

**Supplementary Table 1.**

#Entitylist : RPKM>0.01 70%

#Interpretation : LMH 96 NOTE: this list has all 96 curated samples

#Experiment: CDX96v1

198 total transcripts

#corrected p-value cut-off:0.001

169 unique non-redundant transcripts

#Selected Test : Oneway ANOVA

#p-value computation: Asymptotic

#Multiple Testing Correction: No Correction

KEY: association with CAD or cardiovascular parameters  
 potential involvement in Treg function or differentiation  
 centrosome related

GeneName	p	Log2 Normalized				Symbol	Description	RefSeq
		FC ([HIGH]	Regulat	FC ([MID] vs Regula	[HIGH]			
uc061drv.1	2.93E-04	1.01 up	-4.97 down	-1.24	-1.25	-3.56	A1BG	alpha-1-B glycoprotein (A1BG), mRNA. (from RefSec NM_130786
uc057ilc.1	5.27E-04	1.86 up	-5.43 down	-1.85	-2.75	-5.19	ABCA4	ATP-binding cassette, sub-family A (ABC1), member NM_000350
uc003wjo.3	4.56E-04	-1.25 down	-1.29 down	0.77	1.09	0.72	ABCF2	ATP-binding cassette, sub-family F (GCN20), member NM_005692
uc064bvu.1	9.54E-04	-1.16 down	-3.83 down	0.03	0.24	-1.70	AC099342.1	uncharacterized LOC101927769, long non-coding RNA NR_110117
uc059xhj.1	3.89E-04	-1.24 down	-1.75 down	1.44	1.74	0.94	ADAT1	adenosine deaminase, tRNA-specific 1 (ADAT1), trar NM_012091
uc021xqj.2	3.37E-04	-1.74 down	-1.70 down	-2.79	-2.00	-2.76	ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma pol NM_0011665
uc063bvy.1	4.06E-07	1.50 up	-11.42 down	-2.18	-2.77	-6.29	AHRR	aryl-hydrocarbon receptor repressor (AHRR), transc NM_0012424
uc063bvz.1	9.62E-05	-1.25 down	-7.08 down	-0.12	0.20	-2.62	AHRR	aryl-hydrocarbon receptor repressor (AHRR), transc NM_0012424
uc062jar.1	3.44E-04	-1.28 down	-1.40 down	-1.82	-1.46	-1.95	ALS2CL	ALS2 C-terminal like NR_033815
uc064mjf.1	8.03E-04	-1.24 down	-1.42 down	-1.50	-1.18	-1.69	AP3M2	adaptor-related protein complex 3, mu 2 subunit (AP3 NM_006803
uc001mdb.4	7.45E-04	-1.29 down	-1.35 down	-1.09	-0.72	-1.15	APBB1	amyloid beta (A4) precursor protein-binding, family B, NM_001164
uc001mdc.3	4.90E-04	-1.29 down	-1.39 down	-0.93	-0.56	-1.04	APBB1	amyloid beta (A4) precursor protein-binding, family B, NM_145689
uc057yvj.1	3.32E-04	-1.32 down	-1.39 down	-1.00	-0.60	-1.07	APBB1	amyloid beta (A4) precursor protein-binding, family B, NM_001164
uc057yjj.1	9.37E-04	-1.29 down	-1.34 down	-1.11	-0.74	-1.16	APBB1	amyloid beta (A4) precursor protein-binding, family B, NM_001164
uc057ykd.1	1.32E-04	-1.57 down	-1.35 down	-1.81	-1.16	-1.59	APBB1	amyloid beta (A4) precursor protein-binding, family B, NM_0012573
uc062dsw.1	6.45E-04	1.01 up	-3.95 down	-2.77	-2.78	-4.76	APOL4	apolipoprotein L, 4 (APOL4), transcript variant a, mRN NM_030643
uc064snu.1	5.81E-04	-1.64 down	-5.31 down	-3.71	-3.00	-5.41	APTX	aprataxin NR_036576
uc064soc.1	7.40E-04	1.10 up	-4.11 down	-0.82	-0.96	-3.00	APTX	aprataxin NR_036577
uc065ahz.1	7.23E-04	-1.34 down	-1.45 down	-0.51	-0.09	-0.62	ARMCX6	armadillo repeat containing, X-linked 6 (ARMCX6), tra NM_0011847
uc064pgy.1	3.53E-04	-3.10 down	-1.70 down	-2.19	-0.56	-1.33	AZIN1-AS1	AZIN1 antisense RNA 1 NR_126339
uc059ulu.1	5.07E-04	-1.57 down	-2.22 down	-0.71	-0.06	-1.21	BBS2	Bardet-Biedl syndrome 2 (BBS2), mRNA. (from RefS NM_031885
uc061wwa.1	6.36E-04	-1.44 down	-1.39 down	-0.29	0.24	-0.23	BLCAP	bladder cancer associated protein (BLCAP), transcript NM_0011678
uc058bon.1	8.72E-04	-1.47 down	-1.32 down	1.12	1.68	1.28	C11orf31	chromosome 11 open reading frame 31 (C11orf31), r NM_170746
uc059tos.1	3.30E-04	-1.19 down	-1.47 down	-1.01	-0.77	-1.33	C16orf58	chromosome 16 open reading frame 58 (C16orf58), r NM_022744
uc063kor.1	2.91E-04	-1.42 down	-6.18 down	-2.22	-1.71	-4.34	C5ORF60	chromosome 5 open reading frame 60 NR_131066
uc063nqr.1	3.79E-04	1.29 up	-3.35 down	-5.67	-6.04	-7.78	C6orf10	chromosome 6 open reading frame 10 (C6orf10), trar NM_0012864
uc064rtg.1	4.78E-04	-1.48 down	-2.36 down	-3.80	-3.23	-4.47	CBWD1	COBW domain containing 1 (CBWD1), transcript vari NM_018491
uc064bwy.1	4.66E-04	-1.67 down	-1.50 down	-1.09	-0.36	-0.95	CDCA7L	cell division cycle associated 7-like (CDCA7L), transc NM_0011273
uc059xrj.1	1.45E-04	-2.97 down	-8.68 down	-2.86	-1.29	-4.41	CDH13	cadherin 13 (CDH13), transcript variant 5, mRNA. (fr NM_0012204
uc061mig.1	6.28E-04	-1.21 down	-3.99 down	-2.78	-2.50	-4.49	CHST10	carbohydrate sulfotransferase 10 (CHST10), mRNA. NM_004854
uc062hvi.1	4.91E-04	-1.33 down	-1.24 down	-0.09	0.33	0.01	CNOT10	CCR4-NOT transcription complex subunit 10 NR_046352
uc064rqz.1	8.12E-04	-1.46 down	-1.57 down	0.09	0.64	-0.01	COMMD5	COMM domain containing 5 (COMMD5), transcript v: NM_0010810

uc057ugl.1	8.07E-04	-1.22 down	-1.81 down	-0.50	-0.20	-1.06	COMTD1	catechol-O-methyltransferase domain containing 1 (C NM_144589
uc001tyn.4	6.14E-04	-1.43 down	-1.01 down	0.12	0.64	0.63	COQ5	coenzyme Q5 homolog, methyltransferase (S. cerevi NM_032314
uc062lwg.1	6.59E-04	-1.37 down	-1.47 down	1.17	1.63	1.07	CPOX	coproporphyrinogen oxidase (CPOX), mRNA. (from FNM_000097
uc010rgn.2	7.67E-04	-1.20 down	-1.19 down	0.61	0.88	0.62	CRY2	cryptochrome circadian clock 2 (CRY2), transcript v <sub>ε</sub> NM_021117
uc058ato.1	7.22E-04	-1.20 down	-1.19 down	0.61	0.88	0.62	CRY2	cryptochrome circadian clock 2 (CRY2), transcript v <sub>ε</sub> NM_021117
uc057oir.1	8.16E-04	-1.23 down	-1.54 down	-0.56	-0.26	-0.89	CSRP1	cysteine-rich protein NM_0011935
uc062ukk.1	9.07E-04	-1.21 down	-1.51 down	0.16	0.43	-0.16	CTBP1	C-terminal binding protein 1 (CTBP1), transcript varia NM_0010126
uc059zqi.1	7.57E-04	-1.56 down	-1.90 down	-0.89	-0.25	-1.17	CTNS	cystinosis, lysosomal cystine transporter (CTNS), tr <sub>ε</sub> NM_004937
uc057jkc.1	6.37E-04	-1.26 down	-1.51 down	-0.35	-0.02	-0.61	CTTNBP2NL	CTTNBP2 N-terminal like (CTTNBP2NL), mRNA. (frc NM_018704
uc061otq.1	1.03E-04	-1.47 down	-1.41 down	-0.17	0.38	-0.11	CYTIP	cytohesin 1 interacting protein (CYTIP), mRNA. (from NM_004288
uc058mlq.1	8.52E-04	-1.44 down	-2.37 down	-1.71	-1.19	-2.43	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 (DD. NM_0012571
uc060zfv.1	6.81E-04	-1.12 down	-1.47 down	0.64	0.81	0.26	DEDD2	death effector domain containing 2 NR_073051
uc021wlp.2	9.01E-05	-1.52 down	-1.48 down	-0.18	0.43	-0.14	DGCR8	DGCR8 microprocessor complex subunit (DGCR8), NM_0011903
uc058pdy.1	7.75E-04	-1.36 down	-1.44 down	-0.26	0.18	-0.34	DGKA	diacylglycerol kinase, alpha 80kDa (DGKA), transcript NM_201554
uc062jfe.1	3.85E-04	-1.73 down	-1.44 down	-0.46	0.34	-0.19	DHX30	DEAH (Asp-Glu-Ala-His) box helicase 30 (DHX30), tr NM_138615
uc059kmk.1	4.82E-04	-2.99 down	-1.26 down	-2.79	-1.21	-1.55	DIS3L	DIS3 like exosome 3'-5' exoribonuclease (DIS3L), tra NM_133375
uc062seb.1	9.10E-04	-1.18 down	-1.57 down	-1.66	-1.41	-2.06	DLG1	discs, large homolog 1 (Drosophila) (DLG1), transcript NM_0012043
uc061cxr.1	2.49E-05	-1.50 down	-6.34 down	-3.46	-2.87	-5.54	DNAAF3	dynein, axonemal, assembly factor 3 (DNAAF3), tran NM_0012567
uc010wnn.2	3.37E-04	-1.32 down	-1.17 down	3.12	3.52	3.30	DYNLL2	dynein, light chain, LC8-type 2 (DYNLL2), mRNA. (frc NM_080677
uc059soq.1	5.83E-04	1.01 up	-1.45 down	1.38	1.36	0.82	EIF3CL	eukaryotic translation initiation factor 3, subunit C-like NM_0010996
uc002gnz.5	8.23E-04	-1.36 down	-1.26 down	-0.62	-0.18	-0.52	ELAC2	elaC ribonuclease Z 2 NM_018127
uc057gll.1	5.73E-04	-1.73 down	-1.27 down	-0.12	0.68	0.34	EPS15	epidermal growth factor receptor pathway substrate NM_001981
uc059fov.1	8.33E-04	-1.40 down	-4.19 down	-3.11	-2.62	-4.69	EXOC3L4	exocyst complex component 3-like 4 (EXOC3L4), mF NM_0010775
uc060vkb.1	8.37E-04	-1.47 down	-1.39 down	-0.54	0.02	-0.45	FAM129C	family with sequence similarity 129, member C (FAM. NM_0010985
uc057bod.1	6.86E-05	-2.70 down	-5.95 down	-5.93	-4.49	-7.07	FAM213B,	family with sequence similarity 213, member B (FAM <sub>2</sub> NM_152371
uc061fvb.1	6.86E-05	-2.70 down	-5.95 down	-5.93	-4.49	-7.07	FAM213B,	family with sequence similarity 213, member B (FAM <sub>2</sub> NM_152371
uc064tfh.1	7.56E-04	-2.00 down	-2.97 down	-3.90	-2.90	-4.47	FAM95B1,	family with sequence similarity 95, member B1 (FAM <sub>9</sub> NM_026759
uc060std.1	7.00E-04	1.21 up	-6.37 down	-2.71	-2.99	-5.66	FBN3	fibrillin 3 (FBN3), mRNA. (from RefSeq NM_032447) NM_032447
uc058fep.1	6.63E-04	-1.37 down	-1.52 down	-0.02	0.43	-0.18	FCHSD2	FCH and double SH3 domains 2 (FCHSD2), mRNA. (NM_014824
uc064glm.1	5.34E-04	-1.41 down	-1.39 down	0.90	1.40	0.92	FIS1	fission 1 (mitochondrial outer membrane) homolog (S NM_016068
uc003djj.3	8.46E-04	-1.23 down	-1.33 down	-0.49	-0.18	-0.59	FLNB	filamin B, beta (FLNB), transcript variant 2, mRNA. (fr NM_001457
uc010hnf.3	7.92E-04	-1.24 down	-1.33 down	-0.48	-0.17	-0.59	FLNB	filamin B, beta (FLNB), transcript variant 4, mRNA. (fr NM_0011643
uc064mrv.1	3.41E-04	-1.14 down	-1.46 down	0.25	0.44	-0.11	FNTA	farnesyltransferase, CAAX box, alpha (FNTA), trans NM_002027
uc063okh.1	1.65E-04	1.12 up	-4.26 down	-1.53	-1.69	-3.78	FOXP4-AS1	FOXP4 antisense RNA 1 NR_126417
uc060atq.1	7.87E-04	-1.33 down	-1.41 down	1.69	2.10	1.60	FXR2	fragile X mental retardation, autosomal homolog 2 (F> NM_004860
uc004doi.6	9.23E-04	-1.76 down	-5.32 down	-3.91	-3.10	-5.51	GAGE13	G antigen 2C (GAGE2C), mRNA. (from RefSeq NM_ NM_001472
uc059yvw.1	3.93E-05	1.16 up	-4.34 down	-2.36	-2.57	-4.68	GAS8	growth arrest-specific 8 (GAS8), transcript variant 4, NM_0012862
uc062dbe.1	3.38E-04	-1.56 down	-3.77 down	-1.37	-0.73	-2.64	GATSL3	GATS protein-like 3 (GATSL3), mRNA. (from RefSeq NM_0010376
uc002whp.2	8.97E-04	-1.89 down	-4.43 down	-1.93	-1.01	-3.16	GNRH2	gonadotropin-releasing hormone 2 (GNRH2), transcr NM_178331
uc057dtw.1	6.14E-04	-1.51 down	-1.64 down	-0.77	-0.18	-0.89	GPATCH3	G patch domain containing 3 (GPATCH3), mRNA. (fr NM_022078
uc059uvj.1	5.04E-04	1.44 up	-4.69 down	-4.07	-4.60	-6.83	GPR56	adhesion G protein-coupled receptor G1 (ADGRG1), NM_0011457
uc064roh.1	8.92E-04	-1.17 down	-2.68 down	-2.36	-2.13	-3.56	GPT	glutamic-pyruvate transaminase (alanine aminotransf NM_005309
uc063ixf.1	3.23E-04	-1.84 down	-3.71 down	-4.06	-3.19	-5.08	GRIA1	glutamate receptor, ionotropic, AMPA 1 (GRIA1), tran NM_0012580
uc002iii.2	3.77E-04	-1.30 down	-1.54 down	-1.01	-0.64	-1.26	HEXIM2	hexamethylene bis-acetamide inducible 2 NM_0013034
uc061afd.1	8.69E-04	-1.88 down	-5.50 down	-2.56	-1.65	-4.11	HIF3A	hypoxia inducible factor 3, alpha subunit (HIF3A), trar NM_152796

uc058uor.1	8.95E-04	-1.38 down	-1.34 down	-0.14	0.33	-0.09	HIP1R	huntingtin interacting protein 1 related (HIP1R), transcr	NM_003959
uc061yty.1	1.48E-04	-1.62 down	-1.49 down	-2.68	-1.99	-2.56	ICOSLG	inducible T-cell costimulator ligand	NM_0012830
uc058pgk.1	8.59E-04	-3.36 down	-3.40 down	-4.45	-2.69	-4.46	IKZF4	IKAROS family zinc finger 4 (Eos) (IKZF4), mRNA. (f	NM_022465
uc063ljh.1	9.84E-04	-1.59 down	-1.63 down	-0.30	0.37	-0.34	IRF4	interferon regulatory factor 4	NM_0011952
uc061nqc.1	8.13E-04	-1.31 down	-1.45 down	-0.04	0.35	-0.19	IWS1	IWS1 homolog (S. cerevisiae) (IWS1), mRNA. (from I	NM_017969
uc063hbv.1	5.15E-04	-1.64 down	-1.58 down	-0.30	0.41	-0.24	JADE2	jade family PHD finger 2 (JADE2), transcript variant 3	NM_015288
uc062lig.1	9.27E-04	-1.18 down	-3.34 down	-0.79	-0.55	-2.29	KBTBD8	kelch repeat and BTB (POZ) domain containing 8 (KE	NM_032505
uc064zso.1	6.27E-04	-1.32 down	-3.69 down	-1.29	-0.89	-2.78	KIF4A	kinesin family member 4A (KIF4A), mRNA. (from Ref:	NM_012310
uc057ohz.1	9.46E-04	-1.89 down	-4.43 down	-2.06	-1.14	-3.29	LAD1	ladinin 1 (LAD1), mRNA. (from RefSeq NM_005558)	NM_005558
uc063epk.1	3.51E-04	-1.29 down	-4.69 down	-0.14	0.22	-2.01	LINC01336	long intergenic non-protein coding RNA 1336 (LINC0	NR_126375
uc063ady.1	5.93E-04	-1.34 down	-1.61 down	0.19	0.61	-0.07	LRBA	LPS-responsive vesicle trafficking, beach and anchor	NM_006726
uc058kne.1	6.65E-04	-1.52 down	-2.57 down	-2.24	-1.64	-3.00	LRRC23	leucine rich repeat containing 23 (LRRC23), transcrip	NM_006992
uc060ltc.1	7.33E-04	-1.18 down	-1.72 down	0.64	0.88	0.09	LRRC45	leucine rich repeat containing 45 (LRRC45), mRNA. (	NM_144999
uc063ecv.1	7.05E-04	-1.02 down	-3.11 down	-1.58	-1.55	-3.19	MAST4	microtubule associated serine/threonine kinase family	NM_0012902
uc062pue.1	5.60E-06	-1.59 down	-8.01 down	-5.26	-4.59	-7.60	MECOM	MDS1 and EVI1 complex locus (MECOM), transcript	NM_0011050
uc032yik.1	4.00E-04	-1.28 down	-10.06 down	-0.31	0.05	-3.28	MIR3135B	microRNA 3135b (MIR3135B), microRNA. (from Ref:	NR_039668
uc032ytr.1	4.00E-04	-1.28 down	-10.06 down	-0.31	0.05	-3.28	MIR3135B	microRNA 3135b (MIR3135B), microRNA. (from Ref:	NR_039668
uc021uqm.1	4.43E-04	-1.30 down	-24.62 down	-0.88	-0.50	-5.12	MIR3188	microRNA 3188 (MIR3188), microRNA. (from RefSec	NR_036155
uc058vgw.1	2.07E-04	-1.69 down	-1.83 down	-2.04	-1.28	-2.15	MMP17	matrix metalloproteinase 17 (membrane-inserted) (MM	NM_016155
uc063sgp.1	7.99E-04	-2.35 down	-6.59 down	-2.57	-1.34	-4.06	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ d	NM_0012427
uc060ehm.1	3.05E-04	-1.15 down	-4.41 down	-2.51	-2.30	-4.44	MYO19	myosin XIX (MYO19), transcript variant 3, mRNA. (fr	NM_0010335
uc064kqr.1	8.65E-04	-2.37 down	-5.37 down	-2.71	-1.46	-3.89	NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferas	NM_0011601
uc057jyz.1	8.12E-04	-1.42 down	-1.53 down	-0.50	0.01	-0.60	NBPF15	neuroblastoma breakpoint family, member 15 (NBPF	NR_173638
uc057jza.1	3.65E-04	-1.52 down	-1.63 down	-0.15	0.46	-0.25	NBPF15	neuroblastoma breakpoint family, member 15 (NBPF	NR_173638
uc061end.1	3.17E-04	-3.02 down	-2.71 down	-6.16	-4.57	-6.01	NLRP2	NLR family, pyrin domain containing 2 (NLRP2), trans	NM_0011740
uc061ctz.1	5.74E-04	-1.21 down	-3.43 down	-5.62	-5.34	-7.12	NLRP7	NLR family, pyrin domain containing 7 (NLRP7), trans	NM_0011272
uc061foc.1	5.74E-04	-1.21 down	-3.43 down	-5.62	-5.34	-7.12	NLRP7	NLR family, pyrin domain containing 7 (NLRP7), trans	NM_0011272
uc061var.1	2.61E-04	-1.38 down	-1.50 down	0.02	0.49	-0.10	NOP56	NOP56 ribonucleoprotein (NOP56), transcript variant	NM_006392
uc061mjc.1	1.47E-04	-1.26 down	-4.39 down	-2.81	-2.48	-4.61	NPAS2	neuronal PAS domain protein 2 (NPAS2), mRNA. (fro	NM_002518
uc058cye.1	1.93E-04	1.08 up	-1.87 down	-1.45	-1.56	-2.46	NRXN2	neurexin 2 (NRXN2), transcript variant beta, mRNA. (	NM_138734
uc059six.1	1.07E-05	-2.04 down	-1.12 down	0.00	1.03	0.87	NSMCE1	non-SMC element 1 homolog (S. cerevisiae) (NSMCE	NM_145080
uc021txo.2	4.75E-06	-1.86 down	-1.54 down	-2.28	-1.39	-2.00	NT5C3B	5'-nucleotidase, cytosolic IIIB (NT5C3B), transcript v	NM_052935
uc060fdr.1	8.67E-04	-1.51 down	-1.46 down	-1.86	-1.27	-1.82	NT5C3B	5'-nucleotidase, cytosolic IIIB (NT5C3B), transcript v	NM_052935
uc061aza.1	3.59E-04	-1.43 down	-2.00 down	0.14	0.66	-0.34	NTF4	neurotrophin 4 (NTF4), mRNA. (from RefSeq NM_00	NM_006179
uc062xlo.1	2.87E-04	-1.15 down	-1.54 down	1.17	1.37	0.74	NUP54	nucleoporin 54kDa	NR_103781
uc062xlr.1	6.18E-04	-1.26 down	-1.47 down	-0.24	0.09	-0.46	NUP54	nucleoporin 54kDa	NR_103782
uc061bmx.1	7.54E-04	-1.45 down	-1.38 down	-0.62	-0.09	-0.55	NUP62	nucleoporin 62kDa (NUP62), transcript variant 1, mR	NM_153719
uc057jvt.1	6.40E-04	-1.51 down	-1.72 down	-1.12	-0.53	-1.31	PHGDH	phosphoglycerate dehydrogenase (PHGDH), mRNA. NM	006623
uc064dvi.1	1.39E-04	-1.47 down	-4.86 down	-2.58	-2.02	-4.30	PHKG1	phosphorylase kinase, gamma 1	NR_047689
uc057xni.1	1.96E-04	-6.37 down	-2.10 down	-4.38	-1.71	-2.78	PIDD1	p53-induced death domain protein 1 (PIDD1), transcr	NM_145887
uc059phr.1	1.70E-04	-1.82 down	-1.62 down	-1.22	-0.36	-1.06	PKD1	polycystic kidney disease 1 (autosomal dominant) (P	NM_000296
uc059rbn.1	8.11E-04	-1.42 down	-1.91 down	1.87	2.38	1.45	PLA2G10,	phospholipase A2, group X (PLA2G10), mRNA. (from	NM_003561
uc062iet.1	4.03E-04	-1.75 down	-1.38 down	-0.98	-0.17	-0.63	PLCD1	phospholipase C, delta 1 (PLCD1), transcript variant	NM_006225
uc061xai.1	5.74E-04	-1.75 down	-1.74 down	-0.55	0.25	-0.54	PLCG1	phospholipase C, gamma 1 (PLCG1), transcript varia	NM_182811
uc062fel.1	1.70E-04	-1.09 down	-1.65 down	-1.30	-1.18	-1.90	PPARA	peroxisome proliferator activated receptor alpha	NM_0010019

