	1.03E-02	2.69E-01	Multiple_Complex
TC1200012755.hg.1	PRR4	proline rich 4 (lacrimal)	1.82	7.72	6.85	0.41	0.39	8.70E-03	2.55E-01	Multiple_Complex
TC1700012239.hg.1	TBC1D3K	TBC1 domain family, member 3K	1.82	6.38	5.52	0.23	0.49	1.33E-02	2.89E-01	Coding
TC2200008425.hg.1	LIF	leukemia inhibitory factor	1.82	6.26	5.4	0.45	0.32	8.70E-03	2.56E-01	Coding
TC0900012153.hg.1	MSANTD3	Myb/SANT-like DNA-binding domain containing 3	1.82	11.2	10.34	0.01	0	1.50E-03	1.34E-01	Multiple_Complex
TC2000007928.hg.1	ZNF831	zinc finger protein 831	1.82	11.13	10.27	0.05	0.37	9.30E-03	2.62E-01	Coding
TC1700012353.hg.1	PER1; MIR6883	period circadian clock 1; microRNA 6883	1.82	5.64	4.77	0.28	0.01	3.40E-03	1.82E-01	Multiple_Complex
TC2200007211.hg.1	RASD2	RASD family, member 2	1.82	5.83	4.96	0	0.33	3.80E-03	1.90E-01	Coding
TC1700010677.hg.1	KRT19	keratin 19, type I	1.82	11.05	10.19	0.09	0.19	2.60E-03	1.64E-01	Multiple_Complex
TC0700012971.hg.1	ZNF425	zinc finger protein 425	1.82	6.97	6.11	0.42	0.42	2.20E-02	3.38E-01	Multiple_Complex
TC0100006994.hg.1	PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) member 2	1.82	10.12	9.26	0.3	0.31	8.30E-03	2.50E-01	Multiple_Complex
TC0600008120.hg.1	TMEM63B	transmembrane protein 63B	1.82	9.98	9.12	0.18	0.02	1.71E-02	3.15E-01	Multiple_Complex
TC1200012240.hg.1	RSRC2	arginine/serine-rich coiled-coil 2	1.82	11.67	10.81	0.09	0.32	3.60E-03	1.86E-01	Multiple_Complex
TC1900007947.hg.1	ZNF382	zinc finger protein 382	1.82	6.22	5.36	0.84	0.51	4.41E-02	4.11E-01	Multiple_Complex
TC2100008143.hg.1	ERG	v-ets avian erythroblastosis virus E26 oncogene homolog	1.82	10	9.14	0.07	0.08	3.62E-02	3.87E-01	Multiple_Complex
TC1400010759.hg.1	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	1.81	7.19	6.33	0.61	0.28	1.58E-02	3.07E-01	NonCoding

TC0900012113.hg.1	IFNA8	interferon, alpha 8	1.81	5.64	4.79	0.11	0.26	1.28E-02	2.87E-01	Coding
TC1600006483.hg.1	MSLN	mesothelin	1.81	9	8.14	0.17	0.28	5.00E-03	2.13E-01	Multiple_Complex
TC1100011338.hg.1	CDK2AP2	cyclin-dependent kinase 2 associated protein 2	1.81	9.83	8.97	0.12	0	1.91E-02	3.26E-01	Multiple_Complex
TC1100011182.hg.1	PYGM	phosphorylase, glycogen, muscle	1.81	4.78	3.93	0	0.2	5.50E-03	2.18E-01	Multiple_Complex
TC0400008271.hg.1	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	1.81	8.35	7.5	0.05	0.35	1.62E-02	3.09E-01	Multiple_Complex
TC1700011917.hg.1	USP36	ubiquitin specific peptidase 36	1.81	12.66	11.8	0.08	0.16	6.60E-03	2.34E-01	Multiple_Complex
TC0100018180.hg.1	CLCNKA	chloride channel, voltage-sensitive Ka	1.81	5.9	5.04	0.24	0.46	3.22E-02	3.73E-01	Multiple_Complex
TC0X00010266.hg.1	PCDH11X	Salzman2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_032968	1.8	5.14	4.29	0.24	0.02	7.40E-03	2.46E-01	NonCoding
TC0800010081.hg.1	RNF122	ring finger protein 122	1.8	5.71	4.85	0.35	0	3.81E-02	3.93E-01	Multiple_Complex
TC1000008716.hg.1	GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	1.8	12.23	11.38	0.21	0.19	3.50E-03	1.84E-01	Multiple_Complex
TC0300009673.hg.1	KLHL24	kelch-like family member 24	1.8	11.27	10.42	0.34	0.13	6.10E-03	2.27E-01	Multiple_Complex
TC0100010017.hg.1	SPRR1A	small proline-rich protein 1A	1.8	6.06	5.21	0.32	0.15	5.60E-03	2.19E-01	Multiple_Complex
TC0300014077.hg.1	WDR49	WD repeat domain 49	1.8	6.72	5.87	0.31	0.03	4.50E-03	2.05E-01	Multiple_Complex
TC0100015680.hg.1	NBPF9	neuroblastoma breakpoint family, member 9	1.8	8.05	7.2	0.17	0.54	4.32E-02	4.07E-01	Multiple_Complex
TC0200014269.hg.1	POTEI	POTE ankyrin domain family, member I	1.8	6.1	5.25	0.71	0.5	3.33E-02	3.79E-01	Multiple_Complex
TC1100008792.hg.1	MED17	mediator complex subunit 17	1.8	10.2	9.36	0.04	0.05	2.90E-03	1.70E-01	Multiple_Complex
TC0X00011102.hg.1	CD99L2	CD99 molecule-like 2	1.8	6.35	5.51	0.31	0.79	2.76E-02	3.59E-01	Multiple_Complex
TC0500009109.hg.1	GPX3	glutathione peroxidase 3	1.8	5.53	4.68	0.3	0.23	4.90E-03	2.13E-01	Multiple_Complex
TC0200015397.hg.1	CLK1	CDC like kinase 1	1.79	14.38	13.54	0.58	0.19	1.92E-02	3.26E-01	Multiple_Complex
TC0200009060.hg.1	STEAP3	STEAP family member 3, metalloreductase	1.79	7.8	6.96	0.31	0.29	1.17E-02	2.82E-01	Multiple_Complex

TC1300007164.hg.1	SETDB2	SET domain, bifurcated 2	1.79	7.15	6.31	0.05	0.43	1.64E-02	3.10E-01	Multiple_Complex
TC1400007478.hg.1	GPHN	gephyrin	1.79	5.5	4.66	0.34	0.75	2.76E-02	3.59E-01	Multiple_Complex
TC0600011487.hg.1	C6orf10	chromosome 6 open reading frame 10	1.79	5.02	4.18	0	0.03	1.80E-03	1.42E-01	Coding
TC0900011199.hg.1	OR2K2	olfactory receptor, family 2, subfamily K, member 2	1.79	5.91	5.07	0.11	0.09	1.23E-02	2.84E-01	Coding
TC1600011325.hg.1	CRAMP1	cramped chromatin regulator homolog 1	1.79	6.91	6.07	0.36	0.04	4.50E-03	2.04E-01	Multiple_Complex
TC0600011534.hg.1	WDR46; MIR6873	WD repeat domain 46; microRNA 6873	1.79	8.43	7.59	0.03	0.07	2.40E-03	1.60E-01	Multiple_Complex
TC2000007202.hg.1	ACSS2	acyl-CoA synthetase short-chain family member 2	1.79	9.2	8.36	0.51	0.03	9.20E-03	2.62E-01	Multiple_Complex
TC0300012048.hg.1	ZBTB20; MIR568	zinc finger and BTB domain containing 20; microRNA 568	1.79	10.45	9.61	0.29	0.02	4.00E-03	1.97E-01	Multiple_Complex
TC1600008505.hg.1	WWOX	WW domain containing oxidoreductase	1.79	5.97	5.13	0.14	0.71	2.57E-02	3.51E-01	Multiple_Complex
TC1700012310.hg.1	MFSD11	major facilitator superfamily domain containing 11	1.79	8.04	7.2	0.66	0.2	2.22E-02	3.39E-01	Multiple_Complex
TC0100013908.hg.1	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	1.79	10.9	10.07	0.1	0.14	4.00E-02	3.98E-01	Multiple_Complex
TC1500008232.hg.1	ISG20	interferon stimulated exonuclease gene 20kDa	1.78	13.25	12.41	0.06	0.03	3.50E-03	1.84E-01	Multiple_Complex
TC1600010006.hg.1	PRSS8	protease, serine, 8	1.78	6.59	5.76	0.36	0.2	7.40E-03	2.46E-01	Multiple_Complex
TC0800008715.hg.1	ZHX2	zinc fingers and homeoboxes 2	1.78	9.31	8.47	0.05	0.02	2.40E-03	1.60E-01	Coding
TC1600011235.hg.1	GALNS	galactosamine (N-acetyl)-6-sulfatase	1.78	11.05	10.22	0.14	0.15	2.27E-02	3.40E-01	Multiple_Complex
TC1200010968.hg.1	DDIT3	DNA-damage-inducible transcript 3	1.78	12.51	11.68	0.2	0.58	1.53E-02	3.04E-01	Coding
TC1700012361.hg.1	CDRT1	CMT1A duplicated region transcript 1	1.78	7.09	6.25	0.3	0.41	2.00E-02	3.29E-01	Multiple_Complex
TC0400007918.hg.1	CXCL13	chemokine (C-X-C motif) ligand 13	1.78	5.08	4.24	0.66	0.37	2.77E-02	3.59E-01	Multiple_Complex
TC0700009676.hg.1	GIMAP7	GTPase, IMAP family member 7	1.78	7.44	6.61	0.1	0.84	3.75E-02	3.92E-01	Coding
TC2000009268.hg.1	ELMO2	engulfment and cell motility 2	1.78	9.69	8.86	0.56	0.04	4.49E-02	4.14E-01	Multiple_Complex

TC0700010348.hg.1	SOSTDC1	sclerostin domain containing 1	1.78	5.84	5	0.2	0.31	9.80E-03	2.65E-01	Coding
TC1300008388.hg.1	MTMR6	Transcript Identified by AceView, Entrez Gene ID(s) 9107	1.78	5.1	4.27	0.5	0.31	1.74E-02	3.16E-01	Unassigned
TC1100013230.hg.1	BCL9L	B-cell CLL/lymphoma 9-like	1.78	9.77	8.94	0.16	0.22	4.80E-03	2.12E-01	Multiple_Complex
TC1100008999.hg.1	ZC3H12C	zinc finger CCCH-type containing 12C	1.78	9.55	8.72	0.03	0.04	4.00E-03	1.98E-01	Multiple_Complex
TC2200007467.hg.1	ZC3H7B	zinc finger CCCH-type containing 7B	1.78	8.78	7.95	0.11	0.1	2.79E-02	3.60E-01	Multiple_Complex
TC1900011642.hg.1	SPPL2B	signal peptide peptidase like 2B	1.78	8.77	7.93	0.01	0.36	8.50E-03	2.54E-01	Multiple_Complex
TC1500008043.hg.1	ABHD17C	abhydrolase domain containing 17C	1.78	8.11	7.28	0.01	0.29	8.60E-03	2.54E-01	Multiple_Complex
TC1500010881.hg.1	TIPIN; RPL9P25	TIMELESS interacting protein; ribosomal protein L9 pseudogene 25	1.78	8.08	7.26	0.25	0.3	1.41E-02	2.94E-01	Multiple_Complex
TC1700006909.hg.1	MYOCD	myocardin	1.78	5.87	5.04	0.1	0.65	1.90E-02	3.26E-01	Multiple_Complex
TC1100008899.hg.1	CEP126	centrosomal protein 126kDa	1.77	6.28	5.45	0.21	0.3	6.20E-03	2.27E-01	Coding
TC0700013390.hg.1	TRIM73	tripartite motif containing 73	1.77	6.82	5.99	0.12	0.26	6.60E-03	2.34E-01	Multiple_Complex
TC2200006718.hg.1	SDF2L1	stromal cell-derived factor 2-like 1	1.77	12.66	11.84	0.22	0.16	6.50E-03	2.33E-01	Multiple_Complex
TC0X00009611.hg.1	SLC38A5	solute carrier family 38, member 5	1.77	11.82	10.99	0.16	0.33	4.42E-02	4.11E-01	Multiple_Complex
TC1200012534.hg.1	POLE	Transcript Identified by AceView, Entrez Gene ID(s) 5426	1.77	5.82	4.99	0.15	0.66	1.95E-02	3.27E-01	Unassigned
TC0200007200.hg.1	LTBP1	latent transforming growth factor beta binding protein 1	1.77	5.45	4.62	0.1	0.18	4.90E-03	2.13E-01	Multiple_Complex
TC1900008020.hg.1	ACTN4	actinin, alpha 4	1.77	13.45	12.62	0.21	0.04	2.93E-02	3.65E-01	Multiple_Complex
TC1700009651.hg.1	TP53	tumor protein p53	1.77	9.83	9.01	0.11	0.01	1.29E-02	2.87E-01	Multiple_Complex
TC1600011358.hg.1	C16orf45	chromosome 16 open reading frame 45	1.77	6.94	6.11	0.14	0.02	2.67E-02	3.58E-01	Multiple_Complex
TC0300008660.hg.1	ALDH1L1-AS1	ALDH1L1 antisense RNA 1	1.77	5.8	4.97	0.18	0.24	2.35E-02	3.43E-01	Multiple_Complex
TC0200008870.hg.1	BCL2L11	BCL2-like 11 (apoptosis facilitator)	1.77	9.1	8.27	0.15	0.32	7.10E-03	2.42E-01	Multiple_Complex

TC0700008141.hg.1	PTPN12	protein tyrosine phosphatase, non-receptor type 12	1.77	9.79	8.96	0.21	0.52	3.23E-02	3.74E-01	Multiple_Complex
TC0X00008836.hg.1	PLXNA3	plexin A3	1.77	6.72	5.9	0.42	0.44	3.84E-02	3.94E-01	Multiple_Complex
TC1100006836.hg.1	MRVI1-AS1	MRVI1 antisense RNA 1	1.77	6.6	5.78	0.39	0.52	2.00E-02	3.29E-01	Multiple_Complex
TC0300006582.hg.1	TATDN2; GHRLOS	TatD DNase domain containing 2; ghrelin opposite strand/antisense RNA	1.77	7.13	6.31	0.09	0.03	2.80E-03	1.69E-01	Multiple_Complex
TC1700010811.hg.1	HDAC5	histone deacetylase 5	1.76	8.71	7.89	0.16	0.04	6.20E-03	2.27E-01	Multiple_Complex
TC1100008029.hg.1	PCNXL3	pecanex-like 3 (Drosophila)	1.76	8.54	7.72	0.47	0.12	3.96E-02	3.96E-01	Multiple_Complex
TSUnmapped00000059.hg.1	HYOU1	hypoxia up-regulated 1	1.76	6.53	5.71	0.29	0.51	2.26E-02	3.40E-01	Coding
TC0600011125.hg.1	HIST1H2AB	histone cluster 1, H2ab	1.76	10.91	10.09	0.22	0.08	3.40E-03	1.83E-01	Coding
TC1000009863.hg.1	FAM107B	family with sequence similarity 107, member B	1.76	8.67	7.85	0.28	0.4	2.51E-02	3.49E-01	Multiple_Complex
TC0800008481.hg.1	CTHRC1	collagen triple helix repeat containing 1	1.76	6.23	5.42	0.04	0.21	2.32E-02	3.42E-01	Multiple_Complex
TC0400007962.hg.1	BMP3	bone morphogenetic protein 3	1.76	5.09	4.28	0.06	0.25	3.13E-02	3.72E-01	Coding
TC1700011761.hg.1	RECQL5	RecQ helicase-like 5	1.76	7.85	7.03	0.01	0.06	5.00E-03	2.13E-01	Multiple_Complex
TC1700006721.hg.1	SLC16A13	solute carrier family 16, member 13	1.76	7	6.19	0.04	0.57	1.75E-02	3.16E-01	Multiple_Complex
TC0X00008712.hg.1	MAMLD1	mastermind-like domain containing 1	1.76	6.25	5.44	0.16	0.43	3.14E-02	3.72E-01	Multiple_Complex
TC1600011501.hg.1	NPIPB3	nuclear pore complex interacting protein family, member B3	1.76	11.89	11.07	0.26	0.17	5.70E-03	2.22E-01	Multiple_Complex
TC0300007596.hg.1	FLNB	filamin B, beta	1.76	10.24	9.43	0.01	0.24	8.90E-03	2.58E-01	Multiple_Complex
TC2100007241.hg.1	ABCG1	ATP binding cassette subfamily G member 1	1.75	8.07	7.26	0.15	0.6	1.89E-02	3.26E-01	Multiple_Complex
TC1200011845.hg.1	SELPLG	selectin P ligand	1.75	6.11	5.3	0.28	0.38	1.55E-02	3.05E-01	Coding
TC0100009950.hg.1	ZNF687	zinc finger protein 687	1.75	10.05	9.24	0.04	0.04	2.80E-03	1.68E-01	Multiple_Complex

TC1100008480.hg.1	UVRAG	UV radiation resistance associated	1.75	11.97	11.16	0.32	0.02	6.20E-03	2.27E-01	Multiple_Complex
TC1200012610.hg.1	SSPN	sarcospan	1.75	4.1	3.29	0	0.52	2.67E-02	3.57E-01	Multiple_Complex
TC0700008747.hg.1	HBP1	HMG-box transcription factor 1	1.75	12.79	11.98	0.2	0.14	3.80E-03	1.90E-01	Multiple_Complex
TC0200016710.hg.1	ANKRD36C	ankyrin repeat domain 36C	1.75	11.38	10.57	0.02	0.77	3.41E-02	3.83E-01	Multiple_Complex
TC0300012166.hg.1	HCLS1	hematopoietic cell-specific Lyn substrate 1	1.75	5.73	4.93	0.12	0.31	2.47E-02	3.48E-01	Multiple_Complex
TC1500006683.hg.1	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2	1.75	6.84	6.03	0.11	0.07	9.00E-03	2.59E-01	Multiple_Complex
TC1900011251.hg.1	NKG7	natural killer cell granule protein 7	1.75	7.39	6.59	0.45	0.18	3.37E-02	3.81E-01	Coding
TSUnmapped00000322.hg.1	HYOU1	hypoxia up-regulated 1	1.75	10.85	10.04	0.15	0.13	1.23E-02	2.84E-01	Coding
TC1900010037.hg.1	SUGP2	SURP and G-patch domain containing 2	1.75	9	8.2	0.05	0.43	8.10E-03	2.49E-01	Multiple_Complex
TC1200010612.hg.1	RHEBL1	Ras homolog enriched in brain like 1	1.75	7.78	6.97	0.3	0.07	3.27E-02	3.76E-01	Multiple_Complex
TC1400006828.hg.1	COCH	cochlin	1.75	5.65	4.84	0.06	0.91	4.96E-02	4.26E-01	Multiple_Complex
TC1900012055.hg.1	VN1R1	vomeronasal 1 receptor 1	1.75	7.62	6.82	0.31	0.16	8.00E-03	2.49E-01	Multiple_Complex
TC0300013971.hg.1	UCN2	urocortin 2	1.75	6.07	5.27	0.15	0.18	3.60E-03	1.88E-01	Coding
TSUnmapped00000135.hg.1	INPP5D	inositol polyphosphate-5-phosphatase D	1.75	4.65	3.84	0.4	0.02	7.00E-03	2.39E-01	Coding
TC1000010509.hg.1	AGAP4	ArfGAP with GTPase domain, ankyrin repeat and PH domain 4	1.75	11.1	10.3	0.13	0.22	5.50E-03	2.18E-01	Multiple_Complex
TC0100006787.hg.1	PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta	1.74	7.62	6.82	0.32	0.27	1.23E-02	2.84E-01	Multiple_Complex
TC0600014228.hg.1	FAM217A	family with sequence similarity 217, member A	1.74	4.81	4.01	0.17	0.43	1.65E-02	3.10E-01	Multiple_Complex
TC0700009066.hg.1	FLNC	filamin C, gamma	1.74	7.04	6.24	0.65	0.54	3.71E-02	3.90E-01	Multiple_Complex

TC1000012471.hg.1	ADIRF; AGAP11; BMS1P3	adipogenesis regulatory factor; ankyrin repeat and GTPase domain Arf GTPase activating protein 11; BMS1 ribosome biogenesis factor pseudogene 3	1.74	6.31	5.5	0.17	0	6.40E-03	2.31E-01	Multiple_Complex
TC2000006561.hg.1	MAVS	mitochondrial antiviral signaling protein	1.74	7.55	6.75	0.06	0.27	1.78E-02	3.20E-01	Multiple_Complex
TC0200016687.hg.1	SFXN5	sideroflexin 5	1.74	6.96	6.16	0.11	0.65	2.95E-02	3.65E-01	Multiple_Complex
TC0300007296.hg.1	SCAP	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_012235	1.74	10.06	9.26	0.12	0.84	3.42E-02	3.83E-01	NonCoding
TC1400009184.hg.1	TXNDC16	thioredoxin domain containing 16	1.74	6.25	5.45	0.53	0.05	2.37E-02	3.45E-01	Multiple_Complex
TC0X00007310.hg.1	TSPYL2	TSPY-like 2	1.74	10.59	9.79	0.07	0.01	3.80E-03	1.90E-01	Multiple_Complex
TC1900006687.hg.1	AC007292.7; MPND	Transcript Identified by AceView, Entrez Gene ID(s) 84954; novel transcript, antisense to STAP2	1.74	8.19	7.39	0.06	0.1	1.19E-02	2.83E-01	NonCoding
TC0100018387.hg.1	CDK11B	cyclin-dependent kinase 11B	1.74	9.22	8.42	0.05	0.26	7.10E-03	2.42E-01	Multiple_Complex
TC0600007480.hg.1	HLA-F	major histocompatibility complex, class I, F	1.74	10.87	10.07	0.07	0.2	1.15E-02	2.81E-01	Multiple_Complex
TC1200009546.hg.1	SLC6A12	solute carrier family 6 (neurotransmitter transporter), member 12	1.74	7.25	6.45	0.11	0.67	2.38E-02	3.46E-01	Multiple_Complex
TC1500010783.hg.1	SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	1.74	6.37	5.57	0.33	0.5	2.30E-02	3.41E-01	Multiple_Complex
TC0500010592.hg.1	C6	complement component 6	1.74	4.82	4.02	0.47	0.1	2.56E-02	3.50E-01	Multiple_Complex
TC2200008682.hg.1	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	1.74	7.49	6.69	0.15	0.13	1.02E-02	2.68E-01	Multiple_Complex
TC0300011502.hg.1	FOXP1; RP11-298C2.1	Transcript Identified by AceView, Entrez Gene ID(s) 27086; novel transcript, sense intronic to FOXP1	1.74	5.33	4.53	0.16	0.09	2.18E-02	3.36E-01	NonCoding

TC0600007610.hg.1	MSH5; MSH5-SAPCD1; SAPCD1	mutS homolog 5; MSH5-SAPCD1 readthrough (NMD candidate); suppressor APC domain containing 1	1.74	8.66	7.86	0.04	0.07	3.90E-03	1.95E-01	Multiple_Complex
TC1900009859.hg.1	BRD4	bromodomain containing 4	1.74	12.27	11.47	0.21	0.19	1.73E-02	3.16E-01	Multiple_Complex
TC1400010776.hg.1	CATSPERB	catsper channel auxiliary subunit beta	1.74	5.23	4.44	0.13	0.03	3.80E-03	1.90E-01	Multiple_Complex
TC0200016224.hg.1	PER2	period circadian clock 2	1.74	5.53	4.73	0.37	0.01	6.90E-03	2.39E-01	Multiple_Complex
TC0700009231.hg.1	AKR1B15	aldo-keto reductase family 1, member B15	1.74	6.54	5.75	0.1	0.02	6.30E-03	2.30E-01	Multiple_Complex
TC0800011974.hg.1	TRAPPC9	trafficking protein particle complex 9	1.73	7.84	7.04	0.3	0.07	6.10E-03	2.27E-01	Multiple_Complex
TC0600009362.hg.1	HEY2	hes-related family bHLH transcription factor with YRPW motif 2	1.73	9.05	8.25	0.33	0.04	5.50E-03	2.18E-01	Multiple_Complex
TC0800012474.hg.1	AGO2	argonaute RISC catalytic component 2	1.73	11.5	10.71	0.08	0.04	1.85E-02	3.24E-01	Multiple_Complex
TC1600011383.hg.1	TMEM265; SRCAP	transmembrane protein 265; Snf2-related CREBBP activator protein	1.73	9.54	8.74	0.1	0.08	3.10E-03	1.73E-01	Multiple_Complex
TC2100006674.hg.1	CHODL	chondrolectin	1.73	6.25	5.46	0.05	0.03	5.50E-03	2.18E-01	Multiple_Complex
TC0900011393.hg.1	TRAF1	TNF receptor-associated factor 1	1.73	5.62	4.83	0.54	0.01	3.41E-02	3.82E-01	Multiple_Complex
TC0200009707.hg.1	KCNJ3	potassium channel, inwardly rectifying subfamily J, member 3	1.73	5.27	4.48	0.27	0.55	3.32E-02	3.79E-01	Multiple_Complex
TC1000012552.hg.1	FAM25G; FAM25C; FAM25BP	family with sequence similarity 25, member G; family with sequence similarity 25, member C; protein FAM25	1.73	7.24	6.44	0.27	0.03	2.26E-02	3.40E-01	Multiple_Complex
TC1700011088.hg.1	COL1A1	collagen, type I, alpha 1	1.73	7.38	6.59	0.2	0.35	6.80E-03	2.38E-01	Multiple_Complex
TC0200011991.hg.1	ADCY3	adenylate cyclase 3	1.73	7.43	6.64	0.08	0.18	1.14E-02	2.80E-01	Multiple_Complex
TC1500008183.hg.1	GOLGA6L3	golgin A6 family-like 3	1.73	8.77	7.98	0.26	0.15	1.67E-02	3.12E-01	Multiple_Complex
TC1300006633.hg.1	PABPC3	poly(A) binding protein, cytoplasmic 3	1.73	8.97	8.18	0.32	0.15	1.23E-02	2.84E-01	Coding
TC0600014111.hg.1	SYNGAP1; MIR5004	synaptic Ras GTPase activating protein 1; microRNA 5004	1.73	9.08	8.29	0.22	0.36	1.23E-02	2.84E-01	Multiple_Complex

TC1500007901.hg.1	SNX33	sorting nexin 33	1.73	6.79	6.01	0.18	0.39	1.16E-02	2.81E-01	Multiple_Complex
TC1200012719.hg.1	WDR66	WD repeat domain 66	1.73	6.71	5.93	0.38	0.02	4.74E-02	4.21E-01	Multiple_Complex
TC1500008485.hg.1	IGF1R	insulin-like growth factor 1 receptor	1.73	12.23	11.44	0.14	0.06	4.70E-03	2.10E-01	Multiple_Complex
TC0X00007504.hg.1	STARD8	StAR-related lipid transfer domain containing 8	1.73	7.03	6.24	0.62	0.08	3.01E-02	3.67E-01	Multiple_Complex
TC0300013864.hg.1	PDIA5; MIR7110	protein disulfide isomerase family A, member 5; microRNA 7110	1.72	9.46	8.67	0.07	0.23	7.80E-03	2.48E-01	Multiple_Complex
TC0200012863.hg.1	SPRED2	sprouty-related, EVH1 domain containing 2	1.72	9.89	9.1	0.16	0.1	1.39E-02	2.93E-01	Multiple_Complex
TC1700009137.hg.1	RPTOR	regulatory associated protein of MTOR, complex 1	1.72	9.62	8.84	0.36	0.7	4.83E-02	4.21E-01	Multiple_Complex
TC1100007637.hg.1	OR8U1; OR8U8	olfactory receptor, family 8, subfamily U, member 1; olfactory receptor, family 8, subfamily U, member 8	1.72	4.58	3.8	0.44	0.04	1.13E-02	2.79E-01	Coding
TC1000010358.hg.1	MTRNR2L7	MT-RNR2-like 7	1.72	9.34	8.56	0.34	0.03	1.02E-02	2.68E-01	Coding
TC0800011533.hg.1	TRPS1	Transcript Identified by AceView, Entrez Gene ID(s) 7227	1.72	4.19	3.4	0.03	0.18	8.10E-03	2.50E-01	Unassigned
TC0700013338.hg.1	GLCCI1	glucocorticoid induced 1	1.72	9.03	8.25	0.14	0.18	4.97E-02	4.26E-01	Multiple_Complex
TC0500012138.hg.1	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	1.72	7.97	7.19	0.19	0.39	1.09E-02	2.74E-01	Multiple_Complex
TC0200006799.hg.1	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	1.72	5.87	5.09	0.02	0.08	5.90E-03	2.25E-01	Coding
TC1000007847.hg.1	MYPN	myopalladin	1.72	11.96	11.18	0.39	0.29	4.38E-02	4.10E-01	Multiple_Complex
TC0300006544.hg.1	SETD5	SET domain containing 5	1.72	11.11	10.33	0.24	0.11	2.21E-02	3.39E-01	Multiple_Complex
TC1100008034.hg.1	KAT5	K(lysine) acetyltransferase 5	1.72	10.25	9.47	0.01	0.41	1.98E-02	3.29E-01	Multiple_Complex
TC1200012860.hg.1	LINC01089	long intergenic non-protein coding RNA 1089	1.72	9.18	8.4	0.23	0.37	1.01E-02	2.68E-01	NonCoding
TC1700006782.hg.1	CNTROB	Transcript Identified by AceView, Entrez Gene ID(s) 116840	1.72	5.35	4.57	0.14	0.34	7.00E-03	2.40E-01	Unassigned

TC2200007043.hg.1	HORMAD2	HORMA domain containing 2	1.72	5.87	5.08	0.3	0.22	1.73E-02	3.16E-01	Multiple_Complex
TC0100009608.hg.1	HAO2	hydroxyacid oxidase 2 (long chain)	1.72	4.51	3.72	0.09	0.65	3.94E-02	3.96E-01	Multiple_Complex
TC0100013949.hg.1	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	1.72	11.05	10.27	0.46	0.11	1.49E-02	3.03E-01	Multiple_Complex
TC0900010056.hg.1	ANKRD18A; FAM95C	ankyrin repeat domain 18A; family with sequence similarity 95, member C	1.72	9.5	8.72	0.03	0.05	4.00E-03	1.98E-01	Multiple_Complex
TC0600013537.hg.1	RAET1G	retinoic acid early transcript 1G	1.72	7.84	7.06	0.25	0.19	1.05E-02	2.69E-01	Multiple_Complex
TC1100007786.hg.1	TMEM132A	transmembrane protein 132A	1.72	10.34	9.56	0.16	0.34	1.32E-02	2.89E-01	Multiple_Complex
TC1500010712.hg.1	GOLGA8N	golgin A8 family, member N	1.72	6.64	5.87	0.07	0.84	4.13E-02	4.01E-01	Multiple_Complex
TC0800010894.hg.1	HEY1	hes-related family bHLH transcription factor with YRPW motif 1	1.72	8.15	7.37	0.12	0.07	3.40E-03	1.83E-01	Multiple_Complex
TC0200016771.hg.1	TNS1	tensin 1	1.71	6.9	6.12	0.71	0.17	2.86E-02	3.63E-01	NonCoding
TC0100010387.hg.1	DDR2	discoidin domain receptor tyrosine kinase 2	1.71	8.3	7.53	0.05	0.39	7.40E-03	2.46E-01	Multiple_Complex
TC1700010910.hg.1	KANSL1	KAT8 regulatory NSL complex subunit 1	1.71	10.89	10.12	0.01	0.59	2.00E-02	3.30E-01	Multiple_Complex
TC1600008034.hg.1	NDRG4	NDRG family member 4	1.71	6.06	5.29	0.11	0.63	3.71E-02	3.90E-01	Multiple_Complex
TC1900012020.hg.1	ZNF432	zinc finger protein 432	1.71	8.27	7.5	0.34	0.37	1.65E-02	3.10E-01	Multiple_Complex
TC1900006508.hg.1	ABCA7	ATP binding cassette subfamily A member 7	1.71	8	7.22	0.17	0.02	8.10E-03	2.49E-01	Multiple_Complex
TC2100006922.hg.1	EVA1C	eva-1 homolog C (C. elegans)	1.71	11	10.23	0.6	0.15	2.41E-02	3.46E-01	Multiple_Complex
TC0100015971.hg.1	GON4L	gon-4-like (C. elegans)	1.71	12.93	12.16	0.11	0.07	4.50E-03	2.04E-01	Multiple_Complex
TSUnmapped00000107.hg.1	DUSP16	dual specificity phosphatase 16	1.71	12.43	11.66	0.16	0.13	4.70E-03	2.10E-01	Coding

TC1000010562.hg.1	SYT15; ABC7-42404400C24.1	Homo sapiens synaptotagmin XV (SYT15), transcript variant a, mRNA.; Homo sapiens synaptotagmin XV (SYT15), transcript variant b, mRNA.; Homo sapiens synaptotagmin XV, mRNA (cDNA clone MGC:164845 IMAGE:40147906), complete cds.; Synaptotagmin-15 [Source:UniProtKB/Swiss-Prot;Acc:Q9BQS2]	1.71	6.01	5.23	0.62	0.26	2.27E-02	3.40E-01	Coding
TC1000008727.hg.1	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	1.71	7.56	6.79	0.57	0.08	2.26E-02	3.40E-01	Multiple_Complex
TC2100007278.hg.1	PKNOX1	PBX/knotted 1 homeobox 1	1.71	13.36	12.59	0.05	0.08	3.60E-03	1.88E-01	Multiple_Complex
TC1200008683.hg.1	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	1.71	11.24	10.47	0.07	0.31	3.48E-02	3.84E-01	Multiple_Complex
TC0200007458.hg.1	EPAS1	endothelial PAS domain protein 1	1.71	13.51	12.74	0.14	0.11	3.90E-03	1.96E-01	Multiple_Complex
TC1400010411.hg.1	BRF1	BRF1, RNA polymerase III transcription initiation factor 90 kDa subunit	1.71	10.47	9.7	0.35	0.03	2.08E-02	3.34E-01	Multiple_Complex
TC1000007761.hg.1	ARID5B	AT rich interactive domain 5B (MRF1-like)	1.71	10.81	10.04	0.15	0.01	6.20E-03	2.27E-01	Multiple_Complex
TC0400012942.hg.1	C4orf36	chromosome 4 open reading frame 36	1.71	6.38	5.61	0.15	0.57	1.89E-02	3.26E-01	Multiple_Complex
TC1700009590.hg.1	KIAA0753	KIAA0753	1.7	6.16	5.39	0.03	0.07	4.00E-03	1.97E-01	Multiple_Complex
TC0600008379.hg.1	MTRNR2L9	MT-RNR2-like 9	1.7	15.18	14.41	0.22	0.08	1.08E-02	2.74E-01	Multiple_Complex
TC0300013384.hg.1	CLCN2	chloride channel, voltage-sensitive 2	1.7	6.18	5.41	0.79	0.11	3.86E-02	3.94E-01	Multiple_Complex
TC1000007598.hg.1	AGAP6	ArfGAP with GTPase domain, ankyrin repeat and PH domain 6	1.7	11.04	10.27	0.03	0.24	6.50E-03	2.31E-01	Multiple_Complex
TC1500010764.hg.1	CLK3	CDC like kinase 3	1.7	9.05	8.28	0.41	0.17	1.07E-02	2.71E-01	Multiple_Complex
TC0500008941.hg.1	ARHGAP26	Rho GTPase activating protein 26	1.7	10.56	9.79	0.03	0.03	1.91E-02	3.26E-01	Multiple_Complex

TC1000009839.hg.1	UCMA	upper zone of growth plate and cartilage matrix associated	1.7	4.89	4.12	0.01	0.13	1.27E-02	2.87E-01	Coding
TC0800009113.hg.1	PTP4A3	protein tyrosine phosphatase type IVA, member 3	1.7	7.99	7.23	0.05	0.07	4.10E-03	2.01E-01	Multiple_Complex
TC0700013425.hg.1	STAG3	stromal antigen 3	1.7	6.17	5.41	0.49	0.01	1.20E-02	2.84E-01	Multiple_Complex
TC0600006442.hg.1	IRF4	interferon regulatory factor 4	1.7	6.86	6.09	0.27	0.36	2.72E-02	3.58E-01	Multiple_Complex
TC0600014106.hg.1	CFB	complement factor B	1.7	9.3	8.54	0.13	0.39	1.00E-02	2.68E-01	Multiple_Complex
TC0700012043.hg.1	CLDN15	claudin 15	1.7	8.14	7.38	0.2	0.24	8.10E-03	2.50E-01	Multiple_Complex
TC0200009883.hg.1	XIRP2	xin actin binding repeat containing 2	1.7	5.03	4.27	0.14	0.36	9.60E-03	2.63E-01	Coding
TC0200016640.hg.1	HS1BP3	HCLS1 binding protein 3	1.7	6.4	5.63	0.17	0.13	5.60E-03	2.19E-01	Coding
TC1500008135.hg.1	UBE2Q2L	ubiquitin conjugating enzyme E2Q family member 2-like	1.7	7.38	6.62	0.2	0.28	1.60E-02	3.08E-01	Coding
TC0600011357.hg.1	TRIM26	tripartite motif containing 26	1.7	8.48	7.71	0.07	0.13	8.30E-03	2.50E-01	Multiple_Complex
TC0700007477.hg.1	UPP1	uridine phosphorylase 1	1.7	8.16	7.4	0.22	0.06	5.60E-03	2.19E-01	Multiple_Complex
TC0100011153.hg.1	C1orf106	chromosome 1 open reading frame 106	1.7	5.6	4.83	0.47	0.04	1.36E-02	2.90E-01	Multiple_Complex
TC0800007461.hg.1	HGSNAT	Transcript Identified by AceView, Entrez Gene ID(s) 138050	1.7	4.94	4.17	0.07	0.01	1.03E-02	2.69E-01	Unassigned
TC0700012099.hg.1	RASA4	Salzman2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_006989	1.7	8.48	7.72	0.13	0.12	1.08E-02	2.74E-01	NonCoding
TC0300013103.hg.1	RPL22L1	ribosomal protein L22-like 1	1.7	14.96	14.2	0.45	0.23	2.41E-02	3.46E-01	Multiple_Complex
TC1600010765.hg.1	COG4	component of oligomeric golgi complex 4	1.7	6.61	5.85	0.08	0.1	2.43E-02	3.46E-01	Multiple_Complex
TC0200015958.hg.1	DNER	delta/notch like EGF repeat containing	1.69	6.69	5.93	0.34	0.48	3.18E-02	3.72E-01	Multiple_Complex
TC0800007016.hg.1	CHMP7	Transcript Identified by AceView, Entrez Gene ID(s) 91782	1.69	10.12	9.36	0.19	0.34	8.90E-03	2.58E-01	Unassigned

