Supplemental Data

The regulation of microRNA expression by DNA methylation in hepatocellular carcinoma

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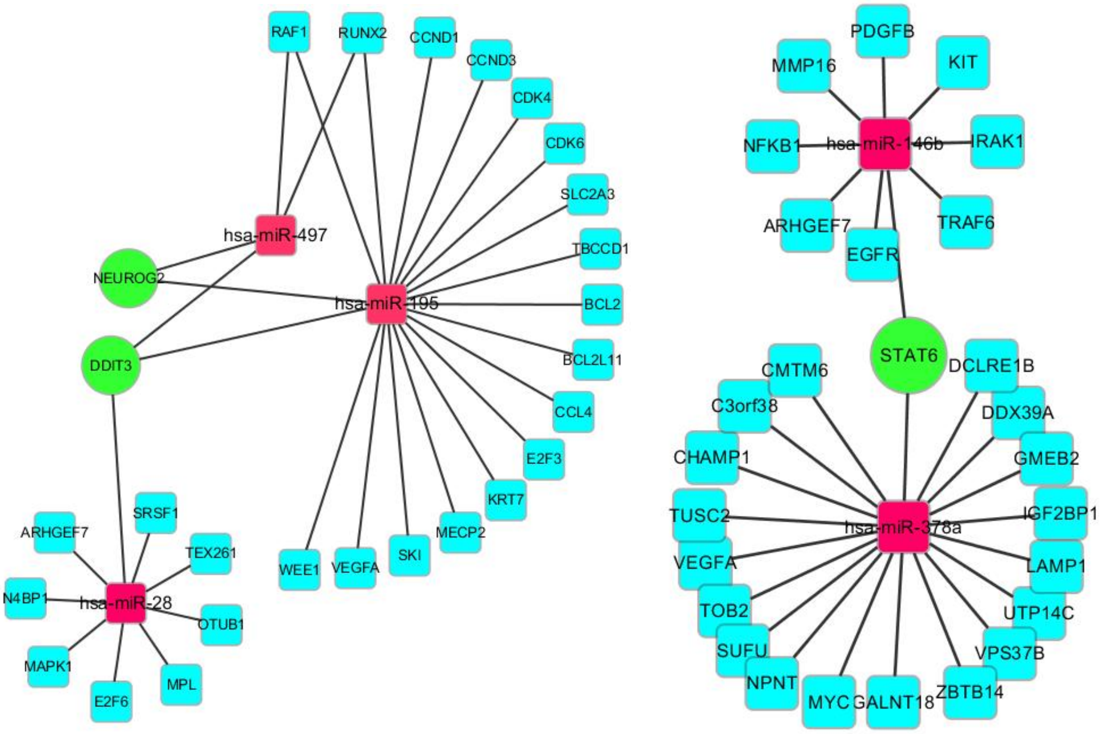

Figure S1. The regulatory network of hypermethylated TFs (left) and hypomethylated TF (right), dysregulated miRNAs regulated by these TFs, and the miRNA targets. Circles in green are TFs, squares in red are miRNAs and others are miRNA target genes. TF regulates miRNAs and miRNAs regulate other target genes.

Table S1. Dysregulated miRNAs between cancerous and normal hepatocytes.

miRNA	Expression change(FC)	p-value
hsa-miR-122	-4049.44	1.85e-05
hsa-miR-122*	-431.92	1.20e-06
hsa-miR-885-5p	-65.13	3.76e-05
hsa-miR-146b-5p	-55.13	1.80e-04
hsa-miR-192	-42.64	0.014
hsa-miR-375	-25.69	1.75e-05
hsa-miR-194	-20.17	0.027
hsa-miR-101	-17.04	1e-04
hsa-miR-215	-15.98	0.020
hsa-miR-195	-15.57	0.001
hsa-miR-768-5p	-15.35	4.46e-04
hsa-miR-768-3p	-13.47	0.004
hsa-miR-148a	-12.58	0.007
hsa-miR-497	-10.31	0.002
hsa-miR-192*	-10.29	2.74e-04
hsa-miR-630	-8.46	0.004
hsa-miR-361-3p	-5.76	0.003
hsa-miR-99a	-5.72	0.003
hsa-miR-26b	-5.22	8.10e-04
hsa-miR-574-3p	-5.14	0.006
hsa-miR-572	-4.99	0.002
hsa-miR-874	-3.51	0.038
hsa-miR-29c	-2.77	0.005
hsa-miR-378	-2.53	0.042
hsa-miR-638	-2.50	0.007
hsa-miR-30e	-2.35	0.017
hsa-miR-30b	-2.17	0.028
hsa-miR-28-5p	-2.15	0.050
hsa-miR-221	28.90	5.47e-04
hsa-miR-99b	27.49	0.033
hsa-miR-181a	5.93	0.025
hsa-miR-93	4.91	8.06e-04
hsa-miR-15b	4.06	0.006
hsa-miR-106b	3.38	0.003
hsa-miR-25	2.99	7.02e-04
hsa-miR-23a	2.85	0.001
hsa-miR-27a	2.58	0.008

