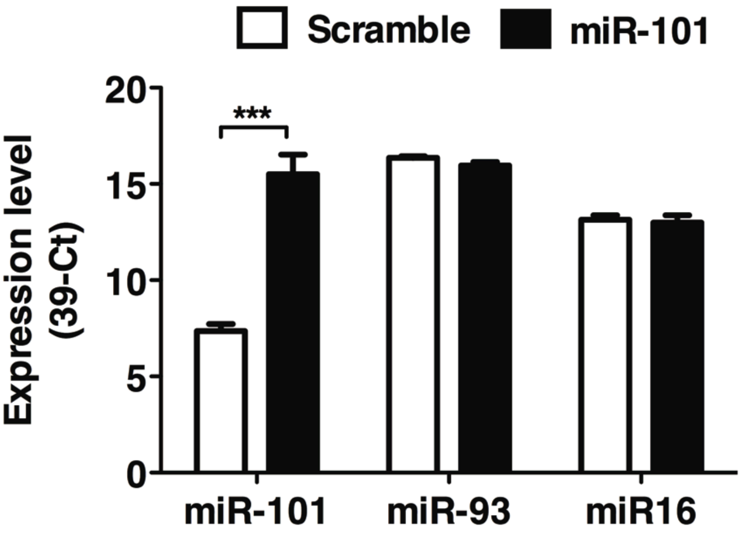
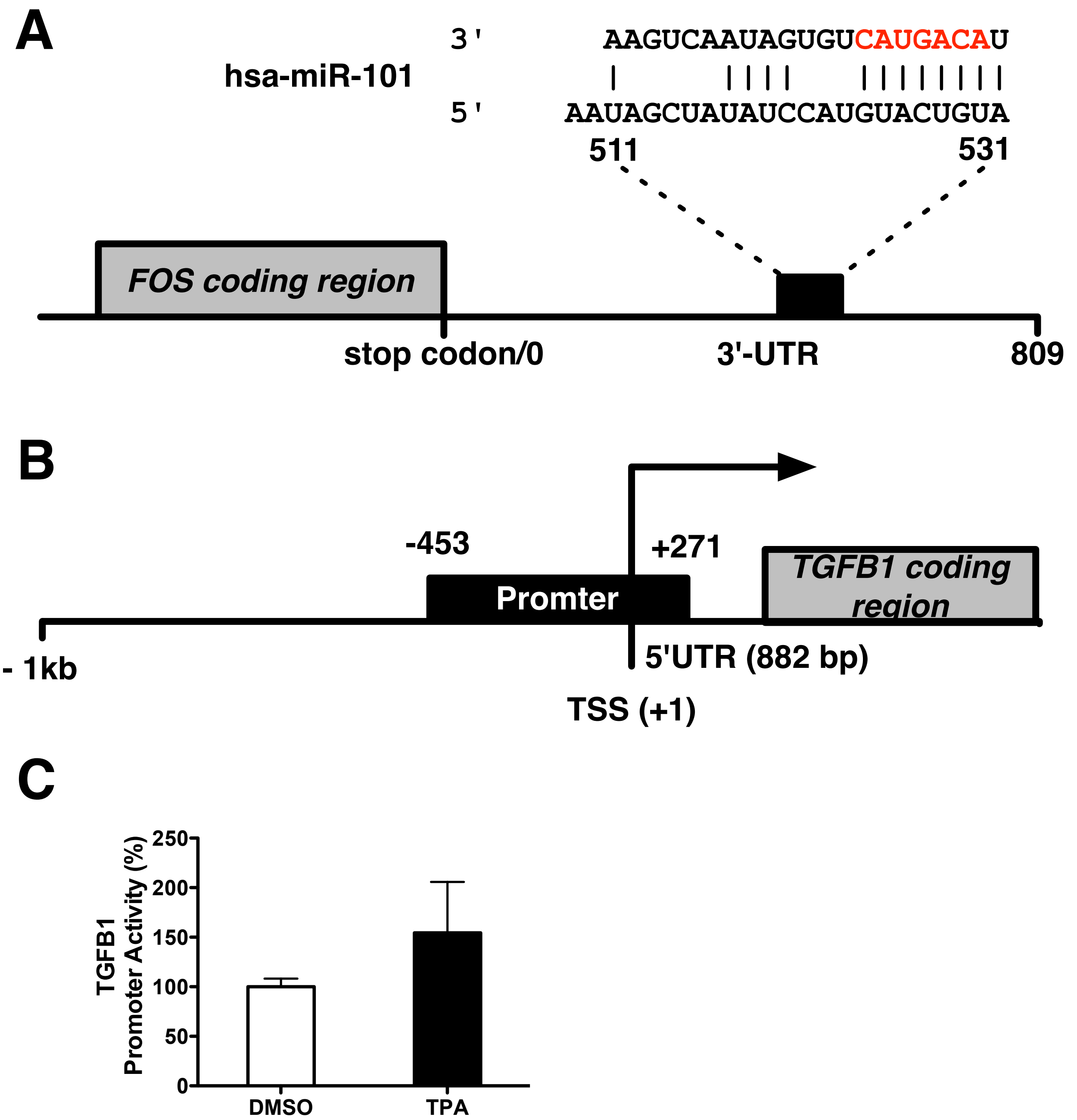
Supplementary figure S1. The expression level of miR-101 determined using a stem-loop qRT-PCR assay in miR-101 over-expressing HepG2 cells. MiRNA expression levels were expressed as 39 – Ct. miR-16 and miR-93 were used as internal control miRNAs. The results are mean ± s.d. of two independent experiments. (*** P-value < 0.001)



Supplementary Figure S2. Genome structure of cloned FOS 3'-UTR region and TGFB1 promoter region. (A) Gray and black boxes indicate the gene body of FOS and hsa-miR-101 putative binding site, respectively. Full length (810 bp) of FOS 3'-UTR was cloned. The nucleotide highlighted with red color indicates the seed region of hsa-miR-101. (B) Black and gray boxes respectively indicate the promoter region and gene body of TGFB1. Upstream 1,000 bp from TSS (transcriptional start site) the full length of 5'UTR (882 bp) of TGFB1 gene was cloned. (C) The TGFB1 promoter c can be activated (1.54-fold changes) by TPA treatment in HepG2 cells.



Supplementary figure S3. Effects of miR-101 on colony-forming activity of cultured HepG2 cells. HepG2 cells were transfected with 15 nM of scrambled oligonucleotides or miR-101 mimetic and seeded onto 6-well plate at 2000 cells/well for 14 days. The cultures were fixed and stained with crystal violet.

Supplementary Table S1 - Gene-specific PCR primers

Gene symbol	Forward Sequence	Reverse Sequence
EEF1A1	CAATGTGGGCTTCAATGTCAA	CATAGCCGGCGCTTATTTG
FOS	CCCTGCCTCTCCTCAAT	GACCCAGATAGGTCCATGT
EGR1	TGCTGGTGGAGACCAGTTA	CCACTGACCAAGCTGAAGA
SP1	GAAGATATGGCACTTCTCCAAC	CCTCTTAGAAGAGGTCTGGTA
CEBPD	GCAACGACCCATACCTCA	TGGTAAGTCCAGGCTGTAG
RELA	AGTGTGTGAAGAAGCGG	ACAGCATTCAGGTCGTAG
STAT3	ACCTATAGCTACATACTCCTGG	AATACAGAAAGGCTATGCTGAT
EZH2	CTTGTGGACCACAGTGTTAC	TGGGCCTGCTACTGTTATT
SUZ12	AGTTAAACCTACTCAAACTATTGCT	GTTGCCTTGTATTGTTGTTATAGAGA
NFYA	TTGAAGAAGAGCCTCTCTACG	CCGAGACTCATGCAGGT
CCND1	TATAACAAGTGTGTCTTACGTGC	CTTCATTGAGATTTGGAGTCTCTTT
CCNE1	CAAATCTTTATACAGATTGCAGAGC	CTTGACACAGTTCTCTATGTCG
CDK4	ACTGGCCTCGAGATGTA	AAAGGCAGAGATTCGCT
CDKN1B	GCTTACTCTGTCCATTTATCCAC	CACAGGTACACTTCAAATGGT
CDKN2A	CTCGGGAAACTTAGATCATCAG	TAAATGGACATTTACGGTAGTGGG
CDKN2B	TGGATCCCACAGTACTATATTACAC	ACAGTATATATTAGGCTGCTGATGA
MCM2	GTGCCCTCTGTGCTTTA	AAACAGTCATGCCAGGT
MCM3	GGAGGGCATTGTCACTAAA	AGATCAGAATAACGTCGCT
MCM4	AGGAACTTTCCAGGAAACC	AATCCTTCCTTGTCCCG
MCM5	CAAGTGTCCACGTTGGAT	TGGGAGCCAATGGCAAA
MCM6	TGTGAAAGAATGGGAGAAAGTG	AAAGAGCATCAGCAGGAC
MCM6	GTGAAAGAATGGGAGAAAGTG	CTTCATCATTGCCATGTATAGTAGG
MCM7	CTCTTTGCTGATGCCGT	TGCTCCATCATTAGCCGA
MDM2	CAACCAATTCAAATGATTGTGCT	GAAGAAATCTATGTGAATTGAGGC

Supplementary table S2. miRNA differentially expressed in normal and HCC samples

microRNA Name	miRNA levels (39-Ct)		Fold-Change (T vs. N)	Paired T-test p-value	Inversely altered
	Normal	Tumor			
miRNA up-modulated in HCC					
miR-10b	5.21 ± 0.73	7.20 ± 1.53	3.98	5.57E-05	Y
miR-18a	6.27 ± 0.80	8.20 ± 1.56	3.82	2.79E-04	N
miR-182	4.49 ± 0.45	6.37 ± 1.76	3.66	6.86E-05	N
miR-221	10.49 ± 0.61	12.26 ± 1.18	3.40	4.86E-06	N
miR-224	6.38 ± 1.21	7.91 ± 1.94	2.88	1.12E-02	N
miR-222	9.45 ± 0.78	10.88 ± 0.88	2.70	1.42E-06	N
miR-15b*	5.59 ± 0.47	7.03 ± 0.83	2.70	2.82E-06	N
miR-93	13.92 ± 0.68	15.32 ± 1.11	2.64	4.48E-06	N
miR-324-5p	9.19 ± 0.29	10.37 ± 0.95	2.27	1.81E-05	N
miR-491-5p	7.56 ± 1.20	8.73 ± 1.44	2.24	1.31E-03	N
miR-135a	5.46 ± 1.38	6.59 ± 1.60	2.19	2.47E-02	N
miR-128b	8.13 ± 0.83	9.17 ± 1.00	2.05	3.83E-05	N
miRNA down-modulated in HCC					
miR-199a-3p	10.83 ± 1.22	7.63 ± 2.29	-9.16	9.02E-06	Y
miR-199a-5p	11.25 ± 0.97	8.31 ± 2.15	-7.71	6.48E-06	N
miR-122	20.79 ± 0.72	18.33 ± 2.93	-5.49	1.10E-03	N
miR-139-5p	12.73 ± 0.47	10.32 ± 1.27	-5.35	1.54E-07	Y
miR-125b	15.54 ± 0.49	13.34 ± 2.26	-4.60	1.50E-04	N
miR-99a	11.30 ± 0.60	9.14 ± 2.16	-4.47	2.12E-04	N
miR-100	12.47 ± 0.83	10.39 ± 2.90	-4.22	5.94E-03	Y
miR-451	11.26 ± 0.84	9.52 ± 1.23	-3.35	1.38E-05	N
miR-378	12.64 ± 0.87	10.94 ± 0.95	-3.25	5.19E-07	N
miR-150	13.63 ± 1.31	11.97 ± 2.21	-3.17	5.01E-03	N
miR-195	9.93 ± 0.53	8.32 ± 1.78	-3.04	1.05E-03	N
miR-10a	8.45 ± 0.71	6.99 ± 1.57	-2.74	1.54E-03	N
miR-486-5p	12.56 ± 0.72	11.11 ± 1.41	-2.74	4.75E-04	N
miR-130a	9.45 ± 1.06	8.10 ± 1.70	-2.54	2.97E-03	N
miR-30a*	9.37 ± 0.35	8.03 ± 1.47	-2.52	4.51E-04	N
miR-29c	9.10 ± 0.64	7.92 ± 1.76	-2.27	3.48E-03	N
miR-215	7.84 ± 0.51	6.66 ± 1.55	-2.27	1.32E-03	N
let-7b	12.88 ± 1.24	11.74 ± 1.75	-2.21	5.47E-03	N
miR-192	14.06 ± 0.65	12.92 ± 1.60	-2.21	7.34E-03	N
miR-223	13.53 ± 0.88	12.41 ± 1.78	-2.18	1.55E-02	N
miR-497	9.93 ± 0.57	8.81 ± 1.10	-2.17	3.82E-05	N
miR-101	6.07 ± 0.84	4.98 ± 0.90	-2.13	1.48E-05	Y
miR-194	14.35 ± 0.64	13.29 ± 1.54	-2.09	8.67E-03	N
miR-22	12.45 ± 1.53	11.41 ± 1.92	-2.06	7.08E-03	Y
miR-548c-5p	5.41 ± 1.10	4.38 ± 0.79	-2.05	2.21E-03	N
miR-450a	8.43 ± 0.47	7.42 ± 0.69	-2.01	2.64E-06	N

Supplementary table S3. miRNA altered by TPA treatment in HepG2 cells

miR Name	miRNA level (39-Ct)		Fold change	Inversely
	DMSO	TPA	TPA / DMSO	altered
miRNA down-modulated by TPA				
miR-486-3p	7.06	3.88	-9.06	N
miR-143	7.28	4.87	-5.33	N
miR-326	10.15	7.91	-4.72	N
miR-455-3p	14.91	12.68	-4.68	N
miR-483-3p	15.33	13.28	-4.16	N
miR-200c*	6.64	4.60	-4.10	N
miR-10b	11.10	9.13	-3.92	Y
miR-674	5.76	3.88	-3.68	N
miR-202	6.31	4.58	-3.32	N
miRNA up-modulated by TPA				
miR-29b	4.67	8.75	16.95	N
miR-100	3.90	7.74	14.36	Y
miR-29a	8.74	12.19	10.91	N
miR-27a	7.28	10.26	7.89	N
miR-29b-1*	6.71	9.53	7.09	N
miR-23a	9.81	12.58	6.84	N
miR-139-5p	6.72	9.25	5.79	Y
miR-199a-3p	4.65	7.02	5.17	Y
miR-24	17.02	19.18	4.47	N
miR-33b	3.90	5.72	3.54	N
miR-31	9.59	11.42	3.54	N
miR-101	5.54	7.28	3.35	Y
miR-221	13.17	14.83	3.17	N
miR-196a*	3.90	5.56	3.16	N
miR-22	6.50	8.09	3.00	Y

Supplementary table S4. Differentially expressed genes in HCC tissues

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
202874_s_at	ATP6V1C1	3.90E-05	2.40
214054_at	DOK2	5.35E-05	-2.71
219146_at	C17orf42	1.02E-04	2.25
207804_s_at	FCN2	1.46E-04	-32.07
226276_at	TMEM167A	1.54E-04	2.26
207654_x_at	DR1	1.70E-04	2.05
209365_s_at	ECM1	2.05E-04	-6.78
216032_s_at	ERGIC3	2.05E-04	2.26
209774_x_at	CXCL2	2.15E-04	-14.92
226980_at	DEPDC1B	2.47E-04	61.36
218918_at	MAN1C1	2.73E-04	-4.97
202579_x_at	HMGN4	2.74E-04	2.56
200977_s_at	TAX1BP1	3.48E-04	2.47
204224_s_at	GCH1	3.63E-04	-7.34
203077_s_at	SMAD2	4.36E-04	3.50
203434_s_at	MME	4.52E-04	-21.57
208270_s_at	RNPEP	4.81E-04	2.19
219330_at	VANGL1	4.96E-04	2.06
213301_x_at	TRIM24	4.98E-04	3.63
217820_s_at	ENAH	5.22E-04	5.54
209165_at	AATF	5.46E-04	2.14
201329_s_at	ETS2	5.48E-04	-3.19
210428_s_at	HGS	5.53E-04	3.94
229349_at	LIN28B	5.62E-04	114.04
223280_x_at	MS4A6A	5.67E-04	-5.77
235783_at	MRTO4	6.33E-04	2.71
213427_at	RPP40	6.71E-04	3.71
222492_at	PDXK	7.35E-04	2.01
221139_s_at	CSAD	7.47E-04	-2.48
201859_at	SRGN	7.51E-04	-2.68
227740_at	UHMK1	7.51E-04	2.13
213670_x_at	NSUN5B	7.52E-04	2.24
238686_at	FBXO3	7.53E-04	2.16
238456_at	LOC100289230	7.61E-04	3.99
217122_s_at	RP11-345P4.4	7.91E-04	2.06
208743_s_at	YWHAB	8.09E-04	2.23
200055_at	TAF10	8.30E-04	2.02
203652_at	MAP3K11	8.44E-04	2.30
205382_s_at	CFD	8.56E-04	-4.20
201405_s_at	COPS6	8.64E-04	2.09
231882_at	FLJ39632	8.70E-04	7.88
217885_at	IPO9	8.82E-04	2.49
218533_s_at	UCKL1	8.84E-04	2.42
212949_at	NCAPH	8.89E-04	15.83
201755_at	MCM5	9.01E-04	4.02
224448_s_at	C6orf125	9.25E-04	2.46
216623_x_at	TOX3	9.54E-04	2.23
1559946_s_at	RUVBL2	9.55E-04	2.22
227796_at	ZFP62	1.03E-03	3.62
212067_s_at	C1R	1.07E-03	-3.97
204547_at	RAB40B	1.09E-03	4.48
205730_s_at	ABLIM3	1.10E-03	-2.06
211052_s_at	TBCD	1.11E-03	2.42
219931_s_at	KLHL12	1.12E-03	2.43
218662_s_at	NCAPG	1.14E-03	24.15
222843_at	FIGNL1	1.14E-03	4.65
226522_at	PODN	1.14E-03	-4.47
211663_x_at	PTGDS	1.16E-03	-3.60
234915_s_at	DENR	1.16E-03	2.36
225808_at	C17orf95	1.18E-03	2.96
225169_at	INTS4	1.21E-03	2.06
225788_at	C6orf153	1.24E-03	3.01
224160_s_at	ACAD9	1.29E-03	2.24
224356_x_at	MS4A6A	1.29E-03	-5.47
206374_at	DUSP8	1.32E-03	3.97
230478_at	OIT3	1.41E-03	-41.84
232893_at	LMBRD2	1.42E-03	2.09
205091_x_at	RECQL	1.49E-03	2.27
1559000_at	C10orf108	1.50E-03	-5.95
209421_at	MSH2	1.50E-03	5.38

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
212474_at	AVL9	1.50E-03	2.52
1555390_at	C14orf21	1.53E-03	2.26
201378_s_at	UBAP2L	1.53E-03	2.48
212899_at	CDC2L6	1.53E-03	2.13
212681_at	EPB41L3	1.57E-03	-2.78
213222_at	PLCB1	1.60E-03	4.62
201555_at	MCM3	1.61E-03	4.45
233013_x_at	LOC220906	1.71E-03	2.83
203819_s_at	IGF2BP3	1.74E-03	24.57
204569_at	ICK	1.74E-03	3.12
217770_at	PIGT	1.74E-03	2.57
200658_s_at	PHB	1.75E-03	2.53
218966_at	MYO5C	1.75E-03	2.63
223649_s_at	SLC25A39	1.76E-03	2.83
218682_s_at	SLC4A1AP	1.80E-03	2.18
201491_at	AHSA1	1.82E-03	3.85
202107_s_at	MCM2	1.86E-03	17.21
204428_s_at	LCAT	1.90E-03	-23.45
1552278_a_at	SLC46A1	1.91E-03	2.36
220266_s_at	KLF4	1.92E-03	-3.71
206429_at	F2RL1	1.96E-03	-2.80
218709_s_at	IFT52	2.00E-03	2.05
230250_at	PTPRB	2.04E-03	-2.27
221452_s_at	TMEM14B	2.08E-03	2.20
226488_at	RCCD1	2.09E-03	2.34
223289_s_at	USP38	2.11E-03	-2.29
217232_x_at	HBB	2.16E-03	-12.99
221983_at	FAM134A	2.17E-03	2.39
201271_s_at	RALY	2.19E-03	2.96
208955_at	DUT	2.21E-03	2.47
205695_at	SDS	2.24E-03	-51.68
217299_s_at	NBN	2.24E-03	2.92
207108_s_at	NIPBL	2.27E-03	3.17
223051_at	SSU72	2.29E-03	3.20
1564521_x_at	PRMT5	2.32E-03	3.27
200020_at	TARDBP	2.41E-03	2.28
220357_s_at	SGK2	2.41E-03	2.94
217839_at	TFG	2.42E-03	2.53
202543_s_at	GMFB	2.47E-03	3.02
203666_at	CXCL12	2.53E-03	-15.50
218424_s_at	STEAP3	2.54E-03	-4.69
214612_x_at	MAGEA6	2.55E-03	150.29
242350_s_at	LOC100128098	2.55E-03	29.89
205440_s_at	NPY1R	2.56E-03	-10.65
224824_at	FAM36A	2.58E-03	2.18
227153_at	IMMP2L	2.60E-03	2.02
209596_at	MXRA5	2.61E-03	-3.42
224341_x_at	TLR4	2.66E-03	-3.71
239989_at	CNTLN	2.66E-03	-3.08
225802_at	TOP1MT	2.72E-03	2.82
203554_x_at	PTTG1	2.75E-03	9.25
227936_at	TMEM68	2.82E-03	2.41
229908_s_at	UNKL	2.83E-03	3.02
226558_at	LOC389834	2.84E-03	2.14
218134_s_at	RBM22	2.90E-03	2.20
208820_at	PTK2	2.91E-03	2.77
1559315_s_at	LOC144481	2.92E-03	-2.26
203943_at	KIF3B	2.94E-03	2.32
209278_s_at	TFPI2	2.96E-03	-15.08
49452_at	ACACB	2.97E-03	-2.85
217840_at	DDX41	2.98E-03	2.76
206344_at	PON1	3.00E-03	-3.04
210481_s_at	CLEC4M	3.03E-03	-115.40
219192_at	UBAP2	3.04E-03	4.52
202528_at	GALE	3.05E-03	2.63
38069_at	CLCN7	3.05E-03	2.11
221928_at	ACACB	3.13E-03	-2.47
204391_x_at	TRIM24	3.14E-03	3.81
221732_at	CANT1	3.14E-03	3.60
225044_at	NT5C3L	3.15E-03	2.19
213006_at	CEBPD	3.18E-03	-8.62

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
200950_at	ARPC1A	3.21E-03	2.16
204026_s_at	ZWINT	3.27E-03	8.43
224724_at	SULF2	3.28E-03	-4.90
204267_x_at	PKMYT1	3.31E-03	2.37
1558201_s_at	SLC4A1AP	3.36E-03	2.10
202953_at	C1QB	3.36E-03	-3.04
211813_x_at	DCN	3.36E-03	-22.79
221541_at	CRISPLD2	3.38E-03	-4.64
220525_s_at	AUP1	3.39E-03	2.53
217932_at	MRPS7	3.46E-03	2.18
206188_at	ZNF623	3.48E-03	5.01
209470_s_at	GPM6A	3.50E-03	-7.18
212212_s_at	INTS1	3.55E-03	2.81
213881_x_at	SUMO2	3.55E-03	2.25
201292_at	TOP2A	3.56E-03	17.48
201061_s_at	STOM	3.62E-03	-4.89
218782_s_at	ATAD2	3.64E-03	4.40
205053_at	PRIM1	3.66E-03	6.60
242915_at	ZNF682	3.69E-03	2.46
201601_x_at	IFITM1	3.74E-03	-5.22
201699_at	PSMC6	3.75E-03	2.07
210915_x_at	TRBC1	3.78E-03	-2.78
201629_s_at	ACP1	3.79E-03	2.14
210559_s_at	CDC2	3.83E-03	11.98
209116_x_at	HBB	3.85E-03	-16.52
213524_s_at	G0S2	3.85E-03	-6.40
231540_at	hCG_1817306	3.86E-03	2.14
225210_s_at	FAM103A1	3.90E-03	2.87
209448_at	HTATIP2	3.91E-03	3.68
204019_s_at	SH3YL1	3.92E-03	-5.90
235576_at	WDR27	3.92E-03	2.71
219979_s_at	C11orf73	3.98E-03	2.50
210097_s_at	NOL7	3.99E-03	2.62
226732_at	RBM33	4.01E-03	2.11
218700_s_at	RAB7L1	4.05E-03	2.23
224308_s_at	INTS2	4.05E-03	3.43
227141_at	TYW3	4.05E-03	2.43
214163_at	HSPB11	4.07E-03	3.55
1559065_a_at	CLEC4G	4.09E-03	-143.33
222484_s_at	CXCL14	4.09E-03	-137.78
218365_s_at	DARS2	4.10E-03	2.50
203213_at	CDC2	4.11E-03	17.44
203732_at	TRIP4	4.17E-03	2.28
201342_at	SNRPC	4.20E-03	3.32
223819_x_at	COMMD5	4.24E-03	2.33
212778_at	PACS2	4.28E-03	2.18
205872_x_at	PDE4DIP	4.30E-03	-4.49
213193_x_at	TRBC1	4.31E-03	-2.39
214774_x_at	TOX3	4.32E-03	2.67
220604_x_at	FTCD	4.40E-03	-4.03
210387_at	HIST1H2BG	4.41E-03	5.33
214198_s_at	DGCR2	4.42E-03	3.01
57532_at	DVL2	4.42E-03	2.49
212141_at	MCM4	4.45E-03	7.17
217832_at	SYNCRIP	4.51E-03	2.22
227350_at	HELLS	4.55E-03	9.65
235590_at	FAM178A	4.59E-03	2.19
215078_at	SOD2	4.61E-03	-9.87
213349_at	TMCC1	4.63E-03	3.63
223077_at	TMOD3	4.63E-03	2.20
226218_at	IL7R	4.64E-03	-3.07
205866_at	FCN3	4.66E-03	-28.19
226287_at	CCDC34	4.66E-03	5.42
219119_at	LSM8	4.71E-03	2.12
204141_at	TUBB2A	4.81E-03	3.46
207396_s_at	ALG3	4.81E-03	2.22
227265_at	FGL2	4.83E-03	-2.28
213330_s_at	STIP1	4.87E-03	4.28
210213_s_at	EIF6	4.94E-03	2.65
238021_s_at	CRNDE	5.02E-03	20.89
201303_at	EIF4A3	5.09E-03	2.13

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
209773_s_at	RRM2	5.15E-03	14.88
37254_at	ZNF133	5.17E-03	2.15
204349_at	MED7	5.24E-03	2.66
201763_s_at	DAXX	5.26E-03	2.05
213025_at	THUMPD1	5.30E-03	2.06
223333_s_at	ANGPTL4	5.32E-03	-2.96
209219_at	RDBP	5.37E-03	6.17
216241_s_at	TCEA1	5.39E-03	2.14
212351_at	EIF2B5	5.41E-03	2.05
222687_s_at	ACER3	5.41E-03	2.17
200007_at	SRP14	5.43E-03	2.01
201459_at	RUVBL2	5.43E-03	3.06
218367_x_at	USP21	5.44E-03	2.77
208813_at	GOT1	5.45E-03	-6.70
217704_x_at	SUZ12P	5.45E-03	2.79
226033_at	USP31	5.47E-03	2.63
1552634_a_at	ZNF101	5.51E-03	2.94
1554830_a_at	STEAP3	5.51E-03	-4.30
202321_at	GGPS1	5.51E-03	2.86
231769_at	FBXO6	5.55E-03	4.46
205107_s_at	EFNA4	5.58E-03	5.05
215691_x_at	HSPB11	5.59E-03	2.69
206513_at	AIM2	5.62E-03	-7.10
220044_x_at	LUC7L3	5.63E-03	2.11
1555175_a_at	PBLD	5.64E-03	-5.76
209821_at	IL33	5.66E-03	-4.74
218962_s_at	TMEM168	5.67E-03	3.22
222037_at	MCM4	5.70E-03	4.08
228393_s_at	ZNF302	5.73E-03	2.32
227084_at	DTNA	5.74E-03	10.38
223784_at	TMEM27	5.79E-03	-16.38
214505_s_at	FHL1	5.80E-03	-2.90
231265_at	COX7B2	5.81E-03	43.53
222251_s_at	GMEB2	5.87E-03	2.58
209935_at	ATP2C1	5.94E-03	2.22
202238_s_at	NNMT	5.96E-03	-66.99
44120_at	ADCK2	5.98E-03	2.44
203714_s_at	TBCE	6.00E-03	3.03
207405_s_at	RAD17	6.01E-03	2.71
201739_at	SGK1	6.04E-03	-5.13
207995_s_at	CLEC4M	6.04E-03	-38.25
231698_at	FLJ36848	6.08E-03	-2.92
223421_at	CYHR1	6.09E-03	2.12
224742_at	ABHD12	6.13E-03	2.50
204787_at	VSIG4	6.15E-03	-9.75
214097_at	RPS21	6.15E-03	3.12
38918_at	SOX13	6.17E-03	2.09
226166_x_at	STK36	6.18E-03	2.62
202095_s_at	BIRC5	6.20E-03	33.56
218185_s_at	ARMC1	6.24E-03	2.45
206632_s_at	APOBEC3B	6.26E-03	21.84
230318_at	SERPINA1	6.28E-03	-6.52
203098_at	CDYL	6.29E-03	3.10
228268_at	FMO2	6.34E-03	-2.57
242001_at	IDH1	6.37E-03	3.56
201893_x_at	DCN	6.39E-03	-14.14
204118_at	CD48	6.40E-03	-2.47
217806_s_at	POLDIP2	6.40E-03	2.10
228930_at	SCARNA15	6.40E-03	3.95
202988_s_at	RGS1	6.43E-03	-2.96
221558_s_at	LEF1	6.45E-03	4.65
213696_s_at	MED8	6.49E-03	2.34
200943_at	HMGN1	6.51E-03	2.49
203087_s_at	KIF2A	6.59E-03	2.47
212588_at	PTPRC	6.70E-03	-2.62
242541_at	ABCA9	6.70E-03	-3.47
220526_s_at	MRPL20	6.73E-03	2.02
224716_at	SLC35B2	6.74E-03	2.56
244293_at	UQCRB	6.82E-03	-2.87
212021_s_at	MKI67	6.85E-03	7.19
200664_s_at	DNAJB1	6.92E-03	-3.28

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
243296_at	NAMPT	6.92E-03	-8.59
220186_s_at	PCDH24	6.94E-03	-19.47
218984_at	PUS7	6.96E-03	3.88
212150_at	EFR3A	6.97E-03	2.09
217917_s_at	DYNLRB1	6.98E-03	2.67
203717_at	DPP4	7.00E-03	4.05
218135_at	ERGIC2	7.00E-03	2.78
221879_at	CALML4	7.02E-03	2.46
223276_at	MST150	7.02E-03	-2.43
205034_at	CCNE2	7.03E-03	7.05
209160_at	AKR1C3	7.06E-03	5.15
208370_s_at	RCAN1	7.07E-03	-5.89
202633_at	TOPBP1	7.11E-03	2.45
34406_at	PACS2	7.11E-03	2.37
206727_at	C9	7.14E-03	-38.13
213684_s_at	PDLIM5	7.23E-03	-2.60
213632_at	DHODH	7.24E-03	-5.68
205301_s_at	OGG1	7.27E-03	2.54
203075_at	SMAD2	7.29E-03	2.63
218480_at	AGBL5	7.30E-03	2.64
221772_s_at	PPP2R2D	7.30E-03	-2.34
228325_at	KIAA0146	7.34E-03	-8.37
216903_s_at	CBARA1	7.40E-03	-2.01
205263_at	BCL10	7.49E-03	2.27
223057_s_at	XPO5	7.50E-03	3.53
233936_s_at	GGNBP2	7.54E-03	2.02
204220_at	GMFG	7.56E-03	-2.07
218578_at	CDC73	7.58E-03	2.33
211767_at	GINS4	7.61E-03	9.63
204282_s_at	FARS2	7.65E-03	2.20
224723_x_at	LOC401397	7.65E-03	2.11
202949_s_at	FHL2	7.67E-03	-6.34
214022_s_at	IFITM1	7.67E-03	-5.01
203428_s_at	ASF1A	7.68E-03	3.20
209736_at	SOX13	7.68E-03	7.98
227647_at	KCNE3	7.68E-03	2.24
219014_at	PLAC8	7.69E-03	-15.03
209035_at	MDK	7.75E-03	7.68
224396_s_at	ASPN	7.76E-03	-2.41
232145_at	C2orf68	7.79E-03	2.20
211696_x_at	HBB	7.85E-03	-14.30
211896_s_at	DCN	7.86E-03	-17.02
223381_at	NUF2	7.87E-03	27.25
230006_s_at	SVIP	7.92E-03	2.53
208837_at	TMED3	7.94E-03	2.89
209071_s_at	RGS5	7.95E-03	6.82
216594_x_at	AKR1C1	8.03E-03	2.58
208697_s_at	EIF3E	8.05E-03	2.40
209655_s_at	TMEM47	8.05E-03	-3.30
205892_s_at	FABP1	8.11E-03	-2.63
218350_s_at	GMNN	8.11E-03	6.60
227679_at	HDAC11	8.11E-03	2.53
210466_s_at	SERBP1	8.13E-03	2.72
201983_s_at	EGFR	8.14E-03	-2.64
238791_at	ZNF100	8.20E-03	2.67
226302_at	ATP8B1	8.25E-03	4.63
214264_s_at	C14orf143	8.36E-03	3.77
201157_s_at	NMT1	8.41E-03	2.45
218061_at	MEA1	8.41E-03	3.91
209220_at	GPC3	8.44E-03	21.78
232449_at	BCO2	8.44E-03	-11.63
214180_at	MAN1C1	8.46E-03	-3.06
202154_x_at	TUBB3	8.48E-03	2.60
201531_at	ZFP36	8.49E-03	-7.48
225026_at	CHD6	8.52E-03	2.26
215773_x_at	PARP2	8.53E-03	2.60
48580_at	CXXC1	8.54E-03	2.21
203545_at	ALG8	8.55E-03	2.25
235670_at	STX11	8.55E-03	-2.31
230326_s_at	C11orf73	8.58E-03	2.02
220491_at	HAMP	8.61E-03	-51.25