TC1700007677.hg.1	DUSP14	dual specificity phosphatase 14	1.69	8.8	8.04	0.03	0.09	5.50E-03	2.18E-01	Coding
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	1.69	9.65	8.89	0.1	0.38	1.48E-02	3.02E-01	Multiple_Complex
TC1100010898.hg.1	UBE2L6	Transcript Identified by AceView, Entrez Gene ID(s) 9246	1.69	7.6	6.85	0.06	0.27	1.61E-02	3.08E-01	Unassigned
TC1900010372.hg.1	CEP89	centrosomal protein 89kDa	1.69	6.77	6.01	0.16	0.55	1.80E-02	3.23E-01	Multiple_Complex
TC0200014303.hg.1	WTH3DI; LOC150786	RAB6C-like; Synthetic construct Homo sapiens clone IMAGE:100016523, MGC:184337 RAB6C-like (LOC150786) mRNA, encodes complete protein.	1.69	6.01	5.26	0.45	0.57	3.94E-02	3.96E-01	Multiple_Complex
TC1700009150.hg.1	BAIAP2	BAI1-associated protein 2	1.69	7.76	7.01	0.29	0.2	2.78E-02	3.59E-01	Multiple_Complex
TC2000009898.hg.1	RP1-122P22.2; RIN2	novel transcript; Transcript Identified by AceView, Entrez Gene ID(s) 54453	1.69	5.42	4.67	0.36	0.28	2.85E-02	3.63E-01	NonCoding
TC2200007495.hg.1	SREBF2	sterol regulatory element binding transcription factor 2	1.69	12.23	11.47	0.38	0.13	2.86E-02	3.63E-01	Multiple_Complex
TC0800007579.hg.1	C8orf22	chromosome 8 open reading frame 22	1.69	12.2	11.44	0.53	0.09	2.29E-02	3.41E-01	Coding
TC0500007465.hg.1	GPBP1	GC-rich promoter binding protein 1	1.69	12.44	11.68	0.31	0.1	9.40E-03	2.62E-01	Multiple_Complex
TC1400008981.hg.1	FOXA1	forkhead box A1	1.69	6.4	5.65	0	0.17	5.10E-03	2.13E-01	Multiple_Complex
TC0600013412.hg.1	HIVEP2	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_006734	1.69	4.93	4.17	0.6	0	2.45E-02	3.47E-01	NonCoding
TC1500010853.hg.1	FSIP1	fibrous sheath interacting protein 1	1.69	5.79	5.04	0.12	0.25	4.69E-02	4.20E-01	Multiple_Complex
TC0100011621.hg.1	TGFB2; TGFB2-OT1	transforming growth factor beta 2; TGFB2 overlapping transcript 1	1.69	5.55	4.8	0.09	0.23	6.00E-03	2.27E-01	Multiple_Complex
TC0900007101.hg.1	TMEM8B	transmembrane protein 8B	1.69	5.23	4.48	0.06	0.16	1.33E-02	2.89E-01	Multiple_Complex

TC1100009833.hg.1	OSBPL5	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_020896	1.69	4.64	3.89	0.31	0.11	7.50E-03	2.46E-01	NonCoding
TC0200010536.hg.1	PARD3B	par-3 family cell polarity regulator beta	1.69	5.1	4.34	0.03	0.03	4.80E-03	2.12E-01	Multiple_Complex
TC0600007789.hg.1	ZNF76	zinc finger protein 76	1.69	10.14	9.38	0.31	0.26	3.92E-02	3.95E-01	Multiple_Complex
TC0700009608.hg.1	ZNF212	zinc finger protein 212	1.69	6.48	5.72	0.13	0.59	2.04E-02	3.32E-01	Coding
TC0100018502.hg.1	GBA	glucosidase, beta, acid	1.69	13.13	12.37	0.08	0.26	3.85E-02	3.94E-01	Multiple_Complex
TC1700012243.hg.1	TBC1D3E	TBC1 domain family, member 3E	1.69	7.28	6.53	0.28	0.07	3.57E-02	3.86E-01	Coding
TC0300009632.hg.1	SOX2	SRY box 2	1.69	6.65	5.9	0.25	0.26	2.71E-02	3.58E-01	Coding
TC1800007201.hg.1	SIGLEC15	sialic acid binding Ig-like lectin 15	1.68	8.88	8.13	0.07	0.19	9.40E-03	2.62E-01	Multiple_Complex
TC1900009007.hg.1	ZSCAN4	zinc finger and SCAN domain containing 4	1.68	6.76	6	0.17	0.16	9.50E-03	2.62E-01	Coding
TC2000009604.hg.1	PMEPA1	prostate transmembrane protein, androgen induced 1	1.68	11.49	10.74	0.16	0.27	9.50E-03	2.62E-01	Multiple_Complex
TC1700008598.hg.1	MILR1	mast cell immunoglobulin-like receptor 1	1.68	6.51	5.76	0.26	0.54	2.81E-02	3.61E-01	Multiple_Complex
TSUnmapped00000492.hg.1	KAT6B	K(lysine) acetyltransferase 6B	1.68	8.79	8.04	0.08	0.03	5.30E-03	2.15E-01	Coding
TC1900011452.hg.1	PTPRH	protein tyrosine phosphatase, receptor type, H	1.68	7.37	6.62	0.39	0.37	1.87E-02	3.25E-01	Multiple_Complex
TC0900008790.hg.1	ZBTB43	zinc finger and BTB domain containing 43	1.68	7.2	6.45	0.05	0.03	1.69E-02	3.12E-01	Multiple_Complex
TC0600011387.hg.1	LINC00243	long intergenic non-protein coding RNA 243	1.68	6.55	5.8	0.03	0.65	3.60E-02	3.87E-01	NonCoding
TC1000010256.hg.1	EPC1	enhancer of polycomb homolog 1 (Drosophila)	1.68	10.55	9.8	0.08	0.09	4.50E-03	2.04E-01	Multiple_Complex
TC1600011364.hg.1	NPIPB5	nuclear pore complex interacting protein family, member B5	1.68	11.68	10.93	0.08	0.04	6.40E-03	2.31E-01	Multiple_Complex
TC1400010748.hg.1	LINC01588	long intergenic non-protein coding RNA 1588	1.68	8.47	7.72	0.65	0.38	4.04E-02	3.99E-01	Multiple_Complex

TC0500012238.hg.1	HBEGF	heparin-binding EGF-like growth factor	1.68	7.96	7.21	0.18	0.43	1.32E-02	2.89E-01	Multiple_Complex
TC0X00008830.hg.1	TAZ	tafazzin	1.68	9.11	8.36	0.02	0.26	1.58E-02	3.07E-01	Multiple_Complex
TC1200008686.hg.1	CHST11	Transcript Identified by AceView, Entrez Gene ID(s) 50515	1.68	5.84	5.09	0.43	0.38	3.84E-02	3.94E-01	Unassigned
TC0900011980.hg.1	SEC16A	SEC16 homolog A, endoplasmic reticulum export factor	1.68	8.47	7.72	0.13	0.3	1.15E-02	2.80E-01	Multiple_Complex
TC0X00009069.hg.1	ARHGAP6	Rho GTPase activating protein 6	1.68	4.67	3.92	0.25	0.06	6.40E-03	2.31E-01	Multiple_Complex
TC1600006645.hg.1	FLYWCH1	Transcript Identified by AceView, Entrez Gene ID(s) 84256	1.68	7.37	6.62	0.6	0.21	2.60E-02	3.52E-01	Unassigned
TC1800006720.hg.1	ANKRD62	ankyrin repeat domain 62	1.68	5.53	4.78	0.19	0.28	2.54E-02	3.49E-01	Multiple_Complex
TC0600011463.hg.1	NEU1	sialidase 1 (lysosomal sialidase)	1.68	12.47	11.73	0.05	0.02	4.60E-03	2.06E-01	Multiple_Complex
TC0400012818.hg.1	CCNG2	cyclin G2	1.68	10.31	9.57	0.03	0.02	1.30E-02	2.88E-01	Multiple_Complex
TC0200015538.hg.1	KLF7	Kruppel-like factor 7 (ubiquitous)	1.68	7.5	6.76	0.7	0.1	2.95E-02	3.65E-01	Multiple_Complex
TC1400006537.hg.1	RNASE3	ribonuclease, RNase A family, 3	1.68	5.72	4.97	0.15	0.7	4.07E-02	4.00E-01	Coding
TC1200007043.hg.1	SLCO1C1	solute carrier organic anion transporter family, member 1C1	1.67	7.12	6.38	0.51	0.54	4.62E-02	4.18E-01	Multiple_Complex
TC0100012006.hg.1	KCNK1	potassium channel, two pore domain subfamily K, member 1	1.67	5.65	4.9	0.25	0.31	2.83E-02	3.62E-01	Multiple_Complex
TSUnmapped00000558.hg.1	HYOU1	hypoxia up-regulated 1	1.67	13.38	12.63	0.14	0.02	4.70E-03	2.10E-01	NonCoding
TC0200011849.hg.1	RAD51AP2	Transcript Identified by AceView, Entrez Gene ID(s) 729475	1.67	4.58	3.83	0.48	0.06	2.66E-02	3.57E-01	Unassigned
TC0X00010473.hg.1	TSC22D3	TSC22 domain family, member 3	1.67	8.66	7.91	0.15	0.05	1.04E-02	2.69E-01	Coding
TC1000011450.hg.1	RBP4	retinol binding protein 4, plasma	1.67	4.62	3.88	0.46	0.08	1.38E-02	2.93E-01	Multiple_Complex
TC0400006656.hg.1	MSX1	msh homeobox 1	1.67	4.58	3.84	0.28	0.06	1.09E-02	2.74E-01	Multiple_Complex

TC1100011011.hg.1	PRPF19	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_014502	1.67	5.48	4.74	0.7	0.27	4.68E-02	4.20E-01	NonCoding
TC1900012046.hg.1	RDH13	retinol dehydrogenase 13 (all-trans/9-cis)	1.67	9.13	8.39	0.02	0.51	4.14E-02	4.01E-01	Multiple_Complex
TC0200008930.hg.1	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	1.67	9.74	9	0.04	0.27	1.53E-02	3.04E-01	Multiple_Complex
TC1400008705.hg.1	SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8	1.67	8.36	7.62	0.02	0.05	2.93E-02	3.65E-01	Multiple_Complex
TC0300013979.hg.1	AMIGO3	adhesion molecule with Ig-like domain 3	1.67	6	5.26	0.2	0.11	6.00E-03	2.26E-01	Coding
TC0100018210.hg.1	SH3D21	SH3 domain containing 21	1.67	5.65	4.91	0.22	0.01	2.77E-02	3.59E-01	Multiple_Complex
TC0700011318.hg.1	ERV3-1; ZNF117	endogenous retrovirus group 3, member 1; zinc finger protein 117	1.67	6.01	5.27	0.38	0.28	1.35E-02	2.89E-01	Multiple_Complex
TC0100010184.hg.1	TTC24	tetratricopeptide repeat domain 24	1.67	10.04	9.3	0.47	0.14	3.00E-02	3.66E-01	Multiple_Complex
TC0800012076.hg.1	ARC	activity-regulated cytoskeleton-associated protein	1.67	6.27	5.53	0.21	0.4	1.62E-02	3.09E-01	Multiple_Complex
TC1700006655.hg.1	ENO3	enolase 3 (beta, muscle)	1.67	7.2	6.47	0	0.45	2.09E-02	3.34E-01	Multiple_Complex
TC2100006554.hg.1	POTED	POTE ankyrin domain family, member D	1.67	5.51	4.77	0.14	0.33	1.04E-02	2.69E-01	Coding
TC1400007154.hg.1	GNG2	guanine nucleotide binding protein (G protein), gamma 2	1.67	5.98	5.25	0.06	0.34	1.30E-02	2.88E-01	Multiple_Complex
TC2200008687.hg.1	TMEM184B	transmembrane protein 184B	1.67	8.05	7.32	0.15	0.63	3.44E-02	3.84E-01	Multiple_Complex
TC1900007108.hg.1	CALR	calreticulin	1.67	15.62	14.88	0.05	0.15	7.50E-03	2.46E-01	Multiple_Complex
TC1600011422.hg.1	CLEC18A	C-type lectin domain family 18, member A	1.67	7.34	6.61	0.28	0.27	2.39E-02	3.46E-01	Multiple_Complex
TC0900012156.hg.1	PALM2	paralemmin 2	1.66	5.01	4.28	0.1	0.35	3.16E-02	3.72E-01	Multiple_Complex
TC1100009248.hg.1	RNF26	ring finger protein 26	1.66	9.18	8.44	0.34	0.13	9.90E-03	2.67E-01	Coding
TC1900007181.hg.1	TECR; MIR639	trans-2,3-enoyl-CoA reductase; microRNA 639	1.66	12.95	12.22	0.24	0.03	7.90E-03	2.49E-01	Multiple_Complex

TC0600007602.hg.1	APOM	apolipoprotein M	1.66	5.86	5.13	0.01	0.26	2.73E-02	3.58E-01	Multiple_Complex
TC0400011053.hg.1	CXCL10	chemokine (C-X-C motif) ligand 10	1.66	5.6	4.86	0.46	0.2	3.88E-02	3.94E-01	Coding
TC2100008357.hg.1	C21orf2	chromosome 21 open reading frame 2	1.66	6.89	6.16	0.02	0.12	5.90E-03	2.25E-01	Multiple_Complex
TC2000009954.hg.1	ZGPAT; LIME1	zinc finger, CCCH-type with G-patch domain; Lck interacting transmembrane adaptor 1	1.66	5.95	5.22	0.23	0.12	8.80E-03	2.57E-01	Multiple_Complex
TC0100018443.hg.1	PLPP3	phospholipid phosphatase 3	1.66	10.74	10.01	0.22	0.24	4.11E-02	4.01E-01	Multiple_Complex
TC0500006648.hg.1	PAPD7	PAP associated domain containing 7	1.66	11.42	10.69	0.25	0.11	2.93E-02	3.65E-01	Multiple_Complex
TC0700011799.hg.1	HEPACAM2	HEPACAM family member 2	1.66	5.02	4.28	0.27	0	4.41E-02	4.11E-01	Multiple_Complex
TC0800009961.hg.1	CLU; MIR6843	clusterin; microRNA 6843	1.66	10.34	9.61	0.13	0.1	8.10E-03	2.50E-01	Multiple_Complex
TC0100018298.hg.1	INTS3	integrator complex subunit 3	1.66	11.9	11.17	0.14	0.17	1.60E-02	3.08E-01	Multiple_Complex
TC2200008932.hg.1	KIAA1644	KIAA1644	1.66	4.96	4.23	0.25	0.02	2.41E-02	3.46E-01	Coding
TC1100011606.hg.1	C2CD3	C2 calcium-dependent domain containing 3	1.66	10.5	9.77	0.27	0.05	1.52E-02	3.04E-01	Multiple_Complex
TC0200012997.hg.1	TGFA	transforming growth factor alpha	1.66	8.43	7.7	0.01	0.37	1.52E-02	3.04E-01	Multiple_Complex
TC0800011452.hg.1	RSPO2	R-spondin 2	1.66	4.94	4.21	0.18	0.31	1.26E-02	2.87E-01	Coding
TC0100013205.hg.1	ECE1	endothelin converting enzyme 1	1.66	13.36	12.63	0.06	0.01	5.50E-03	2.18E-01	Multiple_Complex
TC1100013229.hg.1	FXYD6; FXYD6-FXYD2; FXYD2	FXYD domain containing ion transport regulator 6; FXYD6-FXYD2 readthrough; FXYD domain containing ion transport regulator 2	1.66	5.68	4.95	0.13	0.28	3.64E-02	3.89E-01	Multiple_Complex
TSUnmapped00000282.hg.1	KAT6B	K(lysine) acetyltransferase 6B	1.66	8.03	7.3	0.04	0.21	1.64E-02	3.10E-01	Coding
TC0700008003.hg.1	CLIP2	CAP-GLY domain containing linker protein 2	1.66	6.41	5.68	0.08	0.53	2.41E-02	3.46E-01	Multiple_Complex
TC0900012067.hg.1	PNPLA7	patatin-like phospholipase domain containing 7	1.66	6.96	6.23	0.09	0.09	6.40E-03	2.31E-01	Multiple_Complex
TC1200012778.hg.1	LMNTD1	lamin tail domain containing 1	1.65	5.83	5.1	0.39	0.04	2.09E-02	3.34E-01	Coding

TC0100014040.hg.1	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	1.65	10.16	9.44	0.27	0.16	1.52E-02	3.04E-01	Multiple_Complex
TC1100013150.hg.1	TPH1	tryptophan hydroxylase 1	1.65	4.56	3.83	0.45	0.13	2.03E-02	3.31E-01	Multiple_Complex
TSUnmapped00000327.hg.1	HYOU1	hypoxia up-regulated 1	1.65	12.13	11.4	0.13	0.03	2.14E-02	3.34E-01	Coding
TC2200007101.hg.1	LINC01521	long intergenic non-protein coding RNA 1521	1.65	8.28	7.56	0.24	0.24	1.54E-02	3.04E-01	NonCoding
TC2000008268.hg.1	SLC23A2	solute carrier family 23 (ascorbic acid transporter), member 2	1.65	8	7.27	0.21	0.13	1.27E-02	2.87E-01	Multiple_Complex
TC0100018403.hg.1	ERRFI1	ERBB receptor feedback inhibitor 1	1.65	10.67	9.94	0.02	0.14	1.36E-02	2.91E-01	Multiple_Complex
TC1000011478.hg.1	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	1.65	3.86	3.14	0.62	0.16	3.27E-02	3.76E-01	Multiple_Complex
TC0100013293.hg.1	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	1.65	12.34	11.62	0.01	0.27	3.45E-02	3.84E-01	Multiple_Complex
TC0200007388.hg.1	LINC01126	long intergenic non-protein coding RNA 1126	1.65	5.21	4.49	0.09	0.06	5.60E-03	2.19E-01	Multiple_Complex
TC0X00007149.hg.1	TIMP1	TIMP metallopeptidase inhibitor 1	1.65	11.85	11.13	0.18	0	3.19E-02	3.72E-01	Multiple_Complex
TC0100016960.hg.1	SYT2	synaptotagmin II	1.65	5.92	5.2	0.7	0.11	4.09E-02	4.00E-01	Multiple_Complex
TC1500007304.hg.1	C15orf65	chromosome 15 open reading frame 65	1.65	9.29	8.57	0.4	0.04	2.52E-02	3.49E-01	Multiple_Complex
TC0200008911.hg.1	ZC3H6	zinc finger CCCH-type containing 6	1.65	7.35	6.63	0.19	0.3	1.94E-02	3.26E-01	Multiple_Complex
TC0Y00006825.hg.1	CDY1	chromodomain protein, Y-linked, 1	1.65	4.78	4.06	0.27	0.12	1.00E-02	2.68E-01	Coding
TC1600009958.hg.1	NPIPB4	nuclear pore complex interacting protein family, member B4	1.65	11.83	11.11	0.27	0.15	1.28E-02	2.87E-01	Multiple_Complex
TC0800010002.hg.1	DUSP4	dual specificity phosphatase 4	1.65	11.76	11.04	0.1	0.09	3.07E-02	3.69E-01	Multiple_Complex
TC1900007005.hg.1	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	1.65	14.8	14.08	0.26	0.11	1.14E-02	2.80E-01	Multiple_Complex

TC0800009865.hg.1	RP11-875O11.1; RHOBTB2	Salzman2013 ANTISENSE, CDS, coding, INTERNAL, intronic, OVCODE, OVERLAPTX, OVEXON, UTR3 best transcript NM_015178; novel transcript, antisense to RHOBTB2	1.65	7.38	6.67	0.25	0.23	3.68E-02	3.90E-01	NonCoding
TC0100009770.hg.1	NBPF12	neuroblastoma breakpoint family, member 12	1.65	10.94	10.22	0.13	0.11	1.53E-02	3.04E-01	Multiple_Complex
TC1000012480.hg.1	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	1.65	5.99	5.27	0.24	0.27	2.09E-02	3.34E-01	Coding
TC0700010181.hg.1	RSPH10B2; RSPH10B	radial spoke head 10 homolog B2 (Chlamydomonas); radial spoke head 10 homolog B (Chlamydomonas)	1.64	6.57	5.85	0.44	0.15	3.38E-02	3.81E-01	Multiple_Complex
TSUnmapped00000383.hg.1	HYOU1	hypoxia up-regulated 1	1.64	11.56	10.84	0.02	0.14	9.50E-03	2.62E-01	Coding
TC1100008010.hg.1	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	1.64	9.71	8.99	0.03	0.22	1.55E-02	3.05E-01	Multiple_Complex
TC1000008798.hg.1	SFR1	SWI5-dependent homologous recombination repair protein 1	1.64	9.09	8.38	0.02	0	8.50E-03	2.54E-01	Multiple_Complex
TC0700009462.hg.1	MTRNR2L6	MT-RNR2-like 6	1.64	10.38	9.66	0.24	0.26	1.62E-02	3.09E-01	Coding
TC0500009464.hg.1	LOC101928093; RP11-779O18.1	uncharacterized LOC101928093; novel transcript	1.64	4.97	4.26	0.33	0.11	1.40E-02	2.93E-01	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]	1.64	6.09	5.37	0.58	0.51	4.53E-02	4.15E-01	Multiple_Complex
TC2200007401.hg.1	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	1.64	4.94	4.22	0.02	0.15	1.21E-02	2.84E-01	Multiple_Complex
TC0600014247.hg.1	FAM65B	family with sequence similarity 65, member B	1.64	4.85	4.14	0.21	0.23	2.22E-02	3.40E-01	Multiple_Complex
TC0600013570.hg.1	ZBTB2	zinc finger and BTB domain containing 2	1.64	10.36	9.65	0.08	0.05	2.29E-02	3.41E-01	Multiple_Complex
TC1600007392.hg.1	SNX29P2; SNX29P1	sorting nexin 29 pseudogene 2; sorting nexin 29 pseudogene 1	1.64	5.82	5.1	0.18	0.11	1.98E-02	3.29E-01	Multiple_Complex

TC0900007029.hg.1	UBAP1	ubiquitin associated protein 1	1.64	10.16	9.45	0.13	0.06	7.20E-03	2.42E-01	Multiple_Complex
TC1100011485.hg.1	SHANK2	SH3 and multiple ankyrin repeat domains 2	1.64	6.51	5.8	0.24	0.1	9.50E-03	2.62E-01	Multiple_Complex
TC1600011372.hg.1	SULT1A4; SULT1A3	sulfotransferase family 1A member 4; sulfotransferase family 1A member 3	1.64	9.85	9.14	0.04	0.04	1.11E-02	2.75E-01	Multiple_Complex
TC1500010862.hg.1	ELL3	elongation factor RNA polymerase II-like 3	1.64	5.79	5.08	0.12	0.24	1.01E-02	2.68E-01	Multiple_Complex
TC1400008362.hg.1	TRAF3	TNF receptor-associated factor 3	1.64	8.78	8.06	0.21	0.62	3.86E-02	3.94E-01	Multiple_Complex
TC0100008366.hg.1	DIO1	deiodinase, iodothyronine, type I	1.64	4.53	3.81	0.06	0.03	1.81E-02	3.23E-01	Multiple_Complex
TC1600010825.hg.1	ZFHX3	zinc finger homeobox 3	1.64	7.04	6.32	0.41	0.13	1.42E-02	2.94E-01	Multiple_Complex
TC0100017500.hg.1	TMEM63A	transmembrane protein 63A	1.64	10.86	10.15	0.07	0.01	6.50E-03	2.31E-01	Multiple_Complex
TC0600007887.hg.1	ZFAND3	zinc finger, AN1-type domain 3	1.64	11.24	10.53	0.07	0.09	6.40E-03	2.31E-01	Multiple_Complex
TSUnmapped00000513.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	1.64	6.97	6.26	0.22	0.46	3.49E-02	3.84E-01	NonCoding
TC1500008695.hg.1	GOLGA8J; GOLGA8IP	golgin A8 family, member J; golgin A8 family, member I, pseudogene	1.64	4.54	3.83	0.34	0.35	4.32E-02	4.07E-01	Multiple_Complex
TC1500007763.hg.1	MYO9A	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_006901	1.64	5.41	4.7	0.49	0.34	2.99E-02	3.66E-01	NonCoding
TC1700010206.hg.1	PROCA1	protein interacting with cyclin A1	1.64	5.99	5.28	0.38	0.07	2.51E-02	3.49E-01	Multiple_Complex
TC0400012948.hg.1	EMCN	endomucin	1.64	5.87	5.16	0.09	0.22	2.03E-02	3.31E-01	Multiple_Complex
TC0200007821.hg.1	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.64	7.39	6.68	0.03	0.21	9.00E-03	2.59E-01	Multiple_Complex
TC1300008708.hg.1	ELF1	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_172373	1.64	5.7	4.99	0.57	0.24	3.23E-02	3.74E-01	NonCoding
TC0200009927.hg.1	MYO3B	myosin IIIB	1.64	4.65	3.94	0.59	0.34	4.90E-02	4.24E-01	Multiple_Complex
TC0800009247.hg.1	HSF1	heat shock transcription factor 1	1.64	7.49	6.78	0.41	0.1	3.91E-02	3.95E-01	Multiple_Complex

TC0100016035.hg.1	ETV3	ets variant 3	1.63	11.43	10.72	0	0.13	7.70E-03	2.48E-01	Multiple_Complex
TC0600010040.hg.1	FNDC1	fibronectin type III domain containing 1	1.63	4.83	4.12	0.16	0.22	8.90E-03	2.58E-01	Multiple_Complex
TC2100008222.hg.1	RIPK4	receptor-interacting serine-threonine kinase 4	1.63	6.46	5.75	0.23	0.19	9.40E-03	2.62E-01	Coding
TC0900010350.hg.1	APBA1	amyloid beta (A4) precursor protein-binding, family A, member 1	1.63	5.5	4.79	0.1	0.26	1.53E-02	3.04E-01	Multiple_Complex
TC0400006689.hg.1	MAN2B2	mannosidase, alpha, class 2B, member 2	1.63	7.91	7.2	0.23	0.4	1.71E-02	3.15E-01	Multiple_Complex
TC0300007257.hg.1	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)	1.63	4.99	4.28	0.36	0.2	2.29E-02	3.41E-01	Multiple_Complex
TC1200009967.hg.1	DUSP16	dual specificity phosphatase 16	1.63	11.97	11.27	0.18	0.13	2.44E-02	3.47E-01	Multiple_Complex
TC0300008532.hg.1	FBXO40	F-box protein 40	1.63	3.87	3.16	0.21	0.22	9.80E-03	2.65E-01	Coding
TC0300007161.hg.1	VIPR1	vasoactive intestinal peptide receptor 1	1.63	5.69	4.98	0.19	0.01	8.20E-03	2.50E-01	Multiple_Complex
TC2100006784.hg.1	JAM2	junctional adhesion molecule 2	1.63	4.58	3.88	0.22	0.51	3.04E-02	3.68E-01	Multiple_Complex
TC0200009393.hg.1	LOC101928161; AC010890.1; NCKAP5; spawfa	uncharacterized LOC101928161; Salzman2013 ANTISENSE, coding, INTERNAL, intronic, OVERLAPTX best transcript NM_207363; novel transcript, antisense to NCKAP5; Transcript Identified by AceView	1.63	6.04	5.33	0.08	0.43	2.27E-02	3.40E-01	NonCoding
TC1200009846.hg.1	LINC00612	long intergenic non-protein coding RNA 612	1.63	5.19	4.48	0.39	0.35	2.54E-02	3.49E-01	Multiple_Complex
TC0900012173.hg.1	GARNL3	GTPase activating Rap/RanGAP domain-like 3	1.63	9.52	8.82	0.42	0.11	1.92E-02	3.26E-01	Multiple_Complex
TC2200008907.hg.1	SCUBE1	signal peptide, CUB domain, EGF-like 1	1.63	5.02	4.31	0.34	0.32	1.84E-02	3.24E-01	Multiple_Complex
TC0500012107.hg.1	CXCL14	chemokine (C-X-C motif) ligand 14	1.63	4.5	3.79	0.58	0.26	3.12E-02	3.72E-01	Multiple_Complex
TC0700009060.hg.1	FAM71F1	family with sequence similarity 71, member F1	1.63	5.62	4.92	0.3	0.23	4.05E-02	3.99E-01	Multiple_Complex
TC1100013186.hg.1	SYVN1	synovial apoptosis inhibitor 1, synoviolin	1.63	11.59	10.89	0.13	0.05	6.40E-03	2.31E-01	Multiple_Complex
TC1200012543.hg.1	ANKLE2	ankyrin repeat and LEM domain containing 2	1.63	8.63	7.92	0.23	0.01	8.00E-03	2.49E-01	Multiple_Complex

TC0800006969.hg.1	DMTN	dematin actin binding protein	1.63	7.05	6.35	0.02	0.31	3.26E-02	3.76E-01	Multiple_Complex
TC0100015445.hg.1	TBX15	T-box 15	1.63	5.49	4.79	0.2	0.27	3.70E-02	3.90E-01	Multiple_Complex
TC0700009493.hg.1	ZYX	zyxin	1.62	10.15	9.45	0.11	0.54	4.42E-02	4.11E-01	Multiple_Complex
TC0400012759.hg.1	FAM193A	family with sequence similarity 193, member A	1.62	9.26	8.56	0.11	0.11	7.70E-03	2.48E-01	Multiple_Complex
TC1900009984.hg.1	UNC13A	unc-13 homolog A (C. elegans)	1.62	4.07	3.37	0.34	0.2	3.34E-02	3.80E-01	Multiple_Complex
TC1100007913.hg.1	MARK2	MAP/microtubule affinity-regulating kinase 2	1.62	7.75	7.05	0.41	0	3.77E-02	3.93E-01	Multiple_Complex
TC1700007780.hg.1	CASC3; MIR6866	cancer susceptibility candidate 3; microRNA 6866	1.62	10.3	9.6	0.3	0.12	1.08E-02	2.74E-01	Multiple_Complex
TC1700009394.hg.1	PRPF8	pre-mRNA processing factor 8	1.62	10.04	9.34	0.09	0.38	1.68E-02	3.12E-01	Multiple_Complex
TC1700009619.hg.1	DLG4	discs, large homolog 4 (Drosophila)	1.62	8.43	7.73	0.38	0.1	2.06E-02	3.32E-01	Multiple_Complex
TC0100018308.hg.1	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	1.62	6.18	5.48	0.3	0.18	1.75E-02	3.16E-01	Multiple_Complex
TC1900008050.hg.1	IFNL2	interferon, lambda 2	1.62	5.04	4.34	0.22	0.1	3.19E-02	3.72E-01	Coding
TSUnmapped00000411.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	1.62	10.27	9.57	0.02	0.42	2.72E-02	3.58E-01	Coding
TC1400009538.hg.1	DCAF5	DDB1 and CUL4 associated factor 5	1.62	8.79	8.1	0.14	0.22	9.20E-03	2.62E-01	Multiple_Complex
TC0200010165.hg.1	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	1.62	7.14	6.45	0.21	0.26	1.17E-02	2.82E-01	Multiple_Complex
TC0600008014.hg.1	MDFI	MyoD family inhibitor	1.62	9.28	8.59	0.14	0.17	2.38E-02	3.46E-01	Multiple_Complex
TSUnmapped00000474.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	1.62	9.48	8.78	0.15	0.28	2.28E-02	3.41E-01	Coding
TC0200014190.hg.1	AMMECR1L	AMMECR1 like	1.62	9.93	9.24	0.46	0.07	1.81E-02	3.23E-01	Multiple_Complex
TC1900006848.hg.1	CAMSAP3	calmodulin regulated spectrin-associated protein family, member 3	1.62	6.14	5.45	0.38	0.32	3.40E-02	3.82E-01	Multiple_Complex
TC2200007556.hg.1	MPPED1	metallophosphoesterase domain containing 1	1.62	5.07	4.37	0.14	0.56	3.53E-02	3.85E-01	Multiple_Complex

TC0900012126.hg.1	ANKRD20A3; ANKRD20A2	ankyrin repeat domain 20 family, member A3; ankyrin repeat domain 20 family, member A2	1.62	4.95	4.26	0.22	0.53	2.71E-02	3.58E-01	Multiple_Complex
TC2200008055.hg.1	PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	1.62	7.65	6.96	0.1	0.24	2.07E-02	3.33E-01	Multiple_Complex
TSUnmapped00000405.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	1.62	9.16	8.47	0.17	0.23	1.00E-02	2.68E-01	Coding
TC1100008045.hg.1	TSGA10IP	testis specific 10 interacting protein	1.62	7.27	6.57	0.41	0.1	4.78E-02	4.21E-01	Multiple_Complex
TC1400006457.hg.1	POTEM; POTEG	POTE ankyrin domain family, member M; POTE ankyrin domain family, member G	1.62	5.45	4.76	0.18	0.09	3.62E-02	3.87E-01	Coding
TC1100006484.hg.1	EPS8L2	EPS8-like 2	1.62	8.24	7.55	0.14	0.52	2.72E-02	3.58E-01	Multiple_Complex
TC1700006547.hg.1	SGSM2	small G protein signaling modulator 2	1.62	9.06	8.37	0.38	0.37	3.07E-02	3.69E-01	Multiple_Complex
TC1700012321.hg.1	TBC1D3B; TBC1D3H; TBC1D3I; TBC1D3F; TBC1D3G	TBC1 domain family, member 3B; TBC1 domain family, member 3H; TBC1 domain family, member 3I; TBC1 domain family, member 3F; TBC1 domain family, member 3G	1.62	5.03	4.34	0.17	0.21	1.49E-02	3.03E-01	Multiple_Complex
TC1900010707.hg.1	SERTAD3	SERTA domain containing 3	1.62	7.88	7.19	0.22	0.11	3.09E-02	3.71E-01	Multiple_Complex
TC1900009964.hg.1	GTPBP3	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001195422	1.62	5.35	4.65	0.43	0.02	3.02E-02	3.67E-01	NonCoding
TC0M00006437.hg.1	COX2	cytochrome c oxidase subunit II	1.61	14.26	13.57	0.08	0.08	7.30E-03	2.44E-01	Multiple_Complex
TC0100009370.hg.1	UBL4B	ubiquitin-like 4B	1.61	6.17	5.48	0.21	0.03	3.43E-02	3.83E-01	Coding
TC1100012651.hg.1	OR10G7	olfactory receptor, family 10, subfamily G, member 7	1.61	4.34	3.64	0.05	0.08	1.59E-02	3.07E-01	Coding
TC0600007792.hg.1	PPARD	peroxisome proliferator-activated receptor delta	1.61	8.98	8.29	0.07	0.03	9.40E-03	2.62E-01	Multiple_Complex
TC0200014771.hg.1	FAP	fibroblast activation protein alpha	1.61	5.22	4.53	0.65	0.18	3.78E-02	3.93E-01	Multiple_Complex
TC1700012383.hg.1	OMG	oligodendrocyte myelin glycoprotein	1.61	5.03	4.34	0.57	0.41	4.21E-02	4.02E-01	Multiple_Complex
TC0100007117.hg.1	ARHGEF10L	Rho guanine nucleotide exchange factor 10 like	1.61	6.41	5.72	0.33	0.55	3.92E-02	3.95E-01	Multiple_Complex

TC1700008539.hg.1	MRC2	mannose receptor, C type 2	1.61	10.78	10.09	0.02	0.43	2.02E-02	3.31E-01	Multiple_Complex
TC0100007556.hg.1	PHACTR4	phosphatase and actin regulator 4	1.61	11.15	10.46	0.1	0.17	1.18E-02	2.83E-01	Multiple_Complex
TC0900008891.hg.1	LRRC8A	leucine rich repeat containing 8 family, member A	1.61	8.75	8.06	0.07	0.43	3.14E-02	3.72E-01	Multiple_Complex
TC1100010998.hg.1	MS4A4E	membrane-spanning 4-domains, subfamily A, member 4E	1.61	6.81	6.12	0.1	0.32	3.06E-02	3.69E-01	Multiple_Complex
TC1100006876.hg.1	MICALCL	MICAL C-terminal like	1.61	5.54	4.85	0.36	0.01	1.33E-02	2.89E-01	Multiple_Complex
TC0700007416.hg.1	RAMP3	receptor (G protein-coupled) activity modifying protein 3	1.61	4.91	4.22	0.35	0.21	1.94E-02	3.26E-01	Coding
TC1400009529.hg.1	ACTN1; HMGN1P3	actinin, alpha 1; high mobility group nucleosome binding domain 1 pseudogene 3	1.61	10.71	10.03	0.1	0.36	2.71E-02	3.58E-01	Multiple_Complex
TC0800008667.hg.1	NOV	nephroblastoma overexpressed	1.61	5.6	4.91	0.25	0.06	1.97E-02	3.29E-01	Multiple_Complex
TC1700008668.hg.1	PRKCA	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_002737	1.61	5.79	5.1	0.1	0.37	1.43E-02	2.95E-01	NonCoding
TC1700008974.hg.1	MGAT5B	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	1.61	6.84	6.15	0.3	0.09	1.32E-02	2.89E-01	Multiple_Complex
TC0300006856.hg.1	RARB	retinoic acid receptor, beta	1.61	3.87	3.18	0.27	0.26	2.70E-02	3.58E-01	Multiple_Complex
TC2100008233.hg.1	ZBTB21	zinc finger and BTB domain containing 21	1.61	12.27	11.58	0.15	0.01	7.90E-03	2.48E-01	Multiple_Complex
TC1600007964.hg.1	MT1B; MT1CP	metallothionein 1B; metallothionein 1C, pseudogene	1.61	9.84	9.16	0.1	0.22	1.00E-02	2.68E-01	Multiple_Complex
TC0600007625.hg.1	CYP21A1P; CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 1 pseudogene; cytochrome P450, family 21, subfamily A, polypeptide 2	1.61	5.9	5.21	0.22	0.02	2.85E-02	3.63E-01	Multiple_Complex