FC: fold change, refers to the alteration of miRNA expression between cancerous and normal hepatocytes, negative value "-" means down-regulation of expression of miRNA.

Table S2. GO and KEGG pathway terms enriched by targets of the ten dysregulated miRNAs and miR-148a.

GO terms enriched by targets of ten dysregulated miRNAs	
Category	**P value**
nucleus(cellular_component)	9.42E-17
negative regulation of transcription from RNA polymerase II promoter(biological_process)	1.61E-16
transcription factor binding(molecular_function)	5.95E-14
G1 phase of mitotic cell cycle(biological_process)	8.13E-14
nucleoplasm(cellular_component)	1.30E-12
protein binding(molecular_function)	2.78E-11
cyclin-dependent protein kinase holoenzyme complex(cellular_component)	8.43E-11
positive regulation of transcription from RNA polymerase II promoter(biological_process)	1.08E-09
transcription initiation from RNA polymerase II promoter(biological_process)	1.02E-08
positive regulation of transcription, DNA-dependent(biological_process)	3.03E-08
protein kinase binding(molecular_function)	3.34E-08
chromatin(cellular_component)	5.36E-08
negative regulation of cell proliferation(biological_process)	6.32E-08
transcription factor complex(cellular_component)	8.16E-08
regulation of lipid kinase activity(biological_process)	8.42E-08
sequence-specific DNA binding transcription factor activity(molecular_function)	1.31E-07
positive regulation of cell proliferation(biological_process)	1.92E-07
identical protein binding(molecular_function)	5.70E-07
negative regulation of transcription, DNA-dependent(biological_process)	6.26E-07
regulation of cell cycle(biological_process)	7.85E-07
positive regulation of gene expression(biological_process)	1.16E-06
regulation of gene expression(biological_process)	1.28E-06
mitotic cell cycle(biological_process)	1.55E-06
cell cycle arrest(biological_process)	1.97E-06
cell proliferation(biological_process)	2.33E-06
positive regulation of osteoblast differentiation(biological_process)	4.06E-06
G1/S transition of mitotic cell cycle(biological_process)	4.62E-06
positive regulation of cyclin-dependent protein kinase activity(biological_process)	4.64E-06
negative regulation of apoptotic process(biological_process)	5.45E-06
neuron apoptotic process(biological_process)	9.04E-06
G2 phase of mitotic cell cycle(biological_process)	9.88E-06
type B pancreatic cell development(biological_process)	9.88E-06
neuron maturation(biological_process)	9.88E-06
transcription corepressor activity(molecular_function)	1.22E-05
response to gamma radiation(biological_process)	1.34E-05
transcription, DNA-dependent(biological_process)	1.49E-05
CXCR chemokine receptor binding(molecular_function)	1.94E-05
PML body(cellular_component)	2.20E-05
sequence-specific DNA binding(molecular_function)	2.68E-05
positive regulation of fibroblast proliferation(biological_process)	2.91E-05