uc063msm.1	2.76E-04	1.41 up	1.21 up	-0.05	-0.54	-0.26	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063twf.1	2.76E-04	1.41 up	1.21 up	-0.05	-0.54	-0.26	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063vcd.1	2.76E-04	1.41 up	1.21 up	-0.05	-0.54	-0.26	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063whs.1	2.76E-04	1.41 up	1.21 up	-0.05	-0.54	-0.26	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063xhb.1	2.76E-04	1.41 up	1.21 up	-0.05	-0.54	-0.26	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063ymx.1	8.50E-04	1.35 up	1.26 up	-0.18	-0.61	-0.28	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063zss.1	2.76E-04	1.41 up	1.21 up	-0.05	-0.54	-0.26	PPP1R10	protein phosphatase 1 regulatory subunit 10	NR_072994
uc063phe.1	5.06E-04	-1.18 down	-3.78 down	-0.54	-0.30	-2.22	PRIM2	primase, DNA, polypeptide 2 (58kDa) (PRIM2), trans	NM_000947
uc010vlg.3	5.44E-04	-1.29 down	-1.32 down	-1.65	-1.29	-1.69	PRMT7	protein arginine methyltransferase 7 (PRMT7), trans	NM_0011848
uc064wqo.1	7.50E-04	-1.36 down	-1.63 down	1.44	1.89	1.18	PRRC2B	proline-rich coiled-coil 2B (PRRC2B), mRNA. (from R	NM_013318
uc063mxz.1	3.53E-04	-4.06 down	-5.22 down	-3.46	-1.44	-3.82	PSORS1C1,	psoriasis susceptibility 1 candidate 1 (PSORS1C1), n	NM_014068
uc058mvt.1	3.69E-04	-1.43 down	-1.54 down	-1.05	-0.53	-1.16	PUS7L	pseudouridylylase 7 homolog (S. cerevisiae)-	NM_0010986
uc058jqr.1	9.54E-04	-1.26 down	-2.85 down	-2.29	-1.96	-3.46	RAD52	RAD52 homolog, DNA repair protein	NM_0012974
uc060sfo.1	7.58E-04	-1.14 down	-2.37 down	-1.38	-1.19	-2.44	RANBP3	RAN binding protein 3 (RANBP3), transcript variant 4	NM_0013008
uc058tuf.1	8.53E-04	-1.64 down	-1.43 down	-1.54	-0.83	-1.34	RFC5	replication factor C subunit 5	NM_0012068
uc059xcn.1	9.57E-04	-1.43 down	-1.59 down	-0.58	-0.06	-0.73	RFWD3	ring finger and WD repeat domain 3 (RFWD3), mRNA	NM_018124
uc064qmg.1	6.26E-04	-2.98 down	1.08 up	-1.20	0.38	0.48	RP11-157E2	uncharacterized LOC101927822 (LOC101927822), l	NR_125424
uc057vee.1	4.89E-04	-1.20 down	-4.26 down	0.24	0.50	-1.59	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	NM_0012843
uc060hiq.1	7.49E-04	-1.21 down	-1.53 down	-0.26	0.01	-0.60	RSAD1	radical S-adenosyl methionine domain containing 1 (F	NM_018346
uc062oaq.1	6.40E-04	-1.39 down	-1.51 down	-0.36	0.11	-0.48	RYK	receptor-like tyrosine kinase (RYK), transcript varian	NM_002958
uc064bpk.1	5.85E-04	-1.30 down	-4.92 down	-1.40	-1.02	-3.32	SCIN	scinderin (SCIN), transcript variant 2, mRNA. (from F	NM_033128
uc063exq.1	4.46E-04	-1.38 down	-1.54 down	1.30	1.76	1.14	SERINC5	serine incorporator 5	NM_0011740
uc062evq.1	7.61E-05	-1.37 down	-1.25 down	-0.76	-0.31	-0.63	SERLH2	serine hydrolase-like 2	NR_104301
uc062evt.1	4.01E-04	-1.42 down	-1.28 down	-0.95	-0.44	-0.80	SERLH2	serine hydrolase-like 2	NR_104300
uc062bvk.1	8.81E-04	-1.52 down	-1.42 down	-0.80	-0.19	-0.69	SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor),	NM_000185
uc062djs.1	4.74E-04	-1.35 down	-1.33 down	-0.73	-0.29	-0.71	SFI1	Sfi1 homolog, spindle assembly associated (yeast) (S	NM_014775
uc001zwr.5	9.10E-04	1.02 up	1.67 up	0.59	0.56	1.30	SLC12A1	solute carrier family 12 (sodium/potassium/chloride tr	NM_000338
uc059wbp.1	5.97E-04	-1.62 down	-1.24 down	-1.68	-0.98	-1.29	SLC12A4	solute carrier family 12 (potassium/chloride transport	NM_0011459
uc064wao.1	3.99E-04	-1.80 down	-1.66 down	-1.08	-0.23	-0.96	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosph	NM_052901
uc063fxo.1	5.55E-04	1.02 up	-1.81 down	0.47	0.44	-0.41	SLC25A46	solute carrier family 25 member 46	NM_0013032
uc062iyj.1	2.16E-04	-2.20 down	-1.14 down	-0.19	0.95	0.76	SLC6A20	solute carrier family 6 (proline IMINO transporter), m	NM_022405
uc002cxt.4	7.09E-04	-1.07 down	-3.14 down	-1.91	-1.81	-3.47	SMIM22	small integral membrane protein 22 (SMIM22), trans	NM_0012537
uc059qjk.1	6.54E-04	-1.24 down	-3.31 down	-1.76	-1.45	-3.18	SMIM22	small integral membrane protein 22 (SMIM22), trans	NM_0012537
uc061ver.1	8.60E-04	-1.43 down	-1.45 down	1.02	1.53	0.99	SMOX	spermine oxidase (SMOX), transcript variant 2, mRN	NM_175840
uc057qye.1	2.67E-04	-1.35 down	-3.32 down	-2.80	-2.37	-4.10	SMYD3	SET and MYND domain containing 3 (SMYD3), trans	NM_022743
uc064hsz.1	1.85E-04	-1.16 down	-1.53 down	1.46	1.67	1.06	SND1	staphylococcal nuclease and tudor domain containin	NM_014390
uc001ffu.2	1.20E-04	1.01 up	-6.60 down	0.68	0.67	-2.05	SNORA53	small nucleolar RNA, H/ACA box 53 (SNORA53), sm	NR_003015
uc064tit.1	1.93E-04	-2.64 down	-7.67 down	-4.13	-2.73	-5.67	SPATA31A7	SPATA31 subfamily A, member 7 (SPATA31A7), mRN	NM_015667
uc063eby.1	8.86E-04	-1.33 down	-1.55 down	0.36	0.77	0.14	SREK1	splicing regulatory glutamine/lysine-rich protein 1 (SR	NM_0012704
uc058mcg.1	4.95E-04	-1.60 down	-2.98 down	-1.23	-0.55	-2.13	SSPN	sarcospan (SSPN), transcript variant 2, mRNA. (from	NM_0011358
uc010rnb.2	9.82E-04	-1.41 down	-1.35 down	1.35	1.84	1.41	STIP1	stress-induced phosphoprotein 1 (STIP1), transcript	NM_0012826
uc057jcy.1	5.62E-04	-1.55 down	-1.35 down	0.07	0.71	0.27	STRIP1	striatin interacting protein 1 (STRIP1), transcript varia	NM_0012707
uc064egv.1	8.06E-04	-1.10 down	-2.56 down	-1.75	-1.61	-2.96	STX1A	syntaxin 1A (brain) (STX1A), transcript variant 2, mR	NM_0011659
uc059pdz.1	4.54E-04	-1.52 down	-1.21 down	-1.20	-0.60	-0.87	TBL3	transducin (beta)-like 3 (TBL3), mRNA. (from RefSeq	NM_006453
uc060rek.1	4.39E-04	-1.39 down	-1.29 down	-0.33	0.14	-0.23	TCF3	transcription factor 3 (TCF3), transcript variant 1, mF	NM_003200

uc061znt.1	5.57E-04	-1.77 down	-1.31 down	-1.83	-1.01	-1.40	TCP10L	t-complex 10-like (TCP10L), mRNA. (from RefSeq NI NM_144659
uc057kyy.1	9.60E-04	-1.30 down	-1.29 down	-2.19	-1.81	-2.17	TDRKH	tudor and KH domain containing (TDRKH), transcript NM_0010839
uc060upn.1	4.93E-04	-1.92 down	-1.60 down	-1.19	-0.25	-0.92	TECR	trans-2,3-enoyl-CoA reductase (TECR), transcript vε NM_138501
uc061ojm.1	9.66E-04	-2.23 down	-6.50 down	-2.10	-0.95	-3.65	TEX41	testis expressed 41 (non-protein coding) (TEX41), lo: NR_033870
uc061irb.1	5.78E-05	-2.01 down	-1.74 down	-1.11	-0.10	-0.91	THADA	thyroid adenoma associated NR_073394
uc061kij.1	8.52E-04	-1.45 down	-1.55 down	0.39	0.92	0.29	TIA1	TIA1 cytotoxic granule-associated RNA binding prote NM_022173
uc060vxm.1	4.76E-06	-3.08 down	-10.76 down	-2.48	-0.86	-4.28	TMEM161A	transmembrane protein 161A (TMEM161A), transcrip NM_0012567
uc062bjc.1	4.17E-05	-1.39 down	-6.22 down	-2.72	-2.25	-4.89	TMEM191B	transmembrane protein 191B (TMEM191B), mRNA. ( NM_0012423
uc058ssh.1	1.51E-05	-1.43 down	-1.62 down	-0.05	0.46	-0.24	TMEM263	transmembrane protein 263 (TMEM263), mRNA. (fro NM_152261
uc064ooz.1	6.35E-04	1.04 up	-3.40 down	-3.32	-3.38	-5.14	TMEM67	transmembrane protein 67 NR_024522
uc064vgq.1	0	-1.00 down	-1.00 down	-1.87	-1.87	-1.87	TNC	tenascin C (TNC), mRNA. (from RefSeq NM_002160 NM_002160
uc061duf.1	4.36E-04	-1.33 down	-1.51 down	1.05	1.46	0.87	TRIM28	tripartite motif containing 28 (TRIM28), mRNA. (from NM_005762
uc058qdh.1	9.20E-04	-1.61 down	-1.36 down	-1.66	-0.97	-1.41	TSFM	Ts translation elongation factor, mitochondrial (TSFM NM_005726
uc062atf.1	8.31E-04	-1.41 down	-1.34 down	0.24	0.73	0.32	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBE2G2), trans NM_003343
uc058dep.1	4.94E-04	-1.37 down	-1.52 down	1.35	1.80	1.19	VPS51	vacuolar protein sorting 51 homolog (S. cerevisiae) ( NM_013265
uc058fld.1	8.78E-05	-1.23 down	-4.33 down	-3.01	-2.72	-4.83	XRRA1	X-ray radiation resistance associated 1 (XRRA1), tra NM_0012703
uc060pua.1	1.92E-04	-1.24 down	-1.59 down	1.15	1.46	0.79	ZCCHC2	zinc finger, CCHC domain containing 2 (ZCCHC2), tr NM_017742
uc063ezp.1	8.63E-04	-1.16 down	-3.86 down	-1.01	-0.80	-2.74	ZCCHC9	zinc finger, CCHC domain containing 9 (ZCCHC9), tr NM_0011310
uc001knl.5	9.98E-04	-1.25 down	-1.23 down	-1.75	-1.43	-1.73	ZDHHC16	zinc finger, DHHC-type containing 16 (ZDHHC16), tr: NM_198043
uc057vfd.1	3.53E-04	-1.65 down	-1.61 down	-1.07	-0.35	-1.04	ZDHHC16	zinc finger, DHHC-type containing 16 (ZDHHC16), tr: NM_0012878
uc061you.1	1.46E-04	-1.45 down	-1.61 down	-0.91	-0.38	-1.07	ZGPAT	zinc finger, CCCH-type with G patch domain (ZGPAT NM_181485
uc010tbw.3	9.73E-04	-1.56 down	-1.40 down	-2.72	-2.09	-2.57	ZNF268	zinc finger protein 268 (ZNF268), transcript variant 5. NM_0011658
uc001ico.4	3.87E-04	-1.34 down	-1.20 down	-0.64	-0.21	-0.47	ZNF496	zinc finger protein 496 (ZNF496), mRNA. (from RefS; NM_032752
uc002mtq.3	7.41E-04	-1.46 down	-1.46 down	-1.27	-0.72	-1.26	ZNF563	zinc finger protein 563 (ZNF563), mRNA. (from RefS; NM_145276
uc060zmo.1	3.04E-04	-1.91 down	-1.59 down	-0.53	0.41	-0.26	ZNF576	zinc finger protein 576 (ZNF576), transcript variant 2. NM_0011453
uc061dni.1	6.00E-04	-1.27 down	-1.63 down	-0.91	-0.56	-1.26	ZNF587	zinc finger protein 587 (ZNF587), transcript variant 2. NM_0012048
uc062iuz.1	1.24E-04	-1.38 down	-1.39 down	-0.68	-0.22	-0.69	ZNF852	zinc finger protein 852 (ZNF852), mRNA. (from RefS; NM_0012873
uc002bkr.4	1.09E-04	-1.43 down	-1.29 down	-2.09	-1.58	-1.94	ZSCAN2	zinc finger and SCAN domain containing 2 (ZSCAN2) NM_181877
uc059mrx.1	4.71E-05	-1.45 down	-1.25 down	-2.04	-1.50	-1.82	ZSCAN2	zinc finger and SCAN domain containing 2 (ZSCAN2) NM_181877
uc059mry.1	9.45E-04	-1.38 down	-1.52 down	-1.07	-0.60	-1.20	ZSCAN2	zinc finger and SCAN domain containing 2 (ZSCAN2) NM_181877
uc059msa.1	1.12E-04	-1.45 down	-1.20 down	-1.64	-1.11	-1.36	ZSCAN2	zinc finger and SCAN domain containing 2 (ZSCAN2) NM_181877

Supplementary Table 2.

GeneName		p		FC (abs)		Regulation		[F](normaliz		[M](normaliz		Symbol		Description		RefSeq
uc064gjl.1	0.01938091	3.9134712	up	-2.2245476	-4.1929965	ACHE	Homo sapiens acetylcholinesterase (Yt blood group) (ACHE), transcript variant 3, m	MM_001282449								
uc010tk.2	0.03062528	3.39541	down	-4.2712855	-2.5076997	ADAMTS16	Homo sapiens ADAM metalloproteinase with thrombospondin type 1 motif, 16 (ADAMTS16)	NR_139056								
uc060emi.1	0.00389895	3.0257018	up	-0.4121704	-2.0094402	ARHGAP23	Homo sapiens Rho GTPase activating protein 23 (ARHGAP23), mRNA. (from RefSeq NM_001199417)	NR_001199417								
uc064phw.1	0.01207369	3.2448657	down	-2.4748294	-0.7766708	BAALC	Homo sapiens brain and acute leukemia, cytoplasmic (BAALC), transcript variant 2, NM_001024372	NM_001024372								
uc062ahg.1	0.02366242	3.1006773	down	-4.0203047	-2.3877213	BACE2	Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant c, mRNA. (from RefSeq NM_138991)	NM_138991								
uc060lv.1	0.01410843	3.1679745	down	-2.760526	-1.0969652	CCDC137	Homo sapiens coiled-coil domain containing 137 (CCDC137), mRNA. (from RefSeq NM_199287)	NM_199287								
uc057tex.1	1.43E-04	4.8776813	down	-5.13456	-2.8483646	CHAT	Homo sapiens choline O-acetyltransferase (CHAT), transcript variant N2, mRNA. (from RefSeq NM_020986)	NM_020986								
uc062nwr.1	0.00653113	3.3447895	down	-5.167503	-3.4255874	CPNE4	Homo sapiens copine IV (CPNE4), transcript variant 2, mRNA. (from RefSeq NM_15153429)	NM_15153429								
uc004fsu.2	5.25E-29	5.0172653	down	-0.817907	1.5089942	DDX3Y	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked (DDX3Y), transcript NM_001122665	NM_001122665								
uc004fsv.3	1.89E-19	4.272347	down	0.9116861	3.006715	DDX3Y	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked (DDX3Y), transcript NM_004660	NM_004660								
uc065crs.1	2.24E-31	7.2224665	down	-2.2035515	0.64894	DDX3Y	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked (DDX3Y), transcript NM_001122665	NM_001122665								
uc002wvp.1	0.00206359	3.7402442	down	-0.8678935	1.035239	DEFB115	Homo sapiens defensin, beta 115 (DEFB115), mRNA. (from RefSeq NM_001033773)	NM_001033773								
uc064bwk.1	0.00406922	3.6024404	down	-3.4191754	-1.5702008	DNAH11	Homo sapiens dynein, axonemal, heavy chain 11 (DNAH11), mRNA. (from RefSeq NM_001277115)	NM_001277115								
uc004fuk.5	6.28E-38	21.4298	down	0.2558369	4.6773834	EIF1AY	Homo sapiens eukaryotic translation initiation factor 1A, Y-linked (EIF1AY), transcript NM_004681	NM_004681								
uc004ful.5	4.38E-26	18.869068	down	-0.9159175	3.3220336	EIF1AY	Homo sapiens eukaryotic translation initiation factor 1A, Y-linked (EIF1AY), transcript NM_001278612	NM_001278612								
uc065cuc.1	3.29E-19	7.0512075	down	-0.5066402	2.3112302	EIF1AY	Homo sapiens eukaryotic translation initiation factor 1A, Y-linked (EIF1AY), transcript NM_004681	NM_004681								
uc065cuc.1	3.04E-25	4.04494	down	-0.9418847	1.0742351	EIF1AY	Homo sapiens eukaryotic translation initiation factor 1A, Y-linked (EIF1AY), transcript NM_001278612	NM_001278612								
uc064owu.1	0.01960526	3.3898225	up	-1.1121063	-2.873316	HRSP12	Homo sapiens heat-responsive protein 12 (HRSP12), mRNA. (from RefSeq NM_005005836)	NM_005005836								
uc059wsc.1	0.0136463	3.0066426	up	-0.7712486	-2.359402	HYDIN	Homo sapiens HYDIN, axonemal central pair apparatus protein (HYDIN), transcript NM_001270974	NM_001270974								
uc004fug.4	1.02E-27	4.0219693	down	-1.6747676	0.3331362	KDM5D	Homo sapiens lysine (K)-specific demethylase 5D (KDM5D), transcript variant 2, mFNM_004653	mFNM_004653								
uc010nwv.4	4.32E-27	3.7597651	down	-1.6782808	0.23236163	KDM5D	Homo sapiens lysine (K)-specific demethylase 5D (KDM5D), transcript variant 3, mFNM_001146706	mFNM_001146706								
uc011naz.3	7.70E-28	3.540423	down	-1.4008155	0.42310765	KDM5D	Homo sapiens lysine (K)-specific demethylase 5D (KDM5D), transcript variant 1, mFNM_001146705	mFNM_001146705								
uc065ctw.1	1.47E-27	4.54361	down	-1.9088793	0.27495986	KDM5D	Homo sapiens lysine (K)-specific demethylase 5D (KDM5D), transcript variant 2, mFNM_004653	mFNM_004653								
uc065cua.1	3.20E-32	9.69576	down	-2.2312317	1.0461223	KDM5D	Homo sapiens lysine (K)-specific demethylase 5D (KDM5D), transcript variant 2, mFNM_004653	mFNM_004653								
uc059sio.1	0.02388188	3.6873474	down	-4.13435	-2.2517664	KDM8	Homo sapiens lysine (K)-specific demethylase 8 (KDM8), transcript variant 1, mFNM_001145348	mFNM_001145348								
uc031tkv.2	1.08E-19	4.9962826	down	0.37769195	2.6985471	LINC00278	Homo sapiens long intergenic non-protein coding RNA 278 (LINC00278), long non-coding RNA. (NR_046502)	NR_046502								
uc065cpm.1	1.70E-10	5.5638766	down	-0.3208716	2.1552188	LINC00278	Homo sapiens long intergenic non-protein coding RNA 278 (LINC00278), long non-coding RNA. (NR_046502)	NR_046502								
uc058vvi.1	0.00283394	3.451988	down	-1.6120982	0.17532915	LINC01046	Homo sapiens long intergenic non-protein coding RNA 1046 (LINC01046), long non-coding RNA. (NR_125745)	NR_125745								
uc058xrv.1	0.00866287	3.8844743	up	-0.5234225	-2.4811418	LMO7DN-IT1	Homo sapiens LMO7DN intronic transcript 1 (LMO7DN-IT1), long non-coding RNA. (NR_126373)	NR_126373								
uc064smd.1	0.00512486	3.2028503	down	-4.4714017	-2.7920454	LRRC19	Homo sapiens leucine rich repeat containing 19 (LRRC19), mRNA. (from RefSeq NM_022901)	NM_022901								
uc032bjl.1	0.04585941	4.1469225	down	-3.0917873	-1.0397455	MIR151B	Homo sapiens microRNA 151b (MIR151B), microRNA. (from RefSeq NR_039601)	NR_039601								
uc011jvw.2	0.03729176	4.2927227	up	-0.6004785	-2.7023714	MIR339	Homo sapiens microRNA 339 (MIR339), microRNA. (from RefSeq NR_029898)	NR_029898								
uc021qaz.1	0.02102952	6.3192425	down	-2.5657182	0.09403343	MIR378C	Homo sapiens microRNA 378c (MIR378C), microRNA. (from RefSeq NR_036180)	NR_036180								
uc033ctu.1	0.03079745	3.9283636	up	-0.2509968	-2.2249253	MIR4477B	Homo sapiens microRNA 4477b (MIR4477B), microRNA. (from RefSeq NR_039689)	NR_039689								
uc032rvy.1	0.01692812	4.686864	up	0.85472345	-1.3738996	MIR548AB	Homo sapiens microRNA 548ab (MIR548AB), microRNA. (from RefSeq NR_039611)	NR_039611								
uc021uev.1	0.03646325	4.269607	up	0.18030404	-1.9137993	MIR657	Homo sapiens microRNA 657 (MIR657), microRNA. (from RefSeq NR_030394)	NR_030394								
uc033ccb.1	0.00573946	6.324716	up	-1.1741376	-3.8351383	MIR6845	Homo sapiens microRNA 6845 (MIR6845), microRNA. (from RefSeq NR_106904)	NR_106904								
uc032dpx.1	0.01469008	5.113097	up	-0.7466453	-3.1008427	MIR8065	Homo sapiens microRNA 8065 (MIR8065), microRNA. (from RefSeq NR_107032)	NR_107032								
uc059ppl.1	0.02914493	4.9069304	down	-3.316861	-1.02204	MIR940	Homo sapiens microRNA 940 (MIR940), microRNA. (from RefSeq NR_030636)	NR_030636								
uc004aul.3	0.00267105	6.402918	down	0.7379887	-1.940741	MIRLET7D	Homo sapiens microRNA let-7d (MIRLET7D), microRNA. (from RefSeq NR_029481)	NR_029481								
uc001fie.4	6.87E-04	4.0007987	down	-6.4688354	-4.4685473	MUC1	Homo sapiens mucin 1, cell surface associated (MUC1), transcript variant N21, mRNA. (from RefSeq NM_001204297)	NM_001204297								
uc011bee.3	0.02034955	4.12627	up	0.17895718	-1.865881	MIRLET7G	microRNA let-7g (from HGNC MIRLET7G)	NR_029660								
uc022ckf.2	1.17E-29	4.245518	down	-2.178438	-0.0924974	n/a	n/a	NR_001258249								
uc022ckg.2	2.45E-29	4.032983	down	-2.2834322	-0.271585	n/a	n/a	NR_001258252								
uc022ckj.2	9.36E-30	4.3056283	down	-2.2440703	-0.1378465	n/a	n/a	NR_001258258								
uc022ckn.2	1.38E-28	4.086316	down	-2.2574725	-0.2266717	n/a	n/a	NR_001258251								
uc022ckq.2	5.92E-29	4.0484033	down	-2.2933328	-0.2759796	n/a	n/a	NR_001258256								
uc033csg.1	0.03073894	3.9783487	up	-0.381549	-2.3737187	n/a	n/a	NR_039688								
uc057ukp.1	0.01872875	3.0890422	down	-1.0552721	0.57188743	n/a	n/a	NR_073447								
uc059mrx.1	0.01835862	3.3524635	up	0.5813638	-1.1638578	n/a	n/a	NR_001303234								
uc059xwj.1	0.03450751	3.166916	down	-2.1777365	-0.5146579	n/a	n/a	NR_001291454								
uc062zko.1	0.00206118	4.854856	up	-1.1580049	-3.4374332	n/a	n/a	NR_075089								
uc064mda.1	0.00944297	3.690986	up	-3.447562	-5.3315682	n/a	n/a	NR_001174066								
uc065cru.1	8.97E-26	8.081257	down	-1.7726135	1.2419664	n/a	n/a	NR_001302552								
uc065cru.1	6.61E-10	4.6437545	down	-0.9508694	1.2644224	n/a	n/a	NR_001302552								
uc065cru.1	2.65E-16	3.205997	down	-0.123269	1.557504	n/a	n/a	NR_001302552								
uc065crz.1	2.67E-20	9.097182	down	-3.7320411	-0.5466213	n/a	n/a	NR_004764								
uc060pnx.1	0.01947117	3.4469218	down	-4.8177285	-3.03242	NEDD4L	Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-l (NEDD4L), transcript variant 1, mRNA. (from RefSeq NM_001243960)	NM_001243960								
uc062vgl.1	0.0038996	3.2986445	up	-1.9106007	-3.632474	PEX5L	Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), transcript variant 7, mRNA. (from RefSeq NM_001256755)	NM_001256755								
uc059xow.1	0.00123614	3.5459275	up	-1.0632253	-2.8893883	PKD1L2	Homo sapiens polycystic kidney disease 1-like 2 (gene/pseudogene) (PKD1L2), transcript variant 1, mRNA. (from RefSeq NM_001278425)	NM_001278425								
uc062zne.1	0.00707994	3.4278123	down	-1.7082833	0.06900481	RP11-420A2.2	Homo sapiens uncharacterized LOC100507487 (LOC100507487), long non-coding RNA. (from RefSeq R1NR_125882)	R1NR_125882								
uc004fqi.4	5.80E-08	6.858584	down	1.8678665	4.645777	RPS4Y1	Homo sapiens ribosomal protein S4, Y-linked 1 (RPS4Y1), mRNA. (from RefSeq NM_0010008)	NM_0010008								
uc065cpc.1	5.29E-26	56.036827	down	-2.8105843	2.997719	RPS4Y1	Homo sapiens ribosomal protein S4, Y-linked 1 (RPS4Y1), mRNA. (from RefSeq NM_0010008)	NM_0010008								
uc065cpd.1	1.03E-16	3.3501081	down	0.06841782	1.8126254	RPS4Y1	Homo sapiens ribosomal protein S4, Y-linked 1 (RPS4Y1), mRNA. (from RefSeq NM_0010008)	NM_0010008								
uc061xll.1	0.01804181	3.123604	down	-2.845503	-1.2022915	SLC12A5	Homo sapiens solute carrier family 12 (potassium/chloride transporter), member 5 (SLC12A5), transcript variant 1, mRNA. (from RefSeq NM_001134771)	NM_001134771								
uc031tdn.2	0.02524371	5.191672	up	-0.6484059	-3.024605	SNORD121B	Homo sapiens small nucleolar RNA, C/D box 121B (SNORD121B), small nucleolar RNA. (from RefSeq NR_00102370)	NR_00102370								
uc057zln.1	0.02050424	4.863273	down	-2.7753856	-0.493458	SNORD14B	Homo sapiens small nucleolar RNA, C/D box 14B (SNORD14B), small nucleolar RNA. (from RefSeq NR_001452)	NR_001452								
uc060hqf.1	0.01399945	3.0946639	down	-2.309882	-0.6800992	TOM1L1	Homo sapiens target of myb1 (chicken)-like 1 (TOM1L1), mRNA. (from RefSeq NM_005486)	NM_005486								
uc065crn.1	2.29E-16	4.51908	down	-0.8411754	1.3348538	TTY15	Homo sapiens testis-specific transcript, Y-linked 15 (non-protein coding) (TTY15), transcript variant 1, mRNA. (from RefSeq NM_001545)	NR_001545								
uc061awx.1	0.02167169	3.129873	down	-3.7801132	-2.1340091	TULP2	Homo sapiens tubby like protein 2 (TULP2), mRNA. (from RefSeq NM_003323)	NM_003323								
uc065crq.1	2.53E-11	3.331889	down	-1.6803708	0.05596946	USPY9	Homo sapiens ubiquitin specific peptidase 9, Y-linked (USPY9), mRNA. (from RefSeq NM_004654)	NM_004654								
uc004fss.3	2.21E-29	4.0840335	down	-2.3133934	-0.2833986	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_182659	NM_182659								
uc004fsy.4	4.22E-27	4.5797243	down	-2.1563802	0.03888058	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_182660	NM_182660								
uc004fss.3	1.70E-21	3.3569968	down	-1.3580545	0.38911662	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_182660	NM_182660								
uc022cjm.2	4.60E-29	4.0109487	down	-2.262525	-0.2586097	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_001258266	NM_001258266								
uc022cjk.2	5.10E-28	3.8581698	down	-2.2205687	-0.2726521	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_001258265	NM_001258265								
uc022cjk.2	8.41E-29	3.992532	down	-2.1967497	-0.1994457	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_001258261	NM_001258261								
uc022cjp.3	3.88E-33	5.529723	down	-2.6395357	-0.1541803	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_001258254	NM_001258254								
uc065csc.1	1.17E-07	3.8994606	down	-1.1526278	0.8106468	UTY	Homo sapiens ubiquitously transcribed tetratricopeptide repeat containing, Y-linked NM_182660	NM_182660								
uc004ebm.3	1.55E-29	4.762518	up	3.2276194	0.975895	XIST	Homo sapiens X inactive specific transcript (non-protein coding) (XIST), long non-coding RNA. (from RefSeq NR_001564)	NR_001564								
uc064zym.1	5.07E-16	3.0539112	up	0.8455181	-0.7651401	XIST	Homo sapiens X inactive specific transcript (non-protein coding) (XIST), long non-coding RNA. (from RefSeq NR_001564)	NR_001564								

uc064zyn.1	4.77E-17	3.903899	up	0.44827378	-1.516642	XIST	Homo sapiens X inactive specific transcript (non-protein coding) (XIST), long non-co NR_001564
uc064zyo.1	1.12E-20	4.9645014	up	0.9907029	-1.3209459	XIST	Homo sapiens X inactive specific transcript (non-protein coding) (XIST), long non-co NR_001564
uc065cpi.1	1.93E-12	4.6426497	down	-1.6081386	0.6068098	ZFY	Homo sapiens zinc finger protein, Y-linked (ZFY), transcript variant 1, mRNA. (from NM_003411