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213095_x_at	AIF1	8.70E-03	-2.17
217834_s_at	SYNCRIP	8.72E-03	3.22
211773_s_at	ZKSCAN3	8.74E-03	2.61
213595_s_at	CDC42BPA	8.74E-03	3.47
217786_at	PRMT5	8.75E-03	2.17
1564520_s_at	PRMT5	8.83E-03	3.48
224169_at	NPFFR2	8.85E-03	40.05
1565681_s_at	DIP2C	8.88E-03	-2.94
217234_s_at	EZR	8.88E-03	-2.22
218415_at	VPS33B	8.90E-03	2.07
200027_at	NARS	9.01E-03	3.12
201327_s_at	CCT6A	9.02E-03	3.10
224452_s_at	C7orf70	9.03E-03	2.51
209927_s_at	C1orf77	9.15E-03	3.01
211992_at	WNK1	9.15E-03	3.12
218636_s_at	MAN1B1	9.19E-03	2.21
238004_at	PGBD2	9.20E-03	2.26
227654_at	FAM65C	9.23E-03	-9.56
241224_x_at	DSCR8	9.24E-03	61.65
218039_at	NUSAP1	9.26E-03	7.12
57539_at	ZGPAT	9.27E-03	-3.10
203593_at	CD2AP	9.29E-03	2.32
224747_at	UBE2Q2	9.33E-03	2.29
209960_at	HGF	9.34E-03	-7.62
213293_s_at	TRIM22	9.34E-03	-6.67
204912_at	IL10RA	9.37E-03	-2.96
207253_s_at	UBN1	9.39E-03	3.09
209627_s_at	OSBPL3	9.43E-03	6.17
203547_at	CD4	9.44E-03	-4.30
53071_s_at	C17orf101	9.44E-03	2.06
230550_at	MS4A6A	9.47E-03	-3.91
219666_at	MS4A6A	9.48E-03	-3.63
213351_s_at	TMCC1	9.49E-03	2.26
219870_at	ATF7IP2	9.49E-03	2.63
203726_s_at	LAMA3	9.56E-03	9.92
224748_at	DCAF7	9.58E-03	2.49
201890_at	RRM2	9.59E-03	20.25
229465_s_at	PTPRS	9.60E-03	-4.71
224972_at	ROMO1	9.61E-03	3.04
204752_x_at	PARP2	9.63E-03	2.81
209408_at	KIF2C	9.64E-03	8.68
200889_s_at	SSR1	9.66E-03	2.74
221488_s_at	CUTA	9.67E-03	2.11
232843_s_at	DOCK8	9.70E-03	-2.49
210253_at	HTATIP2	9.78E-03	3.58
219640_at	CLDN15	9.82E-03	5.41
225933_at	CCDC137	9.82E-03	5.20
1567214_a_at	PNN	9.86E-03	2.07
219777_at	GIMAP6	9.86E-03	-2.13
202187_s_at	PPP2R5A	9.88E-03	2.36
224815_at	COMMD7	9.90E-03	2.54
228088_at	SESTD1	9.91E-03	2.31
235542_at	TET3	9.91E-03	2.04
205017_s_at	MBNL2	9.93E-03	-2.67
214220_s_at	ALMS1	9.95E-03	3.95
208979_at	NCOA6	9.96E-03	2.49
233842_x_at	C20orf43	9.97E-03	2.12
225068_at	KLHL12	9.98E-03	2.50
223229_at	UBE2T	1.00E-02	13.00
212856_at	GRAMD4	1.01E-02	-2.94
214710_s_at	CCNB1	1.01E-02	13.97
216237_s_at	MCM5	1.01E-02	3.53
223502_s_at	TNFSF13B	1.01E-02	-2.47
227001_at	NIPAL2	1.01E-02	3.59
209276_s_at	GLRX	1.03E-02	-2.71
212568_s_at	DLAT	1.03E-02	3.84
226087_at	LZIC	1.03E-02	2.94
202591_s_at	SSBP1	1.04E-02	2.26
213988_s_at	SAT1	1.04E-02	-5.56
217815_at	SUPT16H	1.04E-02	2.26
222105_s_at	NKIRAS2	1.04E-02	3.17

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225929_s_at	RNF213	1.04E-02	2.60
203291_at	CNOT4	1.05E-02	2.75
214086_s_at	PARP2	1.05E-02	3.63
218137_s_at	SMAP1	1.05E-02	2.20
228488_at	TBC1D16	1.05E-02	3.03
201464_x_at	JUN	1.06E-02	-2.22
203095_at	MTIF2	1.06E-02	2.36
203888_at	THBD	1.06E-02	-3.63
215690_x_at	GPAA1	1.06E-02	3.40
217918_at	DYNLRB1	1.06E-02	2.72
223526_at	C18orf21	1.06E-02	2.83
232136_s_at	CTTNBP2	1.06E-02	-12.11
1560469_at	NR5A2	1.07E-02	-4.07
224217_s_at	FAF1	1.07E-02	2.66
226536_at	NSMCE2	1.07E-02	2.73
36865_at	ANGEL1	1.07E-02	2.19
1557754_at	LOC401068	1.08E-02	7.61
202326_at	EHMT2	1.08E-02	4.76
202715_at	CAD	1.08E-02	2.20
205357_s_at	AGTR1	1.09E-02	-3.58
209795_at	CD69	1.09E-02	-7.59
211610_at	KLF6	1.09E-02	-2.08
218710_at	TTC27	1.09E-02	2.43
202237_at	NNMT	1.10E-02	-32.92
224963_at	SLC26A2	1.10E-02	2.27
225083_at	GTF3C6	1.10E-02	2.10
225477_s_at	NR2C2	1.10E-02	2.21
204563_at	SELL	1.11E-02	-3.42
208926_at	NEU1	1.11E-02	2.67
209070_s_at	RGS5	1.11E-02	4.75
211714_x_at	TUBB	1.11E-02	2.49
212094_at	PEG10	1.11E-02	29.31
218543_s_at	PARP12	1.11E-02	2.96
1557080_s_at	ITGBL1	1.12E-02	-2.68
203068_at	KLHL21	1.12E-02	2.28
223163_s_at	ZC3HC1	1.12E-02	3.01
229937_x_at	LILRB1	1.12E-02	-2.14
238974_at	C2orf69	1.12E-02	2.05
202347_s_at	UBE2K	1.13E-02	2.67
202992_at	C7	1.13E-02	-13.27
209189_at	FOS	1.13E-02	-28.38
213049_at	GARNL1	1.13E-02	2.03
202487_s_at	H2AFV	1.14E-02	2.45
219935_at	ADAMTS5	1.14E-02	2.40
222906_at	FLVCR1	1.14E-02	2.35
223056_s_at	XPO5	1.15E-02	3.32
203310_at	STXBP3	1.16E-02	2.14
207687_at	INHBC	1.16E-02	-3.73
214642_x_at	MAGEA5	1.16E-02	27.23
1553296_at	GPR128	1.17E-02	-4.69
205220_at	NIACR2	1.18E-02	-2.51
218504_at	FAHD2A	1.18E-02	-2.19
224985_at	NRAS	1.18E-02	2.62
210720_s_at	NECAB3	1.19E-02	6.11
212857_x_at	SUB1	1.19E-02	2.80
223274_at	TCF19	1.19E-02	5.15
225297_at	HAUS1	1.19E-02	3.14
225851_at	FNTB	1.19E-02	2.31
202635_s_at	POLR2K	1.20E-02	3.37
212063_at	CD44	1.20E-02	-2.77
226792_s_at	KIFC2	1.20E-02	3.71
1557905_s_at	CD44	1.21E-02	-2.24
201539_s_at	FHL1	1.21E-02	-2.39
210054_at	HAUS3	1.21E-02	2.07
218983_at	C1RL	1.21E-02	-3.15
219610_at	RGNEF	1.21E-02	3.40
200744_s_at	GNB1	1.22E-02	2.46
226414_s_at	ANAPC11	1.22E-02	2.89
202705_at	CCNB2	1.23E-02	25.79
203960_s_at	HSPB11	1.23E-02	2.30
204142_at	ENOSF1	1.24E-02	4.63

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211060_x_at	GPAA1	1.24E-02	3.33
218541_s_at	C8orf4	1.24E-02	-9.67
238581_at	GBP5	1.24E-02	-3.44
243539_at	KIAA1841	1.24E-02	2.07
47608_at	TJAP1	1.24E-02	2.56
214960_at	API5	1.25E-02	2.11
225689_at	C3orf39	1.25E-02	2.66
227530_at	AKAP12	1.25E-02	-6.53
228596_at	LOC728377	1.25E-02	2.40
203519_s_at	UPF2	1.26E-02	2.30
208079_s_at	AURKA	1.26E-02	5.43
213194_at	ROBO1	1.26E-02	17.08
217919_s_at	MRPL42	1.26E-02	2.47
218683_at	PTBP2	1.26E-02	2.71
218858_at	DEPDC6	1.26E-02	3.44
231845_at	AARS2	1.26E-02	4.23
202232_s_at	EIF3M	1.27E-02	2.29
213068_at	DPT	1.27E-02	-6.10
212556_at	SCRIB	1.28E-02	4.26
225557_at	CSRNP1	1.28E-02	-3.90
226001_at	KLHL5	1.28E-02	2.40
215108_x_at	TOX3	1.29E-02	3.35
218405_at	ABT1	1.29E-02	2.22
223053_x_at	SSU72	1.29E-02	2.27
235158_at	TMEM209	1.29E-02	2.03
202295_s_at	CTSH	1.30E-02	2.29
217856_at	RBM8A	1.30E-02	-2.20
218991_at	HEATR6	1.30E-02	6.90
220801_s_at	HAO2	1.30E-02	-9.18
1568638_a_at	IDO2	1.31E-02	-15.94
203270_at	DTYMK	1.31E-02	3.02
209572_s_at	EED	1.31E-02	2.65
212659_s_at	IL1RN	1.31E-02	-2.42
226269_at	GDAP1	1.31E-02	4.21
238214_at	LRRC69	1.31E-02	4.56
202998_s_at	LOXL2	1.32E-02	2.32
204740_at	CNKSR1	1.32E-02	3.90
206350_at	APCS	1.32E-02	-15.63
224560_at	TIMP2	1.32E-02	-3.68
225102_at	MGLL	1.32E-02	-2.38
228648_at	LRG1	1.33E-02	-8.00
212687_at	LIMS1	1.34E-02	2.14
222162_s_at	ADAMTS1	1.34E-02	-4.34
210467_x_at	MAGEA12	1.35E-02	230.75
221970_s_at	NOL11	1.35E-02	2.33
243916_x_at	UBLCP1	1.35E-02	2.17
201644_at	TSTA3	1.36E-02	2.65
204306_s_at	CD151	1.37E-02	2.32
204587_at	SLC25A14	1.37E-02	2.20
206613_s_at	TAF1A	1.37E-02	3.56
207556_s_at	DGKZ	1.37E-02	2.17
209132_s_at	COMMD4	1.37E-02	2.83
224497_x_at	HSD17B14	1.37E-02	2.79
226813_at	C1orf57	1.37E-02	2.51
219402_s_at	DERL1	1.38E-02	2.57
234726_s_at	TMEM168	1.38E-02	2.03
220206_at	ZMYM1	1.39E-02	4.00
232224_at	MASP1	1.39E-02	-5.96
201323_at	EBNA1BP2	1.40E-02	2.36
205237_at	FCN1	1.40E-02	-3.01
222551_s_at	C8orf33	1.40E-02	2.54
223620_at	GPR34	1.41E-02	-2.01
201060_x_at	STOM	1.42E-02	-5.49
229353_s_at	NUCKS1	1.42E-02	2.79
1559577_at	FCN2	1.43E-02	-56.95
209614_at	ADH1B	1.43E-02	-19.91
218940_at	C14orf138	1.43E-02	2.08
222740_at	ATAD2	1.43E-02	4.33
230120_s_at	PLGLB2	1.43E-02	-9.51
203040_s_at	HMBS	1.44E-02	2.01
204962_s_at	CENPA	1.44E-02	19.33

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
210125_s_at	BANF1	1.44E-02	2.27
222218_s_at	PILRA	1.44E-02	-2.15
230032_at	OSGEPL1	1.44E-02	2.05
201068_s_at	PSMC2	1.45E-02	2.31
215088_s_at	SDHC	1.45E-02	2.20
218062_x_at	CDC42EP4	1.45E-02	2.80
222433_at	ENAH	1.45E-02	6.08
227657_at	RNF150	1.45E-02	-16.23
236313_at	CDKN2B	1.45E-02	4.48
1554459_s_at	CFHR3	1.46E-02	-29.45
218988_at	SLC35E3	1.46E-02	2.20
221268_s_at	SGPP1	1.46E-02	-2.79
223979_x_at	FTCD	1.46E-02	-3.68
224988_at	C6orf89	1.46E-02	2.34
235125_x_at	FAM73A	1.46E-02	2.34
1552621_at	POLR2J2	1.47E-02	2.17
242945_at	FAM20A	1.47E-02	-3.49
211742_s_at	EVI2B	1.48E-02	-2.79
1555759_a_at	CCL5	1.49E-02	-3.42
201282_at	OGDH	1.50E-02	2.32
203473_at	SLCO2B1	1.50E-02	-3.02
214100_x_at	NSUN5B	1.50E-02	3.01
218187_s_at	C8orf33	1.50E-02	3.45
202259_s_at	N4BP2L2	1.51E-02	-2.56
214435_x_at	RALA	1.51E-02	5.14
219343_at	CDC37L1	1.51E-02	-5.65
1554974_at	ACY3	1.52E-02	-2.14
226031_at	CCDC132	1.52E-02	2.44
204057_at	IRF8	1.53E-02	-3.68
213072_at	CYHR1	1.53E-02	2.23
213599_at	OIP5	1.53E-02	13.81
215506_s_at	DIRAS3	1.53E-02	-5.31
222713_s_at	FANCF	1.53E-02	2.16
227561_at	DDR2	1.53E-02	-2.04
204175_at	ZNF593	1.54E-02	2.24
213631_x_at	DHODH	1.54E-02	-4.16
214474_at	PRKAB2	1.54E-02	3.90
215617_at	SPATS2L	1.54E-02	-3.06
221797_at	C17orf90	1.54E-02	3.03
201291_s_at	TOP2A	1.55E-02	37.72
203076_s_at	SMAD2	1.55E-02	2.67
205063_at	SIP1	1.55E-02	2.47
217561_at	CALCA	1.55E-02	-6.47
219918_s_at	ASPM	1.55E-02	33.83
225114_at	AGPS	1.55E-02	2.25
203625_x_at	SKP2	1.56E-02	3.32
209820_s_at	TBL3	1.56E-02	2.05
227968_at	PDDC1	1.56E-02	2.16
201397_at	PHGDH	1.57E-02	-5.05
201930_at	MCM6	1.57E-02	3.92
202666_s_at	ACTL6A	1.57E-02	2.51
202870_s_at	CDC20	1.57E-02	66.37
206626_x_at	SSX1	1.57E-02	130.08
211150_s_at	DLAT	1.57E-02	3.83
223844_at	ADAMTS13	1.57E-02	-6.11
225931_s_at	RNF213	1.57E-02	3.29
227594_at	ZMYM6	1.57E-02	2.76
205943_at	TDO2	1.58E-02	-4.31
227055_at	METTL7B	1.58E-02	-2.34
229232_at	LRRC57	1.58E-02	3.15
36936_at	TSTA3	1.58E-02	3.06
46167_at	TTC4	1.58E-02	2.51
203015_s_at	SSX2IP	1.59E-02	3.25
213007_at	FANCI	1.59E-02	3.53
1554588_a_at	TTC30B	1.60E-02	2.89
202686_s_at	AXL	1.60E-02	-3.83
219819_s_at	MRPS28	1.60E-02	2.04
227370_at	FAM171B	1.60E-02	2.61
205119_s_at	FPR1	1.61E-02	-4.55
213043_s_at	MED24	1.61E-02	3.79
223699_at	CNDP1	1.61E-02	-125.52

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207165_at	HMMR	1.62E-02	56.87
209146_at	SC4MOL	1.62E-02	-2.19
229831_at	CNTN3	1.63E-02	-68.73
203061_s_at	MDC1	1.64E-02	2.17
204204_at	SLC31A2	1.64E-02	-2.30
209304_x_at	GADD45B	1.64E-02	-18.38
225521_at	ANAPC7	1.64E-02	2.05
226710_at	C8orf82	1.64E-02	2.69
1557049_at	LOC149478	1.65E-02	-5.42
204507_s_at	PPP3R1	1.65E-02	2.65
207501_s_at	FGF12	1.65E-02	21.57
218564_at	RFWD3	1.65E-02	2.02
203730_s_at	ZKSCAN5	1.66E-02	2.02
204768_s_at	FEN1	1.66E-02	2.97
204836_at	GLDC	1.66E-02	-2.88
215440_s_at	BEX4	1.66E-02	-2.06
215253_s_at	RCAN1	1.67E-02	-4.53
44111_at	VPS33B	1.67E-02	2.23
207325_x_at	MAGEA1	1.68E-02	68.40
225437_s_at	C7orf27	1.68E-02	2.40
218079_s_at	GGNBP2	1.69E-02	2.00
238447_at	RBMS3	1.69E-02	-2.48
226705_at	FGFR1	1.70E-02	-2.55
229144_at	RP1-21O18.1	1.70E-02	-2.03
204472_at	GEM	1.71E-02	-4.28
233604_at	FLJ22763	1.71E-02	-10.37
236181_at	LOC100132181	1.71E-02	2.18
213428_s_at	COL6A1	1.72E-02	-3.53
215232_at	RICH2	1.73E-02	4.06
223180_s_at	C18orf55	1.73E-02	2.18
232520_s_at	NSFL1C	1.73E-02	2.52
203415_at	PDCD6	1.74E-02	2.13
205502_at	CYP17A1	1.74E-02	12.13
222654_at	IMPAD1	1.74E-02	2.73
227567_at	LOC651250	1.74E-02	2.57
238122_at	RBM12B	1.74E-02	3.33
1555539_at	SDS	1.75E-02	-20.23
202231_at	EIF3M	1.75E-02	2.00
205984_at	CRHBP	1.75E-02	-72.73
207104_x_at	LILRB1	1.75E-02	-2.56
213149_at	DLAT	1.75E-02	3.11
227256_at	USP31	1.75E-02	2.66
203262_s_at	FAM50A	1.76E-02	2.88
207513_s_at	ZNF189	1.76E-02	3.04
207469_s_at	PIR	1.77E-02	4.18
209925_at	OCLN	1.77E-02	3.52
231838_at	PABPC1L	1.77E-02	2.55
213608_s_at	SRRD	1.78E-02	2.05
228135_at	C1orf52	1.78E-02	2.10
228713_s_at	HSD17B14	1.78E-02	3.25
207574_s_at	GADD45B	1.79E-02	-13.26
208808_s_at	HMGB2	1.79E-02	3.80
211737_x_at	PTN	1.79E-02	-3.16
222883_at	C1orf163	1.79E-02	3.32
225073_at	PPHLN1	1.79E-02	2.30
225705_at	CCDC45	1.79E-02	2.07
33736_at	STOML1	1.79E-02	3.06
223839_s_at	SCD	1.80E-02	2.41
203989_x_at	F2R	1.81E-02	-2.54
204524_at	PDPK1	1.81E-02	2.20
206688_s_at	CPSF4	1.81E-02	2.47
212058_at	SR140	1.81E-02	2.36
222291_at	FAM149A	1.81E-02	-4.08
1560916_a_at	DPY19L1	1.82E-02	2.12
202421_at	IGSF3	1.82E-02	8.02
203192_at	ABCB6	1.82E-02	3.35
209156_s_at	COL6A2	1.82E-02	-2.55
219020_at	HS1BP3	1.82E-02	2.33
203472_s_at	SLCO2B1	1.83E-02	-2.39
213105_s_at	C16orf42	1.83E-02	2.86
231307_at	LOC100130725	1.83E-02	19.81

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204121_at	GADD45G	1.84E-02	-3.53
210997_at	HGF	1.84E-02	-3.02
212449_s_at	LYPLA1	1.84E-02	2.18
223054_at	DNAJB11	1.84E-02	2.19
214715_x_at	ZNF160	1.85E-02	2.14
213577_at	SQLE	1.86E-02	2.08
225879_at	TSEN54	1.86E-02	2.86
212871_at	MAPKAPK5	1.87E-02	2.34
235405_at	GSTA4	1.87E-02	26.25
212852_s_at	TROVE2	1.88E-02	2.11
1554899_s_at	FCER1G	1.89E-02	-3.26
215380_s_at	GGCT	1.89E-02	2.42
228357_at	UNK	1.89E-02	2.77
208893_s_at	DUSP6	1.90E-02	-7.19
224447_s_at	C17orf37	1.90E-02	2.92
228941_at	ALG10B	1.90E-02	2.53
202276_at	SHFM1	1.91E-02	2.71
46323_at	CANT1	1.91E-02	3.38
1568765_at	SERPINE1	1.92E-02	-23.92
224479_s_at	MRPL45	1.92E-02	2.14
225903_at	PIGU	1.92E-02	2.70
201592_at	EIF3H	1.93E-02	2.94
204208_at	RNGTT	1.93E-02	2.93
223721_s_at	DNAJC12	1.93E-02	-89.96
210095_s_at	IGFBP3	1.94E-02	-8.37
218549_s_at	FAM82B	1.94E-02	2.51
209358_at	TAF11	1.95E-02	2.05
225056_at	SIPA1L2	1.95E-02	3.10
201471_s_at	SQSTM1	1.96E-02	3.58
203973_s_at	CEBPD	1.96E-02	-2.41
204127_at	RFC3	1.96E-02	3.20
213093_at	PRKCA	1.96E-02	2.25
223133_at	TMEM14B	1.96E-02	2.63
225600_at	C8orf83	1.96E-02	2.90
228095_at	PHF14	1.96E-02	3.14
235443_at	LOC100131067	1.96E-02	3.09
201325_s_at	EMP1	1.97E-02	-2.44
207027_at	HGFAC	1.97E-02	-24.49
208726_s_at	EIF2S2	1.97E-02	2.12
210497_x_at	SSX2	1.97E-02	136.78
219007_at	NUP43	1.97E-02	2.99
219681_s_at	RAB11FIP1	1.97E-02	5.43
221011_s_at	LBH	1.97E-02	-2.40
37278_at	TAZ	1.97E-02	2.53
204835_at	POLA1	1.98E-02	7.26
206324_s_at	DAPK2	1.98E-02	8.59
218795_at	ACP6	1.98E-02	2.21
219494_at	RAD54B	1.98E-02	6.86
220668_s_at	DNMT3B	1.98E-02	4.69
202672_s_at	ATF3	1.99E-02	-3.94
218797_s_at	SIRT7	1.99E-02	3.10
227722_at	RPS23	1.99E-02	-2.24
202882_x_at	NOL7	2.00E-02	2.47
204484_at	PIK3C2B	2.00E-02	3.16
221984_s_at	FAM134A	2.00E-02	3.09
224517_at	POLR2J4	2.00E-02	2.04
204972_at	OAS2	2.01E-02	-3.15
212265_at	QKI	2.02E-02	2.01
216930_at	HNF1A	2.02E-02	2.90
227099_s_at	LOC387763	2.02E-02	-4.38
203385_at	DGKA	2.03E-02	-2.37
205647_at	RAD52	2.03E-02	2.18
213842_x_at	NSUN5C	2.03E-02	2.67
218910_at	ANO10	2.03E-02	3.14
218917_s_at	ARID1A	2.03E-02	2.91
227937_at	MYPOP	2.03E-02	2.49
200054_at	ZNF259	2.04E-02	3.33
203931_s_at	MRPL12	2.04E-02	3.40
208688_x_at	EIF3B	2.04E-02	2.69
226319_s_at	THOC4	2.04E-02	2.75
227353_at	TMC8	2.04E-02	-2.97

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207855_s_at	CLCC1	2.05E-02	2.43
203837_at	MAP3K5	2.06E-02	-2.92
219428_s_at	PXMP4	2.06E-02	3.10
201349_at	SLC9A3R1	2.07E-02	2.29
203448_s_at	TERF1	2.07E-02	2.31
209912_s_at	KIAA0415	2.07E-02	3.03
221060_s_at	TLR4	2.07E-02	-3.59
205530_at	ETFDH	2.08E-02	-2.08
209942_x_at	MAGEA3	2.08E-02	88.28
223961_s_at	CISH	2.08E-02	-4.33
203462_x_at	EIF3B	2.09E-02	2.62
211971_s_at	LRPPRC	2.09E-02	2.24
212921_at	SMYD2	2.09E-02	3.29
223167_s_at	USP25	2.09E-02	-2.47
44673_at	SIGLEC1	2.09E-02	-2.48
205089_at	ZNF7	2.10E-02	2.13
205649_s_at	FGA	2.10E-02	-5.18
218228_s_at	TNKS2	2.10E-02	-2.99
203738_at	C5orf22	2.11E-02	2.32
209484_s_at	NSL1	2.11E-02	2.26
210233_at	IL1RAP	2.11E-02	-18.56
230238_at	ANKRD43	2.11E-02	5.44
1555964_at	ARL17P1	2.12E-02	5.46
201858_s_at	SRGN	2.12E-02	-5.16
220607_x_at	TH1L	2.12E-02	2.10
225955_at	METRNL	2.12E-02	-2.43
226670_s_at	PABPC1L	2.12E-02	2.32
201508_at	IGFBP4	2.13E-02	-2.13
207666_x_at	SSX3	2.13E-02	88.18
212327_at	LIMCH1	2.13E-02	-2.30
64486_at	CORO1B	2.13E-02	2.16
216471_x_at	SSX2	2.14E-02	107.52
231984_at	MTAP	2.14E-02	-2.06
201956_s_at	GNPAT	2.15E-02	3.56
208393_s_at	RAD50	2.15E-02	2.09
209577_at	PCYT2	2.15E-02	2.90
224061_at	INMT	2.15E-02	-13.39
201745_at	TWF1	2.16E-02	2.02
219873_at	COLEC11	2.16E-02	-3.34
223234_at	MAD2L2	2.16E-02	2.52
205819_at	MARCO	2.17E-02	-49.84
206618_at	IL18R1	2.17E-02	-3.27
214721_x_at	CDC42EP4	2.17E-02	3.28
219990_at	E2F8	2.17E-02	17.52
222550_at	ARMC1	2.17E-02	2.19
226778_at	C8orf42	2.17E-02	-2.93
231270_at	CA13	2.17E-02	-2.29
223363_at	PSMG3	2.18E-02	3.32
232068_s_at	TLR4	2.18E-02	-2.76
235119_at	TAF3	2.18E-02	2.77
203249_at	EZH1	2.19E-02	2.36
218788_s_at	SMYD3	2.19E-02	3.52
227255_at	PDIK1L	2.19E-02	2.24
201177_s_at	UBA2	2.20E-02	2.16
203211_s_at	MTMR2	2.20E-02	2.98
205851_at	NME6	2.20E-02	2.11
219362_at	MAK10	2.20E-02	2.68
219526_at	C14orf169	2.20E-02	2.06
201255_x_at	BAT3	2.21E-02	2.57
203894_at	TUBG2	2.21E-02	3.19
207981_s_at	ESRRG	2.21E-02	-30.08
208906_at	BSCL2	2.21E-02	2.45
209696_at	FBP1	2.21E-02	-6.75
218002_s_at	CXCL14	2.21E-02	-71.13
226939_at	CPEB2	2.21E-02	2.10
200703_at	DYNLL1	2.22E-02	2.03
205863_at	S100A12	2.22E-02	-4.33
209196_at	WDR46	2.22E-02	2.89
212828_at	SYNJ2	2.22E-02	2.15
204011_at	SPRY2	2.23E-02	-2.93
205395_s_at	MRE11A	2.23E-02	2.54

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208034_s_at	PROZ	2.23E-02	-5.56
209252_at	HARS2	2.23E-02	2.38
212637_s_at	WWP1	2.23E-02	2.44
223032_x_at	PRELID1	2.23E-02	2.73
244313_at	CR1	2.23E-02	-4.57
219862_s_at	NARF	2.24E-02	3.45
223062_s_at	PSAT1	2.24E-02	-4.56
235145_at	ZBTB7B	2.24E-02	2.31
1554082_a_at	NOL9	2.25E-02	3.41
200083_at	USP22	2.25E-02	2.58
207238_s_at	PTPRC	2.25E-02	-3.95
218482_at	ENY2	2.25E-02	2.57
224726_at	MIB1	2.25E-02	3.67
203658_at	SLC25A20	2.26E-02	-3.10
212657_s_at	IL1RN	2.26E-02	-4.20
215470_at	GTF2H2B	2.26E-02	2.47
218757_s_at	UPF3B	2.26E-02	2.51
223029_s_at	TRAF7	2.26E-02	2.39
228729_at	CCNB1	2.26E-02	14.45
233637_at	DCAF8	2.26E-02	2.27
202376_at	SERPINA3	2.27E-02	-4.88
202391_at	BASP1	2.27E-02	-4.09
205054_at	NEB	2.27E-02	10.42
209685_s_at	PRKCB	2.27E-02	-3.23
210293_s_at	SEC23B	2.27E-02	2.31
244132_x_at	ZNF518A	2.27E-02	3.69
50374_at	C17orf90	2.27E-02	3.47
212917_x_at	RECQL	2.28E-02	2.18
223173_at	SPNS1	2.28E-02	2.63
227012_at	SLC25A40	2.28E-02	2.43
228050_at	UTP15	2.28E-02	2.84
229560_at	TLR8	2.28E-02	-2.31
231691_at	C3P1	2.28E-02	-13.74
212645_x_at	BRE	2.29E-02	2.21
222958_s_at	DEPDC1	2.30E-02	11.34
226791_at	KIFC2	2.30E-02	3.56
228397_at	TUG1	2.30E-02	2.00
1552280_at	TIMD4	2.31E-02	-30.06
1553099_at	TIGD1	2.31E-02	2.45
201091_s_at	CBX3	2.31E-02	2.51
208805_at	PSMA6	2.31E-02	2.40
212155_at	RNF187	2.31E-02	3.74
218631_at	AVPI1	2.31E-02	-3.03
206380_s_at	CFP	2.32E-02	-40.94
207697_x_at	LILRB2	2.32E-02	-2.37
212526_at	SPG20	2.32E-02	-3.28
235126_at	LQK1	2.32E-02	3.13
200594_x_at	HNRNPU	2.33E-02	2.04
203923_s_at	CYBB	2.33E-02	-3.51
203802_x_at	NSUN5	2.34E-02	3.29
209422_at	PHF20	2.34E-02	2.58
209586_s_at	PRUNE	2.34E-02	4.21
218921_at	SIGIRR	2.34E-02	-4.67
225268_at	KPNA4	2.34E-02	2.10
203372_s_at	SOCS2	2.35E-02	-14.20
208795_s_at	MCM7	2.35E-02	2.49
209687_at	CXCL12	2.35E-02	-22.32
242546_at	FLJ39632	2.35E-02	13.18
205077_s_at	PIGF	2.36E-02	2.19
213715_s_at	KANK3	2.36E-02	-2.03
205250_s_at	CEP290	2.37E-02	2.44
212143_s_at	IGFBP3	2.37E-02	-13.33
242056_at	TRIM45	2.37E-02	3.06
200045_at	ABCF1	2.38E-02	2.07
221873_at	ZNF143	2.38E-02	2.05
222401_s_at	TMEM50A	2.38E-02	2.30
223480_s_at	MRPL47	2.38E-02	2.11
209242_at	PEG3	2.39E-02	-7.51
209923_s_at	BRAP	2.39E-02	2.06
207262_at	APOF	2.40E-02	-19.39
218901_at	PLSCR4	2.40E-02	-3.61

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
218911_at	YEATS4	2.40E-02	2.52
233555_s_at	SULF2	2.40E-02	-4.53
218977_s_at	TRNAU1AP	2.41E-02	2.55
213404_s_at	RHEB	2.42E-02	2.21
224962_at	C9orf69	2.42E-02	2.00
238653_at	LRIG2	2.42E-02	2.45
201762_s_at	PSME2	2.43E-02	2.44
209827_s_at	IL16	2.43E-02	-2.20
218395_at	ACTR6	2.43E-02	3.62
220016_at	AHNAK	2.43E-02	-2.51
222606_at	ZWILCH	2.44E-02	2.48
224987_at	C6orf89	2.44E-02	5.10
209901_x_at	AIF1	2.45E-02	-2.24
220060_s_at	C12orf48	2.45E-02	4.57
228561_at	CDC37L1	2.45E-02	-5.14
202265_at	BMI1	2.46E-02	2.76
202664_at	WIPF1	2.46E-02	-2.11
203716_s_at	DPP4	2.46E-02	3.42
226422_at	ERGIC2	2.46E-02	2.78
228299_at	KCTD20	2.46E-02	2.02
1555638_a_at	SAMSN1	2.47E-02	-2.94
208821_at	SNRPB	2.47E-02	2.79
225655_at	UHRF1	2.47E-02	8.58
235763_at	SLC44A5	2.47E-02	147.76
223922_x_at	MS4A6A	2.48E-02	-3.49
227297_at	ITGA9	2.48E-02	-3.49
218560_s_at	JMJD4	2.50E-02	2.96
224827_at	UBTD2	2.50E-02	2.52
225865_x_at	TH1L	2.50E-02	2.65
209709_s_at	HMMR	2.51E-02	5.85
212934_at	UBXN2B	2.51E-02	2.60
218315_s_at	CDK5RAP1	2.51E-02	2.23
218883_s_at	MLF1IP	2.51E-02	10.91
224314_s_at	EGLN1	2.51E-02	2.55
205234_at	SLC16A4	2.52E-02	-4.01
208734_x_at	RAB2A	2.52E-02	2.01
216025_x_at	CYP2C9	2.52E-02	-8.69
220116_at	KCNN2	2.52E-02	-44.37
209066_x_at	UQCRB	2.54E-02	3.72
212149_at	EFR3A	2.54E-02	2.75
210208_x_at	BAT3	2.55E-02	2.42
213243_at	VPS13B	2.55E-02	2.30
225599_s_at	C8orf83	2.55E-02	2.49
201335_s_at	ARHGEF12	2.56E-02	-2.60
204444_at	KIF11	2.56E-02	10.69
222664_at	KCTD15	2.56E-02	-3.89
225444_at	UBN2	2.56E-02	2.02
1553145_at	FLJ39653	2.57E-02	2.85
205189_s_at	FANCC	2.57E-02	-2.72
216598_s_at	CCL2	2.58E-02	-8.35
228157_at	ZNF207	2.58E-02	3.92
243009_at	LOC441242	2.58E-02	2.10
206854_s_at	MAP3K7	2.59E-02	2.63
212809_at	NFATC2IP	2.59E-02	3.24
224494_x_at	HSD17B14	2.59E-02	4.76
225766_s_at	TNPO1	2.59E-02	2.33
32259_at	EZH1	2.59E-02	2.13
202366_at	ACADS	2.60E-02	-2.41
210592_s_at	SAT1	2.60E-02	-2.67
223337_at	SDCCAG10	2.61E-02	2.50
240846_at	PCBD2	2.61E-02	2.28
206734_at	JRKL	2.62E-02	2.37
226261_at	ZNRF2	2.62E-02	2.03
234107_s_at	DTD1	2.62E-02	2.20
210983_s_at	MCM7	2.63E-02	3.67
204834_at	FGL2	2.64E-02	-2.50
220496_at	CLEC1B	2.64E-02	-60.62
239562_at	MTHFD2L	2.64E-02	-3.98
214512_s_at	SUB1	2.65E-02	4.05
219885_at	SLFN12	2.65E-02	2.50
222514_at	RRAGC	2.65E-02	2.48