TC0700012960.hg.1	EZH2	Transcript Identified by AceView, Entrez Gene ID(s) 2146	1.6	4.95	4.27	0.35	0.24	3.39E-02	3.81E-01	Unassigned
TC2200008594.hg.1	MYH9	myosin, heavy chain 9, non-muscle	1.6	11.47	10.79	0.15	0.2	1.22E-02	2.84E-01	Multiple_Complex
TC1100011658.hg.1	MAP6	microtubule associated protein 6	1.6	7.11	6.43	0.4	0.18	3.93E-02	3.96E-01	Multiple_Complex
TC0700008617.hg.1	SH2B2	SH2B adaptor protein 2	1.6	4.33	3.65	0.09	0.45	2.24E-02	3.40E-01	Multiple_Complex
TC0100015698.hg.1	HIST2H3D	histone cluster 2, H3d	1.6	10.45	9.76	0.26	0.23	2.48E-02	3.48E-01	Coding
TC0700007370.hg.1	AEBP1; MIR4649	AE binding protein 1; microRNA 4649	1.6	7.58	6.9	0.08	0.29	4.49E-02	4.14E-01	Multiple_Complex
TC1700010563.hg.1	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	1.6	9.14	8.46	0.23	0.04	1.69E-02	3.13E-01	Multiple_Complex
TC0600012670.hg.1	SIM1	single-minded family bHLH transcription factor 1	1.6	5.13	4.45	0.1	0.27	1.31E-02	2.89E-01	Multiple_Complex
TC0100015629.hg.1	FMO5	flavin containing monooxygenase 5	1.6	4.29	3.61	0.44	0.25	4.03E-02	3.98E-01	Multiple_Complex
TC1100008188.hg.1	PPP6R3	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001164162	1.6	8.09	7.41	0.26	0.52	3.28E-02	3.76E-01	NonCoding
TC1000011596.hg.1	DNMBP	dynamin binding protein	1.6	10.09	9.41	0.15	0.17	1.27E-02	2.87E-01	Multiple_Complex
TC1900011106.hg.1	NUCB1	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_006184	1.6	5.54	4.86	0.22	0.26	1.33E-02	2.89E-01	NonCoding
TC0300008183.hg.1	CEP97	Transcript Identified by AceView, Entrez Gene ID(s) 79598	1.6	6.88	6.2	0.09	0.2	9.50E-03	2.62E-01	Unassigned
TC0X00011364.hg.1	ZNF630	zinc finger protein 630	1.6	5.22	4.55	0.08	0.32	1.39E-02	2.93E-01	Multiple_Complex
TC1700006740.hg.1	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	1.6	7.73	7.06	0.14	0.01	3.59E-02	3.87E-01	Multiple_Complex
TC1000011445.hg.1	MYOF	myoferlin	1.6	9.18	8.5	0.13	0	4.60E-02	4.18E-01	Multiple_Complex
TC0200011503.hg.1	PXDN	peroxidasin	1.6	12.25	11.57	0.02	0.11	9.50E-03	2.62E-01	Multiple_Complex
TC1300006643.hg.1	ATP8A2	ATPase, aminophospholipid transporter, class I, type 8A, member 2	1.6	5.89	5.21	0.07	0.41	2.19E-02	3.37E-01	Multiple_Complex

TC0100013636.hg.1	RNF19B	ring finger protein 19B	1.6	7.28	6.61	0.44	0.07	1.91E-02	3.26E-01	Multiple_Complex
TC1200010011.hg.1	HIST4H4	histone cluster 4, H4	1.6	6.91	6.24	0.24	0.02	1.52E-02	3.04E-01	Multiple_Complex
TC0200015865.hg.1	SCG2	secretogranin II	1.6	5.3	4.62	0.13	0.42	2.54E-02	3.49E-01	Coding
TC1400010771.hg.1	ANGEL1	angel homolog 1 (Drosophila)	1.6	6.98	6.31	0.03	0.58	3.53E-02	3.85E-01	Multiple_Complex
TC1100008120.hg.1	KDM2A	lysine (K)-specific demethylase 2A	1.6	9.53	8.85	0.09	0	1.87E-02	3.25E-01	Multiple_Complex
TC2000008231.hg.1	SPEF1	sperm flagellar 1	1.6	6.32	5.64	0.12	0.57	3.42E-02	3.83E-01	Multiple_Complex
TC1000007024.hg.1	KIAA1217	KIAA1217	1.6	4.67	3.99	0.24	0.01	1.02E-02	2.68E-01	Multiple_Complex
TC1700009809.hg.1	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	1.6	5.79	5.12	0.09	0.36	2.27E-02	3.40E-01	Coding
TC1700011205.hg.1	C17orf67	chromosome 17 open reading frame 67	1.6	6.82	6.14	0.15	0.17	2.82E-02	3.61E-01	Multiple_Complex
TC1500008187.hg.1	AKAP13; MIR7706	A kinase (PRKA) anchor protein 13; microRNA 7706	1.6	10.96	10.29	0.08	0.24	1.28E-02	2.87E-01	Multiple_Complex
TC0300010077.hg.1	LMLN	leishmanolysin-like (metallopeptidase M8 family)	1.6	7.05	6.37	0	0.27	1.37E-02	2.93E-01	Multiple_Complex
TC1100010885.hg.1	TNKS1BP1	tankyrase 1 binding protein 1	1.6	7.84	7.17	0.04	0.08	2.52E-02	3.49E-01	Multiple_Complex
TC0100008653.hg.1	IL12RB2	interleukin 12 receptor, beta 2	1.6	5.93	5.25	0.03	0.27	1.95E-02	3.27E-01	Multiple_Complex
TC1100013109.hg.1	GRAMD1B	GRAM domain containing 1B	1.6	13.02	12.35	0.15	0.04	1.03E-02	2.69E-01	Multiple_Complex
TC0400009526.hg.1	C4orf47	chromosome 4 open reading frame 47	1.59	8.04	7.37	0.33	0.14	1.92E-02	3.26E-01	Multiple_Complex
TSUnmapped00000374.hg.1	DUSP16	dual specificity phosphatase 16	1.59	10.69	10.01	0.15	0.14	2.75E-02	3.59E-01	Coding
TC0400009258.hg.1	PALLD	palladin, cytoskeletal associated protein	1.59	12.18	11.51	0.14	0.04	1.09E-02	2.74E-01	Multiple_Complex
TC1400007444.hg.1	PPP1R36	protein phosphatase 1, regulatory subunit 36	1.59	5.79	5.12	0.16	0.39	3.51E-02	3.85E-01	Multiple_Complex
TC1600011505.hg.1	NPIPB4	nuclear pore complex interacting protein family, member B4	1.59	11.35	10.68	0.23	0.11	2.31E-02	3.41E-01	Multiple_Complex

TC1900011382.hg.1	MYADM	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_001020819	1.59	8.47	7.8	0.14	0.05	1.19E-02	2.83E-01	NonCoding
TC0100012849.hg.1	CASZ1	castor zinc finger 1	1.59	6.78	6.11	0.17	0.42	2.45E-02	3.47E-01	Multiple_Complex
TC1900011639.hg.1	STK11	serine/threonine kinase 11	1.59	7.04	6.37	0.27	0.28	1.67E-02	3.12E-01	Multiple_Complex
TC1100007448.hg.1	DGKZ	diacylglycerol kinase, zeta	1.59	5.82	5.15	0.29	0.04	2.02E-02	3.31E-01	Multiple_Complex
TC1200009890.hg.1	CLEC1A	C-type lectin domain family 1, member A	1.59	4.79	4.12	0.53	0.12	3.52E-02	3.85E-01	Coding
TC0300007529.hg.1	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3	1.59	7.1	6.43	0	0.33	4.53E-02	4.15E-01	Multiple_Complex
TC2100007263.hg.1	PDE9A	phosphodiesterase 9A	1.59	9.25	8.58	0.2	0.28	1.87E-02	3.25E-01	Multiple_Complex
TC1900010538.hg.1	ZNF790	zinc finger protein 790	1.59	6.14	5.47	0.34	0.13	2.48E-02	3.48E-01	Coding
TC1500010072.hg.1	SIN3A	SIN3 transcription regulator family member A	1.59	11.97	11.3	0.21	0.15	1.23E-02	2.84E-01	Multiple_Complex
TC0200007362.hg.1	MTA3	Transcript Identified by AceView, Entrez Gene ID(s) 57504	1.59	5.72	5.05	0.26	0.09	3.56E-02	3.86E-01	Unassigned
TC0700010412.hg.1	SP8	Sp8 transcription factor	1.59	5.46	4.8	0.25	0.2	2.10E-02	3.34E-01	Coding
TC0300010949.hg.1	LTF	lactotransferrin	1.59	5.59	4.92	0.03	0.31	1.68E-02	3.12E-01	Multiple_Complex
TC0600007700.hg.1	KIFC1	kinesin family member C1	1.59	9.18	8.52	0.13	0.02	1.54E-02	3.04E-01	Multiple_Complex
TC0200016775.hg.1	ATG9A	autophagy related 9A	1.59	10.97	10.31	0	0.13	3.09E-02	3.71E-01	Multiple_Complex
TC0800009626.hg.1	DEFB134	defensin, beta 134	1.59	5.31	4.65	0.12	0	3.78E-02	3.93E-01	Coding
TC1200010562.hg.1	COL2A1	collagen, type II, alpha 1	1.58	6.78	6.12	0.1	0.24	2.24E-02	3.40E-01	Multiple_Complex
TSUnmapped00000310.hg.1	HYOU1	hypoxia up-regulated 1	1.58	10.11	9.45	0.07	0.04	8.60E-03	2.54E-01	Coding
TC1700007116.hg.1	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	1.58	8.38	7.72	0.13	0.12	3.90E-02	3.95E-01	Multiple_Complex
TC0400008879.hg.1	GAB1	GRB2-associated binding protein 1	1.58	9.67	9	0.26	0.04	1.85E-02	3.24E-01	Multiple_Complex

TC0Y00007319.hg.1	AKAP17A; SFRS17A	Homo sapiens A kinase (PRKA) anchor protein 17A (AKAP17A), transcript variant 1, mRNA.; Homo sapiens A kinase (PRKA) anchor protein 17A (AKAP17A), transcript variant 2, non-coding RNA.; A kinase (PRKA) anchor protein 17A [Source:HGNC Symbol;Acc:HGNC:18783]; Homo sapiens splicing factor, arginine/serine-rich 17A, mRNA (cDNA clone MGC:39904 IMAGE:5217247), complete cds.; Homo sapiens splicing factor, arginine/serine-rich 17A, mRNA (cDNA clone MGC:125365 IMAGE:40007662), complete cds.; Homo sapiens splicing factor, arginine/serine-rich 17A, mRNA (cDNA clone MGC:125366 IMAGE:40007663), complete cds.; Jeck2013 ANNOTATED, INTERNAL, ncRNA, OVCODE, OVEXON best transcript NR_027383	1.58	6.51	5.85	0.26	0.26	1.86E-02	3.25E-01	Multiple_Complex
TC1100013012.hg.1	STX3	syntaxin 3	1.58	10.4	9.74	0.05	0.12	3.03E-02	3.68E-01	Multiple_Complex
TC0200008904.hg.1	FBLN7	fibulin 7	1.58	4.52	3.86	0.43	0.33	3.36E-02	3.80E-01	Multiple_Complex
TC0600011876.hg.1	YIPF3	Yip1 domain family member 3	1.58	12.2	11.54	0.33	0.15	1.86E-02	3.25E-01	Multiple_Complex
TC0100018490.hg.1	LINGO4	leucine rich repeat and Ig domain containing 4	1.58	6.82	6.16	0.13	0.41	2.30E-02	3.41E-01	Coding
TC1200011727.hg.1	IGF1	insulin-like growth factor 1 (somatomedin C)	1.58	6.2	5.54	0.39	0.22	4.14E-02	4.01E-01	Multiple_Complex
TC0100013610.hg.1	FAM229A	family with sequence similarity 229, member A	1.58	5.5	4.84	0.02	0.02	1.14E-02	2.80E-01	Multiple_Complex
TC1900008075.hg.1	LGALS16	lectin, galactoside-binding, soluble, 16	1.58	4.23	3.57	0.03	0.09	1.94E-02	3.26E-01	Coding

TC1100009521.hg.1	APLP2	amyloid beta (A4) precursor-like protein 2	1.58	11.08	10.42	0.01	0.33	1.56E-02	3.06E-01	Multiple_Complex
TC0100012816.hg.1	CLSTN1	calsyntenin 1	1.58	9.62	8.96	0.13	0.43	2.39E-02	3.46E-01	Multiple_Complex
TC0300007679.hg.1	ATXN7	ataxin 7	1.58	10.38	9.72	0.19	0.31	2.36E-02	3.44E-01	Multiple_Complex
TC0900008740.hg.1	OLFML2A	olfactomedin like 2A	1.58	7.89	7.23	0.23	0.12	1.34E-02	2.89E-01	Coding
TC0600007832.hg.1	BRPF3	bromodomain and PHD finger containing 3	1.58	8.04	7.38	0.05	0.04	1.32E-02	2.89E-01	Multiple_Complex
TC0800012173.hg.1	EPPK1	epiplakin 1	1.58	11.35	10.69	0.03	0.11	3.46E-02	3.84E-01	Coding
TC1100007453.hg.1	MDK	midkine (neurite growth-promoting factor 2)	1.58	8.81	8.16	0.04	0.11	1.60E-02	3.08E-01	Multiple_Complex
TC0900007064.hg.1	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	1.58	7.05	6.39	0.18	0	1.57E-02	3.06E-01	Coding
TC0200012009.hg.1	DTNB	dystrobrevin beta	1.58	7.89	7.23	0.19	0.3	2.84E-02	3.63E-01	Multiple_Complex
TC1500008360.hg.1	SLCO3A1	solute carrier organic anion transporter family, member 3A1	1.58	10.4	9.74	0.47	0	2.54E-02	3.49E-01	Multiple_Complex
TC1900010581.hg.1	LOC100631378; AC016582.2; LOC728853	uncharacterized 100631378; Transcript Identified by AceView, Entrez Gene ID(s) 728853; novel transcript	1.58	4.55	3.89	0.16	0.13	1.45E-02	2.99E-01	NonCoding
TC2100006982.hg.1	LINC00649	long intergenic non-protein coding RNA 649	1.58	5.92	5.26	0.25	0.11	2.75E-02	3.59E-01	Multiple_Complex
TC1600006525.hg.1	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	1.58	6.19	5.53	0.06	0.38	3.79E-02	3.93E-01	Multiple_Complex
TC0200016481.hg.1	CTNNA2	catenin (cadherin-associated protein), alpha 2	1.58	4.44	3.79	0.08	0.25	2.72E-02	3.58E-01	NonCoding
TC0100016360.hg.1	SELL	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_000655	1.58	4.95	4.29	0.23	0.38	3.56E-02	3.86E-01	NonCoding
TC0100011269.hg.1	LINC00260	long intergenic non-protein coding RNA 260	1.58	6.52	5.86	0.17	0.14	3.69E-02	3.90E-01	Multiple_Complex
TC1900011328.hg.1	ZNF160	Transcript Identified by AceView, Entrez Gene ID(s) 90338	1.58	14.09	13.43	0.19	0.41	3.78E-02	3.93E-01	Coding

TC2200007309.hg.1	SH3BP1; PDXP	SH3-domain binding protein 1; pyridoxal (pyridoxine, vitamin B6) phosphatase	1.58	6.37	5.71	0.34	0.4	4.04E-02	3.99E-01	Multiple_Complex
TC2000007670.hg.1	SNAI1	snail family zinc finger 1	1.58	6.02	5.36	0.36	0.32	2.76E-02	3.59E-01	Coding
TC1200009768.hg.1	LPCAT3	lysophosphatidylcholine acyltransferase 3	1.58	9.97	9.31	0.32	0.3	2.30E-02	3.41E-01	Multiple_Complex
TC1900010943.hg.1	RTN2	reticulon 2	1.57	7.78	7.13	0.21	0.17	1.72E-02	3.16E-01	Multiple_Complex
TC1100008025.hg.1	SCYL1	SCY1-like, kinase-like 1	1.57	10.62	9.97	0	0.18	1.35E-02	2.89E-01	Multiple_Complex
TC1200011591.hg.1	NTN4	netrin 4	1.57	7.51	6.85	0.54	0.11	4.19E-02	4.02E-01	Multiple_Complex
TC0100009936.hg.1	BNIPL	BCL2/adenovirus E1B 19kD interacting protein like	1.57	5.34	4.68	0.14	0.07	1.26E-02	2.87E-01	Multiple_Complex
TC1700011390.hg.1	10-Mar	membrane associated ring finger 10	1.57	4.98	4.33	0.54	0.04	3.34E-02	3.80E-01	Multiple_Complex
TC1900006470.hg.1	BSG	basigin (Ok blood group)	1.57	15.29	14.64	0.21	0.2	1.40E-02	2.93E-01	Multiple_Complex
TC0100013437.hg.1	AHDC1	AT hook, DNA binding motif, containing 1	1.57	6.47	5.81	0.26	0.03	2.97E-02	3.65E-01	Multiple_Complex
TC0600013179.hg.1	OR2A4	olfactory receptor, family 2, subfamily A, member 4	1.57	4.16	3.51	0.26	0.34	2.32E-02	3.42E-01	Coding
TC1900008544.hg.1	RCN3	reticulocalbin 3, EF-hand calcium binding domain	1.57	8.3	7.65	0.46	0.38	4.54E-02	4.15E-01	Multiple_Complex
TC0100016296.hg.1	GPA33	glycoprotein A33 (transmembrane)	1.57	5.54	4.89	0.09	0.29	2.56E-02	3.50E-01	Multiple_Complex
TC0300007044.hg.1	GOLGA4	golgin A4	1.57	9.47	8.82	0.3	0.41	3.32E-02	3.79E-01	Multiple_Complex
TSUnmapped00000289.hg.1	RPL7A	ribosomal protein L7a	1.57	7.58	6.93	0.05	0.05	1.27E-02	2.87E-01	NonCoding
TC0700007392.hg.1	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	1.57	12.9	12.25	0.31	0.23	2.30E-02	3.41E-01	Multiple_Complex
TC0400007495.hg.1	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4	1.57	12.29	11.64	0.53	0.31	4.16E-02	4.01E-01	Multiple_Complex
TC0100006683.hg.1	HES3	hes family bHLH transcription factor 3	1.57	5.4	4.75	0.1	0.2	2.80E-02	3.60E-01	Coding
TC0200016494.hg.1	CNNM4	cyclin and CBS domain divalent metal cation transport mediator 4	1.57	7.4	6.75	0.23	0.43	2.94E-02	3.65E-01	Multiple_Complex

TC0300007438.hg.1	RBM15B	RNA binding motif protein 15B	1.57	8.47	7.82	0.14	0.2	2.26E-02	3.40E-01	Coding
TC0400007988.hg.1	THAP9	THAP domain containing 9	1.57	5.5	4.85	0.25	0.16	1.68E-02	3.12E-01	Multiple_Complex
TC0100015471.hg.1	ZNF697	zinc finger protein 697	1.57	6.34	5.69	0.16	0.36	2.80E-02	3.60E-01	Multiple_Complex
TC1900010502.hg.1	NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	1.57	5.32	4.68	0.23	0.04	2.13E-02	3.34E-01	Multiple_Complex
TC1900006978.hg.1	ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	1.57	5.6	4.95	0.06	0.36	2.06E-02	3.33E-01	Multiple_Complex
TC1700006709.hg.1	XAF1	XIAP associated factor 1	1.57	5.38	4.73	0.03	0.1	2.23E-02	3.40E-01	Multiple_Complex
TC1700010865.hg.1	PLCD3	phospholipase C, delta 3	1.57	9.61	8.97	0.07	0.13	3.05E-02	3.68E-01	Multiple_Complex
TC1000010312.hg.1	CUL2; RP11-297A16.2	Transcript Identified by AceView, Entrez Gene ID(s) 8453; novel transcript	1.57	5.61	4.97	0.09	0.12	2.21E-02	3.38E-01	NonCoding
TC1200007887.hg.1	MBD6	methyl-CpG binding domain protein 6	1.57	9.54	8.89	0.24	0.28	1.84E-02	3.24E-01	Multiple_Complex
TC1700007791.hg.1	RARA	retinoic acid receptor, alpha	1.56	8	7.36	0.14	0.17	1.35E-02	2.89E-01	Multiple_Complex
TC1600011522.hg.1	ZNF747	zinc finger protein 747	1.56	6.72	6.07	0.5	0.04	3.48E-02	3.84E-01	Multiple_Complex
TC0500013277.hg.1	MAML1	mastermind-like transcriptional coactivator 1	1.56	7.99	7.34	0.03	0.01	2.25E-02	3.40E-01	Multiple_Complex
TC1600011368.hg.1	LAT	linker for activation of T-cells	1.56	6.38	5.73	0.03	0.3	4.35E-02	4.08E-01	Multiple_Complex
TSUnmapped00000389.hg.1	KAT6B	K(lysine) acetyltransferase 6B	1.56	6.49	5.85	0.26	0.25	1.95E-02	3.27E-01	Coding
TC1500010889.hg.1	CELF6	CUGBP, Elav-like family member 6	1.56	4.38	3.74	0.43	0.38	4.09E-02	4.00E-01	Multiple_Complex
TC0900012231.hg.1	SHB	Src homology 2 domain containing adaptor protein B	1.56	9.01	8.37	0.08	0.04	1.03E-02	2.69E-01	Multiple_Complex
TC0X00006460.hg.1	ASMT; AKAP17A	acetylserotonin O-methyltransferase; A kinase (PRKA) anchor protein 17A	1.56	5.12	4.48	0.03	0.17	1.64E-02	3.10E-01	Multiple_Complex

TC0Y00007320.hg.1	ASMT; SFRS17AandASMT	Homo sapiens acetylserotonin O-methyltransferase (ASMT), transcript variant 1, mRNA.; Homo sapiens acetylserotonin O-methyltransferase (ASMT), transcript variant 3, mRNA.; acetylserotonin O-methyltransferase [Source:HGNC Symbol;Acc:HGNC:750]; Homo sapiens acetylserotonin O-methyltransferase, mRNA (cDNA clone MGC:2145 IMAGE:3356470), complete cds.; Transcript Identified by AceView, Entrez Gene ID(s) 438; 8227, RefSeq ID(s) NM_001171038	1.56	5.12	4.48	0.03	0.17	1.64E-02	3.10E-01	Multiple_Complex
TC1500010752.hg.1	TLN2	talin 2	1.56	5.43	4.79	0.22	0.24	4.03E-02	3.98E-01	NonCoding
TC2000010009.hg.1	BLCAP	bladder cancer associated protein	1.56	5.54	4.89	0.21	0.15	3.14E-02	3.72E-01	NonCoding
TSUnmapped00000172.hg.1	TGM4	transglutaminase 4	1.56	5.11	4.47	0.43	0.26	3.40E-02	3.82E-01	Coding
TC1600007967.hg.1	MT1IP	metallothionein 1I, pseudogene	1.56	5.58	4.94	0.16	0.07	2.17E-02	3.35E-01	Multiple_Complex
TC0800011621.hg.1	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.56	5.11	4.47	0	0.07	4.88E-02	4.24E-01	NonCoding
TC2100006433.hg.1	ICOSLG	inducible T-cell co-stimulator ligand	1.56	6.04	5.4	0.04	0.05	1.00E-02	2.68E-01	Coding
TC1900007410.hg.1	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	1.56	6.86	6.22	0.31	0.03	1.95E-02	3.27E-01	Multiple_Complex
TC0100011920.hg.1	GALNT2	polypeptide N-acetylgalactosaminyltransferase 2	1.56	9.45	8.8	0.01	0.04	3.70E-02	3.90E-01	Multiple_Complex
TC0900009333.hg.1	FAM157B	family with sequence similarity 157, member B	1.56	8.05	7.41	0.43	0.04	3.47E-02	3.84E-01	Multiple_Complex
TC1900010043.hg.1	TMEM161A	transmembrane protein 161A	1.56	7.19	6.55	0.1	0.11	4.32E-02	4.07E-01	Multiple_Complex

TC1600009731.hg.1	COG7	component of oligomeric golgi complex 7	1.56	9	8.36	0.12	0.22	2.69E-02	3.58E-01	Multiple_Complex
TC0400012868.hg.1	STOX2	storkhead box 2	1.56	10.17	9.53	0.1	0.25	2.33E-02	3.42E-01	Multiple_Complex
TC0300012190.hg.1	KPNA1	Transcript Identified by AceView, Entrez Gene ID(s) 3836	1.56	8.59	7.95	0.04	0.15	1.91E-02	3.26E-01	Unassigned
TC0700012584.hg.1	UBE2H	ubiquitin conjugating enzyme E2H	1.56	11.68	11.04	0.05	0.17	1.36E-02	2.91E-01	Multiple_Complex
TC1700012241.hg.1	TBC1D3L; TBC1D3E	TBC1 domain family, member 3L; TBC1 domain family, member 3E	1.56	6.99	6.35	0.12	0.61	4.73E-02	4.21E-01	Coding
TC1500009787.hg.1	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	1.56	5.01	4.37	0.18	0.27	1.82E-02	3.23E-01	Coding
TC1200009547.hg.1	SLC6A13	solute carrier family 6 (neurotransmitter transporter), member 13	1.56	5.72	5.08	0.08	0.46	4.15E-02	4.01E-01	Multiple_Complex
TC1100011083.hg.1	AHNAK	AHNAK nucleoprotein	1.56	6.71	6.07	0.11	0.22	4.21E-02	4.02E-01	Multiple_Complex
TC0X00009603.hg.1	SSX9	synovial sarcoma, X breakpoint 9	1.56	4.49	3.85	0.26	0.32	3.17E-02	3.72E-01	Multiple_Complex
TC0300008787.hg.1	RHO	rhodopsin	1.56	5.4	4.76	0.41	0.13	3.68E-02	3.90E-01	Multiple_Complex
TC0700010665.hg.1	NEUROD6	neuronal differentiation 6	1.56	4.26	3.62	0.15	0.1	4.15E-02	4.01E-01	Coding
TC0700008072.hg.1	RHBDD2	rhomboid domain containing 2	1.56	10.4	9.77	0.09	0.07	2.88E-02	3.64E-01	Multiple_Complex
TC1200010865.hg.1	ITGA7	integrin alpha 7	1.56	6.27	5.63	0.12	0.22	2.11E-02	3.34E-01	Multiple_Complex
TC1600007317.hg.1	KIAA0556	KIAA0556	1.56	8.68	8.05	0.12	0.04	3.50E-02	3.84E-01	Multiple_Complex
TC0100017258.hg.1	BATF3	basic leucine zipper transcription factor, ATF-like 3	1.55	6.12	5.48	0.18	0.1	1.48E-02	3.02E-01	Multiple_Complex
TC0600011441.hg.1	BAG6	BCL2 associated athanogene 6	1.55	13.36	12.73	0.15	0.08	3.03E-02	3.68E-01	Multiple_Complex
TC0600013341.hg.1	GVQW2	GVQW motif containing 2	1.55	7.62	6.98	0.21	0.29	2.78E-02	3.59E-01	Multiple_Complex
TC0X00011168.hg.1	BCAP31	B-cell receptor-associated protein 31	1.55	11.58	10.95	0.3	0.13	1.90E-02	3.26E-01	Multiple_Complex
TSUnmapped00000324.hg.1	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	1.55	6.52	5.89	0.08	0.05	2.82E-02	3.61E-01	Coding

TC1900010802.hg.1	LIPE	lipase, hormone-sensitive	1.55	5.03	4.4	0.5	0.09	4.54E-02	4.15E-01	Multiple_Complex
TC0900011523.hg.1	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.55	15.27	14.64	0.05	0.09	1.23E-02	2.84E-01	Multiple_Complex
TC1500010788.hg.1	CHD2; MIR3175	chromodomain helicase DNA binding protein 2; microRNA 3175	1.55	14.07	13.44	0.11	0.06	1.29E-02	2.87E-01	Multiple_Complex
TC0300011446.hg.1	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	1.55	4.57	3.94	0.15	0.05	1.49E-02	3.03E-01	Multiple_Complex
TC0800009072.hg.1	CHRAC1	Transcript Identified by AceView, Entrez Gene ID(s) 54108	1.55	4.41	3.78	0.07	0.47	3.21E-02	3.73E-01	Unassigned
TC2000007114.hg.1	KIF3B	kinesin family member 3B	1.55	6.49	5.86	0.08	0.22	3.54E-02	3.86E-01	Multiple_Complex
TC2200008781.hg.1	MKL1	megakaryoblastic leukemia (translocation) 1	1.55	9.03	8.4	0.18	0.29	2.58E-02	3.51E-01	Multiple_Complex
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	1.55	6.65	6.02	0.11	0.34	2.38E-02	3.46E-01	NonCoding

TC1100011331.hg.1	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme	1.55	12.46	11.82	0.04	0.08	1.62E-02	3.09E-01	Multiple_Complex
TC0400011535.hg.1	DKK2	dickkopf WNT signaling pathway inhibitor 2	1.55	5.48	4.84	0.05	0.07	1.75E-02	3.16E-01	Multiple_Complex
TC0300013123.hg.1	PLD1	phospholipase D1, phosphatidylcholine-specific	1.55	6.24	5.61	0.08	0.54	3.97E-02	3.96E-01	Multiple_Complex
TC1500007602.hg.1	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	1.55	6.6	5.97	0.1	0.28	2.45E-02	3.47E-01	Multiple_Complex
TC0700006636.hg.1	ANKRD61	ankyrin repeat domain 61	1.55	4.11	3.48	0.37	0.24	3.48E-02	3.84E-01	Coding
TC1700011818.hg.1	JMJD6	jumonji domain containing 6	1.55	11.3	10.67	0.13	0.07	2.52E-02	3.49E-01	Multiple_Complex
TC1700009385.hg.1	SLC43A2	solute carrier family 43 (amino acid system L transporter), member 2	1.55	10.14	9.51	0.36	0.28	2.73E-02	3.58E-01	Multiple_Complex
TC1600006965.hg.1	SHISA9	shisa family member 9	1.55	7.41	6.78	0.49	0.07	4.50E-02	4.14E-01	Multiple_Complex
TC1900011920.hg.1	ZNF98	zinc finger protein 98	1.55	8.46	7.83	0.3	0.33	3.04E-02	3.68E-01	Multiple_Complex
TC1600007007.hg.1	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	1.55	10.35	9.72	0.53	0.02	4.25E-02	4.04E-01	Multiple_Complex
TC0800009237.hg.1	GPAA1	glycosylphosphatidylinositol anchor attachment 1	1.55	12.54	11.91	0.07	0.12	1.25E-02	2.87E-01	Multiple_Complex
TC1900010499.hg.1	PRODH2	proline dehydrogenase (oxidase) 2	1.55	5.69	5.06	0.19	0.14	2.92E-02	3.65E-01	Multiple_Complex
TC0100015947.hg.1	THBS3	Salzman2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_007112	1.55	14.5	13.88	0.07	0.33	2.16E-02	3.34E-01	NonCoding
TC1000009397.hg.1	DPYSL4	dihydropyrimidinase-like 4	1.54	4.7	4.08	0.11	0.23	2.53E-02	3.49E-01	Multiple_Complex
TC0600012502.hg.1	GJB7	gap junction protein beta 7	1.54	5.4	4.77	0.07	0.07	1.60E-02	3.08E-01	Multiple_Complex
TC1100012473.hg.1	MPZL3	myelin protein zero-like 3	1.54	9.26	8.63	0.33	0.36	3.80E-02	3.93E-01	Multiple_Complex
TSUnmapped00000437.hg.1	DGKD	diacylglycerol kinase, delta 130kDa	1.54	8.96	8.33	0.3	0.24	2.98E-02	3.66E-01	Coding
TC1600011451.hg.1	TCF25	transcription factor 25 (basic helix-loop-helix)	1.54	11	10.37	0.07	0.1	1.74E-02	3.16E-01	Multiple_Complex

TC1000006466.hg.1	WDR37	WD repeat domain 37	1.54	10.15	9.53	0.32	0.43	3.79E-02	3.93E-01	Multiple_Complex
TC0X00010445.hg.1	ESX1	ESX homeobox 1	1.54	5.1	4.47	0	0.28	2.45E-02	3.47E-01	Coding
TC0100015561.hg.1	NBPF15	neuroblastoma breakpoint family, member 15	1.54	8.45	7.82	0.4	0.24	3.60E-02	3.87E-01	Multiple_Complex
TC1900006999.hg.1	DNM2	Transcript Identified by AceView, Entrez Gene ID(s) 1785	1.54	10.7	10.08	0.07	0.25	2.08E-02	3.34E-01	Unassigned
TC1600008156.hg.1	LRRC36	leucine rich repeat containing 36	1.54	4.42	3.79	0.03	0.04	3.38E-02	3.81E-01	Multiple_Complex
TC0800011697.hg.1	FER1L6-AS1	FER1L6 antisense RNA 1	1.54	6.09	5.46	0.21	0.03	1.55E-02	3.05E-01	Multiple_Complex
TC1800008584.hg.1	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	1.54	10.25	9.63	0.58	0.15	4.82E-02	4.21E-01	Multiple_Complex
TC0X00008646.hg.1	TMEM257	transmembrane protein 257	1.54	4.41	3.78	0.11	0.06	1.33E-02	2.89E-01	Coding
TC0100015830.hg.1	FLG	filaggrin	1.54	4.51	3.88	0.08	0.41	2.92E-02	3.65E-01	Multiple_Complex
TC0200016382.hg.1	PDCD1	programmed cell death 1	1.54	8.14	7.52	0.12	0.37	3.20E-02	3.72E-01	Coding
TC1700010241.hg.1	NUFIP2; rerdy	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_020772; Transcript Identified by AceView	1.54	6.31	5.69	0.3	0.31	4.31E-02	4.07E-01	Multiple_Complex
TC0600013395.hg.1	NMBR	neuromedin B receptor	1.54	5.1	4.48	0.06	0.03	2.65E-02	3.56E-01	Multiple_Complex
TC1900011756.hg.1	PVR	poliovirus receptor	1.54	9.34	8.72	0.21	0.13	1.76E-02	3.17E-01	Multiple_Complex
TC1900011930.hg.1	U2AF1L4	U2 small nuclear RNA auxiliary factor 1-like 4	1.54	9.74	9.12	0.14	0.34	2.93E-02	3.65E-01	Multiple_Complex
TC2200008888.hg.1	A4GALT	alpha 1,4-galactosyltransferase	1.54	6.17	5.55	0.16	0.07	1.99E-02	3.29E-01	Multiple_Complex
TC0500012450.hg.1	TIGD6	tigger transposable element derived 6	1.54	4.94	4.32	0.17	0.03	2.55E-02	3.50E-01	Multiple_Complex
TC1200009103.hg.1	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	1.54	11.16	10.54	0.36	0.22	2.86E-02	3.63E-01	Multiple_Complex

TC1900008051.hg.1	IFNL1	interferon, lambda 1	1.54	5.82	5.19	0.01	0.22	2.85E-02	3.63E-01	Coding
TC1000008081.hg.1	KAT6B	K(lysine) acetyltransferase 6B	1.54	9.12	8.5	0.09	0.23	2.11E-02	3.34E-01	Multiple_Complex
TC0M00006443.hg.1	CYTB	cytochrome b	1.54	15.14	14.52	0.04	0.03	1.34E-02	2.89E-01	Multiple_Complex
TSUnmapped00000088.hg.1	DUSP16	dual specificity phosphatase 16	1.54	10.66	10.05	0.36	0.21	4.25E-02	4.04E-01	Coding
TC0400009137.hg.1	FNIP2	folliculin interacting protein 2	1.54	8.72	8.1	0.31	0.22	4.82E-02	4.21E-01	Multiple_Complex
TC0100011552.hg.1	VASH2	vasohibin 2	1.54	5.83	5.21	0.34	0.03	4.25E-02	4.04E-01	Multiple_Complex
TC1600008189.hg.1	PLA2G15	phospholipase A2, group XV	1.54	9.58	8.96	0.01	0.02	1.47E-02	3.02E-01	Multiple_Complex
TC2100008355.hg.1	ICOSLG	inducible T-cell co-stimulator ligand	1.54	5.5	4.88	0.05	0.19	2.97E-02	3.65E-01	Multiple_Complex
TC1900007356.hg.1	KCNN1	potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 1	1.54	6.17	5.55	0.38	0.05	4.76E-02	4.21E-01	Multiple_Complex
TC1200012714.hg.1	HSPB8	heat shock 22kDa protein 8	1.53	9.71	9.09	0.04	0.04	3.82E-02	3.94E-01	Multiple_Complex
TC0800009529.hg.1	PPP1R3B	protein phosphatase 1, regulatory subunit 3B	1.53	6.45	5.83	0.28	0.23	2.34E-02	3.43E-01	Coding
TC1900010856.hg.1	PLAUR	plasminogen activator, urokinase receptor	1.53	10.26	9.65	0.27	0.3	4.98E-02	4.27E-01	Multiple_Complex
TC1100011514.hg.1	DHCR7	7-dehydrocholesterol reductase	1.53	14.09	13.47	0.1	0.13	4.11E-02	4.01E-01	Multiple_Complex
TC0700010437.hg.1	RAPGEF5	Rap guanine nucleotide exchange factor 5	1.53	4.89	4.28	0.17	0.57	4.71E-02	4.21E-01	Multiple_Complex
TC1000010439.hg.1	HNRNPF	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001098207	1.53	3.61	2.99	0.49	0.12	3.60E-02	3.87E-01	NonCoding
TC1700012483.hg.1	MAFG	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog G	1.53	5.47	4.85	0.27	0	2.08E-02	3.34E-01	Multiple_Complex
TC1200009676.hg.1	AKAP3	A kinase (PRKA) anchor protein 3	1.53	4.71	4.1	0.11	0.22	1.82E-02	3.23E-01	Multiple_Complex
TC1100007168.hg.1	ARL14EP	ADP-ribosylation factor like GTPase 14 effector protein	1.53	11.93	11.32	0.25	0.03	2.90E-02	3.64E-01	Multiple_Complex