Supplementary Table 3. ANOVA analysis of TRACS

GeneName	p	Regulation	FC (abs)	FC	Log FC	Log2 RPKM Expression			Description	RefSeq
						[LOW]	[norm [MID+]]	[norm Symbol		
uc060kqb.1	9.52E-04	DOWN	1.4337534	1.4337534	0.51979685	-0.185121	-0.7049179	SEPTIN9	Homo sapiens septin 9 (SEPT9), transcript variant 9, mRNA. (from RefSeq NM_001293696)	NM_001293696
uc003wjo.3	9.21E-05	DOWN	1.2744105	1.2744105	0.34983003	1.0920848	0.74225473	ABCF2	Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), transcript variant 2, NM_005692	
uc064jff.1	7.85E-04	DOWN	1.2906467	1.2906467	0.3680941	0.6617042	0.2936101	ABCF2	Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), transcript variant 2, NM_005692	
uc057wcy.1	8.08E-04	DOWN	1.3010219	1.3010219	0.3796453	-0.053218	-0.4328632	ABLIM1	Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 1, mRNA. (from RefSeq NM_0022313)	
uc057bbq.1	4.81E-04	DOWN	1.3252088	1.3252088	0.40621966	1.2488762	0.84265655	ACAP3	Homo sapiens ArfGAP with coiled-coil, ankyrin repeat and PH domains 3 (ACAP3), mRNA. (from RefSeq NM_030649)	
uc064mff.1	9.69E-04	DOWN	2.3338773	2.3338773	1.2227287	-2.3129778	-3.5357065	ADAM32	Homo sapiens ADAM metalloproteinase domain 32 (ADAM32), mRNA. (from RefSeq NM_145004)	NM_145004
uc002zgr.3	6.60E-04	DOWN	1.3100791	1.3100791	0.38965392	-0.7031987	-1.0928526	ADARB1	Homo sapiens adenosine deaminase, RNA-specific, B1 (ADARB1), transcript variant 3, mRNA. (from NM_015834)	
uc059xhj.1	6.69E-04	DOWN	1.5142472	1.5142472	0.59860075	1.7449799	1.463791	ADAT1	Homo sapiens adenosine deaminase, tRNA-specific 1 (ADAT1), transcript variant 1, mRNA. (from RefSeq NM_012091)	
uc021xqj.2	6.12E-05	DOWN	1.7142575	1.7142575	0.7775838	-1.9975505	-2.7751343	ADH7	Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7), transcript variant 1, mRNA. (from RefSeq NM_001166504)	
uc002bmt.3	9.57E-04	DOWN	1.2088468	1.2088468	0.27363142	1.1450907	0.8714593	AEN	Homo sapiens apoptosis enhancing nuclease (AEN), mRNA. (from RefSeq NM_022767)	NM_022767
uc062apr.1	5.21E-04	DOWN	1.3921204	1.3921204	0.47728395	0.42026684	-0.0570171	AGPAT3	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 3 (AGPAT3), transcript variant 2, mRNA. (from RefSeq NM_001037553)	
uc011kox.3	7.76E-04	DOWN	1.2946298	1.2946298	0.37253964	-0.6687162	-1.0412558	AHCYL2	Homo sapiens adenosylhomocysteinase-like 2 (AHCYL2), transcript variant 3, mRNA. (from RefSeq NM_001130722)	
uc064uzz.1	8.86E-04	DOWN	1.3878013	1.3878013	0.472801	-0.4984947	-0.9712957	AKAP2	Homo sapiens A kinase (PRKA) anchor protein 2 (AKAP2), transcript variant 2, mRNA. (from RefSeq NM_001136562)	
uc064ieo.1	4.98E-04	DOWN	1.260167	1.260167	0.33361495	0.13701719	-0.1965978	AKR1B1	Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA. (from RefSeq NM_001628)	
uc001ukx.3	4.25E-04	DOWN	1.2933732	1.2933732	0.37113863	1.04623	0.6750913	ANKLE2	Homo sapiens ankyrin repeat and LEM domain containing 2 (ANKLE2), mRNA. (from RefSeq NM_015114)	
uc061lxq.1	4.91E-04	DOWN	1.416466	1.416466	0.502296	-0.9948019	-1.497098	ANKRD23	Homo sapiens ankyrin repeat domain 23 (ANKRD23), mRNA. (from RefSeq NM_144994)	NM_144994
uc064mjf.1	3.22E-04	DOWN	1.3409983	1.3409983	0.4233074	-1.183571	-1.6068784	AP3M2	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (AP3M2), transcript variant 2, mRNA. (from RefSeq NM_006803)	
uc001mdb.4	1.54E-04	DOWN	1.3240794	1.3240794	0.40498963	-0.7239344	-1.128924	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001164)	
uc001mdc.3	1.14E-04	DOWN	1.3491114	1.3491114	0.43200952	-0.5606896	-0.9926991	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_145689)	
uc001mdd.6	4.39E-04	DOWN	1.3442086	1.3442086	0.42675704	-1.2639574	-1.6907145	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001257323)	
uc057yjt.1	5.44E-04	DOWN	1.3164849	1.3164849	0.396691	-1.6357287	-2.0324197	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001257321)	
uc057yiv.1	6.77E-05	DOWN	1.3608962	1.3608962	0.44455707	-0.5966111	-1.0411681	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001164)	
uc057yjj.1	1.95E-04	DOWN	1.3163289	1.3163289	0.39652	-0.7434836	-1.1400036	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001164)	
uc057yka.1	3.43E-04	DOWN	1.3295468	1.3295468	0.41093457	-0.5385923	-0.9495268	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001164)	
uc057ykb.1	4.13E-04	DOWN	1.3299803	1.3299803	0.41140482	-1.632174	-2.0435789	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001257321)	
uc057ykd.1	5.06E-05	DOWN	1.4381772	1.4381772	0.52424145	-1.1580667	-1.6823082	APBB1	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1), transcript variant 1, mRNA. (from RefSeq NM_001257320)	
uc061yli.1	8.04E-04	DOWN	1.5089302	1.5089302	0.59352607	-0.3083625	-0.9018886	ARFGAP1	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), transcript variant 1, mRNA. (from RefSeq NM_018209)	
uc065ahz.1	1.71E-04	DOWN	1.4031242	1.4031242	0.48864272	-0.0871896	-0.5758323	ARMCX6	Homo sapiens armadillo repeat containing, X-linked 6 (ARMCX6), transcript variant 3, mRNA. (from RefSeq NM_001184768)	
uc003cgd.4	5.36E-04	DOWN	4.2413015	4.2413015	2.084507	-4.205631	-6.290138	ARPP21	Homo sapiens cAMP-regulated phosphoprotein, 21kDa (ARPP21), transcript variant 7, mRNA. (from RefSeq NM_001267618)	
uc059zrw.1	2.96E-04	DOWN	1.3435875	1.3435875	0.4260903	1.8983804	1.47229	ATP2A3	Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), transcript variant 7, mRNA. (from RefSeq NM_174958)	
uc002jfh.4	3.81E-04	DOWN	1.4512465	1.4512465	0.5372926	-0.6264079	-1.1637005	AXIN2	Homo sapiens axin 2 (AXIN2), mRNA. (from RefSeq NM_004655)	NM_004655
uc001ynh.3	8.47E-04	DOWN	1.3201435	1.3201435	0.4006947	1.1346888	0.73399335	BAG5	Homo sapiens BCL2-associated athanogene 5 (BAG5), transcript variant 1, mRNA. (from RefSeq NM_001015049)	
uc059ulu.1	2.64E-04	DOWN	1.9204495	1.9204495	0.94144404	-0.0587493	-1.0001934	BBS2	Homo sapiens Bardet-Biedl syndrome 2 (BBS2), mRNA. (from RefSeq NM_031885)	NM_031885
uc061wwa.1	1.26E-04	DOWN	1.4126246	1.4126246	0.49837813	0.24412708	-0.2542511	BLCAP	Homo sapiens bladder cancer associated protein (BLCAP), transcript variant 2, mRNA. (from RefSeq NM_001167820)	
uc061wwb.1	8.95E-04	DOWN	1.3646924	1.3646924	0.44857585	0.1648186	-0.2837572	BLCAP	Homo sapiens bladder cancer associated protein (BLCAP), transcript variant 2, mRNA. (from RefSeq NM_001167820)	
uc064kgd.1	7.42E-04	DOWN	1.3937876	1.3937876	0.47901073	0.83950424	0.36049345	BLK	Homo sapiens BLK proto-oncogene, Src family tyrosine kinase (BLK), mRNA. (from RefSeq NM_001715)	
uc063hjk.1	9.02E-04	DOWN	1.332296	1.332296	0.41391465	-0.6734464	-1.087361	BRD8	Homo sapiens bromodomain containing 8 (BRD8), transcript variant 6, mRNA. (from RefSeq NM_001300962)	
uc003dzb.5	4.12E-04	DOWN	1.7705259	1.7705259	0.824178	0.9693076	0.14512964	BTLA	Homo sapiens B and T lymphocyte associated (BTLA), transcript variant 2, mRNA. (from RefSeq NM_001085357)	
uc058bon.1	2.60E-04	DOWN	1.3815451	1.3815451	0.4662826	1.6815842	1.2153016	C11orf31	Homo sapiens chromosome 11 open reading frame 31 (C11orf31), mRNA. (from RefSeq NM_17074)	NM_17074
uc058usc.1	9.80E-04	DOWN	1.4553193	1.4553193	0.5413357	-0.7864534	-1.3277892	C12orf65	Homo sapiens chromosome 12 open reading frame 65 (C12orf65), transcript variant 1, mRNA. (from RefSeq NM_152269)	
uc059tos.1	3.95E-04	DOWN	1.3457203	1.3457203	0.42837858	-0.768739	-1.1971176	C16orf58	Homo sapiens chromosome 16 open reading frame 58 (C16orf58), mRNA. (from RefSeq NM_02274)	NM_02274
uc021tna.1	3.01E-04	DOWN	1.3925934	1.3925934	0.47777405	0.6382703	0.16049625	C17orf97	Homo sapiens chromosome 17 open reading frame 97 (C17orf97), mRNA. (from RefSeq NM_0010101)	NM_0010101
uc002rjt.4	8.56E-04	DOWN	1.2446817	1.2446817	0.31577685	0.35971102	0.04393421	CAD	Homo sapiens carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (CAD), transcript variant 1, mRNA. (from RefSeq NM_004341)	
uc063fyf.1	6.94E-04	DOWN	1.3283268	1.3283268	0.40961015	0.848183	0.4385728	CAMK4	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA. (from RefSeq NM_001744)	
uc010nbg.4	8.59E-04	DOWN	1.1643348	1.1643348	0.21950592	0.099172	-0.1203339	CAMSAP1	Homo sapiens calmodulin regulated spectrin-associated protein 1 (CAMSAP1), mRNA. (from RefSeq NM_015447)	
uc064rtg.1	4.80E-04	DOWN	1.9413694	1.9413694	0.95707464	-3.2309866	-4.188061	CBWD1	Homo sapiens COB domain containing 1 (CBWD1), transcript variant 1, mRNA. (from RefSeq NM_0018491)	
uc021wxn.3	6.08E-04	DOWN	1.3152108	1.3152108	0.39529407	-0.3335028	-0.7287969	CCDC51	Homo sapiens coiled-coil domain containing 51 (CCDC51), transcript variant 3, mRNA. (from RefSeq NM_001256965)	
uc010atx.4	4.81E-04	DOWN	1.3128444	1.3128444	0.39269593	2.970372	2.577676	CCDC88C	Homo sapiens coiled-coil domain containing 88C (CCDC88C), mRNA. (from RefSeq NM_001080414)	
uc058mhe.1	9.03E-04	DOWN	1.414445	1.414445	0.5002361	1.3163532	0.8161171	CCDC91	Homo sapiens coiled-coil domain containing 91 (CCDC91), mRNA. (from RefSeq NM_018318)	NM_018318
uc063myg.1	4.14E-04	DOWN	2.0276597	2.0276597	1.0198154	-5.231518	-6.251333	CCHCR1	Homo sapiens coiled-coil alpha-helical rod protein 1 (CCHCR1), transcript variant 3, mRNA. (from RefSeq NM_019052)	
uc060xci.1	5.68E-04	DOWN	1.5151955	1.5151955	0.59950393	-0.6206064	-1.2201103	CD22	Homo sapiens CD22 molecule (CD22), transcript variant 5, mRNA. (from RefSeq NM_001278417)	NM_001278417



uc064bww.1	7.87E-04	DOWN	1.4893333	1.4893333	0.5746666	-0.4312408	-1.0059074	CDCA7L	Homo sapiens cell division cycle associated 7-like (CDCA7L), transcript variant 3, mRNA. (from RefSeq NM_001127371)
uc064bwy.1	1.07E-04	DOWN	1.5699714	1.5699714	0.6507383	-0.3568905	-1.0076288	CDCA7L	Homo sapiens cell division cycle associated 7-like (CDCA7L), transcript variant 2, mRNA. (from RefSeq NM_001127370)
uc059xrx.1	1.26E-04	DOWN	5.5537534	5.5537534	2.473463	-1.2926244	-3.7660873	CDH13	Homo sapiens cadherin 13 (CDH13), transcript variant 5, mRNA. (from RefSeq NM_001220491)
uc060awd.1	8.00E-04	DOWN	1.6806908	1.6806908	0.7490543	2.506842	1.7577876	CHD3	Homo sapiens chromodomain helicase DNA binding protein 3 (CHD3), transcript variant 2, mRNA. (from RefSeq NM_005852)
uc064ldx.1	7.20E-04	DOWN	1.3877572	1.3877572	0.47275516	0.6397034	0.16694826	CHMP7	Homo sapiens charged multivesicular body protein 7 (CHMP7), mRNA. (from RefSeq NM_152272)
uc059ljk.1	5.54E-04	DOWN	1.3671507	1.3671507	0.45117223	0.8071874	0.35601518	CLK3	Homo sapiens CDC-like kinase 3 (CLK3), transcript variant 2, mRNA. (from RefSeq NM_003992)
uc064kms.1	7.10E-04	DOWN	1.3634907	1.3634907	0.44730484	1.4489573	1.0016525	CNOT7	Homo sapiens CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 2, mRNA. (from RefSeq NM_054026)
uc063jat.1	2.72E-04	DOWN	1.5294986	1.5294986	0.61305875	0.32510754	-0.2879512	CNOT8	Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), transcript variant 3, mRNA. (from RefSeq NM_001301074)
uc057egb.1	5.95E-04	DOWN	5.4626527	5.4626527	2.4496017	-1.4775615	-3.9271631	COL16A1	Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA. (from RefSeq NM_001856)
uc064rqz.1	1.73E-04	DOWN	1.5200763	1.5200763	0.60414374	0.6395183	0.03537459	COMMD5	Homo sapiens COMM domain containing 5 (COMMD5), transcript variant 3, mRNA. (from RefSeq NM_001081004)
uc064ofx.1	5.48E-04	DOWN	1.6919246	1.6919246	0.75866526	0.70704895	-0.0516163	CPNE3	Homo sapiens copine III (CPNE3), mRNA. (from RefSeq NM_003909)
uc062lwg.1	1.45E-04	DOWN	1.4263507	1.4263507	0.51232874	1.625692	1.1133633	CPOX	Homo sapiens coproporphyrinogen oxidase (CPOX), mRNA. (from RefSeq NM_000097)
uc009voy.2	6.80E-04	DOWN	1.4515594	1.4515594	0.5376036	2.3564265	1.8188229	CROCC	Homo sapiens ciliary rootlet coiled-coil, rootletin (CROCC), mRNA. (from RefSeq NM_014675)
uc009ykw.4	3.53E-04	DOWN	1.2723478	1.2723478	0.30749308	1.02051815	-0.226975	CRY2	Homo sapiens cryptochrome circadian clock 2 (CRY2), transcript variant 2, mRNA. (from RefSeq NM_001127457)
uc010rgn.2	1.46E-04	DOWN	1.19535	1.19535	0.25743315	0.8755804	0.6181472	CRY2	Homo sapiens cryptochrome circadian clock 2 (CRY2), transcript variant 1, mRNA. (from RefSeq NM_021117)
uc058ato.1	1.38E-04	DOWN	1.1960957	1.1960957	0.25833282	0.8766598	0.618327	CRY2	Homo sapiens cryptochrome circadian clock 2 (CRY2), transcript variant 1, mRNA. (from RefSeq NM_021117)
uc062ukk.1	8.32E-04	DOWN	1.3743054	1.3743054	0.4587026	0.43223295	-0.0264697	CTBP1	Homo sapiens C-terminal binding protein 1 (CTBP1), transcript variant 2, mRNA. (from RefSeq NM_001012614)
uc059zqi.1	2.29E-04	DOWN	1.7476925	1.7476925	0.80545133	-0.2479629	-1.0534142	CTNS	Homo sapiens cystinosis, lysosomal cystine transporter (CTNS), transcript variant 2, mRNA. (from RefSeq NM_004937)
uc057jkc.1	3.39E-04	DOWN	1.4018576	1.4018576	0.48733982	-0.0166596	-0.5039994	CTTNBP2NL	Homo sapiens CTTNBP2 N-terminal like (CTTNBP2NL), mRNA. (from RefSeq NM_018704)
uc002leq.5	4.03E-04	DOWN	1.2371509	1.2371509	0.3070215	0.2981659	-0.0088556	CXCC1	Homo sapiens CXXC finger protein 1 (CXCC1), transcript variant 2, mRNA. (from RefSeq NM_014593)
uc063hsz.1	9.93E-04	DOWN	1.2923493	1.2923493	0.3699961	-0.3193838	-0.6893799	CXXC5	Homo sapiens CXXC finger protein 5 (CXXC5), mRNA. (from RefSeq NM_016463)
uc058ccb.1	3.72E-04	DOWN	1.5803254	1.5803254	0.66022164	-0.0946591	-0.7548807	CYB561A3	Homo sapiens cytochrome b561 family, member A3 (CYB561A3), transcript variant 4, mRNA. (from RefSeq NM_001300763)
uc059zsi.1	7.55E-04	DOWN	1.3452644	1.3452644	0.4278898	-0.7224397	-1.1503295	CYB5D2	Homo sapiens cytochrome b5 domain containing 2 (CYB5D2), transcript variant 2, mRNA. (from RefSeq NM_001254755)
uc061otq.1	1.87E-05	DOWN	1.4315364	1.4315364	0.51756436	0.38363758	-0.1339269	CYTIIP	Homo sapiens cytohesin 1 interacting protein (CYTIIP), mRNA. (from RefSeq NM_004288)
uc060trt.1	6.73E-04	DOWN	1.6379657	1.6379657	0.7119051	2.3080022	1.5960971	DAPK3	Homo sapiens death-associated protein kinase 3 (DAPK3), mRNA. (from RefSeq NM_001348)
uc002tux.2	8.79E-04	DOWN	1.2755452	1.2755452	0.35111406	3.121397	2.770283	DARS	Homo sapiens aspartyl-tRNA synthetase (DARS), transcript variant 1, mRNA. (from RefSeq NM_0011349)
uc058mlq.1	9.58E-04	DOWN	1.923227	1.923227	0.943529	-1.1854318	-2.1289608	DDX11	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 (DDX11), transcript variant 5, mRNA. (from RefSeq NM_001257145)
uc057jjs.1	7.91E-04	DOWN	1.3948647	1.3948647	0.48012516	0.2522162	-0.227909	DDX20	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (DDX20), mRNA. (from RefSeq NM_007204)
uc058utt.1	4.44E-04	DOWN	1.3347564	1.3347564	0.41657645	-1.2244805	-1.6410569	DDX55	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (DDX55), mRNA. (from RefSeq NM_020909)
uc021wlp.2	1.54E-05	DOWN	1.4976513	1.4976513	0.5827018	0.42528155	-0.1574202	DGCR8	Homo sapiens DGCR8 microprocessor complex subunit (DGCR8), transcript variant 2, mRNA. (from RefSeq NM_001190326)
uc058pdr.1	8.60E-04	DOWN	1.8234607	1.8234607	0.8666791	0.07406825	-0.7926108	DGKA	Homo sapiens diacylglycerol kinase, alpha 80kDa (DGKA), transcript variant 4, mRNA. (from RefSeq NM_201554)
uc058pdy.1	1.65E-04	DOWN	1.4035074	1.4035074	0.48903662	0.18466794	-0.3043687	DGKA	Homo sapiens diacylglycerol kinase, alpha 80kDa (DGKA), transcript variant 4, mRNA. (from RefSeq NM_201554)
uc060uba.1	4.56E-04	DOWN	1.4090039	1.4090039	0.49467555	0.12977083	-0.3649048	DHPS	Homo sapiens deoxyhypusine synthase (DHPS), transcript variant 1, mRNA. (from RefSeq NM_001930)
uc062jfe.1	1.41E-04	DOWN	1.5565609	1.5565609	0.638362	0.33597872	-0.3023833	DHX30	Homo sapiens DEAD/H (Asp-Glu-Ala-His) box helicase 30 (DHX30), transcript variant 1, mRNA. (from RefSeq NM_138615)
uc058xkw.1	6.03E-04	DOWN	1.4960788	1.4960788	0.5811862	0.79466057	0.21347432	DIS3	Homo sapiens DIS3 exosome endoribonuclease and 3'-5' exoribonuclease (DIS3), transcript variant 1, mRNA. (from RefSeq NM_014953)
uc061cxr.1	4.42E-04	DOWN	3.4806626	3.4806626	1.799362	-2.874132	-4.673494	DNAAF3	Homo sapiens dynein, axonemal, assembly factor 3 (DNAAF3), transcript variant 1, mRNA. (from RefSeq NM_001256714)
uc062eiv.1	2.90E-04	DOWN	1.9544363	1.9544363	0.9667525	0.49695006	-0.4698025	DNAL4	Homo sapiens dynein, axonemal, light chain 4 (DNAL4), mRNA. (from RefSeq NM_005740)
uc059zkr.1	2.37E-04	DOWN	1.7925972	1.7925972	0.8420513	1.6935285	0.8514772	DPH1	Homo sapiens diphthamide biosynthesis 1 (DPH1), mRNA. (from RefSeq NM_001383)
uc063iju.1	3.26E-04	DOWN	3.0620632	3.0620632	1.6145041	-2.5977495	-4.2122536	DPYSL3	Homo sapiens dihydropyrimidinase-like 3 (DPYSL3), transcript variant 2, mRNA. (from RefSeq NM_001387)
uc002kwk.5	4.97E-04	UP	1.5694616	-1.5694616	-0.6502697	2.0402553	2.690525	DSC2	Homo sapiens desmocollin 2 (DSC2), transcript variant Dsc2b, mRNA. (from RefSeq NM_004949)
uc059jbx.1	9.32E-04	DOWN	2.828315	2.828315	1.4999428	-0.5355427	-2.0354855	DTWD1	Homo sapiens DTW domain containing 1 (DTWD1), transcript variant 2, mRNA. (from RefSeq NM_001144955)
uc060sdo.1	9.03E-04	DOWN	1.3031578	1.3031578	0.3820118	0.08413836	-0.2978735	DUS3L	Homo sapiens dihydrouridine synthase 3-like (S. cerevisiae) (DUS3L), transcript variant 1, mRNA. (from RefSeq NM_020175)
uc060sds.1	2.85E-04	DOWN	1.4717858	1.4717858	0.5575677	0.5148777	-0.0426907	DUS3L	Homo sapiens dihydrouridine synthase 3-like (S. cerevisiae) (DUS3L), transcript variant 1, mRNA. (from RefSeq NM_020175)
uc010wnn.2	2.46E-04	DOWN	1.2284846	1.2284846	0.2968798	3.522628	3.2257483	DYNLL2	Homo sapiens dynein, light chain, LC8-type 2 (DYNLL2), mRNA. (from RefSeq NM_080677)
uc060ttv.1	6.18E-04	DOWN	1.3899735	1.3899735	0.4750574	0.64705426	0.1719969	ECSIT	Homo sapiens ECSIT signalling integrator (ECSIT), transcript variant 3, mRNA. (from RefSeq NM_0011424265)
uc059fjp.1	7.23E-04	DOWN	1.3500446	1.3500446	0.43300706	0.6690862	0.23607916	EIF5	Homo sapiens eukaryotic translation initiation factor 5 (EIF5), transcript variant 1, mRNA. (from RefSeq NM_001969)
uc064zht.1	6.55E-04	DOWN	3.4123712	3.4123712	1.7707746	-2.9005659	-4.6713405	ELN	Homo sapiens elastin (ELN), transcript variant 3, mRNA. (from RefSeq NM_001081753)
uc057wfo.1	8.12E-04	DOWN	2.9038887	2.9038887	1.5379862	-0.2584959	-1.7964821	EMX2OS	Homo sapiens EMX2 opposite strand/antisense RNA (EMX2OS), long non-coding RNA. (from RefSeq NR_002791)
uc062xsy.1	9.11E-04	DOWN	1.4225762	1.4225762	0.50850594	1.066101	0.557595	ENOPH1	Homo sapiens enolase-phosphatase 1 (ENOPH1), transcript variant 1, mRNA. (from RefSeq NM_0212204)
uc062xsz.1	9.13E-04	DOWN	1.2292796	1.2292796	0.29781315	0.61124355	0.31343034	ENOPH1	Homo sapiens enolase-phosphatase 1 (ENOPH1), transcript variant 2, mRNA. (from RefSeq NM_001292017)
uc060mtq.1	5.20E-04	DOWN	1.3539106	1.3539106	0.43713245	0.26639283	-0.1707396	ENOSF1	Homo sapiens enolase superfamily member 1 (ENOSF1), transcript variant 2, mRNA. (from RefSeq NM_001126123)
uc065bcs.1	4.02E-04	DOWN	1.4150074	1.4150074	0.50080955	-0.0309631	-0.5317727	ENOX2	Homo sapiens ecto-NOX disulfide-thiol exchanger 2 (ENOX2), transcript variant 1, mRNA. (from RefSeq NM_006375)
uc058vib.1	7.03E-04	DOWN	1.2665782	1.2665782	0.34093615	0.23307593	-0.1078602	EP400	Homo sapiens E1A binding protein p400 (EP400), mRNA. (from RefSeq NM_015409)