induction of apoptosis(biological_process)	2.91E-05
nuclear chromatin(cellular_component)	3.57E-05
negative regulation of epithelial cell proliferation(biological_process)	4.67E-05
apoptotic process(biological_process)	4.74E-05
response to DNA damage stimulus(biological_process)	5.06E-05
ovarian follicle development(biological_process)	5.10E-05
negative regulation of transcription involved in G1/S phase of mitotic cell cycle(biological_process)	5.81E-05
DNA-methyltransferase activity(molecular_function)	5.81E-05
cytoplasm(cellular_component)	5.66E-05
camera-type eye morphogenesis(biological_process)	5.47E-05
T cell homeostasis(biological_process)	6.55E-05
cell division(biological_process)	6.67E-05
transcription regulatory region DNA binding(molecular_function)	8.09E-05
core promoter binding(molecular_function)	9.09E-05
negative regulation of smoothened signaling pathway(biological_process)	9.09E-05
post-embryonic camera-type eye development(biological_process)	1.16E-04
DNA (cytosine-5-)-methyltransferase activity(molecular_function)	1.16E-04
acetylcholine receptor binding(molecular_function)	1.16E-04
Rb-E2F complex(cellular_component)	1.16E-04
RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription(molecular_function)	1.36E-04
negative regulation of fibroblast proliferation(biological_process)	1.40E-04
regulation of translation(biological_process)	1.45E-04
S phase of mitotic cell cycle(biological_process)	1.53E-04
cytosol(cellular_component)	1.53E-04
Notch signaling pathway(biological_process)	1.66E-04
negative regulation of histone H3-K9 methylation(biological_process)	1.93E-04
B cell lineage commitment(biological_process)	1.93E-04
gland morphogenesis(biological_process)	1.93E-04
positive regulation of peptidyl-tyrosine phosphorylation(biological_process)	1.87E-04
transforming growth factor beta receptor signaling pathway(biological_process)	1.94E-04
MAPK cascade(biological_process)	1.98E-04
repressing transcription factor binding(molecular_function)	2.03E-04
DNA binding(molecular_function)	2.12E-04
blood coagulation(biological_process)	2.10E-04
positive regulation of cell differentiation(biological_process)	2.28E-04
response to stress(biological_process)	2.44E-04
negative regulation of cell aging(biological_process)	2.88E-04
T cell differentiation in thymus(biological_process)	2.83E-04
RNA polymerase II transcription factor binding(molecular_function)	2.83E-04
positive regulation of protein metabolic process(biological_process)	2.88E-04
epidermal growth factor receptor signaling pathway(biological_process)	2.92E-04
nuclear body(cellular_component)	3.13E-04
dendrite development(biological_process)	3.46E-04

protein kinase activity(molecular_function)	3.44E-04
cyclin-dependent protein kinase activity(molecular_function)	3.46E-04
chromatin binding(molecular_function)	3.65E-04
unmethylated CpG binding(molecular_function)	4.02E-04
prostate gland growth(biological_process)	4.02E-04
methyl-CpG binding(molecular_function)	4.02E-04
negative regulation of epithelial cell differentiation(biological_process)	4.02E-04
nerve growth factor receptor signaling pathway(biological_process)	4.08E-04
positive regulation of protein phosphorylation(biological_process)	4.62E-04
negative regulation of osteoblast differentiation(biological_process)	4.97E-04
transcription coactivator activity(molecular_function)	5.18E-04
mammary gland epithelial cell proliferation(biological_process)	5.35E-04
cellular response to amino acid stimulus(biological_process)	5.87E-04
cell maturation(biological_process)	6.35E-04
adult locomotory behavior(biological_process)	6.35E-04
negative regulation of phosphatidylinositol 3-kinase cascade(biological_process)	6.86E-04
positive regulation of histone H3-K4 methylation(biological_process)	6.86E-04
ear development(biological_process)	6.86E-04
dendritic spine morphogenesis(biological_process)	6.86E-04
nuclear membrane(cellular_component)	6.69E-04
response to ethanol(biological_process)	7.18E-04
mitotic cell cycle G1/S transition DNA damage checkpoint(biological_process)	8.55E-04
axon regeneration(biological_process)	8.55E-04
protein phosphorylation(biological_process)	8.39E-04
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway(biological_process)	8.53E-04
positive regulation of peptidyl-serine phosphorylation(biological_process)	8.53E-04
branching involved in ureteric bud morphogenesis(biological_process)	9.14E-04
chromatin modification(biological_process)	9.84E-04

KEGG pathways enriched by targets of the ten dysregulated miRNAs

Category	**Pvalue**
Cell cycle	3.27E-14
Bladder cancer	8.21E-13
Non-small cell lung cancer	1.24E-11
Pancreatic cancer	1.86E-10
Small cell lung cancer	1.69E-09
Glioma	2.21E-09
Melanoma	4.95E-09
Chronic myeloid leukemia	6.37E-09
Prostate cancer	3.77E-08
HTLV-I infection	1.52E-07
Endometrial cancer	1.91E-07
Pathways in cancer	2.85E-07
Focal adhesion	5.60E-07

p53 signaling pathway	1.25E-06
Colorectal cancer	1.10E-05
Measles	1.16E-04
Adipocytokine signaling pathway	2.54E-04
Neurotrophin signaling pathway	6.13E-04