TC0100010066.hg.1	UBAP2L	ubiquitin associated protein 2 like	1.53	12.66	12.05	0.08	0.18	1.99E-02	3.29E-01	Multiple_Complex
TC2000007830.hg.1	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	1.53	7.59	6.98	0.2	0.21	1.92E-02	3.26E-01	Coding
TC1700009679.hg.1	AURKB	aurora kinase B	1.53	13.05	12.44	0.09	0.09	1.55E-02	3.05E-01	Multiple_Complex
TC0100008033.hg.1	ERMAP	erythroblast membrane-associated protein (Scianna blood group)	1.53	5.83	5.22	0.18	0.35	3.75E-02	3.92E-01	Multiple_Complex
TC0200016423.hg.1	SPDYA	speedy/RINGO cell cycle regulator family member A	1.53	7.36	6.75	0.3	0.05	2.15E-02	3.34E-01	Multiple_Complex
TC1700007319.hg.1	WSB1	WD repeat and SOCS box containing 1	1.53	10.9	10.28	0.03	0.11	1.74E-02	3.16E-01	Multiple_Complex
TC0800006769.hg.1	ZNF705D	zinc finger protein 705D	1.53	7.01	6.4	0.03	0.06	2.22E-02	3.39E-01	Coding
TC0400007901.hg.1	SHROOM3	shroom family member 3	1.53	9.34	8.73	0.27	0.09	2.18E-02	3.36E-01	Multiple_Complex
TC0400008103.hg.1	RP11-10L7.1; HERC6	Transcript Identified by AceView, Entrez Gene ID(s) 55008; novel transcript	1.53	6.42	5.81	0.24	0.22	3.12E-02	3.72E-01	NonCoding
TC1900011777.hg.1	CYTH2	cytohesin 2	1.53	10.67	10.06	0.08	0.07	2.36E-02	3.45E-01	Multiple_Complex
TC2100008461.hg.1	SPATC1L	spermatogenesis and centriole associated 1-like	1.53	5.91	5.3	0.08	0.04	2.92E-02	3.65E-01	Coding
TC0100015580.hg.1	NBPF20	neuroblastoma breakpoint family, member 20	1.53	11.08	10.47	0.03	0.11	1.76E-02	3.17E-01	Coding
TC0100009876.hg.1	HIST2H2AA3; HIST2H2AA4	histone cluster 2, H2aa3; histone cluster 2, H2aa4	1.53	13.44	12.83	0.19	0.06	2.14E-02	3.34E-01	Coding
TC1200012327.hg.1	SCARB1	scavenger receptor class B, member 1	1.53	9.85	9.24	0.14	0.07	2.42E-02	3.46E-01	Multiple_Complex
TC1100013132.hg.1	INS; INS-IGF2	insulin; INS-IGF2 readthrough	1.53	4.25	3.64	0.33	0.08	4.67E-02	4.20E-01	Multiple_Complex
TC0300007336.hg.1	ATRIP; TREX1	ATR interacting protein; three prime repair exonuclease 1	1.53	10.12	9.51	0.44	0.19	3.56E-02	3.86E-01	Multiple_Complex
TC0300013471.hg.1	BCL6	B-cell CLL/lymphoma 6	1.53	9.94	9.33	0.2	0.22	2.89E-02	3.64E-01	Multiple_Complex
TC0200016673.hg.1	RTN4	reticulon 4	1.52	7.69	7.08	0.19	0.26	2.32E-02	3.42E-01	Multiple_Complex
TC1600007504.hg.1	SETD1A	SET domain containing 1A	1.52	9.69	9.08	0.06	0.1	2.00E-02	3.29E-01	Multiple_Complex

TSUnmapped00000138.hg.1	HYOU1	hypoxia up-regulated 1	1.52	12.78	12.17	0.02	0.22	2.72E-02	3.58E-01	Coding
TC0400010058.hg.1	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	1.52	5.18	4.57	0.35	0.02	4.28E-02	4.06E-01	Coding
TC2000009624.hg.1	APCDD1L	adenomatosis polyposis coli down-regulated 1-like	1.52	6.76	6.15	0.14	0.01	1.81E-02	3.23E-01	Multiple_Complex
TC0600014266.hg.1	TNXB	tenascin XB	1.52	5.34	4.73	0.05	0.29	2.54E-02	3.49E-01	Multiple_Complex
TC1900009052.hg.1	ZNF324B	zinc finger protein 324B	1.52	5.88	5.28	0.03	0.14	2.13E-02	3.34E-01	Coding
TC0100009215.hg.1	CDC14A	cell division cycle 14A	1.52	9.66	9.05	0.25	0.32	3.39E-02	3.81E-01	Multiple_Complex
TC1000008758.hg.1	CNNM2	cyclin and CBS domain divalent metal cation transport mediator 2	1.52	11.03	10.43	0.13	0.01	1.53E-02	3.04E-01	Multiple_Complex
TC0100007243.hg.1	ALPL	alkaline phosphatase, liver/bone/kidney	1.52	13.29	12.69	0.44	0.29	4.24E-02	4.04E-01	Multiple_Complex
TC1000010744.hg.1	TMEM26	transmembrane protein 26	1.52	5.02	4.41	0.26	0.25	2.63E-02	3.54E-01	Multiple_Complex
TC0200012488.hg.1	LOC100506142; RP11-417F21.1; RHOQ	uncharacterized LOC100506142; Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_012249; novel transcript	1.52	4.19	3.58	0.12	0.35	2.62E-02	3.53E-01	NonCoding
TC2200008637.hg.1	IL2RB	interleukin 2 receptor, beta	1.52	6	5.4	0.08	0.24	4.79E-02	4.21E-01	Multiple_Complex
TSUnmapped00000044.hg.1	AC208162.1		1.52	6.6	5.99	0.02	0.2	2.21E-02	3.38E-01	Coding
TC0X00008828.hg.1	EMD	emerin	1.52	9.65	9.05	0.15	0.28	4.79E-02	4.21E-01	Multiple_Complex
TC1200009796.hg.1	SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	1.52	14.19	13.59	0.25	0.07	2.53E-02	3.49E-01	Multiple_Complex
TC0700013332.hg.1	RBAK; RBAK-RBAKDN; RBAKDN	RB-associated KRAB zinc finger; RBAK-RBAKDN readthrough; RBAK downstream neighbor (non-protein coding)	1.52	11.96	11.36	0.09	0.2	2.05E-02	3.32E-01	Multiple_Complex
TC0300008563.hg.1	DIRC2	disrupted in renal carcinoma 2	1.52	11.05	10.45	0.14	0.01	1.61E-02	3.08E-01	Multiple_Complex

TC1200009183.hg.1	SETD1B	SET domain containing 1B	1.52	8.57	7.97	0.29	0.04	2.47E-02	3.48E-01	Multiple_Complex
TC0100011205.hg.1	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	1.52	6.47	5.87	0.31	0.23	3.41E-02	3.82E-01	Multiple_Complex
TC0200006725.hg.1	GREB1	growth regulation by estrogen in breast cancer 1	1.52	4.29	3.69	0.12	0.2	4.79E-02	4.21E-01	Multiple_Complex
TC1200010592.hg.1	ADCY6; MIR4701	adenylate cyclase 6; microRNA 4701	1.52	8.39	7.79	0.29	0.17	3.30E-02	3.78E-01	Multiple_Complex
TSUnmapped00000706.hg.1	HYOU1	hypoxia up-regulated 1	1.52	10.13	9.53	0.05	0.01	3.80E-02	3.93E-01	NonCoding
TC0600014198.hg.1	TULP4	tubby like protein 4	1.52	10.69	10.09	0.22	0.07	3.12E-02	3.72E-01	Multiple_Complex
TC0X00010895.hg.1	ZNF75D	zinc finger protein 75D	1.52	8.76	8.16	0.05	0.06	2.15E-02	3.34E-01	Multiple_Complex
TC0200016676.hg.1	WDPCP	WD repeat containing planar cell polarity effector	1.52	8.36	7.76	0.2	0.15	4.21E-02	4.02E-01	Multiple_Complex
TC1300007752.hg.1	CLDN10	claudin 10	1.51	5.17	4.57	0.34	0.21	3.17E-02	3.72E-01	Multiple_Complex
TC1900008982.hg.1	USP29	ubiquitin specific peptidase 29	1.51	4.29	3.69	0.43	0.28	4.67E-02	4.20E-01	Coding
TC1900008053.hg.1	SAMD4B	sterile alpha motif domain containing 4B	1.51	11.94	11.34	0.21	0.2	2.17E-02	3.36E-01	Multiple_Complex
TC0800009309.hg.1	OR4F21	olfactory receptor, family 4, subfamily F, member 21	1.51	6	5.4	0.23	0.45	4.52E-02	4.15E-01	Coding
TC0X00011381.hg.1	KCNE5; ACSL4	potassium channel, voltage gated subfamily E regulatory beta subunit 5; acyl-CoA synthetase long-chain family member 4	1.51	5.49	4.89	0.06	0.26	3.60E-02	3.87E-01	Multiple_Complex
TC1100012510.hg.1	HYOU1	hypoxia up-regulated 1	1.51	15.06	14.46	0.15	0	1.78E-02	3.20E-01	Multiple_Complex
TC2000009058.hg.1	TGM2	transglutaminase 2	1.51	7.64	7.04	0.28	0.09	4.29E-02	4.06E-01	Multiple_Complex
TC1700008134.hg.1	TBKBP1	TBK1 binding protein 1	1.51	5.45	4.85	0.16	0.27	4.07E-02	4.00E-01	Coding
TC1800009306.hg.1	RNF152	ring finger protein 152	1.51	4.81	4.22	0.17	0.04	2.24E-02	3.40E-01	Multiple_Complex
TC0700008809.hg.1	LRRN3	leucine rich repeat neuronal 3	1.51	6.1	5.5	0.26	0.06	2.77E-02	3.59E-01	Multiple_Complex
TC1500008317.hg.1	CRTC3	CREB regulated transcription coactivator 3	1.51	11.04	10.44	0.16	0.04	1.90E-02	3.26E-01	Multiple_Complex

TC0600007194.hg.1	KAAG1	kidney associated antigen 1	1.51	4.73	4.13	0.23	0.01	2.39E-02	3.46E-01	Coding
TC1300009515.hg.1	DZIP1	Transcript Identified by AceView, Entrez Gene ID(s) 22873	1.51	5.78	5.19	0.19	0.15	2.29E-02	3.41E-01	Unassigned
TC1900011869.hg.1	RGL3	ral guanine nucleotide dissociation stimulator-like 3	1.51	6.86	6.27	0.03	0.18	3.65E-02	3.89E-01	Multiple_Complex
TC0100007562.hg.1	TRNAU1AP	tRNA selenocysteine 1 associated protein 1	1.51	7.95	7.36	0.01	0.37	2.85E-02	3.63E-01	Multiple_Complex
TC0300006694.hg.1	NR2C2	nuclear receptor subfamily 2, group C, member 2	1.51	10.83	10.24	0.13	0.06	1.81E-02	3.23E-01	Multiple_Complex
TC0500007875.hg.1	BHMT2	betaine--homocysteine S-methyltransferase 2	1.51	6.85	6.25	0.23	0.12	4.94E-02	4.25E-01	Multiple_Complex
TC1200012574.hg.1	TULP3	tubby like protein 3	1.51	11.65	11.06	0.24	0.02	2.01E-02	3.31E-01	Multiple_Complex
TC0500012587.hg.1	TIMD4	T-cell immunoglobulin and mucin domain containing 4	1.51	4.33	3.74	0.17	0.36	3.14E-02	3.72E-01	Coding
TC1700009402.hg.1	SMYD4	SET and MYND domain containing 4	1.51	9.84	9.25	0.34	0.17	4.40E-02	4.10E-01	Multiple_Complex
TC0200010120.hg.1	PLEKHA3	Transcript Identified by AceView, Entrez Gene ID(s) 65977	1.51	5.08	4.49	0.21	0.32	4.28E-02	4.06E-01	Unassigned
TC0500012312.hg.1	SPRY4	sprouty RTK signaling antagonist 4	1.51	5.08	4.49	0.17	0.18	3.13E-02	3.72E-01	Multiple_Complex
TC1900011766.hg.1	MARK4	MAP/microtubule affinity-regulating kinase 4	1.51	10.1	9.51	0.05	0.14	1.75E-02	3.17E-01	Multiple_Complex
TC1900006660.hg.1	ATCAY	ataxia, cerebellar, Cayman type	1.51	5.26	4.67	0.02	0.07	3.29E-02	3.77E-01	Multiple_Complex
TC0X00010005.hg.1	CXCR3	chemokine (C-X-C motif) receptor 3	1.51	6.21	5.62	0.03	0.29	4.85E-02	4.23E-01	Coding
TSUnmapped00000777.hg.1	HYOU1	hypoxia up-regulated 1	1.51	13.17	12.58	0.07	0.18	2.50E-02	3.49E-01	Coding
TC2200006637.hg.1	DGCR8	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_022720	1.5	5.89	5.3	0	0.37	4.83E-02	4.21E-01	NonCoding
TC1000007013.hg.1	PTF1A	pancreas specific transcription factor, 1a	1.5	5.74	5.15	0.31	0.05	2.46E-02	3.47E-01	Coding
TC1300008125.hg.1	LAMP1	lysosomal-associated membrane protein 1	1.5	9.01	8.42	0.11	0.02	1.65E-02	3.10E-01	Multiple_Complex

TC1600009185.hg.1	MEFV	Mediterranean fever	1.5	5.02	4.43	0.32	0.15	3.71E-02	3.90E-01	Multiple_Complex
TC0900011501.hg.1	NR6A1	nuclear receptor subfamily 6, group A, member 1	1.5	5.39	4.8	0.03	0.29	3.81E-02	3.93E-01	Multiple_Complex
TC0700012734.hg.1	CREB3L2	cAMP responsive element binding protein 3-like 2	1.5	10.17	9.58	0.05	0.12	1.78E-02	3.20E-01	Multiple_Complex
TC1700012073.hg.1	P4HB	prolyl 4-hydroxylase, beta polypeptide	1.5	12.3	11.72	0.11	0.02	2.22E-02	3.39E-01	Multiple_Complex
TC0100018366.hg.1	CHRM3	cholinergic receptor, muscarinic 3	1.5	5.72	5.13	0.04	0.42	4.79E-02	4.21E-01	NonCoding
TC1900008286.hg.1	BCAM	basal cell adhesion molecule (Lutheran blood group)	1.5	5.5	4.91	0.12	0.22	4.72E-02	4.21E-01	Multiple_Complex
TC0100017260.hg.1	NSL1	NSL1, MIS12 kinetochore complex component	-1.5	12.43	13.01	0.22	0.12	3.02E-02	3.67E-01	Multiple_Complex
TC1900010011.hg.1	LSM4	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated	-1.5	11.17	11.75	0.03	0.01	1.63E-02	3.09E-01	Multiple_Complex
TC0100006627.hg.1	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	-1.5	7.4	7.99	0.12	0.38	3.56E-02	3.86E-01	Multiple_Complex
TC1800006841.hg.1	MIB1	mindbomb E3 ubiquitin protein ligase 1	-1.5	10.1	10.69	0.07	0.31	3.61E-02	3.87E-01	Multiple_Complex
TC1700007189.hg.1	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	-1.5	9.03	9.61	0.29	0	3.18E-02	3.72E-01	Multiple_Complex
TC0200013902.hg.1	RGPD5; RGPD8	RANBP2-like and GRIP domain containing 5; RANBP2-like and GRIP domain containing 8	-1.5	9.29	9.88	0.03	0.09	1.85E-02	3.24E-01	Multiple_Complex
TC1900011867.hg.1	TMEM205	transmembrane protein 205	-1.5	10.78	11.37	0.44	0	3.74E-02	3.92E-01	Multiple_Complex
TC0700011876.hg.1	ASNS	asparagine synthetase (glutamine-hydrolyzing)	-1.5	11.14	11.73	0.22	0.2	2.68E-02	3.58E-01	Multiple_Complex
TC0800007308.hg.1	ERLIN2	ER lipid raft associated 2	-1.5	8.6	9.19	0.02	0.18	3.69E-02	3.90E-01	Multiple_Complex
TC0800010138.hg.1	RAB11FIP1	RAB11 family interacting protein 1 (class I)	-1.5	8.42	9.01	0.01	0.1	4.02E-02	3.98E-01	Multiple_Complex
TC0900007752.hg.1	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	-1.5	4.27	4.85	0.31	0.01	3.17E-02	3.72E-01	Multiple_Complex
TC1100007866.hg.1	UQCC3	ubiquinol-cytochrome c reductase complex assembly factor 3	-1.5	12.33	12.92	0.01	0.06	1.83E-02	3.24E-01	Multiple_Complex

TC1700012384.hg.1	RAD51L3-RFFL	RAD51L3-RFFL readthrough; HCG2039718, isoform CRA_g; Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:K7EN88]	-1.5	6.86	7.45	0.11	0.24	2.83E-02	3.62E-01	Multiple_Complex
TC0X00008694.hg.1	HSFX1	heat shock transcription factor family, X-linked 1	-1.5	4.22	4.81	0.02	0.1	4.54E-02	4.15E-01	Coding
TC0600007301.hg.1	BTN3A2	butyrophilin, subfamily 3, member A2	-1.5	12.8	13.39	0.05	0.13	3.00E-02	3.66E-01	Multiple_Complex
TC0600011562.hg.1	LEMD2	LEM domain containing 2	-1.51	6.41	7	0.18	0.06	2.25E-02	3.40E-01	Multiple_Complex
TSUnmapped00000239.hg.1	ATG16L1	autophagy related 16-like 1	-1.51	4.85	5.44	0.3	0.23	3.64E-02	3.88E-01	NonCoding
TC0200011013.hg.1	FBXO36	F-box protein 36	-1.51	6.33	6.92	0.23	0.01	2.51E-02	3.49E-01	Multiple_Complex
TC1000008193.hg.1	PPIF	peptidylprolyl isomerase F	-1.51	8.42	9.01	0.1	0	2.89E-02	3.64E-01	Multiple_Complex
TC1700008465.hg.1	CLTC	clathrin, heavy chain (Hc)	-1.51	13.64	14.23	0.16	0.07	2.59E-02	3.51E-01	Multiple_Complex
TC0200014345.hg.1	ANKRD30BL	ankyrin repeat domain 30B-like	-1.51	4.3	4.89	0.16	0.05	2.30E-02	3.41E-01	Multiple_Complex
TC1200009217.hg.1	DENR	density-regulated protein	-1.51	12	12.59	0.21	0.24	2.51E-02	3.49E-01	Multiple_Complex
TC1300008894.hg.1	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	-1.51	4.43	5.02	0.04	0.14	2.29E-02	3.41E-01	Multiple_Complex
TC0400008329.hg.1	GSTCD	glutathione S-transferase, C-terminal domain containing	-1.51	10.51	11.1	0.07	0.19	2.15E-02	3.34E-01	Multiple_Complex
TC0200007907.hg.1	GKN1	gastrokine 1	-1.51	4.92	5.52	0.16	0.31	3.87E-02	3.94E-01	Multiple_Complex
TC0800012146.hg.1	PYCRL	pyrroline-5-carboxylate reductase-like	-1.51	8.05	8.65	0.05	0.27	3.26E-02	3.76E-01	Multiple_Complex
TC1400009295.hg.1	EXOC5	exocyst complex component 5	-1.51	9.07	9.66	0.19	0.15	4.41E-02	4.11E-01	Multiple_Complex
TC1000008574.hg.1	PGAM1	phosphoglycerate mutase 1 (brain)	-1.51	13.76	14.35	0.18	0.16	3.00E-02	3.66E-01	Multiple_Complex
TC1700007754.hg.1	PNMT	phenylethanolamine N-methyltransferase	-1.51	5.96	6.56	0.17	0.09	2.39E-02	3.46E-01	Multiple_Complex

TC0100010340.hg.1	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	-1.51	10.52	11.11	0.1	0.17	2.72E-02	3.58E-01	Multiple_Complex
TC0700008662.hg.1	ARMC10	armadillo repeat containing 10	-1.51	8.29	8.88	0.35	0.17	2.95E-02	3.65E-01	Multiple_Complex
TC0X00006957.hg.1	XK	X-linked Kx blood group	-1.51	6.5	7.09	0.16	0.22	2.10E-02	3.34E-01	Multiple_Complex
TC2100007362.hg.1	LRRC3	leucine rich repeat containing 3	-1.51	5.35	5.95	0.15	0.18	4.66E-02	4.20E-01	Coding
TC1700012352.hg.1	TRAPPC1	trafficking protein particle complex 1	-1.51	9.45	10.05	0.13	0.02	1.61E-02	3.08E-01	Multiple_Complex
TSUnmapped00000493.hg.1	TRAPPC4	trafficking protein particle complex 4	-1.51	6.53	7.12	0.15	0.17	2.13E-02	3.34E-01	Coding
TC1100007600.hg.1	OR4P4	olfactory receptor, family 4, subfamily P, member 4	-1.51	3.62	4.22	0.08	0.45	4.02E-02	3.98E-01	Coding
TC0700009329.hg.1	TTC26	tetratricopeptide repeat domain 26	-1.51	9.66	10.25	0.22	0.04	2.34E-02	3.43E-01	Multiple_Complex
TC0500008014.hg.1	RASA1	RAS p21 protein activator (GTPase activating protein) 1	-1.51	6.57	7.16	0.06	0.14	3.10E-02	3.71E-01	Multiple_Complex
TC0X00008147.hg.1	ZCCHC16	zinc finger, CCHC domain containing 16	-1.51	3.7	4.29	0.13	0.31	2.87E-02	3.63E-01	Coding
TC0300006462.hg.1	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	-1.51	7.56	8.16	0.19	0.48	4.59E-02	4.18E-01	Multiple_Complex
TC0900010485.hg.1	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	-1.51	7.65	8.24	0.22	0.39	3.83E-02	3.94E-01	Multiple_Complex
TC0600012432.hg.1	PGM3	phosphoglucomutase 3	-1.51	10.53	11.12	0.32	0.37	3.93E-02	3.96E-01	Multiple_Complex
TC0200009134.hg.1	TSN	translin	-1.51	13.27	13.87	0.03	0.1	1.64E-02	3.10E-01	Multiple_Complex
TC0900009758.hg.1	TUSC1	tumor suppressor candidate 1	-1.51	6.06	6.66	0.12	0.21	3.48E-02	3.84E-01	Coding
TC2000007502.hg.1	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	-1.51	9.98	10.58	0.01	0.23	3.04E-02	3.68E-01	Multiple_Complex
TC0200015779.hg.1	DNPEP	aspartyl aminopeptidase	-1.51	6.36	6.96	0.09	0.08	3.28E-02	3.76E-01	Multiple_Complex
TC1600011356.hg.1	MPV17L	MPV17 mitochondrial membrane protein-like	-1.51	5.18	5.78	0.19	0.1	4.20E-02	4.02E-01	Multiple_Complex

TC1900011857.hg.1	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	-1.51	11.03	11.63	0.34	0.15	4.70E-02	4.21E-01	Multiple_Complex
TC0400007593.hg.1	SRP72	signal recognition particle 72kDa	-1.52	13.77	14.37	0.03	0.01	2.49E-02	3.49E-01	Multiple_Complex
TC0700013065.hg.1	ABCF2	ATP binding cassette subfamily F member 2	-1.52	7.91	8.51	0.28	0.26	4.80E-02	4.21E-01	Multiple_Complex
TC1500010256.hg.1	BTBD1	BTB (POZ) domain containing 1	-1.52	9.77	10.38	0.2	0.11	2.47E-02	3.48E-01	Multiple_Complex
TC1500007671.hg.1	FEM1B	fem-1 homolog b (C. elegans)	-1.52	10.79	11.4	0.07	0.23	2.71E-02	3.58E-01	Coding
TC0400010886.hg.1	UBA6	ubiquitin-like modifier activating enzyme 6	-1.52	7.65	8.26	0.16	0.44	4.51E-02	4.15E-01	Multiple_Complex
TC0700012148.hg.1	SRPK2	SRSF protein kinase 2	-1.52	4.76	5.36	0.08	0.24	2.26E-02	3.40E-01	Multiple_Complex
TC0800008279.hg.1	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	-1.52	7.39	7.99	0.39	0.16	3.88E-02	3.94E-01	Multiple_Complex
TSUnmapped00000523.hg.1	RPS25	ribosomal protein S25	-1.52	9.98	10.58	0.15	0.15	2.73E-02	3.58E-01	NonCoding
TC1900011807.hg.1	ZNF583	zinc finger protein 583	-1.52	3.94	4.54	0.15	0.3	4.17E-02	4.01E-01	Multiple_Complex
TC1400009784.hg.1	VIPAS39	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog	-1.52	9.32	9.92	0.45	0.23	4.00E-02	3.98E-01	Multiple_Complex
TC1800007490.hg.1	CDH20	cadherin 20, type 2	-1.52	3.77	4.37	0.07	0.25	2.14E-02	3.34E-01	Multiple_Complex
TC0100015925.hg.1	KCNN3	potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 3	-1.52	5.28	5.88	0.22	0.31	2.72E-02	3.58E-01	Multiple_Complex
TC0100009580.hg.1	WDR3	WD repeat domain 3	-1.52	9.38	9.98	0.26	0.23	3.55E-02	3.86E-01	Multiple_Complex
TC0100013748.hg.1	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	-1.52	11.7	12.3	0.22	0.12	2.08E-02	3.34E-01	Multiple_Complex
TC0200007176.hg.1	SLC30A6	solute carrier family 30 (zinc transporter), member 6	-1.52	13.23	13.84	0.37	0.07	3.72E-02	3.91E-01	Multiple_Complex
TC1200012613.hg.1	MED21	mediator complex subunit 21	-1.52	4.46	5.06	0.25	0.18	4.88E-02	4.24E-01	NonCoding

TC0X00009218.hg.1	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	-1.52	5.55	6.16	0.16	0.14	3.43E-02	3.83E-01	Multiple_Complex
TC0100016676.hg.1	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	-1.52	8.82	9.43	0.38	0.17	3.46E-02	3.84E-01	Multiple_Complex
TC0300013772.hg.1	IQCG	IQ motif containing G	-1.52	6.21	6.82	0.09	0.23	2.50E-02	3.49E-01	Multiple_Complex
TSUnmapped00000155.hg.1	SURF2	surfeit 2 [Source:HGNC Symbol;Acc:HGNC:11475]	-1.52	5.82	6.43	0.03	0.18	3.27E-02	3.76E-01	NonCoding
TC1600011407.hg.1	CMTM1	CKLF-like MARVEL transmembrane domain containing 1	-1.52	5.63	6.24	0.03	0.52	4.73E-02	4.21E-01	Coding
TC0100007447.hg.1	CEP85	centrosomal protein 85kDa	-1.52	6.37	6.98	0.09	0.2	2.97E-02	3.65E-01	Multiple_Complex
TC0100014403.hg.1	KANK4	KN motif and ankyrin repeat domains 4	-1.52	6.83	7.44	0.12	0.21	4.86E-02	4.23E-01	Multiple_Complex
TC0X00011205.hg.1	UBL4A	ubiquitin-like 4A	-1.53	6.54	7.15	0.22	0.16	1.91E-02	3.26E-01	Multiple_Complex
TC1500006962.hg.1	RPUSD2	RNA pseudouridylate synthase domain containing 2	-1.53	5.92	6.53	0.04	0.25	2.90E-02	3.64E-01	Multiple_Complex
TC0300014075.hg.1	TRIM59	tripartite motif containing 59	-1.53	10.22	10.83	0.11	0.07	1.88E-02	3.25E-01	Coding
TC0400009129.hg.1	RXFP1	relaxin/insulin-like family peptide receptor 1	-1.53	3.82	4.43	0.19	0.41	3.11E-02	3.71E-01	Multiple_Complex
TC1000008019.hg.1	NUDT13	nudix hydrolase 13	-1.53	7.38	7.99	0.4	0.04	2.75E-02	3.59E-01	Multiple_Complex
TC1200010407.hg.1	KIF21A	kinesin family member 21A	-1.53	9.99	10.6	0.25	0.07	2.32E-02	3.42E-01	Multiple_Complex
TC0200010119.hg.1	PLEKHA3	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	-1.53	10.09	10.7	0.14	0.02	1.59E-02	3.08E-01	Multiple_Complex
TC1800007059.hg.1	DTNA	dystrobrevin, alpha	-1.53	8.05	8.66	0.01	0.26	2.57E-02	3.51E-01	Multiple_Complex
TC1900011635.hg.1	CHMP2A	charged multivesicular body protein 2A	-1.53	8.72	9.33	0.28	0.12	2.03E-02	3.31E-01	Multiple_Complex
TC0700009483.hg.1	TAS2R40	taste receptor, type 2, member 40	-1.53	3.02	3.63	0.07	0.51	3.81E-02	3.93E-01	Coding
TC0200013943.hg.1	SLC35F5	solute carrier family 35, member F5	-1.53	9.33	9.94	0.34	0	2.98E-02	3.66E-01	Multiple_Complex
TC1800007850.hg.1	COLEC12	collectin sub-family member 12	-1.53	4.39	5.01	0.15	0.16	4.48E-02	4.14E-01	Multiple_Complex

TC1800006935.hg.1	PSMA8	proteasome subunit alpha 8	-1.53	3.47	4.09	0.01	0.03	1.29E-02	2.88E-01	Coding
TC2100008000.hg.1	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	-1.53	13.3	13.91	0.08	0.03	1.27E-02	2.87E-01	Multiple_Complex
TC0200009973.hg.1	ITGA6	integrin alpha 6	-1.53	6.63	7.24	0.25	0.04	2.37E-02	3.45E-01	Multiple_Complex
TC0900009768.hg.1	CAAP1	caspase activity and apoptosis inhibitor 1	-1.53	9.37	9.99	0.04	0.39	2.59E-02	3.51E-01	Multiple_Complex
TC0600012883.hg.1	TUBE1	tubulin, epsilon 1	-1.53	11.64	12.25	0.29	0.05	1.98E-02	3.29E-01	Multiple_Complex
TC0200016308.hg.1	MYEOV2	myeloma overexpressed 2	-1.53	11.2	11.81	0.07	0.04	1.28E-02	2.87E-01	Multiple_Complex
TC1200011916.hg.1	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	-1.53	13.29	13.9	0.2	0.04	2.10E-02	3.34E-01	Multiple_Complex
TC0X00011313.hg.1	GPRASP2	G protein-coupled receptor associated sorting protein 2	-1.53	4.42	5.04	0.28	0.29	2.96E-02	3.65E-01	Multiple_Complex
TC1600007959.hg.1	MT1E	metallothionein 1E	-1.53	8.85	9.46	0.01	0.02	1.68E-02	3.12E-01	Multiple_Complex
TC0700011847.hg.1	SLC25A13	solute carrier family 25 (aspartate/glutamate carrier), member 13	-1.53	8.89	9.51	0.29	0.24	3.45E-02	3.84E-01	Multiple_Complex
TC0900012229.hg.1	EXOSC3	exosome component 3	-1.53	9.95	10.57	0.16	0.3	3.01E-02	3.67E-01	Multiple_Complex
TC0400011291.hg.1	HERC6	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_001165136	-1.53	6.68	7.29	0.23	0.13	1.77E-02	3.19E-01	NonCoding
TC1200008678.hg.1	EID3	EP300 interacting inhibitor of differentiation 3	-1.53	6.88	7.5	0.09	0.13	2.86E-02	3.63E-01	Coding
TC0500013226.hg.1	CDC42SE2	CDC42 small effector 2	-1.53	11.63	12.25	0.05	0.04	2.76E-02	3.59E-01	Multiple_Complex
TC1600009184.hg.1	ZNF200	Transcript Identified by AceView, Entrez Gene ID(s) 7752	-1.53	5.25	5.87	0.01	0.4	3.70E-02	3.90E-01	Unassigned
TC0900011254.hg.1	CDC26	cell division cycle 26	-1.53	13.82	14.44	0.06	0	1.35E-02	2.90E-01	Multiple_Complex
TC1400006890.hg.1	SRP54	signal recognition particle 54kDa	-1.53	10.03	10.64	0.14	0.14	4.23E-02	4.04E-01	Multiple_Complex

TC0X00008866.hg.1	VBP1	von Hippel-Lindau binding protein 1	-1.54	9.21	9.83	0.43	0.08	2.86E-02	3.63E-01	Multiple_Complex
TC1500009861.hg.1	ITGA11	integrin alpha 11	-1.54	3.84	4.45	0.03	0.11	1.65E-02	3.10E-01	Multiple_Complex
TC1400009351.hg.1	SIX1	SIX homeobox 1	-1.54	7.09	7.71	0.03	0.07	2.15E-02	3.34E-01	Multiple_Complex
TC1600006493.hg.1	FAM173A	family with sequence similarity 173, member A	-1.54	10.44	11.06	0.13	0.05	3.84E-02	3.94E-01	Multiple_Complex
TC0600014127.hg.1	RPL7L1	ribosomal protein L7-like 1	-1.54	10.81	11.43	0.01	0.05	1.26E-02	2.87E-01	Multiple_Complex
TC0100018453.hg.1	ARHGAP29	Rho GTPase activating protein 29	-1.54	3.78	4.4	0.21	0.03	2.04E-02	3.32E-01	NonCoding
TC1400006543.hg.1	METTL17	methyltransferase like 17	-1.54	5.01	5.63	0.16	0.2	3.61E-02	3.87E-01	Multiple_Complex
TC1300006767.hg.1	USPL1	ubiquitin specific peptidase like 1	-1.54	9.66	10.28	0.07	0.19	1.87E-02	3.25E-01	Multiple_Complex
TC1000008988.hg.1	TRUB1	TruB pseudouridine (psi) synthase family member 1	-1.54	10.05	10.67	0.15	0.05	2.14E-02	3.34E-01	Multiple_Complex
TC0700012203.hg.1	COG5	component of oligomeric golgi complex 5	-1.54	9.32	9.94	0.07	0.39	3.74E-02	3.92E-01	Multiple_Complex
TC1500007910.hg.1	UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	-1.54	6.15	6.77	0.11	0.25	4.31E-02	4.07E-01	Multiple_Complex
TC1600010181.hg.1	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	-1.54	11.89	12.52	0.2	0.13	1.89E-02	3.26E-01	Multiple_Complex
TC1400010700.hg.1	SIVA1	SIVA1, apoptosis-inducing factor	-1.54	10.61	11.23	0.26	0.16	2.13E-02	3.34E-01	Multiple_Complex
TC1400010632.hg.1	GPATCH2L	G-patch domain containing 2 like	-1.54	8.97	9.59	0.12	0.16	1.45E-02	2.98E-01	Multiple_Complex
TC0600009279.hg.1	ASF1A	anti-silencing function 1A histone chaperone	-1.54	10.66	11.28	0.05	0.13	1.48E-02	3.02E-01	Multiple_Complex
TC0700009513.hg.1	OR2F2	olfactory receptor, family 2, subfamily F, member 2	-1.54	3.72	4.35	0.36	0.2	3.44E-02	3.84E-01	Coding
TC1400010723.hg.1	TM9SF1	transmembrane 9 superfamily member 1	-1.54	10.4	11.03	0.15	0.07	4.25E-02	4.04E-01	Multiple_Complex
TC0500013336.hg.1	SSBP2	single-stranded DNA binding protein 2	-1.54	8.62	9.25	0.16	0.1	2.24E-02	3.40E-01	Multiple_Complex
TC0800012307.hg.1	RRS1	ribosome biogenesis regulator homolog	-1.54	9.39	10.01	0.08	0.05	2.37E-02	3.45E-01	Coding
TC1700011319.hg.1	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.54	6.7	7.33	0.07	0.04	1.35E-02	2.89E-01	Multiple_Complex
TC1700006652.hg.1	C17orf107	chromosome 17 open reading frame 107	-1.54	5.38	6.01	0.07	0.23	2.02E-02	3.31E-01	Multiple_Complex