uc063rjd.1	3.70E-04	DOWN	1.5517591	1.5517591	0.63390464	-1.7924179	-2.4263225	EPB41L2	Homo sapiens erythrocyte membrane protein band 4.1-like 2 (EPB41L2), transcript variant 2, mRNA. (from RefSeq NM_001135555)
uc064iwe.1	3.28E-04	DOWN	1.3043476	1.3043476	0.3833284	0.30906773	-0.0742608	EPHA1	Homo sapiens EPH receptor A1 (EPHA1), mRNA. (from RefSeq NM_005232)
uc060uys.1	3.92E-04	DOWN	1.2193388	1.2193388	0.28609902	1.4997584	1.2136594	EPS15L1	Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), transcript v. NM_001258375
uc060vkb.1	1.79E-04	DOWN	1.4217726	1.4217726	0.5076907	0.02209011	-0.4856006	FAM129C	Homo sapiens family with sequence similarity 129, member C (FAM129C), transcript variant 2, mRNA. (from RefSeq NM_001098524)
uc060vkc.1	4.39E-04	DOWN	1.3720957	1.3720957	0.4563811	-0.1605814	-0.6169626	FAM129C	Homo sapiens family with sequence similarity 129, member C (FAM129C), transcript variant 2, mRNA. (from RefSeq NM_001098524)
uc057bod.1	4.52E-05	DOWN	4.2857165	4.2857165	2.0995364	-4.4922795	-6.591816	FAM213B	Homo sapiens family with sequence similarity 213, member B (FAM213B), transcript variant 2, mRNA. (from RefSeq NM_152371)
uc061fvb.1	4.52E-05	DOWN	4.2857165	4.2857165	2.0995364	-4.4922795	-6.591816	FAM213B	Homo sapiens family with sequence similarity 213, member B (FAM213B), transcript variant 2, mRNA. (from RefSeq NM_152371)
uc064tfh.1	2.82E-04	DOWN	2.5153918	2.5153918	1.3307831	-2.90459	-4.235373	FAM95B1	Homo sapiens family with sequence similarity 95, member B1 (FAM95B1), long non-coding RNA. (from RefSeq NR_026759)
uc002rpa.2	8.82E-04	DOWN	1.2223758	1.2223758	0.2896878	0.0637974	-0.2258904	FAM98A	Homo sapiens family with sequence similarity 98, member A (FAM98A), transcript variant 1, mRNA. (from RefSeq NM_015475)
uc010jnv.2	9.66E-04	DOWN	1.2734643	1.2734643	0.34875855	0.6780751	0.32931653	FARS2	Homo sapiens phenylalanyl-tRNA synthetase 2, mitochondrial (FARS2), mRNA. (from RefSeq NM_00106567)
uc060lwd.1	4.84E-04	DOWN	1.5184833	1.5184833	0.60263103	0.78219837	0.17956735	FASN	Homo sapiens fatty acid synthase (FASN), mRNA. (from RefSeq NM_004104)
uc060ynr.1	6.15E-04	DOWN	1.4972541	1.4972541	0.5823191	1.4468273	0.86450815	FBL	Homo sapiens fibrillarin (FBL), mRNA. (from RefSeq NM_001436)
uc058ttr.1	4.78E-04	DOWN	1.3824271	1.3824271	0.4672034	0.706743	0.23953962	FBXO21	Homo sapiens F-box protein 21 (FBXO21), transcript variant 1, mRNA. (from RefSeq NM_033624)
uc060suj.1	6.55E-04	DOWN	1.3777107	1.3777107	0.46227297	0.07015614	-0.3921169	FCER2	Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23) (FCER2), transcript variant 1, mRNA. (from RefSeq NM_002002)
uc060sqm.1	5.48E-04	DOWN	1.4911617	1.4911617	0.5764367	0.11143559	-0.4650012	FCER2	Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23) (FCER2), transcript variant 1, mRNA. (from RefSeq NM_002002)
uc058fep.1	1.75E-04	DOWN	1.4564477	1.4564477	0.5424539	0.4302286	-0.1122253	FCHSD2	Homo sapiens FCH and double SH3 domains 2 (FCHSD2), mRNA. (from RefSeq NM_014824)
uc064glm.1	1.00E-04	DOWN	1.4015203	1.4015203	0.4869926	1.3968903	0.90989774	FIS1	Homo sapiens fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae) (FIS1), mRNA. (from RefSeq NM_016068)
uc003djj.3	2.21E-04	DOWN	1.2875259	1.2875259	0.36760143	-0.1843731	-0.5489746	FLNB	Homo sapiens filamin B, beta (FLNB), transcript variant 2, mRNA. (from RefSeq NM_001457)
uc003djk.3	2.56E-04	DOWN	1.2852204	1.2852204	0.36201575	-0.181928	-0.5439437	FLNB	Homo sapiens filamin B, beta (FLNB), transcript variant 3, mRNA. (from RefSeq NM_001164318)
uc003djm.3	9.95E-04	DOWN	1.2445667	1.2445667	0.31564352	-0.159998	-0.4756416	FLNB	Homo sapiens filamin B, beta (FLNB), transcript variant 4, mRNA. (from RefSeq NM_001164319)
uc010hne.3	5.21E-04	DOWN	1.3080819	1.3080819	0.38745284	-0.1450327	-0.5324855	FLNB	Homo sapiens filamin B, beta (FLNB), transcript variant 1, mRNA. (from RefSeq NM_001164317)
uc010hnf.3	2.03E-04	DOWN	1.29133	1.29133	0.3688577	-0.1743539	-0.5432116	FLNB	Homo sapiens filamin B, beta (FLNB), transcript variant 4, mRNA. (from RefSeq NM_001164319)
uc062kyo.1	5.42E-04	DOWN	1.1885079	1.1885079	0.24915151	-0.0901803	-0.3393317	FLNB	Homo sapiens filamin B, beta (FLNB), transcript variant 4, mRNA. (from RefSeq NM_001164319)
uc059prq.1	8.53E-04	DOWN	1.2842814	1.2842814	0.36096132	-0.7828972	-1.1438586	FLYWCH1	Homo sapiens FLYWCH-type zinc finger 1 (FLYWCH1), transcript variant 1, mRNA. (from RefSeq NM_0032296)
uc064muv.1	7.62E-04	DOWN	1.3168805	1.3168805	0.39712438	0.43809152	0.0409671	FNTA	Homo sapiens farnesyltransferase, CAAX box, alpha (FNTA), transcript variant 1, mRNA. (from RefSeq NM_002027)
uc064vxp.1	8.95E-04	DOWN	1.3649472	1.3649472	0.44884515	-0.9141061	-1.3629512	FPGS	Homo sapiens folylpolyglutamate synthase (FPGS), transcript variant 1, mRNA. (from RefSeq NM_0004957)
uc064vyr.1	2.34E-04	DOWN	1.4879673	1.4879673	0.57334274	-0.9706222	-1.543965	FPGS	Homo sapiens folylpolyglutamate synthase (FPGS), transcript variant 1, mRNA. (from RefSeq NM_0004957)
uc058djl.1	6.44E-04	DOWN	1.4106445	1.4106445	0.4963545	0.21383233	-0.2825221	FRMD8	Homo sapiens FERM domain containing 8 (FRMD8), transcript variant 1, mRNA. (from RefSeq NM_0031904)
uc058djm.1	3.80E-04	DOWN	1.4113189	1.4113189	0.497044	0.4372523	-0.0597917	FRMD8	Homo sapiens FERM domain containing 8 (FRMD8), transcript variant 2, mRNA. (from RefSeq NM_00103300832)
uc060atq.1	1.75E-04	DOWN	1.3747438	1.3747438	0.4591628	2.0954998	1.6363369	FXR2	Homo sapiens fragile X mental retardation, autosomal homolog 2 (FXR2), mRNA. (from RefSeq NM_004860)
uc062daw.1	6.98E-04	DOWN	1.2820716	1.2820716	0.35847682	-1.822708	-2.1811848	GATSL3	Homo sapiens GATS protein-like 3 (GATSL3), mRNA. (from RefSeq NM_001037666)
uc062dbe.1	8.67E-04	DOWN	2.6110659	2.6110659	1.3846388	-0.7264488	-1.2110876	GATSL3	Homo sapiens GATS protein-like 3 (GATSL3), mRNA. (from RefSeq NM_001037666)
uc058tzd.1	5.97E-04	DOWN	1.3484395	1.3484395	0.43129075	0.9592147	0.5279239	GCN1L1	Homo sapiens GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (GCN1L1), mRNA. (from RefSeq NM_006836)
uc063ymk.1	9.71E-04	DOWN	1.2795461	1.2795461	0.35563216	-1.1937543	-1.5493865	GNL1	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA. (from RefSeq NM_005275)
uc002whp.2	9.74E-04	DOWN	3.1071494	3.1071494	1.6355916	-1.011351	-2.6469426	GNRH2	Homo sapiens gonadotropin-releasing hormone 2 (GNRH2), transcript variant 3, mRNA. (from RefSeq NM_178331)
uc057dtw.1	1.33E-04	DOWN	1.5824472	1.5824472	0.66215736	-0.1753319	-0.8374892	GPATCH3	Homo sapiens G patch domain containing 3 (GPATCH3), mRNA. (from RefSeq NM_022078)
uc063ixf.1	3.28E-04	DOWN	2.7667317	2.7667317	1.4681828	-3.18731	-4.655493	GRIA1	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), transcript variant 7, mRNA. (from RefSeq NM_001258023)
uc057idf.1	7.14E-04	DOWN	1.5648838	1.5648838	0.6460556	0.6933504	0.04729484	GTF2B	Homo sapiens general transcription factor IIB (GTF2B), mRNA. (from RefSeq NM_001514)
uc058waz.1	9.32E-04	DOWN	1.4175823	1.4175823	0.50343245	1.590342	1.0869095	GTF3A	Homo sapiens general transcription factor IIIA (GTF3A), mRNA. (from RefSeq NM_002097)
uc064wsm.1	5.19E-04	DOWN	1.3935853	1.3935853	0.47880134	0.7353887	0.25658733	GTF3C4	Homo sapiens general transcription factor IIIC, polypeptide 4, 90kDa (GTF3C4), mRNA. (from RefSeq NM_012204)
uc004cci.5	7.15E-04	DOWN	1.2272269	1.2272269	0.29540196	0.06520756	-0.2301944	GTF3C5	Homo sapiens general transcription factor IIIC, polypeptide 5, 63kDa (GTF3C5), transcript variant 2, mRNA. (from RefSeq NM_012087)
uc033dju.2	4.19E-04	DOWN	1.2532845	1.2532845	0.3257139	-0.0266291	-0.352343	GTF3C5	Homo sapiens general transcription factor IIIC, polypeptide 5, 63kDa (GTF3C5), transcript variant 3, mRNA. (from RefSeq NM_001286709)
uc057reu.1	8.73E-04	DOWN	1.4814469	1.4814469	0.5670069	1.2631001	0.69609326	GTPBP4	Homo sapiens GTP binding protein 4 (GTPBP4), mRNA. (from RefSeq NM_012341)
uc062kga.1	5.79E-04	DOWN	1.3277055	1.3277055	0.40893516	-1.03673	-1.4456652	HEMK1	Homo sapiens HemK methyltransferase family member 1 (HEMK1), mRNA. (from RefSeq NM_0161173)
uc061aff.1	4.05E-04	DOWN	5.606754	5.606754	2.4871657	-2.5747898	-5.0619555	HIF3A	Homo sapiens hypoxia inducible factor 3, alpha subunit (HIF3A), transcript variant 4, mRNA. (from RefSeq NM_152796)
uc001udj.2	3.14E-04	DOWN	1.3390192	1.3390192	0.4211766	1.4725891	1.0514125	HIP1R	Homo sapiens huntingtin interacting protein 1 related (HIP1R), transcript variant 1, mRNA. (from RefSeq NM_003959)
uc058uor.1	1.81E-04	DOWN	1.3555408	1.3555408	0.4388685	0.32607898	-0.1127895	HIP1R	Homo sapiens huntingtin interacting protein 1 related (HIP1R), transcript variant 1, mRNA. (from RefSeq NM_003959)
uc058uot.1	8.22E-04	DOWN	1.376099	1.376099	0.46058425	0.25862607	-0.2019582	HIP1R	Homo sapiens huntingtin interacting protein 1 related (HIP1R), transcript variant 1, mRNA. (from RefSeq NM_003959)
uc057zqa.1	7.13E-04	DOWN	1.2905959	1.2905959	0.36803734	-0.5494239	-0.9174612	HP55	Homo sapiens Hermansky-Pudlak syndrome 5 (HP55), transcript variant 3, mRNA. (from RefSeq NM_181508)
uc063gye.1	6.47E-04	DOWN	1.553354	1.553354	0.63538665	1.3144798	0.6790931	HSPA4	Homo sapiens heat shock 70kDa protein 4 (HSPA4), mRNA. (from RefSeq NM_002154)
uc057uwb.1	7.47E-04	DOWN	1.2488009	1.2488009	0.32054344	0.2864841	-0.0340594	IDE	Homo sapiens insulin-degrading enzyme (IDE), transcript variant 2, mRNA. (from RefSeq NM_00116165946)
uc064sma.1	8.58E-04	DOWN	1.7223176	1.7223176	0.78435117	-0.1169544	-0.9013056	IFT74	Homo sapiens intraflagellar transport 74 (IFT74), transcript variant 4, mRNA. (from RefSeq NM_001001099224)
uc058pgk.1	1.65E-04	DOWN	3.3863482	3.3863482	1.7597303	-2.6947336	-4.454464	IKZF4	Homo sapiens IKAROS family zinc finger 4 (Eos) (IKZF4), mRNA. (from RefSeq NM_022465)

uc060tla.1	6.58E-04	DOWN	1.2897521	1.2897521	0.36709383	0.50788546	0.14079161	ILF3	Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 4, mRNA. (from NM_017620	
uc060urt.1	2.12E-04	DOWN	1.5014273	1.5014273	0.5863346	-1.6479577	-2.2342923	ILVBL	Homo sapiens ilvB (bacterial acetolactate synthase)-like (ILVBL), mRNA. (from RefSeq NM_006844)	NM_006844
uc057wqx.1	8.12E-04	DOWN	1.4821254	1.4821254	0.5676675	0.66837925	0.10071168	INPP5A	Homo sapiens inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA. (from RefSeq NM_00	NM_005539
uc065cai.1	9.36E-04	DOWN	1.3765228	1.3765228	0.4610285	0.7418396	0.28081113	IRAK1	Homo sapiens interleukin-1 receptor-associated kinase 1 (IRAK1), transcript variant 2, mRNA. (from NM_001025242	
uc057sqo.1	8.11E-04	DOWN	1.2761558	1.2761558	0.3518045	0.99496365	0.64315915	ITGB1	Homo sapiens integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2,	NM_033668
uc061nqc.1	2.18E-04	DOWN	1.3883929	1.3883929	0.4734159	0.34611484	-0.1273011	IWS1	Homo sapiens IWS1 homolog (S. cerevisiae) (IWS1), mRNA. (from RefSeq NM_017969)	NM_017969
uc063hbu.1	3.33E-04	DOWN	1.3825978	1.3825978	0.46738154	1.1864761	0.7190946	JADE2	Homo sapiens jade family PHD finger 2 (JADE2), transcript variant 3, mRNA. (from RefSeq NM_015	NM_015288
uc063hbu.1	9.85E-05	DOWN	1.6018566	1.6018566	0.67974496	0.4113808	-0.2683642	JADE2	Homo sapiens jade family PHD finger 2 (JADE2), transcript variant 3, mRNA. (from RefSeq NM_015	NM_015288
uc061lwd.1	4.05E-04	DOWN	1.5455755	1.5455755	0.62814415	-0.2712648	-0.8994089	KANSL3	Homo sapiens KAT8 regulatory NSL complex subunit 3 (KANSL3), transcript variant 7, non-coding RN	NR_047658
uc058dom.1	7.30E-04	DOWN	1.2990743	1.2990743	0.37748393	-0.4537181	-0.831202	KAT5	Homo sapiens K(llysine) acetyltransferase 5 (KAT5), transcript variant 2, mRNA. (from RefSeq NM_0	NM_006388
uc060jxt.1	5.19E-04	DOWN	1.8570356	1.8570356	0.8930015	-0.7108379	-1.6038394	KIAA0195	Homo sapiens KIAA0195 (KIAA0195), mRNA. (from RefSeq NM_014738)	NM_014738
uc059auf.1	5.86E-04	DOWN	1.333917	1.333917	0.4156689	-0.4526337	-0.8683025	KIAA0391	Homo sapiens KIAA0391 (KIAA0391), transcript variant 2, mRNA. (from RefSeq NM_001256678)	NM_001256678
uc059bik.1	5.09E-04	DOWN	1.456567	1.456567	0.5425721	-1.3735608	-1.9161329	L2HGDH	Homo sapiens L-2-hydroxyglutarate dehydrogenase (L2HGDH), mRNA. (from RefSeq NM_024884)	NM_024884
uc011cfk.3	3.76E-04	DOWN	1.3542188	1.3542188	0.4374609	1.3142334	0.87677246	LEF1	Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), transcript variant 4, mRNA. (from RefSeq NM_0011666119	
uc057otb.1	7.08E-04	DOWN	2.4232428	2.4232428	1.2769389	-1.8144094	-3.0913484	LEMD1	Homo sapiens LEM domain containing 1 (LEMD1), transcript variant 4, mRNA. (from RefSeq NM_00	NM_001199052
uc057otc.1	9.06E-04	DOWN	2.3645246	2.3645246	1.2415501	-1.8387089	-3.080259	LEMD1	Homo sapiens LEM domain containing 1 (LEMD1), transcript variant 4, mRNA. (from RefSeq NM_00	NM_001199052
uc058ujc.1	8.13E-04	DOWN	1.5301507	1.5301507	0.6136737	0.20963831	-0.4040354	LINC01089	Homo sapiens long intergenic non-protein coding RNA 1089 (LINC01089), long non-coding RNA. (fro	NR_002809
uc057lwf.1	7.53E-04	DOWN	1.3924829	1.3924829	0.47765958	-0.5281399	-1.0052795	LMNA	Homo sapiens lamin A/C (LMNA), transcript variant 3, mRNA. (from RefSeq NM_170708)	NM_170708
uc058bpn.1	8.80E-04	DOWN	1.465787	1.465787	0.5516755	2.4074094	1.8557339	LPXN	Homo sapiens leupaxin (LPXN), transcript variant 2, mRNA. (from RefSeq NM_004811)	NM_004811
uc063ady.1	2.43E-04	DOWN	1.4906352	1.4906352	0.5759272	0.6129604	0.03703318	LRBA	Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), transcript vari	NM_006726
uc058kne.1	6.80E-04	DOWN	2.0665438	2.0665438	1.04722	-1.6357126	-2.6829326	LRRC23	Homo sapiens leucine rich repeat containing 23 (LRRC23), transcript variant 2, mRNA. (from RefSeq NM_006992	
uc001akx.2	5.95E-04	DOWN	1.1888478	1.1888478	0.249564	2.672828	2.423264	LRRC47	Homo sapiens leucine rich repeat containing 47 (LRRC47), mRNA. (from RefSeq NM_020710)	NM_020710
uc064cq.1	7.30E-04	DOWN	1.5036224	1.5036224	0.5884423	-0.5690464	-1.1574887	LSMS5	Homo sapiens LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSMS5), transcript va	NM_012322
uc057vlt.1	5.84E-04	DOWN	1.4735569	1.4735569	0.55930275	-0.6038199	-1.1631227	LZTS2	Homo sapiens leucine zipper, putative tumor suppressor 2 (LZTS2), mRNA. (from RefSeq NM_03242	NM_032422
uc059ian.1	4.97E-04	DOWN	1.4599111	1.4599111	0.5458805	-0.4585696	-1.0044502	MAPKBP1	Homo sapiens mitogen-activated protein kinase binding protein 1 (MAPKBP1), transcript variant 3, n	NM_001265611
uc003fle.4	4.63E-04	DOWN	1.2460678	1.2460678	0.3173825	-1.1091388	-1.4265214	MCCC1	Homo sapiens methylcrotonoyl-CoA carboxylase 1 (alpha) (MCCC1), transcript variant 1, mRNA. (fro	NM_020166
uc062qnd.1	5.07E-04	DOWN	1.2288607	1.2288607	0.2973214	-1.1339347	-1.4312562	MCCC1	Homo sapiens methylcrotonoyl-CoA carboxylase 1 (alpha) (MCCC1), transcript variant 1, mRNA. (fro	NM_020166
uc062qne.1	3.54E-04	DOWN	1.240623	1.240623	0.31106478	-1.1042471	-1.4153118	MCCC1	Homo sapiens methylcrotonoyl-CoA carboxylase 1 (alpha) (MCCC1), transcript variant 1, mRNA. (fro	NM_020166
uc003pnn.2	7.47E-04	DOWN	1.2560745	1.2560745	0.3289221	1.6296577	1.3007356	MDN1	Homo sapiens MDN1, midasin homolog (yeast) (MDN1), mRNA. (from RefSeq NM_014611)	NM_014611
uc063qcd.1	9.47E-04	DOWN	1.3042611	1.3042611	0.38323268	1.5583802	1.1751475	MDN1	Homo sapiens MDN1, midasin homolog (yeast) (MDN1), mRNA. (from RefSeq NM_014611)	NM_014611
uc062pue.1	1.81E-04	DOWN	4.079837	4.079837	2.0285115	-4.594736	-6.6232476	MECOM	Homo sapiens MDS1 and EVI1 complex locus (MECOM), transcript variant 3, mRNA. (from RefSeq N	NM_001105078
uc064ged.1	2.79E-04	DOWN	1.4110893	1.4110893	0.49680927	0.7099866	0.21317732	MEPCE	Homo sapiens methylphosphate capping enzyme (MEPCE), transcript variant 4, mRNA. (from RefSe	NM_001194992
uc059znk.1	6.16E-04	DOWN	1.3454988	1.3454988	0.4281411	-0.032758	-0.4608991	METTL16	Homo sapiens methyltransferase like 16 (METTL16), mRNA. (from RefSeq NM_024086)	NM_024086
uc060ccx.1	8.12E-04	DOWN	1.4379041	1.4379041	0.52396744	-1.4459757	-1.9699432	MIEF2	Homo sapiens mitochondrial elongation factor 2 (MIEF2), transcript variant 1, mRNA. (from RefSeq	NM_139162
uc064bkt.1	3.14E-04	DOWN	1.4664329	1.4664329	0.55231106	0.43986157	-0.1124495	MIOS	Homo sapiens missing oocyte, meiosis regulator, homolog (Drosophila) (MIOS), mRNA. (from RefSe	NM_019005
uc058vgw.1	3.97E-05	DOWN	1.7731789	1.7731789	0.8263381	-1.2798477	-2.106186	MMP17	Homo sapiens matrix metalloproteinase 17 (membrane-inserted) (MMP17), mRNA. (from RefSeq NI	NM_016155
uc057vfm.1	6.57E-04	DOWN	1.3661103	1.3661103	0.450074	0.26967993	-0.180394	MMS19	Homo sapiens MMS19 nucleotide excision repair homolog (S. cerevisiae) (MMS19), transcript variar	NM_001289403
uc059lni.1	5.86E-04	DOWN	1.6071565	1.6071565	0.6845104	-0.0592606	-0.7437711	MPI	Homo sapiens mannose phosphate isomerase (MPI), transcript variant 2, mRNA. (from RefSeq NM_	NM_001289155
uc060fve.1	7.30E-04	DOWN	4.313879	4.313879	2.1089857	-3.324458	-5.4334435	MPP2	Homo sapiens membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2), tran	NM_001278381
uc059mwq.1	3.05E-04	DOWN	1.7236552	1.7236552	0.7854712	-1.5743408	-2.359812	MRPL46	Homo sapiens mitochondrial ribosomal protein L46 (MRPL46), mRNA. (from RefSeq NM_022163)	NM_022163
uc001yqy.4	4.37E-04	DOWN	1.2514856	1.2514856	0.32364166	-0.9097973	-1.233439	MTA1	Homo sapiens metastasis associated 1 (MTA1), transcript variant 2, mRNA. (from RefSeq NM_0012	NM_001203258
uc061ipp.1	9.01E-04	DOWN	2.817037	2.817037	1.4941785	-2.2645373	-3.7587159	MTA3	Homo sapiens metastasis associated 1 family, member 3 (MTA3), transcript variant 3, mRNA. (from	NM_020744
uc057dns.1	9.79E-04	DOWN	1.446597	1.446597	0.53266305	-0.863583	-1.3962461	MTFR1L	Homo sapiens mitochondrial fission regulator 1-like (MTFR1L), transcript variant 1, mRNA. (from	Re NM_019557
uc063sgp.1	7.58E-04	DOWN	4.284698	4.284698	2.0991936	-1.3402783	-3.439472	MTHFD1L	Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (MTHFD1L), tra	NM_001242768
uc058xpe.1	8.43E-04	DOWN	1.3325596	1.3325596	0.41420004	4.2407594	3.8265593	MYCBP2	Homo sapiens MYC binding protein 2, E3 ubiquitin protein ligase (MYCBP2), mRNA. (from RefSeq NI	NM_015057
uc001udy.2	4.55E-04	DOWN	1.3060995	1.3060995	0.38526484	-2.370269	-2.755534	n/a	n/a	NM_001304835
uc002gnz.5	2.10E-04	DOWN	1.3026936	1.3026936	0.3814978	-0.1807804	-0.5622781	n/a	n/a	NM_018127
uc002iii.2	1.67E-04	DOWN	1.4330951	1.4330951	0.51913434	-0.6375163	-1.1566507	n/a	n/a	NM_001303442
uc003zjz.4	5.30E-04	DOWN	1.2690427	1.2690427	0.34374064	0.7658224	0.4220818	n/a	n/a	NR_046386
uc010dzm.2	8.73E-04	DOWN	1.3376595	1.3376595	0.4197109	-0.3204994	-0.7402104	n/a	n/a	NR_046366
uc010lyy.3	9.18E-04	DOWN	1.3024448	1.3024448	0.38122225	0.2236887	-0.1575335	n/a	n/a	NM_001271287
uc032qsv.2	6.25E-04	DOWN	1.2440816	1.2440816	0.31508112	-2.0031366	-2.3182178	n/a	n/a	NR_034118
uc032qyp.2	4.80E-04	DOWN	1.248422	1.248422	0.3201057	-1.9956144	-2.31572	n/a	n/a	NR_034118