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
213460_x_at	NSUN5C	2.67E-02	2.41
204266_s_at	CHKA	2.68E-02	2.09
204514_at	DPH2	2.68E-02	3.84
203640_at	MBNL2	2.69E-02	-2.34
212445_s_at	NEDD4L	2.69E-02	4.99
221230_s_at	ARID4B	2.69E-02	2.45
204439_at	IFI44L	2.70E-02	-2.52
209410_s_at	GRB10	2.71E-02	2.04
212709_at	NUP160	2.71E-02	2.11
221737_at	GNA12	2.71E-02	2.29
1560116_a_at	NEDD1	2.72E-02	2.66
214017_s_at	DHX34	2.72E-02	7.17
226982_at	ELL2	2.72E-02	-4.79
203708_at	PDE4B	2.73E-02	-2.59
203959_s_at	ZBTB40	2.73E-02	3.86
209813_x_at	TARP	2.74E-02	-2.71
218385_at	MRPS18A	2.74E-02	2.76
204092_s_at	AURKA	2.75E-02	6.36
210324_at	C8G	2.75E-02	-2.44
220750_s_at	LEPRE1	2.75E-02	2.45
222683_at	RNF20	2.75E-02	2.23
227803_at	ENPP5	2.75E-02	3.57
210361_s_at	ELF2	2.76E-02	-2.56
210473_s_at	GPR125	2.76E-02	-4.09
222701_s_at	CHCHD7	2.76E-02	2.79
204023_at	RFC4	2.77E-02	5.55
229025_s_at	IMMP1L	2.77E-02	2.73
237346_at	TGDS	2.77E-02	-2.21
212247_at	NUP205	2.78E-02	2.77
219539_at	GEMIN6	2.78E-02	2.71
221434_s_at	C14orf156	2.78E-02	2.30
221640_s_at	LRDD	2.78E-02	2.04
227246_at	PLRG1	2.78E-02	-2.04
231358_at	MRO	2.78E-02	-3.23
235299_at	SLC41A2	2.78E-02	-2.65
1554095_at	RBM33	2.79E-02	2.24
207039_at	CDKN2A	2.81E-02	3.60
229521_at	FLJ36031	2.81E-02	-2.46
207874_s_at	CFHR4	2.82E-02	-19.60
225205_at	KIF3B	2.82E-02	2.45
226300_at	MED19	2.82E-02	2.27
227388_at	TUSC1	2.82E-02	-2.96
212399_s_at	VGLL4	2.83E-02	2.03
217774_s_at	TRMT112	2.83E-02	2.54
219487_at	BBS10	2.83E-02	2.32
221570_s_at	METTL5	2.83E-02	2.92
213528_at	C1orf156	2.84E-02	2.19
209356_x_at	EFEMP2	2.85E-02	-2.05
224586_x_at	SUB1	2.85E-02	3.42
1554628_at	ZNF57	2.86E-02	2.38
203755_at	BUB1B	2.86E-02	7.45
204999_s_at	ATF5	2.86E-02	-7.62
1569112_at	SLC44A5	2.87E-02	14.41
202446_s_at	PLSCR1	2.87E-02	-2.12
205729_at	OSMR	2.87E-02	-2.73
209469_at	GPM6A	2.87E-02	-9.09
226267_at	JDP2	2.87E-02	-2.30
202813_at	TARBP1	2.88E-02	4.10
204449_at	PDCL	2.88E-02	2.56
211339_s_at	ITK	2.88E-02	-3.56
218829_s_at	CHD7	2.88E-02	2.56
202957_at	HCLS1	2.89E-02	-2.74
213008_at	FANCI	2.89E-02	13.35
213485_s_at	ABCC10	2.89E-02	2.43
239001_at	MGST1	2.89E-02	2.74
223452_s_at	ATL3	2.90E-02	2.77
201477_s_at	RRM1	2.91E-02	2.79
202872_at	ATP6V1C1	2.91E-02	3.03
222666_s_at	RCL1	2.91E-02	-8.31
223395_at	ABI3BP	2.91E-02	-3.61
203645_s_at	CD163	2.92E-02	-5.28

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206052_s_at	SLBP	2.92E-02	2.17
220108_at	GNA14	2.92E-02	-3.86
1554455_at	LINS1	2.93E-02	2.48
201453_x_at	RHEB	2.93E-02	2.46
201774_s_at	NCAPD2	2.93E-02	8.80
227378_x_at	C16orf13	2.93E-02	2.03
227978_s_at	ZADH2	2.93E-02	-2.10
218544_s_at	RCL1	2.94E-02	-5.21
200064_at	HSP90AB1	2.95E-02	3.26
206918_s_at	CPNE1	2.95E-02	2.32
208722_s_at	ANAPC5	2.95E-02	2.03
219519_s_at	SIGLEC1	2.95E-02	-9.22
205773_at	CPEB3	2.96E-02	-3.30
213733_at	MYO1F	2.96E-02	-2.58
219620_x_at	C9orf167	2.96E-02	-3.38
58696_at	EXOSC4	2.96E-02	2.68
210306_at	L3MBTL	2.97E-02	2.69
224896_s_at	TTL	2.97E-02	2.64
225006_x_at	TH1L	2.97E-02	3.16
201512_s_at	TOMM70A	2.98E-02	2.13
226572_at	SOCS7	2.98E-02	2.87
202037_s_at	SFRP1	2.99E-02	-5.87
202647_s_at	NRAS	2.99E-02	4.62
209409_at	GRB10	2.99E-02	2.43
212897_at	CDC2L6	2.99E-02	2.51
217880_at	CDC27	2.99E-02	2.37
235496_at	HRCT1	2.99E-02	8.56
203830_at	C17orf75	3.00E-02	4.68
208973_at	ERI3	3.00E-02	2.32
212983_at	HRAS	3.00E-02	3.66
57163_at	ELOVL1	3.00E-02	2.56
217408_at	MRPS18B	3.01E-02	2.93
230270_at	PRPF38B	3.01E-02	2.51
203840_at	BLZF1	3.02E-02	2.43
226436_at	RASSF4	3.02E-02	3.82
201714_at	TUBG1	3.03E-02	4.01
203511_s_at	TRAPPC3	3.03E-02	2.12
223702_x_at	FTCD	3.03E-02	-3.34
203104_at	CSF1R	3.04E-02	-2.62
209380_s_at	ABCC5	3.04E-02	2.63
223330_s_at	SUGT1	3.04E-02	2.10
226225_at	MCC	3.04E-02	-7.91
212148_at	PBX1	3.06E-02	-3.72
238756_at	GAS2L3	3.06E-02	3.60
244569_at	C8orf37	3.06E-02	2.19
224300_x_at	FTCD	3.07E-02	-3.62
228047_at	SNORA72	3.07E-02	3.03
201170_s_at	BHLHE40	3.08E-02	-4.88
215049_x_at	CD163	3.08E-02	-5.03
218838_s_at	TTC31	3.08E-02	2.36
220018_at	CBLL1	3.08E-02	2.36
225510_at	OAF	3.08E-02	-2.50
217739_s_at	NAMPT	3.09E-02	-5.24
219512_at	DSN1	3.09E-02	2.85
218622_at	NUP37	3.10E-02	3.16
223758_s_at	GTF2H2	3.10E-02	3.59
205449_at	SAC3D1	3.11E-02	9.08
206205_at	MPHOSPH9	3.11E-02	2.29
227697_at	SOCS3	3.11E-02	-10.36
1555167_s_at	NAMPT	3.12E-02	-7.35
203362_s_at	MAD2L1	3.12E-02	6.00
210609_s_at	TP53I3	3.12E-02	7.67
212355_at	KIAA0323	3.12E-02	2.76
225082_at	CPSF3	3.12E-02	2.44
208002_s_at	ACOT7	3.13E-02	2.51
209026_x_at	TUBB	3.13E-02	2.23
201300_s_at	PRNP	3.14E-02	-4.31
204818_at	HSD17B2	3.14E-02	-4.04
209699_x_at	AKR1C2	3.14E-02	2.69
209335_at	DCN	3.15E-02	-8.23
225031_at	CHD6	3.15E-02	2.34

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228662_at	SOCS7	3.15E-02	2.88
201144_s_at	EIF2S1	3.16E-02	2.28
203131_at	PDGFRA	3.16E-02	-10.48
207628_s_at	WBSCR22	3.16E-02	2.16
210543_s_at	PRKDC	3.16E-02	4.01
213056_at	FRMD4B	3.16E-02	-3.37
218585_s_at	DTL	3.16E-02	18.01
219581_at	TSEN2	3.16E-02	2.44
208016_s_at	AGTR1	3.17E-02	-4.68
210859_x_at	CLN3	3.17E-02	2.52
213009_s_at	TRIM37	3.17E-02	2.76
200909_s_at	RPLP2	3.18E-02	2.13
201809_s_at	ENG	3.18E-02	-3.21
214719_at	SLC46A3	3.18E-02	-8.64
216038_x_at	DAXX	3.18E-02	2.24
228330_at	ZUFSP	3.18E-02	2.05
213773_x_at	NSUN5	3.19E-02	2.26
221498_at	SNX27	3.19E-02	3.22
218046_s_at	MRPS16	3.20E-02	2.42
225203_at	PPP1R16A	3.20E-02	4.00
204731_at	TGFBR3	3.21E-02	-2.91
211557_x_at	SLCO2B1	3.21E-02	-2.10
214140_at	SLC25A16	3.21E-02	2.18
239085_at	JDP2	3.21E-02	-2.34
203502_at	BPGM	3.22E-02	2.79
209034_at	PNRC1	3.22E-02	-2.86
219700_at	PLXDC1	3.22E-02	2.56
225912_at	TP53INP1	3.22E-02	2.13
228189_at	BAG4	3.22E-02	2.09
1553984_s_at	DTYMK	3.24E-02	3.41
205909_at	POLE2	3.24E-02	4.27
226483_at	TMEM68	3.24E-02	2.87
203501_at	PGCP	3.25E-02	2.18
216071_x_at	MED12	3.25E-02	2.26
203225_s_at	RFK	3.26E-02	2.38
218106_s_at	MRPS10	3.26E-02	3.18
221802_s_at	KIAA1598	3.26E-02	3.06
230964_at	FREM2	3.26E-02	-21.96
212922_s_at	SMYD2	3.27E-02	3.03
215462_at	PLK3	3.27E-02	-3.94
218859_s_at	ESF1	3.27E-02	4.97
52731_at	AMBRA1	3.27E-02	2.40
201672_s_at	USP14	3.28E-02	2.25
212486_s_at	FYN	3.28E-02	-3.60
226801_s_at	AIDA	3.28E-02	2.30
201041_s_at	DUSP1	3.29E-02	-5.28
220786_s_at	SLC38A4	3.29E-02	-3.35
228384_s_at	PYROXD2	3.29E-02	-5.49
209786_at	HMGN4	3.30E-02	2.40
216295_s_at	CLTA	3.30E-02	2.56
219878_s_at	KLF13	3.30E-02	3.99
225642_at	KTI12	3.30E-02	2.34
227898_s_at	ZFP41	3.30E-02	16.25
204150_at	STAB1	3.31E-02	-3.34
223258_s_at	G2E3	3.31E-02	3.81
225196_s_at	MRPS26	3.31E-02	2.04
218252_at	CKAP2	3.32E-02	3.43
223270_at	CTDSPL2	3.32E-02	3.17
212918_at	RECQL	3.33E-02	2.10
209505_at	NR2F1	3.34E-02	-3.67
237350_at	TTC36	3.34E-02	-11.47
218234_at	ING4	3.35E-02	2.33
201566_x_at	ID2	3.36E-02	-8.85
205821_at	KLRK1	3.36E-02	-3.21
200610_s_at	NCL	3.37E-02	2.03
209657_s_at	HSF2	3.37E-02	3.58
221474_at	MYL12B	3.37E-02	2.23
226707_at	NAPRT1	3.37E-02	2.19
201498_at	USP7	3.38E-02	2.59
206662_at	GLRX	3.38E-02	-4.04
223055_s_at	XPO5	3.38E-02	2.87

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201694_s_at	EGR1	3.40E-02	-6.48
207543_s_at	P4HA1	3.40E-02	-2.85
38290_at	RGS14	3.40E-02	2.15
226936_at	C6orf173	3.41E-02	6.76
1555501_s_at	RSRC1	3.42E-02	2.97
205687_at	UBFD1	3.42E-02	2.23
221637_s_at	C11orf48	3.42E-02	2.46
223448_x_at	MRPS22	3.42E-02	2.40
227558_at	CBX4	3.42E-02	3.93
231671_at	FGA	3.42E-02	-3.06
44146_at	GMEB2	3.42E-02	2.33
203953_s_at	CLDN3	3.43E-02	2.71
231926_at	EPS15L1	3.43E-02	2.64
203887_s_at	THBD	3.44E-02	-2.75
229980_s_at	SNX5	3.44E-02	2.16
200960_x_at	CLTA	3.45E-02	3.36
232873_at	ZNF33A	3.45E-02	3.33
201720_s_at	LAPTM5	3.46E-02	-2.08
207541_s_at	EXOSC10	3.46E-02	2.06
212097_at	CAV1	3.46E-02	2.29
1558700_s_at	ZNF260	3.48E-02	2.01
201377_at	UBAP2L	3.48E-02	4.02
204334_at	KLF7	3.49E-02	-2.83
223110_at	KIAA1429	3.49E-02	2.18
228124_at	ABHD12	3.49E-02	2.25
228469_at	PPID	3.49E-02	-4.78
201797_s_at	VARS	3.50E-02	2.65
221842_s_at	ZNF131	3.50E-02	2.81
230435_at	LOC375190	3.50E-02	3.02
232216_at	YME1L1	3.50E-02	2.02
221887_s_at	DFNB31	3.51E-02	3.30
204955_at	SRPX	3.52E-02	-10.43
204970_s_at	MAFG	3.52E-02	2.99
205307_s_at	KMO	3.52E-02	-27.46
219258_at	TIPIN	3.52E-02	3.76
238295_at	C17orf42	3.53E-02	2.93
206541_at	KLKB1	3.54E-02	-6.29
217286_s_at	NDRG3	3.54E-02	2.25
202227_s_at	BRD8	3.55E-02	2.76
202230_s_at	CHERP	3.55E-02	2.18
222493_s_at	ZFAND3	3.55E-02	2.35
200608_s_at	RAD21	3.56E-02	2.65
201892_s_at	IMPDH2	3.56E-02	2.32
204862_s_at	NME3	3.56E-02	2.27
225694_at	CRKRS	3.56E-02	2.02
226750_at	LARP1B	3.56E-02	-2.96
242956_at	IDH1	3.56E-02	3.69
217934_x_at	STUB1	3.57E-02	2.36
225301_s_at	MYO5B	3.57E-02	3.76
204767_s_at	FEN1	3.58E-02	4.17
205543_at	HSPA4L	3.58E-02	-3.26
211009_s_at	ZNF271	3.58E-02	2.16
225765_at	TNPO1	3.58E-02	2.83
229172_at	HSPA12B	3.58E-02	3.34
231857_s_at	AGBL5	3.58E-02	2.51
217947_at	CMTM6	3.59E-02	-2.09
205437_at	ZNF211	3.60E-02	2.12
209305_s_at	GADD45B	3.60E-02	-19.70
224598_at	MGAT4B	3.60E-02	3.06
1554424_at	FIP1L1	3.61E-02	-2.26
210386_s_at	MTX1	3.61E-02	2.05
211548_s_at	HPGD	3.61E-02	-7.87
218870_at	ARHGAP15	3.61E-02	-2.78
228821_at	ST6GAL2	3.61E-02	-9.24
1558304_s_at	TSEN54	3.62E-02	2.84
201169_s_at	BHLHE40	3.62E-02	-5.45
223411_at	MIF4GD	3.62E-02	2.42
202893_at	UNC13B	3.63E-02	3.06
221515_s_at	LCMT1	3.63E-02	2.14
201618_x_at	GPAA1	3.64E-02	3.12
207096_at	SAA4	3.64E-02	-11.69

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
202503_s_at	KIAA0101	3.65E-02	10.92
208678_at	ATP6V1E1	3.65E-02	2.13
218617_at	TRIT1	3.65E-02	2.08
230912_at	ASPDH	3.65E-02	-2.68
209063_x_at	PAIP1	3.66E-02	2.00
215947_s_at	FAM136A	3.66E-02	2.60
226426_at	ADNP	3.66E-02	2.31
34210_at	CD52	3.66E-02	-2.61
203073_at	COG2	3.67E-02	2.33
204988_at	FGB	3.67E-02	-2.80
207401_at	PROX1	3.67E-02	-2.67
230788_at	GCNT2	3.67E-02	-3.03
202200_s_at	SRPK1	3.68E-02	2.08
202679_at	NPC1	3.68E-02	2.36
202737_s_at	LSM4	3.68E-02	3.24
213131_at	OLFM1	3.68E-02	-2.65
204595_s_at	STC1	3.69E-02	3.57
206009_at	ITGA9	3.69E-02	-2.16
206932_at	CH25H	3.69E-02	-3.11
201503_at	G3BP1	3.70E-02	2.16
219293_s_at	OLA1	3.70E-02	2.04
211040_x_at	GTSE1	3.71E-02	2.22
219644_at	CCDC41	3.71E-02	2.18
239742_at	TULP4	3.71E-02	3.75
202040_s_at	KDM5A	3.72E-02	2.24
209656_s_at	TMEM47	3.72E-02	-3.02
209902_at	ATR	3.72E-02	2.33
203410_at	AP3M2	3.73E-02	2.05
213927_at	MAP3K9	3.73E-02	3.95
226329_s_at	MITD1	3.73E-02	2.40
228186_s_at	RSPO3	3.73E-02	-10.40
236027_at	C10orf78	3.73E-02	3.06
212448_at	NEDD4L	3.75E-02	4.27
217741_s_at	ZFAND5	3.75E-02	-2.84
235033_at	NPEPL1	3.75E-02	2.20
217738_at	NAMPT	3.76E-02	-4.57
1554080_at	RQCD1	3.77E-02	3.96
224468_s_at	C19orf48	3.77E-02	2.87
227103_s_at	ECE2	3.77E-02	2.72
243_g_at	MAP4	3.77E-02	2.08
207330_at	PZP	3.78E-02	-12.98
212638_s_at	WWP1	3.78E-02	2.05
203612_at	BYSL	3.79E-02	3.23
205024_s_at	RAD51	3.79E-02	2.87
214061_at	WDR67	3.79E-02	3.34
204771_s_at	TTF1	3.80E-02	2.96
227541_at	WDR20	3.80E-02	2.16
217559_at	RPL10L	3.81E-02	4.55
218637_at	IMPACT	3.81E-02	2.28
225538_at	ZCCHC9	3.81E-02	3.37
231579_s_at	TIMP2	3.81E-02	-2.28
204050_s_at	CLTA	3.82E-02	3.08
213626_at	CBR4	3.82E-02	-2.86
215235_at	SPTAN1	3.82E-02	2.16
221705_s_at	SIKE1	3.82E-02	2.10
225520_at	MTHFD1L	3.82E-02	2.89
232195_at	GPR158	3.82E-02	45.52
216088_s_at	PSMA7	3.83E-02	2.23
221829_s_at	TNPO1	3.83E-02	2.96
224299_x_at	FTCD	3.83E-02	-3.54
209540_at	IGF1	3.84E-02	-15.35
209899_s_at	PUF60	3.84E-02	2.61
212349_at	POFUT1	3.84E-02	2.03
222637_at	COMMD10	3.84E-02	2.22
1557226_a_at	ASPG	3.85E-02	-2.78
201795_at	LBR	3.85E-02	2.83
204055_s_at	CTAGE5	3.85E-02	2.80
207571_x_at	C1orf38	3.85E-02	-2.39
213226_at	CCNA2	3.85E-02	18.52
230100_x_at	PAK1	3.85E-02	2.02
205554_s_at	DNASE1L3	3.86E-02	-15.38

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
213104_at	C16orf42	3.87E-02	2.22
218287_s_at	EIF2C1	3.87E-02	2.03
230165_at	SGOL2	3.87E-02	5.37
201473_at	JUNB	3.88E-02	-4.14
211713_x_at	KIAA0101	3.88E-02	2.11
226165_at	C8orf59	3.88E-02	3.66
230288_at	FGF14	3.88E-02	14.26
53720_at	C19orf66	3.88E-02	-2.52
205674_x_at	FXYD2	3.89E-02	-3.32
209523_at	TAF2	3.89E-02	3.06
209541_at	IGF1	3.89E-02	-20.00
222380_s_at	PDCD6	3.89E-02	2.05
203721_s_at	UTP18	3.90E-02	2.41
202846_s_at	PIGC	3.91E-02	2.52
207098_s_at	MFN1	3.91E-02	2.07
223879_s_at	OXR1	3.91E-02	3.77
231188_at	ZSCAN2	3.91E-02	2.87
201652_at	COPS5	3.92E-02	2.24
214617_at	PRF1	3.92E-02	-2.28
214948_s_at	TMF1	3.92E-02	2.71
1556126_s_at	GPATCH2	3.93E-02	2.00
201044_x_at	DUSP1	3.93E-02	-12.44
203358_s_at	EZH2	3.93E-02	14.43
215017_s_at	FNBP1L	3.93E-02	2.38
218353_at	RGS5	3.93E-02	3.41
218695_at	EXOSC4	3.93E-02	3.23
226992_at	NOSTRIN	3.93E-02	-2.11
227719_at	SMAD9	3.95E-02	-3.27
1563445_x_at	CTSLL3	3.96E-02	-2.64
205187_at	SMAD5	3.96E-02	2.07
215230_x_at	EIF3C	3.96E-02	2.84
218448_at	C20orf11	3.98E-02	2.95
218907_s_at	LRRC61	3.98E-02	4.03
223556_at	HELLS	3.98E-02	8.43
202087_s_at	CTSL1	3.99E-02	-2.12
209853_s_at	PSME3	3.99E-02	2.29
211302_s_at	PDE4B	3.99E-02	-2.21
218087_s_at	SORBS1	3.99E-02	-2.67
220155_s_at	BRD9	3.99E-02	2.72
51228_at	RBM12B	3.99E-02	2.84
225968_at	PRICKLE2	4.00E-02	-2.27
201704_at	ENTPD6	4.01E-02	2.59
211470_s_at	SULT1C2	4.01E-02	41.42
220017_x_at	CYP2C9	4.01E-02	-7.64
203879_at	PIK3CD	4.02E-02	-3.79
219456_s_at	RIN3	4.02E-02	-2.10
1555758_a_at	CDKN3	4.03E-02	18.21
201675_at	AKAP1	4.03E-02	2.22
204829_s_at	FOLR2	4.04E-02	-2.62
207231_at	DZIP3	4.04E-02	2.39
219131_at	UBIAD1	4.04E-02	3.44
232164_s_at	EPPK1	4.04E-02	7.15
1556060_a_at	ZNF451	4.05E-02	2.45
202242_at	TSPAN7	4.05E-02	-3.15
225020_at	DAB2IP	4.05E-02	2.57
235132_at	LOC254128	4.06E-02	2.14
202883_s_at	PPP2R1B	4.07E-02	-2.02
205167_s_at	CDC25C	4.07E-02	21.35
209606_at	CYTIP	4.07E-02	-2.49
228160_at	LOC339290	4.08E-02	2.07
203536_s_at	CIAO1	4.09E-02	2.11
203562_at	FEZ1	4.09E-02	-4.27
204579_at	FGFR4	4.09E-02	2.38
227029_at	FAM177A1	4.09E-02	2.45
201565_s_at	ID2	4.10E-02	-5.66
202288_at	MTOR	4.10E-02	2.19
203035_s_at	PIAS3	4.10E-02	3.52
215160_x_at	LOC642236	4.10E-02	2.21
396_f_at	EPOR	4.10E-02	-2.18
218205_s_at	MKNK2	4.11E-02	2.10
223605_at	SLC25A18	4.11E-02	-10.95

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
225701_at	AKNA	4.11E-02	-2.29
238441_at	PRKAA2	4.12E-02	9.52
1553510_s_at	RQCD1	4.13E-02	2.56
200827_at	PLOD1	4.13E-02	2.15
201485_s_at	RCN2	4.13E-02	2.66
208975_s_at	KPNB1	4.13E-02	2.78
218009_s_at	PRC1	4.13E-02	42.66
232165_at	EPPK1	4.13E-02	11.18
208694_at	PRKDC	4.14E-02	3.50
219230_at	TMEM100	4.14E-02	-6.95
221725_at	WASF2	4.14E-02	2.20
202111_at	SLC4A2	4.15E-02	2.61
218979_at	RMI1	4.15E-02	2.93
210143_at	ANXA10	4.16E-02	-19.07
210629_x_at	LST1	4.16E-02	-2.62
211582_x_at	LST1	4.16E-02	-3.67
218512_at	WDR12	4.16E-02	2.33
222388_s_at	VPS35	4.16E-02	2.29
225316_at	MFSD2	4.16E-02	-13.63
224782_at	ZMAT2	4.17E-02	2.42
225638_at	C1orf31	4.17E-02	2.30
230873_at	TTLL3	4.17E-02	2.18
206030_at	ASPA	4.18E-02	-9.00
217362_x_at	HLA-DRB6	4.18E-02	-3.15
227863_at	CTSD	4.18E-02	-3.71
203954_x_at	CLDN3	4.19E-02	2.86
208784_s_at	KLHDC3	4.19E-02	3.27
226632_at	CYGB	4.19E-02	-2.31
229963_at	BEX5	4.19E-02	-2.72
202144_s_at	ADSL	4.20E-02	2.63
206219_s_at	VAV1	4.20E-02	-2.43
226629_at	SLC43A2	4.20E-02	2.69
208991_at	STAT3	4.21E-02	-2.21
216661_x_at	MUTYH	4.21E-02	-11.03
223515_s_at	COQ3	4.21E-02	2.48
201730_s_at	TPR	4.22E-02	2.80
220114_s_at	STAB2	4.22E-02	-28.19
200021_at	CFL1	4.23E-02	2.72
204700_x_at	C1orf107	4.23E-02	2.28
224986_s_at	PDPK1	4.23E-02	2.12
226278_at	SVIP	4.23E-02	2.83
203956_at	MORC2	4.24E-02	2.05
207434_s_at	FXYD2	4.24E-02	-3.53
214735_at	IPCEF1	4.24E-02	-2.05
224738_x_at	RPL7L1	4.24E-02	2.04
200783_s_at	STMN1	4.25E-02	2.72
229312_s_at	GKAP1	4.25E-02	2.39
223467_at	RASD1	4.27E-02	-6.84
204459_at	CSTF2	4.28E-02	4.64
200837_at	BCAP31	4.29E-02	2.70
203302_at	DCK	4.29E-02	2.29
204108_at	NFYA	4.29E-02	2.41
213911_s_at	H2AFZ	4.29E-02	3.26
218643_s_at	CRIPT	4.29E-02	3.09
225170_at	WDR5	4.29E-02	2.11
201656_at	ITGA6	4.30E-02	5.40
226818_at	MPEG1	4.30E-02	-2.79
201841_s_at	HSPB1	4.31E-02	4.95
204240_s_at	SMC2	4.31E-02	3.51
218895_at	GPATCH3	4.31E-02	2.58
242577_at	LOC389834	4.31E-02	7.47
201540_at	FHL1	4.32E-02	-4.25
203160_s_at	RNF8	4.32E-02	3.23
211501_s_at	EIF3B	4.32E-02	2.52
219612_s_at	FGG	4.32E-02	-2.22
204924_at	TLR2	4.33E-02	-3.62
206218_at	MAGEB2	4.33E-02	11.97
212187_x_at	PTGDS	4.33E-02	-7.62
215425_at	BTG3	4.33E-02	3.00
227404_s_at	EGR1	4.34E-02	-9.43
242923_at	ZNF678	4.34E-02	4.26

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201663_s_at	SMC4	4.35E-02	3.06
201817_at	UBE3C	4.36E-02	2.46
202075_s_at	PLTP	4.36E-02	-3.59
203914_x_at	HPGD	4.36E-02	-7.06
208131_s_at	PTGIS	4.36E-02	-8.66
212554_at	CAP2	4.36E-02	14.33
217994_x_at	CPSF3L	4.36E-02	2.01
227070_at	GLT8D2	4.36E-02	-4.02
57516_at	ZNF764	4.36E-02	4.23
202330_s_at	UNG	4.37E-02	2.16
210999_s_at	GRB10	4.37E-02	2.82
204489_s_at	CD44	4.38E-02	-2.08
225319_s_at	FAM104A	4.39E-02	2.79
204825_at	MELK	4.40E-02	53.26
213452_at	ZNF184	4.40E-02	2.58
213566_at	RNASE6	4.40E-02	-2.11
222589_at	NLK	4.40E-02	2.02
203318_s_at	ZNF148	4.41E-02	2.12
219228_at	ZNF331	4.41E-02	-2.68
219000_s_at	DSCC1	4.42E-02	6.69
224632_at	GPATCH4	4.42E-02	2.69
37424_at	CCHCR1	4.43E-02	4.44
200882_s_at	PSMD4	4.44E-02	3.72
218698_at	APIP	4.44E-02	2.38
233587_s_at	SIPA1L2	4.44E-02	3.30
200618_at	LASP1	4.45E-02	2.89
201777_s_at	KIAA0494	4.45E-02	2.25
1555250_a_at	CPEB3	4.46E-02	-4.92
209291_at	ID4	4.46E-02	-2.84
205019_s_at	VIPR1	4.47E-02	-10.96
212807_s_at	SORT1	4.47E-02	5.11
218263_s_at	ZBED5	4.47E-02	2.04
220371_s_at	SLC12A9	4.47E-02	2.05
1569189_at	TTC9C	4.48E-02	2.15
203231_s_at	ATXN1	4.48E-02	2.32
220137_at	FLJ20674	4.48E-02	2.27
220994_s_at	STXBP6	4.48E-02	22.33
213320_at	PRMT3	4.49E-02	2.40
225439_at	NUDCD1	4.49E-02	2.60
227804_at	TLCD1	4.49E-02	4.73
202444_s_at	ERLIN1	4.50E-02	-5.14
205436_s_at	H2AFX	4.50E-02	2.84
226789_at	EMB	4.50E-02	-3.36
215563_s_at	MSTP9	4.51E-02	-2.25
218854_at	DSE	4.51E-02	-2.41
223037_at	PDZD11	4.51E-02	2.59
227179_at	STAU2	4.51E-02	3.36
227718_at	PURB	4.51E-02	2.84
204510_at	CDC7	4.52E-02	2.81
205116_at	LAMA2	4.52E-02	-2.15
218479_s_at	XPO4	4.52E-02	2.76
207727_s_at	MUTYH	4.53E-02	2.04
228707_at	CLDN23	4.53E-02	2.23
205269_at	LCP2	4.54E-02	-2.45
210982_s_at	HLA-DRA	4.55E-02	-2.18
203665_at	HMOX1	4.56E-02	-4.76
218247_s_at	MEX3C	4.56E-02	2.13
33494_at	ETFDH	4.56E-02	-2.24
204301_at	KBTBD11	4.57E-02	-14.17
209466_x_at	PTN	4.58E-02	-2.22
219113_x_at	HSD17B14	4.58E-02	2.64
223040_at	NAT5	4.58E-02	3.52
202495_at	TBCC	4.59E-02	3.56
226324_s_at	IFT172	4.59E-02	2.51
229742_at	C15orf61	4.59E-02	2.37
244455_at	KCNT2	4.59E-02	-2.90
206643_at	HAL	4.60E-02	-13.22
233924_s_at	EXOC6	4.60E-02	2.01
212724_at	RND3	4.61E-02	-4.89
209233_at	EMG1	4.62E-02	3.54
203967_at	CDC6	4.63E-02	4.91

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235071_at	WDR92	4.63E-02	2.08
1566785_x_at	LOC728806	4.64E-02	2.09
201066_at	CYC1	4.64E-02	2.49
209662_at	CETN3	4.64E-02	2.03
43427_at	ACACB	4.64E-02	-2.12
209188_x_at	DR1	4.65E-02	2.11
218361_at	GOLPH3L	4.66E-02	4.29
202670_at	MAP2K1	4.68E-02	-2.60
200636_s_at	PTPRF	4.69E-02	2.11
227598_at	C7orf29	4.69E-02	2.35
231663_s_at	ARG1	4.69E-02	-2.13
209891_at	SPC25	4.70E-02	3.48
211609_x_at	PSMD4	4.70E-02	3.59
213869_x_at	THY1	4.71E-02	2.48
201109_s_at	THBS1	4.72E-02	-3.89
160020_at	MMP14	4.73E-02	2.31
206150_at	CD27	4.73E-02	-2.14
211776_s_at	EPB41L3	4.74E-02	-3.21
214597_at	SSTR2	4.74E-02	-2.47
206441_s_at	COMMD4	4.75E-02	2.30
231776_at	EOMES	4.75E-02	-2.10
202961_s_at	ATP5J2	4.76E-02	2.06
232012_at	CAPN1	4.76E-02	2.11
235979_at	C7	4.76E-02	-4.49
201683_x_at	TOX4	4.77E-02	2.82
206102_at	GINS1	4.77E-02	11.91
208650_s_at	CD24	4.77E-02	9.05
220391_at	ZBTB3	4.77E-02	2.28
222025_s_at	OPLAH	4.77E-02	2.04
227529_s_at	AKAP12	4.77E-02	-3.85
209835_x_at	CD44	4.78E-02	-2.00
218516_s_at	IMPAD1	4.78E-02	2.06
219203_at	FAM158A	4.78E-02	3.55
226485_at	FLJ20674	4.78E-02	6.16
225390_s_at	KLF13	4.79E-02	2.97
205930_at	GTF2E1	4.80E-02	2.26
202184_s_at	NUP133	4.81E-02	2.09
208891_at	DUSP6	4.81E-02	-4.29
214098_at	KIAA1107	4.82E-02	3.26
230871_at	DHX30	4.82E-02	3.03
217814_at	CCDC47	4.83E-02	2.28
218524_at	E4F1	4.83E-02	2.30
228868_x_at	CDT1	4.83E-02	3.26
200661_at	CTSA	4.84E-02	3.72
225235_at	TSPAN17	4.84E-02	2.70
225394_s_at	ZCRB1	4.84E-02	2.28
202168_at	TAF9	4.85E-02	2.76
207907_at	TNFSF14	4.85E-02	-13.65
208894_at	HLA-DRA	4.85E-02	-2.36
210649_s_at	ARID1A	4.85E-02	2.10
214328_s_at	HSP90AA1	4.85E-02	2.08
217907_at	MRPL18	4.85E-02	2.30
224513_s_at	UBQLN4	4.85E-02	2.70
227174_at	WDR72	4.85E-02	-7.63
230024_at	AARS2	4.85E-02	4.32
242169_at	BHMT2	4.85E-02	2.12
204103_at	CCL4	4.86E-02	-4.06
213302_at	PFAS	4.86E-02	2.42
222668_at	KCTD15	4.86E-02	-3.86
206507_at	ZSCAN12	4.87E-02	3.87
225442_at	DDR2	4.87E-02	-2.37
212137_at	LARP1	4.88E-02	2.09
226129_at	FAM83H	4.88E-02	8.09
226241_s_at	MRPL52	4.88E-02	2.18
202510_s_at	TNFAIP2	4.89E-02	-2.17
202628_s_at	SERPINE1	4.89E-02	-9.98
220800_s_at	TMOD3	4.89E-02	4.03
239377_at	EIF1AD	4.89E-02	2.11
214889_at	FAM149A	4.91E-02	-3.92
204998_s_at	ATF5	4.92E-02	-8.52
213681_at	CYHR1	4.92E-02	2.26