TC1000011798.hg.1	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-1.54	10.92	11.54	0.04	0.25	1.92E-02	3.26E-01	Multiple_Complex
TC0100012872.hg.1	MTOR	mechanistic target of rapamycin (serine/threonine kinase)	-1.54	9.78	10.41	0.04	0.11	1.20E-02	2.84E-01	Multiple_Complex
TC0200013063.hg.1	EGR4	early growth response 4	-1.54	4.06	4.68	0.3	0.19	3.07E-02	3.69E-01	Coding
TC0900008902.hg.1	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	-1.54	9.72	10.35	0.14	0.03	1.54E-02	3.04E-01	Multiple_Complex
TC0500012781.hg.1	DOCK2	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_004946	-1.54	7.01	7.64	0.35	0.15	3.16E-02	3.72E-01	NonCoding
TC1000012139.hg.1	CTBP2	C-terminal binding protein 2	-1.54	8.6	9.23	0.32	0.18	2.85E-02	3.63E-01	Multiple_Complex
TC1100010400.hg.1	LGR4	leucine-rich repeat containing G protein-coupled receptor 4	-1.55	7.62	8.25	0.39	0	2.87E-02	3.63E-01	Multiple_Complex
TC0700011050.hg.1	FIGNL1	fidgetin-like 1	-1.55	8.09	8.72	0.36	0.19	2.59E-02	3.51E-01	Multiple_Complex
TC2100008534.hg.1	PCBP3	poly(rC) binding protein 3	-1.55	5.96	6.59	0.09	0.15	2.55E-02	3.49E-01	NonCoding
TC0700012917.hg.1	TPK1	thiamin pyrophosphokinase 1	-1.55	6	6.63	0.05	0.33	2.19E-02	3.37E-01	Multiple_Complex
TC0200007712.hg.1	PEX13	peroxisomal biogenesis factor 13	-1.55	10.57	11.2	0.3	0.22	3.49E-02	3.84E-01	Multiple_Complex
TC0100018329.hg.1	CFHR1	complement factor H-related 1	-1.55	3.44	4.07	0.09	0.42	3.84E-02	3.94E-01	Multiple_Complex
TC0400010965.hg.1	GRSF1	G-rich RNA sequence binding factor 1	-1.55	12.38	13.01	0.06	0.04	1.09E-02	2.74E-01	Multiple_Complex
TC0200016681.hg.1	WDR92	WD repeat domain 92	-1.55	8.04	8.67	0.11	0.08	1.60E-02	3.08E-01	Multiple_Complex
TC0200011745.hg.1	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	-1.55	12.07	12.7	0.01	0.15	1.22E-02	2.84E-01	Multiple_Complex
TC0300008088.hg.1	CRYBG3	crystallin beta-gamma domain containing 3	-1.55	5.97	6.6	0.26	0.25	4.21E-02	4.02E-01	Multiple_Complex
TC2100008537.hg.1	C21orf33	chromosome 21 open reading frame 33	-1.55	8.12	8.75	0.17	0.28	3.19E-02	3.72E-01	Multiple_Complex
TC1600007183.hg.1	UQCRC2	ubiquinol-cytochrome c reductase core protein II	-1.55	12.15	12.78	0.02	0.08	2.13E-02	3.34E-01	Multiple_Complex
TC0400009132.hg.1	ETFDH	electron-transferring-flavoprotein dehydrogenase	-1.55	5.79	6.43	0.43	0.14	4.25E-02	4.04E-01	Multiple_Complex

TC0500009481.hg.1	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	-1.55	14.57	15.2	0.04	0.19	1.27E-02	2.87E-01	Multiple_Complex
TC0500013271.hg.1	LOC728554; THOC3	THO complex 3 pseudogene; Homo sapiens THO complex 3, mRNA (cDNA clone MGC:5469 IMAGE:3451612), complete cds.; Homo sapiens THO complex 3, mRNA (cDNA clone MGC:87233 IMAGE:5262880), complete cds.; Salzman2013 ANNOTATED, INTERNAL, ncRNA, OVERLAPTX, OVEXON best transcript NR_003615; Transcript Identified by AceView, Entrez Gene ID(s) 728554	-1.55	11.98	12.61	0.02	0.09	1.22E-02	2.84E-01	Multiple_Complex
TC0100009561.hg.1	TTF2	transcription termination factor, RNA polymerase II	-1.55	8.66	9.29	0.03	0.03	2.11E-02	3.34E-01	Multiple_Complex
TC0800011312.hg.1	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	-1.55	9.2	9.83	0.03	0.02	1.57E-02	3.06E-01	Multiple_Complex
TC1400010068.hg.1	DICER1	dicer 1, ribonuclease type III	-1.55	10.57	11.21	0.2	0.01	1.40E-02	2.93E-01	Multiple_Complex
TC0X00009101.hg.1	GPM6B	glycoprotein M6B	-1.55	6.65	7.28	0.29	0.05	2.04E-02	3.32E-01	Multiple_Complex
TC1700012089.hg.1	DCXR	dicarbonyl/L-xylulose reductase	-1.55	12.09	12.73	0.23	0.2	3.81E-02	3.93E-01	Multiple_Complex
TC1400007139.hg.1	TMX1	thioredoxin-related transmembrane protein 1	-1.55	12.42	13.05	0.15	0.14	1.84E-02	3.24E-01	Multiple_Complex
TC0200010056.hg.1	MTX2	metaxin 2	-1.55	9.36	9.99	0.18	0.37	3.60E-02	3.87E-01	Multiple_Complex
TC0800010298.hg.1	THAP1	THAP domain containing, apoptosis associated protein 1	-1.55	7.82	8.46	0	0.02	2.58E-02	3.51E-01	Multiple_Complex
TC0100009738.hg.1	GPR89A	G protein-coupled receptor 89A	-1.55	10.01	10.65	0.12	0.01	1.88E-02	3.26E-01	Multiple_Complex
TC0X00008405.hg.1	RBMX2	RNA binding motif protein, X-linked 2	-1.55	9.94	10.57	0.29	0.19	1.89E-02	3.26E-01	Multiple_Complex
TC1000008908.hg.1	SHOC2	SHOC2 leucine-rich repeat scaffold protein	-1.55	11.84	12.48	0.18	0.17	2.26E-02	3.40E-01	Multiple_Complex
TC0700006649.hg.1	ZDHHC4	zinc finger, DHHC-type containing 4	-1.55	10.01	10.64	0.39	0.03	2.48E-02	3.48E-01	Multiple_Complex

TC2000007942.hg.1	FAM217B	family with sequence similarity 217, member B	-1.55	7.28	7.91	0.1	0.17	2.37E-02	3.45E-01	Multiple_Complex
TC0900007775.hg.1	NAA35	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	-1.55	10.52	11.16	0.15	0.13	1.86E-02	3.25E-01	Multiple_Complex
TC0600009667.hg.1	VTA1	vesicle (multivesicular body) trafficking 1	-1.56	11.42	12.05	0.19	0.31	2.92E-02	3.65E-01	Multiple_Complex
TC0600011733.hg.1	KCNK5	potassium channel, two pore domain subfamily K, member 5	-1.56	6.06	6.69	0.08	0.12	1.61E-02	3.08E-01	Multiple_Complex
TC0X00010046.hg.1	DMRTC1B; DMRTC1	DMRT-like family C1B; DMRT-like family C1	-1.56	4.87	5.5	0.04	0.41	2.50E-02	3.49E-01	Multiple_Complex
TSUnmapped00000654.hg.1	FMN1	formin 1	-1.56	4.26	4.9	0.11	0.02	2.09E-02	3.34E-01	NonCoding
TC0600007446.hg.1	OR2J1	olfactory receptor, family 2, subfamily J, member 1 (gene/pseudogene)	-1.56	3.42	4.06	0.22	0.07	1.95E-02	3.27E-01	Pseudogene
TC0800012233.hg.1	ZNF251	zinc finger protein 251	-1.56	6.07	6.71	0.05	0.14	4.64E-02	4.19E-01	Multiple_Complex
TC0100016470.hg.1	MRPS14	mitochondrial ribosomal protein S14	-1.56	13.78	14.41	0.08	0.07	1.09E-02	2.74E-01	Multiple_Complex
TC0100018080.hg.1	AHCTF1	AT hook containing transcription factor 1	-1.56	11.03	11.67	0	0.05	1.41E-02	2.93E-01	Multiple_Complex
TC0100018430.hg.1	SMIM12	small integral membrane protein 12	-1.56	12.51	13.15	0.14	0.26	1.59E-02	3.07E-01	Coding
TC0700008252.hg.1	CROT	carnitine O-octanoyltransferase	-1.56	5.53	6.17	0.33	0.38	4.66E-02	4.20E-01	Multiple_Complex
TC0700013491.hg.1	GIMAP1-GIMAP5; GIMAP5; GIMAP1	GIMAP1-GIMAP5 readthrough; GTPase, IMAP family member 5; GTPase, IMAP family member 1	-1.56	3.98	4.62	0.1	0.34	3.38E-02	3.81E-01	Multiple_Complex
TC1500006930.hg.1	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	-1.56	9.7	10.34	0.25	0.08	2.14E-02	3.34E-01	Multiple_Complex
TC0800011172.hg.1	MTERF3	mitochondrial transcription termination factor 3	-1.56	10.1	10.74	0.11	0.07	1.20E-02	2.83E-01	Multiple_Complex
TC1900006956.hg.1	PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	-1.56	8.34	8.98	0.36	0.47	4.91E-02	4.24E-01	Multiple_Complex
TC0900009897.hg.1	FAM219A	family with sequence similarity 219, member A	-1.56	5.61	6.25	0.39	0.27	3.39E-02	3.81E-01	Coding

TC0700011626.hg.1	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-1.56	9.17	9.81	0.02	0.37	2.41E-02	3.46E-01	Multiple_Complex
TC1700010826.hg.1	SLC25A39	solute carrier family 25, member 39	-1.56	7.62	8.26	0.29	0.26	2.61E-02	3.52E-01	Multiple_Complex
TC0400007276.hg.1	KLHL5	kelch-like family member 5	-1.56	10.18	10.82	0.03	0	1.38E-02	2.93E-01	Multiple_Complex
TC0200007348.hg.1	PKDCC	protein kinase domain containing, cytoplasmic	-1.56	8.74	9.39	0.05	0.04	1.22E-02	2.84E-01	Multiple_Complex
TC0300007677.hg.1	C3orf49	chromosome 3 open reading frame 49	-1.56	4.74	5.38	0.27	0.11	2.34E-02	3.43E-01	Multiple_Complex
TC1500009370.hg.1	FAM227B	family with sequence similarity 227, member B	-1.56	6.94	7.59	0.26	0.27	2.92E-02	3.65E-01	Multiple_Complex
TC0200015431.hg.1	TMEM237	transmembrane protein 237	-1.56	10.23	10.87	0.14	0.31	2.59E-02	3.51E-01	Multiple_Complex
TC0400011202.hg.1	COQ2	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase	-1.56	9.75	10.39	0.25	0.19	1.93E-02	3.26E-01	Multiple_Complex
TC1500007912.hg.1	FBXO22	F-box protein 22	-1.56	10.15	10.8	0.06	0.14	1.16E-02	2.81E-01	Multiple_Complex
TC1600010475.hg.1	CFAP20	cilia and flagella associated protein 20	-1.56	12.17	12.82	0.21	0.01	1.34E-02	2.89E-01	Multiple_Complex
TC0X00008084.hg.1	COL4A5	collagen, type IV, alpha 5	-1.56	6.07	6.72	0.46	0.37	3.79E-02	3.93E-01	Multiple_Complex
TC0200008819.hg.1	SOWAHC	sosondowah ankyrin repeat domain family member C	-1.56	7.04	7.68	0.04	0.05	3.91E-02	3.95E-01	Coding
TC0500008296.hg.1	MAN2A1	mannosidase, alpha, class 2A, member 1	-1.56	11.54	12.19	0.28	0.18	2.15E-02	3.34E-01	Multiple_Complex
TC1000012025.hg.1	MCMBP	minichromosome maintenance complex binding protein	-1.56	10.36	11.01	0.06	0.27	1.56E-02	3.06E-01	Multiple_Complex
TC1500007691.hg.1	GLCE	glucuronic acid epimerase	-1.56	8.54	9.19	0.31	0.19	2.58E-02	3.51E-01	Multiple_Complex
TC0300010357.hg.1	CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	-1.56	9.38	10.03	0.43	0.02	2.37E-02	3.45E-01	Multiple_Complex
TC0200007886.hg.1	PNO1	partner of NOB1 homolog	-1.56	9.29	9.93	0.18	0.03	1.52E-02	3.04E-01	Multiple_Complex
TSUnmapped00000529.hg.1	FMN1	formin 1	-1.57	5.94	6.58	0.27	0.19	2.79E-02	3.60E-01	Coding
TSUnmapped00000785.hg.1	ZNF780B	zinc finger protein 780B	-1.57	4.8	5.45	0.3	0.16	1.94E-02	3.26E-01	Coding

TC0700009256.hg.1	C7orf73	chromosome 7 open reading frame 73	-1.57	9.15	9.8	0.03	0.47	3.73E-02	3.92E-01	Multiple_Complex
TC1200007835.hg.1	COQ10A	coenzyme Q10A	-1.57	9.73	10.38	0.02	0.04	1.17E-02	2.82E-01	Multiple_Complex
TC1500010756.hg.1	RAB11A	RAB11A, member RAS oncogene family	-1.57	4.04	4.69	0.37	0.11	2.73E-02	3.58E-01	NonCoding
TC0300008369.hg.1	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	-1.57	10.51	11.15	0.03	0.01	1.92E-02	3.26E-01	Multiple_Complex
TC2200008018.hg.1	TRMT2A	tRNA methyltransferase 2 homolog A	-1.57	11.7	12.35	0.1	0.02	1.43E-02	2.96E-01	Multiple_Complex
TC0600012413.hg.1	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-1.57	10.83	11.48	0.11	0.23	1.49E-02	3.02E-01	Multiple_Complex
TC1300009799.hg.1	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	-1.57	10.31	10.96	0.2	0.17	3.66E-02	3.90E-01	Multiple_Complex
TC1700012287.hg.1	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.57	8.59	9.24	0.01	0.31	2.86E-02	3.63E-01	Multiple_Complex
TC0200007257.hg.1	NDUFAF7	NADH dehydrogenase (ubiquinone) complex I, assembly factor 7	-1.57	10.18	10.83	0.55	0.03	5.00E-02	4.27E-01	Multiple_Complex
TC0600011809.hg.1	CCND3	cyclin D3	-1.57	11.54	12.19	0.18	0.25	1.65E-02	3.10E-01	Multiple_Complex
TC1400007647.hg.1	ACOT2	acyl-CoA thioesterase 2	-1.57	7.55	8.2	0.52	0.09	4.44E-02	4.11E-01	Multiple_Complex
TC1300009293.hg.1	MYCBP2	MYC binding protein 2, E3 ubiquitin protein ligase	-1.57	11.79	12.44	0.09	0.24	1.39E-02	2.93E-01	Multiple_Complex
TC1500010855.hg.1	EPB42	erythrocyte membrane protein band 4.2	-1.57	4.44	5.09	0.01	0.07	2.96E-02	3.65E-01	NonCoding
TC1900007508.hg.1	ZNF430	zinc finger protein 430	-1.57	8.64	9.29	0.2	0.23	4.32E-02	4.07E-01	Multiple_Complex
TC0100013561.hg.1	FABP3	fatty acid binding protein 3, muscle and heart	-1.57	7.79	8.44	0.35	0.19	4.01E-02	3.98E-01	Multiple_Complex
TC1200009459.hg.1	PUS1	pseudouridylate synthase 1	-1.57	6.03	6.68	0.03	0.64	4.82E-02	4.21E-01	Multiple_Complex
TC1000011659.hg.1	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	-1.57	7.53	8.18	0.36	0.25	3.37E-02	3.81E-01	Multiple_Complex
TC1700006587.hg.1	EMC6	ER membrane protein complex subunit 6	-1.57	10.48	11.13	0.44	0.11	2.75E-02	3.59E-01	Coding
TC0600012566.hg.1	MAP3K7	mitogen-activated protein kinase kinase kinase 7	-1.57	7.84	8.49	0.07	0.09	1.14E-02	2.79E-01	Multiple_Complex
TC1100012717.hg.1	PUS3	pseudouridylate synthase 3	-1.57	7.78	8.43	0.32	0.28	2.41E-02	3.46E-01	Coding

TC1200012737.hg.1	ZNF268	zinc finger protein 268	-1.57	6.44	7.09	0.41	0.05	2.33E-02	3.42E-01	Multiple_Complex
TC1100013075.hg.1	DDIAS	DNA damage-induced apoptosis suppressor	-1.57	7.43	8.08	0.42	0.04	2.46E-02	3.47E-01	Multiple_Complex
TC1900011952.hg.1	ZNF780A	zinc finger protein 780A	-1.57	9.74	10.39	0.16	0.17	1.22E-02	2.84E-01	Multiple_Complex
TC0400012916.hg.1	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-1.57	4.4	5.05	0.12	0.21	3.06E-02	3.69E-01	NonCoding
TC1100009234.hg.1	TRAPPC4; MIR3656	trafficking protein particle complex 4; microRNA 3656	-1.57	11.8	12.45	0.03	0.3	4.44E-02	4.11E-01	Multiple_Complex
TC1300010025.hg.1	RNF6	ring finger protein (C3H2C3 type) 6	-1.57	8.28	8.93	0.23	0.16	4.55E-02	4.15E-01	Multiple_Complex
TC1000011125.hg.1	KCNMA1	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001014797	-1.57	4.37	5.02	0.08	0.28	1.78E-02	3.20E-01	NonCoding
TC0100010244.hg.1	IFI16	interferon, gamma-inducible protein 16	-1.57	11.55	12.2	0.12	0.23	1.34E-02	2.89E-01	Multiple_Complex
TC0400012251.hg.1	C4orf46	chromosome 4 open reading frame 46	-1.57	11.34	11.99	0.13	0.09	1.38E-02	2.93E-01	Multiple_Complex
TC1700009850.hg.1	PMP22	peripheral myelin protein 22	-1.57	10.21	10.86	0.07	0.02	1.59E-02	3.08E-01	Multiple_Complex
TC2000009973.hg.1	ZNF343	zinc finger protein 343	-1.57	5.82	6.48	0.08	0.42	3.27E-02	3.76E-01	Multiple_Complex
TC0Y00006574.hg.1	TSPY10	testis specific protein, Y-linked 10	-1.57	3.41	4.06	0.34	0.33	4.35E-02	4.08E-01	Multiple_Complex
TSUnmapped00000747.hg.1	CCDC84	coiled-coil domain containing 84	-1.57	7.11	7.76	0.15	0.47	3.00E-02	3.66E-01	NonCoding
TC0500008125.hg.1	RHOBTB3	Rho-related BTB domain containing 3	-1.57	7.53	8.18	0.18	0.31	1.74E-02	3.16E-01	Multiple_Complex
TC0800009872.hg.1	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	-1.57	6.9	7.56	0.57	0.12	3.73E-02	3.92E-01	Coding
TC0800010103.hg.1	LSM12	Homo sapiens LSM12 homolog (S. cerevisiae), mRNA (cDNA clone MGC:57206 IMAGE:4794614), complete cds.	-1.57	12.68	13.33	0.01	0.01	1.05E-02	2.70E-01	Multiple_Complex
TC0100014501.hg.1	INSL5	insulin-like 5	-1.57	3.15	3.81	0.08	0.08	3.48E-02	3.84E-01	Coding

TC0X00009044.hg.1	GPR143	G protein-coupled receptor 143	-1.57	3.54	4.2	0.03	0.44	2.20E-02	3.38E-01	Multiple_Complex
TC0100010314.hg.1	LY9	lymphocyte antigen 9	-1.57	4.78	5.44	0.4	0.13	2.29E-02	3.41E-01	Multiple_Complex
TC0700012416.hg.1	TSPAN12	tetraspanin 12	-1.57	9.01	9.67	0.02	0.05	1.57E-02	3.06E-01	Multiple_Complex
TC0700012115.hg.1	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	-1.58	6.29	6.94	0.17	0.1	1.33E-02	2.89E-01	Multiple_Complex
TC0100015310.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	-1.58	13.1	13.76	0.24	0.1	2.14E-02	3.34E-01	Multiple_Complex
TC0300008477.hg.1	TIMMDC1	translocase of inner mitochondrial membrane domain containing 1	-1.58	10.77	11.43	0.01	0.12	1.54E-02	3.04E-01	Multiple_Complex
TC0100015061.hg.1	DBT	dihydrolipoamide branched chain transacylase E2	-1.58	9.46	10.11	0.18	0.02	4.65E-02	4.19E-01	Multiple_Complex
TC1900010479.hg.1	DMKN	dermokine	-1.58	9.84	10.5	0.15	0.24	1.32E-02	2.89E-01	Multiple_Complex
TC0200013308.hg.1	IMMT	inner membrane protein, mitochondrial	-1.58	11.48	12.14	0.06	0.13	1.25E-02	2.86E-01	Multiple_Complex
TC0400007775.hg.1	ODAM	odontogenic, ameloblast asssociated	-1.58	5.1	5.76	0.49	0.07	4.34E-02	4.07E-01	Multiple_Complex
TC1900011379.hg.1	NLRP12	NLR family, pyrin domain containing 12	-1.58	3.72	4.38	0.16	0.04	3.33E-02	3.79E-01	Multiple_Complex
TC0700013371.hg.1	ZNF138	zinc finger protein 138	-1.58	9.58	10.23	0.17	0.01	1.18E-02	2.83E-01	Multiple_Complex
TC0200015019.hg.1	KIAA1715	KIAA1715	-1.58	7.93	8.59	0.21	0.28	3.69E-02	3.90E-01	Multiple_Complex
TC0700013370.hg.1	ZNF107; MIR6839	zinc finger protein 107; microRNA 6839	-1.58	8.49	9.15	0.19	0.07	1.32E-02	2.89E-01	Multiple_Complex
TC0X00009793.hg.1	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	-1.58	4.02	4.68	0.06	0.14	1.09E-02	2.74E-01	Multiple_Complex
TC1000012585.hg.1	CHUK	conserved helix-loop-helix ubiquitous kinase	-1.58	10.96	11.62	0.4	0.16	2.63E-02	3.54E-01	Multiple_Complex
TC1300007549.hg.1	CLN5	ceroid-lipofuscinosis, neuronal 5	-1.58	8.65	9.31	0.21	0.18	3.74E-02	3.92E-01	Multiple_Complex
TC0700013502.hg.1	SNX8; MIR6836	sorting nexin 8; microRNA 6836	-1.58	7.6	8.26	0.31	0.05	2.10E-02	3.34E-01	Multiple_Complex

TC0Y00006569.hg.1	TSPY3; TSPY4; TSPY8; TSPY1	testis specific protein, Y-linked 3; testis specific protein, Y-linked 4; testis specific protein, Y-linked 8; testis specific protein, Y-linked 1	-1.58	3.52	4.18	0.33	0.35	4.50E-02	4.14E-01	Multiple_Complex
TSUnmapped00000682.hg.1	HMBS	hydroxymethylbilane synthase	-1.58	5.43	6.09	0.13	0.17	4.14E-02	4.01E-01	Coding
TC0400012640.hg.1	CCDC110	coiled-coil domain containing 110	-1.58	7.62	8.28	0.39	0.3	2.91E-02	3.65E-01	Coding
TC0100011963.hg.1	SPRTN	SprT-like N-terminal domain	-1.58	9.75	10.42	0.21	0.25	2.48E-02	3.48E-01	Multiple_Complex
TC0X00010462.hg.1	RBM41	RNA binding motif protein 41	-1.58	8.23	8.89	0.23	0.06	2.44E-02	3.47E-01	Multiple_Complex
TC0200007297.hg.1	GEMIN6	gem nuclear organelle associated protein 6	-1.58	12.65	13.32	0.63	0.03	4.80E-02	4.21E-01	Multiple_Complex
TC0400008376.hg.1	SEC24B	SEC24 homolog B, COPII coat complex component	-1.59	8.72	9.38	0.19	0.14	1.57E-02	3.06E-01	Multiple_Complex
TC0600009439.hg.1	TMEM200A	transmembrane protein 200A	-1.59	4.42	5.09	0.14	0.23	4.68E-02	4.20E-01	Coding
TC0100013920.hg.1	C1orf210	chromosome 1 open reading frame 210	-1.59	6	6.66	0.02	0.3	3.24E-02	3.75E-01	Coding
TC1400008760.hg.1	SDR39U1	short chain dehydrogenase/reductase family 39U, member 1	-1.59	10.96	11.63	0.08	0.01	1.18E-02	2.83E-01	Multiple_Complex
TC1200008224.hg.1	GLIPR1	GLI pathogenesis-related 1	-1.59	4.11	4.78	0.23	0.26	2.77E-02	3.59E-01	Multiple_Complex
TC1400010764.hg.1	VTI1B	vesicle transport through interaction with t-SNAREs 1B	-1.59	11.93	12.59	0.01	0.18	2.69E-02	3.58E-01	Multiple_Complex
TC1700012437.hg.1	SRSF1	serine/arginine-rich splicing factor 1	-1.59	10.03	10.7	0.06	0.18	1.35E-02	2.89E-01	Multiple_Complex
TC0Y00007117.hg.1	CDY2B; CDY2A	chromodomain protein, Y-linked, 2B; chromodomain protein, Y-linked, 2A	-1.59	4.64	5.31	0.23	0.43	4.12E-02	4.01E-01	Coding
TC0100006723.hg.1	VAMP3	vesicle associated membrane protein 3	-1.59	6.94	7.61	0.09	0.34	1.71E-02	3.15E-01	Multiple_Complex
TC1000009684.hg.1	GDI2	GDP dissociation inhibitor 2	-1.59	12.17	12.84	0.24	0.11	1.48E-02	3.02E-01	Multiple_Complex
TC1300006785.hg.1	B3GLCT	beta 3-glucosyltransferase	-1.59	6.24	6.91	0.35	0.09	1.83E-02	3.24E-01	Multiple_Complex
TC0600014283.hg.1	NUDT3	nudix hydrolase 3	-1.59	9.56	10.23	0.13	0.11	1.17E-02	2.82E-01	Multiple_Complex

TC0600012647.hg.1	FBXL4	F-box and leucine-rich repeat protein 4	-1.59	7.98	8.65	0.27	0.02	2.43E-02	3.46E-01	Multiple_Complex
TC0100018233.hg.1	FPGT	fucose-1-phosphate guanylyltransferase	-1.59	9.95	10.62	0.61	0.06	3.70E-02	3.90E-01	Coding
TC0900011432.hg.1	RBM18	RNA binding motif protein 18	-1.59	10.45	11.12	0.08	0.31	1.39E-02	2.93E-01	Multiple_Complex
TC0700009996.hg.1	C7orf50	chromosome 7 open reading frame 50	-1.59	6.78	7.45	0.02	0.31	2.14E-02	3.34E-01	Multiple_Complex
TC0200016516.hg.1	TMEM177	transmembrane protein 177	-1.59	7.16	7.83	0.31	0.07	2.89E-02	3.64E-01	Multiple_Complex
TC0200016413.hg.1	FKBP1B	FK506 binding protein 1B	-1.59	6.28	6.95	0.57	0.2	4.64E-02	4.19E-01	Multiple_Complex
TC1600008003.hg.1	ADGRG5	adhesion G protein-coupled receptor G5	-1.59	5.45	6.12	0.07	0.16	4.02E-02	3.98E-01	Multiple_Complex
TC1600011428.hg.1	TERF2IP	telomeric repeat binding factor 2, interacting protein	-1.59	9.41	10.09	0.12	0.02	8.60E-03	2.54E-01	Coding
TC1900011752.hg.1	ZNF223	zinc finger protein 223	-1.59	6.19	6.86	0.35	0.55	4.03E-02	3.98E-01	Multiple_Complex
TC1500009221.hg.1	TP53BP1	tumor protein p53 binding protein 1	-1.59	10.77	11.45	0.12	0.12	2.63E-02	3.54E-01	Multiple_Complex
TC0100015160.hg.1	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	-1.59	7.69	8.37	0.31	0.03	2.40E-02	3.46E-01	Multiple_Complex
TC0800011071.hg.1	TMEM64	transmembrane protein 64	-1.59	7.64	8.31	0.42	0.26	2.41E-02	3.46E-01	Multiple_Complex
TC0800008916.hg.1	EFR3A	EFR3 homolog A	-1.59	8.3	8.97	0.46	0.01	2.26E-02	3.40E-01	Multiple_Complex
TC0X00010426.hg.1	MORF4L2	mortality factor 4 like 2	-1.59	11.85	12.52	0.13	0.09	1.09E-02	2.74E-01	Multiple_Complex
TC0100013458.hg.1	EYA3	EYA transcriptional coactivator and phosphatase 3	-1.59	5.78	6.45	0.27	0.17	3.05E-02	3.68E-01	Multiple_Complex
TC0900011385.hg.1	PSMD5	proteasome 26S subunit, non-ATPase 5	-1.59	10.61	11.29	0.05	0.22	4.33E-02	4.07E-01	Multiple_Complex
TC1100010932.hg.1	OR10W1	olfactory receptor, family 10, subfamily W, member 1	-1.59	4.39	5.06	0.08	0.11	9.50E-03	2.62E-01	Coding
TC1200012666.hg.1	TMEM19	transmembrane protein 19	-1.59	9.55	10.22	0.08	0.11	9.00E-03	2.60E-01	Multiple_Complex
TC0700010719.hg.1	TBX20	T-box 20	-1.59	8.39	9.07	0.29	0.19	2.12E-02	3.34E-01	Multiple_Complex
TC1900009805.hg.1	SAMD1	sterile alpha motif domain containing 1	-1.6	8.8	9.47	0.07	0.19	4.04E-02	3.99E-01	Multiple_Complex

TC1200007759.hg.1	COPZ1	coatomer protein complex subunit zeta 1	-1.6	10.39	11.06	0.07	0.12	9.40E-03	2.62E-01	Multiple_Complex
TC0600007306.hg.1	BTN3A3	butyrophilin, subfamily 3, member A3	-1.6	10.19	10.87	0.21	0.21	2.43E-02	3.46E-01	Multiple_Complex
TC0700006781.hg.1	BZW2	basic leucine zipper and W2 domains 2	-1.6	9.33	10	0.33	0.14	2.75E-02	3.59E-01	Multiple_Complex
TC1400010728.hg.1	HEATR5A	HEAT repeat containing 5A	-1.6	9	9.68	0.08	0.17	2.42E-02	3.46E-01	Multiple_Complex
TC0700008246.hg.1	DMTF1	cyclin D binding myb-like transcription factor 1	-1.6	9.93	10.61	0.06	0.21	2.82E-02	3.62E-01	Multiple_Complex
TC0900008888.hg.1	ENDOG	endonuclease G	-1.6	7.92	8.59	0.64	0.25	4.24E-02	4.04E-01	Coding
TC1200009876.hg.1	CD69	CD69 molecule	-1.6	3.66	4.33	0.47	0.19	2.34E-02	3.43E-01	Multiple_Complex
TC1700010723.hg.1	PTRF	polymerase I and transcript release factor	-1.6	9.5	10.18	0.48	0.26	3.34E-02	3.80E-01	Multiple_Complex
TC0100015931.hg.1	PMVK	phosphomevalonate kinase	-1.6	6.64	7.32	0.05	0.07	2.80E-02	3.60E-01	Multiple_Complex
TC0X00010169.hg.1	BRWD3	bromodomain and WD repeat domain containing 3	-1.6	10.62	11.3	0.31	0.26	1.81E-02	3.23E-01	Multiple_Complex
TC0700009398.hg.1	TAS2R3	taste receptor, type 2, member 3	-1.6	4.9	5.58	0.15	0.37	2.53E-02	3.49E-01	Coding
TC1500006902.hg.1	FAM98B	family with sequence similarity 98, member B	-1.6	6.73	7.41	0.42	0.25	4.58E-02	4.17E-01	Multiple_Complex
TC0100010661.hg.1	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	-1.6	10.71	11.39	0.24	0.03	1.02E-02	2.68E-01	Multiple_Complex
TC0100010664.hg.1	ZBTB37	zinc finger and BTB domain containing 37	-1.6	4.4	5.08	0.01	0.24	1.19E-02	2.83E-01	Multiple_Complex
TC0900006560.hg.1	PDCD1LG2	programmed cell death 1 ligand 2	-1.6	5.15	5.83	0.43	0.07	2.56E-02	3.50E-01	Multiple_Complex
TC1600008214.hg.1	TANGO6	transport and golgi organization 6 homolog	-1.6	5.99	6.67	0.25	0	3.83E-02	3.94E-01	Multiple_Complex
TC1400006521.hg.1	PNP	purine nucleoside phosphorylase	-1.6	11.38	12.06	0.13	0.04	1.06E-02	2.71E-01	Multiple_Complex
TC0900007733.hg.1	IDNK	idnK, gluconokinase homolog (E. coli)	-1.6	4.85	5.53	0.19	0.25	3.34E-02	3.80E-01	Multiple_Complex
TC2200008609.hg.1	TXN2	thioredoxin 2	-1.6	11.7	12.38	0.4	0.14	4.16E-02	4.01E-01	Multiple_Complex
TC0900009918.hg.1	FAM205A	family with sequence similarity 205, member A	-1.6	3.8	4.48	0.26	0.64	4.54E-02	4.15E-01	Coding
TC0200013878.hg.1	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	-1.6	10.72	11.4	0.06	0.13	1.46E-02	3.00E-01	Multiple_Complex
TC0100014937.hg.1	FAM69A	family with sequence similarity 69, member A	-1.6	5.01	5.69	0.28	0.2	1.98E-02	3.29E-01	Coding

TC2000007507.hg.1	ZSWIM1	zinc finger, SWIM-type containing 1	-1.6	7.26	7.94	0.11	0.29	3.17E-02	3.72E-01	Multiple_Complex
TC1500009192.hg.1	LRRC57	leucine rich repeat containing 57	-1.6	6.78	7.46	0.2	0.25	1.58E-02	3.07E-01	Multiple_Complex
TC0800012165.hg.1	SCRIB; MIR937	scribbled planar cell polarity protein; microRNA 937	-1.6	7.86	8.54	0.1	0.17	8.80E-03	2.57E-01	Multiple_Complex
TC1300009993.hg.1	BIVM	basic, immunoglobulin-like variable motif containing	-1.6	7	7.69	0.22	0.31	1.56E-02	3.05E-01	Multiple_Complex
TC0200015894.hg.1	DOCK10	Transcript Identified by AceView, Entrez Gene ID(s) 55619	-1.6	4.84	5.52	0.11	0.44	4.58E-02	4.17E-01	Unassigned
TC0100013998.hg.1	HECTD3	HECT domain containing E3 ubiquitin protein ligase 3	-1.61	8.78	9.47	0.01	0.23	1.38E-02	2.93E-01	Multiple_Complex
TC1600007723.hg.1	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	-1.61	8	8.68	0.06	0.15	3.20E-02	3.72E-01	Multiple_Complex
TC1300007137.hg.1	RB1	retinoblastoma 1	-1.61	8.67	9.35	0.11	0.25	2.66E-02	3.57E-01	Multiple_Complex
TC1500010883.hg.1	SNAPC5	small nuclear RNA activating complex polypeptide 5	-1.61	9.07	9.75	0.25	0.1	1.64E-02	3.10E-01	Coding
TC0600014086.hg.1	ZNF391	zinc finger protein 391	-1.61	6.92	7.61	0.09	0.46	2.02E-02	3.31E-01	Multiple_Complex
TC0900010352.hg.1	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-1.61	10.85	11.54	0.23	0.06	1.23E-02	2.84E-01	Multiple_Complex
TC1500007975.hg.1	IREB2	iron responsive element binding protein 2	-1.61	9.23	9.92	0.03	0.01	2.25E-02	3.40E-01	Multiple_Complex
TC1000011992.hg.1	SFXN4	sideroflexin 4	-1.61	6.76	7.44	0.38	0.07	4.83E-02	4.21E-01	Multiple_Complex
TC1100007384.hg.1	ALKBH3; SEC14L1P1	alkB homolog 3, alpha-ketoglutarate-dependent dioxygenase; SEC14-like 1 pseudogene 1	-1.61	7.44	8.13	0.4	0.11	2.96E-02	3.65E-01	Multiple_Complex
TC0600012199.hg.1	EYS	eyes shut homolog (Drosophila)	-1.61	4.82	5.51	0.53	0.24	4.59E-02	4.18E-01	Multiple_Complex
TC0600008873.hg.1	UFL1	UFM1-specific ligase 1	-1.61	7.02	7.71	0.44	0.03	1.88E-02	3.26E-01	Multiple_Complex
TC0100008132.hg.1	TMEM69	transmembrane protein 69	-1.61	9.94	10.63	0.05	0.03	8.30E-03	2.50E-01	Multiple_Complex
TC0900007106.hg.1	LINC00961	long intergenic non-protein coding RNA 961	-1.61	4.93	5.62	0.16	0.28	1.73E-02	3.16E-01	NonCoding

TC1100011829.hg.1	CREBZF	CREB/ATF bZIP transcription factor	-1.61	9.32	10.01	0.13	0.22	1.13E-02	2.78E-01	Multiple_Complex
TC0300011801.hg.1	MINA	MYC induced nuclear antigen	-1.61	10.22	10.9	0.23	0.19	2.08E-02	3.34E-01	Multiple_Complex
TC0X00007781.hg.1	ZNF711	zinc finger protein 711	-1.61	4.81	5.5	0.09	0.03	1.88E-02	3.26E-01	Multiple_Complex
TC1900011573.hg.1	ZNF416	zinc finger protein 416	-1.61	4.29	4.98	0.09	0.36	2.12E-02	3.34E-01	Coding
TC0200016505.hg.1	CCDC138	coiled-coil domain containing 138	-1.61	6.22	6.91	0.07	0.11	1.38E-02	2.93E-01	NonCoding
TC1100012667.hg.1	OR8B3	olfactory receptor, family 8, subfamily B, member 3	-1.62	4.25	4.95	0.13	0.68	4.15E-02	4.01E-01	Coding
TC1400009422.hg.1	RAB15	RAB15, member RAS oncogene family	-1.62	4.67	5.36	0.23	0.24	1.94E-02	3.26E-01	Multiple_Complex
TC1600011343.hg.1	CLUAP1	clusterin associated protein 1	-1.62	6.17	6.87	0	0.14	1.59E-02	3.07E-01	Multiple_Complex
TC1500008511.hg.1	LRRC28	leucine rich repeat containing 28	-1.62	8.16	8.86	0.11	0.07	1.69E-02	3.13E-01	Multiple_Complex
TC1700006592.hg.1	GSG2	germ cell associated 2 (haspin)	-1.62	7.34	8.04	0.28	0.02	1.69E-02	3.12E-01	Coding
TC0100015764.hg.1	FAM63A	family with sequence similarity 63, member A	-1.62	5.31	6.01	0.03	0.04	6.70E-03	2.34E-01	Multiple_Complex
TC0200016498.hg.1	LIPT1	lipoyltransferase 1	-1.62	5.46	6.15	0.11	0.3	5.00E-02	4.27E-01	Multiple_Complex
TC0700008397.hg.1	DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1	-1.62	3.56	4.25	0.16	0.01	1.26E-02	2.87E-01	Multiple_Complex
TC0400010939.hg.1	UGT2A2; UGT2A1	UDP glucuronosyltransferase 2 family, polypeptide A2; UDP glucuronosyltransferase 2 family, polypeptide A1, complex locus	-1.62	3.63	4.33	0.02	0.71	4.23E-02	4.03E-01	Multiple_Complex
TC0800011314.hg.1	UBR5	ubiquitin protein ligase E3 component n-recognin 5	-1.62	6.33	7.02	0.08	0.13	9.80E-03	2.65E-01	Multiple_Complex
TC1200008213.hg.1	ATXN7L3B	ataxin 7-like 3B	-1.62	8.04	8.73	0.44	0.2	2.40E-02	3.46E-01	Multiple_Complex
TC0300013727.hg.1	NCBP2	nuclear cap binding protein subunit 2	-1.62	10.69	11.38	0.02	0.18	2.73E-02	3.58E-01	Multiple_Complex
TC0300009468.hg.1	PRKCI	protein kinase C, iota	-1.62	11.65	12.35	0.07	0.05	9.70E-03	2.65E-01	Multiple_Complex
TC0200012804.hg.1	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	-1.62	7.32	8.02	0.13	0.07	1.31E-02	2.89E-01	Multiple_Complex
TC0400010612.hg.1	NFXL1	nuclear transcription factor, X-box binding-like 1	-1.62	8.86	9.56	0.22	0.15	1.29E-02	2.87E-01	Multiple_Complex