uc032tgw.1	3.46E-04	DOWN	1.3213444	1.3213444	0.4020065	-0.0667328	-0.4687394	n/a	n/a	NM_001278363
uc057hsg.1	2.08E-04	DOWN	1.3992146	1.3992146	0.48461726	-0.562811	-1.0474283	n/a	n/a	NR_073562
uc057oir.1	6.77E-04	DOWN	1.4009339	1.4009339	0.48638883	-0.2627614	-0.7491502	n/a	n/a	NM_001193570
uc058tuf.1	2.47E-04	DOWN	1.5127581	1.5127581	0.5971813	-0.8257096	-1.422891	n/a	n/a	NM_001206801
uc058uon.1	9.24E-04	DOWN	1.3786023	1.3786023	0.4632063	0.87075204	0.4075457	n/a	n/a	NM_001303097
uc058upr.1	8.84E-04	DOWN	1.3141855	1.3141855	0.3941689	-1.99234	-2.386509	n/a	n/a	NM_001304834
uc059aun.1	6.11E-04	DOWN	1.5369658	1.5369658	0.6200851	0.47703028	-0.1430549	n/a	n/a	NR_104110
uc059otm.1	6.89E-04	DOWN	2.245546	2.245546	1.1670663	-0.8134839	-1.9805502	n/a	n/a	NR_033645
uc060fvx.1	5.82E-04	DOWN	1.5452799	1.5452799	0.6278681	-1.2433196	-1.8711878	n/a	n/a	NM_001304814
uc060hxx.1	8.55E-04	DOWN	1.382876	1.382876	0.46767184	0.21683846	-0.2508334	n/a	n/a	NR_038416
uc060myc.1	2.53E-04	DOWN	1.4927839	1.4927839	0.5780053	-1.0690707	-1.647076	n/a	n/a	NM_001278684
uc060nfo.1	7.90E-04	DOWN	1.5328991	1.5328991	0.6162628	1.4752246	0.8589618	n/a	n/a	NM_001083625
uc061irb.1	1.25E-05	DOWN	1.848503	1.848503	0.88635737	-0.1049546	-0.991312	n/a	n/a	NR_073394
uc061sne.1	9.73E-04	DOWN	2.2861962	2.2861962	1.1929492	-1.8364338	-3.029383	n/a	n/a	NM_001079866
uc061xwg.1	5.98E-04	DOWN	1.3093083	1.3093083	0.38880482	-0.2577944	-0.6465992	n/a	n/a	NM_198433
uc061xwh.1	2.95E-04	DOWN	1.3791691	1.3791691	0.46379936	0.08060125	-0.3831982	n/a	n/a	NM_198433
uc061yty.1	3.04E-05	DOWN	1.5428617	1.5428617	0.62560874	-1.9878901	-2.613499	n/a	n/a	NM_001283052
uc062evq.1	2.26E-05	DOWN	1.2992173	1.2992173	0.37764278	-0.3089729	-0.6866157	n/a	n/a	NR_104110
uc062evt.1	1.31E-04	DOWN	1.3366652	1.3366652	0.4186381	-0.4444166	-0.8630547	n/a	n/a	NR_104300
uc062hvi.1	1.28E-04	DOWN	1.2769156	1.2769156	0.3526631	0.32500753	-0.0276556	n/a	n/a	NR_046352
uc062jao.1	5.59E-04	DOWN	1.3062011	1.3062011	0.38537702	-1.5060563	-1.8914334	n/a	n/a	NR_033815
uc062jaq.1	8.53E-04	DOWN	1.245694	1.245694	0.31694975	-0.8807747	-1.1977245	n/a	n/a	NR_033815
uc062jar.1	9.22E-05	DOWN	1.3510718	1.3510718	0.43410438	-1.4584565	-1.892561	n/a	n/a	NR_033815
uc062lut.1	8.45E-04	DOWN	1.5484262	1.5484262	0.6308026	-0.1032705	-0.7340731	n/a	n/a	NM_001261829
uc062qnh.1	5.26E-04	DOWN	1.2573651	1.2573651	0.33040363	-1.2823358	-1.6127394	n/a	n/a	NR_102639
uc062xlo.1	8.12E-04	DOWN	1.3678064	1.3678064	0.45186406	1.3719277	0.9200637	n/a	n/a	NR_103781
uc062xlr.1	2.60E-04	DOWN	1.3787224	1.3787224	0.46333203	0.09416642	-0.3691656	n/a	n/a	NR_103782
uc063exq.1	1.13E-04	DOWN	1.4738429	1.4738429	0.5595827	1.7643167	1.204734	n/a	n/a	NM_001174071
uc063ljh.1	1.93E-04	DOWN	1.6148275	1.6148275	0.6913801	0.365051	-0.326329	n/a	n/a	NM_001195286
uc063msm.1	1.83E-04	UP	1.290776	-1.290776	-0.3682387	-0.5414801	-0.1732414	n/a	n/a	NR_072994
uc063twf.1	1.83E-04	UP	1.290776	-1.290776	-0.3682387	-0.5414801	-0.1732414	n/a	n/a	NR_072994
uc063vcd.1	1.83E-04	UP	1.290776	-1.290776	-0.3682387	-0.5414801	-0.1732414	n/a	n/a	NR_072994
uc063whs.1	1.83E-04	UP	1.290776	-1.290776	-0.3682387	-0.5414801	-0.1732414	n/a	n/a	NR_072994
uc063xhb.1	1.83E-04	UP	1.290776	-1.290776	-0.3682387	-0.5414801	-0.1732414	n/a	n/a	NR_072994
uc063ymx.1	2.12E-04	UP	1.296198	-1.296198	-0.3742861	-0.6125109	-0.2382247	n/a	n/a	NR_072994
uc063zss.1	1.83E-04	UP	1.290776	-1.290776	-0.3682387	-0.5414801	-0.1732414	n/a	n/a	NR_072994
uc064dvi.1	9.93E-04	DOWN	2.9565728	2.9565728	1.5639257	-2.0152664	-3.5791922	n/a	n/a	NR_047689
uc064efz.1	4.38E-04	DOWN	1.5643185	1.5643185	0.6455343	-0.9788129	-1.6243472	n/a	n/a	NR_045512
uc064pgy.1	4.83E-04	DOWN	2.1829476	2.1829476	1.1262776	-0.5619285	-1.6882058	n/a	n/a	NR_126339
uc064rdj.1	3.14E-04	DOWN	2.5641959	2.5641959	1.3585064	-3.039708	-4.3982143	n/a	n/a	NR_110193
uc064voi.1	9.36E-04	DOWN	1.5573264	1.5573264	0.6390714	-0.0684742	-0.7075455	n/a	n/a	NR_033234
uc059bwu.1	8.27E-04	DOWN	1.4354949	1.4354949	0.5215482	1.0612817	0.5397335	NAA30	Homo sapiens N(alpha)-acetyltransferase 30, NatC catalytic subunit (NAA30), mRNA. (from RefSeq NM_001011713	
uc059qle.1	8.63E-04	DOWN	1.5101768	1.5101768	0.59471744	-0.675169	-1.2698864	NAGPA	Homo sapiens N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (NAGPA), mRNA NM_016256	
uc064kqr.1	5.70E-04	DOWN	3.8234951	3.8234951	1.934892	-1.4622906	-3.3971827	NAT1	Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), transcript variant 4, mRNA NM_001160173	
uc057jyz.1	1.78E-04	DOWN	1.4817319	1.4817319	0.5672844	0.01036535	-0.556919	NBPF15	Homo sapiens neuroblastoma breakpoint family, member 15 (NBPF15), transcript variant 2, mRNA. NM_173638	
uc057jza.1	7.35E-05	DOWN	1.5859307	1.5859307	0.66532975	0.4592986	-0.2060311	NBPF15	Homo sapiens neuroblastoma breakpoint family, member 15 (NBPF15), transcript variant 2, mRNA. NM_173638	
uc062jqk.1	5.92E-04	DOWN	1.3335292	1.3335292	0.41524944	-0.0118366	-0.427086	NCKIPSD	Homo sapiens NCK interacting protein with SH3 domain (NCKIPSD), transcript variant 2, mRNA. (from RefSeq NM_184231	
uc064ipg.1	8.92E-04	DOWN	1.445949	1.445949	0.53201663	0.47285008	-0.0591665	NDUFB2	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa (NDUFB2), mRNA. (from RefSeq NM_004546	
uc057mpx.1	3.84E-04	DOWN	1.3569298	1.3569298	0.44034606	-0.0668979	-0.5072439	NDUFS2	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) (NDUFS2), mRNA. (from RefSeq NM_004550	
uc062yok.1	4.26E-04	DOWN	1.2873061	1.2873061	0.36435512	1.2260548	0.86169964	NFKB1	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1), transcript variant 1, mRNA. (from RefSeq NM_003998	
uc061end.1	5.97E-05	DOWN	2.8327382	2.8327382	1.5021973	-4.5717025	-6.0738997	NLRP2	Homo sapiens NLR family, pyrin domain containing 2 (NLRP2), transcript variant 2, mRNA. (from RefSeq NM_001174081	
uc061var.1	5.75E-05	DOWN	1.446402	1.446402	0.5324685	0.48531654	-0.047152	NOP56	Homo sapiens NOP56 ribonucleoprotein (NOP56), transcript variant 1, mRNA. (from RefSeq NM_001006392	
uc032awd.2	7.10E-04	DOWN	1.2948493	1.2948493	0.37278417	1.1093647	0.7365806	NOP9	Homo sapiens NOP9 nucleolar protein (NOP9), transcript variant 2, mRNA. (from RefSeq NM_001286367	

uc021txo.2	1.75E-06	DOWN	1.6627548	1.6627548	0.7335754	-1.3857993	-2.1193748	NT5C3B	Homo sapiens 5'-nucleotidase, cytosolic IIIB (NT5C3B), transcript variant 1, mRNA. (from RefSeq NM_052935	
uc060fdr.1	1.71E-04	DOWN	1.4781127	1.4781127	0.5637563	-1.2732315	-1.8370777	NT5C3B	Homo sapiens 5'-nucleotidase, cytosolic IIIB (NT5C3B), transcript variant 1, mRNA. (from RefSeq NM_052935	
uc061aza.1	2.60E-04	DOWN	1.7418319	1.7418319	0.8006054	0.66143537	-0.13917	NTF4	Homo sapiens neurotrophin 4 (NTF4), mRNA. (from RefSeq NM_006179)	NM_006179
uc058qqv.1	5.41E-04	DOWN	1.4575303	1.4575303	0.5435258	-0.3868452	-0.930371	NUP107	Homo sapiens nucleoporin 107kDa (NUP107), mRNA. (from RefSeq NM_020401)	NM_020401
uc061bmx.1	1.57E-04	DOWN	1.4055872	1.4055872	0.49117294	-0.087938	-0.579111	NUP62	Homo sapiens nucleoporin 62kDa (NUP62), transcript variant 1, mRNA. (from RefSeq NM_153719)	NM_153719
uc060jui.1	5.97E-04	DOWN	1.3628567	1.3628567	0.4466339	-0.3735092	-0.820143	NUP85	Homo sapiens nucleoporin 85kDa (NUP85), transcript variant 1, mRNA. (from RefSeq NM_024844)	NM_024844
uc002gbo.3	3.72E-04	DOWN	1.237186	1.237186	0.30706236	0.6628111	0.3557488	NUP88	Homo sapiens nucleoporin 88kDa (NUP88), mRNA. (from RefSeq NM_002532)	NM_002532
uc057qeh.1	2.25E-04	DOWN	1.4150653	1.4150653	0.5008686	-0.540885	-1.0417535	OBSCN	Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), transcript va	NM_001271223
uc011mbf.3	7.49E-04	DOWN	1.2250093	1.2250093	0.29279274	-0.8481388	-1.1409315	ODF2	Homo sapiens outer dense fiber of sperm tails 2 (ODF2), transcript variant 7, mRNA. (from RefSeq NM_153440	NM_153440
uc057fbq.1	8.30E-04	DOWN	1.3984331	1.3984331	0.48381123	0.2718339	-0.2119774	PABPC4	Homo sapiens poly(A) binding protein, cytoplasmic 4 (inducible form) (PABPC4), transcript variant 3, NM_001135654	NM_001135654
uc003aks.4	7.61E-04	DOWN	1.2578754	1.2578754	0.33098906	0.7356434	0.40465438	PATZ1	Homo sapiens POZ (BTB) and AT hook containing zinc finger 1 (PATZ1), transcript variant 4, mRNA. NM_032051	NM_032051
uc010mls.3	5.64E-04	DOWN	1.4451263	1.4451263	0.5311956	-1.0197122	-1.5509171	PAX5	Homo sapiens paired box 5 (PAX5), transcript variant 5, mRNA. (from RefSeq NM_001280550)	NM_001280550
uc064kpk.1	8.79E-04	DOWN	1.4384214	1.4384214	0.52448636	1.3690842	0.8445979	PCM1	Homo sapiens pericentriolar material 1 (PCM1), mRNA. (from RefSeq NM_006197)	NM_006197
uc062mbe.1	8.46E-04	DOWN	1.3801694	1.3801694	0.46484533	1.777595	1.3127497	PCNP	Homo sapiens PEST proteolytic signal containing nuclear protein (PCNP), mRNA. (from RefSeq NM_1020357	NM_1020357
uc060wvu.1	9.69E-04	DOWN	1.4061683	1.4061683	0.4917693	-0.0943106	-0.5860799	PDCD2L	Homo sapiens programmed cell death 2-like (PDCD2L), mRNA. (from RefSeq NM_032346)	NM_032346
uc001emh.3	6.42E-04	DOWN	1.2513936	1.2513936	0.32353556	0.80455637	0.48102078	PDE4DIP	Homo sapiens phosphodiesterase 4D interacting protein (PDE4DIP), transcript variant 5, mRNA. (fro	NM_001002811
uc062alz.1	9.24E-04	DOWN	2.8799474	2.8799474	1.5260425	-4.1637044	-5.689747	PDE9A	Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 2, mRNA. (from RefSeq NM_00100	NM_001001567
uc060baa.1	5.24E-04	DOWN	1.3054589	1.3054589	0.38455704	-0.1416681	-0.5262252	PFAS	Homo sapiens phosphoribosylformylglycinamide synthase (PFAS), mRNA. (from RefSeq NM_0123	NM_012393
uc057jvt.1	1.61E-04	DOWN	1.6271101	1.6271101	0.7023119	-0.5270156	-1.2293276	PHGDH	Homo sapiens phosphoglycerate dehydrogenase (PHGDH), mRNA. (from RefSeq NM_006623)	NM_006623
uc003try.3	4.05E-04	DOWN	1.296422	1.296422	0.3745354	-0.0550644	-0.4295999	PHKG1	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1), transcript variant 2, mRNA. (from	NM_006213
uc021lyz.2	3.78E-04	DOWN	1.2906355	1.2906355	0.36808157	0.19874375	-0.1693379	PI16	Homo sapiens peptidase inhibitor 16 (PI16), transcript variant 2, mRNA. (from RefSeq NM_0011991	NM_001199159
uc057xni.1	5.85E-04	DOWN	3.3347383	3.3347383	1.7375735	-1.7080282	-3.4456017	PIDD1	Homo sapiens p53-induced death domain protein 1 (PIDD1), transcript variant 3, mRNA. (from RefS	NM_145887
uc057xnk.1	8.87E-04	DOWN	1.6087366	1.6087366	0.68592817	-0.6246703	-1.3105985	PIDD1	Homo sapiens p53-induced death domain protein 1 (PIDD1), transcript variant 3, mRNA. (from RefS	NM_145887
uc059php.1	3.39E-04	DOWN	1.2870557	1.2870557	0.36407453	-0.428887	-0.7929616	PKD1	Homo sapiens polycystic kidney disease 1 (autosomal dominant) (PKD1), transcript variant 2, mRNA	NM_000296
uc059phr.1	3.64E-05	DOWN	1.7017137	1.7017137	0.76698834	-0.359971	-1.1269593	PKD1	Homo sapiens polycystic kidney disease 1 (autosomal dominant) (PKD1), transcript variant 2, mRNA	NM_000296
uc059rhn.1	4.55E-04	DOWN	1.6877521	1.6877521	0.75510305	2.3829587	1.6278557	PLA2G10	Homo sapiens phospholipase A2, group X (PLA2G10), mRNA. (from RefSeq NM_003561),	NM_003561
uc009ypi.4	3.34E-04	DOWN	1.4851621	1.4851621	0.5706204	0.7913184	0.22069792	PLCB3	Homo sapiens phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3), transcript variant 1, n	NM_000932
uc062iet.1	2.54E-04	DOWN	1.521547	1.521547	0.60553885	-0.1730668	-0.7786057	PLCD1	Homo sapiens phospholipase C, delta 1 (PLCD1), transcript variant 2, mRNA. (from RefSeq NM_006	NM_006225
uc061xae.1	1.07E-04	DOWN	1.7400681	1.7400681	0.79914373	0.25267655	-0.5464672	PLCG1	Homo sapiens phospholipase C, gamma 1 (PLCG1), transcript variant 2, mRNA. (from RefSeq NM_1	NM_182811
uc059vsr.1	2.18E-04	DOWN	1.3588929	1.3588929	0.44243178	-1.5788502	-2.021282	PLEKHG4	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 4 (f	NM_001129729
uc062erg.1	5.67E-04	DOWN	1.6051593	1.6051593	0.6827164	-0.4386688	-1.1213852	PMM1	Homo sapiens phosphomannomutase 1 (PMM1), mRNA. (from RefSeq NM_002676)	NM_002676
uc064bfu.1	7.43E-04	DOWN	1.297185	1.297185	0.37538418	0.449991	0.07460678	PMS2	Homo sapiens PMS2 postmeiotic segregation increased 2 (S. cerevisiae) (PMS2), transcript variant 1	NM_000535
uc062avx.1	5.29E-04	DOWN	1.4505265	1.4505265	0.5365766	-1.348824	-1.8854007	POFUT2	Homo sapiens protein O-fucosyltransferase 2 (POFUT2), transcript variant 3, mRNA. (from RefSeq	NM_133635
uc062uom.1	3.79E-04	DOWN	2.7521698	2.7521698	1.4605695	-1.5645882	-3.0251577	POLN	Homo sapiens polymerase (DNA directed) nu (POLN), mRNA. (from RefSeq NM_181808)	NM_181808
uc057kca.1	7.84E-04	DOWN	1.3388258	1.3388258	0.42096826	1.2649206	0.84395236	POLR3GL	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like (POLR3GL), mRNA. (fr	NM_032305
uc003baf.5	7.24E-04	DOWN	1.1986835	1.1986835	0.26145077	0.3619145	0.10046375	POLR3H	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide H (22.9kD) (POLR3H), transcript vari	NM_138338
uc062eqw.1	3.06E-04	DOWN	1.3954544	1.3954544	0.48073497	-0.283875	-0.76461	POLR3H	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide H (22.9kD) (POLR3H), transcript vari	NM_001018050
uc064emi.1	2.27E-04	DOWN	1.4989387	1.4989387	0.58394134	1.5621787	0.97823733	POM121C	Homo sapiens POM121 transmembrane nucleoporin C (POM121C), mRNA. (from RefSeq NM_00105	NM_001099415
uc061isf.1	5.45E-04	DOWN	1.2608339	1.2608339	0.33437818	0.6451784	0.31080022	PPM1B	Homo sapiens protein phosphatase, Mg2+/Mn2+ dependent, 1B (PPM1B), transcript variant 1, mRN	NM_002706
uc058tfv.1	9.85E-04	DOWN	1.451177	1.451177	0.5372235	1.7413245	1.2041011	PPP1CC	Homo sapiens protein phosphatase 1, catalytic subunit, gamma isozyme (PPP1CC), transcript variant	NM_002710
uc058enj.1	9.40E-04	DOWN	1.4143714	1.4143714	0.500161	0.5976357	0.09747469	PPP6R3	Homo sapiens protein phosphatase 6, regulatory subunit 3 (PPP6R3), transcript variant 3, mRNA. (fr	NM_001164164
uc058enm.1	9.88E-04	DOWN	1.4273974	1.4273974	0.513387	0.3181437	-0.1952433	PPP6R3	Homo sapiens protein phosphatase 6, regulatory subunit 3 (PPP6R3), transcript variant 3, mRNA. (fr	NM_001164164
uc064yij.1	9.54E-04	DOWN	1.3761176	1.3761176	0.46060374	0.3719382	-0.0886656	PRDX4	Homo sapiens peroxiredoxin 4 (PRDX4), mRNA. (from RefSeq NM_006406)	NM_006406
uc010smd.3	5.58E-04	DOWN	1.3640354	1.3640354	0.44788104	0.21469362	-0.2331875	PRKAG1	Homo sapiens protein kinase, AMP-activated, gamma 1 non-catalytic subunit (PRKAG1), transcript v	NM_001206710
uc010vlg.3	1.05E-04	DOWN	1.3053896	1.3053896	0.3844805	-1.2878727	-1.6723531	PRMT7	Homo sapiens protein arginine methyltransferase 7 (PRMT7), transcript variant 2, mRNA. (from Ref	NM_001184824
uc059wfw.1	8.99E-04	DOWN	1.275288	1.275288	0.35082307	-1.3989285	-1.7497516	PRMT7	Homo sapiens protein arginine methyltransferase 7 (PRMT7), transcript variant 1, mRNA. (from Ref	NM_019023
uc057knz.1	5.59E-04	DOWN	1.3038893	1.3038893	0.38282135	2.0640752	1.6812539	PRPF3	Homo sapiens pre-mRNA processing factor 3 (PRPF3), mRNA. (from RefSeq NM_004698)	NM_004698
uc059zhu.1	9.42E-04	DOWN	1.4483182	1.4483182	0.53437865	1.2172068	0.68282825	PRPF8	Homo sapiens pre-mRNA processing factor 8 (PRPF8), mRNA. (from RefSeq NM_006445),	NM_006445
uc064wqp.1	2.85E-04	DOWN	1.5161586	1.5161586	0.60042065	1.8911299	1.2907091	PRRC2B	Homo sapiens proline-rich coiled-coil 2B (PRRC2B), mRNA. (from RefSeq NM_013318)	NM_013318
uc060irr.1	4.01E-04	DOWN	1.2625949	1.2625949	0.33639187	0.5422088	0.20581692	PSMCS	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMCS), transcript varian	NM_002805
uc063mxz.1	7.17E-05	DOWN	4.6986156	4.6986156	2.2322357	-1.4356651	-3.6679008	PSORS1C1	Homo sapiens psoriasis susceptibility 1 candidate 1 (PSORS1C1), mRNA. (from RefSeq NM_014068)	NM_014068
uc060qrc.1	2.06E-04	DOWN	1.292369	1.292369	0.37001806	0.46050623	0.09048816	PTBP1	Homo sapiens polypyrimidine tract binding protein 1 (PTBP1), transcript variant 2, mRNA. (from Ref	NM_031990
uc060qrh.1	2.20E-04	DOWN	1.3203248	1.3203248	0.40089285	0.04292854	-0.3579643	PTBP1	Homo sapiens polypyrimidine tract binding protein 1 (PTBP1), transcript variant 1, mRNA. (from Ref	NM_002819