Affy Probe ID	Gene Symbol	Paired T-test p-value	Fold Change T / N
213910_at	IGFBP7	4.92E-02	-2.62
218460_at	HEATR2	4.93E-02	2.47
221522_at	ANKRD27	4.94E-02	3.94
209096_at	UBE2V2	4.95E-02	2.23
218073_s_at	TMEM48	4.95E-02	3.79
222347_at	LOC644450	4.96E-02	11.82
266_s_at	CD24	4.96E-02	6.27
205463_s_at	PDGFA	4.98E-02	3.18
217897_at	FXYD6	4.98E-02	-2.83
218718_at	PDGFC	4.98E-02	-2.36
224464_s_at	NUDT22	4.98E-02	2.06
201415_at	GSS	4.99E-02	3.12
201599_at	OAT	4.99E-02	-7.63
203017_s_at	SSX2IP	4.99E-02	2.15
219953_s_at	C11orf17	4.99E-02	2.33
228272_at	DNLZ	4.99E-02	2.26

Supplementary Table S5. Predicted targets and enrichement score of 10 random miRNA sets

miRNA	predicted target count							Fisher's Exact p-value					
	C1	C2	C3	C4	C5	C6	Total	C1	C2	C3	C4	C5	C6
RS1_let-7a	6	3	1	6	13	4	33	3.49E-02	8.02E-01	7.25E-01	1.00E+00	2.11E-03	2.61E-01
RS1_miR-148a	5	9	1	12	9	20	56	6.00E-01	3.22E-01	3.85E-01	4.12E-01	7.24E-01	3.81E-02
RS1_miR-188-3p	3	2	3	8	11	15	42	1.00E+00	1.33E-01	7.59E-01	1.00E+00	1.75E-01	1.55E-01
RS1_miR-526b	1	9	6	16	6	11	49	2.66E-01	1.30E-01	5.46E-02	1.02E-02	8.48E-01	7.49E-01
RS1_miR-660	6	7	0	3	5	7	28	2.36E-02	1.05E-01	2.67E-01	3.83E-01	8.13E-01	8.47E-01
RS1_miR-95	0	0	0	2	3	3	8	1.00E+00	1.00E+00	1.00E+00	1.80E-01	2.86E-02	7.38E-02
RS2_miR-1	5	9	2	15	8	15	54	4.41E-01	3.13E-01	7.73E-01	9.26E-02	1.00E+00	3.73E-01
RS2_miR-140-3p	4	5	0	15	7	17	48	7.90E-01	8.37E-01	7.74E-02	6.11E-02	1.00E+00	1.29E-01
RS2_miR-208b	1	1	0	4	8	9	23	1.00E+00	7.32E-01	6.31E-01	5.78E-01	8.18E-03	3.99E-02
RS2_miR-217	5	6	7	14	5	18	55	5.99E-01	1.00E+00	4.36E-02	1.83E-01	2.87E-01	1.04E-01
RS2_miR-423-5p	3	7	1	8	5	5	29	1.00E+00	3.64E-01	5.22E-01	8.50E-01	8.39E-01	1.79E-01
RS2_miR-550	4	4	3	4	4	10	29	3.27E-01	1.00E+00	4.71E-01	5.38E-01	8.25E-01	4.65E-01
RS3_miR-142-5p	16	19	6	23	21	32	117	3.68E-03	7.85E-02	1.00E+00	2.76E-01	1.91E-01	8.27E-02
RS3_miR-15b	11	14	4	20	10	26	85	2.34E-02	1.21E-01	1.00E+00	6.62E-02	7.61E-01	3.11E-02
RS3_miR-183	3	6	5	9	4	7	34	1.00E+00	6.52E-01	1.10E-01	5.74E-01	4.22E-01	5.07E-01
RS3_miR-214	6	13	1	10	5	14	49	4.79E-01	9.75E-02	1.89E-01	7.62E-01	1.05E-01	1.00E+00
RS3_miR-23b	12	17	4	19	13	39	104	1.29E-01	2.47E-01	4.11E-01	1.00E+00	4.39E-01	2.68E-03
RS3_miR-362-5p	5	6	1	8	5	10	35	9.02E-02	3.03E-01	1.00E+00	3.94E-01	1.00E+00	3.44E-01
RS4_miR-151-5p	0	1	1	0	0	0	2	1.00E+00	5.66E-01	3.34E-01	6.37E-01	6.29E-01	4.10E-01
RS4_miR-299-3p	3	6	0	5	6	9	29	4.86E-01	2.81E-01	2.67E-01	1.00E+00	4.76E-01	4.31E-01
RS4_miR-34c-5p	4	4	2	15	3	14	42	7.82E-01	5.32E-01	1.00E+00	3.66E-02	1.29E-01	3.51E-01
RS4_miR-452	10	12	1	18	10	25	76	1.36E-01	5.21E-01	6.31E-02	4.20E-01	4.71E-01	1.52E-01
RS4_miR-196b	6	3	1	2	6	5	23	8.84E-03	1.00E+00	1.00E+00	3.34E-01	2.84E-01	1.00E+00
RS4_miR-19a	6	7	4	22	6	28	73	8.24E-01	6.09E-01	1.00E+00	2.42E-02	9.46E-02	1.16E-02
RS5_miR-107	5	6	1	17	3	16	48	4.22E-01	1.00E+00	3.75E-01	1.54E-02	9.54E-02	1.72E-01
RS5_miR-146b-5p	3	5	2	9	4	17	40	1.00E+00	1.00E+00	1.00E+00	5.80E-01	4.24E-01	3.03E-02
RS5_miR-18b	1	5	1	6	8	9	30	1.00E+00	2.67E-01	1.00E+00	4.84E-01	7.00E-02	2.10E-01
RS5_miR-299-5p	2	6	4	16	2	12	42	1.00E+00	4.59E-01	1.69E-01	7.89E-04	1.87E-01	1.53E-01
RS5_miR-421	6	9	4	14	18	22	73	8.24E-01	1.00E+00	1.00E+00	8.88E-01	6.67E-02	2.11E-01
RS5_miR-510	2	7	1	8	8	4	30	1.00E+00	2.36E-01	7.30E-01	5.56E-01	3.91E-01	1.57E-01
RS6_let-7g	6	2	1	5	12	4	30	3.53E-02	4.47E-01	7.25E-01	8.36E-01	5.92E-03	2.62E-01
RS6_miR-1	5	9	2	15	8	15	54	4.41E-01	3.13E-01	7.73E-01	9.26E-02	1.00E+00	3.73E-01
RS6_miR-126	0	0	0	0	1	1	2	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.29E-01	1.84E-01
RS6_miR-127-3p	0	1	0	0	0	0	1	1.00E+00	2.68E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00
RS6_miR-143	3	5	2	10	7	14	41	1.00E+00	8.36E-01	7.71E-01	7.30E-01	1.00E+00	3.61E-01
RS6_miR-625	3	11	4	10	7	21	56	6.30E-01	1.90E-01	7.88E-01	8.77E-01	5.04E-01	7.01E-02
RS7_miR-181a	8	18	7	28	14	40	115	6.92E-01	6.89E-02	5.19E-01	1.14E-02	1.00E+00	1.93E-04
RS7_miR-214	6	13	1	10	5	14	49	4.79E-01	9.75E-02	1.89E-01	7.62E-01	1.05E-01	1.00E+00
RS7_miR-455-3p	4	4	4	11	3	6	32	3.58E-01	1.00E+00	2.92E-01	1.13E-01	2.93E-01	4.84E-01
RS7_miR-532-5p	4	7	2	8	6	10	37	3.67E-01	2.47E-01	1.00E+00	6.95E-01	1.00E+00	6.04E-01
RS7_miR-876-5p	4	6	6	7	12	14	49	7.97E-01	1.00E+00	1.41E-01	5.06E-01	2.07E-01	5.54E-01
RS7_miR-877	2	4	1	5	5	8	25	1.00E+00	7.86E-01	1.00E+00	1.00E+00	8.09E-01	5.52E-01
RS8_miR-18b	1	5	1	6	8	9	30	1.00E+00	2.68E-01	1.00E+00	4.85E-01	7.05E-02	2.11E-01
RS8_miR-335	3	4	4	6	6	11	34	7.69E-01	1.00E+00	3.09E-01	8.48E-01	1.00E+00	4.96E-01
RS8_miR-9	8	10	4	12	6	20	60	6.94E-02	2.41E-01	5.86E-01	5.19E-01	4.84E-01	5.97E-02
RS8_miR-92b	5	7	6	7	10	13	48	4.01E-01	5.31E-01	6.77E-02	7.26E-01	3.41E-01	4.38E-01
RS8_miR-96	2	6	3	11	7	10	39	5.88E-01	1.00E+00	7.68E-01	3.86E-01	1.00E+00	8.77E-01
RS8_miR-202	2	2	1	9	4	10	28	1.00E+00	5.92E-01	1.00E+00	1.16E-01	1.00E+00	2.31E-01
RS9_miR-142-3p	4	3	2	4	3	10	26	1.17E-01	1.00E+00	6.68E-01	1.00E+00	1.00E+00	8.70E-02
RS9_miR-146a	3	5	2	9	4	17	40	1.00E+00	1.00E+00	1.00E+00	5.77E-01	4.23E-01	2.97E-02
RS9_miR-149	5	7	1	8	3	12	36	2.48E-01	3.81E-01	5.24E-01	8.54E-01	1.68E-01	4.16E-01
RS9_miR-33b	3	4	2	10	6	14	39	1.00E+00	6.69E-01	1.00E+00	5.96E-01	8.49E-01	3.45E-01
RS9_miR-502-3p	3	6	2	2	6	11	30	4.47E-01	1.49E-01	6.76E-01	2.48E-01	3.12E-01	5.74E-02
RS9_miR-532-3p	4	3	5	8	9	12	41	7.85E-01	2.96E-01	2.28E-01	8.65E-01	5.79E-01	7.61E-01
RSJ_miR-143	3	5	2	10	7	14	41	1.00E+00	8.36E-01	7.71E-01	7.30E-01	1.00E+00	4.42E-01
RSJ_miR-187	0	0	0	1	3	3	7	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.00E-02	1.44E-01
RSJ_miR-26b	5	13	3	16	14	25	76	8.12E-01	9.70E-02	1.00E+00	2.24E-01	1.92E-01	1.00E-02
RSJ_miR-30b	6	15	6	27	16	30	100	1.00E+00	2.82E-01	8.26E-01	1.49E-02	6.80E-01	5.37E-02
RSJ_miR-499-5p	3	3	4	10	6	15	41	1.00E+00	3.83E-01	3.53E-01	4.71E-01	8.48E-01	1.47E-01
RSJ_miR-106b	4	15	1	22	15	35	92	5.28E-01	1.43E-01	6.31E-02	7.91E-02	5.61E-01	4.59E-04

Supplementary table S6. Topological properties of whole network for cluster C6 network

GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Betweenness		# of Interactions (Degree)			
						Value	Rank*	Total	In	Out	Rank*
AP-1	FOS	TF		101, 139-5p, 199-3p	101, 139-5p, 199a-3p	249208.61	0.14%	291	112	179	0.14%
EGR1	EGR1	TF	✓		101, 139-5p, 199a-3p	72295.33	0.27%	125	32	93	0.28%
miR-101	miR-101					56924.00	0.41%	77	4	73	0.42%
HNF4-alpha	HNF4A	TF			101, 139-5p	44757.16	0.54%	69	8	61	0.56%
miR-139-5p	miR-139-5p					30350.00	0.68%	50	1	49	0.99%
c-Myc	MYC	TF			101, 139-5p, 199a-3p	26864.92	0.82%	63	25	38	1.41%
SP1/SP3 complex	SP1	TF		199-3p	101, 139-5p, 199a-3p	26196.43	0.95%	70	14	56	0.70%
NF-Y	NF-Y				199a-3p	25680.85	1.09%	63	12	51	0.85%
Tcf(Lef)	LEF1	TF			101, 139-5p, 199a-3p	22192.08	1.22%	59	24	35	1.55%
ESR1 (nuclear)	ESR1	TF			101, 139-5p, 199a-3p	21792.08	1.36%	54	22	32	1.83%
p53	TP53	TF			101, 139-5p, 199a-3p	21048.43	1.50%	57	28	29	2.11%
IGF-1	IGF-1				101, 139-5p, 199a-3p	20782.87	1.63%	46	36	10	7.46%
KLF4	KLF4	TF	✓		101, 139-5p	20556.33	1.77%	55	25	30	1.97%
C/EBPdelta	CEBPD	TF	✓		101, 139-5p, 199a-3p	19309.54	1.90%	61	36	25	2.54%
miR-199a-3p	miR-199a-3p					18887.15	2.04%	55	13	42	1.13%
NF-kB	RELA	TF			101, 139-5p	17556.05	2.18%	41	15	26	2.39%
ERK1/2	ERK1/2					16240.25	2.31%	27	13	14	4.93%
EZH2	EZH2	EPIGENES	✓	101	101, 139-5p, 199a-3p	15792.27	2.45%	53	13	40	1.27%
Androgen receptor	AR	TF			101, 139-5p	13974.19	2.59%	40	20	20	3.24%
JAK2	JAK2			101	101, 139-5p	13876.60	2.72%	26	11	15	4.65%
c-Src	SRC				101, 139-5p	13570.23	2.86%	22	13	9	9.01%
MEKK1(MAP3K1)	MAP3K1					12517.24	2.99%	10	7	3	24.08%
N-CoR	NCOR1	TF	✓		101, 139-5p	12444.68	3.13%	47	14	33	1.69%
STAT3	STAT3	TF			101, 139-5p	12201.45	3.27%	28	12	16	4.08%
p16INK4	CDKN2A	TF	✓		101, 139-5p, 199a-3p	11640.78	3.40%	45	41	4	18.17%
mTOR	MTOR		✓		101, 139-5p	9691.05	3.54%	30	20	10	7.46%
SUZ12	SUZ12	EPIGENES	✓		199a-3p	9046.93	3.67%	40	12	28	2.25%
Caspase-3	CASP3			101, 139-5p	101, 139-5p	8983.41	3.81%	12	3	9	9.01%
IRF8	IRF8	TF	✓			8469.37	3.95%	35	12	23	2.82%
Ubiquitin	UBB				101, 139-5p, 199a-3p	8159.22	4.08%	31	9	22	2.96%
LRH1	NR5A2	TF	✓	139-5p	101, 139-5p	7736.99	4.22%	38	27	11	6.34%
ATF-3	ATF3	TF	✓		101, 139-5p, 199a-3p	7376.23	4.35%	39	22	17	3.94%
Cathepsin L	Cathepsin L				101, 139-5p, 199a-3p	7358.72	4.49%	26	22	4	18.17%
ZNF143	ZNF143	TF	✓	101		7337.00	4.63%	15	5	10	7.46%
MMP-14	MMP14		✓		101, 139-5p	7296.47	4.76%	28	16	12	5.92%
PRNP	PRNP		✓		101, 139-5p, 199a-3p	7214.45	4.90%	15	10	5	15.92%
COUP-TFI	NR2F1	TF	✓		101, 139-5p, 199a-3p	7047.94	5.03%	24	14	10	7.46%
Beta-catenin	CTNNB1	TF			101, 139-5p	7046.22	5.17%	23	14	9	9.01%
c-Myb	MYB			101	101, 139-5p	6864.78	5.31%	14	8	6	14.08%
BMI-1	BMI1	EPIGENES	✓		101, 139-5p, 199a-3p	6854.58	5.44%	25	12	13	5.49%
Calpain 1(mu)	CAPN1		✓		101, 139-5p	6720.80	5.58%	27	5	22	2.96%
p27KIP1	CDKN1B				101, 139-5p	6647.14	5.71%	14	12	2	34.37%
E2F1	E2F1	TF				6475.78	5.85%	32	8	24	2.68%
p14ARF	CDKN2A	TF	✓		101, 139-5p, 199a-3p	6423.89	5.99%	39	19	20	3.24%
MMP-12	MMP12				101, 139-5p	6420.77	6.12%	16	4	12	5.92%
Endoglin	ENG		✓		101, 139-5p	5934.46	6.26%	25	21	4	18.17%
SOD2	SOD2		✓		101, 139-5p, 199a-3p	5795.24	6.39%	25	25	0	100.00%
Shc	SHC1			139-5p	101, 139-5p	5776.25	6.53%	20	13	7	11.55%
MCM4/6/7 complex	MCM4/6/7 complex				199a-3p	5613.03	6.67%	28	28	0	100.00%
DAXX	DAXX		✓		101, 139-5p	5435.93	6.80%	34	14	20	3.24%
SMAD3	SMAD3	TF				5142.22	6.94%	17	10	7	11.55%
Cyclin D1	CCND1				101, 139-5p, 199a-3p	5065.37	7.07%	20	19	1	52.82%
JNK(MAPK8-10)	JNK(MAPK8-10)				101, 139-5p	4982.53	7.21%	11	8	3	24.08%
Mi-2 alpha	CHD3	EPIGENES			101, 139-5p	4968.91	7.35%	3	2	1	52.82%
Fibronectin	FN1			101, 199-3p	199a-3p	4904.44	7.48%	14	9	5	15.92%
STAT1	STAT1	TF				4872.05	7.62%	21	12	9	9.01%
c-Raf-1	RAF1				101, 139-5p	4403.77	7.76%	13	10	3	24.08%
HIF1A	HIF1A	TF			101, 139-5p, 199a-3p	4331.88	7.89%	19	8	11	6.34%
PI3K reg class IA	PI3K reg class IA					4305.55	8.03%	10	5	5	15.92%
ASK1 (MAP3K5)	MAP3K5			101, 139-5p, 199-3p	101, 139-5p, 199a-3p	4168.41	8.16%	10	6	4	18.17%
RAR-alpha/RXR-alpha	RAR-alpha/RXR-alpha	TF			101, 139-5p	3861.93	8.30%	29	19	10	7.46%
STAT5	STAT5					3796.84	8.44%	13	6	7	11.55%
CDK4	CDK4				101, 139-5p	3757.32	8.57%	8	5	3	24.08%
AML1 (RUNX1)	RUNX1	TF		101, 139-5p, 199-3p	101, 139-5p, 199a-3p	3672.90	8.71%	16	9	7	11.55%
FHL2	FHL2		✓		199a-3p	3515.95	8.84%	20	7	13	5.49%
PBX1	PBX1	TF	✓			3501.58	8.98%	25	9	16	4.08%
Oct-3/4	POU5F1	TF			101, 139-5p, 199a-3p	3410.92	9.12%	23	9	14	4.93%
TIF1-beta	TRIM28	EPIGENES				3396.95	9.25%	4	1	3	24.08%
TITF1	NKX2-1	TF			101, 139-5p	3379.24	9.39%	26	17	9	9.01%
G-protein alpha-i family	G-protein alpha-i family				101, 139-5p	3375.94	9.52%	8	6	2	34.37%
EED	EED	EPIGENES	✓	101	199a-3p	3335.05	9.66%	19	9	10	7.46%
RIPK1	RIPK1			101		3312.39	9.80%	5	3	2	34.37%
MMP-9	MMP9				101, 139-5p	3290.01	9.93%	8	6	2	34.37%
c-IAP1	BIRC2					3276.97	10.07%	4	3	1	52.82%
TNF-alpha	TNF				101, 139-5p	3260.44	10.20%	12	10	2	34.37%
FasR(CD95)	FAS				101, 139-5p	3247.13	10.34%	7	4	3	24.08%
VEGF-A	VEGFA				101, 139-5p	3212.41	10.48%	9	4	5	15.92%
p300	EP300	EPIGENES			101, 139-5p	3145.85	10.61%	16	6	10	7.46%
Eomesodermin	EOMES	TF	✓		101, 139-5p, 199a-3p	3040.45	10.75%	13	12	1	52.82%
Sequestosome 1(p62)	SQSTM1		✓		101, 139-5p, 199a-3p	2971.85	10.88%	16	12	4	18.17%
GSK3 beta	GSK3B				101, 139-5p	2942.77	11.02%	8	4	4	18.17%
KLF6	KLF6	TF	✓		101, 139-5p	2912.91	11.16%	29	17	12	5.92%
GFRalpha1	GFRA1			101		2890.87	11.29%	3	2	1	52.82%
Rb protein	RB1	TF		199-3p	101, 139-5p, 199a-3p	2878.64	11.43%	14	9	5	15.92%
RBB2	KDM5A	EPIGENES	✓		101, 139-5p	2877.53	11.56%	18	4	14	4.93%
GRB2	GRB2				101, 139-5p	2840.76	11.70%	13	10	3	24.08%
RAP-1A	RAP1A			101		2829.36	11.84%	5	3	2	34.37%
SUMO-3	SUMO3		✓	101, 199-3p	199a-3p	2783.02	11.97%	19	3	16	4.08%
MKK7 (MAP2K7)	MAP2K7				101, 139-5p	2769.72	12.11%	6	5	1	52.82%
M-CSF receptor	CSF1R		✓		101, 139-5p	2743.84	12.24%	19	18	1	52.82%
MCM3	MCM3		✓		101, 139-5p	2717.49	12.38%	18	17	1	52.82%
HNF1-alpha	HNF1A	TF			101, 139-5p	2691.58	12.52%	12	1	11	6.34%
CD40(TNFRSF5)	CD40					2680.08	12.65%	6	3	3	24.08%
JAB1	COPS5		✓			2664.54	12.79%	22	7	15	4.65%
HSF1	HSF1	TF			101, 139-5p, 199a-3p	2561.07	12.93%	11	4	7	11.55%
p63	TP63	TF				2557.72	13.06%	14	5	9	9.01%
ETS1	ETS1	TF		139-5p	101, 139-5p	2550.00	13.20%	15	4	11	6.34%
CREB1	CREB1	TF				2544.86	13.33%	20	1	19	3.66%
GDNF	GDNF					2472.75	13.47%	5	3	2	34.37%
c-Cbl	CBL	TF				2472.08	13.61%	9	5	4	18.17%
HSF2	HSF2	TF	✓		199a-3p	2436.74	13.74%	13	2	11	6.34%
SRF	SRF	TF			101, 139-5p	2420.60	13.88%	17	7	10	7.46%
Tyk2	TYK2					2388.38	14.01%	7	3	4	18.17%
Thrombospondin 1	THBS1			139-5p	101, 139-5p	2324.28	14.15%	6	4	2	34.37%
CDK1 (p34)	CDK1				101, 139-5p	2286.27	14.29%	13	6	7	11.55%
GCR-alpha	NR3C1	TF				2281.48	14.42%	15	6	9	9.01%
SUMO-1	SUMO1					2265.75	14.56%	9	3	6	14.08%
G-protein beta/gamma	G-protein beta/gamma					2258.62	14.69%	5	3	2	34.37%
RNA polymerase II	RNA polymerase II				199a-3p	2257.31	14.83%	11	8	3	24.08%
NANOG	NANOG	TF			101, 139-5p, 199a-3p	2252.87	14.97%	12	5	7	11.55%
TAZ	WWTR1			101		2206.86	15.10%	14	5	9	9.01%
C/EBPbeta	CEBPB	TF			101, 139-5p	2114.83	15.24%	22	6	16	4.08%
CBP	CREBBP	EPIGENES				2061.01	15.37%	16	5	11	6.34%
p73	TP73	TF				2055.31	15.51%	8	6	2	34.37%
BMP4	BMP4				101, 139-5p	2046.02	15.65%	6	4	2	34.37%
PIAS3	PIAS3		✓			2033.25	15.78%	22	3	19	3.66%
AHR	AHR	TF			101, 139-5p	2023.02	15.92%	5	1	4	18.17%
NRSF	REST				101, 139-5p	2012.40	16.05%	5	3	2	34.37%
Elk-1	ELK1	TF				1947.78	16.19%	9	2	7	11.55%

GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Betweenness		# of Interactions (Degree)			
						Value	Rank*	Total	In	Out	Rank*
MYOD	MYOD1	TF			101, 139-5p, 199a-3p	1941.44	16.33%	16	6	10	7.46%
ATR	ATR					1845.45	16.46%	5	2	3	24.08%
IGF-1 receptor	IGF1R					1837.09	16.60%	10	1	9	9.01%
Rac1	RAC1			101		1818.00	16.73%	6	3	3	24.08%
Bcl-2	BCL2			139-5p	101, 139-5p	1813.22	16.87%	3	2	1	52.82%
PAK1	PAK1					1808.69	17.01%	2	1	1	52.82%
GATA-3	GATA3	TF			199a-3p	1803.64	17.14%	5	1	4	18.17%
OGG1	OGG1		✓			1794.14	17.28%	10	10	0	100.00%
IL-4	IL4				101, 139-5p, 199a-3p	1781.53	17.41%	7	5	2	34.37%
IL-18	IL18				101, 139-5p	1781.30	17.55%	3	2	1	52.82%
TIF1-alpha	TRIM24	EPIGENES	✓	101, 139-5p	101, 139-5p, 199a-3p	1751.65	17.69%	12	6	6	14.08%
ABT1	ABT1		✓			1742.88	17.82%	4	3	1	52.82%
ERK5 (MAPK7)	MAPK7					1736.16	17.96%	4	2	2	34.37%
Rad51	RAD51					1705.49	18.10%	3	2	1	52.82%
Karyopherin alpha 3	KPNA3					1701.13	18.23%	3	2	1	52.82%
STAT4	STAT4	TF			101, 139-5p	1688.37	18.37%	7	4	3	24.08%
BMP2	BMP2				199a-3p	1681.77	18.50%	10	6	4	18.17%
NLK	NLK		✓	101, 199-3p	199a-3p	1678.09	18.64%	13	7	6	14.08%
Nucleophosmin	NPM1					1672.67	18.78%	6	3	3	24.08%
XBP1	XBP1	TF			101, 139-5p	1669.79	18.91%	5	2	3	24.08%
HIPK2	HIPK2					1663.11	19.05%	5	3	2	34.37%
hnRNP K	HNRNPK					1655.62	19.18%	4	2	2	34.37%
MCM2	MCM2		✓		101, 139-5p	1649.51	19.32%	15	14	1	52.82%
Raptor	RPTOR				101, 139-5p	1640.80	19.46%	3	2	1	52.82%
PACAP	ADCYAP1			101	101, 139-5p	1577.55	19.59%	5	3	2	34.37%
IKK-gamma	IKBKG					1575.90	19.73%	6	4	2	34.37%
YY1	YY1	TF			101, 139-5p, 199a-3p	1545.87	19.86%	11	4	7	11.55%
SERTAD1	SERTAD1					1489.82	20.00%	2	1	1	52.82%
FOXP3	FOXP3	TF			101, 139-5p	1487.35	20.14%	7	2	5	15.92%
RET	RET					1475.98	20.27%	3	2	1	52.82%
SMAD5	SMAD5	TF	✓		199a-3p	1453.86	20.41%	18	12	6	14.08%
FOXO3A	FOXO3	TF			101, 139-5p	1431.97	20.54%	9	3	6	14.08%
SAT-1	SLC26A1				101, 139-5p, 199a-3p	1401.61	20.68%	9	9	0	100.00%
MEK4(MAP2K4)	MAP2K4				101, 139-5p	1376.40	20.82%	5	4	1	52.82%
IRF1	IRF1	TF				1371.98	20.95%	8	3	5	15.92%
WNT5A	WNT5A				101, 139-5p, 199a-3p	1356.63	21.09%	6	4	2	34.37%
VEGF-D	FIGF			139-5p	101, 139-5p	1338.77	21.22%	5	3	2	34.37%
FAK1	PTK2					1335.75	21.36%	10	6	4	18.17%
MYOG	MYOG	TF			101, 139-5p, 199a-3p	1303.52	21.50%	9	5	4	18.17%
UFO	AXL		✓	139-5p	101, 139-5p	1301.98	21.63%	8	6	2	34.37%
ZNF148	ZNF148	TF	✓			1300.69	21.77%	17	3	14	4.93%
ATAD2	ATAD2	EPIGENES	✓		101, 139-5p	1259.51	21.90%	12	5	7	11.55%
PC4	SUB1		✓	101	101, 139-5p, 199a-3p	1250.22	22.04%	11	6	5	15.92%
microRNA 155	miR-155				101, 139-5p	1243.62	22.18%	3	1	2	34.37%
Galpha(s)-specific calcitonin GPCRs	Galpha(s)-specific calcitonin GPCRs					1228.82	22.31%	6	3	3	24.08%
Sortilin	SORT1		✓		101, 139-5p	1225.98	22.45%	4	4	0	100.00%
IL-2	IL2				101, 139-5p	1211.11	22.59%	4	3	1	52.82%
CCL2	CCL2					1201.70	22.72%	4	3	1	52.82%
NCOA1 (SRC1)	NCOA1	EPIGENES				1201.47	22.86%	10	4	6	14.08%
Prolactin	PRL				101, 139-5p	1195.18	22.99%	6	4	2	34.37%
TTF1	TTF1		✓		101, 139-5p	1187.73	23.13%	8	6	2	34.37%
MRK	ICK		✓	101, 139-5p	101, 139-5p	1186.23	23.27%	5	3	2	34.37%
IL-8	IL8					1184.42	23.40%	5	4	1	52.82%
Endothelin-1	EDN1					1156.50	23.54%	8	5	3	24.08%
FGL2	FGL2		✓	199-3p	101, 139-5p, 199a-3p	1147.69	23.67%	11	10	1	52.82%
PRMT5	PRMT5	EPIGENES	✓			1142.29	23.81%	13	3	10	7.46%
Progesterone receptor	PGR	TF			101, 139-5p, 199a-3p	1142.14	23.95%	10	8	2	34.37%
alpha-3/beta-1 integrin	alpha-3/beta-1 integrin				101, 139-5p, 199a-3p	1124.28	24.08%	5	4	1	52.82%
MAPKAPK5	MAPKAPK5		✓		101, 139-5p	1100.77	24.22%	8	5	3	24.08%
ENA-78	ENA-78					1095.85	24.35%	4	3	1	52.82%
Caspase-9	CASP9					1094.16	24.49%	2	1	1	52.82%
VEGFR-2	KDR				101, 139-5p	1092.16	24.63%	12	8	4	18.17%
Urocortin	UCN					1091.34	24.76%	2	1	1	52.82%
EWS/FLI1 fusion protein	EWS/FLI1 fusion protein					1088.48	24.90%	9	2	7	11.55%
Neuropilin-1	NRP1			101		1069.29	25.03%	7	5	2	34.37%
BAT3	BAT3		✓		101, 139-5p	1065.73	25.17%	8	5	3	24.08%
Epo receptor	EPOR					1052.18	25.31%	8	1	7	11.55%
c-Abl	ABL1				101, 139-5p	1046.51	25.44%	4	1	3	24.08%
HMG2	HMGB2	EPIGENES	✓			1038.87	25.58%	11	6	5	15.92%
40452	POU2F1	TF				1025.45	25.71%	14	1	13	5.49%
TFIIE, alpha subunit	GTF2E1		✓	101	101, 139-5p	1011.62	25.85%	8	6	2	34.37%
TMF1	TMF1		✓	101, 139-5p	101, 139-5p	1009.53	25.99%	7	4	3	24.08%
Aggrecanase-2	ADAMTS5		✓	101		1005.74	26.12%	11	7	4	18.17%
CDK2	CDK2				101, 139-5p	1005.14	26.26%	11	4	7	11.55%
OAS2	OAS2		✓			997.19	26.39%	7	7	0	100.00%
GATA-4	GATA4	TF			101, 139-5p	996.67	26.53%	8	3	5	15.92%
UHRF1	UHRF1	TF	✓			981.94	26.67%	12	5	7	11.55%
POLA1	POLA1		✓		101, 139-5p	966.91	26.80%	10	10	0	100.00%
ERR3	ESRRG	TF	✓	139-5p	101, 139-5p	960.94	26.94%	17	7	10	7.46%
14-3-3 zeta/delta	YWHAZ			199-3p	101, 139-5p, 199a-3p	933.72	27.07%	5	3	2	34.37%
TRAF2	TRAF2					932.80	27.21%	8	2	6	14.08%
Cystatin A	CSTA				101, 139-5p	918.24	27.35%	4	1	3	24.08%
GATA-1	GATA1	TF			199a-3p	905.18	27.48%	14	3	11	6.34%
PROX1	PROX1	TF	✓			895.04	27.62%	10	5	5	15.92%
BRG1	SMARCA4	EPIGENES		101		876.26	27.76%	11	2	9	9.01%
IL-5	IL5				101, 139-5p	853.93	27.89%	2	1	1	52.82%
PMGE	BPGM		✓			849.97	28.03%	5	5	0	100.00%
PPARGC1 (PGC1-alpha)	PPARGC1A			139-5p	101, 139-5p	838.33	28.16%	10	7	3	24.08%
RUNX2	RUNX2	TF			101, 139-5p	819.46	28.30%	15	7	8	10.99%
MCM5	MCM5		✓			812.44	28.44%	14	12	2	34.37%
NF-AT1(NFATC2)	NFATC2	TF				801.74	28.57%	5	2	3	24.08%
H-Ras	HRAS				101, 139-5p	800.67	28.71%	6	2	4	18.17%
TGF-beta receptor type I	TGFBR1			101		794.70	28.84%	7	3	4	18.17%
TGF-beta receptor type II	TGFBR2				101, 139-5p	794.11	28.98%	10	7	3	24.08%
Neprilysin	MME		✓			786.11	29.12%	10	7	3	24.08%
alpha-V/beta-3 integrin	alpha-V/beta-3 integrin				101, 139-5p	773.35	29.25%	6	5	1	52.82%
TGF-beta 1	TGFB1			139-5p	101, 139-5p, 199a-3p	772.28	29.39%	8	6	2	34.37%
E2F8	E2F8	TF	✓			770.38	29.52%	7	4	3	24.08%
FKHR	FOXO1	TF			101, 139-5p	763.45	29.66%	9	3	6	14.08%
MAFG	MAFG	TF	✓		101, 139-5p	757.29	29.80%	8	5	3	24.08%
G-protein alpha-q/11	G-protein alpha-q/11				101, 139-5p	750.93	29.93%	4	3	1	52.82%
ACACB	ACACB		✓		101, 139-5p, 199a-3p	747.67	30.07%	13	13	0	100.00%
AP-2A	TFAP2A	TF				744.50	30.20%	9	1	8	10.99%
Pc2	CBX4	EPIGENES	✓			741.64	30.34%	10	4	6	14.08%
G-protein alpha-s	GNAS					733.27	30.48%	4	3	1	52.82%
AKT(PKB)	AKT(PKB)				101, 139-5p	725.41	30.61%	7	3	4	18.17%
Cystatin B	CSTB				101, 139-5p	724.13	30.75%	3	1	2	34.37%
SSAT	SAT1		✓		101, 139-5p	723.63	30.88%	13	11	2	34.37%
EGFR	EGFR					717.74	31.02%	8	4	4	18.17%
IL-10	IL10					715.10	31.16%	3	2	1	52.82%
Galpha(q)-specific frizzled GPCRs	Galpha(q)-specific frizzled GPCRs				101, 139-5p	709.43	31.29%	4	3	1	52.82%
Fyn	FYN					699.33	31.43%	6	3	3	24.08%
BAF250A	ARID1A	EPIGENES	✓	101		696.16	31.56%	9	2	7	11.55%
E2F3	E2F3	TF				695.30	31.70%	9	1	8	10.99%
BRD8	BRD8	EPIGENES	✓			693.95	31.84%	5	4	1	52.82%
NCOA6 (TRBP)	NCOA6		✓			693.13	31.97%	13	2	11	6.34%
PTEN	PTEN			139-5p	101, 139-5p, 199a-3p	690.66	32.11%	7	6	1	52.82%
JAK1	JAK1					686.69	32.24%	9	5	4	18.17%
Galectin-3	LGALS3				101, 139-5p	682.08	32.38%	3	2	1	52.82%
ERR1	ESRRA	TF			101, 139-5p	678.72	32.52%	5	2	3	24.08%

GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Betweenness		# of Interactions (Degree)			
						Value	Rank*	Total	In	Out	Rank*
ZNF302	ZNF302		✓	139-5p	101, 139-5p	678.05	32.65%	7	7	0	100.00%
SALL4	SALL4					675.71	32.79%	9	3	6	14.08%
DR1	DR1		✓	101		672.90	32.93%	4	3	1	52.82%
E2I	UBE2I					672.65	33.06%	9	2	7	11.55%
C/EBPalpha	CEBPA	TF		101	101, 139-5p	658.67	33.20%	12	5	7	11.55%
N-Myc	MYCN	TF		101		656.29	33.33%	11	3	8	10.99%
DNMT3A	DNMT3A	EPIGENES		101, 199-3p	199a-3p	649.24	33.47%	8	5	3	24.08%
VEGFR-3	FLT4				101, 139-5p	645.81	33.61%	8	5	3	24.08%
Enkephalin A	PENK					641.39	33.74%	2	1	1	52.82%
HNF3-beta	FOXA2	TF			101, 139-5p	624.98	33.88%	12	3	9	9.01%
IL-9	IL9				101, 139-5p	621.14	34.01%	2	1	1	52.82%
CDK11	CDK19		✓			601.10	34.15%	5	2	3	24.08%
PU.1	SPI1	TF			101, 139-5p	590.40	34.29%	11	2	9	9.01%
HDAC1	HDAC1	EPIGENES				577.09	34.42%	10	3	7	11.55%
Collagen IV	Collagen IV				101, 139-5p, 199a-3p	566.13	34.56%	5	3	2	34.37%
E2F2	E2F2	TF				564.13	34.69%	11	2	9	9.01%
MEK1(MAP2K1)	MAP2K1					557.77	34.83%	4	3	1	52.82%
Bcl-6	BCL6	TF				553.47	34.97%	7	3	4	18.17%
IL-1 beta	IL1B				101, 139-5p	548.79	35.10%	7	4	3	24.08%
RAIDD	CRADD					539.29	35.24%	2	1	1	52.82%
SMAD4	SMAD4	TF				528.35	35.37%	9	4	5	15.92%
NCOA2 (GRIP1/TIF2)	NCOA2					520.37	35.51%	5	2	3	24.08%
PLK3 (CNK)	PLK3		✓		199a-3p	516.90	35.65%	6	3	3	24.08%
PNRC1	PNRC1		✓	101, 199-3p	199a-3p	514.27	35.78%	7	6	1	52.82%
ARID4B	ARID4B		✓	101, 199-3p	199a-3p	506.25	35.92%	6	5	1	52.82%
TARBP1	TARBP1		✓		101, 139-5p	499.54	36.05%	7	6	1	52.82%
NF-AT2(NFATC1)	NFATC1	TF		139-5p	101, 139-5p	489.02	36.19%	4	2	2	34.37%
SDF-1	CXCL12				199a-3p	484.09	36.33%	7	6	1	52.82%
PKC-alpha	PRKCA			139-5p	101, 139-5p	482.12	36.46%	3	2	1	52.82%
GABP alpha	GABPA	TF			101, 139-5p	481.68	36.60%	4	2	2	34.37%
Brca1	BRCA1				101, 139-5p	472.38	36.73%	6	4	2	34.37%
SMAD9 (SMAD8)	SMAD9	TF	✓		199a-3p	471.34	36.87%	10	7	3	24.08%
TIP30	HTATIP2		✓		101, 139-5p	462.40	37.01%	7	1	6	14.08%
APEX	APEX1				101, 139-5p	461.09	37.14%	6	3	3	24.08%
AATC	GOT1		✓		101, 139-5p	458.61	37.28%	8	8	0	100.00%
TFIIH	TFIIH				101, 139-5p, 199a-3p	457.89	37.41%	6	4	2	34.37%
CDC42	CDC42					451.17	37.55%	3	1	2	34.37%
HDAC2	HDAC2	EPIGENES		139-5p	101, 139-5p	451.00	37.69%	6	2	4	18.17%
HUTH	HAL		✓			449.74	37.82%	7	7	0	100.00%
ATF-5	ATF5	TF	✓			447.98	37.96%	8	3	5	15.92%
SHP-2	PTPN11				101, 139-5p	445.82	38.10%	5	3	2	34.37%
MEF2D	MEF2D	TF				442.33	38.23%	4	2	2	34.37%
CD40L(TNFSF5)	CD40LG					435.64	38.37%	3	2	1	52.82%
VAV-1	VAV1	TF				433.83	38.50%	4	2	2	34.37%
CrkL	CRKL					433.24	38.64%	5	4	1	52.82%
CAPER	RBM39		✓			432.89	38.78%	8	4	4	18.17%
IL-12 receptor	IL-12 receptor					432.55	38.91%	4	2	2	34.37%
PDGF-A	PDGFA				101, 139-5p	430.56	39.05%	3	2	1	52.82%
MDM2	MDM2				101, 139-5p	429.24	39.18%	8	7	1	52.82%
HMGI/Y	HMGA1	EPIGENES			101, 139-5p	422.36	39.32%	7	4	3	24.08%
PCNA	PCNA				101, 139-5p	416.98	39.46%	5	3	2	34.37%
EPAS1	EPAS1	TF		199-3p	199a-3p	412.26	39.59%	6	2	4	18.17%
Ataxin-1	ATXN1			101, 139-5p	101, 139-5p	411.99	39.73%	3	2	1	52.82%
KLF13	KLF13		✓	199-3p	199a-3p	411.87	39.86%	8	5	3	24.08%
Somatotropin	GH1					411.69	40.00%	4	2	2	34.37%
SREBP1 (nuclear)	SREBP1 (nuclear)	TF				411.63	40.14%	6	2	4	18.17%
DJ-1	PARK7				101, 139-5p	407.99	40.27%	3	2	1	52.82%
VDR	VDR	TF			101, 139-5p	406.22	40.41%	8	5	3	24.08%
TFIID 31 kDa subunit	TAF9		✓			405.01	40.54%	8	4	4	18.17%
TRAP230	MED12		✓			402.56	40.68%	8	4	4	18.17%
JDP2	JDP2	TF	✓	101	101, 139-5p	400.60	40.82%	10	4	6	14.08%
IRS-1	IRS1					400.34	40.95%	6	2	4	18.17%
CYLD	CYLD			101		399.92	41.09%	3	2	1	52.82%
ZNF331	ZNF331		✓	139-5p	101, 139-5p	397.80	41.22%	4	4	0	100.00%
ID1	ID1				101, 139-5p	396.89	41.36%	8	7	1	52.82%
PSF	SFPQ			101	101, 139-5p	394.94	41.50%	4	3	1	52.82%
QKI	QKI		✓	101, 199-3p	199a-3p	394.10	41.63%	5	4	1	52.82%
SMAD7	SMAD7	TF			101, 139-5p	387.79	41.77%	6	5	1	52.82%
SOS	SOS				101, 139-5p	380.71	41.90%	6	3	3	24.08%
Sry	SRY	TF			101, 139-5p	373.44	42.04%	4	1	3	24.08%
DKK1	DKK1				199a-3p	373.13	42.18%	5	4	1	52.82%
Adrenomedullin	ADM				101, 139-5p	365.72	42.31%	3	2	1	52.82%
SNAIL1	SNAI1				101, 139-5p	361.80	42.45%	6	5	1	52.82%
GAB1	GAB1				101, 139-5p	359.24	42.59%	4	3	1	52.82%
VEGFR-1	FLT1					358.75	42.72%	6	3	3	24.08%
Syk	SYK					358.04	42.86%	7	3	4	18.17%
MAP3K3	MAP3K3				101, 139-5p	353.48	42.99%	3	2	1	52.82%
TNF-R1	TNFRSF1A					347.90	43.13%	2	1	1	52.82%
SMAD2	SMAD2	TF		139-5p	101, 139-5p	344.83	43.27%	6	4	2	34.37%
IL-12	IL-12				101, 139-5p	335.66	43.40%	3	2	1	52.82%
PAX3	PAX3	TF			101, 139-5p, 199a-3p	332.82	43.54%	6	5	1	52.82%
alpha-5/beta-1 integrin	alpha-5/beta-1 integrin				101, 139-5p	326.77	43.67%	7	4	3	24.08%
Laminin 1	Laminin 1					325.89	43.81%	5	3	2	34.37%
HoxC13	HOXC13	TF			199a-3p	320.73	43.95%	4	3	1	52.82%
CXCR4	CXCR4			139-5p	101, 139-5p	319.59	44.08%	4	2	2	34.37%
ELF3	ELF3	TF			101, 139-5p	319.09	44.22%	4	2	2	34.37%
PKA-cat beta	PRKACB			139-5p	101, 139-5p	316.74	44.35%	4	3	1	52.82%
Paxillin	PXN					311.23	44.49%	4	3	1	52.82%
microRNA 21	miR-21				101, 139-5p	310.45	44.63%	5	2	3	24.08%
TBP	TBP	TF			199a-3p	307.08	44.76%	3	2	1	52.82%
GFRalpha2	GFRA2					307.04	44.90%	2	1	1	52.82%
IL-13	IL13			101		306.08	45.03%	4	3	1	52.82%
I-kB	I-kB				101, 139-5p	305.70	45.17%	7	4	3	24.08%
TR4	NR2C2	TF	✓			305.03	45.31%	9	4	5	15.92%
p130	RBL2			101		304.56	45.44%	6	3	3	24.08%
FOXF1	FOXF1	TF			199a-3p	304.06	45.58%	5	4	1	52.82%
ELAVL1 (HuR)	ELAVL1				101, 139-5p	303.28	45.71%	7	3	4	18.17%
BMP7	BMP7				199a-3p	303.18	45.85%	4	2	2	34.37%
ELF1	ELF1	TF			101, 139-5p	299.67	45.99%	4	1	3	24.08%
Importin (karyopherin)-beta	Importin (karyopherin)-beta				101, 139-5p	299.05	46.12%	4	3	1	52.82%
IL-2 receptor	IL-2 receptor					298.71	46.26%	5	1	4	18.17%
CENP-50	MLF1IP		✓		199a-3p	296.89	46.39%	5	5	0	100.00%
cKrox	ZBTB7B	TF	✓			294.63	46.53%	5	2	3	24.08%
SOX9	SOX9	TF		101		288.07	46.67%	6	4	2	34.37%
Golgin-45 (BLZF1)	BLZF1	TF	✓		101, 139-5p	287.62	46.80%	9	8	1	52.82%
FKBP8	FKBP8					282.34	46.94%	4	2	2	34.37%
ZNF451	ZNF451		✓	101		281.51	47.07%	3	2	1	52.82%
Leptin	LEP				101, 139-5p	281.44	47.21%	3	2	1	52.82%
Epo	EPO					281.39	47.35%	2	1	1	52.82%
BMPR1B	BMPR1B					280.03	47.48%	7	4	3	24.08%
GATA-6	GATA6	TF			199a-3p	278.96	47.62%	6	3	3	24.08%
IBP5	IGFBP5			101, 139-5p	101, 139-5p	272.32	47.76%	4	3	1	52.82%
PCY2	PCYT2		✓		101, 139-5p, 199a-3p	268.87	47.89%	9	9	0	100.00%
CTCF	CTCF	TF		101		267.34	48.03%	5	3	2	34.37%
PP2A catalytic	PP2A catalytic				101, 139-5p, 199a-3p	264.98	48.16%	5	3	2	34.37%
PCAF	KAT2B	EPIGENES				261.55	48.30%	5	2	3	24.08%
ZNF217	ZNF217	TF		101, 199-3p	199a-3p	259.63	48.44%	5	4	1	52.82%
NCK1	NCK1					249.73	48.57%	2	1	1	52.82%
ESR2	ESR2	TF				248.41	48.71%	7	2	5	15.92%
SMAD1	SMAD1	TF				247.11	48.84%	5	3	2	34.37%

						Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Value	Rank*	Total	In	Out	Rank*
PML	PML					240.56	48.98%	4	1	3	24.08%
ErbB2	ERBB2				101, 139-5p	237.07	49.12%	3	1	2	34.37%
IL-4R type II	IL-4R type II				199a-3p	236.74	49.25%	4	3	1	52.82%
NOTCH1 (NICD)	NOTCH1 (NICD)				101, 139-5p	235.03	49.39%	4	3	1	52.82%
Cyclin E	CCNE1				101, 139-5p	232.94	49.52%	8	6	2	34.37%
ITF2	TCF4	TF				230.52	49.66%	4	2	2	34.37%
WWP1	WWP1		✓			230.14	49.80%	9	0	9	9.01%
GSTM1	GSTM1					229.82	49.93%	4	2	2	34.37%
E4F1	E4F1	TF	✓		199a-3p	229.42	50.07%	8	4	4	18.17%
CtBP2	CTBP2				101, 139-5p	226.58	50.20%	4	3	1	52.82%
Ephrin-A5	EFNA5					225.51	50.34%	2	1	1	52.82%
FOXF2	FOXF2	TF				219.58	50.48%	4	2	2	34.37%
SLC38A1	SLC38A1			199-3p	199a-3p	218.06	50.61%	4	4	0	100.00%
ACM3	CHRM3				101, 139-5p	217.40	50.75%	4	3	1	52.82%
Granzyme B	GZMB				101, 139-5p	215.00	50.88%	5	2	3	24.08%
DCK	DCK		✓			214.36	51.02%	5	5	0	100.00%
Cathepsin A	CTSA		✓			212.49	51.16%	4	2	2	34.37%
IFN-beta	IFNB1					210.52	51.29%	2	1	1	52.82%
P4HA1	P4HA1		✓		101, 139-5p, 199a-3p	208.88	51.43%	8	8	0	100.00%
PDGF-R-alpha	PDGFRA			199-3p	199a-3p	208.79	51.56%	3	2	1	52.82%
NRF2	NFE2L2	TF		101		207.65	51.70%	7	3	4	18.17%
ELL2	ELL2		✓	139-5p	101, 139-5p	201.50	51.84%	5	5	0	100.00%
RUVBL2	RUVBL2		✓			200.76	51.97%	6	3	3	24.08%
HGK(MAP4K4)	MAP4K4					199.95	52.11%	3	1	2	34.37%
PPP2R5A	PPP2R5A		✓			197.85	52.24%	2	0	2	34.37%
c-MPL	MPL			199-3p	199a-3p	196.52	52.38%	3	2	1	52.82%
CDYL	CDYL	EPIGENES	✓	101	101, 139-5p	196.52	52.52%	6	6	0	100.00%
ZNF207	ZNF207	TF	✓	101		196.39	52.65%	2	2	0	100.00%
GCK(MAP4K2)	MAP4K2					195.56	52.79%	3	1	2	34.37%
MSX1	MSX1	TF		101	101, 139-5p	193.27	52.93%	4	3	1	52.82%
PARP-1	PARP1					191.72	53.06%	4	1	3	24.08%
B-Raf	BRAF					190.82	53.20%	5	2	3	24.08%
EGF	EGF				101, 139-5p	190.33	53.33%	3	1	2	34.37%
CRK	CRK					188.22	53.47%	3	2	1	52.82%
Bax	BAX				101, 139-5p	185.29	53.61%	3	1	2	34.37%
RIP140	NRIP1			199-3p	199a-3p	184.30	53.74%	5	3	2	34.37%
ROR-alpha	RORA	TF				183.38	53.88%	6	4	2	34.37%
Ski	SKI				101, 139-5p	180.59	54.01%	5	1	4	18.17%
p15	CDKN2B				199a-3p	178.80	54.15%	4	3	1	52.82%
ZNF189	ZNF189	TF	✓		199a-3p	174.20	54.29%	6	6	0	100.00%
HMGA2	HMGA2	EPIGENES				173.42	54.42%	4	2	2	34.37%
MSH6	MSH6				101, 139-5p	173.25	54.56%	2	1	1	52.82%
Cathepsin V	CTSL1		✓		101, 139-5p	172.75	54.69%	4	4	0	100.00%
Cystatin C	CST3					172.16	54.83%	3	1	2	34.37%
Tat (HIV-1)	Tat (HIV-1)					171.21	54.97%	5	2	3	24.08%
Vitronectin	VTN					170.13	55.10%	4	3	1	52.82%
HSP27	HSPB1				101, 139-5p, 199a-3p	169.72	55.24%	6	5	1	52.82%
SF1	NR5A1	TF				168.14	55.37%	4	3	1	52.82%
MITF	MITF	TF		101	101, 139-5p	165.50	55.51%	6	5	1	52.82%
SMRT	NCOR2					164.76	55.65%	5	1	4	18.17%
BMAL1	ARNTL	TF			101, 139-5p	164.02	55.78%	4	2	2	34.37%
SHP-1	PTPN6				101, 139-5p	163.38	55.92%	4	2	2	34.37%
MYF5	MYF5	TF			101, 139-5p	162.86	56.05%	3	2	1	52.82%
ZNRF2	ZNRF2		✓	101, 199-3p	199a-3p	162.62	56.19%	4	3	1	52.82%
Amyloid beta	Amyloid beta					162.00	56.33%	3	2	1	52.82%
TGT	USP14		✓	101		159.36	56.46%	4	3	1	52.82%
GLI-3	GLI3	TF				157.28	56.60%	3	1	2	34.37%
TFIID 30 kDa subunit	TAF10	TF	✓			156.85	56.73%	3	1	2	34.37%
C14orf169	C14orf169		✓		199a-3p	154.93	56.87%	4	1	3	24.08%
HB-EGF	HBEGF				101, 139-5p	154.73	57.01%	3	2	1	52.82%
FOXP1	FOXP1	TF		139-5p, 199-3p	101, 139-5p, 199a-3p	153.28	57.14%	4	3	1	52.82%
IL-22	IL22				199a-3p	152.88	57.28%	4	3	1	52.82%
ARHGAP15	ARHGAP15		✓		199a-3p	152.67	57.41%	3	2	1	52.82%
PAX6	PAX6	TF				151.69	57.55%	5	3	2	34.37%
TrkA	NTRK1				101, 139-5p	151.10	57.69%	3	2	1	52.82%
Pin1	PIN1					149.62	57.82%	5	3	2	34.37%
TIMP1	TIMP1				101, 139-5p	149.41	57.96%	5	3	2	34.37%
NFATC2IP	NFATC2IP		✓			147.24	58.10%	4	3	1	52.82%
RD protein	RDBP		✓			146.89	58.23%	4	3	1	52.82%
CDK3	CDK3					144.75	58.37%	2	1	1	52.82%
IRF4	IRF4	TF			101, 139-5p	142.31	58.50%	3	1	2	34.37%
DNMT1	DNMT1	EPIGENES			101, 139-5p, 199a-3p	139.44	58.64%	6	4	2	34.37%
p19	CDKN2D					139.43	58.78%	3	2	1	52.82%
DAPK1	DAPK1				101, 139-5p	138.33	58.91%	5	3	2	34.37%
IL-1RI	IL1R1			101		137.50	59.05%	3	2	1	52.82%
SHP	NR0B2	TF			101, 139-5p	137.17	59.18%	9	5	4	18.17%
Cathepsin D	CTSD					136.24	59.32%	4	3	1	52.82%
Pitx2	PITX2	TF				133.41	59.46%	2	1	1	52.82%
CIITA	CIITA	EPIGENES			101, 139-5p	133.25	59.59%	6	5	1	52.82%
TAFI48	TAF1A		✓		101, 139-5p, 199a-3p	132.46	59.73%	5	5	0	100.00%
Huntingtin	HTT					132.26	59.86%	5	1	4	18.17%
HNF1-beta	HNF1B	TF				129.56	60.00%	2	1	1	52.82%
UBF	UBTF				101, 139-5p	129.28	60.14%	3	1	2	34.37%
HOXB3	HOXB3	TF		139-5p	101, 139-5p	128.68	60.27%	3	2	1	52.82%
HDAC3	HDAC3	EPIGENES				127.74	60.41%	6	3	3	24.08%
Casein kinase II, alpha chain (CSNK2A1)	CSNK2A1					126.31	60.54%	4	1	3	24.08%
CSF1	CSF1					125.96	60.68%	5	4	1	52.82%
Chk1	CHEK1					123.39	60.82%	2	1	1	52.82%
Protein kinase G1 alpha	PRKG1				199a-3p	121.81	60.95%	5	3	2	34.37%
RUNX3	RUNX3	TF				121.74	61.09%	4	3	1	52.82%
ERM	ETV5	TF		101	101, 139-5p	121.10	61.22%	4	3	1	52.82%
ZNF306	ZKSCAN3	TF	✓			120.54	61.36%	6	1	5	15.92%
alpha-11/beta-1 integrin	alpha-11/beta-1 integrin				101, 139-5p	118.97	61.50%	4	3	1	52.82%
BLIMP1 (PRDI-BF1)	PRDM1	EPIGENES				118.81	61.63%	3	2	1	52.82%
MNK2(GPRK7)	MKNK2		✓		199a-3p	118.59	61.77%	5	3	2	34.37%
JMJD2A	KDM4A	EPIGENES			101, 139-5p	118.48	61.90%	3	1	2	34.37%
ZAP70	ZAP70				101, 139-5p	117.66	62.04%	4	3	1	52.82%
Btk	BTK					116.72	62.18%	3	2	1	52.82%
AUF1	HNRNPD					115.83	62.31%	3	1	2	34.37%
PKC-lambda/iota	PRKCI			199-3p	199a-3p	114.64	62.45%	4	3	1	52.82%
PLAU (UPA)	PLAU				101, 139-5p, 199a-3p	113.79	62.59%	4	3	1	52.82%
IKK (cat)	IKK (cat)					113.60	62.72%	4	2	2	34.37%
Pdx-1 (IPF1)	PDX1	TF				111.47	62.86%	4	2	2	34.37%
ASF1A	ASF1A	EPIGENES	✓	139-5p	101, 139-5p	108.94	62.99%	2	2	0	100.00%
HSP90	HSP90				199a-3p	108.48	63.13%	4	2	2	34.37%
Collagen I	Collagen I					108.45	63.27%	4	3	1	52.82%
TOP1	TOP1			139-5p	101, 139-5p	108.14	63.40%	3	2	1	52.82%
Insulin receptor	INSR					107.51	63.54%	3	1	2	34.37%
NEUR1	NEU1		✓		199a-3p	106.91	63.67%	4	4	0	100.00%
NCOA3 (pCIP/SRC3)	NCOA3	EPIGENES				106.88	63.81%	5	2	3	24.08%
Ep-CAM	EPCAM				199a-3p	106.35	63.95%	4	2	2	34.37%
TRADD	TRADD					104.48	64.08%	3	1	2	34.37%
SOX2	SOX2	TF				103.50	64.22%	4	2	2	34.37%
IL-22 receptor	IL-22 receptor					103.36	64.35%	3	1	2	34.37%
IL8RA	CXCR1					101.74	64.49%	3	2	1	52.82%
dUTPase (DUT)	DUT		✓		199a-3p	101.62	64.63%	6	5	1	52.82%
PRMT1	PRMT1	EPIGENES				99.46	64.76%	3	1	2	34.37%
HRPT2	CDC73		✓			97.67	64.90%	5	1	4	18.17%
Prohibitin	PHB					94.64	65.03%	4	1	3	24.08%
14-3-3 beta/alpha	YWHAB					91.64	65.17%	3	1	2	34.37%

						Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Value	Rank*	Total	In	Out	Rank*
CDK5	CDK5					91.42	65.31%	3	1	2	34.37%
VEGF-B	VEGFB					90.57	65.44%	3	1	2	34.37%
MutYH	MUTYH		✓			90.24	65.58%	4	4	0	100.00%
IBP2	IGFBP2				199a-3p	89.99	65.71%	3	2	1	52.82%
Clusterin	CLU					89.49	65.85%	4	3	1	52.82%
HIP-2	UBE2K		✓			89.20	65.99%	5	1	4	18.17%
PAX5	PAX5	TF				88.35	66.12%	5	3	2	34.37%
CGI-141	GOLT1B					87.55	66.26%	2	1	1	52.82%
GHR	GHR					86.70	66.39%	2	1	1	52.82%
WNT3A	WNT3A				199a-3p	86.18	66.53%	3	2	1	52.82%
IBP4	IGFBP4					85.85	66.67%	3	2	1	52.82%
LIN-28B	LIN28B		✓	101, 199-3p	199a-3p	85.47	66.80%	3	3	0	100.00%
Versican	VCAN				101, 139-5p, 199a-3p	84.47	66.94%	4	3	1	52.82%
ATF-1	ATF1	TF			199a-3p	83.55	67.07%	4	1	3	24.08%
MLK3(MAP3K11)	MAP3K11					83.54	67.21%	4	2	2	34.37%
MYF6	MYF6	TF			101, 139-5p	82.74	67.35%	4	2	2	34.37%
Sin3A	SIN3A			101		81.69	67.48%	4	3	1	52.82%
CHERP	CHERP		✓			81.16	67.62%	3	3	0	100.00%
GRO-1	CXCL1					81.11	67.76%	2	1	1	52.82%
NEURL1	NEURL				101, 139-5p, 199a-3p	80.88	67.89%	3	3	0	100.00%
NEIL1	NEIL1				101, 139-5p	80.17	68.03%	2	1	1	52.82%
HPK38	MELK		✓			79.22	68.16%	3	3	0	100.00%
Granzyme A	GZMA					78.96	68.30%	3	2	1	52.82%
Ephrin-B receptor 1	EPHB1					78.36	68.44%	2	1	1	52.82%
Sirtuin7	SIRT7		✓		101, 139-5p	77.26	68.57%	6	5	1	52.82%
YAP1 (YAp65)	YAP1			199-3p	101, 139-5p, 199a-3p	74.60	68.71%	3	2	1	52.82%
CITED2	CITED2	TF		199-3p	199a-3p	74.32	68.84%	4	2	2	34.37%
Furin	FURIN					72.26	68.98%	4	1	3	24.08%
EGR2 (Krox20)	EGR2	TF				71.04	69.12%	3	2	1	52.82%
MEK2(MAP2K2)	MAP2K2					70.57	69.25%	3	2	1	52.82%
PAR1	F2R					70.12	69.39%	3	2	1	52.82%
Calreticulin	CALR					69.96	69.52%	2	1	1	52.82%
MEF2C	MEF2C	TF				69.82	69.66%	3	1	2	34.37%
ECE2	ECE2		✓			69.04	69.80%	2	1	1	52.82%
PKC-delta	PRKCD				101, 139-5p	67.94	69.93%	2	1	1	52.82%
FBXW7	FBXW7	EPIGENES			101, 139-5p	67.94	69.93%	2	1	1	52.82%
MTAP	MTAP		✓		199a-3p	67.73	70.20%	4	4	0	100.00%
TAFII28	TAF11		✓		101, 139-5p	67.57	70.34%	4	3	1	52.82%
LCKBP1	HCLS1	TF	✓		101, 139-5p	65.46	70.48%	3	3	0	100.00%
DMTF1	DMTF1	TF			101, 139-5p	63.48	70.61%	4	1	3	24.08%
PACE4	PCSK6				101, 139-5p	63.39	70.75%	2	1	1	52.82%
UNG1	UNG		✓	101		59.14	70.88%	3	3	0	100.00%
DOK1	DOK1					58.71	71.02%	2	1	1	52.82%
microRNA 106a	miR-106a					58.30	71.16%	2	1	1	52.82%
NIPP-1	PPP1R8				199a-3p	57.35	71.29%	3	2	1	52.82%
USP25	USP25		✓	199-3p	199a-3p	57.16	71.43%	5	5	0	100.00%
SIAHBP1	PUF60		✓			55.51	71.56%	3	2	1	52.82%
KLF7	KLF7	TF	✓			55.34	71.70%	4	3	1	52.82%
G-CSF	CSF3				101, 139-5p, 199a-3p	54.72	71.84%	3	2	1	52.82%
SNSR4	MRGPRX1					54.39	71.97%	3	1	2	34.37%
IRS-2	IRS2					54.23	72.11%	3	1	2	34.37%
FTHFSDC1	MTHFD1L		✓		199a-3p	53.82	72.24%	3	3	0	100.00%
PAK3	PAK3					53.36	72.38%	2	1	1	52.82%
DAX1	NR0B1	TF			101, 139-5p	51.55	72.52%	5	2	3	24.08%
DREAM	KCNIP3					51.51	72.65%	2	1	1	52.82%
Miz-1	ZBTB17	TF				51.50	72.79%	3	1	2	34.37%
14-3-3 sigma	SFN				101, 139-5p	51.48	72.93%	3	2	1	52.82%
RENT2	UPF2		✓	199-3p	199a-3p	50.94	73.06%	2	1	1	52.82%
BAF53A	ACTL6A	EPIGENES	✓			50.79	73.20%	5	4	1	52.82%
beta-TrCP	BTRC			199-3p	199a-3p	50.07	73.33%	3	2	1	52.82%
IBP3	IGFBP3				199a-3p	49.43	73.47%	3	2	1	52.82%
PI3K cat class IB (p110-gamma)	PIK3CG					48.72	73.61%	3	2	1	52.82%
URKL1	UCKL1		✓			48.41	73.74%	2	2	0	100.00%
CHD7	CHD7	EPIGENES	✓	139-5p	101, 139-5p	47.38	73.88%	2	2	0	100.00%
TCP1	TCP1				101, 139-5p, 199a-3p	46.98	74.01%	3	2	1	52.82%
PPP2R2D	PPP2R2D		✓			46.77	74.15%	2	1	1	52.82%
FOXC1	FOXC1	TF				46.75	74.29%	2	1	1	52.82%
Tip60	KAT5	EPIGENES				46.48	74.42%	4	1	3	24.08%
GADD45 beta	GADD45B					45.98	74.56%	3	1	2	34.37%
TAF3	TAF3		✓			45.41	74.69%	3	0	3	24.08%
SRPK1	SRPK1		✓	139-5p	101, 139-5p	45.41	74.83%	2	1	1	52.82%
PIAS4	PIAS4				101, 139-5p	45.39	74.97%	5	1	4	18.17%
PELP1	PELP1				101, 139-5p	45.36	75.10%	2	1	1	52.82%
Hamartin	TSC1				199a-3p	44.81	75.24%	3	2	1	52.82%
L3MBTL	L3MBTL	TF	✓			44.71	75.37%	3	0	3	24.08%
Calcineurin A (catalytic)	Calcineurin A (catalytic)					44.65	75.51%	2	1	1	52.82%
E7 protein (HPV16)	E7 protein (HPV16)				101, 139-5p	44.65	75.51%	2	1	1	52.82%
KNG	KNG1				101, 139-5p	44.65	75.51%	2	1	1	52.82%
IQGAP1	IQGAP1					44.00	75.92%	2	1	1	52.82%
NF-AT3(NFATC4)	NFATC4	TF				44.00	75.92%	2	1	1	52.82%
STAT2	STAT2	TF				41.53	76.19%	3	2	1	52.82%
SUPT5H	SUPT5H					40.96	76.33%	2	1	1	52.82%
PDGF-R-beta	PDGFRB					39.76	76.46%	2	1	1	52.82%
TWIST1	TWIST1				101, 139-5p, 199a-3p	39.17	76.60%	4	3	1	52.82%
RASSF1	RASSF1					38.86	76.73%	4	2	2	34.37%
NEPH2	KIRREL3					38.83	76.87%	2	1	1	52.82%
TIMP4	TIMP4				101, 139-5p	38.83	76.87%	2	1	1	52.82%
TIMP2	TIMP2				101, 139-5p	38.83	76.87%	2	1	1	52.82%
NF-E2 (45 kDa)	NFE2	TF				38.68	77.28%	4	2	2	34.37%
Casein kinase I alpha	CSNK1A1					37.84	77.41%	2	1	1	52.82%
PARP-2	PARP2					36.59	77.55%	2	1	1	52.82%
IL-5 receptor	IL-5 receptor					35.82	77.69%	2	1	1	52.82%
Calcitonin	CALCA					35.06	77.82%	2	1	1	52.82%
DDX41	DDX41		✓			34.95	77.96%	2	1	1	52.82%
GBL	MLST8				199a-3p	34.82	78.10%	2	1	1	52.82%
GRP78	HSPA5					34.73	78.23%	2	1	1	52.82%
Lyn	LYN					34.46	78.37%	5	1	4	18.17%
Sirtuin1	SIRT1	EPIGENES			199a-3p	34.37	78.50%	3	1	2	34.37%
RAGE	AGER					34.30	78.64%	2	1	1	52.82%
MBD1	MBD1	EPIGENES				34.02	78.78%	3	2	1	52.82%
Nucleolin	NCL					33.80	78.91%	4	1	3	24.08%
PI3K cat class IA	PI3K cat class IA					33.58	79.05%	2	1	1	52.82%
TRIP6	TRIP6					33.18	79.18%	2	1	1	52.82%
Claudin-1	CLDN1					33.04	79.32%	2	1	1	52.82%
EZH1	EZH1	EPIGENES	✓			32.68	79.46%	4	0	4	18.17%
VIP receptor 1	VIPR1					32.28	79.59%	2	1	1	52.82%
LL37	CAMP				101, 139-5p	31.97	79.73%	4	3	1	52.82%
CRM1	XPO1					31.93	79.86%	3	1	2	34.37%
GMF-gamma	GMFG		✓		101, 139-5p	31.84	80.00%	5	5	0	100.00%
CBF beta	CBFB	TF			101, 139-5p	31.16	80.14%	2	1	1	52.82%
GC1QBP	C1QBP				101, 139-5p	31.16	80.14%	2	1	1	52.82%
ZFP36(Tristetraprolin)	ZFP36					31.07	80.41%	3	1	2	34.37%
KLF5	KLF5	TF				30.77	80.54%	3	2	1	52.82%
ZNF593	ZNF593		✓			30.75	80.68%	2	2	0	100.00%
Thimet oligopeptidase	THOP1					30.45	80.82%	3	1	2	34.37%
EGLN1	EGLN1		✓		199a-3p	29.90	80.95%	5	2	3	24.08%
Rap1GAP1	RAP1GAP				101, 139-5p	29.56	81.09%	2	1	1	52.82%
Thrombin	F2					29.23	81.22%	3	1	2	34.37%
alpha-4/beta-1 integrin	alpha-4/beta-1 integrin				101, 139-5p	27.68	81.36%	2	1	1	52.82%
p21	CDKN1A				199a-3p	27.48	81.50%	3	2	1	52.82%

GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Betweenness		# of Interactions (Degree)			
						Value	Rank*	Total	In	Out	Rank*
Pyk2(FAK2)	PTK2B					27.06	81.63%	2	1	1	52.82%
microRNA 222	miR-222				101, 139-5p	27.00	81.77%	2	1	1	52.82%
microRNA 221	miR-221				101, 139-5p	27.00	81.77%	2	1	1	52.82%
HDAC4	HDAC4	EPIGENES				26.79	82.04%	3	1	2	34.37%
LCMR1	MED19		✓			26.69	82.18%	2	1	1	52.82%
ARPC4	ARPC4		✓		101, 139-5p	26.44	82.31%	3	3	0	100.00%
Talin	Talin					26.39	82.45%	2	1	1	52.82%
IBP6	IGFBP6					26.32	82.59%	2	1	1	52.82%
CTIP1	BCL11A					26.30	82.72%	2	1	1	52.82%
ATF-6 alpha	ATF6	TF			199a-3p	25.62	82.86%	3	1	2	34.37%
ZFPM1 (FOG)	ZFPM1					25.34	82.99%	2	1	1	52.82%
METTL7B	METTL7B		✓			25.15	83.13%	2	2	0	100.00%
HOXA2	HOXA2	TF				25.14	83.27%	2	1	1	52.82%
POU3F2 (BRN2)	POU3F2	TF			101, 139-5p	25.09	83.40%	4	3	1	52.82%
MAP2K5 (MEK5)	MAP2K5					24.74	83.54%	2	1	1	52.82%
GLUT4	SLC2A4					24.46	83.67%	2	1	1	52.82%
DRAP1	DRAP1	TF				24.26	83.81%	3	1	2	34.37%
Plakoglobin	JUP					24.06	83.95%	2	1	1	52.82%
AMPK alpha 2 subunit	PRKAA2		✓			23.91	84.08%	2	0	2	34.37%
Collectrin	TMEM27		✓			23.39	84.22%	2	2	0	100.00%
TRRAP	TRRAP					22.95	84.35%	3	1	2	34.37%
CtBP1	CTBP1	TF				22.93	84.49%	3	1	2	34.37%
AUP1	AUP1		✓			21.86	84.63%	2	2	0	100.00%
N-cadherin	CDH2					21.63	84.76%	2	1	1	52.82%
JAK3	JAK3					21.43	84.90%	3	1	2	34.37%
MLK2(MAP3K10)	MAP3K10					21.26	85.03%	2	1	1	52.82%
IL-4R type I	IL-4R type I					21.05	85.17%	2	1	1	52.82%
PIT1	POU1F1	TF			101, 139-5p	21.01	85.31%	4	3	1	52.82%
A-FABP	FABP4				101, 139-5p	20.55	85.44%	3	2	1	52.82%
CRSP9	MED7		✓			20.34	85.58%	2	2	0	100.00%
SR140	SR140		✓	199-3p	199a-3p	20.23	85.71%	2	2	0	100.00%
SOX15	SOX15	TF			199a-3p	20.17	85.85%	3	2	1	52.82%
IAP	ALPI					19.92	85.99%	3	2	1	52.82%
Prolactin receptor	PRLR					19.86	86.12%	2	1	1	52.82%
Caspase-2	CASP2					19.45	86.26%	2	1	1	52.82%
HGFA	HGFAC		✓		199a-3p	19.27	86.39%	2	2	0	100.00%
ALK-2	ACVR1					19.21	86.53%	4	3	1	52.82%
PDE4B	PDE4B		✓	199-3p	199a-3p	18.60	86.67%	2	2	0	100.00%
ALK-1	ACVRL1					18.29	86.80%	3	1	2	34.37%
PAX8	PAX8	TF				18.10	86.94%	2	1	1	52.82%
Schwannomin (NF2)	NF2					18.06	87.07%	2	1	1	52.82%
PLK1	PLK1					18.05	87.21%	2	1	1	52.82%
CXXC1	CXXC1		✓			17.96	87.35%	2	2	0	100.00%
SOCS1	SOCS1					17.93	87.48%	2	1	1	52.82%
FasL(TNFSF6)	FASLG				101, 139-5p	17.87	87.62%	4	3	1	52.82%
C3G	RAPGEF1					16.76	87.76%	2	1	1	52.82%
p107	RBL1					16.55	87.89%	3	1	2	34.37%
FAT10	UBD		✓		101, 139-5p, 199a-3p	16.31	88.03%	3	3	0	100.00%
CCR1	CCR1					16.26	88.16%	2	1	1	52.82%
Peg10	PEG10					16.09	88.30%	2	1	1	52.82%
Max	MAX	TF				16.09	88.30%	2	1	1	52.82%
Leukocyte elastase	ELANE					15.99	88.57%	2	1	1	52.82%
Leptin receptor	LEPR					15.92	88.71%	3	1	2	34.37%
PNRC2	PNRC2					15.87	88.84%	2	1	1	52.82%
TRAF7	TRAF7		✓			15.70	88.98%	3	2	1	52.82%
AXUD1	CSRNP1	TF	✓		101, 139-5p	15.64	89.12%	3	3	0	100.00%
CILP	CILP					15.64	89.25%	2	1	1	52.82%
CDX2	CDX2	TF				15.63	89.39%	2	1	1	52.82%
IL8RB	CXCR2					15.03	89.52%	2	1	1	52.82%
DNMT3B	DNMT3B	EPIGENES			199a-3p	14.96	89.66%	4	2	2	34.37%
MUC1	MUC1					14.77	89.80%	2	1	1	52.82%
MJD (ataxin-3)	ATXN3				101, 139-5p	14.77	89.93%	2	1	1	52.82%
IRF2	IRF2	TF				14.73	90.07%	2	1	1	52.82%
TBX2	TBX2	TF				14.51	90.20%	2	1	1	52.82%
ERCC6	ERCC6	EPIGENES				14.22	90.34%	2	1	1	52.82%
RCD1	RQCD1		✓			14.00	90.48%	3	1	2	34.37%
Calponin-3	CNN3					13.97	90.61%	2	1	1	52.82%
HOXC6	HOXC6	TF			199a-3p	13.93	90.75%	2	1	1	52.82%
ROR2	ROR2					13.39	90.88%	2	1	1	52.82%
Plasmin	Plasmin					13.06	91.02%	2	1	1	52.82%
Caveolin-1	CAV1					13.06	91.02%	2	1	1	52.82%
GMF	GMFB		✓			12.93	91.29%	2	1	1	52.82%
IL-9 receptor	IL-9 receptor					12.41	91.43%	2	1	1	52.82%
DDC	DDC					12.33	91.56%	2	1	1	52.82%
UBE2T	UBE2T		✓			12.33	91.70%	2	1	1	52.82%
Fibrillin 1	FBN1					12.02	91.84%	2	1	1	52.82%
GRK2	ADRBK1					11.94	91.97%	2	1	1	52.82%
40453	POU2F2	TF				11.76	92.11%	2	1	1	52.82%
SLIRP	C14orf156		✓			11.76	92.24%	2	1	1	52.82%
FLASH	CASP8AP2					11.72	92.38%	2	1	1	52.82%
ADAM17	ADAM17					11.08	92.52%	2	1	1	52.82%
A1U	UBQLN4		✓		101, 139-5p	11.02	92.65%	2	2	0	100.00%
LRP6	LRP6					10.95	92.79%	2	1	1	52.82%
NGF	NGF					10.79	92.93%	2	1	1	52.82%
IFN-alpha/beta receptor	IFN-alpha/beta receptor					10.67	93.06%	2	1	1	52.82%
CLIP170	CLIP1					10.62	93.20%	2	1	1	52.82%
GOLT1A	GOLT1A					10.36	93.33%	2	2	0	100.00%
ILK	ILK					9.95	93.47%	2	1	1	52.82%
Smac/Diablo	DIABLO					9.81	93.61%	2	1	1	52.82%
HtrA2	HTRA2					9.81	93.61%	2	1	1	52.82%
HSP60	HSPD1					9.65	93.88%	2	1	1	52.82%
Cullin 4A	CUL4A					9.37	94.01%	2	1	1	52.82%
Rictor	RICTOR					9.30	94.15%	2	1	1	52.82%
microRNA 214	miR-214				199a-3p	9.16	94.29%	3	2	1	52.82%
SATB2	SATB2	TF				9.16	94.42%	2	1	1	52.82%
TAK1(MAP3K7)	MAP3K7					9.14	94.56%	3	1	2	34.37%
PLC-gamma 1	PLCG1					8.83	94.69%	2	1	1	52.82%
HCF1	HCFC1	TF				8.80	94.83%	2	1	1	52.82%
BMP receptor 2	BMPR2					8.59	94.97%	3	2	1	52.82%
TXNIP (VDUP1)	TXNIP					8.48	95.10%	3	2	1	52.82%
SP4	SP4	TF				8.43	95.24%	2	1	1	52.82%
HES1	HES1					8.37	95.37%	2	1	1	52.82%
LRP130	LRPPRC		✓			8.14	95.51%	2	1	1	52.82%
Twinfilin	TWF1		✓			7.76	95.65%	2	2	0	100.00%
ACY2	ASPA		✓			7.57	95.78%	2	2	0	100.00%
40457	POU3F1	TF				7.48	95.92%	2	1	1	52.82%
IL-10 receptor	IL-10 receptor					7.35	96.05%	2	1	1	52.82%
WNT11	WNT11					6.96	96.19%	2	1	1	52.82%
PLOD1	PLOD1		✓			6.65	96.33%	2	2	0	100.00%
EDF1	EDF1	TF				6.62	96.46%	2	1	1	52.82%
SREBP2 precursor	SREBF2	TF				6.62	96.46%	2	1	1	52.82%
RBMS1	RBMS1				199a-3p	6.59	96.73%	2	1	1	52.82%
ETS2	ETS2	TF			101, 139-5p	6.53	96.87%	4	1	3	24.08%
CRHR1	CRHR1					6.29	97.01%	2	1	1	52.82%
ING1	ING1					6.17	97.14%	2	1	1	52.82%
TRAF6	TRAF6					6.15	97.28%	2	1	1	52.82%
Staf-50	TRIM22	TF	✓		199a-3p	5.71	97.41%	2	1	1	52.82%
Casein kinase II, alpha' chain (CSNK2A2)	CSNK2A2					5.69	97.55%	2	1	1	52.82%
N-Ras	NRAS					5.58	97.69%	2	1	1	52.82%
K-RAS	KRAS					5.58	97.69%	2	1	1	52.82%

						Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	miRNA Subnetwork**	Value	Rank*	Total	In	Out	Rank*
NFE2L1	NFE2L1	TF				5.52	97.96%	2	1	1	52.82%
Neuropilin-2	NRP2					5.26	98.10%	3	1	2	34.37%
Tuberin	TSC2					4.95	98.23%	2	1	1	52.82%
Cathepsin H	CTSH		✓			4.78	98.37%	3	3	0	100.00%
CDC18L (CDC6)	CDC6					4.58	98.50%	2	1	1	52.82%
PURB	PURB	TF	✓			4.28	98.64%	2	0	2	34.37%
PKC-zeta	PRKCZ					4.22	98.78%	2	1	1	52.82%
ATP2C1	ATP2C1		✓			3.83	98.91%	2	2	0	100.00%
Tafazzin	TAZ		✓			3.36	99.05%	2	1	1	52.82%
SETDB1	SETDB1	EPIGENES				3.06	99.18%	2	1	1	52.82%
GPI	GPI				199a-3p	3.00	99.32%	2	2	0	100.00%
ZNF57	ZNF57		✓			2.97	99.46%	2	2	0	100.00%
L1CAM	L1CAM					2.79	99.59%	3	1	2	34.37%
CDC25A	CDC25A					1.89	99.73%	2	1	1	52.82%
RIG-G	IFIT3					1.75	99.86%	2	1	1	52.82%
ENY2	ENY2		✓			0.00	100.00%	1	1	0	100.00%
SBDS	SBDS					0.00	100.00%	1	1	0	100.00%
ZNF133	ZNF133	TF	✓			0.00	100.00%	1	1	0	100.00%
TH1L	TH1L		✓			0.00	100.00%	1	1	0	100.00%
Ms4a6b	MS4A6A		✓			0.00	100.00%	1	1	0	100.00%
RNF138	RNF138					0.00	100.00%	1	1	0	100.00%
UBE2Q2	UBE2Q2		✓			0.00	100.00%	1	1	0	100.00%
COQ3	COQ3		✓			0.00	100.00%	1	1	0	100.00%
ABTAP	ESF1		✓			0.00	100.00%	1	1	0	100.00%
ZNF131	ZNF131	TF	✓			0.00	100.00%	1	1	0	100.00%
JRKL	JRKL		✓			0.00	100.00%	1	0	1	52.82%
C20orf104	PHF20		✓			0.00	100.00%	1	1	0	100.00%
TGF-beta 3	TGFB3					0.00	100.00%	2	1	1	52.82%
YME1L1	YME1L1		✓			0.00	100.00%	1	0	1	52.82%
CDK6	CDK6					0.00	100.00%	1	1	0	100.00%
TGM2	TGM2					0.00	100.00%	1	0	1	52.82%
p130CAS	BCAR1					0.00	100.00%	2	1	1	52.82%
GLK(MAP4K3)	MAP4K3					0.00	100.00%	2	0	2	34.37%
GCKR(MAP4K5)	MAP4K5					0.00	100.00%	1	1	0	100.00%
TCL1A	TCL1A					0.00	100.00%	1	1	0	100.00%
CD43	SPN					0.00	100.00%	1	0	1	52.82%
Elk-4	ELK4	TF				0.00	100.00%	1	0	1	52.82%
SOCS3	SOCS3					0.00	100.00%	2	1	1	52.82%
MEF2A	MEF2A	TF				0.00	100.00%	2	1	1	52.82%
HAND2	HAND2	TF				0.00	100.00%	1	0	1	52.82%
ELF2	ELF2	TF	✓			0.00	100.00%	1	1	0	100.00%
TARDBP (TDP43)	TARDBP	TF	✓			0.00	100.00%	1	1	0	100.00%
SC1	TCF19	TF	✓			0.00	100.00%	1	1	0	100.00%
GAS41	YEATS4	TF	✓			0.00	100.00%	1	1	0	100.00%
VGLL4	VGLL4		✓			0.00	100.00%	1	1	0	100.00%
PMS2L1	PMS2L1		✓			0.00	100.00%	1	0	1	52.82%
P3H1	LEPRE1		✓			0.00	100.00%	2	1	1	52.82%
ACY3	ACY3		✓			0.00	100.00%	1	0	1	52.82%
PRMT3	PRMT3		✓			0.00	100.00%	2	1	1	52.82%
PMS2L8	PMS2L1		✓			0.00	100.00%	1	1	0	100.00%
ZBTB40	ZBTB40		✓			0.00	100.00%	1	1	0	100.00%
Ciao 1	CIAO1		✓			0.00	100.00%	1	1	0	100.00%
C16orf35	C16orf35					0.00	100.00%	1	1	0	100.00%
AKNA	AKNA		✓			0.00	100.00%	1	1	0	100.00%
FAHD2A	FAHD2A		✓			0.00	100.00%	2	1	1	52.82%
ZNF101	ZNF101		✓			0.00	100.00%	1	1	0	100.00%
SAE2	UBA2		✓			0.00	100.00%	1	0	1	52.82%
CNOT4	CNOT4		✓			0.00	100.00%	1	1	0	100.00%
ZFP95	ZKSCAN5	TF	✓			0.00	100.00%	1	0	1	52.82%
WBSCR22	WBSCR22		✓			0.00	100.00%	1	1	0	100.00%
SARA	ZFYVE9					0.00	100.00%	1	1	0	100.00%
HELLS (Lsh)	HELLS	EPIGENES	✓			0.00	100.00%	1	1	0	100.00%
DAB2	DAB2					0.00	100.00%	1	1	0	100.00%
TRAP100	MED24		✓			0.00	100.00%	1	1	0	100.00%
SURF5	MED22					0.00	100.00%	2	1	1	52.82%
RagC	RRAGC		✓			0.00	100.00%	2	1	1	52.82%
AMYP	AMY2A					0.00	100.00%	1	1	0	100.00%
USP48	USP48					0.00	100.00%	1	1	0	100.00%
PDIK1L	PDIK1L		✓			0.00	100.00%	1	1	0	100.00%
RNASEH2A	RNASEH2A					0.00	100.00%	1	1	0	100.00%
CHD6	CHD6	EPIGENES	✓	101		0.00	100.00%	1	1	0	100.00%
RAD54B	RAD54B	EPIGENES	✓			0.00	100.00%	1	0	1	52.82%
PRIM1	PRIM1		✓			0.00	100.00%	1	1	0	100.00%
Fbxo3	FBXO3		✓			0.00	100.00%	1	1	0	100.00%
ZNF764	ZNF764		✓			0.00	100.00%	1	1	0	100.00%
Pirin	PIR		✓			0.00	100.00%	2	1	1	52.82%
ZNF33A	ZNF33A	TF	✓	101		0.00	100.00%	2	1	1	52.82%
ZNF96	ZSCAN12	TF	✓			0.00	100.00%	4	2	2	34.37%
SULF2	SULF2		✓		199a-3p	0.00	100.00%	2	1	1	52.82%
C/EBP zeta	DDIT3	TF			101, 139-5p	0.00	100.00%	2	1	1	52.82%
USP31	USP31		✓		101, 139-5p	0.00	100.00%	2	1	1	52.82%
GFER	GFER				101, 139-5p	0.00	100.00%	2	1	1	52.82%
GSK3 alpha	GSK3A				101, 139-5p	0.00	100.00%	2	1	1	52.82%
ADNP	ADNP	TF	✓		101, 139-5p	0.00	100.00%	2	1	1	52.82%
Ifi202a	Ifi202a				101, 139-5p	0.00	100.00%	2	1	1	52.82%
microRNA 206	miR-206				101, 139-5p	0.00	100.00%	2	1	1	52.82%
Thioredoxin	TXN				101, 139-5p	0.00	100.00%	2	1	1	52.82%
ZNF160	ZNF160		✓	139-5p	101, 139-5p	0.00	100.00%	2	1	1	52.82%
S100A7	S100A7				101, 139-5p	0.00	100.00%	2	1	1	52.82%
Pinin	PNN		✓	139-5p	101, 139-5p	0.00	100.00%	1	1	0	100.00%
MED8	MED8		✓	139-5p	101, 139-5p	0.00	100.00%	1	1	0	100.00%
ODP2	DLAT		✓		101, 139-5p	0.00	100.00%	2	2	0	100.00%

* Rank percentile

** The componets in specific miRNA-subnetworks

† Predicted by TargetScan and context score < -0.2

Supplementary table S7. Topological properties of miR-101 sub-network for cluster C6 network

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Value	Rank*	Total	In	Out	Rank*
AP-1	FOS	TF		101, 139-5p, 199-3p	88207.05	0.78%	190	11	179	0.72%
miR-101	miR-101				74861.48	1.56%	77	4	73	1.44%
EZH2	EZH2	EPIGENES	✓	101	16024.90	2.34%	42	2	40	2.16%
JAK2	JAK2			101	9490.86	3.13%	17	2	15	3.60%
NF-kB	RELA	TF			8920.23	3.91%	28	2	26	2.88%
ZNF143	ZNF143	TF	✓	101	6005.86	4.69%	12	2	10	5.04%
SUMO-3	SUMO3		✓	101, 199-3p	5966.60	5.47%	17	1	16	3.60%
Caspase-3	CASP3			101, 139-5p	5910.47	6.25%	10	1	9	7.91%
mTOR	MTOR		✓		4266.82	7.03%	11	1	10	6.47%
Fibronectin	FN1			101, 199-3p	3780.00	7.81%	7	2	5	13.67%
TAZ	WWTR1			101	3126.90	8.59%	11	2	9	6.47%
PC4	SUB1		✓	101	3067.21	9.38%	6	1	5	15.83%
EED	EED	EPIGENES	✓	101	3004.33	10.16%	12	2	10	5.04%
AML1 (RUNX1)	RUNX1	TF		101, 139-5p, 199-3p	2706.87	10.94%	9	2	7	10.07%
NLK	NLK		✓	101, 199-3p	2395.73	11.72%	7	1	6	13.67%
BRG1 (SMARCA4)	SMARCA4	EPIGENES		101	2375.62	12.50%	10	1	9	7.91%
ASK1 (MAP3K5)	MAP3K5			101, 139-5p, 199-3p	2357.77	13.28%	5	1	4	19.42%
c-Myb	MYB			101	2133.98	14.06%	10	4	6	7.91%
BAF250A (ARID1A)	ARID1A	EPIGENES	✓	101	2037.98	14.84%	8	1	7	12.23%
STAT3	STAT3	TF			1925.07	15.63%	4	4	0	25.90%
p53	TP53	TF			1787.75	16.41%	6	6	0	15.83%
TGF-beta receptor type I	TGFBR1			101	1759.01	17.19%	5	1	4	19.42%
Aggrecanase-2	ADAMTS5		✓	101	1635.72	17.97%	5	1	4	19.42%
Rac1	RAC1			101	1629.72	18.75%	4	1	3	25.90%
Galpha(s)-specific calcitonin GPCRs	Galpha(s)-specific calcitonin GPCRs				1518.00	19.53%	4	1	3	25.90%
Neuropilin-1	NRP1			101	1518.00	19.53%	4	2	2	25.90%
RIPK1	RIPK1			101	1518.00	19.53%	3	1	2	38.13%
RAP-1A	RAP1A			101	1518.00	19.53%	3	1	2	38.13%
G-protein beta/gamma	G-protein beta/gamma				1518.00	19.53%	4	2	2	25.90%
N-Myc	MYCN	TF		101	1300.43	23.44%	9	1	8	10.07%
TIF1-alpha	TRIM24	EPIGENES	✓	101, 139-5p	1294.57	24.22%	7	1	6	13.67%
STAT4	STAT4	TF			1290.21	25.00%	2	2	0	62.59%
RNA polymerase II	RNA polymerase II				1162.64	25.78%	4	1	3	25.90%
MRK	ICK		✓	101, 139-5p	1128.87	26.56%	3	1	2	38.13%
Tcf(Lef)	LEF1	TF			1107.00	27.34%	5	5	0	19.42%
C/EBPalpha	CEBPA	TF		101	1061.86	28.13%	9	2	7	10.07%
c-Myc	MYC	TF			1052.22	28.91%	5	5	0	19.42%
JDP2	JDP2	TF	✓	101	1016.74	29.69%	8	2	6	12.23%
DNMT3A	DNMT3A	EPIGENES		101, 199-3p	900.93	30.47%	6	3	3	15.83%
CTCF	CTCF	TF		101	878.63	31.25%	4	2	2	25.90%
TFIIE, alpha subunit	GTF2E1		✓	101	799.21	32.03%	4	2	2	25.90%
GABP alpha	GABPA	TF			775.13	32.81%	2	2	0	62.59%
PACAP	ADCYAP1			101	760.00	33.59%	4	2	2	25.90%
ENA-78	ENA-78				760.00	33.59%	2	1	1	62.59%
Amyloid beta	Amyloid beta				760.00	33.59%	2	1	1	62.59%
NOTCH1 (NICD)	NOTCH1 (NICD)				760.00	33.59%	2	1	1	62.59%
MSX1	MSX1	TF		101	760.00	33.59%	3	2	1	38.13%
GFRalpha1	GFRA1			101	760.00	33.59%	2	1	1	62.59%
DR1	DR1		✓	101	760.00	33.59%	2	1	1	62.59%
IL-13	IL13			101	760.00	33.59%	3	2	1	38.13%
Galpha(q)-specific frizzled GPCRs	Galpha(q)-specific frizzled GPCRs				760.00	33.59%	2	1	1	62.59%
IL-1RI	IL1R1			101	760.00	33.59%	2	1	1	62.59%
Ataxin-1	ATXN1			101, 139-5p	760.00	33.59%	2	1	1	62.59%
CYLD	CYLD			101	760.00	33.59%	2	1	1	62.59%
IL-12 receptor	IL-12 receptor				760.00	33.59%	3	1	2	38.13%
Importin (karyopherin)-beta	Importin (karyopherin)-beta				760.00	33.59%	2	1	1	62.59%
ESR1 (nuclear)	ESR1	TF			692.76	44.53%	4	4	0	25.90%
Beta-catenin	CTNNB1	TF			670.47	45.31%	4	4	0	25.90%
C/EBPdelta	CEBPD	TF	✓		652.40	46.09%	5	5	0	19.42%
p130	RBL2			101	564.79	46.88%	5	2	3	19.42%
IL-4	IL4				556.57	47.66%	3	3	0	38.13%
DNMT1	DNMT1	EPIGENES			556.57	47.66%	3	3	0	38.13%
Endoglin	ENG		✓		480.13	49.22%	3	3	0	38.13%
RAR-alpha/RXR-alpha	RAR-alpha/RXR-alpha	TF			468.96	50.00%	4	4	0	25.90%
AKT(PKB)	AKT(PKB)				466.74	50.78%	2	2	0	62.59%
Androgen receptor	AR	TF			453.59	51.56%	5	5	0	19.42%
Versican	VCAN				422.01	52.34%	2	2	0	62.59%
JNK(MAPK8-10)	JNK(MAPK8-10)				422.01	52.34%	2	2	0	62.59%
PAX3	PAX3	TF			418.36	53.91%	3	3	0	38.13%
Progesterone receptor	PGR	TF			340.08	56.25%	3	3	0	38.13%
IGF-1	IGF-1				392.12	55.47%	5	5	0	19.42%
Cyclin D1	CCND1				340.08	56.25%	3	3	0	38.13%
CIITA	CIITA	EPIGENES			317.61	57.81%	2	2	0	62.59%
NRF2	NFE2L2	TF		101	313.76	62.50%	6	2	4	15.83%
SNAIL1	SNAI1				317.61	57.81%	2	2	0	62.59%
14-3-3 sigma	SFN				317.61	57.81%	2	2	0	62.59%
TNF-alpha	TNF				317.61	57.81%	2	2	0	62.59%
WNT5A	WNT5A				317.61	57.81%	2	2	0	62.59%
PTEN	PTEN			139-5p	317.61	57.81%	2	2	0	62.59%
ERM	ETV5	TF		101	269.40	63.28%	4	3	1	25.90%
Oct-3/4	POU5F1	TF			215.30	64.84%	2	2	0	62.59%
Cathepsin L	Cathepsin L				215.39	64.06%	4	4	0	25.90%
YY1	YY1	TF			212.76	65.63%	3	2	1	38.13%
RUNX2	RUNX2	TF			207.55	66.41%	2	2	0	62.59%
SMAD7	SMAD7	TF			207.55	66.41%	2	2	0	62.59%
Eomesodermin	EOMES	TF	✓		153.21	72.66%	3	3	0	38.13%
TMF1	TMF1		✓	101, 139-5p	195.12	67.97%	4	1	3	25.90%
TGT	USP14		✓	101	192.84	68.75%	2	1	1	62.59%
ZNRF2	ZNRF2		✓	101, 199-3p	192.84	68.75%	2	1	1	62.59%
PCY2	PCYT2		✓		187.14	70.31%	3	3	0	38.13%
Thrombospondin 1	THBS1			139-5p	173.08	71.09%	2	2	0	62.59%
CDK1 (p34)	CDK1				173.08	71.09%	2	2	0	62.59%
SOX9	SOX9	TF		101	100.79	76.56%	3	1	2	38.13%
p27KIP1	CDKN1B				140.67	73.44%	2	2	0	62.59%
SMAD3	SMAD3	TF			77.14	77.34%	3	3	0	38.13%
QKI	QKI		✓	101, 199-3p	113.06	75.00%	2	1	1	62.59%
Sin3A	SIN3A			101	105.91	75.78%	3	2	1	38.13%
ZNF217	ZNF217	TF		101, 199-3p	73.88	78.13%	2	1	1	62.59%
MAFG	MAFG	TF	✓		64.85	79.69%	3	3	0	38.13%
STAT1	STAT1	TF			63.69	82.03%	2	2	0	62.59%
PNRC1	PNRC1		✓	101, 199-3p	67.76	78.91%	3	2	1	38.13%
SSAT	SAT1		✓		64.85	79.69%	3	3	0	38.13%
Sequestosome 1(p62)	SQSTM1		✓		64.85	79.69%	3	3	0	38.13%
ATF-3	ATF3	TF	✓		61.43	83.59%	3	3	0	38.13%
MITF	MITF	TF		101	45.71	86.72%	4	3	1	25.90%
EWS/FLI1 fusion protein	EWS/FLI1 fusion protein				61.97	82.81%	2	2	0	62.59%
DNMT3B	DNMT3B	EPIGENES			26.20	89.84%	2	2	0	62.59%

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Value	Rank*	Total	In	Out	Rank*
IBP5	IGFBP5			101, 139-5p	50.63	84.38%	2	1	1	62.59%
PSF	SFPQ			101	50.63	84.38%	2	1	1	62.59%
ZNF451	ZNF451		✓	101	48.63	85.94%	2	1	1	62.59%
TITF1	NKX2-1	TF			19.92	92.19%	3	3	0	38.13%
MCM2	MCM2		✓		41.30	87.50%	4	4	0	25.90%
MCM5	MCM5		✓		33.79	88.28%	3	3	0	38.13%
MCM3	MCM3		✓		32.66	89.06%	2	2	0	62.59%
NIPP-1	PPP1R8				26.20	89.84%	2	2	0	62.59%
EGR1	EGR1	TF	✓		13.06	93.75%	3	3	0	38.13%
CSF1	CSF1				24.47	91.41%	2	2	0	62.59%
KLF4	KLF4	TF	✓		5.52	95.31%	3	3	0	38.13%
BAT3	BAT3		✓		17.33	92.97%	2	2	0	62.59%
KLF6	KLF6	TF	✓		4.75	96.09%	3	3	0	38.13%
Ubiquitin	UBB				7.04	94.53%	3	3	0	38.13%
BMI-1	BMI1	EPIGENES	✓		2.33	99.22%	2	2	0	62.59%
ADNP	ADNP	TF	✓		0.00	100.00%	1	1	0	100.00%
M-CSF receptor	CSF1R		✓		2.69	96.88%	3	3	0	38.13%
Sirtuin7	SIRT7		✓		2.69	96.88%	2	2	0	62.59%
MCM4/6/7 complex	MCM4/6/7 complex				2.43	98.44%	3	3	0	38.13%
AHR	AHR	TF			0.00	100.00%	1	1	0	100.00%
FGL2	FGL2		✓	199-3p	0.00	100.00%	1	1	0	100.00%
Pyk2(FAK2)	PTK2B				0.00	100.00%	1	1	0	100.00%
POLA1	POLA1		✓		0.00	100.00%	1	1	0	100.00%
Cathepsin V	CTSL1		✓		0.00	100.00%	1	1	0	100.00%
GSTM1	GSTM1				0.00	100.00%	1	1	0	100.00%
RET	RET				0.00	100.00%	1	1	0	100.00%
Bcl-2	BCL2			139-5p	0.00	100.00%	1	1	0	100.00%
USP25	USP25		✓	199-3p	0.00	100.00%	1	1	0	100.00%
AP-2A	TFAP2A	TF			0.00	100.00%	1	1	0	100.00%
CDK5	CDK5				0.00	100.00%	1	1	0	100.00%
AXUD1	CSRNP1	TF	✓		0.00	100.00%	1	1	0	100.00%
PAK3	PAK3				0.00	100.00%	1	1	0	100.00%
ErbB2	ERBB2				0.00	100.00%	1	1	0	100.00%
BMAL1	ARNTL	TF			0.00	100.00%	2	2	0	62.59%
TGF-beta receptor type II	TGFBR2				0.00	100.00%	1	1	0	100.00%
TIMP4	TIMP4				0.00	100.00%	1	1	0	100.00%
FasL(TNFSF6)	FASLG				0.00	100.00%	1	1	0	100.00%
C/EBP zeta	DDIT3	TF			0.00	100.00%	1	1	0	100.00%
C/EBPbeta	CEBPB	TF			0.00	100.00%	3	2	1	38.13%
DAB2	DAB2				0.00	100.00%	1	1	0	100.00%
VIP receptor 1	VIPR1				0.00	100.00%	1	1	0	100.00%
Raptor	RPTOR				0.00	100.00%	1	1	0	100.00%
Karyopherin alpha 3	KPNA3				0.00	100.00%	1	1	0	100.00%
S100A7	S100A7				0.00	100.00%	1	1	0	100.00%
CBF beta	CBFB	TF			0.00	100.00%	1	1	0	100.00%
LL37	CAMP				0.00	100.00%	1	1	0	100.00%
COUP-TFI	NR2F1	TF	✓		0.00	100.00%	1	1	0	100.00%
ODP2	DLAT		✓		0.00	100.00%	1	1	0	100.00%
microRNA 206	miR-206				0.00	100.00%	1	1	0	100.00%
VEGF-D	FIGF			139-5p	0.00	100.00%	1	1	0	100.00%
DMTF1	DMTF1	TF			0.00	100.00%	1	1	0	100.00%
PDGF-A	PDGFA				0.00	100.00%	1	1	0	100.00%
MKK7 (MAP2K7)	MAP2K7				0.00	100.00%	1	1	0	100.00%
NEIL1	NEIL1				0.00	100.00%	1	1	0	100.00%
DRAP1	DRAP1	TF			0.00	100.00%	1	1	0	100.00%
TWIST1	TWIST1				0.00	100.00%	1	1	0	100.00%
Casein kinase I alpha	CSNK1A1				0.00	100.00%	1	1	0	100.00%
UNG1	UNG		✓	101	0.00	100.00%	1	1	0	100.00%
RASSF1	RASSF1				0.00	100.00%	1	1	0	100.00%
Leptin	LEP				0.00	100.00%	1	1	0	100.00%
HSP27	HSPB1				0.00	100.00%	1	1	0	100.00%
PACE4	PCSK6				0.00	100.00%	1	1	0	100.00%
E2F1	E2F1	TF			0.00	100.00%	1	1	0	100.00%
EGR2 (Krox20)	EGR2	TF			0.00	100.00%	1	1	0	100.00%
Adrenomedullin	ADM				0.00	100.00%	1	1	0	100.00%
ELF1	ELF1	TF			0.00	100.00%	1	1	0	100.00%
RNF138	RNF138				0.00	100.00%	1	1	0	100.00%
FAK1	PTK2				0.00	100.00%	1	1	0	100.00%
ELF3	ELF3	TF			0.00	100.00%	1	1	0	100.00%
Elk-1	ELK1	TF			0.00	100.00%	1	1	0	100.00%
PKA-cat beta	PRKACB			139-5p	0.00	100.00%	1	1	0	100.00%
ERR1	ESRRA	TF			0.00	100.00%	1	1	0	100.00%
DAXX	DAXX		✓		0.00	100.00%	1	1	0	100.00%
Tyk2	TYK2				0.00	100.00%	1	1	0	100.00%
ETS1	ETS1	TF		139-5p	0.00	100.00%	2	2	0	62.59%
STAT5	STAT5				0.00	100.00%	1	1	0	100.00%
GRK2	ADRBK1				0.00	100.00%	1	1	0	100.00%
c-IAP1	BIRC2				0.00	100.00%	1	1	0	100.00%
SAT-1	SLC26A1				0.00	100.00%	1	1	0	100.00%
c-Abl	ABL1				0.00	100.00%	1	1	0	100.00%
G-CSF	CSF3				0.00	100.00%	1	1	0	100.00%
ETS2	ETS2	TF			0.00	100.00%	1	1	0	100.00%
Rad51	RAD51				0.00	100.00%	1	1	0	100.00%
microRNA 214	miR-214				0.00	100.00%	1	1	0	100.00%
FKHR	FOXO1	TF			0.00	100.00%	1	1	0	100.00%
OAS2	OAS2		✓		0.00	100.00%	1	1	0	100.00%
p15	CDKN2B				0.00	100.00%	1	1	0	100.00%
FOXF1	FOXF1	TF			0.00	100.00%	1	1	0	100.00%
DAPK1	DAPK1				0.00	100.00%	1	1	0	100.00%
G-protein alpha-q/11	G-protein alpha-q/11				0.00	100.00%	1	1	0	100.00%
FOXF2	FOXF2	TF			0.00	100.00%	1	1	0	100.00%
MMP-12	MMP12				0.00	100.00%	1	1	0	100.00%
YAP1 (YAp65)	YAP1			199-3p	0.00	100.00%	1	1	0	100.00%
FOXO3A	FOXO3	TF			0.00	100.00%	1	1	0	100.00%
PELP1	PELP1				0.00	100.00%	1	1	0	100.00%
SHP-1	PTPN6				0.00	100.00%	1	1	0	100.00%
FHL2	FHL2		✓		0.00	100.00%	1	1	0	100.00%
PP2A catalytic	PP2A catalytic				0.00	100.00%	1	1	0	100.00%
CILP	CILP				0.00	100.00%	1	1	0	100.00%
ELL2	ELL2		✓	139-5p	0.00	100.00%	1	1	0	100.00%
Clusterin	CLU				0.00	100.00%	1	1	0	100.00%
FOXP1	FOXP1	TF		139-5p, 199-3p	0.00	100.00%	1	1	0	100.00%
GC1QBP	C1QBP				0.00	100.00%	1	1	0	100.00%
FOXP3	FOXP3	TF			0.00	100.00%	1	1	0	100.00%
TIMP2	TIMP2				0.00	100.00%	1	1	0	100.00%
PI3K cat class IB (p110-gamma)	PIK3CG				0.00	100.00%	1	1	0	100.00%
GATA-6	GATA6	TF			0.00	100.00%	1	1	0	100.00%
Golgin-45 (BLZF1)	BLZF1	TF	✓		0.00	100.00%	2	2	0	62.59%

GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Betweenness Value	Betweenness Rank*	# of Interactions (Degree) Total	In	Out	Rank*
DJ-1	PARK7				0.00	100.00%	1	1	0	100.00%
TAFII28	TAF11		✓		0.00	100.00%	1	1	0	100.00%
HNF4-alpha	HNF4A	TF			0.00	100.00%	1	1	0	100.00%
MAP3K3	MAP3K3				0.00	100.00%	1	1	0	100.00%
TIMP1	TIMP1				0.00	100.00%	1	1	0	100.00%
TAFI48	TAF1A		✓		0.00	100.00%	1	1	0	100.00%
TRIP6	TRIP6				0.00	100.00%	1	1	0	100.00%
HOXB3	HOXB3	TF		139-5p	0.00	100.00%	1	1	0	100.00%
SARA	ZFYVE9				0.00	100.00%	1	1	0	100.00%
GSK3 beta	GSK3B				0.00	100.00%	1	1	0	100.00%
MSH6	MSH6				0.00	100.00%	1	1	0	100.00%
CLIP170	CLIP1				0.00	100.00%	1	1	0	100.00%
HSF1	HSF1	TF			0.00	100.00%	1	1	0	100.00%
A-FABP	FABP4				0.00	100.00%	1	1	0	100.00%
FBXW7	FBXW7	EPIGENES			0.00	100.00%	1	1	0	100.00%
ID1	ID1				0.00	100.00%	1	1	0	100.00%
ERK1/2	ERK1/2				0.00	100.00%	1	1	0	100.00%
MJD (ataxin-3)	ATXN3				0.00	100.00%	1	1	0	100.00%
CtBP2	CTBP2				0.00	100.00%	1	1	0	100.00%
Cystatin A	CSTA				0.00	100.00%	1	1	0	100.00%
HSF2	HSF2	TF	✓		0.00	100.00%	1	1	0	100.00%
IRF1	IRF1	TF			0.00	100.00%	1	1	0	100.00%
RAGE	AGER				0.00	100.00%	1	1	0	100.00%
HB-EGF	HBEGF				0.00	100.00%	1	1	0	100.00%
p14ARF	CDKN2A		✓		137.24	74.22%	3	3	0	38.13%
PRMT1	PRMT1	EPIGENES			0.00	100.00%	1	1	0	100.00%
BMP4	BMP4				0.00	100.00%	1	1	0	100.00%
p16INK4	CDKN2A		✓		395.15	54.69%	6	6	0	15.83%
IRF4	IRF4	TF			0.00	100.00%	1	1	0	100.00%
CDK4	CDK4				0.00	100.00%	1	1	0	100.00%
TARBP1	TARBP1		✓		0.00	100.00%	1	1	0	100.00%
microRNA 221	miR-221				0.00	100.00%	1	1	0	100.00%
DKK1	DKK1				0.00	100.00%	1	1	0	100.00%
p300	EP300	EPIGENES			0.00	100.00%	1	1	0	100.00%
WNT3A	WNT3A				0.00	100.00%	1	1	0	100.00%
LCKBP1	HCLS1	TF	✓		0.00	100.00%	1	1	0	100.00%
TRAF7	TRAF7		✓		0.00	100.00%	1	1	0	100.00%
MEF2A	MEF2A	TF			0.00	100.00%	1	1	0	100.00%
MEF2C	MEF2C	TF			0.00	100.00%	1	1	0	100.00%
Twinfilin	TWF1		✓		0.00	100.00%	1	1	0	100.00%
A1U	UBQLN4		✓		0.00	100.00%	1	1	0	100.00%
Cyclin E	CCNE1				0.00	100.00%	1	1	0	100.00%
MEF2D	MEF2D	TF			0.00	100.00%	1	1	0	100.00%
Brca1	BRCA1				0.00	100.00%	1	1	0	100.00%
MYF5	MYF5	TF			0.00	100.00%	1	1	0	100.00%
RAIDD	CRADD				0.00	100.00%	1	1	0	100.00%
MYF6	MYF6	TF			0.00	100.00%	1	1	0	100.00%
MYOD	MYOD1	TF			0.00	100.00%	1	1	0	100.00%
MYOG	MYOG	TF			0.00	100.00%	1	1	0	100.00%
CRK	CRK				0.00	100.00%	1	1	0	100.00%
PCNA	PCNA				0.00	100.00%	1	1	0	100.00%
Shc	SHC1			139-5p	0.00	100.00%	1	1	0	100.00%
N-CoR	NCOR1	TF	✓		0.00	100.00%	1	1	0	100.00%
VEGFR-3	FLT4				0.00	100.00%	1	1	0	100.00%
Prolactin	PRL				0.00	100.00%	1	1	0	100.00%
SOD2	SOD2		✓		0.00	100.00%	2	2	0	62.59%
NANOG	NANOG	TF			0.00	100.00%	1	1	0	100.00%
GFER	GFER				0.00	100.00%	1	1	0	100.00%
GRB2	GRB2				0.00	100.00%	1	1	0	100.00%
PIAS4	PIAS4				0.00	100.00%	1	1	0	100.00%
14-3-3 zeta/delta	YWHAZ			199-3p	0.00	100.00%	1	1	0	100.00%
Cystatin B	CSTB				0.00	100.00%	1	1	0	100.00%
BMP2	BMP2				0.00	100.00%	1	1	0	100.00%
NF-AT3(NFATC4)	NFATC4	TF			0.00	100.00%	1	1	0	100.00%
c-Raf-1	RAF1				0.00	100.00%	1	1	0	100.00%
microRNA 21	miR-21				0.00	100.00%	1	1	0	100.00%
NF-Y	NF-Y				0.00	100.00%	1	1	0	100.00%
MMP-14	MMP14		✓		0.00	100.00%	1	1	0	100.00%
p130CAS	BCAR1				0.00	100.00%	1	1	0	100.00%
Galectin-3	LGALS3				0.00	100.00%	1	1	0	100.00%
ARID4B	ARID4B		✓	101, 199-3p	0.00	100.00%	2	1	1	62.59%
FasR(CD95)	FAS				0.00	100.00%	1	1	0	100.00%
HDAC2	HDAC2	EPIGENES		139-5p	0.00	100.00%	1	1	0	100.00%
I-kB	I-kB				0.00	100.00%	1	1	0	100.00%
Pc2 (CBX4)	CBX4	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
E7 protein (HPV16)	E7 protein (HPV16)				0.00	100.00%	1	1	0	100.00%
ACM3	CHRM3				0.00	100.00%	1	1	0	100.00%
G-protein alpha-i family	G-protein alpha-i family				0.00	100.00%	1	1	0	100.00%
alpha-V/beta-3 integrin	alpha-V/beta-3 integrin				0.00	100.00%	1	1	0	100.00%
MBD1	MBD1	EPIGENES			0.00	100.00%	1	1	0	100.00%
Sortilin	SORT1		✓		0.00	100.00%	1	1	0	100.00%
Ifi202a	Ifi202a				0.00	100.00%	1	1	0	100.00%
EGF	EGF				0.00	100.00%	1	1	0	100.00%
PAX8	PAX8	TF			0.00	100.00%	1	1	0	100.00%
IKK-gamma	IKBKG				0.00	100.00%	1	1	0	100.00%
IL-18	IL18				0.00	100.00%	1	1	0	100.00%
APEX	APEX1				0.00	100.00%	1	1	0	100.00%
VEGF-A	VEGFA				0.00	100.00%	1	1	0	100.00%
LIN-28B	LIN28B		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
CDYL	CDYL	EPIGENES	✓	101	0.00	100.00%	1	1	0	100.00%
JMJD2A	KDM4A	EPIGENES			0.00	100.00%	1	1	0	100.00%
Mi-2 alpha	CHD3	EPIGENES			0.00	100.00%	1	1	0	100.00%
BRD8	BRD8	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
alpha-11/beta-1 integrin	alpha-11/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
PPARGC1 (PGC1-alpha)	PPARGC1A			139-5p	0.00	100.00%	1	1	0	100.00%
IRS-1	IRS1				0.00	100.00%	1	1	0	100.00%
IL-5	IL5				0.00	100.00%	1	1	0	100.00%
PLAU (UPA)	PLAU				0.00	100.00%	1	1	0	100.00%
IL-12	IL-12				0.00	100.00%	1	1	0	100.00%
MEK4(MAP2K4)	MAP2K4				0.00	100.00%	1	1	0	100.00%
Pdx-1 (IPF1)	PDX1	TF			0.00	100.00%	1	1	0	100.00%
IL-4R type II	IL-4R type II				0.00	100.00%	1	1	0	100.00%
TGF-beta 1	TGFB1			139-5p	0.00	100.00%	1	1	0	100.00%
HMGI/Y	HMGA1	EPIGENES			0.00	100.00%	2	1	1	62.59%
PIT1	POU1F1	TF			0.00	100.00%	2	2	0	62.59%
POU3F2 (BRN2)	POU3F2	TF			0.00	100.00%	1	1	0	100.00%
MMP-9	MMP9				0.00	100.00%	1	1	0	100.00%
IL-2	IL2				0.00	100.00%	1	1	0	100.00%

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	**Mapped Gene Symbol**	**Molecular Function**	**DEGs**	**Predicted Targets †**	**Value**	**Rank***	**Total**	**In**	**Out**	**Rank***
PU.1	SPI1	TF			0.00	100.00%	1	1	0	100.00%
microRNA 155	miR-155				0.00	100.00%	1	1	0	100.00%
Rb protein	RB1	TF		199-3p	0.00	100.00%	1	1	0	100.00%
MAPKAPK5	MAPKAPK5		✓		0.00	100.00%	1	1	0	100.00%
SDF-1	CXCL12				0.00	100.00%	1	1	0	100.00%
VEGFR-2	KDR				0.00	100.00%	1	1	0	100.00%
RD protein	RDBP		✓		0.00	100.00%	1	1	0	100.00%
B-Raf	BRAF				0.00	100.00%	1	1	0	100.00%
RUNX3	RUNX3	TF			0.00	100.00%	1	1	0	100.00%
GSK3 alpha	GSK3A				0.00	100.00%	1	1	0	100.00%
SATB2	SATB2	TF			0.00	100.00%	1	1	0	100.00%
MDM2	MDM2				0.00	100.00%	1	1	0	100.00%
Btk	BTK				0.00	100.00%	1	1	0	100.00%
SHP	NR0B2	TF			0.00	100.00%	1	1	0	100.00%
RBB2	KDM5A	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
miR-199-3p	miR-199-3p				0.00	100.00%	1	1	0	100.00%
Thioredoxin	TXN				0.00	100.00%	1	1	0	100.00%
SMAD2	SMAD2	TF		139-5p	0.00	100.00%	1	1	0	100.00%
SMAD4	SMAD4	TF			0.00	100.00%	1	1	0	100.00%
CCL2	CCL2				0.00	100.00%	1	1	0	100.00%
CrkL	CRKL				0.00	100.00%	1	1	0	100.00%
BMPR1B	BMPR1B				0.00	100.00%	1	1	0	100.00%
HDAC1	HDAC1	EPIGENES			0.00	100.00%	1	1	0	100.00%
UFO	AXL		✓	139-5p	0.00	100.00%	1	1	0	100.00%
SMAD5	SMAD5	TF	✓		0.00	100.00%	1	1	0	100.00%
SP1/SP3 complex	SP1	TF		199-3p	0.00	100.00%	3	2	1	38.13%
PKC-delta	PRKCD				0.00	100.00%	1	1	0	100.00%
SRF	SRF	TF			0.00	100.00%	1	1	0	100.00%
PRNP	PRNP		✓		0.00	100.00%	1	1	0	100.00%
ELAVL1 (HuR)	ELAVL1				0.00	100.00%	1	1	0	100.00%
PARP-2	PARP2				0.00	100.00%	1	1	0	100.00%
microRNA 222	miR-222				0.00	100.00%	1	1	0	100.00%
IL-1 beta	IL1B				0.00	100.00%	1	1	0	100.00%
IL8RB	CXCR2				0.00	100.00%	1	1	0	100.00%
KNG	KNG1				0.00	100.00%	1	1	0	100.00%
Sry	SRY	TF			0.00	100.00%	1	1	0	100.00%
alpha-5/beta-1 integrin	alpha-5/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
P4HA1	P4HA1		✓		0.00	100.00%	2	2	0	62.59%
STAT2	STAT2	TF			0.00	100.00%	1	1	0	100.00%
CHD6	CHD6	EPIGENES	✓	101	0.00	100.00%	2	1	1	62.59%
UBF	UBTF				0.00	100.00%	1	1	0	100.00%
VDR	VDR	TF			0.00	100.00%	1	1	0	100.00%
G-protein alpha-s	GNAS				0.00	100.00%	1	1	0	100.00%
GMF-gamma	GMFG		✓		0.00	100.00%	1	1	0	100.00%
TrkA	NTRK1				0.00	100.00%	1	1	0	100.00%
IL-9	IL9				0.00	100.00%	1	1	0	100.00%
alpha-3/beta-1 integrin	alpha-3/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
XBP1	XBP1	TF			0.00	100.00%	1	1	0	100.00%
IKK (cat)	IKK (cat)				0.00	100.00%	1	1	0	100.00%
Granzyme B	GZMB				0.00	100.00%	1	1	0	100.00%
SUZ12	SUZ12	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
Protein kinase G1 alpha	PRKG1				0.00	100.00%	1	1	0	100.00%
ARPC4	ARPC4		✓		0.00	100.00%	1	1	0	100.00%
ZNF207	ZNF207	TF	✓	101	0.00	100.00%	1	1	0	100.00%
SETDB1	SETDB1	EPIGENES			0.00	100.00%	1	1	0	100.00%
Ski	SKI				0.00	100.00%	1	1	0	100.00%
ZNF33A	ZNF33A	TF	✓	101	0.00	100.00%	1	1	0	100.00%
HDAC3	HDAC3	EPIGENES			0.00	100.00%	1	1	0	100.00%
L1CAM	L1CAM				0.00	100.00%	1	1	0	100.00%

* Rank percentile

† Predicted by TargetScan and context score < -0.2

Supplementary table S8. Topological properties of miR-139-5p sub-network for cluster C6 network

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Value	Rank*	Total	In	Out	Rank*
AP-1	FOS	TF		101, 139-5p, 199-3p	65132.05	1.35%	184	5	179	1.18%
miR-139-5p	miR-139-5p				35929.06	2.70%	50	1	49	2.35%
LRH1	NR5A2	TF	✓	139-5p	4249.50	4.05%	14	3	11	3.53%
Caspase-3	CASP3			101, 139-5p	3954.45	5.41%	10	1	9	7.06%
Shc	SHC1			139-5p	3014.50	6.76%	8	1	7	8.24%
ETS1	ETS1	TF		139-5p	2548.65	8.11%	13	2	11	4.71%
ERR3	ESRRG	TF	✓	139-5p	2475.56	9.46%	12	2	10	5.88%
ASK1 (MAP3K5)	MAP3K5			101, 139-5p, 199-3p	2268.00	10.81%	5	1	4	16.47%
AKT(PKB)	AKT(PKB)				2150.87	12.16%	6	2	4	12.94%
AML1 (RUNX1)	RUNX1	TF		101, 139-5p, 199-3p	2074.74	13.51%	8	1	7	8.24%
TIF1-alpha	TRIM24	EPIGENES	✓	101, 139-5p	1622.79	14.86%	7	1	6	10.59%
FKHR	FOXO1	TF			1335.49	16.22%	7	1	6	10.59%
Collagen IV	Collagen IV				1138.00	17.57%	3	1	2	23.53%
PP2A catalytic	PP2A catalytic				1138.00	17.57%	3	1	2	23.53%
TFIIH	TFIIH				1138.00	17.57%	3	1	2	23.53%
Thrombospondin 1	THBS1			139-5p	1138.00	17.57%	4	2	2	17.65%
VEGF-D	FIGF			139-5p	1029.07	22.97%	4	2	2	17.65%
CXCR4	CXCR4			139-5p	845.83	24.32%	3	1	2	23.53%
MRK	ICK		✓	101, 139-5p	842.51	25.68%	3	1	2	23.53%
G-protein alpha-i family	G-protein alpha-i family				753.67	27.03%	3	1	2	23.53%
PPARGC1 (PGC1-alpha)	PPARGC1A			139-5p	734.78	28.38%	6	3	3	12.94%
SHP	NR0B2	TF			672.52	29.73%	3	3	0	23.53%
HDAC2	HDAC2	EPIGENES		139-5p	658.63	31.08%	6	2	4	12.94%
TGF-beta 1	TGFB1			139-5p	643.40	32.43%	4	2	2	17.65%
NF-AT2(NFATC1)	NFATC1	TF		139-5p	607.58	33.78%	3	1	2	23.53%
Ataxin-1	ATXN1			101, 139-5p	570.00	35.14%	2	1	1	45.88%
Bcl-2	BCL2			139-5p	570.00	35.14%	2	1	1	45.88%
Galpha(q)-specific frizzled GPCRs	Galpha(q)-specific frizzled GPCRs				570.00	35.14%	2	1	1	45.88%
Importin (karyopherin)-beta	Importin (karyopherin)-beta				570.00	35.14%	2	1	1	45.88%
NRSF	REST				570.00	35.14%	2	0	2	45.88%
PKC-alpha	PRKCA			139-5p	570.00	35.14%	2	1	1	45.88%
PTEN	PTEN			139-5p	570.00	35.14%	3	2	1	23.53%
SRPK1	SRPK1		✓	139-5p	570.00	35.14%	2	1	1	45.88%
UFO	AXL		✓	139-5p	462.00	45.95%	3	1	2	23.53%
HOXB3	HOXB3	TF		139-5p	460.40	47.30%	3	2	1	23.53%
Beta-catenin	CTNNB1	TF			418.32	48.65%	3	3	0	23.53%
Cyclin D1	CCND1				418.32	48.65%	2	2	0	45.88%
c-Myc	MYC	TF			418.32	48.65%	2	2	0	45.88%
Androgen receptor	AR	TF			366.78	52.70%	3	3	0	23.53%
KLF4	KLF4	TF	✓		343.41	54.05%	3	3	0	23.53%
EGR1	EGR1	TF	✓		335.00	55.41%	4	4	0	17.65%
SOD2	SOD2		✓		329.22	56.76%	3	3	0	23.53%
ESR1 (nuclear)	ESR1	TF			280.93	58.11%	2	2	0	45.88%
p53	TP53	TF			280.93	58.11%	2	2	0	45.88%
ERR1	ESRRA	TF			218.86	60.81%	2	2	0	45.88%
RAR-alpha/RXR-alpha	RAR-alpha/RXR-alpha	TF			218.86	60.81%	2	2	0	45.88%
RUNX2	RUNX2	TF			218.86	60.81%	2	2	0	45.88%
YY1	YY1	TF			218.86	60.81%	2	2	0	45.88%
TMF1	TMF1		✓	101, 139-5p	199.57	66.22%	4	1	3	17.65%
M-CSF receptor	CSF1R		✓		161.53	67.57%	3	3	0	23.53%
IGF-1	IGF-1				156.40	68.92%	2	2	0	45.88%
TARBP1	TARBP1		✓		156.40	68.92%	2	2	0	45.88%
NOTCH1 (NICD)	NOTCH1 (NICD)				152.62	71.62%	2	1	1	45.88%
PKA-cat beta	PRKACB			139-5p	107.60	72.97%	2	1	1	45.88%
alpha-V/beta-3 integrin	alpha-V/beta-3 integrin				106.93	74.32%	2	1	1	45.88%
PAX3	PAX3	TF			79.12	75.68%	2	2	0	45.88%
STAT3	STAT3	TF			79.12	75.68%	2	2	0	45.88%
SMAD2	SMAD2	TF		139-5p	73.40	78.38%	3	1	2	23.53%
IBP5	IGFBP5			101, 139-5p	72.73	79.73%	2	1	1	45.88%
TCP1	TCP1				72.73	79.73%	2	1	1	45.88%
FOXP1	FOXP1	TF		139-5p, 199-3p	49.83	82.43%	2	1	1	45.88%
N-CoR	NCOR1	TF	✓		33.33	83.78%	2	2	0	45.88%
Cathepsin V	CTSL1		✓		29.70	85.14%	2	2	0	45.88%
c-Src	SRC				19.17	86.49%	3	3	0	23.53%
BAT3	BAT3		✓		16.67	87.84%	2	2	0	45.88%
TAFII28	TAF11		✓		12.77	89.19%	2	2	0	45.88%
ZAP70	ZAP70				12.33	90.54%	2	2	0	45.88%
GMF-gamma	GMFG		✓		10.67	91.89%	2	2	0	45.88%
p300	EP300	EPIGENES			7.17	93.24%	2	2	0	45.88%
p16INK4	CDKN2A	TF	✓		4.67	94.59%	3	3	0	23.53%
SHP-2	PTPN11				3.83	95.95%	2	2	0	45.88%
VEGFR-2	KDR				2.00	97.30%	2	2	0	45.88%
TITF1	NKX2-1	TF			1.00	98.65%	2	2	0	45.88%
14-3-3 sigma	SFN				0.00	100.00%	1	1	0	100.00%
14-3-3 zeta/delta	YWHAZ			199-3p	0.00	100.00%	1	1	0	100.00%
A-FABP	FABP4				0.00	100.00%	1	1	0	100.00%
A1U	UBQLN4		✓		0.00	100.00%	1	1	0	100.00%
AATC	GOT1		✓		0.00	100.00%	1	1	0	100.00%
ACACB	ACACB		✓		0.00	100.00%	1	1	0	100.00%
ACM3	CHRM3				0.00	100.00%	1	1	0	100.00%
ADNP	ADNP	TF	✓		0.00	100.00%	1	1	0	100.00%
AHR	AHR	TF			0.00	100.00%	1	1	0	100.00%
APEX	APEX1				0.00	100.00%	1	1	0	100.00%
ARPC4	ARPC4		✓		0.00	100.00%	1	1	0	100.00%
ASF1A	ASF1A	EPIGENES	✓	139-5p	0.00	100.00%	1	1	0	100.00%
ATAD2	ATAD2	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
ATF-3	ATF3	TF	✓		0.00	100.00%	1	1	0	100.00%
AXUD1	CSRNP1	TF	✓		0.00	100.00%	1	1	0	100.00%
Adrenomedullin	ADM				0.00	100.00%	1	1	0	100.00%
BMAL1	ARNTL	TF			0.00	100.00%	1	1	0	100.00%
BMI-1	BMI1	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
BMP4	BMP4				0.00	100.00%	1	1	0	100.00%
Bax	BAX				0.00	100.00%	1	1	0	100.00%
Brca1	BRCA1				0.00	100.00%	1	1	0	100.00%
C/EBP zeta	DDIT3	TF			0.00	100.00%	1	1	0	100.00%
C/EBPalpha	CEBPA	TF		101	0.00	100.00%	1	1	0	100.00%
C/EBPbeta	CEBPB	TF			0.00	100.00%	2	2	0	45.88%
C/EBPdelta	CEBPD	TF	✓		0.00	100.00%	1	1	0	100.00%
CBF beta	CBFB	TF			0.00	100.00%	1	1	0	100.00%

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Value	Rank*	Total	In	Out	Rank*
CDK1 (p34)	CDK1				0.00	100.00%	1	1	0	100.00%
CDK2	CDK2				0.00	100.00%	1	1	0	100.00%
CDK4	CDK4				0.00	100.00%	1	1	0	100.00%
CDYL	CDYL	EPIGENES	✓	101	0.00	100.00%	1	1	0	100.00%
CHD7	CHD7	EPIGENES	✓	139-5p	0.00	100.00%	1	1	0	100.00%
CIITA	CIITA	EPIGENES			0.00	100.00%	1	1	0	100.00%
COUP-TFI	NR2F1	TF	✓		0.00	100.00%	1	1	0	100.00%
Calpain 1(mu)	CAPN1		✓		0.00	100.00%	1	1	0	100.00%
Cathepsin L	Cathepsin L				0.00	100.00%	1	1	0	100.00%
CtBP2	CTBP2				0.00	100.00%	1	1	0	100.00%
Cyclin E	CCNE1				0.00	100.00%	1	1	0	100.00%
Cystatin A	CSTA				0.00	100.00%	1	1	0	100.00%
Cystatin B	CSTB				0.00	100.00%	1	1	0	100.00%
DAPK1	DAPK1				0.00	100.00%	1	1	0	100.00%
DAX1	NR0B1	TF			0.00	100.00%	1	1	0	100.00%
DAXX	DAXX		✓		0.00	100.00%	1	1	0	100.00%
DJ-1	PARK7				0.00	100.00%	1	1	0	100.00%
DMTF1	DMTF1	TF			0.00	100.00%	1	1	0	100.00%
DNMT1	DNMT1	EPIGENES			0.00	100.00%	1	1	0	100.00%
E7 protein (HPV16)	E7 protein (HPV16)				0.00	100.00%	1	1	0	100.00%
EGF	EGF				0.00	100.00%	1	1	0	100.00%
ELAVL1 (HuR)	ELAVL1				0.00	100.00%	1	1	0	100.00%
ELF1	ELF1	TF			0.00	100.00%	1	1	0	100.00%
ELF3	ELF3	TF			0.00	100.00%	1	1	0	100.00%
ELL2	ELL2		✓	139-5p	0.00	100.00%	1	1	0	100.00%
ERM	ETV5	TF		101	0.00	100.00%	1	1	0	100.00%
ETS2	ETS2	TF			0.00	100.00%	1	1	0	100.00%
EZH2	EZH2	EPIGENES	✓	101	0.00	100.00%	1	1	0	100.00%
Endoglin	ENG		✓		0.00	100.00%	2	2	0	45.88%
Eomesodermin	EOMES	TF	✓		0.00	100.00%	1	1	0	100.00%
ErbB2	ERBB2				0.00	100.00%	1	1	0	100.00%
FAT10	UBD		✓		0.00	100.00%	1	1	0	100.00%
FBXW7	FBXW7	EPIGENES			0.00	100.00%	1	1	0	100.00%
FGL2	FGL2		✓	199-3p	0.00	100.00%	2	2	0	45.88%
FOXO3A	FOXO3	TF			0.00	100.00%	1	1	0	100.00%
FOXP3	FOXP3	TF			0.00	100.00%	1	1	0	100.00%
FasL(TNFSF6)	FASLG				0.00	100.00%	1	1	0	100.00%
FasR(CD95)	FAS				0.00	100.00%	1	1	0	100.00%
G-CSF	CSF3				0.00	100.00%	1	1	0	100.00%
G-protein alpha-q/11	G-protein alpha-q/11				0.00	100.00%	1	1	0	100.00%
GAB1	GAB1				0.00	100.00%	1	1	0	100.00%
GABP alpha	GABPA	TF			0.00	100.00%	1	1	0	100.00%
GATA-4	GATA4	TF			0.00	100.00%	1	1	0	100.00%
GC1QBP	C1QBP				0.00	100.00%	1	1	0	100.00%
GFER	GFER				0.00	100.00%	1	1	0	100.00%
GRB2	GRB2				0.00	100.00%	1	1	0	100.00%
GSK3 alpha	GSK3A				0.00	100.00%	1	1	0	100.00%
GSK3 beta	GSK3B				0.00	100.00%	1	1	0	100.00%
Galectin-3	LGALS3				0.00	100.00%	1	1	0	100.00%
Golgin-45 (BLZF1)	BLZF1	TF	✓		0.00	100.00%	1	1	0	100.00%
Granzyme B	GZMB				0.00	100.00%	1	1	0	100.00%
H-Ras	HRAS				0.00	100.00%	1	1	0	100.00%
HB-EGF	HBEGF				0.00	100.00%	1	1	0	100.00%
HIF1A	HIF1A	TF			0.00	100.00%	1	1	0	100.00%
HMGI/Y	HMGA1	EPIGENES			0.00	100.00%	1	1	0	100.00%
HNF1-alpha	HNF1A	TF			0.00	100.00%	1	1	0	100.00%
HNF3-beta	FOXA2	TF			0.00	100.00%	1	1	0	100.00%
HNF4-alpha	HNF4A	TF			0.00	100.00%	1	1	0	100.00%
HSF1	HSF1	TF			0.00	100.00%	1	1	0	100.00%
HSP27	HSPB1				0.00	100.00%	1	1	0	100.00%
I-kB	I-kB				0.00	100.00%	1	1	0	100.00%
ID1	ID1				0.00	100.00%	1	1	0	100.00%
IL-1 beta	IL1B				0.00	100.00%	1	1	0	100.00%
IL-12	IL-12				0.00	100.00%	1	1	0	100.00%
IL-18	IL18				0.00	100.00%	1	1	0	100.00%
IL-2	IL2				0.00	100.00%	1	1	0	100.00%
IL-4	IL4				0.00	100.00%	1	1	0	100.00%
IL-5	IL5				0.00	100.00%	1	1	0	100.00%
IL-9	IL9				0.00	100.00%	1	1	0	100.00%
IRF4	IRF4	TF			0.00	100.00%	1	1	0	100.00%
Ifi202a	Ifi202a				0.00	100.00%	1	1	0	100.00%
JAK2	JAK2			101	0.00	100.00%	1	1	0	100.00%
JDP2	JDP2	TF	✓	101	0.00	100.00%	1	1	0	100.00%
JMJD2A	KDM4A	EPIGENES			0.00	100.00%	1	1	0	100.00%
JNK(MAPK8-10)	JNK(MAPK8-10)				0.00	100.00%	1	1	0	100.00%
KLF6	KLF6	TF	✓		0.00	100.00%	2	2	0	45.88%
KNG	KNG1				0.00	100.00%	1	1	0	100.00%
LCKBP1	HCLS1	TF	✓		0.00	100.00%	1	1	0	100.00%
LL37	CAMP				0.00	100.00%	1	1	0	100.00%
Leptin	LEP				0.00	100.00%	1	1	0	100.00%
MAFG	MAFG	TF	✓		0.00	100.00%	1	1	0	100.00%
MAP3K3	MAP3K3				0.00	100.00%	1	1	0	100.00%
MAPKAPK5	MAPKAPK5		✓		0.00	100.00%	1	1	0	100.00%
MCM2	MCM2		✓		0.00	100.00%	1	1	0	100.00%
MCM3	MCM3		✓		0.00	100.00%	1	1	0	100.00%
MDM2	MDM2				0.00	100.00%	1	1	0	100.00%
MED8	MED8		✓	139-5p	0.00	100.00%	1	1	0	100.00%
MEK4(MAP2K4)	MAP2K4				0.00	100.00%	1	1	0	100.00%
MITF	MITF	TF		101	0.00	100.00%	1	1	0	100.00%
MJD (ataxin-3)	ATXN3				0.00	100.00%	1	1	0	100.00%
MKK7 (MAP2K7)	MAP2K7				0.00	100.00%	1	1	0	100.00%
MMP-12	MMP12				0.00	100.00%	1	1	0	100.00%
MMP-14	MMP14		✓		0.00	100.00%	1	1	0	100.00%
MMP-9	MMP9				0.00	100.00%	1	1	0	100.00%
MSH6	MSH6				0.00	100.00%	1	1	0	100.00%
MSX1	MSX1	TF		101	0.00	100.00%	1	1	0	100.00%
MYF5	MYF5	TF			0.00	100.00%	1	1	0	100.00%
MYF6	MYF6	TF			0.00	100.00%	1	1	0	100.00%
MYOD	MYOD1	TF			0.00	100.00%	1	1	0	100.00%
MYOG	MYOG	TF			0.00	100.00%	1	1	0	100.00%

GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Betweenness		# of Interactions (Degree)			
					Value	Rank*	Total	In	Out	Rank*
Mi-2 alpha	CHD3	EPIGENES			0.00	100.00%	1	1	0	100.00%
NANOG	NANOG	TF			0.00	100.00%	1	1	0	100.00%
NEIL1	NEIL1				0.00	100.00%	1	1	0	100.00%
NEURL1	NEURL				0.00	100.00%	1	1	0	100.00%
NF-kB	RELA	TF			0.00	100.00%	1	1	0	100.00%
ODP2	DLAT		✓		0.00	100.00%	1	1	0	100.00%
Oct-3/4	POU5F1	TF			0.00	100.00%	1	1	0	100.00%
P4HA1	P4HA1		✓		0.00	100.00%	1	1	0	100.00%
PACAP	ADCYAP1			101	0.00	100.00%	1	1	0	100.00%
PACE4	PCSK6				0.00	100.00%	1	1	0	100.00%
PC4	SUB1		✓	101	0.00	100.00%	1	1	0	100.00%
PCNA	PCNA				0.00	100.00%	1	1	0	100.00%
PCY2	PCYT2		✓		0.00	100.00%	1	1	0	100.00%
PDGF-A	PDGFA				0.00	100.00%	1	1	0	100.00%
PELP1	PELP1				0.00	100.00%	1	1	0	100.00%
PIAS4	PIAS4				0.00	100.00%	1	1	0	100.00%
PIT1	POU1F1	TF			0.00	100.00%	2	2	0	45.88%
PKC-delta	PRKCD				0.00	100.00%	1	1	0	100.00%
PLAU (UPA)	PLAU				0.00	100.00%	1	1	0	100.00%
POLA1	POLA1		✓		0.00	100.00%	1	1	0	100.00%
POU3F2 (BRN2)	POU3F2	TF			0.00	100.00%	1	1	0	100.00%
PRNP	PRNP		✓		0.00	100.00%	1	1	0	100.00%
PSF	SFPQ			101	0.00	100.00%	1	1	0	100.00%
PU.1	SPI1	TF			0.00	100.00%	1	1	0	100.00%
Pinin	PNN		✓	139-5p	0.00	100.00%	1	1	0	100.00%
Progesterone receptor	PGR	TF			0.00	100.00%	1	1	0	100.00%
Prolactin	PRL				0.00	100.00%	1	1	0	100.00%
RBB2	KDM5A	EPIGENES	✓		0.00	100.00%	1	1	0	100.00%
Rap1GAP1	RAP1GAP				0.00	100.00%	1	1	0	100.00%
Raptor	RPTOR				0.00	100.00%	1	1	0	100.00%
Rb protein	RB1	TF		199-3p	0.00	100.00%	1	1	0	100.00%
S100A7	S100A7				0.00	100.00%	1	1	0	100.00%
SAT-1	SLC26A1				0.00	100.00%	1	1	0	100.00%
SHP-1	PTPN6				0.00	100.00%	1	1	0	100.00%
SMAD7	SMAD7	TF			0.00	100.00%	1	1	0	100.00%
SNAIL1	SNAI1				0.00	100.00%	1	1	0	100.00%
SOS	SOS				0.00	100.00%	1	1	0	100.00%
SP1/SP3 complex	SP1	TF		199-3p	0.00	100.00%	2	2	0	45.88%
SRF	SRF	TF			0.00	100.00%	1	1	0	100.00%
SSAT	SAT1		✓		0.00	100.00%	1	1	0	100.00%
STAT4	STAT4	TF			0.00	100.00%	1	1	0	100.00%
Sequestosome 1(p62)	SQSTM1		✓		0.00	100.00%	2	2	0	45.88%
Sirtuin7	SIRT7		✓		0.00	100.00%	1	1	0	100.00%
Ski	SKI				0.00	100.00%	1	1	0	100.00%
Sortilin	SORT1		✓		0.00	100.00%	1	1	0	100.00%
Sry	SRY	TF			0.00	100.00%	1	1	0	100.00%
TAFI48	TAF1A		✓		0.00	100.00%	1	1	0	100.00%
TFIIE, alpha subunit	GTF2E1		✓	101	0.00	100.00%	1	1	0	100.00%
TGF-beta receptor type II	TGFBR2				0.00	100.00%	2	2	0	45.88%
TIMP1	TIMP1				0.00	100.00%	1	1	0	100.00%
TIMP2	TIMP2				0.00	100.00%	1	1	0	100.00%
TIMP4	TIMP4				0.00	100.00%	1	1	0	100.00%
TIP30	HTATIP2		✓		0.00	100.00%	1	1	0	100.00%
TNF-alpha	TNF				0.00	100.00%	1	1	0	100.00%
TOP1	TOP1			139-5p	0.00	100.00%	2	1	1	45.88%
TTF1	TTF1		✓		0.00	100.00%	1	1	0	100.00%
TWIST1	TWIST1				0.00	100.00%	1	1	0	100.00%
Tcf(Lef)	LEF1	TF			0.00	100.00%	2	2	0	45.88%
Thioredoxin	TXN				0.00	100.00%	1	1	0	100.00%
TrkA	NTRK1				0.00	100.00%	1	1	0	100.00%
UBF	UBTF				0.00	100.00%	1	1	0	100.00%
USP31	USP31		✓		0.00	100.00%	1	1	0	100.00%
Ubiquitin	UBB				0.00	100.00%	1	1	0	100.00%
VDR	VDR	TF			0.00	100.00%	1	1	0	100.00%
VEGF-A	VEGFA				0.00	100.00%	1	1	0	100.00%
VEGFR-3	FLT4				0.00	100.00%	1	1	0	100.00%
Versican	VCAN				0.00	100.00%	1	1	0	100.00%
WNT5A	WNT5A				0.00	100.00%	1	1	0	100.00%
XBP1	XBP1	TF			0.00	100.00%	1	1	0	100.00%
YAP1 (YAp65)	YAP1			199-3p	0.00	100.00%	1	1	0	100.00%
ZNF160	ZNF160		✓	139-5p	0.00	100.00%	1	1	0	100.00%
ZNF302	ZNF302		✓	139-5p	0.00	100.00%	2	2	0	45.88%
ZNF331	ZNF331		✓	139-5p	0.00	100.00%	1	1	0	100.00%
alpha-11/beta-1 integrin	alpha-11/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
alpha-3/beta-1 integrin	alpha-3/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
alpha-4/beta-1 integrin	alpha-4/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
alpha-5/beta-1 integrin	alpha-5/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
c-Abl	ABL1				0.00	100.00%	1	1	0	100.00%
c-Myb	MYB			101	0.00	100.00%	1	1	0	100.00%
c-Raf-1	RAF1				0.00	100.00%	1	1	0	100.00%
mTOR	MTOR		✓		0.00	100.00%	1	1	0	100.00%
microRNA 155	miR-155				0.00	100.00%	1	1	0	100.00%
microRNA 206	miR-206				0.00	100.00%	1	1	0	100.00%
microRNA 21	miR-21				0.00	100.00%	1	1	0	100.00%
microRNA 221	miR-221				0.00	100.00%	1	1	0	100.00%
microRNA 222	miR-222				0.00	100.00%	1	1	0	100.00%
p14ARF	CDKN2A	TF	✓		0.00	100.00%	1	1	0	100.00%
p27KIP1	CDKN1B				0.00	100.00%	1	1	0	100.00%

* Rank percentile

† Predicted by TargetScan and context score < -0.2

Supplementary table S9. Topological properties of miR-199-3p sub-network for cluster C6 network

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	Mapped Gene Symbol	Molecular Function	DEGs	Predicted Targets †	Value	Rank*	Total	In	Out	Rank*
miR-199a-3p	miR-199a-3p				15340.51	3.70%	55	13	42	3.03%
p53	TP53	TF			6041.00	7.41%	29	0	29	6.06%
SUZ12	SUZ12	EPIGENES	✓		5872.51	11.11%	28	0	28	9.09%
BMI-1	BMI1	EPIGENES	✓		2602.05	14.81%	13	0	13	12.12%
HSF2	HSF2	TF	✓		2295.58	18.52%	11	0	11	18.18%
HIF1A	HIF1A	TF			2015.61	22.22%	12	1	11	15.15%
MYOD	MYOD1	TF			1720.13	25.93%	10	0	10	21.21%
EED	EED	EPIGENES	✓	101	1689.18	29.63%	10	0	10	21.21%
MYOG	MYOG	TF			463.45	33.33%	4	0	4	27.27%
C/EBPdelta	CEBPD	TF	✓		392.59	37.04%	2	2	0	39.39%
EZH2	EZH2	EPIGENES	✓	101	392.59	37.04%	2	2	0	39.39%
ATF-6 alpha	ATF6	TF			280.00	44.44%	2	0	2	39.39%
p16INK4	CDKN2A	TF	✓		254.21	48.15%	3	3	0	33.33%
AP-1	FOS	TF		101, 139-5p, 199-3p	224.89	51.85%	4	4	0	27.27%
ATF-3	ATF3	TF	✓		197.33	55.56%	2	2	0	39.39%
ATF-1	ATF1	TF			189.50	59.26%	3	0	3	33.33%
DKK1	DKK1				161.44	62.96%	2	2	0	39.39%
IGF-1	IGF-1				110.42	66.67%	2	2	0	39.39%
PRNP	PRNP		✓		110.42	66.67%	2	2	0	39.39%
GATA-6	GATA6	TF			101.90	74.07%	2	2	0	39.39%
c-Myc	MYC	TF			101.90	74.07%	2	2	0	39.39%
BMP2	BMP2				97.50	81.48%	2	2	0	39.39%
microRNA 214	miR-214				70.17	85.19%	2	2	0	39.39%
ACACB	ACACB		✓		18.11	88.89%	2	2	0	39.39%
EGR1	EGR1	TF	✓		16.50	92.59%	2	2	0	39.39%
SOD2	SOD2		✓		16.50	92.59%	2	2	0	39.39%
14-3-3 zeta/delta	YWHAZ			199-3p	0.00	100.00%	1	1	0	100.00%
AML1 (RUNX1)	RUNX1	TF		101, 139-5p, 199-3p	0.00	100.00%	2	2	0	39.39%
ARHGAP15	ARHGAP15		✓		0.00	100.00%	1	1	0	100.00%
ARID4B	ARID4B		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
ASK1 (MAP3K5)	MAP3K5			101, 139-5p, 199-3p	0.00	100.00%	1	1	0	100.00%
BMP7	BMP7				0.00	100.00%	1	1	0	100.00%
C14orf169	C14orf169		✓		0.00	100.00%	1	1	0	100.00%
CENP-50	MLF1IP		✓		0.00	100.00%	1	1	0	100.00%
CITED2	CITED2	TF		199-3p	0.00	100.00%	1	1	0	100.00%
COUP-TFI	NR2F1	TF	✓		0.00	100.00%	1	1	0	100.00%
Cathepsin L	Cathepsin L				0.00	100.00%	1	1	0	100.00%
Collagen IV	Collagen IV				0.00	100.00%	1	1	0	100.00%
Cyclin D1	CCND1				0.00	100.00%	1	1	0	100.00%
DNMT1	DNMT1	EPIGENES			0.00	100.00%	1	1	0	100.00%
DNMT3A	DNMT3A	EPIGENES		101, 199-3p	0.00	100.00%	2	2	0	39.39%
DNMT3B	DNMT3B	EPIGENES			0.00	100.00%	1	1	0	100.00%
E4F1	E4F1	TF	✓		0.00	100.00%	1	1	0	100.00%
EGLN1	EGLN1		✓		0.00	100.00%	1	1	0	100.00%
EPAS1	EPAS1	TF		199-3p	0.00	100.00%	1	1	0	100.00%
ESR1 (nuclear)	ESR1	TF			0.00	100.00%	1	1	0	100.00%
Eomesodermin	EOMES	TF	✓		0.00	100.00%	1	1	0	100.00%
Ep-CAM	EPCAM				0.00	100.00%	1	1	0	100.00%
FAT10	UBD		✓		0.00	100.00%	1	1	0	100.00%
FGL2	FGL2		✓	199-3p	0.00	100.00%	1	1	0	100.00%
FHL2	FHL2		✓		0.00	100.00%	1	1	0	100.00%
FOXF1	FOXF1	TF			0.00	100.00%	1	1	0	100.00%
FOXP1	FOXP1	TF		139-5p, 199-3p	0.00	100.00%	1	1	0	100.00%
FTHFSDC1	MTHFD1L		✓		0.00	100.00%	1	1	0	100.00%
Fibronectin	FN1			101, 199-3p	0.00	100.00%	1	1	0	100.00%
G-CSF	CSF3				0.00	100.00%	1	1	0	100.00%
GATA-1	GATA1	TF			0.00	100.00%	1	1	0	100.00%
GATA-3	GATA3	TF			0.00	100.00%	1	1	0	100.00%
GBL	MLST8				0.00	100.00%	1	1	0	100.00%
GPI	GPI				0.00	100.00%	1	1	0	100.00%
HGFA	HGFAC		✓		0.00	100.00%	1	1	0	100.00%
HOXC6	HOXC6	TF			0.00	100.00%	1	1	0	100.00%
HSF1	HSF1	TF			0.00	100.00%	1	1	0	100.00%
HSP27	HSPB1				0.00	100.00%	1	1	0	100.00%
HSP90	HSP90				0.00	100.00%	1	1	0	100.00%
Hamartin	TSC1				0.00	100.00%	1	1	0	100.00%
HoxC13	HOXC13	TF			0.00	100.00%	1	1	0	100.00%
IBP2	IGFBP2				0.00	100.00%	1	1	0	100.00%
IBP3	IGFBP3				0.00	100.00%	1	1	0	100.00%
IL-22	IL22				0.00	100.00%	1	1	0	100.00%
IL-4	IL4				0.00	100.00%	1	1	0	100.00%
IL-4R type II	IL-4R type II				0.00	100.00%	1	1	0	100.00%
KLF13	KLF13		✓	199-3p	0.00	100.00%	1	1	0	100.00%
LIN-28B	LIN28B		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
MCM4/6/7 complex	MCM4/6/7 complex				0.00	100.00%	1	1	0	100.00%
MNK2(GPRK7)	MKNK2		✓		0.00	100.00%	1	1	0	100.00%
MTAP	MTAP		✓		0.00	100.00%	1	1	0	100.00%
NANOG	NANOG	TF			0.00	100.00%	1	1	0	100.00%
NEUR1	NEU1		✓		0.00	100.00%	1	1	0	100.00%
NEURL1	NEURL				0.00	100.00%	1	1	0	100.00%
NF-Y	NF-Y				0.00	100.00%	1	1	0	100.00%
NIPP-1	PPP1R8				0.00	100.00%	1	1	0	100.00%
NLK	NLK		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
Oct-3/4	POU5F1	TF			0.00	100.00%	1	1	0	100.00%
P4HA1	P4HA1		✓		0.00	100.00%	1	1	0	100.00%
PAX3	PAX3	TF			0.00	100.00%	1	1	0	100.00%
PC4	SUB1		✓	101	0.00	100.00%	1	1	0	100.00%
PCY2	PCYT2		✓		0.00	100.00%	1	1	0	100.00%
PDE4B	PDE4B		✓	199-3p	0.00	100.00%	1	1	0	100.00%
PDGF-R-alpha	PDGFRA			199-3p	0.00	100.00%	1	1	0	100.00%
PKC-lambda/iota	PRKCI			199-3p	0.00	100.00%	1	1	0	100.00%
PLAU (UPA)	PLAU				0.00	100.00%	1	1	0	100.00%
PLK3 (CNK)	PLK3		✓		0.00	100.00%	1	1	0	100.00%
PNRC1	PNRC1		✓	101, 199-3p	0.00	100.00%	2	2	0	39.39%

					Betweenness		# of Interactions (Degree)			
GeneGO Object Name	**Mapped Gene Symbol**	**Molecular Function**	**DEGs**	**Predicted Targets †**	**Value**	**Rank***	**Total**	**In**	**Out**	**Rank***
PP2A catalytic	PP2A catalytic				0.00	100.00%	1	1	0	100.00%
PTEN	PTEN			139-5p	0.00	100.00%	1	1	0	100.00%
Progesterone receptor	PGR	TF			0.00	100.00%	1	1	0	100.00%
Protein kinase G1 alpha	PRKG1				0.00	100.00%	1	1	0	100.00%
QKI	QKI		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
RBMS1	RBMS1				0.00	100.00%	1	1	0	100.00%
RENT2	UPF2		✓	199-3p	0.00	100.00%	1	1	0	100.00%
RIP140	NRIP1			199-3p	0.00	100.00%	1	1	0	100.00%
RNA polymerase II	RNA polymerase II				0.00	100.00%	1	1	0	100.00%
Rb protein	RB1	TF		199-3p	0.00	100.00%	2	2	0	39.39%
SAT-1	SLC26A1				0.00	100.00%	1	1	0	100.00%
SDF-1	CXCL12				0.00	100.00%	1	1	0	100.00%
SLC38A1	SLC38A1			199-3p	0.00	100.00%	1	1	0	100.00%
SMAD5	SMAD5	TF	✓		0.00	100.00%	1	1	0	100.00%
SMAD9 (SMAD8)	SMAD9	TF	✓		0.00	100.00%	1	1	0	100.00%
SOX15	SOX15	TF			0.00	100.00%	1	1	0	100.00%
SP1/SP3 complex	SP1	TF		199-3p	0.00	100.00%	1	1	0	100.00%
SR140	SR140		✓	199-3p	0.00	100.00%	1	1	0	100.00%
SULF2	SULF2		✓		0.00	100.00%	1	1	0	100.00%
SUMO-3	SUMO3		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
Sequestosome 1(p62)	SQSTM1		✓		0.00	100.00%	1	1	0	100.00%
Sirtuin1	SIRT1	EPIGENES			0.00	100.00%	1	1	0	100.00%
Staf-50	TRIM22	TF	✓		0.00	100.00%	1	1	0	100.00%
TAFI48	TAF1A		✓		0.00	100.00%	1	1	0	100.00%
TBP	TBP	TF			0.00	100.00%	1	0	1	100.00%
TCP1	TCP1				0.00	100.00%	1	1	0	100.00%
TFIIH	TFIIH				0.00	100.00%	1	1	0	100.00%
TGF-beta 1	TGFB1			139-5p	0.00	100.00%	1	1	0	100.00%
TIF1-alpha	TRIM24	EPIGENES	✓	101, 139-5p	0.00	100.00%	1	1	0	100.00%
TWIST1	TWIST1				0.00	100.00%	1	0	1	100.00%
Tcf(Lef)	LEF1	TF			0.00	100.00%	1	1	0	100.00%
USP25	USP25		✓	199-3p	0.00	100.00%	1	1	0	100.00%
Ubiquitin	UBB				0.00	100.00%	1	1	0	100.00%
Versican	VCAN				0.00	100.00%	2	1	1	39.39%
WNT3A	WNT3A				0.00	100.00%	1	1	0	100.00%
WNT5A	WNT5A				0.00	100.00%	1	1	0	100.00%
YAP1 (YAp65)	YAP1			199-3p	0.00	100.00%	1	1	0	100.00%
YY1	YY1	TF			0.00	100.00%	1	1	0	100.00%
ZNF189	ZNF189	TF	✓		0.00	100.00%	1	1	0	100.00%
ZNF217	ZNF217	TF		101, 199-3p	0.00	100.00%	2	2	0	39.39%
ZNRF2	ZNRF2		✓	101, 199-3p	0.00	100.00%	1	1	0	100.00%
alpha-3/beta-1 integrin	alpha-3/beta-1 integrin				0.00	100.00%	1	1	0	100.00%
beta-TrCP	BTRC			199-3p	0.00	100.00%	1	1	0	100.00%
c-MPL	MPL			199-3p	0.00	100.00%	1	1	0	100.00%
dUTPase (DUT)	DUT		✓		0.00	100.00%	1	1	0	100.00%
p14ARF	CDKN2A	TF	✓		0.00	100.00%	1	1	0	100.00%
p15	CDKN2B				0.00	100.00%	1	1	0	100.00%
p21	CDKN1A				0.00	100.00%	1	1	0	100.00%

* Rank percentile

† Predicted by TargetScan and context score < -0.2

Supplementary Table S10. Experimentally validated targets of AP1

1st neighbor	Mechanism	Effect	2nd neighbor	Object Type	Mapped gene symbol	Experimental type	Reference
AP-1	***Transcription regulation***	***Activation***	ATF-3	Transcription factor	ATF3	ChIP	(1)
			Beta-catenin	Generic binding protein	CTNNB1	EMSA	(2)
			C/EBP zeta	Transcription factor	DDIT3	CAT, SEQ	(3-5)
			Cathepsin L	Generic protease	Cathepsin L	SEQ	(6-8)
			CIITA	Generic binding protein	CIITA	SEQ	(9)
			Cyclin D1	Generic binding protein	CCND1	EMSA	(10-14)
			DMTF1	Transcription factor	DMTF1	TAS	(15, 16)
			E7 protein (HPV16)	Protein	E7 protein (HPV16)	EMSA	(17, 18)
			EGR1	Transcription factor	EGR1	ChIP	(19)
			ELAVL1 (HuR)	Generic binding protein	ELAVL1	SEQ	(20)
			ELF1	Transcription factor	ELF1	EMSA	(21)
			ERR1	Transcription factor	ESRRA	ChIP	(22)
			FasL(TNFSF6)	Receptor ligand	FASLG	EMSA, SEQ	(23-26, 6, 27)
			FOXP3	Transcription factor	FOXP3	SEQ	(28-31)
			Granzyme B	Generic protease	GZMB	SEQ	(32-35)
			HB-EGF	Receptor ligand	HBEGF	SEQ	(36-40, 6, 41)
			HSP27	Generic binding protein	HSPB1	TAS	(42)
			IGF-1	Receptor ligand	IGF-1	EMSA	(43)
			IL-1 beta	Receptor ligand	IL1B	EMSA	(44, 45)
			IL-18	Receptor ligand	IL18	SEQ	(46, 47)
			IL-2	Receptor ligand	IL2	EMSA	(48-55)
			IL-4	Receptor ligand	IL4	TAS	(56, 19)
			IL-5	Receptor ligand	IL5	SEQ	(57-63)
			MDM2	Generic enzyme	MDM2	SEQ	(64, 65)
			MMP-12	Metalloprotease	MMP12	SEQ	(66-69)
			MMP-9	Metalloprotease	MMP9	EMSA, SEQ	(70-98)
			MYOD	Transcription factor	MYOD1	TAS	(99)
			PLAU (UPA)	Generic protease	PLAU	EMSA	(100-102)
			PLAU (UPA)	Generic protease	PLAU	ChIP	(103)
			Prolactin	Receptor ligand	PRL	SEQ	(104-110)
			SAT-1	Transporter	SLC26A1	SEQ	(111-113)
			SMAD7	Generic binding protein	SMAD7	SEQ	(114-116)
			SNAIL1	Transcription factor	SNAI1	SEQ	(117)
			SOD2	Generic enzyme	SOD2	EMSA	(118, 119)
			TGF-beta 1	Receptor ligand	TGFB1	EMSA	(120-123, 19, 124, 125)
			TIMP1	Generic binding protein	TIMP1	SEQ	(126, 127, 88, 128, 94)
			TIMP2	Generic binding protein	TIMP2	SEQ	(129, 94)
			TNF-alpha	Receptor ligand	TNF	SEQ	(130-133)
			TNF-alpha	Receptor ligand	TNF	EMSA	(134, 135, 19, 136, 137)
			VEGF-A	Receptor ligand	VEGFA	EMSA, SEQ	(138-149)
			VEGF-D	Receptor ligand	FIGF	EMSA	(150)
		Inhibition	c-Myc	Transcription factor	MYC	EMSA	(151, 152)
			MYOD	Transcription factor	MYOD1	EMSA	(153)
			PIT1	Transcription factor	POU1F1	EMSA	(154, 155)
			Progesterone receptor	Transcription factor	PGR	ChIP	(156)
		Unspecified	Cyclin D1	Generic binding protein	CCND1	SEQ	(27, 157)
			EGR1	Transcription factor	EGR1	SEQ	(158)
			G-CSF	Receptor ligand	CSF3	SEQ	(159)
			GFER	Generic binding protein	GFER	SEQ	(160)
			IL-2	Receptor ligand	IL2	SEQ	(161)
			IL-4	Receptor ligand	IL4	TAS	(162)
			IL-5	Receptor ligand	IL5	EMSA	(163)
			KLF4	Transcription factor	KLF4	SEQ	(164)
			LL37	Receptor ligand	CAMP	ChIP-chip, SEQ	(165)
			M-CSF receptor	Generic receptor	CSF1R	EMSA	(166)
			microRNA 221	RNA	miR-221	SEQ	(167)
			microRNA 222	RNA	miR-222	SEQ	(167)
			PCNA	Generic binding protein	PCNA	SEQ	(168)
			PCY2	Generic enzyme	PCYT2	SEQ	(169)
			PLAU (UPA)	Generic protease	PLAU	SEQ	(100)
			SHP-1	Protein phosphatase	PTPN6	SEQ	(170)
			SSAT	Generic enzyme	SAT1	TAS	(171, 172)
			Thrombospondin 1	Receptor ligand	THBS1	SEQ	(173)
			TrkA	Receptor with enzyme activity	NTRK1	SEQ	(174)

CAT: chloramphenicol acetyl transferase assay; ChIP: chromatin immunoprecipitation assays; ChIP-chip: chromatin immunoprecipitation array; Co-IP: coimmunoprecipitation; SEQ: sequence analysis; TAS: Traceable Author Statement

Supplementary Table S11. Experimentally validated targets of EZH2

1st neighbor	Mechanism	Effect	2nd neighbor	Object Type	Mapped HGNC Symbol	Interaction validation	Reference
EZH2	***Binding***	***Activation***	DNMT1	Generic enzyme	DNMT1	Co-IP	(175-177)
			DNMT3A	Generic enzyme	DNMT3A	Co-IP	(175, 176)
			DNMT3B	Generic enzyme	DNMT3B	Co-IP	(175, 176, 178)
			ESR1 (nuclear)	Transcription factor	ESR1	Co-IP	(179)
	Transcription regulation	***Activation***	c-Myc	Transcription factor	MYC	ChIP	(179)
			Cyclin D1	Generic binding protein	CCND1	ChIP	(179, 180)
			PAX3	Transcription factor	PAX3	ChIP	(181-183)
			WNT3A	Receptor ligand	WNT3A	ChIP	(182)
		Inhibition	14-3-3 sigma	Generic binding protein	SFN	ChIP	(184)
			BMP2	Receptor ligand	BMP2	ChIP, SEQ	(181, 185)
			BMPR1B	Receptor with enzyme activity	BMPR1B	ChIP	(186)
			C/EBPdelta	Transcription factor	CEBPD	ChIP	(187)
			CIITA	Generic binding protein	CIITA	ChIP	(188)
			DKK1	Receptor ligand	DKK1	ChIP	(189-191)
			FOXP1	Transcription factor	FOXP1	ChIP	(184)
			HOXD13	Transcription factor	HOXD13	ChIP	(181, 192)
			IL-13	Receptor ligand	IL13	ChIP	(193)
			IL-4	Receptor ligand	IL4	ChIP	(193, 194)
			Lef-1	Transcription factor	LEF1	ChIP	(185)
			NANOG	Transcription factor	NANOG	ChIP	(182, 195)
			Oct-3/4	Transcription factor	POU5F1	ChIP	(182, 189, 196)
			p14ARF	Generic binding protein	CDKN2A	ChIP	(197-199)
			p15	Generic binding protein	CDKN2B	ChIP	(197, 198, 192)
			p53	Transcription factor	TP53	ChIP	(191)
			p73	Transcription factor	TP73	ChIP	(200)
			PKA-cat beta	Protein kinase	PRKACB	ChIP	(184)
			Progesterone receptor	Transcription factor	PGR	ChIP, ChIP-chip	(181, 201)
			PTEN	Lipid phosphatase	PTEN	ChIP	(202, 203)
			RASSF1	Generic binding protein	RASSF1	ChIP	(178)
			RUNX3	Transcription factor	RUNX3	ChIP	(181, 204, 205)
			SDF-1	Receptor ligand	CXCL12	ChIP, ChIP-chip	(181, 206)
		Unspecified	IFN-gamma	Receptor ligand	IFNG	ChIP	(194)

ChIP: chromatin immunoprecipitation assays; ChIP-chip: chromatin immunoprecipitation array; Co-IP: coimmunoprecipitation; SEQ: sequence analysis

Supplmentary table S12: Significantly enriched pathways enriched by secondary nodes in miR-101 subnet

KEGG pathway enrichment by 162 secondary nodes in miR-101 subnet

Term	Count	%	Fold Enrichment	P-Value	Benjamini	FDR
hsa04110:Cell cycle	24	8.08	6.03	3.28E-12	9.09E-11	3.71E-09
hsa04350:TGF-beta signaling pathway	18	6.06	6.49	1.01E-09	1.87E-08	1.15E-06
hsa04510:Focal adhesion	26	8.75	4.06	2.35E-09	3.26E-08	2.66E-06
hsa04010:MAPK signaling pathway	30	10.10	3.53	2.68E-09	3.30E-08	3.03E-06
hsa04722:Neurotrophin signaling pathway	20	6.73	5.06	7.34E-09	8.14E-08	8.30E-06
hsa04060:Cytokine-cytokine receptor interaction	28	9.43	3.35	3.21E-08	3.24E-07	3.63E-05
hsa04012:ErbB signaling pathway	15	5.05	5.41	4.21E-07	3.60E-06	4.77E-04
hsa04062:Chemokine signaling pathway	21	7.07	3.52	1.31E-06	9.70E-06	1.48E-03
hsa04520:Adherens junction	12	4.04	4.89	2.50E-05	1.46E-04	2.82E-02
hsa04630:Jak-STAT signaling pathway	17	5.72	3.44	2.54E-05	1.41E-04	2.87E-02
hsa04310:Wnt signaling pathway	16	5.39	3.33	7.21E-05	3.64E-04	8.16E-02
hsa04210:Apoptosis	12	4.04	4.33	7.95E-05	3.84E-04	9.00E-02
hsa04660:T cell receptor signaling pathway	12	4.04	3.49	5.52E-04	2.55E-03	6.23E-01
hsa04115:p53 signaling pathway	9	3.03	4.15	1.25E-03	5.52E-03	1.40E+00
hsa04664:Fc epsilon RI signaling pathway	9	3.03	3.62	3.02E-03	1.19E-02	3.37E+00
hsa04910:Insulin signaling pathway	12	4.04	2.79	3.43E-03	1.31E-02	3.81E+00
hsa04340:Hedgehog signaling pathway	7	2.36	3.92	8.05E-03	2.95E-02	8.74E+00
hsa04650:Natural killer cell mediated cytotoxicity	11	3.70	2.60	9.08E-03	3.21E-02	9.81E+00
hsa04912:GnRH signaling pathway	9	3.03	2.88	1.19E-02	4.08E-02	1.27E+01
hsa04620:Toll-like receptor signaling pathway	9	3.03	2.80	1.41E-02	4.68E-02	1.49E+01
hsa04360:Axon guidance	10	3.37	2.43	2.05E-02	6.53E-02	2.09E+01
hsa04662:B cell receptor signaling pathway	7	2.36	2.93	3.06E-02	8.91E-02	2.97E+01
hsa04370:VEGF signaling pathway	7	2.36	2.93	3.06E-02	8.91E-02	2.97E+01
hsa04670:Leukocyte transendothelial migration	9	3.03	2.39	3.27E-02	9.25E-02	3.13E+01
hsa04916:Melanogenesis	8	2.69	2.54	3.66E-02	9.82E-02	3.44E+01
hsa04940:Type I diabetes mellitus	5	1.68	3.74	4.26E-02	1.11E-01	3.89E+01
hsa04320:Dorso-ventral axis formation	4	1.35	5.02	4.30E-02	1.10E-01	3.92E+01

BioCarta pathway enrichment by 144 secondary nodes in miR-101 subnet

Term	Count	%	Fold Enrichment	PValue	Benjamini	FDR
h_g1Pathway:Cell Cycle: G1/S Check Point	15	5.05	5.16	1.06E-07	2.36E-05	1.35E-04
h_p38mapkPathway:p38 MAPK Signaling Pathway	15	5.05	4.54	7.85E-07	8.75E-05	1.00E-03
h_tgfbPathway:TGF beta signaling pathway	9	3.03	5.28	8.89E-05	6.58E-03	1.13E-01
h_etsPathway:METS affect on Macrophage Differentiation	8	2.69	4.99	4.43E-04	2.44E-02	5.64E-01
h_keratinocytePathway:Keratinocyte Differentiation	12	4.04	3.15	7.31E-04	3.21E-02	9.29E-01
h_cellcyclePathway:Cyclins and Cell Cycle Regulation	9	3.03	3.59	1.97E-03	7.07E-02	2.49E+00
h_mapkPathway:MAPKinase Signaling Pathway	17	5.72	2.12	3.91E-03	1.17E-01	4.88E+00
h_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	8	2.69	3.63	3.95E-03	1.04E-01	4.92E+00
h_p53Pathway:p53 Signaling Pathway	7	2.36	4.11	4.29E-03	1.01E-01	5.33E+00
h_prc2Pathway:The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone Tails	6	2.02	4.61	6.06E-03	1.27E-01	7.46E+00
h_arfPathway:Tumor Suppressor Arf Inhibits Ribosomal Biogenesis	6	2.02	4.61	6.06E-03	1.27E-01	7.46E+00
h_hsp27Pathway:Stress Induction of HSP Regulation	6	2.02	4.28	8.68E-03	1.62E-01	1.05E+01
h_ctcfPathway:CTCF: First Multivalent Nuclear Factor	7	2.36	3.49	1.04E-02	1.77E-01	1.25E+01
h_inflamPathway:Cytokines and Inflammatory Response	8	2.69	3.07	1.08E-02	1.70E-01	1.30E+01
h_pmlPathway:Regulation of transcriptional activity by PML	6	2.02	3.99	1.20E-02	1.75E-01	1.43E+01
h_At1rPathway:Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	8	2.69	2.96	1.34E-02	1.82E-01	1.58E+01
h_alkPathway:ALK in cardiac myocytes	9	3.03	2.64	1.52E-02	1.93E-01	1.78E+01
h_RacCycDPathway:Influence of Ras and Rho proteins on G1 to S Transition	7	2.36	2.91	2.59E-02	2.92E-01	2.85E+01
h_nthiPathway:NFkB activation by Nontypeable Hemophilus influenzae	7	2.36	2.91	2.59E-02	2.92E-01	2.85E+01
h_carm-erPathway:CARM1 and Regulation of the Estrogen Receptor	7	2.36	2.79	3.14E-02	3.27E-01	3.34E+01
h_wntPathway:WNT Signaling Pathway	7	2.36	2.79	3.14E-02	3.27E-01	3.34E+01
h_pdgfPathway:PDGF Signaling Pathway	7	2.36	2.79	3.14E-02	3.27E-01	3.34E+01
h_HivnefPathway:HIV-I Nef: negative effector of Fas and TNF	11	3.70	2.07	3.17E-02	3.15E-01	3.37E+01
h_egfPathway:EGF Signaling Pathway	7	2.36	2.69	3.76E-02	3.48E-01	3.87E+01
h_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	8	2.69	2.42	3.89E-02	3.44E-01	3.97E+01
h_cytokinePathway:Cytokine Network	6	2.02	2.99	4.12E-02	3.47E-01	4.16E+01

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