TC0200006831.hg.1	VSNL1	visinin like 1	-1.62	5.24	5.94	0.18	0.22	1.11E-02	2.75E-01	Multiple_Complex
TC1600007234.hg.1	DCTN5	dynactin 5 (p25)	-1.62	8.99	9.69	0.25	0.24	2.15E-02	3.34E-01	Multiple_Complex
TC0300011182.hg.1	GLT8D1	glycosyltransferase 8 domain containing 1	-1.62	11.08	11.78	0.05	0.02	7.40E-03	2.46E-01	Multiple_Complex
TC1100010859.hg.1	OR5M8	olfactory receptor, family 5, subfamily M, member 8	-1.62	3.98	4.68	0.27	0.5	2.44E-02	3.47E-01	Coding
TC0X00007668.hg.1	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	-1.62	6.97	7.67	0.03	0.18	2.15E-02	3.34E-01	Multiple_Complex
TC2200008829.hg.1	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	-1.62	8.75	9.45	0.06	0.13	9.80E-03	2.65E-01	Multiple_Complex
TC0500011705.hg.1	NREP	neuronal regeneration related protein	-1.63	9.24	9.94	0.13	0.14	1.01E-02	2.68E-01	Multiple_Complex
TC1700008452.hg.1	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	-1.63	10.14	10.84	0.67	0.11	3.78E-02	3.93E-01	Multiple_Complex
TC0300012670.hg.1	ATR	ATR serine/threonine kinase	-1.63	10.09	10.79	0.24	0.12	1.12E-02	2.77E-01	Multiple_Complex
TC1400006853.hg.1	AKAP6	A kinase (PRKA) anchor protein 6	-1.63	5.64	6.34	0.25	0.12	1.51E-02	3.04E-01	Multiple_Complex
TC1000008502.hg.1	TBC1D12	TBC1 domain family, member 12	-1.63	6.43	7.13	0.27	0.11	1.21E-02	2.84E-01	Multiple_Complex
TC1700007108.hg.1	MIEF2	mitochondrial elongation factor 2	-1.63	4.83	5.53	0.1	0.27	1.42E-02	2.94E-01	Multiple_Complex
TC1700008256.hg.1	RSAD1	radical S-adenosyl methionine domain containing 1	-1.63	7.46	8.16	0.25	0.04	2.04E-02	3.32E-01	Multiple_Complex
TC0100016364.hg.1	SCYL3	SCY1-like, kinase-like 3	-1.63	6.63	7.34	0.04	0.33	1.39E-02	2.93E-01	Multiple_Complex
TC1700008820.hg.1	C17orf80	chromosome 17 open reading frame 80	-1.63	10.35	11.05	0.37	0.04	2.04E-02	3.32E-01	Multiple_Complex
TC1000010727.hg.1	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-1.63	4.13	4.83	0.12	0.52	2.56E-02	3.50E-01	Multiple_Complex
TC0400011538.hg.1	PAPSS1	3-phosphoadenosine 5-phosphosulfate synthase 1	-1.63	7.13	7.84	0.18	0.65	4.96E-02	4.26E-01	Multiple_Complex
TC0100009428.hg.1	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	-1.63	9.84	10.55	0.12	0.04	1.98E-02	3.29E-01	Multiple_Complex
TC1700007360.hg.1	TMEM97	transmembrane protein 97	-1.63	12.69	13.4	0.03	0.02	1.74E-02	3.16E-01	Coding

TC0700010435.hg.1	CDCA7L	cell division cycle associated 7-like	-1.63	10.7	11.41	0.22	0.08	1.20E-02	2.84E-01	Multiple_Complex
TC1900006603.hg.1	ZNF556	zinc finger protein 556	-1.63	8.37	9.08	0.05	0.03	7.60E-03	2.48E-01	Coding
TC1400009709.hg.1	MLH3	mutL homolog 3	-1.63	8.78	9.49	0.15	0.33	2.71E-02	3.58E-01	Multiple_Complex
TC0100010012.hg.1	SMCP	sperm mitochondria-associated cysteine-rich protein	-1.63	3.54	4.25	0.22	0.09	1.51E-02	3.04E-01	Coding
TC0300014081.hg.1	TMEM41A	transmembrane protein 41A	-1.63	6.11	6.82	0.32	0.1	1.46E-02	3.00E-01	Multiple_Complex
TC0600009365.hg.1	NCOA7	Transcript Identified by AceView, Entrez Gene ID(s) 135112	-1.63	6.19	6.9	0.02	0.04	2.06E-02	3.33E-01	Unassigned
TC0200014164.hg.1	CYP27C1	cytochrome P450, family 27, subfamily C, polypeptide 1	-1.63	3.67	4.38	0.68	0.15	3.70E-02	3.90E-01	Coding
TC0100014505.hg.1	SLC35D1	solute carrier family 35 (UDP-GlcA/UDP-GalNAc transporter), member D1	-1.63	7.39	8.1	0.04	0.09	1.68E-02	3.12E-01	Multiple_Complex
TSUnmapped00000749.hg.1	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	-1.63	4.51	5.22	0.03	0.71	4.39E-02	4.10E-01	NonCoding
TC1600011047.hg.1	HSDL1	hydroxysteroid dehydrogenase like 1	-1.64	8.64	9.35	0.3	0.12	3.57E-02	3.86E-01	Multiple_Complex
TC1300008716.hg.1	KBTBD7	kelch repeat and BTB (POZ) domain containing 7	-1.64	5.6	6.31	0.02	0.02	9.10E-03	2.60E-01	Coding
TC0400012933.hg.1	NAAA	N-acylethanolamine acid amidase	-1.64	7.08	7.79	0.14	0.12	7.30E-03	2.46E-01	Multiple_Complex
TC0300006791.hg.1	KAT2B	K(lysine) acetyltransferase 2B	-1.64	6.81	7.52	0.14	0.02	1.09E-02	2.74E-01	Multiple_Complex
TC0100016137.hg.1	CD84	CD84 molecule	-1.64	3.49	4.2	0.17	0.06	7.10E-03	2.41E-01	Multiple_Complex
TC0400012905.hg.1	QDPR	quinoid dihydropteridine reductase	-1.64	9.45	10.16	0.08	0.12	1.74E-02	3.16E-01	Multiple_Complex
TC0500007048.hg.1	C5orf22	chromosome 5 open reading frame 22	-1.64	7.62	8.33	0.43	0.16	4.15E-02	4.01E-01	Multiple_Complex
TC1400010715.hg.1	AJUBA	ajuba LIM protein	-1.64	11.9	12.61	0.21	0.03	2.24E-02	3.40E-01	Multiple_Complex
TC1200009307.hg.1	TMEM132B	transmembrane protein 132B	-1.64	4.52	5.23	0.19	0.3	1.08E-02	2.74E-01	Multiple_Complex
TC0500008664.hg.1	HSPA4	heat shock 70kDa protein 4	-1.64	12.02	12.73	0.04	0.05	5.70E-03	2.22E-01	Multiple_Complex

TC1800006635.hg.1	TWSG1	twisted gastrulation BMP signaling modulator 1	-1.64	9.44	10.15	0.19	0.43	1.84E-02	3.24E-01	Multiple_Complex
TC1100008541.hg.1	AAMDC	adipogenesis associated, Mth938 domain containing	-1.64	10.82	11.54	0.06	0.13	6.20E-03	2.27E-01	Multiple_Complex
TC0400009217.hg.1	KLHL2	kelch-like family member 2	-1.64	6.84	7.55	0.56	0.07	3.27E-02	3.76E-01	Multiple_Complex
TC0800008626.hg.1	UTP23	UTP23, small subunit (SSU) processome component, homolog (yeast)	-1.64	9.34	10.05	0.15	0.07	1.24E-02	2.85E-01	Multiple_Complex
TC1000012549.hg.1	PARG	poly (ADP-ribose) glycohydrolase	-1.64	6.98	7.69	0.21	0.43	3.49E-02	3.84E-01	Multiple_Complex
TC1700010692.hg.1	KLHL11	kelch-like family member 11	-1.64	7.06	7.78	0.15	0.43	3.83E-02	3.94E-01	Multiple_Complex
TC0100015866.hg.1	S100A4	S100 calcium binding protein A4	-1.64	12.79	13.51	0.04	0.06	1.16E-02	2.81E-01	Multiple_Complex
TC1000012428.hg.1	AKR1C3	aldo-keto reductase family 1, member C3	-1.64	5.9	6.61	0.17	0.63	4.07E-02	4.00E-01	Multiple_Complex
TC1300008371.hg.1	CENPJ	centromere protein J	-1.64	8.71	9.43	0.29	0.19	3.18E-02	3.72E-01	Multiple_Complex
TC0100013623.hg.1	SYNC	syncoilin, intermediate filament protein	-1.64	4.18	4.9	0.29	0.55	3.60E-02	3.87E-01	Multiple_Complex
TC0100007564.hg.1	RAB42	RAB42, member RAS oncogene family	-1.64	8.11	8.82	0.57	0.5	4.56E-02	4.16E-01	Multiple_Complex
TC0900011454.hg.1	ZBTB26	zinc finger and BTB domain containing 26	-1.64	7.12	7.84	0.21	0.3	1.10E-02	2.74E-01	Coding
TC1900007456.hg.1	ZNF253	zinc finger protein 253	-1.64	10.2	10.91	0.38	0.07	4.01E-02	3.98E-01	Multiple_Complex
TC0100010369.hg.1	ATF6	activating transcription factor 6	-1.64	12.24	12.96	0.01	0.27	8.30E-03	2.50E-01	Multiple_Complex
TC0100010341.hg.1	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	-1.64	5.29	6.01	0.29	0	1.10E-02	2.74E-01	Multiple_Complex
TC1300009008.hg.1	NEK3	NIMA-related kinase 3	-1.65	8.28	9	0.09	0.24	1.27E-02	2.87E-01	Multiple_Complex
TC0X00008833.hg.1	FAM50A	family with sequence similarity 50, member A	-1.65	6.62	7.34	0.02	0.19	4.26E-02	4.05E-01	Multiple_Complex
TC1800009278.hg.1	TCEB3CL	transcription elongation factor B polypeptide 3C-like	-1.65	4.72	5.44	0.35	0.08	1.19E-02	2.83E-01	Coding
TC0800012454.hg.1	ZHX1	zinc fingers and homeoboxes 1	-1.65	10.9	11.62	0.09	0.08	7.70E-03	2.48E-01	Multiple_Complex
TC1900011902.hg.1	SMIM7; MED26	small integral membrane protein 7; mediator complex subunit 26	-1.65	12.95	13.67	0	0.1	7.90E-03	2.49E-01	Multiple_Complex

TSUnmapped00000242.hg.1	KIF15	kinesin family member 15	-1.65	7.14	7.86	0.25	0.18	9.20E-03	2.62E-01	Coding
TC1100012990.hg.1	MIR670HG; HSD17B12	MIR670 host gene; hydroxysteroid (17-beta) dehydrogenase 12	-1.65	4.52	5.24	0.16	0.08	9.60E-03	2.63E-01	Multiple_Complex
TC0200012299.hg.1	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	-1.65	8.94	9.66	0.23	0.43	3.44E-02	3.84E-01	Multiple_Complex
TC1700007796.hg.1	IGFBP4	insulin like growth factor binding protein 4	-1.65	7.46	8.18	0.16	0.24	1.90E-02	3.26E-01	Multiple_Complex
TC0100008450.hg.1	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	-1.65	7.86	8.58	0.27	0.11	2.98E-02	3.66E-01	Multiple_Complex
TC1200006604.hg.1	CD9	CD9 molecule	-1.65	7.37	8.1	0.32	0.03	1.70E-02	3.14E-01	Multiple_Complex
TC0500013316.hg.1	CD180	CD180 molecule	-1.65	4.14	4.86	0.59	0.27	2.89E-02	3.64E-01	Multiple_Complex
TC0200014775.hg.1	KCNH7	potassium channel, voltage gated eag related subfamily H, member 7	-1.65	3.81	4.54	0.28	0.54	2.52E-02	3.49E-01	Multiple_Complex
TC1300006989.hg.1	AKAP11	A kinase (PRKA) anchor protein 11	-1.65	9.71	10.44	0.26	0.25	1.41E-02	2.94E-01	Multiple_Complex
TC1000011050.hg.1	AP3M1	adaptor-related protein complex 3, mu 1 subunit	-1.65	11.92	12.64	0.2	0.24	1.76E-02	3.17E-01	Multiple_Complex
TC0900009707.hg.1	IFNA2	interferon, alpha 2	-1.65	5.01	5.73	0.42	0.19	3.46E-02	3.84E-01	Coding
TC1300008329.hg.1	SACS	sacsin molecular chaperone	-1.65	7.58	8.31	0.16	0.03	1.19E-02	2.83E-01	Multiple_Complex
TC0800007137.hg.1	FZD3	frizzled class receptor 3	-1.66	6.86	7.58	0.18	0.29	1.18E-02	2.83E-01	Multiple_Complex
TC0800006681.hg.1	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-1.66	4.48	5.21	0.44	0.16	2.17E-02	3.36E-01	NonCoding
TC1600009063.hg.1	MRPS34	mitochondrial ribosomal protein S34	-1.66	9.18	9.91	0.07	0.25	9.20E-03	2.62E-01	Multiple_Complex
TC1900011814.hg.1	ZNF17	zinc finger protein 17	-1.66	9.67	10.4	0.17	0.34	4.67E-02	4.20E-01	Multiple_Complex
TC0100010877.hg.1	TSEN15	TSEN15 tRNA splicing endonuclease subunit	-1.66	9.12	9.85	0.1	0.12	7.60E-03	2.48E-01	Multiple_Complex
TC0500009803.hg.1	EXOC3	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript NM_007277	-1.66	6.13	6.86	0.19	0.2	2.16E-02	3.34E-01	NonCoding

TC0900011146.hg.1	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	-1.66	9.49	10.21	0.09	0.15	9.20E-03	2.62E-01	Multiple_Complex
TC0800006557.hg.1	MCPH1	microcephalin 1	-1.66	8.34	9.07	0.44	0.13	1.97E-02	3.29E-01	Multiple_Complex
TC0700013324.hg.1	GET4	golgi to ER traffic protein 4	-1.66	7.85	8.58	0.19	0.05	2.16E-02	3.35E-01	Multiple_Complex
TC0200008351.hg.1	RPIA	ribose 5-phosphate isomerase A	-1.66	5.82	6.55	0.45	0.02	3.35E-02	3.80E-01	Multiple_Complex
TC0200008500.hg.1	CIAO1	cytosolic iron-sulfur assembly component 1	-1.66	7.45	8.18	0.07	0.04	5.20E-03	2.14E-01	Multiple_Complex
TC1300007070.hg.1	COG3	component of oligomeric golgi complex 3	-1.66	10.91	11.64	0.21	0.05	1.70E-02	3.14E-01	Multiple_Complex
TC1900011141.hg.1	PIH1D1	PIH1 domain containing 1	-1.66	11.13	11.86	0.12	0.36	1.39E-02	2.93E-01	Multiple_Complex
TC0200012219.hg.1	FAM98A	family with sequence similarity 98, member A	-1.66	11.33	12.06	0.04	0.08	6.90E-03	2.39E-01	Multiple_Complex
TC0100008410.hg.1	LEXM	lymphocyte expansion molecule	-1.66	3.96	4.69	0.18	0.15	1.06E-02	2.71E-01	Coding
TC0900008967.hg.1	EXOSC2	exosome component 2	-1.66	13.21	13.95	0.04	0.11	4.90E-03	2.13E-01	Multiple_Complex
TC0800007985.hg.1	GDAP1	ganglioside induced differentiation associated protein 1	-1.66	7.35	8.08	0.66	0	3.79E-02	3.93E-01	Multiple_Complex
TC0500012070.hg.1	CDKN2AIPNL	CDKN2A interacting protein N-terminal like	-1.66	10.45	11.19	0.23	0.02	6.90E-03	2.39E-01	Coding
TC1300010007.hg.1	TMEM255B	transmembrane protein 255B	-1.66	3.94	4.67	0.13	0.46	1.55E-02	3.05E-01	Multiple_Complex
TC0200013096.hg.1	MOB1A	MOB kinase activator 1A	-1.66	11.23	11.96	0.21	0.09	8.10E-03	2.49E-01	Multiple_Complex
TC0100014226.hg.1	C1orf123	chromosome 1 open reading frame 123	-1.66	11.85	12.58	0.09	0.03	6.00E-03	2.27E-01	Multiple_Complex
TC0900006892.hg.1	IFNK	interferon, kappa	-1.66	3.34	4.07	0.08	0.04	4.70E-03	2.09E-01	Coding
TC1100009049.hg.1	C11orf57	chromosome 11 open reading frame 57	-1.66	10.7	11.43	0.13	0.21	8.70E-03	2.55E-01	Multiple_Complex
TC0300006575.hg.1	FANCD2	Fanconi anemia complementation group D2	-1.66	10.23	10.96	0.17	0.11	9.50E-03	2.62E-01	Multiple_Complex
TC1600011347.hg.1	ALG1; NAGPA-AS1	ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase; NAGPA antisense RNA 1	-1.66	9.05	9.78	0.04	0.33	1.97E-02	3.28E-01	Multiple_Complex

TC0X00006590.hg.1	WWC3	WWC family member 3	-1.67	5.54	6.27	0.05	0.35	9.90E-03	2.67E-01	Multiple_Complex
TC0800011565.hg.1	RAD21; MIR3610	RAD21 cohesin complex component; microRNA 3610	-1.67	8.75	9.48	0.29	0.09	1.32E-02	2.89E-01	Multiple_Complex
TC0100017666.hg.1	ABCB10	ATP binding cassette subfamily B member 10	-1.67	6.98	7.72	0.25	0.17	1.79E-02	3.21E-01	Multiple_Complex
TC1200010038.hg.1	EPS8	epidermal growth factor receptor pathway substrate 8	-1.67	6.42	7.15	0.23	0.09	1.02E-02	2.68E-01	Multiple_Complex
TC1200008671.hg.1	HCFC2	host cell factor C2	-1.67	8.76	9.49	0.11	0.02	7.20E-03	2.43E-01	Multiple_Complex
TC1700008879.hg.1	ICT1	immature colon carcinoma transcript 1	-1.67	9.51	10.25	0.32	0.36	2.08E-02	3.34E-01	Multiple_Complex
TC0900007667.hg.1	PSAT1	phosphoserine aminotransferase 1	-1.67	10.87	11.61	0.05	0.08	4.90E-03	2.13E-01	Multiple_Complex
TC0X00007923.hg.1	CSTF2	cleavage stimulation factor, 3 pre-RNA, subunit 2	-1.67	8	8.74	0.11	0.03	8.80E-03	2.57E-01	Multiple_Complex
TC0800012350.hg.1	MTBP	MDM2 binding protein	-1.67	4.04	4.77	0.08	0.03	1.56E-02	3.05E-01	NonCoding
TC0700008857.hg.1	MDFIC	MyoD family inhibitor domain containing	-1.67	4.22	4.95	0.16	0.25	1.16E-02	2.81E-01	Multiple_Complex
TC1500010234.hg.1	EFTUD1	elongation factor Tu GTP binding domain containing 1	-1.67	9	9.74	0.07	0.14	1.38E-02	2.93E-01	Multiple_Complex
TC0Y00006632.hg.1	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked	-1.67	3.7	4.44	0.06	0.56	1.93E-02	3.26E-01	Multiple_Complex
TC0600011600.hg.1	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	-1.67	9.86	10.6	0.1	0.29	1.14E-02	2.80E-01	Multiple_Complex
TC0500011163.hg.1	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-1.67	9.35	10.09	0.08	0.13	6.10E-03	2.27E-01	Multiple_Complex
TC0200016767.hg.1	MREG	melanoregulin	-1.67	5.65	6.39	0.27	0.29	1.30E-02	2.88E-01	Multiple_Complex
TC1700010303.hg.1	TEFM	transcription elongation factor, mitochondrial	-1.67	8.6	9.34	0.68	0.31	4.09E-02	4.00E-01	Multiple_Complex
TC1100009540.hg.1	C11orf44	chromosome 11 open reading frame 44	-1.68	4.07	4.82	0.2	0.01	9.20E-03	2.62E-01	Multiple_Complex
TC0400011748.hg.1	CCNA2	cyclin A2	-1.68	12.92	13.66	0.01	0.16	6.20E-03	2.27E-01	Multiple_Complex
TC0300009313.hg.1	GFM1	G elongation factor, mitochondrial 1	-1.68	10.79	11.53	0.05	0.09	8.20E-03	2.50E-01	Multiple_Complex

TC1900008323.hg.1	CD3EAP	CD3e molecule, epsilon associated protein	-1.68	6.57	7.32	0.28	0.33	1.27E-02	2.87E-01	Multiple_Complex
TC1400008838.hg.1	STRN3	striatin, calmodulin binding protein 3	-1.68	6.96	7.71	0.08	0.03	3.53E-02	3.85E-01	Multiple_Complex
TC0500013238.hg.1	ZMAT2	zinc finger, matrin-type 2	-1.68	10.61	11.36	0.09	0.18	6.70E-03	2.35E-01	Coding
TC1900007040.hg.1	CNN1	calponin 1, basic, smooth muscle	-1.68	6.11	6.86	0.12	0.06	4.40E-03	2.04E-01	Multiple_Complex
TC1200012629.hg.1	DAZAP2	DAZ associated protein 2	-1.68	9.67	10.42	0.1	0.24	6.90E-03	2.39E-01	Multiple_Complex
TC0X00011334.hg.1	BRCC3	BRCA1/BRCA2-containing complex subunit 3	-1.68	9.11	9.86	0.1	0.1	1.07E-02	2.71E-01	Multiple_Complex
TC0X00008028.hg.1	FAM199X	family with sequence similarity 199, X-linked	-1.68	7.08	7.83	0.17	0.38	2.71E-02	3.58E-01	Multiple_Complex
TC0300006631.hg.1	MKRN2	makorin ring finger protein 2	-1.68	9.08	9.83	0.23	0.1	6.70E-03	2.34E-01	Multiple_Complex
TC0400008803.hg.1	RAB33B	RAB33B, member RAS oncogene family	-1.68	8.53	9.28	0.44	0.02	1.67E-02	3.12E-01	Multiple_Complex
TC0200007174.hg.1	SPAST	spastin	-1.68	9.54	10.29	0.3	0	2.68E-02	3.58E-01	Multiple_Complex
TC0300008518.hg.1	GTF2E1	general transcription factor IIE subunit 1	-1.68	10.55	11.3	0.29	0.15	1.51E-02	3.04E-01	Multiple_Complex
TC0500007935.hg.1	ZCCHC9	zinc finger, CCHC domain containing 9	-1.68	10.79	11.54	0.22	0.34	1.28E-02	2.87E-01	Multiple_Complex
TC0300008506.hg.1	LRRC58	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, intronic, UTR3 best transcript NM_001099678	-1.68	6.75	7.5	0.08	0.36	1.40E-02	2.93E-01	NonCoding
TC0300007220.hg.1	ZNF502	zinc finger protein 502	-1.68	3.45	4.2	0.42	0.24	2.86E-02	3.63E-01	Coding
TC0X00010409.hg.1	BEX2	brain expressed X-linked 2	-1.68	4.5	5.25	0.15	0.31	2.47E-02	3.48E-01	Coding
TC2100007032.hg.1	CBR1	carbonyl reductase 1	-1.69	10.3	11.05	0.15	0.15	1.01E-02	2.68E-01	Multiple_Complex
TC0600013531.hg.1	NUP43	nucleoporin 43kDa	-1.69	11.71	12.47	0.22	0.03	1.14E-02	2.80E-01	Multiple_Complex
TC0X00009929.hg.1	OPHN1	oligophrenin 1	-1.69	6.21	6.96	0.27	0.31	3.18E-02	3.72E-01	Multiple_Complex
TC0200009933.hg.1	ERICH2	glutamate rich 2	-1.69	4.83	5.58	0.3	0.21	1.11E-02	2.75E-01	Multiple_Complex
TC0200011919.hg.1	LDAH	lipid droplet associated hydrolase	-1.69	9.34	10.09	0.55	0.33	4.52E-02	4.15E-01	Multiple_Complex
TC1600010168.hg.1	SHCBP1	SHC SH2-domain binding protein 1	-1.69	9.5	10.25	0.45	0.26	4.78E-02	4.21E-01	Multiple_Complex

TC0400008924.hg.1	LSM6	Transcript Identified by AceView, Entrez Gene ID(s) 11157	-1.69	5.8	6.56	0.55	0.33	2.35E-02	3.44E-01	Unassigned
TC1700011247.hg.1	MKS1	Meckel syndrome, type 1	-1.69	5.63	6.39	0.26	0	1.90E-02	3.26E-01	Multiple_Complex
TC1500010672.hg.1	TARSL2	threonyl-tRNA synthetase-like 2	-1.69	6.06	6.81	0.18	0.1	3.68E-02	3.90E-01	Multiple_Complex
TC2000007435.hg.1	IFT52	intraflagellar transport 52	-1.69	9.13	9.89	0.63	0.33	4.91E-02	4.24E-01	Multiple_Complex
TC0100009568.hg.1	MAN1A2	mannosidase, alpha, class 1A, member 2	-1.69	12.77	13.53	0.11	0.18	7.80E-03	2.48E-01	Multiple_Complex
TC1000011555.hg.1	MORN4	MORN repeat containing 4	-1.69	5.1	5.85	0.32	0.2	1.05E-02	2.70E-01	Multiple_Complex
TC1900007957.hg.1	ZNF568	zinc finger protein 568	-1.69	5.44	6.19	0.48	0.14	4.86E-02	4.23E-01	Multiple_Complex
TC0900007129.hg.1	MELK	maternal embryonic leucine zipper kinase	-1.69	10.55	11.31	0.17	0.14	1.17E-02	2.82E-01	Multiple_Complex
TC0200016115.hg.1	ARL4C	ADP-ribosylation factor like GTPase 4C	-1.69	4.88	5.64	0.44	0.25	1.65E-02	3.10E-01	Multiple_Complex
TC1900009511.hg.1	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	-1.69	9.71	10.47	0.14	0.06	5.90E-03	2.25E-01	Multiple_Complex
TC0100018156.hg.1	ATAD3B	ATPase family, AAA domain containing 3B	-1.69	8.06	8.82	0.15	0.28	6.90E-03	2.39E-01	Multiple_Complex
TC0600010305.hg.1	C6orf120	chromosome 6 open reading frame 120	-1.69	6.38	7.14	0.39	0.34	1.94E-02	3.26E-01	Coding
TC0700010899.hg.1	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	-1.69	5.64	6.39	0.26	0	1.06E-02	2.71E-01	Multiple_Complex
TC1200011862.hg.1	ALKBH2	alkB homolog 2, alpha-ketoglutarate-dependent dioxygenase	-1.69	9.23	9.99	0.04	0.19	5.30E-03	2.15E-01	Multiple_Complex
TC0100017059.hg.1	RBBP5	retinoblastoma binding protein 5	-1.69	10.19	10.94	0.17	0.02	5.40E-03	2.18E-01	Multiple_Complex
TC1300009674.hg.1	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	-1.69	10.29	11.05	0.25	0.29	1.11E-02	2.75E-01	Multiple_Complex
TC1900006882.hg.1	CERS4	ceramide synthase 4	-1.69	8.81	9.57	0.21	0.15	6.50E-03	2.32E-01	Multiple_Complex
TC1000009221.hg.1	ZRANB1	zinc finger, RAN-binding domain containing 1	-1.69	8.11	8.87	0.17	0.11	5.00E-03	2.13E-01	Multiple_Complex
TC1700009554.hg.1	ZNF594	zinc finger protein 594	-1.69	5.36	6.12	0.25	0.31	9.60E-03	2.63E-01	Coding
TC1200012700.hg.1	C12orf75	chromosome 12 open reading frame 75	-1.7	11.17	11.93	0.21	0.24	6.30E-03	2.30E-01	Multiple_Complex

TC0800007641.hg.1	RGS20	regulator of G-protein signaling 20	-1.7	5.56	6.32	0.59	0.3	3.17E-02	3.72E-01	Multiple_Complex
TC0600012952.hg.1	FRK	fyn-related Src family tyrosine kinase	-1.7	5.31	6.08	0.09	0.65	3.02E-02	3.67E-01	Coding
TC1100007805.hg.1	TMEM216	transmembrane protein 216	-1.7	6.8	7.57	0.52	0.45	3.15E-02	3.72E-01	Multiple_Complex
TC1100006644.hg.1	RRM1	ribonucleotide reductase M1	-1.7	11.96	12.73	0.12	0.16	4.90E-03	2.13E-01	Multiple_Complex
TC0200010182.hg.1	DUSP19	dual specificity phosphatase 19	-1.7	8.08	8.84	0.05	0.14	1.19E-02	2.83E-01	Multiple_Complex
TC0100013818.hg.1	PPT1	palmitoyl-protein thioesterase 1	-1.7	10.76	11.53	0.01	0.26	3.82E-02	3.94E-01	Multiple_Complex
TC1900008569.hg.1	ZNF473	zinc finger protein 473	-1.7	8.34	9.1	0.2	0.37	1.51E-02	3.04E-01	Multiple_Complex
TC0600006611.hg.1	WRNIP1	Werner helicase interacting protein 1	-1.7	9.41	10.18	0.16	0.31	3.52E-02	3.85E-01	Multiple_Complex
TC1000008800.hg.1	GSTO1	glutathione S-transferase omega 1	-1.7	10.37	11.14	0.02	0.42	1.54E-02	3.04E-01	Multiple_Complex
TC1200009649.hg.1	CRACR2A	calcium release activated channel regulator 2A	-1.7	4.89	5.66	0.64	0.21	3.12E-02	3.71E-01	Multiple_Complex
TC2000006628.hg.1	MCM8	minichromosome maintenance 8 homologous recombination repair factor	-1.7	9.15	9.92	0.33	0.12	2.50E-02	3.49E-01	Multiple_Complex
TC0500011483.hg.1	MCTP1	multiple C2 domains, transmembrane 1	-1.7	4.8	5.56	0.09	0.19	8.40E-03	2.52E-01	Multiple_Complex
TC0500007421.hg.1	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	-1.7	7.71	8.48	0.02	0.2	4.70E-03	2.08E-01	Multiple_Complex
TC1600009646.hg.1	KNOP1	lysine-rich nucleolar protein 1	-1.7	10.62	11.39	0.32	0.37	1.16E-02	2.81E-01	Multiple_Complex
TC0100006501.hg.1	CPTP	ceramide-1-phosphate transfer protein	-1.7	4.85	5.61	0.53	0.37	2.82E-02	3.62E-01	Multiple_Complex
TC1100013227.hg.1	FDXACB1	ferredoxin-fold anticodon binding domain containing 1	-1.7	3.44	4.21	0.03	0.21	5.40E-03	2.17E-01	Multiple_Complex
TC0300012216.hg.1	CCDC14	coiled-coil domain containing 14	-1.7	10.9	11.67	0.11	0.23	7.40E-03	2.46E-01	Multiple_Complex
TC1200008606.hg.1	UTP20	UTP20 small subunit (SSU) processome component	-1.7	10.8	11.56	0	0.21	4.40E-03	2.04E-01	Multiple_Complex
TC1500007644.hg.1	C15orf61	chromosome 15 open reading frame 61	-1.7	6.94	7.71	0.42	0.24	2.07E-02	3.34E-01	Multiple_Complex

TC1200006778.hg.1	KLRF2	killer cell lectin-like receptor subfamily F, member 2	-1.7	3.31	4.08	0.18	0.33	7.40E-03	2.46E-01	Coding
TC1800006748.hg.1	SEH1L	SEH1-like nucleoporin	-1.71	10.21	10.98	0.24	0.06	1.94E-02	3.26E-01	Multiple_Complex
TC0100011461.hg.1	DIEXF	digestive organ expansion factor homolog (zebrafish)	-1.71	8.85	9.62	0.2	0.11	6.20E-03	2.28E-01	Multiple_Complex
TC0600007836.hg.1	KCTD20	potassium channel tetramerization domain containing 20	-1.71	10.3	11.07	0.01	0.17	4.20E-03	2.02E-01	Multiple_Complex
TC1200010901.hg.1	RNF41	ring finger protein 41, E3 ubiquitin protein ligase	-1.71	10.08	10.85	0.05	0.04	3.20E-03	1.79E-01	Multiple_Complex
TC0500010865.hg.1	DEPDC1B	DEP domain containing 1B	-1.71	9.99	10.76	0.32	0.24	1.10E-02	2.75E-01	Multiple_Complex
TC0200013894.hg.1	ANAPC1	anaphase promoting complex subunit 1	-1.71	10.39	11.16	0.11	0.17	7.20E-03	2.42E-01	Multiple_Complex
TC0100016969.hg.1	KLHL12	kelch-like family member 12	-1.71	7.96	8.73	0.51	0.05	3.10E-02	3.71E-01	Multiple_Complex
TC1200007906.hg.1	XRCC6BP1	XRCC6 binding protein 1	-1.71	10.04	10.81	0.41	0.03	1.87E-02	3.25E-01	Multiple_Complex
TC0100018442.hg.1	CYB5RL	cytochrome b5 reductase-like	-1.71	6.63	7.4	0.33	0.1	1.23E-02	2.84E-01	Multiple_Complex
TC0800009204.hg.1	TIGD5	tigger transposable element derived 5	-1.71	6.89	7.67	0.32	0.31	9.80E-03	2.65E-01	Multiple_Complex
TC0100008559.hg.1	ANGPTL3	angiopoietin like 3	-1.71	5.23	6	0.27	0.13	1.43E-02	2.95E-01	Multiple_Complex
TC0100017935.hg.1	RGS7	regulator of G-protein signaling 7	-1.71	3.73	4.51	0.03	0.27	8.80E-03	2.57E-01	Multiple_Complex
TC0300012924.hg.1	VEPH1	ventricular zone expressed PH domain containing 1	-1.71	7.33	8.11	0.32	0.09	3.60E-02	3.87E-01	Multiple_Complex
TC0500010680.hg.1	PARP8	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, intronic best transcript NM_001178056	-1.71	7.62	8.39	0.01	0.4	1.82E-02	3.23E-01	NonCoding
TC1200011224.hg.1	LRRC10	leucine rich repeat containing 10	-1.71	4.03	4.81	0.23	0.46	2.02E-02	3.31E-01	Coding
TC1200006555.hg.1	CCND2	cyclin D2	-1.71	9.7	10.48	0.44	0.06	9.60E-03	2.64E-01	Multiple_Complex
TC0300008989.hg.1	SLC25A36	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	-1.71	13.13	13.91	0.16	0.19	6.00E-03	2.26E-01	Multiple_Complex
TC0900009437.hg.1	AK3	adenylate kinase 3	-1.71	8.75	9.52	0.57	0.15	2.97E-02	3.65E-01	Multiple_Complex