uc064umt.1	8.19E-04	DOWN	2.0232575	2.0232575	1.0166799	-2.7186441	-3.7353241	PTCH1	Homo sapiens patched 1 (PTCH1), transcript variant 1d, mRNA. (from RefSeq NM_001083606)	NM_001083606
uc064unb.1	3.59E-04	DOWN	3.1931295	3.1931295	1.6749711	-3.068345	-4.743316	PTCH1	Homo sapiens patched 1 (PTCH1), transcript variant 1c', mRNA. (from RefSeq NM_001083605)	NM_001083605
uc057ofm.1	4.21E-04	DOWN	1.3871766	1.3871766	0.4721515	-0.8639333	-1.3360848	PTPN7	Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7), transcript variant 1, mRNA. (from RefSeq NM_002832)	NM_002832
uc058mvt.1	7.78E-05	DOWN	1.4958481	1.4958481	0.5809636	-0.5292943	-1.110258	PUS7L	Homo sapiens pseudouridylate synthase 7 homolog (S. cerevisiae)-like (PUS7L), transcript variant 2, NM_001098614	NM_001098614
uc062aqk.1	9.50E-04	DOWN	1.5196857	1.5196857	0.603773	1.3084248	0.70465183	PWP2	Homo sapiens PWP2 periodic tryptophan protein homolog (yeast) (PWP2), mRNA. (from RefSeq NM_005049)	NM_005049
uc058fzr.1	7.95E-04	DOWN	1.594856	1.594856	0.67342615	-1.209675	-1.8831011	RAB30	Homo sapiens RAB30, member RAS oncogene family (RAB30), transcript variant 2, mRNA. (from RefSeq NM_014488)	NM_014488
uc060uuc.1	3.13E-04	DOWN	1.4480727	1.4480727	0.534134	0.85487753	0.32074356	RASAL3	Homo sapiens RAS protein activator like 3 (RASAL3), mRNA. (from RefSeq NM_022904)	NM_022904
uc004dhf.4	5.01E-04	DOWN	1.2375112	1.2375112	0.30744153	1.3686744	1.0612328	RBM10	Homo sapiens RNA binding motif protein 10 (RBM10), transcript variant 1, mRNA. (from RefSeq NM_005676)	NM_005676
uc004dhi.4	5.18E-04	DOWN	1.2458704	1.2458704	0.31715393	1.4672886	1.1501347	RBM10	Homo sapiens RNA binding motif protein 10 (RBM10), transcript variant 5, mRNA. (from RefSeq NM_001204468)	NM_001204468
uc001tvm.5	3.05E-04	DOWN	1.2246418	1.2246418	0.29235983	0.42723038	0.149944	RBM19	Homo sapiens RNA binding motif protein 19 (RBM19), transcript variant 3, mRNA. (from RefSeq NM_001146698)	NM_001146698
uc057kbj.1	2.70E-04	DOWN	1.3268416	1.3268416	0.40799615	1.4242088	1.0162126	RBM8A	Homo sapiens RNA binding motif protein 8A (RBM8A), mRNA. (from RefSeq NM_005105)	NM_005105
uc058acp.1	6.77E-04	DOWN	1.4084407	1.4084407	0.4940988	-0.7304082	-1.224507	RCN1	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA. (from RefSeq NM_002901)	NM_002901
uc062vzw.1	7.82E-04	DOWN	1.3807817	1.3807817	0.4654852	0.57894766	0.11346246	RFC1	Homo sapiens replication factor C (activator 1) 1, 145kDa (RFC1), transcript variant 1, mRNA. (from RefSeq NM_002913)	NM_002913
uc059xnc.1	2.30E-04	DOWN	1.5203614	1.5203614	0.60441434	-0.0619525	-0.6663668	RFWD3	Homo sapiens ring finger and WD repeat domain 3 (RFWD3), mRNA. (from RefSeq NM_018124)	NM_018124
uc032tgs.1	2.09E-04	DOWN	1.3263673	1.3263673	0.4074803	-0.1065364	-0.5140167	RHOH	Homo sapiens ras homolog family member H (RHOH), transcript variant 4, mRNA. (from RefSeq NM_001278362)	NM_001278362
uc032tgt.1	2.67E-04	DOWN	1.315562	1.315562	0.39567924	-0.0874111	-0.4830904	RHOH	Homo sapiens ras homolog family member H (RHOH), transcript variant 1, mRNA. (from RefSeq NM_001278359)	NM_001278359
uc032tgu.1	6.28E-04	DOWN	1.2880341	1.2880341	0.36517078	-0.1437313	-0.508902	RHOH	Homo sapiens ras homolog family member H (RHOH), transcript variant 3, mRNA. (from RefSeq NM_001278361)	NM_001278361
uc032tgv.1	3.47E-04	DOWN	1.3125197	1.3125197	0.39233905	-0.047764	-0.440103	RHOH	Homo sapiens ras homolog family member H (RHOH), transcript variant 2, mRNA. (from RefSeq NM_001278360)	NM_001278360
uc002jys.5	3.68E-04	DOWN	1.3271444	1.3271444	0.4083253	0.15025906	-0.2580662	RPTOR	Homo sapiens regulatory associated protein of MTOR, complex 1 (RPTOR), transcript variant 2, mRNA. (from RefSeq NM_001163034)	NM_001163034
uc010wuf.2	9.99E-04	DOWN	1.3079842	1.3079842	0.38734514	0.27418116	-0.113164	RPTOR	Homo sapiens regulatory associated protein of MTOR, complex 1 (RPTOR), transcript variant 2, mRNA. (from RefSeq NM_001163034)	NM_001163034
uc003znj.4	4.50E-04	DOWN	1.2600447	1.2600447	0.3334749	2.897482	2.564007	RRAGA	Homo sapiens Ras-related GTP binding A (RRAGA), mRNA. (from RefSeq NM_006570)	NM_006570
uc001mf.5	4.41E-04	DOWN	1.411432	1.411432	0.49715966	0.8156739	0.3185142	RRAS2	Homo sapiens related RAS viral (r-ras) oncogene homolog 2 (RRAS2), transcript variant 1, mRNA. (from RefSeq NM_012250)	NM_012250
uc060hiq.1	7.17E-04	DOWN	1.3859949	1.3859949	0.47092196	0.01118546	-0.4597365	RSAD1	Homo sapiens radical S-adenosyl methionine domain containing 1 (RSAD1), transcript variant 1, mRNA. (from RefSeq NM_018346)	NM_018346
uc062oaq.1	1.48E-04	DOWN	1.4572004	1.4572004	0.5431993	0.11373038	-0.4294689	RYK	Homo sapiens receptor-like tyrosine kinase (RYK), transcript variant 2, mRNA. (from RefSeq NM_002958)	NM_002958
uc061akp.1	9.04E-04	DOWN	1.2700317	1.2700317	0.3448645	0.53511864	0.19025409	SAE1	Homo sapiens SUMO1 activating enzyme subunit 1 (SAE1), transcript variant 1, mRNA. (from RefSeq NM_005500)	NM_005500
uc010swx.2	3.49E-04	DOWN	1.2962941	1.2962941	0.37439305	0.9367518	0.5623587	SART3	Homo sapiens squamous cell carcinoma antigen recognized by T cells 3 (SART3), mRNA. (from RefSeq NM_014706)	NM_014706
uc058suo.1	4.11E-04	DOWN	1.2769626	1.2769626	0.3527163	0.61272655	0.2645602	SART3	Homo sapiens squamous cell carcinoma antigen recognized by T cells 3 (SART3), mRNA. (from RefSeq NM_014706)	NM_014706
uc062xkn.1	9.64E-04	DOWN	1.4737791	1.4737791	0.5595203	1.5154352	0.9559149	SDAD1	Homo sapiens SDA1 domain containing 1 (SDAD1), transcript variant 1, mRNA. (from RefSeq NM_018115)	NM_018115
uc059ahe.1	8.49E-04	DOWN	1.2069174	1.2069174	0.27132696	-0.8409004	-1.1122273	SDR39U1	Homo sapiens short chain dehydrogenase/reductase family 39U, member 1 (SDR39U1), transcript variant 1, mRNA. (from RefSeq NM_020195)	NM_020195
uc062bvk.1	1.94E-04	DOWN	1.4599779	1.4599779	0.5459465	-0.1899279	-0.7358744	SERPIND1	Homo sapiens serpin peptidase inhibitor, clade D (heparin cofactor), member 1 (SERPIND1), mRNA. (from RefSeq NM_000185)	NM_000185
uc058fon.1	9.08E-04	DOWN	1.6135396	1.6135396	0.69022894	-0.5334949	-1.2237239	SERPINH1	Homo sapiens serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding) (SERPINH1), mRNA. (from RefSeq NM_001207014)	NM_001207014
uc058zcs.1	7.69E-04	DOWN	1.4519949	1.4519949	0.53803635	0.74744505	0.20940872	SF1	Homo sapiens splicing factor 1 (SF1), transcript variant 5, mRNA. (from RefSeq NM_001178031)	NM_001178031
uc003alf.5	2.22E-04	DOWN	1.2294629	1.2294629	0.29802814	-0.3474678	-0.645496	SF11	Homo sapiens Sfi1 homolog, spindle assembly associated (yeast) (SF11), transcript variant 2, mRNA. (from RefSeq NM_014775)	NM_014775
uc062djn.1	2.90E-04	DOWN	1.238267	1.238267	0.30832237	-0.373285	-0.6816074	SF11	Homo sapiens Sfi1 homolog, spindle assembly associated (yeast) (SF11), transcript variant 1, mRNA. (from RefSeq NM_001007467)	NM_001007467
uc062djs.1	8.84E-05	DOWN	1.338568	1.338568	0.4206904	-0.2944833	-0.7151737	SF11	Homo sapiens Sfi1 homolog, spindle assembly associated (yeast) (SF11), transcript variant 2, mRNA. (from RefSeq NM_014775)	NM_014775
uc061kon.1	2.51E-04	DOWN	1.350485	1.350485	0.43347758	-1.6922766	-2.125754	SFXN5	Homo sapiens sideroflexin 5 (SFXN5), mRNA. (from RefSeq NM_144579)	NM_144579
uc058hsd.1	9.84E-04	DOWN	1.4435725	1.4435725	0.5296436	-0.0018167	-0.5314603	SIDT2	Homo sapiens SID1 transmembrane family, member 2 (SIDT2), mRNA. (from RefSeq NM_00104045)	NM_00104045
uc059wbp.1	9.20E-04	DOWN	1.3850757	1.3850757	0.4699648	-0.9814606	-1.4514254	SLC12A4	Homo sapiens solute carrier family 12 (potassium/chloride transporter), member 4 (SLC12A4), transcript variant 1, mRNA. (from RefSeq NM_001145964)	NM_001145964
uc064wao.1	8.04E-05	DOWN	1.7162374	1.7162374	0.77924913	-0.233956	-1.0132052	SLC25A25	Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 (SLC25A25), transcript variant 1, mRNA. (from RefSeq NM_052901)	NM_052901
uc002gku.1	6.72E-04	DOWN	1.2737942	1.2737942	0.34913218	-0.1626447	-0.5117768	SLC25A35	Homo sapiens solute carrier family 25, member 35 (SLC25A35), mRNA. (from RefSeq NM_201520)	NM_201520
uc003etr.3	9.13E-04	DOWN	1.2488834	1.2488834	0.32063875	-0.4139556	-0.7345943	SLC25A36	Homo sapiens solute carrier family 25 (pyrimidine nucleotide carrier), member 36 (SLC25A36), transcript variant 1, mRNA. (from RefSeq NM_001104647)	NM_001104647
uc062okh.1	5.48E-04	DOWN	1.5024016	1.5024016	0.5872705	-0.638229	-1.2254995	SLC25A36	Homo sapiens solute carrier family 25 (pyrimidine nucleotide carrier), member 36 (SLC25A36), transcript variant 2, mRNA. (from RefSeq NM_018155)	NM_018155
uc062kbt.1	4.06E-04	DOWN	3.7354627	3.7354627	1.9301287	-1.2004913	-3.1017783	SLC38A3	Homo sapiens solute carrier family 38, member 3 (SLC38A3), mRNA. (from RefSeq NM_006841)	NM_006841
uc002gur.3	2.37E-04	DOWN	1.2505794	1.2505794	0.3225966	0.63603765	0.313441	SLC5A10	Homo sapiens solute carrier family 5 (sodium/sugar cotransporter), member 10 (SLC5A10), transcript variant 1, mRNA. (from RefSeq NM_001282417)	NM_001282417
uc033eer.2	6.09E-04	DOWN	1.4189857	1.4189857	0.50486004	0.7264187	0.22155859	SMC1A	Homo sapiens structural maintenance of chromosomes 1A (SMC1A), transcript variant 1, mRNA. (from RefSeq NM_006306)	NM_006306
uc061ver.1	1.67E-04	DOWN	1.4434175	1.4434175	0.5294887	1.5320424	1.0025537	SMOX	Homo sapiens spermine oxidase (SMOX), transcript variant 2, mRNA. (from RefSeq NM_175840)	NM_175840
uc001sff.3	2.94E-04	DOWN	1.298578	1.298578	0.37693268	-1.2101015	-1.5870342	SMUG1	Homo sapiens single-strand-selective monofunctional uracil-DNA glycosylase 1 (SMUG1), transcript variant 1, mRNA. (from RefSeq NM_014311)	NM_014311
uc058ouu.1	8.45E-04	DOWN	1.2666962	1.2666962	0.34107056	-1.1676779	-1.5087484	SMUG1	Homo sapiens single-strand-selective monofunctional uracil-DNA glycosylase 1 (SMUG1), transcript variant 2, mRNA. (from RefSeq NM_014311)	NM_014311
uc064hsz.1	5.23E-04	DOWN	1.3600539	1.3600539	0.4436638	1.671265	1.2276012	SND1	Homo sapiens staphylococcal nuclease and tudor domain containing 1 (SND1), mRNA. (from RefSeq NM_014390)	NM_014390
uc002dby.6	3.75E-04	DOWN	1.2043747	1.2043747	0.26828426	2.2939608	2.0256765	SNX29	Homo sapiens sorting nexin 29 (SNX29), mRNA. (from RefSeq NM_032167)	NM_032167
uc064pbh.1	8.48E-04	DOWN	1.5363804	1.5363804	0.61953545	-0.249683	-0.8692184	SNX31	Homo sapiens sorting nexin 31 (SNX31), mRNA. (from RefSeq NM_152628)	NM_152628
uc064kzy.1	9.63E-04	DOWN	1.5874264	1.5874264	0.6666897	-0.9390299	-1.6057196	SORBS3	Homo sapiens sorbin and SH3 domain containing 3 (SORBS3), transcript variant 1, mRNA. (from RefSeq NM_005775)	NM_005775
uc064szm.1	7.92E-04	DOWN	1.5565406	1.5565406	0.6383432	-1.0379893	-1.6763325	SPAG8	Homo sapiens sperm associated antigen 8 (SPAG8), transcript variant 1, mRNA. (from RefSeq NM_001039592)	NM_001039592

uc064tit.1	1.96E-04	DOWN	4.9173074	4.9173074	2.2978685	-2.7281444	-5.026013	SPATA31A7	Homo sapiens SPATA31 subfamily A, member 7 (SPATA31A7), mRNA. (from RefSeq NM_015667)	NM_015667
uc001qrl.4	5.75E-04	DOWN	1.3101797	1.3101797	0.3897647	0.44171762	0.05195296	SPSB2	Homo sapiens spla/ryanodine receptor domain and SOCS box containing 2 (SPSB2), transcript variant 1 (SPSB2), transcript variant 1 (SPSB2), transcript variant 1 (SPSB2)	NM_001146316
uc001qrm.4	3.64E-04	DOWN	1.3169955	1.3169955	0.3972504	0.4247893	0.0275389	SPSB2	Homo sapiens spla/ryanodine receptor domain and SOCS box containing 2 (SPSB2), transcript variant 1 (SPSB2), transcript variant 1 (SPSB2), transcript variant 1 (SPSB2)	NM_032641
uc063eby.1	3.09E-04	DOWN	1.4520903	1.4520903	0.5381311	0.7738885	0.23575735	SREK1	Homo sapiens splicing regulatory glutamine/lysine-rich protein 1 (SREK1), transcript variant 4, mRNA. (from RefSeq NM_001270493)	NM_001270493
uc059cww.1	4.53E-04	DOWN	1.6296676	1.6296676	0.70457774	1.7157656	1.0111878	SRSF5	Homo sapiens serine/arginine-rich splicing factor 5 (SRSF5), transcript variant 2, mRNA. (from RefSeq NM_006925)	NM_006925
uc002kvn.4	8.22E-04	DOWN	1.3419981	1.3419981	0.42438263	0.2535786	-0.1708041	SS18	Homo sapiens synovial sarcoma translocation, chromosome 18 (SS18), transcript variant 2, mRNA. (from RefSeq NM_005637)	NM_005637
uc058mcg.1	5.83E-04	DOWN	2.3022642	2.3022642	1.2030534	-0.5542331	-1.7572865	SSPN	Homo sapiens sarcospan (SSPN), transcript variant 2, mRNA. (from RefSeq NM_001135823)	NM_001135823
uc064qlp.1	7.84E-04	DOWN	1.3147906	1.3147906	0.39483306	1.9079814	1.5131483	ST3GAL1	Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 1 (ST3GAL1), transcript variant 2, mRNA. (from RefSeq NM_173344)	NM_173344
uc010rmb.2	2.05E-04	DOWN	1.3715278	1.3715278	0.45578384	1.8385347	1.3827509	STIP1	Homo sapiens stress-induced phosphoprotein 1 (STIP1), transcript variant 3, mRNA. (from RefSeq NM_001282653)	NM_001282653
uc003nyo.4	5.77E-04	DOWN	2.892846	2.892846	1.5324895	-3.682356	-5.2148457	STK19	Homo sapiens serine/threonine kinase 19 (STK19), transcript variant 3, non-coding RNA. (from RefSeq NR_026717)	NM_026717
uc061uro.1	4.79E-04	DOWN	1.4358821	1.4358821	0.52193725	-0.4958884	-1.0178257	STK25	Homo sapiens serine/threonine kinase 25 (STK25), transcript variant 4, mRNA. (from RefSeq NM_001066374)	NM_001066374
uc057jcy.1	1.87E-04	DOWN	1.4310664	1.4310664	0.5170906	0.70703584	0.18994522	STRIP1	Homo sapiens striatin interacting protein 1 (STRIP1), transcript variant 2, mRNA. (from RefSeq NM_001270768)	NM_001270768
uc060vzi.1	4.07E-04	DOWN	1.3941176	1.3941176	0.47935227	-0.6710272	-1.1503794	SUGP1	Homo sapiens SURP and G patch domain containing 1 (SUGP1), mRNA. (from RefSeq NM_172231)	NM_172231
uc060vzm.1	3.18E-04	DOWN	1.4322947	1.4322947	0.51832837	-0.7515937	-1.269922	SUGP1	Homo sapiens SURP and G patch domain containing 1 (SUGP1), mRNA. (from RefSeq NM_172231)	NM_172231
uc057yyi.1	3.18E-04	DOWN	1.4614923	1.4614923	0.5474422	0.6499431	0.10250086	SWAP70	Homo sapiens SWAP switching B-cell complex 70kDa subunit (SWAP70), transcript variant 1, mRNA. (from RefSeq NM_015055)	NM_015055
uc059cwr.1	2.10E-04	DOWN	1.4609756	1.4609756	0.5469321	0.7396915	0.19275932	SYNJ2BP	Homo sapiens synaptojanin 2 binding protein (SYNJ2BP), mRNA. (from RefSeq NM_018373)	NM_018373
uc002kvt.5	3.64E-04	DOWN	1.2995728	1.2995728	0.37803748	-0.21532	-0.5933575	TAF4B	Homo sapiens TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa (TAF4B), transcript variant 5, mRNA. (from RefSeq NM_001293725)	NM_001293725
uc062vjo.1	5.50E-04	DOWN	1.3021791	1.3021791	0.3809279	0.78185314	0.40092528	TAPT1	Homo sapiens transmembrane anterior posterior transformation 1 (TAPT1), mRNA. (from RefSeq NM_153365)	NM_153365
uc062dbn.1	5.92E-04	DOWN	1.47967	1.47967	0.5652755	0.32357368	-0.2417019	TBC1D10A	Homo sapiens TBC1 domain family, member 10A (TBC1D10A), transcript variant 2, mRNA. (from RefSeq NM_031937)	NM_031937
uc059pdz.1	6.61E-04	DOWN	1.3326174	1.3326174	0.41426262	-0.5980837	-1.0123463	TBL3	Homo sapiens transducin (beta)-like 3 (TBL3), mRNA. (from RefSeq NM_006453)	NM_006453
uc060rek.1	1.03E-04	DOWN	1.3305947	1.3305947	0.41207114	0.13917707	-0.2728941	TCF3	Homo sapiens transcription factor 3 (TCF3), transcript variant 1, mRNA. (from RefSeq NM_003200)	NM_003200
uc061znt.1	7.03E-04	DOWN	1.4835258	1.4835258	0.56903	-1.0095584	-1.5785884	TCP10L	Homo sapiens t-complex 10-like (TCP10L), mRNA. (from RefSeq NM_144659)	NM_144659
uc009wnb.2	4.04E-04	DOWN	1.2925551	1.2925551	0.37022576	-1.1198666	-1.4900924	TDRKH	Homo sapiens tudor and KH domain containing (TDRKH), transcript variant 3, mRNA. (from RefSeq NM_0006862)	NM_0006862
uc057kyy.1	1.87E-04	DOWN	1.2944707	1.2944707	0.37236226	-1.8051876	-2.1775498	TDRKH	Homo sapiens tudor and KH domain containing (TDRKH), transcript variant 2, mRNA. (from RefSeq NM_001083963)	NM_001083963
uc060upn.1	1.44E-04	DOWN	1.7235485	1.7235485	0.7853819	-0.249048	-1.0344299	TECR	Homo sapiens trans-2,3-enoyl-CoA reductase (TECR), transcript variant 1, mRNA. (from RefSeq NM_138501)	NM_138501
uc057lnm.1	7.68E-04	DOWN	2.6156912	2.6156912	1.3871922	-0.9821219	-2.3693142	THBS3	Homo sapiens thrombospondin 3 (THBS3), transcript variant 3, mRNA. (from RefSeq NM_00125260)	NM_00125260
uc061kij.1	1.82E-04	DOWN	1.5086564	1.5086564	0.5932642	0.92305785	0.3297936	TIA1	Homo sapiens TIA1 cytotoxic granule-associated RNA binding protein (TIA1), transcript variant 2, mRNA. (from RefSeq NM_022173)	NM_022173
uc060vxx.1	9.17E-06	DOWN	6.3920336	6.3920336	2.676275	-0.8566036	-3.5328786	TMEM161A	Homo sapiens transmembrane protein 161A (TMEM161A), transcript variant 2, mRNA. (from RefSeq NM_001256766)	NM_001256766
uc002ocx.3	7.29E-04	DOWN	1.3421794	1.3421794	0.42457753	1.0684067	0.64382917	TMEM186	Homo sapiens transmembrane protein 186 (TMEM186), mRNA. (from RefSeq NM_015421)	NM_015421
uc058qzc.1	4.84E-04	DOWN	1.4507658	1.4507658	0.5368147	0.22629212	-0.3105226	TMEM19	Homo sapiens transmembrane protein 19 (TMEM19), mRNA. (from RefSeq NM_018279)	NM_018279
uc062bjc.1	9.17E-04	DOWN	3.3256276	3.3256276	1.7336266	-2.2503574	-3.983984	TMEM191B	Homo sapiens transmembrane protein 191B (TMEM191B), mRNA. (from RefSeq NM_001242313)	NM_001242313
uc058ssh.1	3.91E-06	DOWN	1.5409752	1.5409752	0.62384367	0.46464792	-0.1591958	TMEM263	Homo sapiens transmembrane protein 263 (TMEM263), mRNA. (from RefSeq NM_152261)	NM_152261
uc057pch.1	8.78E-04	DOWN	1.4623923	1.4623923	0.5483304	1.9409966	1.3926662	TRAF3IP3	Homo sapiens TRAF3 interacting protein 3 (TRAF3IP3), transcript variant 2, mRNA. (from RefSeq NM_001287754)	NM_001287754
uc060dem.1	9.16E-04	DOWN	1.3961633	1.3961633	0.48146772	-0.4331847	-0.9146524	TRAF4	Homo sapiens TNF receptor-associated factor 4 (TRAF4), mRNA. (from RefSeq NM_004295)	NM_004295
uc011ekt.3	6.76E-04	DOWN	1.8590623	1.8590623	0.8945751	-5.1601963	-6.0547714	TRIM26	Homo sapiens tripartite motif containing 26 (TRIM26), transcript variant 1, mRNA. (from RefSeq NM_003449)	NM_003449
uc011exk.3	7.58E-04	DOWN	1.5816913	1.5816913	0.661468	-4.2868767	-4.9483447	TRIM26	Homo sapiens tripartite motif containing 26 (TRIM26), transcript variant 1, mRNA. (from RefSeq NM_003449)	NM_003449
uc011fvx.3	6.76E-04	DOWN	1.8590623	1.8590623	0.8945751	-5.1601963	-6.0547714	TRIM26	Homo sapiens tripartite motif containing 26 (TRIM26), transcript variant 1, mRNA. (from RefSeq NM_003449)	NM_003449
uc011ihz.3	6.76E-04	DOWN	1.8590623	1.8590623	0.8945751	-5.1601963	-6.0547714	TRIM26	Homo sapiens tripartite motif containing 26 (TRIM26), transcript variant 1, mRNA. (from RefSeq NM_003449)	NM_003449
uc061dud.1	5.87E-04	DOWN	1.3993151	1.3993151	0.4847209	1.599368	1.114647	TRIM28	Homo sapiens tripartite motif containing 28 (TRIM28), mRNA. (from RefSeq NM_005762)	NM_005762
uc061dud.1	1.33E-04	DOWN	1.4319136	1.4319136	0.51794446	1.4607326	0.9427881	TRIM28	Homo sapiens tripartite motif containing 28 (TRIM28), mRNA. (from RefSeq NM_005762)	NM_005762
uc059pfx.1	4.33E-04	DOWN	1.3908731	1.3908731	0.47599077	-0.7714217	-1.2474126	TSC2	Homo sapiens tuberous sclerosis 2 (TSC2), transcript variant 4, mRNA. (from RefSeq NM_00107718)	NM_00107718
uc058qdh.1	3.68E-04	DOWN	1.457643	1.457643	0.54363745	-0.9739726	-1.5176101	TSFM	Homo sapiens Ts translation elongation factor, mitochondrial (TSFM), transcript variant 2, mRNA. (from RefSeq NM_005726)	NM_005726
uc064ebm.1	2.61E-04	DOWN	1.3691713	1.3691713	0.45330292	-0.3239483	-0.772512	TYW1	Homo sapiens tRNA-yW synthesizing protein 1 homolog (S. cerevisiae) (TYW1), mRNA. (from RefSeq NM_018264)	NM_018264
uc010gpe.4	6.41E-04	DOWN	1.2603626	1.2603626	0.33383888	0.6372262	0.3033874	UBASH3A	Homo sapiens ubiquitin associated and SH3 domain containing A (UBASH3A), transcript variant 3, mRNA. (from RefSeq NM_001243467)	NM_001243467
uc062atf.1	1.78E-04	DOWN	1.3657991	1.3657991	0.44974524	0.73383886	0.28409365	UBE2G2	Homo sapiens ubiquitin-conjugating enzyme E2G 2 (UBE2G2), transcript variant 1, mRNA. (from RefSeq NM_003343)	NM_003343
uc060kwg.1	2.83E-04	DOWN	1.2708144	1.2708144	0.34575337	-0.2679234	-0.6136767	USP36	Homo sapiens ubiquitin specific peptidase 36 (USP36), mRNA. (from RefSeq NM_025090)	NM_025090
uc061lir.1	8.90E-04	DOWN	1.2361414	1.2361414	0.30584383	0.01851674	-0.287327	USP39	Homo sapiens ubiquitin specific peptidase 39 (USP39), transcript variant 2, mRNA. (from RefSeq NM_001256725)	NM_001256725
uc001xss.4	4.40E-04	DOWN	1.3755202	1.3755202	0.45997736	0.10258385	-0.3573935	VASH1	Homo sapiens vasohibin 1 (VASH1), mRNA. (from RefSeq NM_014909)	NM_014909
uc001ucd.4	8.90E-04	DOWN	1.2559216	1.2559216	0.3287464	2.1484215	1.8196751	VPS33A	Homo sapiens vacuolar protein sorting 33 homolog A (S. cerevisiae) (VPS33A), mRNA. (from RefSeq NM_002916)	NM_002916
uc058deo.1	8.74E-04	DOWN	1.3332107	1.3332107	0.4149048	1.3796762	0.96477145	VPS51	Homo sapiens vacuolar protein sorting 51 homolog (S. cerevisiae) (VPS51), transcript variant 1, mRNA. (from RefSeq NM_013265)	NM_013265
uc058dep.1	1.26E-04	DOWN	1.4589694	1.4589694	0.5449496	1.801518	1.2565684	VPS51	Homo sapiens vacuolar protein sorting 51 homolog (S. cerevisiae) (VPS51), transcript variant 1, mRNA. (from RefSeq NM_013265)	NM_013265
uc058des.1	3.86E-04	DOWN	1.4673897	1.4673897	0.55325204	2.1826818	1.6294297	VPS51	Homo sapiens vacuolar protein sorting 51 homolog (S. cerevisiae) (VPS51), transcript variant 1, mRNA. (from RefSeq NM_013265)	NM_013265
uc057ixb.1	3.09E-04	DOWN	1.4779993	1.4779993	0.5636456	0.5589262	-0.0047194	WDR47	Homo sapiens WD repeat domain 47 (WDR47), transcript variant 3, mRNA. (from RefSeq NM_001142551)	NM_001142551

uc060plz.1	8.10E-04	DOWN	1.4390806	1.4390806	0.5251474	0.4197742	-0.1053732	WDR7	Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. (from RefSeq NM_052834)	NM_052834
uc062unn.1	5.56E-04	DOWN	2.5743792	2.5743792	1.3642246	-1.6938831	-3.0581076	WHSC1	Homo sapiens Wolf-Hirschhorn syndrome candidate 1 (WHSC1), transcript variant 3, mRNA. (from RNM_133335)	NM_133335
uc059qwg.1	7.51E-04	DOWN	1.4578638	1.4578638	0.54385597	0.18383855	-0.3600174	ZC3H7A	Homo sapiens zinc finger CCHC-type containing 7A (ZC3H7A), mRNA. (from RefSeq NM_014153)	NM_014153
uc060pua.1	2.15E-04	DOWN	1.431236	1.431236	0.5172616	1.455643	0.93838143	ZCCHC2	Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), transcript variant 1, mRNA. (from RefSeq NM_017742)	NM_017742
uc001knl.5	1.98E-04	DOWN	1.2404679	1.2404679	0.31088442	-1.4266387	-1.7375231	ZDHHC16	Homo sapiens zinc finger, DHHC-type containing 16 (ZDHHC16), transcript variant 2, mRNA. (from RefSeq NM_198043)	NM_198043
uc001knn.5	2.20E-04	DOWN	1.2567183	1.2567183	0.32966128	-1.4043833	-1.7340446	ZDHHC16	Homo sapiens zinc finger, DHHC-type containing 16 (ZDHHC16), transcript variant 4, mRNA. (from RefSeq NM_198045)	NM_198045
uc001knn.5	2.96E-04	DOWN	1.2478478	1.2478478	0.31944197	-1.4134797	-1.7329217	ZDHHC16	Homo sapiens zinc finger, DHHC-type containing 16 (ZDHHC16), transcript variant 3, mRNA. (from RefSeq NM_198044)	NM_198044
uc057vfd.1	6.44E-05	DOWN	1.6282582	1.6282582	0.7033295	-0.3471101	-1.0504397	ZDHHC16	Homo sapiens zinc finger, DHHC-type containing 16 (ZDHHC16), transcript variant 7, mRNA. (from RefSeq NM_001287804)	NM_001287804
uc059ygx.1	3.41E-04	DOWN	1.5172886	1.5172886	0.6014955	-0.2331409	-0.8346365	ZFPM1	Homo sapiens zinc finger protein, FOG family member 1 (ZFPM1), mRNA. (from RefSeq NM_15381)	NM_15381
uc010qpb.3	7.77E-04	DOWN	1.2197018	1.2197018	0.28652844	-0.3717222	-0.6582506	ZFYVE27	Homo sapiens zinc finger, FYVE domain containing 27 (ZFYVE27), transcript variant 6, mRNA. (from RefSeq NM_001174121)	NM_001174121
uc061you.1	3.34E-05	DOWN	1.538955	1.538955	0.621951	-0.3797532	-1.0017042	ZGPAT	Homo sapiens zinc finger, CCCH-type with G patch domain (ZGPAT), transcript variant 3, mRNA. (from RefSeq NM_181485)	NM_181485
uc004aum.2	2.64E-04	DOWN	1.3094375	1.3094375	0.38894722	-0.0145963	-0.4035435	ZNF169	Homo sapiens zinc finger protein 169 (ZNF169), transcript variant 2, mRNA. (from RefSeq NM_1943)	NM_1943
uc010tbw.3	2.49E-04	DOWN	1.4636956	1.4636956	0.54961556	-2.0871649	-2.6367805	ZNF268	Homo sapiens zinc finger protein 268 (ZNF268), transcript variant 5, mRNA. (from RefSeq NM_0011)	NM_0011
uc064fyo.1	6.80E-04	DOWN	1.4893813	1.4893813	0.5747132	-1.0091217	-1.5838348	ZNF3	Homo sapiens zinc finger protein 3 (ZNF3), transcript variant 1, mRNA. (from RefSeq NM_017715)	NM_017715
uc002nvr.3	9.95E-04	DOWN	1.2547241	1.2547241	0.32737023	-0.7882028	-1.1155729	ZNF302	Homo sapiens zinc finger protein 302 (ZNF302), transcript variant 3, mRNA. (from RefSeq NM_0012)	NM_0012
uc060xsx.1	3.28E-04	DOWN	1.3566679	1.3566679	0.44006756	-0.0882812	-0.5283487	ZNF383	Homo sapiens zinc finger protein 383 (ZNF383), mRNA. (from RefSeq NM_152604)	NM_152604
uc001ico.4	1.86E-04	DOWN	1.2566826	1.2566826	0.32962036	-0.2125391	-0.5421595	ZNF496	Homo sapiens zinc finger protein 496 (ZNF496), mRNA. (from RefSeq NM_032752)	NM_032752
uc002mtq.3	1.41E-04	DOWN	1.4632297	1.4632297	0.5491562	-0.7157932	-1.2649494	ZNF563	Homo sapiens zinc finger protein 563 (ZNF563), mRNA. (from RefSeq NM_145276)	NM_145276
uc060zmo.1	9.09E-05	DOWN	1.7175585	1.7175585	0.7803592	0.4081181	-0.3722412	ZNF576	Homo sapiens zinc finger protein 576 (ZNF576), transcript variant 2, mRNA. (from RefSeq NM_0011)	NM_0011
uc061dnb.1	5.18E-04	DOWN	1.5809321	1.5809321	0.6607754	0.41471407	-0.2460613	ZNF586	Homo sapiens zinc finger protein 586 (ZNF586), transcript variant 2, mRNA. (from RefSeq NM_001)	NM_001
uc061dnf.1	9.71E-04	DOWN	1.51933	1.51933	0.6034353	-0.3240847	-0.92752	ZNF587	Homo sapiens zinc finger protein 587 (ZNF587), transcript variant 1, mRNA. (from RefSeq NM_0328)	NM_0328
uc061dng.1	9.64E-04	DOWN	1.7451968	1.7451968	0.8033897	-0.2446956	-1.0480853	ZNF587	Homo sapiens zinc finger protein 587 (ZNF587), transcript variant 2, mRNA. (from RefSeq NM_0012)	NM_0012
uc061dnh.1	5.39E-04	DOWN	1.4637096	1.4637096	0.54962933	-0.3309494	-0.8805787	ZNF587	Homo sapiens zinc finger protein 587 (ZNF587), transcript variant 2, mRNA. (from RefSeq NM_0012)	NM_0012
uc061dni.1	4.60E-04	DOWN	1.4697145	1.4697145	0.555536	-0.5591287	-1.1146647	ZNF587	Homo sapiens zinc finger protein 587 (ZNF587), transcript variant 2, mRNA. (from RefSeq NM_0012)	NM_0012
uc060weu.1	2.74E-04	DOWN	1.75261	1.75261	0.809505	0.68229747	-0.1272075	ZNF626	Homo sapiens zinc finger protein 626 (ZNF626), transcript variant 2, mRNA. (from RefSeq NM_1452)	NM_1452
uc059tkg.1	7.93E-04	DOWN	2.61518	2.61518	1.3869102	-1.3806344	-2.7675447	ZNF668	Homo sapiens zinc finger protein 668 (ZNF668), transcript variant 2, mRNA. (from RefSeq NM_0247)	NM_0247
uc057fla.1	5.33E-04	DOWN	1.3146166	1.3146166	0.39464206	-1.5912694	-1.9859115	ZNF691	Homo sapiens zinc finger protein 691 (ZNF691), transcript variant 1, mRNA. (from RefSeq NM_0012)	NM_0012
uc011kuo.3	5.63E-04	DOWN	1.1895795	1.1895795	0.25045168	1.8345261	1.5840744	ZNF783	Homo sapiens zinc finger family member 783 (ZNF783), mRNA. (from RefSeq NM_001195220)	NM_001195220
uc060tys.1	8.33E-04	DOWN	1.734782	1.734782	0.7947543	0.78073627	-0.0140181	ZNF799	Homo sapiens zinc finger protein 799 (ZNF799), mRNA. (from RefSeq NM_001080821)	NM_001080821
uc010ygn.3	5.09E-04	DOWN	1.2656769	1.2656769	0.3399091	1.6741399	1.3342308	ZNF835	Homo sapiens zinc finger protein 835 (ZNF835), mRNA. (from RefSeq NM_001005850)	NM_001005850
uc061cbj.1	3.95E-04	DOWN	1.4309256	1.4309256	0.51694864	0.8439073	0.32695857	ZNF841	Homo sapiens zinc finger protein 841 (ZNF841), mRNA. (from RefSeq NM_001136499)	NM_001136499
uc062iuy.1	4.36E-04	DOWN	1.3225425	1.3225425	0.40331414	-0.3897847	-0.7930989	ZNF852	Homo sapiens zinc finger protein 852 (ZNF852), mRNA. (from RefSeq NM_001287349)	NM_001287349
uc062iuz.1	2.11E-05	DOWN	1.3880543	1.3880543	0.47306395	-0.2150409	-0.6881048	ZNF852	Homo sapiens zinc finger protein 852 (ZNF852), mRNA. (from RefSeq NM_001287349)	NM_001287349
uc002bkr.4	3.45E-05	DOWN	1.346895	1.346895	0.42963737	-1.5751795	-2.0048168	ZSCAN2	Homo sapiens zinc finger and SCAN domain containing 2 (ZSCAN2), transcript variant 1, mRNA. (from RefSeq NM_181877)	NM_181877
uc059mrx.1	3.03E-05	DOWN	1.3308383	1.3308383	0.4123353	-1.501401	-1.9137362	ZSCAN2	Homo sapiens zinc finger and SCAN domain containing 2 (ZSCAN2), transcript variant 1, mRNA. (from RefSeq NM_181877)	NM_181877
uc059mry.1	2.32E-04	DOWN	1.4622391	1.4622391	0.54817927	-0.5980268	-1.146206	ZSCAN2	Homo sapiens zinc finger and SCAN domain containing 2 (ZSCAN2), transcript variant 1, mRNA. (from RefSeq NM_181877)	NM_181877
uc059msa.1	1.76E-04	DOWN	1.2959998	1.2959998	0.37406546	-1.1061901	-1.4802556	ZSCAN2	Homo sapiens zinc finger and SCAN domain containing 2 (ZSCAN2), transcript variant 1, mRNA. (from RefSeq NM_181877)	NM_181877
uc032wpp.2	6.69E-04	DOWN	1.255474	1.255474	0.3282321	-0.3200883	-0.6483204	ZSCAN26	Homo sapiens zinc finger and SCAN domain containing 26 (ZSCAN26), transcript variant d, mRNA. (from RefSeq NM_001287421)	NM_001287421
uc059pye.1	7.08E-04	DOWN	1.2240224	1.2240224	0.29162994	-1.0684617	-1.3600916	ZSCAN32	Homo sapiens zinc finger and SCAN domain containing 32 (ZSCAN32), transcript variant 3, mRNA. (from RefSeq NM_001284528)	NM_001284528



**Supplementary Table 4. Summary of published manuscripts linking progenitor cell changes to atherosclerosis.**

First	Last	Journal	Year	Source	Method	Endnote	DOI/PMID	
Vasa et al	Dimmeler	Circ Res	2001	blood	EPC isolated by adhesion	KDR+/CD34+ by flow	EPC reduced in CAD, - correlation w risks	10.1161/hh1301.093953
D'Ippolito	Schiller	J. Cell Science	2004	marrow	MIAMI, marrow isolated adult multilineage indi	adhesion	CD81 positive, CD34 neg!	10.1242/jcs.01103
Damani	Topol	Sci. Trans Med	2012	blood	3 channel microscopy	Circ Endo Cells	multinuclear predict acute MI	10.1126/scitranslmed.3003451
Bielak	Peysers	Clinical Medicine	2009	blood	flow	CD34+ cell count	correlates with Ca score	
Hill	Finkel	NEJM	2003	blood	colony forming units from 45 men	EPC, vascular function, cv risk (-0.47) and vasodilation (0.	25966	10.1056/NEJMoa022287
Schmidt-Lucke	Dimmeler	Circulation	2005	blood	flow for CD34+/KDR+	reduced EPC associated with higher events, 43 con vs 44 with stable cad		
Schmidt-Lucke	Dimmeler	Atherosclerosis	2010	blood	flow for CD34+/KDR+ and apop EPC	statins, not ezetimibe reduced EPC apop		
Hristov	Weber	Atherosclerosis	2007	blood	flow for CD34+/KDR+	statins reduced EPC numbers		
Schmidt-Lucke	Dimmeler	PLOS One	2010	blood	ISHAGE gating on flow for CD45(dim)/CD34+/Kt	confirm reduced EPC in CAD and statin effect	25967	10.1371/journal.pone.0013790
Werner	Nickenig	NEJM	2005	blood	flow for CD34+/KDR+	high EPC had lower event rate, but not predictive of MI		
Chen	Chang	Int Heart J	2006	blood	flow CD34+/KDR+ and CD62E or CD31	no age related change in healthy subjects 20-61	16479045	
Laufs		Circulation	2004	blood		physical training increases EPC numbers		
Heiss		JACC	2005	blood		EPC in age related dysfunction		
Kunz		Am Ht Journal	2006	blood		EPC predict CAD severity		
Fadini		Stroke	2006	blood	flow CD34+/KDR+	EPC predicts subclinical atherosclerosis		
Rauscher		Circulation	2003	blood	BM EPC treatment prevents athero in Apo E mice		10.1161/01.CIR.0000082924.75945.48	
Fadini	Werner	PLOS One	2010	blood	meta-analysis of 1,057 patients	CPC helped predict MACE in high risk patients	10.1371/journal.pone.0011488	
Pirro	Mannarino	Atherosclerosis	2008	blood	flow CD34+/KDR+	EPC, and EPC microparticles reduced with high risk		
Bonello	Sabatier	J Thromb Haem	2012	blood	flow CD34+/KDR+	EPC changes, not level, predict restenosis after BMS	10.1111/j.1538-7836.2012.04854.x	
Chen	Zhu	Clinical Science	2004	blood	adhesion to FN	EPC levels lower in hypercholesterolemia		
Muller-Ehmsen	Flesch	Eur Heart Jour	2008	blood	CD34 and KDR, and AC133	CPC lower in obesity	10.1093/eurheartj/ehn213	
Boos	Lip	J Thromb Haem	2008	blood	immunobeads, vWF, sEel, sFas, sFasL Elisa	CEC associated with MACE and CV death	10.1111/j.1538-7836.2008.03148.x	
<b>Arrays</b>								
Liu et al		Physiol Gen	2011		CD34+ immunomagnetic, Isolex300i	CD34+ differentiated with cytokines	10.1152/physiolgenomics.00099.2011	
Ahrens	Agrotis	PLOS One	2011		EPC isolation improved by culture method	Cord blood elevated II-37, PDK4, A2M	10.1371/journal.pone.0023210	
Cheng	Lee	BMC Medical Ger	2012		leukocyt divided by high risk, ie FH, vs low risk	found 56 biomarkers of risk	http://www.biomedcentral.com/1755-8794/5/2	
Huang CC	MESA	Physiol Genomics	2011	PBL	females divided by Ca score, about 300	409 transcripts found race associate genes also	10.1152/physiolgenomics.00243.2010	
Colombo	Marina Cam	Thr. Res	2011		platelets stable angina vs non ST coronary	45 transcripts found GP1BB	10.1016/j.thromres.2011.02.012	
Brinch	Kolvraa	Prenatal Diagnosi	2012		materna magnetic sorting, microarray	28 transcripts mmp14, mcam, kcnq4, cldn6, F3		
Kraan	Horrevoets	BMC Genomics	2010	blood	magnetic beads for CD34, CD14, CD4, 60 ml	Illumina BeadChip retinoic acid signature	http://www.biomedcentral.com/1471-2164/11/388	



Supplementary Table 6. Correlations of TRACs with known Treg markers.

Gene Symbol	FOXP3	PSORS	AHRR	DLG1	IL12A	ICOSLG	PDCD1	CD88	TRIM28	TCF3	CD68	IKZF4	DGKA	CD27	B3GAT1	SMYD3	B3GAT1	ICOS	PTPRC	RUNX1	ICOS	CD8A	CD4	CD27	IL2RA		
IL2RA	0.220	0.135	0.035	0.166	-0.240	0.179	-0.011	0.160	0.085	0.130	0.211	0.080	0.294	0.368	-0.111	0.111	0.061	0.596	0.100	0.413	0.619	0.177	0.184	0.285	1	IL2RA	
CD27	0.083	-0.106	0.006	-0.099	-0.081	0.255	0.272	0.115	0.163	0.133	0.349	-0.269	0.072	0.594	0.300	-0.129	0.240	0.233	-0.345	0.214	0.189	0.214	0.504	1.000		CD27	
CD4	-0.073	-0.237	-0.202	-0.128	-0.229	0.066	0.109	0.092	0.198	-0.150	0.606	-0.176	0.078	0.363	0.065	-0.087	-0.103	0.311	-0.158	0.167	0.273	0.093	1.000			CD4	
CD8A	0.534	0.056	0.380	0.245	0.009	0.299	0.390	0.517	0.430	0.031	0.266	0.042	0.114	0.462	0.065	0.062	0.224	0.150	-0.212	0.358	0.075	1.000				CD8A	
ICOS	0.115	0.167	0.024	0.272	-0.263	0.024	-0.090	0.473	0.156	0.006	0.187	0.039	0.468	0.261	-0.128	0.091	-0.097	0.874	0.223	0.171	1.000					ICOS	
RUNX1	0.363	-0.029	0.084	0.044	-0.057	0.189	0.113	0.012	-0.037	-0.311	0.499	-0.078	-0.142	0.099	0.105	0.129	0.484	0.247	-0.185	1.000						RUNX1	
PTPRC	-0.309	0.035	-0.188	0.235	-0.191	-0.214	-0.459	0.095	-0.042	-0.015	-0.086	0.228	0.227	-0.028	-0.476	0.113	-0.449	0.050	1.000							PTPRC	
ICOS	0.231	0.179	0.059	0.266	-0.214	0.041	0.066	0.412	0.134	-0.057	0.203	0.011	0.351	0.280	0.031	0.054	0.053	1.000								ICOS	
B3GAT1	0.353	0.107	0.299	-0.136	0.042	0.069	0.349	-0.181	-0.107	-0.118	0.176	-0.129	-0.241	-0.149	0.638	0.017	1.000									B3GAT1	
SMYD3	0.082	0.263	0.030	0.196	-0.086	-0.065	-0.091	0.123	-0.015	0.004	-0.079	0.002	0.042	-0.044	-0.034	1.000										SMYD3	
B3GAT1	0.165	0.098	0.244	-0.209	0.083	0.105	0.589	-0.091	-0.119	-0.106	0.003	-0.147	-0.253	-0.166	1.000											B3GAT1	
CD27	0.187	-0.031	0.090	0.212	-0.186	0.268	0.052	0.416	0.518	0.216	0.305	-0.011	0.387	1.000												CD27	
DGKA	0.178	0.042	0.341	0.288	-0.311	0.330	-0.034	0.382	0.346	0.197	-0.073	0.214	1.000													DGKA	
IKZF4	0.130	0.254	0.197	0.182	-0.003	0.039	-0.022	0.028	0.291	0.218	-0.189	1.000														IKZF4	
CD68	0.075	-0.093	-0.140	-0.118	-0.163	0.020	0.081	0.141	0.169	-0.163	1.000																CD68
TCF3	0.061	0.189	0.163	0.176	-0.127	0.121	0.096	0.108	0.308	1.000																	TCF3
TRIM28	0.213	0.010	0.208	0.085	-0.171	0.207	0.180	0.394	1.000																		TRIM28
CD88	0.203	0.186	0.224	0.412	-0.176	0.076	0.075	1.000																			CD88
PDCD1	0.480	0.186	0.444	0.086	0.135	0.288	1.000																				PDCD1
ICOSLG	0.407	0.010	0.387	0.088	0.000	1.000																					ICOSLG
IL12A	0.151	0.080	0.164	-0.058	1.000																						IL12A
DLG1	0.315	0.283	0.279	1.000																							DLG1
AHRR	0.722	0.480	1.000																								AHRR
PSORS1C1	0.352	1.000																									PSORS1C1
FOXP3	1.000																										FOXP3
correlation w. FOXP3		PSORS	AHRR	DLG1	IL12A	ICOSLG	PDCD1	CD88	TRIM28	TCF3	CD68	IKZF4	DGKA	CD27	B3GAT1	SMYD3	B3GAT1	ICOS	PTPRC	RUNX1	ICOS	CD8A	CD4	CD27	IL2RA		

Supplementary Table 7. DEG common to Discovery and Validation Cohorts.