TC1500010715.hg.1	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	-1.71	10.33	11.11	0.08	0.16	5.20E-03	2.13E-01	Multiple_Complex
TC0800007210.hg.1	WRN	Transcript Identified by AceView, Entrez Gene ID(s) 7486	-1.72	4.34	5.12	0	0.03	8.30E-03	2.50E-01	Coding
TC0100013760.hg.1	SF3A3	splicing factor 3a subunit 3	-1.72	11.23	12	0.18	0.1	9.30E-03	2.62E-01	Multiple_Complex
TC1900011935.hg.1	ZFP30	ZFP30 zinc finger protein	-1.72	5.44	6.22	0.03	0.56	1.84E-02	3.24E-01	Multiple_Complex
TC0100015943.hg.1	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	-1.72	11.03	11.81	0.14	0.28	8.50E-03	2.53E-01	Multiple_Complex
TC1500009782.hg.1	PDCD7	programmed cell death 7	-1.72	8.31	9.09	0.31	0.3	1.89E-02	3.26E-01	Multiple_Complex
TC1100010216.hg.1	PLEKHA7	pleckstrin homology domain containing, family A member 7	-1.72	5.16	5.94	0.4	0.64	4.70E-02	4.21E-01	Multiple_Complex
TC0600013147.hg.1	ARHGAP18	Rho GTPase activating protein 18	-1.72	10.31	11.09	0.04	0.19	2.05E-02	3.32E-01	Multiple_Complex
TC0100008584.hg.1	ALG6	ALG6, alpha-1,3-glucosyltransferase	-1.72	8.65	9.43	0.82	0.15	4.81E-02	4.21E-01	Multiple_Complex
TC1100010483.hg.1	CSTF3	cleavage stimulation factor, 3 pre-RNA, subunit 3	-1.72	11.16	11.94	0.2	0.28	7.90E-03	2.49E-01	Multiple_Complex
TC1600009952.hg.1	YPEL3	yippee like 3	-1.72	5.03	5.81	0.04	0.22	4.40E-03	2.04E-01	Multiple_Complex
TC1100009700.hg.1	PDDC1	Parkinson disease 7 domain containing 1	-1.72	8.89	9.67	0.53	0.1	2.33E-02	3.42E-01	Multiple_Complex
TC1100008477.hg.1	DGAT2	diacylglycerol O-acyltransferase 2	-1.72	5.95	6.74	0.06	0.29	6.30E-03	2.30E-01	Multiple_Complex
TC2000008573.hg.1	CRNKL1	crooked neck pre-mRNA splicing factor 1	-1.72	9.6	10.39	0.31	0.2	7.70E-03	2.48E-01	Multiple_Complex
TC0200015741.hg.1	RNF25	ring finger protein 25	-1.72	8.93	9.72	0.05	0.18	1.59E-02	3.07E-01	Multiple_Complex
TC1700011294.hg.1	PTRH2	peptidyl-tRNA hydrolase 2	-1.72	12.07	12.85	0.61	0.07	2.01E-02	3.30E-01	Multiple_Complex
TC0300007164.hg.1	SS18L2	synovial sarcoma translocation gene on chromosome 18-like 2	-1.73	12.26	13.05	0.38	0.08	1.34E-02	2.89E-01	Multiple_Complex
TC1900006827.hg.1	ADGRE1	adhesion G protein-coupled receptor E1	-1.73	3.75	4.54	0.37	0.12	1.49E-02	3.02E-01	Multiple_Complex
TC0100007954.hg.1	SMAP2	small ArfGAP2	-1.73	11.18	11.97	0.06	0.16	5.10E-03	2.13E-01	Multiple_Complex
TC0100016076.hg.1	OR6K2	olfactory receptor, family 6, subfamily K, member 2	-1.73	3.66	4.45	0.18	0.17	3.08E-02	3.70E-01	Coding

TC0100016476.hg.1	KIAA0040	KIAA0040	-1.73	6.51	7.3	0.02	0.26	7.70E-03	2.48E-01	Multiple_Complex
TC0900006758.hg.1	DENND4C	DENN/MADD domain containing 4C	-1.73	8.11	8.91	0.06	0.13	7.90E-03	2.49E-01	Multiple_Complex
TC0300011450.hg.1	TMF1	TATA element modulatory factor 1	-1.73	6.9	7.7	0.3	0.21	8.10E-03	2.49E-01	Multiple_Complex
TC0500011881.hg.1	CEP120	centrosomal protein 120kDa	-1.73	7.45	8.24	0.28	0.05	7.80E-03	2.48E-01	Multiple_Complex
TC1100013185.hg.1	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	-1.74	12.52	13.32	0.03	0.34	1.99E-02	3.29E-01	Multiple_Complex
TC1200011495.hg.1	LUM	lumican	-1.74	6.04	6.83	0.21	0.03	7.50E-03	2.46E-01	Multiple_Complex
TC1100006840.hg.1	CTR9	CTR9 homolog, Paf1/RNA polymerase II complex component	-1.74	12.38	13.18	0.03	0	4.60E-03	2.06E-01	Multiple_Complex
TC0X00010099.hg.1	ABCB7	ATP binding cassette subfamily B member 7	-1.74	10.34	11.14	0.02	0.01	3.00E-03	1.72E-01	Multiple_Complex
TC1400008070.hg.1	SERPINA13P	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 13, pseudogene	-1.74	4.66	5.46	0.48	0.36	2.47E-02	3.48E-01	Multiple_Complex
TC0500009274.hg.1	FABP6	fatty acid binding protein 6, ileal	-1.74	4.95	5.75	0.04	0.58	3.89E-02	3.95E-01	Multiple_Complex
TC1000008377.hg.1	LIPJ	lipase, family member J	-1.74	3.73	4.52	0.05	0.82	3.45E-02	3.84E-01	Multiple_Complex
TC1700010701.hg.1	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	-1.74	7.73	8.53	0.19	0.67	2.48E-02	3.48E-01	NonCoding
TC2000010001.hg.1	PIGU	phosphatidylinositol glycan anchor biosynthesis class U	-1.74	9.62	10.42	0.28	0.15	5.20E-03	2.13E-01	Multiple_Complex
TC0200016447.hg.1	ACYP2	acylphosphatase 2, muscle type	-1.74	8.76	9.56	0.11	0.02	2.90E-03	1.71E-01	Multiple_Complex
TC0500008437.hg.1	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	-1.74	7.99	8.79	0.15	0.25	2.45E-02	3.47E-01	Multiple_Complex
TC1500009504.hg.1	PYGO1	pygopus family PHD finger 1	-1.74	6.81	7.61	0.22	0.25	8.50E-03	2.54E-01	Multiple_Complex
TC1700010763.hg.1	BRCA1	breast cancer 1, early onset	-1.74	7.57	8.37	0.61	0.06	2.78E-02	3.59E-01	Multiple_Complex
TC1500008225.hg.1	MRPS11	mitochondrial ribosomal protein S11	-1.74	9.53	10.33	0.06	0.19	3.30E-03	1.80E-01	Multiple_Complex
TC1100011374.hg.1	KMT5B	lysine (K)-specific methyltransferase 5B	-1.74	7.3	8.1	0.06	0.41	1.02E-02	2.68E-01	Multiple_Complex

TC1100013144.hg.1	ZBED5	zinc finger, BED-type containing 5	-1.74	10.93	11.74	0.12	0.24	5.10E-03	2.13E-01	Multiple_Complex
TC0300008846.hg.1	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.75	9.11	9.92	0.1	0.01	3.30E-03	1.80E-01	Multiple_Complex
TC0400011791.hg.1	ANKRD50	ankyrin repeat domain 50	-1.75	7.12	7.93	0.12	0.28	1.13E-02	2.78E-01	Multiple_Complex
TC0900010814.hg.1	ZNF484	zinc finger protein 484	-1.75	9.1	9.91	0.07	0.11	7.50E-03	2.46E-01	Multiple_Complex
TC0200012652.hg.1	PNPT1	polyribonucleotide nucleotidyltransferase 1	-1.75	9.93	10.73	0.38	0.02	3.23E-02	3.74E-01	Multiple_Complex
TC1200010264.hg.1	IPO8	importin 8	-1.75	7.93	8.74	0.26	0.21	9.40E-03	2.62E-01	Multiple_Complex
TC1000008351.hg.1	MINPP1	multiple inositol-polyphosphate phosphatase 1	-1.75	8.96	9.76	0.11	0.26	1.41E-02	2.94E-01	Multiple_Complex
TC1700008463.hg.1	DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	-1.75	9.56	10.36	0.36	0.18	3.15E-02	3.72E-01	Multiple_Complex
TC1400008844.hg.1	HECTD1	HECT domain containing E3 ubiquitin protein ligase 1	-1.75	11.63	12.44	0.18	0.02	4.20E-03	2.01E-01	Multiple_Complex
TC0100016916.hg.1	PHLDA3	pleckstrin homology-like domain, family A, member 3	-1.75	9.15	9.96	0.09	0.05	1.44E-02	2.97E-01	Multiple_Complex
TC1800007355.hg.1	C18orf54	chromosome 18 open reading frame 54	-1.75	4.42	5.23	0.71	0.22	3.70E-02	3.90E-01	Multiple_Complex
TC0900010946.hg.1	TSTD2	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	-1.75	6.97	7.78	0.01	0.29	5.10E-03	2.13E-01	Multiple_Complex
TC0900008574.hg.1	TRIM32	tripartite motif containing 32	-1.75	6.3	7.11	0.47	0.2	3.77E-02	3.92E-01	Coding
TC0400012496.hg.1	AGA	aspartylglucosaminidase	-1.75	9.36	10.17	0.12	0.06	4.40E-03	2.04E-01	Multiple_Complex
TC1100009419.hg.1	EI24	etoposide induced 2.4	-1.75	9.77	10.58	0.11	0.08	4.10E-03	2.01E-01	Multiple_Complex
TC1200009834.hg.1	MFAP5	microfibrillar associated protein 5	-1.75	8.33	9.14	0.17	0.08	5.70E-03	2.21E-01	Multiple_Complex
TC1100007727.hg.1	FAM111B	family with sequence similarity 111, member B	-1.76	9.47	10.28	0.04	0.49	1.18E-02	2.83E-01	Multiple_Complex
TSUnmapped00000758.hg.1	KIF15	kinesin family member 15	-1.76	3.34	4.15	0.11	0.67	2.64E-02	3.55E-01	NonCoding
TC0800011061.hg.1	NBN	nibrin	-1.76	6.81	7.62	0.19	0.48	2.14E-02	3.34E-01	Multiple_Complex
TC0600013054.hg.1	SERINC1	serine incorporator 1	-1.76	10.76	11.57	0.2	0.08	8.20E-03	2.50E-01	Multiple_Complex

TC1200010569.hg.1	ASB8	ankyrin repeat and SOCS box containing 8	-1.76	10.61	11.42	0.39	0.13	6.80E-03	2.38E-01	Multiple_Complex
TC2000009673.hg.1	SYCP2	synaptonemal complex protein 2	-1.76	4.62	5.44	0.8	0.07	4.88E-02	4.24E-01	Multiple_Complex
TC1100012358.hg.1	USP28	ubiquitin specific peptidase 28	-1.76	5.99	6.8	0.28	0.16	1.62E-02	3.09E-01	Multiple_Complex
TC0600010095.hg.1	MAP3K4	mitogen-activated protein kinase kinase kinase 4	-1.76	7.43	8.25	0.15	0.28	2.00E-02	3.30E-01	Multiple_Complex
TC0200011898.hg.1	SDC1	syndecan 1	-1.76	6.26	7.08	0.27	0.37	1.45E-02	2.98E-01	Multiple_Complex
TC0400008483.hg.1	UGT8	UDP glycosyltransferase 8	-1.76	8.2	9.02	0	0.23	3.50E-03	1.84E-01	Multiple_Complex
TC0700010926.hg.1	TMED4	transmembrane p24 trafficking protein 4	-1.76	11.88	12.69	0.13	0.07	1.27E-02	2.87E-01	Multiple_Complex
TC0400007399.hg.1	GUF1	GUF1 homolog, GTPase	-1.76	9.75	10.57	0.19	0.11	2.77E-02	3.59E-01	Multiple_Complex
TC0300011054.hg.1	CCDC71	coiled-coil domain containing 71	-1.76	7.32	8.14	0.04	0.15	5.30E-03	2.17E-01	Coding
TC1100010948.hg.1	GLYAT	glycine-N-acyltransferase	-1.76	4.06	4.87	0.08	0.5	1.24E-02	2.84E-01	Multiple_Complex
TC0500006436.hg.1	PLEKHG4B	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_052909	-1.76	4.44	5.26	0.36	0.04	5.80E-03	2.23E-01	NonCoding
TC0400008902.hg.1	ABCE1	ATP binding cassette subfamily E member 1	-1.77	11.36	12.18	0.14	0.23	5.00E-03	2.13E-01	Multiple_Complex
TC0200016626.hg.1	MBOAT2	membrane bound O-acyltransferase domain containing 2	-1.77	7.66	8.48	0.05	0.1	3.20E-03	1.79E-01	Multiple_Complex
TC1400010738.hg.1	KLHL28	kelch-like family member 28	-1.77	5	5.82	0.33	0.85	3.82E-02	3.94E-01	NonCoding
TC2000009053.hg.1	TTI1	TELO2 interacting protein 1	-1.77	9.24	10.06	0.11	0.3	4.60E-03	2.05E-01	Multiple_Complex
TC1500010723.hg.1	CHAC1	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	-1.77	7.66	8.48	0.47	0.11	1.11E-02	2.75E-01	Multiple_Complex
TC1700010747.hg.1	COA3	cytochrome c oxidase assembly factor 3	-1.77	10.85	11.67	0.11	0.01	7.30E-03	2.44E-01	Multiple_Complex
TC0700006783.hg.1	TSPAN13	tetraspanin 13	-1.77	10.86	11.68	0.25	0.11	1.05E-02	2.69E-01	Multiple_Complex
TC0300006577.hg.1	BRK1	BRICK1, SCAR/WAVE actin-nucleating complex subunit	-1.77	9.14	9.96	0.01	0.14	2.50E-03	1.61E-01	Multiple_Complex
TC0100017368.hg.1	BPNT1	3(2), 5-bisphosphate nucleotidase 1	-1.77	11.11	11.93	0.69	0.02	2.11E-02	3.34E-01	Multiple_Complex

TC0800008321.hg.1	LAPTM4B	lysosomal protein transmembrane 4 beta	-1.77	9.89	10.71	0.11	0.01	7.90E-03	2.49E-01	Multiple_Complex
TC0200008259.hg.1	MAT2A	methionine adenosyltransferase II, alpha	-1.77	10.99	11.81	0.18	0.03	2.90E-03	1.70E-01	Multiple_Complex
TC0800009266.hg.1	MFSD3	major facilitator superfamily domain containing 3	-1.77	12.29	13.11	0.57	0.03	1.17E-02	2.82E-01	Multiple_Complex
TC1100008804.hg.1	ANKRD49	ankyrin repeat domain 49	-1.77	9.05	9.88	0.23	0.31	1.54E-02	3.04E-01	Multiple_Complex
TC0400012864.hg.1	ADAM29	ADAM metallopeptidase domain 29	-1.77	3.83	4.65	0.21	0.14	3.70E-03	1.90E-01	NonCoding
TC0100017947.hg.1	OPN3	opsin 3	-1.77	8.15	8.98	0.25	0.37	7.20E-03	2.42E-01	Multiple_Complex
TC0600010647.hg.1	ECI2	enoyl-CoA delta isomerase 2	-1.77	11.14	11.97	0.29	0.12	5.00E-03	2.13E-01	Multiple_Complex
TC2200007361.hg.1	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	-1.78	9.2	10.03	0.01	0.19	3.20E-03	1.76E-01	Multiple_Complex
TC0X00010355.hg.1	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	-1.78	8.19	9.02	0.51	0.15	3.47E-02	3.84E-01	Multiple_Complex
TC0800009619.hg.1	CTSB	cathepsin B	-1.78	5.94	6.77	0.52	0.13	4.57E-02	4.16E-01	Multiple_Complex
TC1200011320.hg.1	BBS10	Bardet-Biedl syndrome 10	-1.78	9.09	9.92	0.13	0.17	1.21E-02	2.84E-01	Coding
TC0600011808.hg.1	MED20	mediator complex subunit 20	-1.78	8.98	9.81	0.34	0.09	8.50E-03	2.54E-01	Multiple_Complex
TC0400012458.hg.1	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-1.78	7.09	7.92	0.28	0.09	1.41E-02	2.94E-01	Multiple_Complex
TC0400009024.hg.1	ARFIP1	ADP-ribosylation factor interacting protein 1	-1.78	9.86	10.69	0.11	0.03	4.30E-03	2.03E-01	Multiple_Complex
TC1200008601.hg.1	ANO4	anoctamin 4	-1.78	3.9	4.73	0.12	0.44	8.90E-03	2.58E-01	Multiple_Complex
TC1100009445.hg.1	FAM118B	family with sequence similarity 118, member B	-1.78	10.86	11.69	0.01	0.23	5.50E-03	2.18E-01	Multiple_Complex
TC0600007303.hg.1	BTN3A1	butyrophilin, subfamily 3, member A1	-1.78	9.34	10.17	0.08	0.29	9.50E-03	2.62E-01	Multiple_Complex
TC1800007326.hg.1	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	-1.78	10.4	11.23	0.07	0.05	8.90E-03	2.58E-01	Multiple_Complex
TC0600008622.hg.1	SH3BGRL2	SH3 domain binding glutamate-rich protein like 2	-1.78	4.79	5.62	0.68	0.28	2.30E-02	3.41E-01	Multiple_Complex

TC0500007772.hg.1	BTF3	basic transcription factor 3	-1.78	10.96	11.8	0.4	0.32	1.50E-02	3.03E-01	Multiple_Complex
TC1200009550.hg.1	KDM5A	lysine (K)-specific demethylase 5A	-1.78	5.89	6.72	0.28	0.44	1.03E-02	2.69E-01	Multiple_Complex
TC0500008766.hg.1	MYOT	myotilin	-1.78	4.74	5.57	0.28	0.07	4.60E-03	2.06E-01	Multiple_Complex
TC0400006756.hg.1	TRMT44	tRNA methyltransferase 44 homolog (S. cerevisiae)	-1.78	5.06	5.89	0.74	0.28	3.92E-02	3.95E-01	Multiple_Complex
TC0200010805.hg.1	BCS1L	BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone	-1.78	8.73	9.56	0.14	0.16	7.50E-03	2.46E-01	Multiple_Complex
TC0X00007696.hg.1	FGF16	fibroblast growth factor 16	-1.78	4.54	5.38	0.06	0.14	7.20E-03	2.43E-01	Coding
TC0500009424.hg.1	FGF18	fibroblast growth factor 18	-1.78	6.08	6.91	0.51	0.11	2.75E-02	3.59E-01	Coding
TC1200012745.hg.1	C1RL	complement component 1, r subcomponent-like	-1.78	6.83	7.67	0.33	0.08	5.00E-03	2.13E-01	Multiple_Complex
TC0500011255.hg.1	MTX3	metaxin 3	-1.79	6.14	6.97	0.14	0.03	1.50E-02	3.04E-01	Multiple_Complex
TC0600014202.hg.1	FGFR1OP	FGFR1 oncogene partner	-1.79	7.6	8.44	0	0.14	4.50E-03	2.04E-01	Multiple_Complex
TC0300013719.hg.1	CEP19	centrosomal protein 19kDa	-1.79	5.51	6.34	0.04	0.13	4.50E-03	2.04E-01	Multiple_Complex
TC2100008486.hg.1	BAGE; BAGE4; BAGE3; BAGE2; BAGE5	B melanoma antigen; B melanoma antigen family, member 4; B melanoma antigen family, member 3; B melanoma antigen family, member 2; B melanoma antigen family, member 5	-1.79	8.25	9.09	0.12	0.02	1.17E-02	2.82E-01	Multiple_Complex
TC1300008338.hg.1	MIPEP	mitochondrial intermediate peptidase	-1.79	10.46	11.3	0.13	0.07	2.80E-03	1.69E-01	Multiple_Complex
TC1600009246.hg.1	ROGDI	rogdi homolog	-1.79	7.79	8.63	0.43	0.46	2.09E-02	3.34E-01	Multiple_Complex
TC0700010749.hg.1	KIAA0895	KIAA0895	-1.79	6.78	7.62	0.03	0.18	3.70E-03	1.90E-01	Multiple_Complex
TC1000011839.hg.1	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	-1.79	7.06	7.91	0.07	0.11	1.37E-02	2.93E-01	Multiple_Complex
TC1300008292.hg.1	MICU2	mitochondrial calcium uptake 2	-1.79	8.49	9.33	0.28	0.16	5.90E-03	2.25E-01	Multiple_Complex
TC1900008036.hg.1	MRPS12	mitochondrial ribosomal protein S12	-1.79	7.62	8.46	0.29	0.23	2.95E-02	3.65E-01	Multiple_Complex

TC0X00011121.hg.1	GABRE; MIR224; MIR452	gamma-aminobutyric acid (GABA) A receptor, epsilon; microRNA 224; microRNA 452	-1.79	7.62	8.46	0.01	0.02	3.10E-03	1.73E-01	Multiple_Complex
TC2000007466.hg.1	KCNK15	potassium channel, two pore domain subfamily K, member 15	-1.79	3.82	4.66	0.34	0.32	7.30E-03	2.45E-01	Multiple_Complex
TC0600008863.hg.1	MANEA	mannosidase, endo-alpha	-1.8	7.33	8.17	0.42	0.1	8.30E-03	2.50E-01	Multiple_Complex
TC1900009002.hg.1	ZNF530	zinc finger protein 530	-1.8	6.24	7.08	0.17	0.02	1.41E-02	2.94E-01	Multiple_Complex
TSUnmapped00000341.hg.1	ZNF780A	zinc finger protein 780A	-1.8	5.02	5.87	0.42	0.45	1.54E-02	3.04E-01	Coding
TC1100008955.hg.1	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-1.8	12.5	13.34	0.24	0.05	3.10E-03	1.73E-01	Multiple_Complex
TSUnmapped00000237.hg.1	ZKSCAN7	zinc finger with KRAB and SCAN domains 7	-1.8	4.27	5.12	0.14	0.46	1.01E-02	2.68E-01	Coding
TC1100009043.hg.1	DIXDC1	DIX domain containing 1	-1.8	6.26	7.11	0.58	0.34	2.51E-02	3.49E-01	Multiple_Complex
TC0100009191.hg.1	AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	-1.8	8.39	9.24	0.33	0.17	5.80E-03	2.25E-01	Multiple_Complex
TC0500010423.hg.1	MTMR12	myotubularin related protein 12	-1.8	8.33	9.18	0.07	0.52	7.90E-03	2.48E-01	Multiple_Complex
TC1100009078.hg.1	TTC12	tetratricopeptide repeat domain 12	-1.8	7.22	8.07	0.25	0.22	4.00E-03	1.97E-01	Multiple_Complex
TC0200010448.hg.1	STRADB	STE20-related kinase adaptor beta	-1.8	10.55	11.41	0.01	0.09	2.20E-03	1.54E-01	Multiple_Complex
TC0100008124.hg.1	MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	-1.81	9.39	10.24	0.09	0.21	7.80E-03	2.48E-01	Multiple_Complex
TC0400008007.hg.1	GPAT3	glycerol-3-phosphate acyltransferase 3	-1.81	5.35	6.2	0.18	0.27	1.21E-02	2.84E-01	Multiple_Complex
TC1800009244.hg.1	HMSD	histocompatibility (minor) serpin domain containing	-1.81	3.7	4.55	0.04	0.56	1.09E-02	2.74E-01	Multiple_Complex
TC1200007842.hg.1	SPRYD4	SPRY domain containing 4	-1.81	8.76	9.62	0.1	0.15	2.60E-03	1.62E-01	Coding
TC2100007668.hg.1	C21orf91; C21orf91-OT1	chromosome 21 open reading frame 91; C21orf91 overlapping transcript 1	-1.81	9.1	9.95	0.07	0.03	2.30E-03	1.59E-01	Multiple_Complex

TC0500012523.hg.1	ATOX1	antioxidant 1 copper chaperone	-1.81	9.3	10.16	0.18	0.11	5.20E-03	2.14E-01	Multiple_Complex
TC0400011108.hg.1	CNOT6L	CCR4-NOT transcription complex subunit 6-like	-1.81	7.93	8.78	0.31	0.29	5.00E-03	2.13E-01	Multiple_Complex
TC1100012186.hg.1	MSANTD4	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils	-1.81	9.01	9.87	0.28	0.09	1.03E-02	2.69E-01	Multiple_Complex
TC0100015049.hg.1	FRRS1	ferric-chelate reductase 1	-1.82	8.44	9.3	0.4	0.05	1.83E-02	3.24E-01	Multiple_Complex
TC1000011605.hg.1	CWF19L1; SNORA12	CWF19-like 1, cell cycle control (S. pombe); small nucleolar RNA, H/ACA box 12	-1.82	7.85	8.71	0.27	0.38	1.68E-02	3.12E-01	Multiple_Complex
TC0700010472.hg.1	TRA2A	transformer 2 alpha homolog (Drosophila)	-1.82	11.78	12.64	0.03	0.17	3.30E-03	1.81E-01	Multiple_Complex
TC0X00010640.hg.1	CXorf56	chromosome X open reading frame 56	-1.82	8.68	9.54	0.24	0.16	8.00E-03	2.49E-01	Multiple_Complex
TC1500007752.hg.1	THSD4	Transcript Identified by AceView, Entrez Gene ID(s) 79875	-1.82	3.52	4.39	0.29	0.08	4.40E-03	2.04E-01	Unassigned
TC1700010221.hg.1	DHRS13	dehydrogenase/reductase (SDR family) member 13	-1.82	7.92	8.78	0.03	0.51	4.10E-02	4.01E-01	Multiple_Complex
TC1600006439.hg.1	MPG	N-methylpurine DNA glycosylase	-1.82	7.23	8.1	0.15	0.24	1.75E-02	3.16E-01	Multiple_Complex
TC1600010171.hg.1	VPS35	VPS35 retromer complex component	-1.82	8.72	9.58	0.58	0.48	2.28E-02	3.41E-01	Multiple_Complex
TC0600012009.hg.1	DEFB114	defensin, beta 114	-1.82	4.01	4.88	0.06	0.3	2.72E-02	3.58E-01	Multiple_Complex
TC0200011514.hg.1	MYT1L	Transcript Identified by AceView, Entrez Gene ID(s) 23040	-1.82	3.28	4.15	0.12	0.08	1.82E-02	3.23E-01	Unassigned
TC1100013001.hg.1	CLP1	cleavage and polyadenylation factor I subunit 1	-1.83	7.8	8.67	0.07	0.16	2.57E-02	3.51E-01	Coding
TC1700010425.hg.1	SLFN12	schlafen family member 12	-1.83	7.72	8.59	0.86	0.17	2.97E-02	3.65E-01	Multiple_Complex
TC1700012401.hg.1	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	-1.83	11.35	12.22	0.16	0.08	4.30E-03	2.04E-01	Multiple_Complex
TC0300008182.hg.1	CEP97	centrosomal protein 97kDa	-1.83	8.85	9.72	0.2	0.24	4.10E-03	2.01E-01	Multiple_Complex
TC1800009222.hg.1	RNF125	ring finger protein 125, E3 ubiquitin protein ligase	-1.83	7.77	8.64	0.31	0.08	2.80E-02	3.60E-01	Multiple_Complex

TC0900009479.hg.1	RANBP6	RAN binding protein 6	-1.83	6.07	6.94	0.41	0.35	7.10E-03	2.41E-01	Coding
TC0500007841.hg.1	AGGF1	angiogenic factor with G-patch and FHA domains 1	-1.83	6.82	7.69	0.22	0.35	8.20E-03	2.50E-01	Multiple_Complex
TC1900009547.hg.1	ZNF414	zinc finger protein 414	-1.83	6.33	7.2	0.41	0.41	1.68E-02	3.12E-01	Multiple_Complex
TC0100013323.hg.1	STPG1	sperm-tail PG-rich repeat containing 1	-1.83	7.83	8.7	0.09	0.11	1.80E-03	1.41E-01	Multiple_Complex
TC0600007092.hg.1	FAM8A1	family with sequence similarity 8, member A1	-1.84	8.73	9.61	0.19	0.19	8.30E-03	2.50E-01	Multiple_Complex
TC0400007285.hg.1	LIAS	lipoic acid synthetase	-1.84	4.49	5.36	0.18	0.74	2.10E-02	3.34E-01	Multiple_Complex
TC1000011400.hg.1	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	-1.84	3.89	4.76	0.38	0.01	1.72E-02	3.15E-01	Multiple_Complex
TC2000006818.hg.1	PET117; CSRP2BP	PET117 homolog; CSRP2 binding protein	-1.84	7.83	8.7	0.02	0.22	2.20E-03	1.54E-01	Multiple_Complex
TC2100008168.hg.1	HMGN1	high mobility group nucleosome binding domain 1	-1.84	9.2	10.08	0.22	0.1	2.00E-03	1.48E-01	Multiple_Complex
TC0600008095.hg.1	POLR1C	polymerase (RNA) I polypeptide C	-1.84	12.51	13.39	0.1	0.13	4.40E-03	2.04E-01	Multiple_Complex
TC1000008875.hg.1	ADD3	adducin 3 (gamma)	-1.84	5.97	6.85	0.24	0.41	1.55E-02	3.05E-01	Multiple_Complex
TC0400010770.hg.1	PPAT	phosphoribosyl pyrophosphate amidotransferase	-1.84	12.81	13.69	0.02	0.11	4.30E-03	2.04E-01	Multiple_Complex
TSUnmapped00000038.hg.1	ZNF780A	zinc finger protein 780A	-1.84	5.01	5.89	0.26	0.09	3.80E-03	1.90E-01	Coding
TC1700010699.hg.1	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	-1.84	10.6	11.48	0.24	0.05	2.10E-03	1.49E-01	Multiple_Complex
TC0600008255.hg.1	EFHC1	EF-hand domain (C-terminal) containing 1	-1.85	7.63	8.51	0.63	0.13	2.53E-02	3.49E-01	Multiple_Complex
TC1400010768.hg.1	MED6	mediator complex subunit 6	-1.85	11.65	12.54	0	0.16	2.70E-03	1.67E-01	Multiple_Complex
TC1900007265.hg.1	FAM32A	family with sequence similarity 32, member A	-1.85	8.88	9.77	0.11	0.11	1.58E-02	3.07E-01	Coding
TC0800012405.hg.1	FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	-1.85	8.35	9.24	0.13	0.34	1.64E-02	3.10E-01	Multiple_Complex
TSUnmapped00000211.hg.1	SERTAD4	SERTA domain containing 4	-1.85	7.91	8.8	0.52	0.34	1.90E-02	3.26E-01	NonCoding

TC1000012510.hg.1	ZNF511	zinc finger protein 511	-1.85	7.19	8.08	0.71	0.05	2.23E-02	3.40E-01	Multiple_Complex
TC1100010513.hg.1	CAT	Memczak2013 ANTISENSE, CDS, coding, INTERNAL, UTR3 best transcript NM_001752	-1.85	4.65	5.54	0.17	0.09	6.00E-03	2.27E-01	NonCoding
TC1500009514.hg.1	RFX7	regulatory factor X, 7	-1.85	7.16	8.05	0.22	0.56	1.19E-02	2.83E-01	Multiple_Complex
TC0200008923.hg.1	POLR1B	polymerase (RNA) I polypeptide B	-1.86	6.74	7.63	0.06	0.27	5.20E-03	2.14E-01	Multiple_Complex
TC1900011824.hg.1	ZNF587B	zinc finger protein 587B	-1.86	6.23	7.12	0.13	0.64	2.06E-02	3.32E-01	Multiple_Complex
TC1600009512.hg.1	NTAN1	N-terminal asparagine amidase	-1.86	7.43	8.33	0.18	0.16	1.00E-02	2.68E-01	Multiple_Complex
TC0200012608.hg.1	PSME4	proteasome activator subunit 4	-1.86	11.92	12.82	0.18	0.04	2.50E-03	1.61E-01	Multiple_Complex
TC0200012092.hg.1	CCDC121	coiled-coil domain containing 121	-1.86	5.69	6.59	0.63	0.1	3.34E-02	3.80E-01	Coding
TC0600007103.hg.1	KDM1B	lysine (K)-specific demethylase 1B	-1.86	10.27	11.17	0.2	0.23	2.90E-03	1.70E-01	Multiple_Complex
TC1900012026.hg.1	ZNF468	zinc finger protein 468	-1.86	9.04	9.94	0.21	0.22	2.20E-03	1.54E-01	Multiple_Complex
TC0X00009493.hg.1	EFHC2	EF-hand domain (C-terminal) containing 2	-1.87	6.04	6.94	0.22	0.57	8.30E-03	2.50E-01	Multiple_Complex
TC0300012191.hg.1	PARP9	poly(ADP-ribose) polymerase family member 9	-1.87	10.58	11.48	0.23	0.29	5.10E-03	2.13E-01	Multiple_Complex
TC0800012256.hg.1	CLN8	ceroid-lipofuscinosis, neuronal 8	-1.87	5.94	6.84	0.7	0.14	1.39E-02	2.93E-01	Multiple_Complex
TC1800007911.hg.1	MYOM1	myomesin 1	-1.87	4.57	5.48	0.49	0.38	1.05E-02	2.70E-01	Multiple_Complex
TC0400012564.hg.1	CLDN22	claudin 22	-1.87	4.46	5.36	0.1	0.13	1.60E-03	1.37E-01	Coding
TC1100007612.hg.1	OR5D18	olfactory receptor, family 5, subfamily D, member 18	-1.87	3.24	4.14	0.14	0.23	2.50E-03	1.61E-01	Coding
TC2200008000.hg.1	TXNRD2	Transcript Identified by AceView, Entrez Gene ID(s) 10587	-1.87	5.24	6.14	0.1	0.13	2.10E-03	1.49E-01	Coding
TC1000010499.hg.1	ZFAND4	zinc finger, AN1-type domain 4	-1.87	6.33	7.24	0.29	0.42	6.20E-03	2.28E-01	Multiple_Complex
TC1900011813.hg.1	ZNF548	zinc finger protein 548	-1.87	7.33	8.24	0.06	0.44	1.56E-02	3.06E-01	Multiple_Complex
TC0400011705.hg.1	C4orf3	chromosome 4 open reading frame 3	-1.87	9.83	10.73	0.09	0.2	1.70E-03	1.40E-01	Multiple_Complex

TC1200012836.hg.1	C12orf73	chromosome 12 open reading frame 73	-1.87	10.26	11.17	0.69	0.26	1.79E-02	3.21E-01	Multiple_Complex
TC0100015864.hg.1	S100A6	S100 calcium binding protein A6	-1.88	11.58	12.49	0.17	0.06	4.80E-03	2.10E-01	Multiple_Complex
TSUnmapped00000229.hg.1	ZKSCAN7	zinc finger with KRAB and SCAN domains 7	-1.88	3.82	4.73	0.24	0.29	2.53E-02	3.49E-01	Coding
TC0200006677.hg.1	RRM2	ribonucleotide reductase M2	-1.88	9.97	10.88	0.16	0.04	1.80E-03	1.42E-01	Multiple_Complex
TC0100007305.hg.1	KDM1A	Transcript Identified by AceView, Entrez Gene ID(s) 23028	-1.88	4.12	5.03	0.22	0.18	2.54E-02	3.49E-01	Unassigned
TC0500012937.hg.1	NOP16	NOP16 nucleolar protein	-1.88	13	13.91	0.04	0.08	3.10E-03	1.73E-01	Multiple_Complex
TC0700011796.hg.1	SAMD9	sterile alpha motif domain containing 9	-1.88	8.53	9.44	0.39	0.25	1.01E-02	2.68E-01	Coding
TC0300007225.hg.1	TMEM42; MIR564	transmembrane protein 42; microRNA 564	-1.88	6.83	7.74	0.27	0.16	2.80E-03	1.69E-01	Multiple_Complex
TC0700010046.hg.1	FTSJ2	FtsJ RNA methyltransferase homolog 2 (E. coli)	-1.88	7.88	8.8	0.19	0.01	9.40E-03	2.62E-01	Multiple_Complex
TC1900011282.hg.1	ZNF614	zinc finger protein 614	-1.89	8.75	9.67	0.6	0.1	8.00E-03	2.49E-01	Multiple_Complex
TC1900011874.hg.1	ZNF878	zinc finger protein 878	-1.89	4.37	5.29	0.3	0.61	1.01E-02	2.68E-01	Coding
TC0300011038.hg.1	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-1.9	7.21	8.14	0.48	0	9.40E-03	2.62E-01	Multiple_Complex
TC1500009189.hg.1	ZNF106	zinc finger protein 106	-1.9	11.22	12.14	0.36	0.07	2.70E-03	1.67E-01	Multiple_Complex
TC0500007607.hg.1	NLN	neurolysin (metallopeptidase M3 family)	-1.9	6.02	6.94	0.1	0.33	5.10E-03	2.13E-01	Multiple_Complex
TC0300010744.hg.1	ACAA1	acetyl-CoA acyltransferase 1	-1.9	7.87	8.79	0.09	0.25	3.40E-03	1.83E-01	Multiple_Complex
TC1300009740.hg.1	LIG4	ligase IV, DNA, ATP-dependent	-1.9	8.92	9.85	0.14	0.02	1.20E-03	1.20E-01	Coding
TC0100012471.hg.1	AURKAIP1	aurora kinase A interacting protein 1	-1.9	11.84	12.77	0.79	0.02	2.99E-02	3.66E-01	Multiple_Complex
TC0900006531.hg.1	RCL1	RNA terminal phosphate cyclase-like 1	-1.9	7.37	8.29	0	0.38	5.40E-03	2.17E-01	Multiple_Complex
TC0200016418.hg.1	ZNF512	zinc finger protein 512	-1.9	7.1	8.03	0.22	0.14	2.40E-03	1.61E-01	Multiple_Complex
TC1100011739.hg.1	ALG8	ALG8, alpha-1,3-glucosyltransferase	-1.9	12.6	13.52	0	0.02	1.40E-03	1.27E-01	Multiple_Complex