UCSC ID	p ([CAD] Vs [Regulation ( FC (abs) ([CA FC ([CAD] Vs Log FC ([CAD [CAD](raw) [LOW](raw) start of trans Description	chr	SeqLL TRACIT3 INOVA HG38 SeqLL	mat STRESS	SeqLL TRACIT1 GWU HG38 SeqLL	SeqLL TRACIT1 GWU HG19 Seqll					
UCSC ID	p ([CAD] Vs [Regulation ( FC (abs) ([CA FC ([CAD] Vs Log FC ([CAD [CAD](raw) [LOW](raw) start of trans Description	chr	Gene Name	mat STRESS	CathDx 599 list	CathDx					
uc061hhh.1	0.00466694 up	3.1491892	3.1491892	1.6549804	0.08496023	0.02697844	26308175	Adhesion G Protein-Coupled Receptor F3. (from Un chr2			
uc063gxp.1	0.00544914 down	1.2519302	-1.2519302	-0.3241542	4.696951	5.8802547	132897203	AF4/FMR2 family, member 4 (from HGNC AFF4) chr5			
uc061wik.1	0.00476174 down	1.4414719	-1.4414719	-0.5275428	0.92420864	1.3322208	34291464	adenosylhomocysteine (from HGNC AHCY) chr20			
uc062bv.1	8.58E-04 down	9.211627	-9.211627	-3.203456	0.0066789	0.06152349	20965176	apoptosis-inducing factor, mitochondrion-associate chr22			
uc062eav.1	1.45E-04 down	9.639785	-9.639785	-3.269001	0.03060729	0.29504773	37833008	Ankyrin Repeat Domain 54. (from UniProt C9JX82) chr22			
uc057shp.1	0.00793906 down	1.3702843	-1.3702843	-0.4544753	0.50020045	0.6854169	24629013	Rho GTPase activating protein 21 (from HGNC ARH chr10			
uc060lgs.1	0.00771698 down	4.540955	-4.540955	-2.1829958	0.037111	0.16851938	81097578	BAI1 Associated Protein 2. (from UniProt I3L0Y9) chr17			
uc059uld.1	0.00893112 down	1.2283325	-1.2283325	-0.2967012	2.237617	2.7485378	56484344	Bardet-Biedl syndrome 2 (from HGNC BBS2) chr16			
uc061hmb.1	0.00518361 down	4.071977	-4.071977	-2.0257294	0.0617337	0.2513782	27241920	Carbamoyl-Phosphate Synthetase 2, Aspartate, Bel chr2			
uc058qob.1	0.00997198 up	3.9418516	3.9418516	1.9788735	0.45921156	0.11649641	67269717	cullin-associated and neddylation-dissociated 1 (frc chr12			
uc058svy.1	0.00836163 down	1.2155546	-1.2155546	-0.281647	3.5544074	4.320576	108658880	Belongs to the WD repeat coronin family. (from Ur chr12			
uc058zud.1	0.00311815 down	3.6590462	-3.6590462	-1.8714676	0.00556233	0.02035282	24071588	copine VI (neuronal) (from HGNC CPNE6) chr14			
uc061oas.1	0.00893666 down	1.251643	-1.251643	-0.3238231	2.9431279	3.6837454	135906823	aspartyl-tRNA synthetase (from HGNC DARS) chr2			
uc062lxl.1	0.00727313 down	3.096001	-3.096001	-1.6304059	0.01418335	0.04391168	98807910	discoidin, CUB and LCCL domain containing 2 (from chr3			
uc063naw.1	0.00208251 down	1.2229795	-1.2229795	-0.2904003	5.738689	7.018299	31530242	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B (from chr6			
uc063hco.1	0.00609706 down	5.3292775	-5.3292775	-2.41394	0.0663546	0.35362202	134773784	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (from chr5			
uc058viq.1	0.00960035 down	2.0436409	-2.0436409	-1.0311416	0.44386658	0.90710384	132139112	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (from chr12			
uc058pcp.1	0.00954773 up	1.4104319	1.4104319	0.49613696	4.2960267	3.0458946		diacylglycerol kinase, alpha 80kDa (from HGNC DGI chr12			
uc002app.4	0.00721339 down	1.2387679	-1.2387679	-0.3089059	1.1705571	1.4500486	66293216	DIS3 like exosome 3'-5' exoribonuclease (DIS3L), tr. chr15			
uc064ljj.1	0.00664018 down	1.44623	-1.44623	-0.5322971	1.3436074	1.9431655	26627214	dihydropyrimidinase-like 2 (from HGNC DPYSL2) chr8			
uc063pfd.1	0.00451893 down	5.760368	-5.760368	-2.526161	0.03775852	0.21750295	56617199	Dystonin. (from UniProt H0YAT7) chr6			
uc058pzo.1	7.35E-04 down	1.4873667	-1.4873667	-0.5727603	0.60503316	0.8999062	57604638	Deltex E3 Ubiquitin Ligase 3. (from UniProt F8VUZ) chr12			
uc059lkd.1	0.00922576 down	1.421449	-1.421449	-0.5073623	0.8373783	1.1902905	74655793	Enhancer Of MRNA Decapping 3. (from UniProt H3) chr15			
uc064lhm.1	0.00821887 down	1.253947	-1.253947	-0.3264764	2.252565	2.824597	28118897	elongator acetyltransferase complex subunit 3 (froi chr8			
uc058bhy.1	0.00430335 down	1.3011535	-1.3011535	-0.3797912	4.9715977	6.468812	47732481	formin binding protein 4 (from HGNC FNBP4) chr11			
uc062llr.1	0.00234395 down	1.2440604	-1.2440604	-0.3150565	7.420352	9.231366	70968847	forkhead box P1 (from HGNC FOXP1) chr3			
uc002utu.4	0.00690295 down	1.2726772	-1.2726772	-0.3478665	1.6410824	2.0885682	196780088	general transcription factor IIIC subunit 3 (GTF3C3) chr2			
uc058igy.1	0.00498888 down	1.2429291	-1.2429291	-0.3137444	0.8698461	1.0811571	119131438	histone H4 transcription factor (from HGNC HINFP) chr11			
uc059vpb.1	0.00656629 down	5.5908747	-5.5908747	-2.483074	0.01402885	0.07843354	67165524	Heat Shock Transcription Factor 4. (from UniProt H chr16			
uc061qzm.1	0.00504353 down	1.420102	-1.420102	-0.5059946	2.0935285	2.9730241	197496890	Heat Shock Protein Family D (Hsp60) Member 1 (cf chr2			
uc059mbz.1	0.00979137 down	4.922826	-4.922826	-2.2994866	0.04578593	0.22539617	78163715	Isocitrate Dehydrogenase 3 (NAD(+)) Alpha. (from chr15			
uc001vnf.2	0.00700541 down	1.237847	-1.237847	-0.307833	1.0729606	1.328161	97976631	Importin 5			
uc057sqt.1	0.0056646 down	1.2380247	-1.2380247	-0.3084001	8.723372	10.799751	32929984	Integrin Subunit Beta 1. (from UniProt C9JNE0) chr10			
uc058nxx.1	1.30E-04 down	1.5037236	-1.5037236	-0.5885394	1.5619553	2.3487492	15048312	LETM1 domain containing 1 (from HGNC LETMD1) chr12			
uc001fnf.3	0.00678139 down	1.2709522	-1.2709522	-0.3459098	1.1653022	1.4810433	156082577	lamin A/C (LMNA), transcript variant 2. mRNA. (frc chr1			
uc064sik.1	0.00679545 down	1.3376278	-1.3376278	-0.4196767	2.030512	2.7160695	20346405	MLLT3 Super Elongation Complex Subunit. (from U chr9			
uc002aze.3	0.0059149 down	1.316997	-1.316997	-0.3972521	1.3843883	1.8232353	74890041	mannose phosphate isomerase (MPI), transcript va chr15			
uc057skx.1	0.00291165 down	1.2832036	-1.2832036	-0.3357501	3.3767724	4.3030865	28054142	Membrane Palmitoylated Protein 7. (from UniProt chr10			
uc060bvl.1	0.00599846 down	1.3389245	-1.3389245	-0.4210746	1.2934629	1.7318492	17179557	Myosin Phosphatase Rho Interacting Protein. (from chr17			
uc057uah.1	0.00393548 down	1.2238083	-1.2238083	-0.2913776	4.7361636	5.796156	73250740	mitochondrial ribosomal protein S16 (from HGNC chr10			
uc061ipi.1	0.00567156 down	5.6448393	-5.6448393	-2.4969325	0.03140524	0.17727755	42568167	metastasis associated 1 family, member 3 (from H chr2			
uc059cjt.1	0.0030653 down	6.661544	-6.661544	-2.7358565	0.02530567	0.16857481	64457996	methylenetetrahydrofolate dehydrogenase (NADP+ chr14			
uc061jge.1	0.00261511 down	1.259208	-1.259208	-0.3325166	1.658834	2.088817	55236620	Mitochondrial Translational Initiation Factor 2 chr2			
uc003wxt.4	0.00769938 down	2.4843318	-2.4843318	-1.3128579	0.05885801	0.14622281	17643803	microtubule associated tumor suppressor 1 (MTUS chr8			
uc059zfb.1	0.00387835 down	5.238711	-5.238711	-2.389212	0.0739109	0.38719785	1468222	myosin IC (from HGNC MYO1C) chr17			
uc061cul.1	0.0098469 down	4.928974	-4.928974	-2.3012874	0.03456391	0.1703646	54973993	NLR Family Pyrin Domain Containing 2. (from UniP chr19			

SeqLL TRACIT3 INOVA HG38 SeqLL	mat STRESS	SeqLL TRACIT1 GWU HG38 SeqLL	SeqLL TRACIT1 GWU HG19 Seqll
Gene Name	mat STRESS	CathDx 599 list	CathDx
Gen80 664 list			
ADGRF3	c	ADGRG3	
AFF4	c	AFF3	
AHCY	a		AHCYL2
AIFM3	a		AIFM3
ANKRD54	a	ANKHD1	ANKRD54
ARHGAP21	a		ARHGAP22
BAIAP2	e	BAIAP2	BAIAP3
BBS2	a		BBS2
CAD	a		CAD
CAND1	a		CAND2
CORO1C	a	CORO1B	CORO6
CPNE6	a		CPNE3
DARS	a	hypoxia	DARS
DCBLD2	c	DCBLD1	
DDX39B	a		DDX39A
DDX46	c	DDX47	DDX42
DDX51	a	DDX50	DDX51
DGKA		DGKA	DGKA
DIS3L	e	DIS3L2	DIS3
DPYSL2	a	DPYSL2	DPYSL3
DST	o	DST	
DTX3	c	DTX3L	DTX1
EDC3	e	EDC3	EDC3
ELP3	c		ELP2
FNBP4	e	FNBP4	
FOXP1	e	FOXP1	FOXP1, 1132
GTF3C3	a	GTF2H4	GTF3C3
HINFP	e	HINFP	
HSF4	a	Heat Shock	HSF4
HSPD1	c	HSPD1	HSPE1
IDH3A	a		IDH1
IPOS	c		IPO11
ITGB1	a	ITGB1	ITGB1
LETMD1	a		LETMD1
LMNA	a	LMNA	LMNA
MLLT3	a		MLLT3
MPI	a		MPI
MPP7	a		MPP2
MPRIP	a	stress fibers	MPRIIP
MRPS16	c		MRPS31
MTA3	a		MTA3
MTHFD1	e	MTHFD1	MTHFD1L
MTIF2	a	hypoxia down	292270
MTUS1	a		MTUS2
MYO1C	e	MYO6	MYO1E
NLRP2	a	aging	NLRP2,

uc002rcy.4	0.00504953	down	1.4440056	-1.4440056	-0.5300763	0.27387014	0.39547002	18555544	NT5C1B-RDH14 readthrough (NT5C1B-RDH14).	trar	chr2
uc004bve.4	0.0090192	down	1.2714772	-1.2714772	-0.3465056	0.6369028	0.8098074	128456918	outer dense fiber of sperm tails 2 (ODF2).	transcrip	chr9
uc058upy.1	0.00163712	down	1.3608307	-1.3608307	-0.4444875	0.9761837	1.3284208	122975241	2-oxoglutarate and iron-dependent oxygenase dom		chr12
uc062htp.1	2.85E-04	down	11.307217	-11.307217	-3.499172	0.02170722	0.24544828	31683968	oxysterol binding protein-like 10 (from HGNC OSBP)		chr3
uc062axf.1	0.00935585	down	3.932247	-3.932247	-1.9753538	0.01675902	0.06590062	45849989	Poly(RC) Binding Protein 3 Contains 3 KH domains		chr21
uc061apt.1	0.00386926	down	5.2680926	-5.2680926	-2.3972807	0.02025118	0.1066851	48097764	phospholipase A2, group IVC (cytosolic, calcium-inc)		chr19
uc002eso.5	0.00228795	down	1.5580505	-1.5580505	-0.639742	0.17257616	0.26888236	67277509	pleckstrin homology and RhoGEF domain containin		chr16
uc060epe.1	0.00396322	down	6.754754	-6.754754	-2.7559032	0.01532278	0.1035016	39072013	plexin domain containing 1 (from HGNC PLXDC1)		chr17
uc060qvd.1	0.00637629	down	1.200787	-1.200787	-0.2639802	5.5362716	6.6478825	1088147	polymerase (RNA) II (DNA directed) polypeptide E.		chr19
uc060ihp.1	0.00965993	down	1.2412302	-1.2412302	-0.3117708	1.7525004	2.1752565	60600182	Protein Phosphatase, Mg2+/Mn2+ Dependent 1D		chr17
uc062rrj.1	0.00865548	down	1.2024927	-1.2024927	-0.2660281	4.875126	5.8623033	195519160	Protein Phosphatase 1 Regulatory Inhibitor Subunit		chr3
uc064zfq.1	0.00463741	down	1.4196897	-1.4196897	-0.5055756	0.43235695	0.6138127	49269842	Glycogen-targeting subunit for protein phosphatase		chrX
uc057ubg.1	0.0052754	down	3.086338	-3.086338	-1.6258961	0.15896747	0.49062735	73496286	PPP3CB antisense RNA 1 (head to head) (from HGNC)		chr10
uc058nma.1	0.00124233	down	1.2204394	-1.2204394	-0.2874007	2.856492	3.4861758	49003809	Protein Kinase AMP-Activated Non-Catalytic Subunit		chr12
uc002dzb.2	0.00304907	down	1.2940506	-1.2940506	-0.371894	1.6394578	2.1215413	30654108	proline rich 14 (from HGNC PRR14)		chr16
uc064wqo.1	0.001422	down	1.3874075	-1.3874075	-0.4723916	4.342514	6.0248365	131473593	Proline Rich Coiled-Coil 2B. (from UniProt Q5JSZ9)		chr9
uc057zit.1	0.00307177	down	1.4568127	-1.4568127	-0.5428155	1.6053652	2.3387163	14610853	proteasome (prosome, macropain) subunit, alpha t		chr11
uc058zoc.1	0.00158443	down	1.4917963	-1.4917963	-0.5770505	1.4193069	2.1173165	23016542	Belongs to the peptidase T1B family. (from UniProt)		chr14
uc060eva.1	0.00102343	down	1.2573454	-1.2573454	-0.3303811	3.3179946	4.171865	39986608	proteasome (prosome, macropain) 26S subunit, no		chr17
uc062hhe.1	0.00257963	down	1.275671	-1.275671	-0.3512563	7.6515155	9.760817	18414948	SATB homeobox 1 (from HGNC SATB1)		chr3
uc002ubx.5	0.00848147	down	2.115307	-2.115307	-1.080867	0.1222189	0.25853053	161624425	Solute carrier family 4 member 10 (SLC4A10).	tran:	chr2
uc064ikc.1	0.00143057	down	1.2051876	-1.2051876	-0.2692577	1.2460814	1.5017617	138460548	Tripartite Motif Containing 24. (from UniProt A0A0)		chr7
uc061qdv.1	0.00461844	up	1.4030657	1.4030657	0.48858255	2.0478244	1.4595356	178528739	TTN antisense RNA 1 (from HGNC TTN-AS1)		chr2
uc064yux.1	0.00753835	down	1.2729685	-1.2729685	-0.3481967	1.1967776	1.5234601	47232865	ubiquitin specific peptidase 11 (USP11). mRNA. (fr		chrX
uc062unl.1	0.00353547	down	1.3544748	-1.3544748	-0.4377335	0.5120621	0.69357514	1939280	Wolf-Hirschhorn syndrome candidate 1 (from HGNC)		chr4
uc059ftl.1	0.00441255	down	6.35512	-6.35512	-2.6679194	0.01124214	0.07144516	103702015	X-ray repair complementing defective repair in Chi		chr14

NT5C1B-RDH14	e	NT5C3A	NT5C3B
ODF2	e	ODF2L	ODF2
OGFOD2	e	OGFOD1	OGFOD2
OSBPL10	e	OSBPL9	OSBPL10
PCBP3	e	PCBP2, PCBP	PCBP1-AS1
PLA2G4C	o		PLA2G10,
PLEKHG4	a		PLEKHG4
PLXDC1	c	PLXNC1	PLXND1
POLR2E	c	POLR2B	POLR2D
PPM1D	a		PPM1B
PPP1R2	c	PPP1R8	PPP1R13B
PPP1R3F	a		PPP1CC
PPP3CB-AS1	e		PPP3CB-AS
PRKAG1	a	PRKCE	PRKAG1
PRR14	c		PRR14L
PRRC2B	a	PRRC2B	PRRC2B
PSMA1	c		PSMA3
PSMB5	a	PSMD2	PSMC5
PSMD3	c	PSMD2	PSMD6
SATB1	c	AGE1	SATB2
SLC4A10	a		SLC5A10
TRIM24	c	TRIM21	TRIM47
TTN-AS1	e		TTN
USP11	e	USP11	USP11
WHSC1	a		WHSC1
XRCC3	a		XRRA1
			XRCC3

**Supplementary Table 8. 26 Transcript exemplars common to both studies  
and to known stress granule transcripts.**

STRESS GRANULE		Discovery HG19	Discovery HG38	Validation HG38	MATCH STRESS
ANKHD1		ANKRD54		ANKRD54	c
CORO1B		CORO6		CORO1C	c
DDX31		DDX39A		DDX39B	c
DDX47		DDX42		DDX46	c
DDX50		DDX51		DDX51	c
DDX58		DDX51		DDX54	c
DIS3L2			DIS3	DIS3L	e
DPYSL2			DPYSL2	DPYSL2	e
DST		DST		DST	e
DTX3L			DTX1	DTX3	e
EDC3			EDC3	EDC3	e
HSF4		HSF4		HSF4	e
HSPD1		HSPB3	HSPE1	HSPD1	e
ITGB1		ITGB1		ITGB1	e
LMNA		LMNA		LMNA	e
MTHFD1			MTHFD1	MTHFD1	e
OGFOD1		OGFOD2	OGFOD2	OGFOD2	e
OSBPL9			OSBPL10	OSBPL10	c
PCBP2, PCBP1			PCBP1-AS1	PCBP3	c
POLR2B		POLR3GL	POLR2D	POLR2E	c
PPP1R8		PPP1R10	PPP1R13B	PPP1R2	c
PRRC2B		PRRC2B		PRRC2B	e
PSMD2			PSMD6	PSMD3	c
SATB1			SATB2	SATB1	e
TRIM21		TRIM28	TRIM47	TRIM24	c
USP11			USP11	USP11	e

Supplementary Table 9. Cilia and/or synapse/immune synapse related transcripts

UCSC ID	p ([CAD] Vs [Regulation (  FC (abs) ([CA FC ([CAD] Vs Log FC ([CAD [CAD](raw) [LOW](raw) start of trans Description	chr	SeqLL	SeqLL	SeqLL								
			TRACIT3	TRACIT1	TRACIT1								
			INOVA	GWU	GWU								
			HG38	HG38	HG19								
			SeqLL	SeqLL	Seqll								
			Gene Name	CathDx	CathDx								
uc061hhh.1	0.00466694 up	3.1491892	3.1491892	1.6549804	0.08496023	0.02697844	26308175	Adhesion G Protein-Coupled Receptor F3. (from chr2	ADGRF3	c		ADGRG3	
uc057shp.1	0.00793906 down	1.3702843	-1.3702843	-0.4544753	0.50020045	0.6854169	24629013	Rho GTPase activating protein 21 (from HGNC chr10	ARHGAP21	a			ARHGAP22
uc059uld.1	0.00893112 down	1.2283325	-1.2283325	-0.2967012	2.237617	2.7485378	56484344	Bardet-Biedl syndrome 2 (from HGNC BBS2) chr16	BBS2	a			BBS2
uc058zuz.1	0.00311815 down	3.6590462	-3.6590462	-1.8714676	0.00556233	0.02035282	24071588	copine VI (neuronal) (from HGNC CPNE6) chr14	CPNE6	a			CPNE3
uc062lxl.1	0.00727313 down	3.096001	-3.096001	-1.6304059	0.01418335	0.04391168	98807910	discoidin, CUB and LCCL domain containing 2 (chr3	DCBLD2	c		DCBLD1	
uc064ljz.1	0.00664018 down	1.44623	-1.44623	-0.5322971	1.3436074	1.9431655	26627214	dihydropyrimidinase-like 2 (from HGNC DPYSL chr8	DPYSL2	a	DPYSL2		DPYSL3
uc063pfd.1	0.00451893 down	5.760368	-5.760368	-2.526161	0.03775852	0.21750295	56617199	Dystonin. (from UniProt HOYAT7) chr6	DST	o	DST	*	
uc003wxt.4	0.00769938 down	2.4843318	-2.4843318	-1.3128579	0.05885801	0.14622281	17643803	microtubule associated tumor suppressor 1 (chr8	MTUS1	a			MTUS2
uc059zfb.1	0.00387835 down	5.238711	-5.238711	-2.389212	0.0739109	0.38719785	1468222	myosin IC (from HGNC MYO1C) chr17	MYO1C	e	MYO6	MYO1E	MYO1D
uc004bve.4	0.0090192 down	1.2714772	-1.2714772	-0.3465056	0.6369028	0.8098074	128456918	outer dense fiber of sperm tails 2 (ODF2). trar chr9	ODF2	e		ODF2L	ODF2
uc064wqo.1	0.001422 down	1.3874075	-1.3874075	-0.4723916	4.342514	6.0248365	131473593	Proline Rich Coiled-Coil 2B. (from UniProt Q5J) chr9	PRRC2B	a	PRRC2B		PRRC2B
uc001bse.3	0.00488237 down	3.3408244	-3.3408244	-1.7402041	0.07455237	0.24906638	30873134	Syndecan 3 (SDC3). mRNA. (from RefSeq NM_ chr1	SDC3	o			

**Supplementary Table 10.****The expression of CardioDx transcripts in the Discovery Cohort quantified by RNAseq.**

GeneName	Gene expression in log2 RPKM		Symbol	Description	RefSeq
	[LOW]	[MID+]			
uc010ugx.2	4.17	4.14	AQP9	aquaporin 9	NM_020980
uc010rva.2	0.01	0.24	CASP5	caspase 5, apoptosis-related cysteine peptidase	NM_004347
uc001pss.2	4.23	3.93	CD3D	CD3d molecule, delta	NM_000732
uc001quo.2	3.19	3.15	CLEC4E	C-type lectin domain family 4, member E	NM_014358
uc061sid.1	2.39	2.70	CXCR2	chemokine (C-X-C motif) receptor 2	NM_001168298
uc002tbx.4	2.13	2.11	IL18RAP	interleukin 18 receptor accessory protein	NM_003853
uc001ovc.4	3.89	4.00	KCNE3	potassium channel, voltage gated subfamily E regulatory beta subunit 3	NM_005472
uc001qye.4	2.12	2.06	KLRC4	killer cell lectin-like receptor subfamily C, member 4	NM_013431
uc003apy.5	2.91	3.03	NCF4	neutrophil cytosolic factor 4, 40kDa	NM_000631
uc002qkv.4	1.08	0.96	RPL28	ribosomal protein L28	NM_000991
uc001fbr.2	5.56	5.86	S100A12	S100 calcium binding protein A12	NM_005621
uc001fbs.3	8.68	8.78	S100A8	S100 calcium binding protein A8	NM_002964
uc001fwq.5	0.06	0.22	SLAMF7	SLAM family member 7	NM_021181
uc004bjz.5	4.04	3.98	TLR4	toll-like receptor 4	NM_138554
uc002jup.3	2.86	2.74	TMC8	transmembrane channel-like 8	NM_152468
uc002txk.3	2.69	2.88	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	NM_007115
uc003xyc.4	5.34	5.45	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy	NM_003841
<b>Mean</b>	<b>3.26</b>	<b>3.31</b>			
<b>t test p value</b>	<b>0.94</b>				