TC1700006733.hg.1	ELP5	elongator acetyltransferase complex subunit 5	-1.9	8.16	9.09	0.19	0.2	2.70E-03	1.64E-01	Multiple_Complex
TC1200010944.hg.1	ZBTB39	zinc finger and BTB domain containing 39	-1.9	6.52	7.45	0.16	0.05	2.20E-03	1.52E-01	Coding
TC2000007016.hg.1	GINS1	GINS complex subunit 1 (Psf1 homolog)	-1.9	9.69	10.61	0.12	0.06	1.10E-03	1.15E-01	Multiple_Complex
TC1400009016.hg.1	FBXO33	F-box protein 33	-1.91	5.94	6.87	0.24	0.35	1.09E-02	2.74E-01	Multiple_Complex
TC0X00008081.hg.1	ATG4A	autophagy related 4A, cysteine peptidase	-1.91	7.66	8.59	0.18	0.26	2.00E-03	1.47E-01	Multiple_Complex
TC1000011363.hg.1	RNLS	renalase, FAD-dependent amine oxidase	-1.91	4.22	5.15	0	0.07	1.20E-03	1.18E-01	Multiple_Complex
TC1600008779.hg.1	JPH3	junctophilin 3	-1.91	4.05	4.98	0.24	0.24	4.20E-03	2.03E-01	Multiple_Complex
TC0200016165.hg.1	IQCA1	Transcript Identified by AceView, Entrez Gene ID(s) 79781	-1.91	2.93	3.86	0.01	0.55	2.31E-02	3.41E-01	Unassigned
TC1700010413.hg.1	NLE1	notchless homolog 1 (Drosophila)	-1.91	7.03	7.97	0.19	0.09	1.80E-03	1.42E-01	Multiple_Complex
TC1700012337.hg.1	P2RX5	purinergic receptor P2X, ligand gated ion channel, 5	-1.92	7.78	8.72	0.15	0.41	5.90E-03	2.25E-01	Multiple_Complex
TC0800008478.hg.1	FZD6	frizzled class receptor 6	-1.92	8.49	9.43	0.05	0.11	2.60E-03	1.64E-01	Coding
TC0500008582.hg.1	ISOC1	isochorismatase domain containing 1	-1.92	8.22	9.16	0.07	0.27	1.60E-03	1.37E-01	Multiple_Complex
TC0X00011139.hg.1	CETN2	centrin 2	-1.92	10.83	11.77	0.16	0.07	1.40E-03	1.31E-01	Multiple_Complex
TC1900011729.hg.1	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	-1.92	9.36	10.31	0.23	0.06	7.70E-03	2.48E-01	Multiple_Complex
TC0800006933.hg.1	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	-1.92	7.37	8.32	0.25	0.46	1.33E-02	2.89E-01	Multiple_Complex
TC0100015192.hg.1	PSRC1	proline/serine-rich coiled-coil 1	-1.93	7.71	8.66	0.01	0.59	1.23E-02	2.84E-01	Multiple_Complex
TC1800008862.hg.1	PIGN	phosphatidylinositol glycan anchor biosynthesis class N	-1.93	9.25	10.2	0.4	0.33	6.10E-03	2.27E-01	Multiple_Complex
TC0800008198.hg.1	OTUD6B	Transcript Identified by AceView, Entrez Gene ID(s) 51633	-1.93	4.53	5.48	0.5	0.11	2.21E-02	3.38E-01	Unassigned
TC1700006640.hg.1	MED11	mediator complex subunit 11	-1.93	6.34	7.29	0.19	0.66	1.24E-02	2.84E-01	Coding

TC1200010832.hg.1	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	-1.93	9.58	10.53	0.73	0.17	2.14E-02	3.34E-01	Multiple_Complex
TC0600014095.hg.1	RPP21	ribonuclease P/MRP 21kDa subunit	-1.93	9.18	10.13	0.65	0.06	1.40E-02	2.93E-01	Multiple_Complex
TC0900011067.hg.1	OR13C2	olfactory receptor, family 13, subfamily C, member 2	-1.93	4.07	5.02	0.04	0.33	2.70E-03	1.66E-01	Coding
TC1100012992.hg.1	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	-1.93	7.87	8.83	0.17	0.09	1.60E-03	1.35E-01	Multiple_Complex
TC1200007706.hg.1	MFSD5	major facilitator superfamily domain containing 5	-1.93	6.32	7.28	0.05	0.77	1.25E-02	2.86E-01	Multiple_Complex
TC0200012433.hg.1	PREPL	prolyl endopeptidase-like	-1.94	10.82	11.77	0.13	0.03	1.50E-03	1.32E-01	Multiple_Complex
TC0200012995.hg.1	FAM136A	family with sequence similarity 136, member A	-1.94	10.88	11.83	0	0.25	3.00E-03	1.73E-01	Multiple_Complex
TC1600009666.hg.1	THUMPD1	THUMP domain containing 1	-1.94	7.92	8.87	0.27	0.04	1.00E-02	2.68E-01	Multiple_Complex
TC0700011835.hg.1	PON2	paraoxonase 2	-1.94	11.56	12.52	0.11	0.07	1.60E-03	1.35E-01	Multiple_Complex
TC0600008539.hg.1	CD109	CD109 molecule	-1.94	5.23	6.18	0.24	0.6	6.70E-03	2.34E-01	Multiple_Complex
TC0500010427.hg.1	ZFR	zinc finger RNA binding protein	-1.95	11.67	12.63	0.24	0.35	1.69E-02	3.12E-01	Multiple_Complex
TC1600008906.hg.1	DEF8	differentially expressed in FDCP 8 homolog (mouse)	-1.95	9.64	10.61	1.11	0.1	3.52E-02	3.85E-01	Multiple_Complex
TC0100017945.hg.1	FH	fumarate hydratase	-1.95	7.96	8.92	0.22	0.1	2.20E-03	1.54E-01	Multiple_Complex
TC1000011379.hg.1	LIPA	Transcript Identified by AceView, Entrez Gene ID(s) 3988	-1.95	3.6	4.56	0.96	0.45	4.92E-02	4.24E-01	Unassigned
TC2000007819.hg.1	CSTF1	cleavage stimulation factor, 3 pre-RNA, subunit 1	-1.95	10.2	11.17	0.58	0.16	5.30E-03	2.15E-01	Multiple_Complex
TC1700011519.hg.1	HELZ	helicase with zinc finger	-1.95	8.9	9.87	0.44	0.13	1.62E-02	3.09E-01	Multiple_Complex
TC0200016753.hg.1	CCDC141	coiled-coil domain containing 141	-1.95	3.69	4.65	0.43	0.55	9.50E-03	2.62E-01	Multiple_Complex
TC0600007196.hg.1	MRS2	MRS2 magnesium transporter	-1.96	7.6	8.56	0.53	0.3	1.48E-02	3.02E-01	Multiple_Complex
TC1900011919.hg.1	ZNF708	zinc finger protein 708	-1.96	8.23	9.19	0.23	0.12	1.80E-03	1.42E-01	Multiple_Complex
TC1600009066.hg.1	HAGH	hydroxyacylglutathione hydrolase	-1.96	9.4	10.37	0.23	0.14	5.40E-03	2.17E-01	Multiple_Complex

TC0600012059.hg.1	GSTA4	glutathione S-transferase alpha 4	-1.96	4.33	5.3	0.27	0.36	4.90E-03	2.13E-01	Multiple_Complex
TC0900011650.hg.1	WDR34	WD repeat domain 34	-1.96	9.82	10.79	0.42	0.12	1.30E-02	2.88E-01	Multiple_Complex
TC0100011940.hg.1	COG2	component of oligomeric golgi complex 2	-1.96	6.77	7.75	0.08	0.27	2.40E-03	1.59E-01	Multiple_Complex
TC1500007860.hg.1	MPI	mannose phosphate isomerase	-1.96	8.78	9.75	0.17	0.1	1.30E-03	1.26E-01	Multiple_Complex
TC1000008961.hg.1	NHLRC2	NHL repeat containing 2	-1.97	11.91	12.89	0.06	0.03	6.00E-04	9.73E-02	Multiple_Complex
TC0X00010482.hg.1	PSMD10	proteasome 26S subunit, non-ATPase 10	-1.97	12.52	13.5	0.11	0.41	2.70E-03	1.65E-01	Multiple_Complex
TC1300006474.hg.1	MPHOSPH8	M-phase phosphoprotein 8	-1.97	6.94	7.92	0.03	0.26	8.20E-03	2.50E-01	Multiple_Complex
TC0100008369.hg.1	LRRC42	leucine rich repeat containing 42	-1.97	8.31	9.29	0.29	0.05	1.90E-03	1.45E-01	Multiple_Complex
TC0700007352.hg.1	BLVRA	biliverdin reductase A	-1.97	8.51	9.49	0.21	0.11	1.10E-03	1.18E-01	Multiple_Complex
TC1500006951.hg.1	KNSTRN	kinetochore-localized astrin/SPAG5 binding protein	-1.98	11.99	12.97	0.01	0.1	1.00E-03	1.14E-01	Multiple_Complex
TC1000010446.hg.1	ZNF239	zinc finger protein 239	-1.98	5.81	6.79	0.03	0.04	1.00E-03	1.13E-01	Multiple_Complex
TC0600014112.hg.1	ZBTB9	zinc finger and BTB domain containing 9	-1.98	6.88	7.87	0.3	0.62	8.60E-03	2.54E-01	Multiple_Complex
TC0700012477.hg.1	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	-1.98	6.13	7.12	0.17	0.49	1.85E-02	3.24E-01	Coding
TC1600008226.hg.1	NIP7	NIP7, nucleolar pre-rRNA processing protein	-1.98	12.13	13.12	0.14	0.14	4.50E-03	2.04E-01	Multiple_Complex
TC0300007711.hg.1	SLC25A26	solute carrier family 25 (S-adenosylmethionine carrier), member 26	-1.99	8.07	9.06	0.38	0.1	2.50E-03	1.61E-01	Multiple_Complex
TC0100009305.hg.1	PRMT6	protein arginine methyltransferase 6	-1.99	6.74	7.73	0.01	0.59	1.58E-02	3.07E-01	Coding
TC0900012218.hg.1	KLHL9	kelch-like family member 9	-1.99	5.21	6.2	0.51	0.25	7.40E-03	2.46E-01	Coding
TC0500007143.hg.1	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	-1.99	11.99	12.98	0.05	0	1.10E-03	1.15E-01	Multiple_Complex
TC0900007663.hg.1	CEP78	centrosomal protein 78kDa	-1.99	8.64	9.63	0.13	0.12	1.00E-03	1.13E-01	Multiple_Complex

TC0200012091.hg.1	ZNF512	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript NM_032434	-2	7.74	8.74	0.59	0.16	5.10E-03	2.13E-01	NonCoding
TC1400007227.hg.1	LGALS3	lectin, galactoside-binding, soluble, 3	-2	8.02	9.02	0.04	0.12	1.46E-02	3.00E-01	Multiple_Complex
TC1300008824.hg.1	SLC25A30	solute carrier family 25, member 30	-2	5.24	6.24	0.11	0.31	1.70E-03	1.38E-01	Multiple_Complex
TC1300008080.hg.1	TUBGCP3	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_006322	-2.01	7.76	8.76	0.18	0.51	5.30E-03	2.16E-01	NonCoding
TC1000011323.hg.1	GLUD1	glutamate dehydrogenase 1	-2.01	10.08	11.08	0.15	0.16	8.00E-04	1.03E-01	Multiple_Complex
TC0200010577.hg.1	ADAM23	ADAM metallopeptidase domain 23	-2.01	3.22	4.23	0.23	0.25	5.40E-03	2.17E-01	Multiple_Complex
TC0600011140.hg.1	HIST1H3F	histone cluster 1, H3f	-2.01	12.91	13.91	0.43	0.01	9.30E-03	2.62E-01	Coding
TC0300010540.hg.1	TOP2B; MIR4442	topoisomerase (DNA) II beta; microRNA 4442	-2.01	8.36	9.36	0.14	0.42	5.60E-03	2.19E-01	Multiple_Complex
TC1700009623.hg.1	PHF23	PHD finger protein 23	-2.01	8.71	9.72	0.01	0.03	8.00E-04	1.04E-01	Multiple_Complex
TC0200013061.hg.1	PRADC1	protease-associated domain containing 1	-2.01	9.06	10.07	0.1	0.06	2.50E-03	1.61E-01	Multiple_Complex
TC1900011236.hg.1	KLK13	kallikrein related peptidase 13	-2.01	4.64	5.65	0.27	0.21	1.34E-02	2.89E-01	Coding
TC1300008713.hg.1	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	-2.01	8.03	9.04	0.01	0.28	8.00E-03	2.49E-01	Multiple_Complex
TC0100008332.hg.1	ZYG11B	zyg-11 family member B, cell cycle regulator	-2.01	8.33	9.34	0.05	0.01	1.30E-03	1.22E-01	Multiple_Complex
TC0700009233.hg.1	BPGM	Transcript Identified by AceView, Entrez Gene ID(s) 669	-2.02	4.99	6	0.38	0.06	4.20E-03	2.03E-01	Unassigned
TC0X00011163.hg.1	FAM58A	family with sequence similarity 58, member A	-2.02	8.03	9.04	0.36	0.17	1.04E-02	2.69E-01	Multiple_Complex
TC0600009235.hg.1	FAM26D	family with sequence similarity 26, member D	-2.02	4.78	5.79	0.11	0.1	1.11E-02	2.75E-01	Coding
TC2200007892.hg.1	CECR5	cat eye syndrome chromosome region, candidate 5	-2.02	7.12	8.14	0.18	0.21	2.00E-02	3.29E-01	Multiple_Complex
TC2200009028.hg.1	CERK	ceramide kinase	-2.02	9.64	10.66	0.24	0.04	8.00E-04	1.07E-01	Multiple_Complex
TC0X00009139.hg.1	AP1S2	adaptor-related protein complex 1 sigma 2 subunit	-2.03	8.17	9.19	0.61	0.18	8.60E-03	2.54E-01	Multiple_Complex
TC0900009579.hg.1	ZDHHC21	zinc finger, DHHC-type containing 21	-2.03	7.13	8.15	0.35	0.2	3.10E-03	1.73E-01	Multiple_Complex

TC0700009232.hg.1	BPGM	2,3-bisphosphoglycerate mutase	-2.03	10.11	11.13	0.1	0.15	6.00E-04	8.99E-02	Coding
TC0900009740.hg.1	ELAVL2	ELAV like neuron-specific RNA binding protein 2	-2.03	8.41	9.44	0.19	0.07	1.10E-03	1.16E-01	Multiple_Complex
TC0400008985.hg.1	RPS3A	Zhang2013 ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001006	-2.03	4.21	5.23	0.47	0.2	3.58E-02	3.87E-01	NonCoding
TC0700010352.hg.1	ANKMY2	ankyrin repeat and MYND domain containing 2	-2.04	8.58	9.61	0.05	0.02	5.00E-04	8.89E-02	Multiple_Complex
TC0900009948.hg.1	ARHGEF39	Rho guanine nucleotide exchange factor 39	-2.04	7.28	8.3	0.25	0.36	1.70E-03	1.39E-01	Multiple_Complex
TC1100007257.hg.1	CAT	catalase	-2.05	8.73	9.77	0.33	0.27	7.90E-03	2.48E-01	Multiple_Complex
TC0200015887.hg.1	CUL3	cullin 3	-2.05	10.33	11.37	0.24	0.21	1.00E-03	1.13E-01	Multiple_Complex
TC1200012748.hg.1	CD163L1	CD163 molecule-like 1	-2.05	7.79	8.83	0.43	0.17	2.40E-03	1.61E-01	Multiple_Complex
TC1100010824.hg.1	OR4C11	olfactory receptor, family 4, subfamily C, member 11	-2.05	3.21	4.25	0.41	0.36	2.50E-03	1.61E-01	Coding
TC0200007746.hg.1	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	-2.05	8.49	9.53	0	0.16	5.00E-04	8.89E-02	Coding
TC0800012363.hg.1	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	-2.05	4.16	5.19	0.61	0.29	1.18E-02	2.83E-01	NonCoding
TC0200010374.hg.1	MARS2	methionyl-tRNA synthetase 2, mitochondrial	-2.05	6.2	7.24	0.41	0.44	5.00E-03	2.13E-01	Coding
TC0X00011136.hg.1	MAGEA6	MAGE family member A6	-2.06	9.2	10.23	0.14	0.12	3.50E-03	1.84E-01	Multiple_Complex
TC0X00008470.hg.1	PHF6	PHD finger protein 6	-2.06	9.92	10.96	0.19	0.01	1.90E-03	1.43E-01	Multiple_Complex
TC0600011697.hg.1	CCDC167	coiled-coil domain containing 167	-2.06	8.63	9.67	0.17	0.54	4.30E-03	2.04E-01	Coding
TC0300013985.hg.1	TUSC2	tumor suppressor candidate 2	-2.06	10.1	11.14	0.23	0.39	1.50E-03	1.34E-01	Multiple_Complex
TC1500010726.hg.1	TMEM62	transmembrane protein 62	-2.06	6.51	7.56	0.49	0.17	2.40E-03	1.59E-01	Multiple_Complex
TC1300007167.hg.1	PHF11	PHD finger protein 11	-2.06	7.31	8.35	0.4	0.22	1.80E-03	1.41E-01	Multiple_Complex
TC1600010780.hg.1	CMTR2	cap methyltransferase 2	-2.07	8.27	9.32	0.42	0.31	6.20E-03	2.27E-01	Multiple_Complex

TC1700010700.hg.1	DNAJC7	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic, OVERLAPTX, OVEXON best transcript NM_003315	-2.08	6.09	7.15	0.04	0.05	2.40E-03	1.59E-01	NonCoding
TC1700007949.hg.1	ARL4D	ADP-ribosylation factor like GTPase 4D	-2.08	5.25	6.3	0.27	0.22	1.00E-03	1.13E-01	Coding
TC0200016618.hg.1	RNASEH1	ribonuclease H1	-2.08	10.88	11.93	0.09	0.18	8.00E-04	1.06E-01	Multiple_Complex
TC0300012764.hg.1	HLTF	helicase-like transcription factor	-2.09	10.01	11.07	0.19	0.4	5.50E-03	2.18E-01	Multiple_Complex
TC2000009890.hg.1	ANKEF1	ankyrin repeat and EF-hand domain containing 1	-2.09	7.18	8.24	0.02	0.05	1.00E-03	1.13E-01	Multiple_Complex
TC0100012788.hg.1	GPR157	G protein-coupled receptor 157	-2.09	5.48	6.54	0.5	0.24	2.90E-03	1.71E-01	Multiple_Complex
TC1200010653.hg.1	CERS5	ceramide synthase 5	-2.09	9.26	10.33	0.31	0.03	1.40E-03	1.26E-01	Multiple_Complex
TC1500010140.hg.1	WDR61	WD repeat domain 61	-2.09	5.96	7.03	0.53	0.37	6.80E-03	2.37E-01	Multiple_Complex
TC0500010731.hg.1	ARL15	ADP-ribosylation factor like GTPase 15	-2.09	7.53	8.59	0.52	0.06	2.41E-02	3.46E-01	Multiple_Complex
TC1900011537.hg.1	ZNF835	Transcript Identified by AceView, Entrez Gene ID(s) 90485	-2.09	4.21	5.28	0.31	0.97	1.64E-02	3.10E-01	Coding
TC0X00009988.hg.1	ZMYM3	zinc finger, MYM-type 3	-2.1	6.42	7.49	0.17	0.27	3.10E-03	1.73E-01	Multiple_Complex
TC0500012568.hg.1	GEMIN5	gem nuclear organelle associated protein 5	-2.1	7.33	8.4	0.02	0.29	6.00E-04	9.73E-02	Multiple_Complex
TC0100017948.hg.1	CHML	choroideremia-like (Rab escort protein 2)	-2.1	7.13	8.2	0.26	0.26	3.35E-02	3.80E-01	Multiple_Complex
TC1100009110.hg.1	NNMT	nicotinamide N-methyltransferase	-2.1	11.42	12.49	0.27	0.46	3.80E-03	1.90E-01	Multiple_Complex
TSUnmapped00000313.hg.1	CCDC84	coiled-coil domain containing 84	-2.1	7.82	8.89	0.13	0.44	5.40E-03	2.18E-01	NonCoding
TC0X00007158.hg.1	ZNF81	zinc finger protein 81	-2.1	7.3	8.37	0.05	0.37	6.20E-03	2.27E-01	Multiple_Complex
TC0300013795.hg.1	OXNAD1	oxidoreductase NAD-binding domain containing 1	-2.1	7.97	9.05	0.03	0.35	1.30E-03	1.22E-01	Multiple_Complex
TC0700007807.hg.1	ZNF92	zinc finger protein 92	-2.1	7.26	8.34	0.64	0.37	1.02E-02	2.68E-01	Multiple_Complex
TC0500013259.hg.1	MFAP3	microfibrillar associated protein 3	-2.11	8.01	9.08	0.02	0.26	9.00E-04	1.11E-01	Multiple_Complex

TC0800010703.hg.1	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	-2.11	8.47	9.55	0.65	0.04	5.70E-03	2.22E-01	Multiple_Complex
TC1100006485.hg.1	TMEM80	transmembrane protein 80	-2.11	6.57	7.65	0.23	0.84	2.39E-02	3.46E-01	Multiple_Complex
TC1200009931.hg.1	TAS2R46	taste receptor, type 2, member 46	-2.12	5.41	6.49	0.64	0.28	1.84E-02	3.24E-01	Coding
TC0400008043.hg.1	PTPN13	Transcript Identified by AceView, Entrez Gene ID(s) 5783	-2.12	3.48	4.56	0.32	0.21	1.30E-03	1.22E-01	Unassigned
TC0X00007707.hg.1	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	-2.12	4.53	5.61	0.39	0.03	9.00E-04	1.09E-01	Multiple_Complex
TC0500012163.hg.1	CDC23	cell division cycle 23	-2.12	9.09	10.18	0.17	0.41	1.85E-02	3.24E-01	Multiple_Complex
TC0100010467.hg.1	UCK2	Jeck2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_012474	-2.12	4.97	6.06	0.38	0.16	1.10E-03	1.16E-01	NonCoding
TC0200012656.hg.1	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	-2.12	8.98	10.07	0.05	0.34	1.53E-02	3.04E-01	Multiple_Complex
TC0400009919.hg.1	MRFAP1L1	Morf4 family associated protein 1-like 1	-2.13	11.87	12.95	0.06	0.02	4.00E-04	8.29E-02	Multiple_Complex
TC0400008725.hg.1	PCDH10	protocadherin 10	-2.13	5.32	6.41	0.48	0.31	2.30E-03	1.58E-01	Multiple_Complex
TC1000008474.hg.1	HHEX	hematopoietically expressed homeobox	-2.13	4.43	5.52	0.02	0.52	1.80E-03	1.41E-01	Multiple_Complex
TC0200010284.hg.1	MYO1B	myosin IB	-2.13	6.44	7.53	0.07	0.02	1.40E-03	1.26E-01	Multiple_Complex
TC1800006731.hg.1	TUBB6	tubulin, beta 6 class V	-2.13	9.15	10.24	0.21	0.12	1.50E-03	1.33E-01	Multiple_Complex
TC0400012956.hg.1	ELOVL6	ELOVL fatty acid elongase 6	-2.13	8.47	9.56	0.58	0.03	3.50E-03	1.84E-01	Multiple_Complex
TC0200015002.hg.1	CHN1	chimerin 1	-2.14	7.43	8.52	0.66	0.23	4.30E-03	2.04E-01	Multiple_Complex
TC1000012577.hg.1	LIPA	lipase A, lysosomal acid, cholesterol esterase	-2.14	8.37	9.46	0.01	0.26	8.00E-04	1.04E-01	Multiple_Complex
TC0700006523.hg.1	PSMG3-AS1	PSMG3 antisense RNA 1 (head to head)	-2.14	6.41	7.51	0.04	0.38	1.30E-03	1.22E-01	NonCoding
TC0200007590.hg.1	CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	-2.15	11.64	12.75	0.25	0.14	1.00E-03	1.13E-01	Coding

TC0600013464.hg.1	SHPRH	SNF2 histone linker PHD RING helicase, E3 ubiquitin protein ligase	-2.15	8.22	9.32	0.28	0.01	1.00E-03	1.13E-01	Multiple_Complex
TC0600009102.hg.1	FIG4	FIG4 phosphoinositide 5-phosphatase	-2.15	6.64	7.74	0.19	0.49	1.90E-03	1.46E-01	Multiple_Complex
TC1100006925.hg.1	PDE3B	phosphodiesterase 3B, cGMP-inhibited	-2.15	4.21	5.32	0.82	0.37	1.04E-02	2.69E-01	NonCoding
TC1700009551.hg.1	ZNF232	zinc finger protein 232	-2.16	8.98	10.09	0.44	0.19	8.20E-03	2.50E-01	Multiple_Complex
TC0600006967.hg.1	EDN1	endothelin 1	-2.16	8.05	9.17	0.04	0.26	1.00E-03	1.13E-01	Multiple_Complex
TSUnmapped00000054.hg.1	ZNF780B	zinc finger protein 780B	-2.16	6.1	7.21	0.64	0.17	4.30E-03	2.03E-01	Coding
TSUnmapped00000177.hg.1	ZNF780B	zinc finger protein 780B	-2.16	6.1	7.21	0.64	0.17	4.30E-03	2.03E-01	Coding
TC0800010506.hg.1	PLAG1	pleiomorphic adenoma gene 1	-2.16	6.09	7.2	0.28	0.42	2.00E-03	1.48E-01	Multiple_Complex
TC0400012641.hg.1	PDLIM3	PDZ and LIM domain 3	-2.17	6.78	7.9	0.2	0.06	9.00E-04	1.10E-01	Multiple_Complex
TC1900007826.hg.1	ZNF30	zinc finger protein 30	-2.17	5.75	6.86	0.17	0.13	1.20E-03	1.20E-01	Multiple_Complex
TC1500007518.hg.1	RAB8B	RAB8B, member RAS oncogene family	-2.17	6	7.11	0.27	0.09	1.40E-03	1.27E-01	Multiple_Complex
TC0100014768.hg.1	MCOLN2	mucolipin 2	-2.18	4.99	6.11	0.65	0.11	3.60E-03	1.88E-01	Multiple_Complex
TC0800011173.hg.1	PTDSS1	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_014754	-2.18	5.08	6.2	0.1	0.11	1.20E-03	1.18E-01	NonCoding
TC1700008104.hg.1	NSF	N-ethylmaleimide-sensitive factor	-2.19	7.58	8.71	0.1	0.46	2.20E-03	1.54E-01	Multiple_Complex
TC1900008655.hg.1	ZNF175	zinc finger protein 175	-2.19	6.75	7.88	0.24	0.2	5.00E-04	8.69E-02	Multiple_Complex
TC1600008942.hg.1	MRPL28	mitochondrial ribosomal protein L28	-2.19	5.67	6.8	0.29	0.23	2.70E-03	1.66E-01	Multiple_Complex
TC0X00008392.hg.1	UTP14A	UTP14A small subunit (SSU) processome component	-2.2	7.2	8.33	0.13	0.4	7.60E-03	2.48E-01	Multiple_Complex
TC0400010132.hg.1	TAPT1	transmembrane anterior posterior transformation 1	-2.2	9.4	10.54	0.25	0.02	1.00E-03	1.13E-01	Multiple_Complex
TC0400009543.hg.1	TLR3	toll-like receptor 3	-2.21	9.38	10.52	0.15	0.32	1.68E-02	3.12E-01	Multiple_Complex
TC0100015850.hg.1	SPRR2B	small proline-rich protein 2B	-2.21	4.4	5.54	0.18	0.08	1.90E-03	1.43E-01	Coding

TC0900008028.hg.1	MFSD14B	major facilitator superfamily domain containing 14B	-2.22	10.61	11.76	0.07	0.05	4.00E-04	8.29E-02	Multiple_Complex
TC0600012958.hg.1	TSPYL4	TSPY-like 4	-2.23	4.5	5.66	0.25	0.19	6.00E-04	8.99E-02	Multiple_Complex
TSUnmapped00000068.hg.1	ZNF780A	zinc finger protein 780A	-2.23	5.19	6.34	0.75	0.53	9.50E-03	2.62E-01	Coding
TC1200008081.hg.1	DYRK2	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-2.23	4.48	5.63	0.12	0.52	1.60E-03	1.37E-01	Multiple_Complex
TC1600009062.hg.1	NME3	NME/NM23 nucleoside diphosphate kinase 3	-2.23	7.11	8.27	0.7	0.23	4.19E-02	4.02E-01	Multiple_Complex
TSUnmapped00000085.hg.1	CCDC84	coiled-coil domain containing 84	-2.23	6.04	7.2	0.04	0.29	7.00E-04	1.02E-01	NonCoding
TC1200012265.hg.1	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	-2.23	7.74	8.9	0.25	0.05	1.90E-03	1.46E-01	Multiple_Complex
TC0100010347.hg.1	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	-2.25	7.84	9.01	0.02	0.24	3.00E-04	7.01E-02	Multiple_Complex
TC1800008952.hg.1	DSEL	dermatan sulfate epimerase-like	-2.26	6.17	7.35	0.02	0.15	1.20E-03	1.22E-01	Coding
TC1700007718.hg.1	CISD3	CDGSH iron sulfur domain 3	-2.26	8.94	10.12	0.19	0.01	2.20E-03	1.54E-01	Multiple_Complex
TC0200010733.hg.1	XRCC5	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_021141	-2.26	6.42	7.6	0.75	0.22	6.80E-03	2.38E-01	NonCoding
TC0100011022.hg.1	RGS2	regulator of G-protein signaling 2	-2.28	11.01	12.2	0.21	0.1	1.80E-03	1.43E-01	Multiple_Complex
TC1600010341.hg.1	AKTIP	AKT interacting protein	-2.28	5.48	6.67	0.31	0.17	5.00E-04	8.89E-02	Multiple_Complex
TC1900007502.hg.1	ZNF85	zinc finger protein 85	-2.29	4.92	6.11	0.68	0.53	7.70E-03	2.48E-01	Multiple_Complex
TC0100008120.hg.1	HPDL	4-hydroxyphenylpyruvate dioxygenase-like	-2.29	7.27	8.47	0.02	0.23	2.00E-04	5.95E-02	Coding
TC0X00006891.hg.1	GK	glycerol kinase	-2.29	5.68	6.88	0.87	0.52	2.15E-02	3.34E-01	Multiple_Complex
TC0400012907.hg.1	ADGRA3	adhesion G protein-coupled receptor A3	-2.31	4.66	5.86	0.95	0.47	1.39E-02	2.93E-01	Multiple_Complex

TC0500011220.hg.1	AP3B1	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_003664	-2.31	3.25	4.46	0.07	0.21	6.60E-03	2.34E-01	NonCoding
TC0400012781.hg.1	STIM2	stromal interaction molecule 2	-2.31	8.42	9.63	0.27	0.2	2.50E-03	1.61E-01	NonCoding
TC1700012286.hg.1	SMG8	SMG8 nonsense mediated mRNA decay factor	-2.32	6.43	7.64	0.01	0.59	1.20E-03	1.19E-01	Multiple_Complex
TC0600007378.hg.1	HIST1H4J	histone cluster 1, H4j	-2.33	9.76	10.98	0.28	0.64	4.90E-03	2.13E-01	Coding
TSUnmapped00000134.hg.1	SLC16A1	solute carrier family 16 (monocarboxylate transporter), member 1	-2.33	9.95	11.17	0.49	0.23	3.80E-03	1.90E-01	NonCoding
TC0600014130.hg.1	RRP36	ribosomal RNA processing 36	-2.33	8.01	9.23	0.01	0.01	8.00E-04	1.06E-01	NonCoding
TSUnmapped00000461.hg.1	ZNF35	zinc finger protein 35	-2.34	8.45	9.68	0.15	0	7.00E-04	1.00E-01	Coding
TC0800007245.hg.1	MAK16	MAK16 homolog	-2.34	9.16	10.39	0.39	0.06	5.00E-04	8.29E-02	Multiple_Complex
TC0500007267.hg.1	CCDC152	coiled-coil domain containing 152	-2.36	5.53	6.77	1.01	0.75	2.05E-02	3.32E-01	Multiple_Complex
TC0600007263.hg.1	HIST1H4A	histone cluster 1, H4a	-2.4	8.13	9.39	0.41	0.32	9.00E-04	1.11E-01	Coding
TC1800007543.hg.1	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	-2.41	8.69	9.96	0.54	0.11	1.00E-03	1.13E-01	Multiple_Complex
TC0600008663.hg.1	DOPEY1	dopey family member 1	-2.42	6.14	7.41	0.07	0.7	4.80E-03	2.12E-01	Multiple_Complex
TC0500010781.hg.1	SLC38A9	Transcript Identified by AceView, Entrez Gene ID(s) 153129	-2.43	3.49	4.77	0.09	1.2	2.42E-02	3.46E-01	Unassigned
TC0700010563.hg.1	HOXA7	homeobox A7	-2.44	8.11	9.4	0.31	0.04	2.00E-04	5.95E-02	Multiple_Complex
TC1500008156.hg.1	SCAND2P	SCAN domain containing 2 pseudogene	-2.47	7.84	9.14	0.19	0.29	9.00E-04	1.10E-01	Multiple_Complex
TC0700013578.hg.1	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	-2.47	4.63	5.94	0.23	0.25	2.00E-04	5.95E-02	Multiple_Complex
TC0400010618.hg.1	TEC	tec protein tyrosine kinase	-2.52	6.15	7.48	0.08	0.01	2.00E-04	5.95E-02	Multiple_Complex
TC1700008342.hg.1	PCTP	phosphatidylcholine transfer protein	-2.52	7.88	9.21	0.42	0.02	4.00E-04	7.50E-02	Multiple_Complex

TC1600011474.hg.1	ANKS3	ankyrin repeat and sterile alpha motif domain containing 3	-2.54	5.31	6.66	0.4	0.67	3.00E-03	1.73E-01	Multiple_Complex
TC0800006887.hg.1	NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	-2.55	5.09	6.45	0.23	0.4	2.00E-04	5.95E-02	Multiple_Complex
TC1600011553.hg.1	PSMB10	proteasome subunit beta 10	-2.57	6.91	8.27	0.71	0.71	4.00E-03	1.98E-01	Multiple_Complex
TSUnmapped00000018.hg.1	ZNF35	zinc finger protein 35	-2.58	7.42	8.78	0.11	0.06	1.00E-04	5.24E-02	Coding
TC0300007435.hg.1	DOCK3	dedicator of cytokinesis 3	-2.58	5.11	6.48	0.41	0.82	2.80E-03	1.67E-01	Multiple_Complex
TC1700010293.hg.1	CRLF3	cytokine receptor-like factor 3	-2.64	7.61	9.01	0.19	0.22	3.00E-04	7.31E-02	Multiple_Complex
TC0600009127.hg.1	AMD1	adenosylmethionine decarboxylase 1	-2.64	10.75	12.15	0.08	0.07	3.93E-05	2.64E-02	Multiple_Complex
TC0X00007851.hg.1	FAM133A	family with sequence similarity 133, member A	-2.66	3.65	5.06	0.37	0.36	7.00E-04	1.02E-01	Coding
TC0900010586.hg.1	C9orf64	chromosome 9 open reading frame 64	-2.67	6.88	8.29	0.3	0.24	2.50E-03	1.61E-01	Multiple_Complex
TC0700013583.hg.1	MTERF1	mitochondrial transcription termination factor 1	-2.71	7	8.44	0.63	0.04	1.00E-03	1.13E-01	Multiple_Complex
TC0900011429.hg.1	NDUFA8	Transcript Identified by AceView, Entrez Gene ID(s) 4702	-2.73	4.09	5.54	0.11	0.11	7.00E-04	1.02E-01	Unassigned
TC1200008346.hg.1	ALX1	ALX homeobox 1	-2.8	5.96	7.45	0.42	0.16	2.00E-04	5.95E-02	Coding
TC0X00010607.hg.1	KLHL13	kelch-like family member 13	-2.88	7.3	8.83	0.35	0.13	1.00E-04	4.80E-02	Multiple_Complex
TC0100018476.hg.1	PEX11B	peroxisomal biogenesis factor 11 beta	-2.9	6.45	7.98	0.23	0.16	4.16E-05	2.70E-02	Multiple_Complex
TC2000008516.hg.1	SNX5	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_152227	-3	4.85	6.44	1.3	0.25	6.90E-03	2.39E-01	NonCoding
TC0700011797.hg.1	SAMD9L	sterile alpha motif domain containing 9-like	-3.07	6.3	7.92	0.25	0.56	8.00E-04	1.06E-01	Multiple_Complex
TC0500011334.hg.1	TMEM167A	Transcript Identified by AceView, Entrez Gene ID(s) 153339	-3.1	5.03	6.67	1.43	0.56	2.69E-02	3.58E-01	Unassigned
TC1000009240.hg.1	EDRF1	erythroid differentiation regulatory factor 1	-3.16	8.11	9.77	0.12	0.11	1.00E-04	5.15E-02	Multiple_Complex

TC1100008886.hg.1	TMEM133	transmembrane protein 133	-3.26	4.82	6.52	0.54	0.26	2.00E-04	6.03E-02	Coding
TC0100009870.hg.1	HIST2H4B; HIST2H4A	histone cluster 2, H4b; histone cluster 2, H4a	-3.27	11.26	12.97	0.36	0.09	2.28E-05	2.10E-02	Coding
TC0200011972.hg.1	C2orf44	chromosome 2 open reading frame 44	-3.31	5.48	7.2	0.04	0.16	1.75E-05	1.99E-02	Coding
TC0100015707.hg.1	HIST2H4A; HIST2H4B	histone cluster 2, H4a; histone cluster 2, H4b	-3.38	11.26	13.02	0.46	0.11	7.44E-05	3.71E-02	Multiple_Complex
TSUnmapped00000705.hg.1	RPS25	ribosomal protein S25	-3.43	10.39	12.17	0.28	0.03	1.45E-05	1.99E-02	NonCoding
TSUnmapped00000222.hg.1	ZNF780A	zinc finger protein 780A	-3.55	7.42	9.25	0.02	0.3	1.00E-04	5.15E-02	Coding
TSUnmapped00000670.hg.1	ZNF780A	zinc finger protein 780A	-3.57	7.62	9.45	0.03	0.3	1.00E-04	4.98E-02	Coding
TC2000007083.hg.1	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-3.65	9.16	11.03	0.09	0.02	7.82E-05	3.72E-02	Multiple_Complex
TSUnmapped00000311.hg.1	ZNF780A	zinc finger protein 780A	-3.69	7.32	9.2	0.14	0.38	4.46E-05	2.79E-02	Coding
TC0600007375.hg.1	HIST1H3H	histone cluster 1, H3h	-3.7	8.13	10.02	0.06	0.22	2.07E-05	2.02E-02	Coding
TC0100009877.hg.1	HIST2H3A	histone cluster 2, H3a	-3.84	8.98	10.92	0.03	0.22	9.82E-06	1.91E-02	Coding
TC0100015701.hg.1	HIST2H3A; HIST2H3C	histone cluster 2, H3a; histone cluster 2, H3c	-4.41	8.83	10.97	0.45	0.1	9.01E-06	1.91E-02	Coding