GO terms enriched by targets of miR-148a

Category	**Pvalue**
DNA (cytosine-5-)-methyltransferase activity(molecular_function)	4.59E-05
DNA-methyltransferase activity(molecular_function)	2.30E-05
negative regulation of histone H3-K9 methylation(biological_process)	7.64E-05
positive regulation of histone H3-K4 methylation(biological_process)	2.73E-04
respiratory chain(cellular_component)	2.73E-04

Table S3. HCC or cancer related genes got from differently methylated genes; targets (protein-coding genes) of differently methylated TFs (DMTFs); targets of dysregulated miRNAs which targeted by differently methylated TFs. Cancer related genes: covered by yellow; HCC related genes: font in red. TF: transcription factor.

Differently methylated genes				
Hypermethyed genes				**Hypomethylated genes**
AEN	EVX1	HOXC13	PRAC	ATG4D
GPR158-AS1	EVX2	HOXC4	PTPLAD2	ATP2B2
AKNA	FAM5B	HOXC5	RASGRF1	CACNA1B
LOC339825	FBXL21	HOXC6	RASGRP2	CALCR
ALDH16A1	FBXL8	HOXC8	RING1	CNPY4
ALG3	FEV	HOXC9	RUNX2	COL27A1
ANK1	GCC1	HOXD1	SHMT2	CTDSPL
ANKRD28	GLB1L	HOXD10	SIX5	DENND1C
ARF5	GPR158	HOXD11	SLC17A7	DIS3L2
ARHGAP9	GRM8	HOXD12	SLC26A10	DPM3
ASTN1	GULP1	HOXD13	SLC39A7	DPRX
ATP8B2	HAS1	HOXD3	SLC6A20	EIF4H
B3GNT9	HLA-DPA1	HOXD4	SLIT2	FAM184A
BAD	HLA-DPB1	HOXD8	SLIT3	FBXL18
BTG4	HOXA10	HOXD9	SPEF1	GPR157
C10orf125	HOXA11	HSF4	STK16	HSD17B8
C11orf20	HOXA13	HTR2C	STK19	HUWE1
C19orf35	HOXA2	IFNA2	TCEA2	IGF2
C1orf61	HOXA3	IFNA8	TLCD1	KIAA1797
C1orf92	HOXA4	IL25	TMEM208	LRP1
C20orf27	HOXA5	ILF3	TNFAIP8L1	MAP2K4
C9orf3	HOXA6	ITCH	TP73	MYH7
C9orf4	HOXA7	LCOR	TRAF4	NOVA2
CACNG7	HOXA9	LHX2	TRIM45	PKHD1
CACNG8	HOXB13	LRCH3	TRIM59	RTL1
CAMK2N2	HOXB3	NDUFA3	TTC9B	SIGLEC14
CDC25B	HOXB4	NEUROG2	TUBA8	SLC11A1
CENPB	HOXB5	NUDT18	UGT8	SLC12A3
CHRM2	HOXB6	OAZ1	UNCX	SMAD5
CILP2	HOXB7	OSCAR	VENTX	STAT6
COL11A2	HOXB8	OSR2	WBP2NL	TAF12
CYHR1	HOXB9	PLCB3	WHSC2	ZCCHC13
DDIT3	HOXC10	PLCD1	ZNF141	ZNF18
DPYS	HOXC11	PNKD	ZNF610	ZNF766
targets(protein-coding genes) of differently methylated TFs				

	hypermethyed TF	**target gene**	**hypermethyed TF**
	DDIT3	AARS	HOXA3
	DDIT3	ADK	HOXA3
	DDIT3	ADSS	HOXA3
	DDIT3	AGER	HOXA3
	DDIT3	AP2A1	HOXA3
	DDIT3	AP2S1	HOXA3

	DDIT3	APBB2	HOXA3
	DDIT3	ATP5G1	HOXA3
	DDIT3	BCL11B	HOXA3
	DDIT3	BHLHB2	HOXA3
	DDIT3	C1orf51	HOXA3
	DDIT3	C6orf138	HOXA3
	DDIT3	C9orf150	HOXA3
	DDIT3	CCL2	HOXA3

	DDIT3	CCS	HOXA3
	DDIT3	CD79A	HOXA3
	DDIT3	CDIPT	HOXA3
	DDIT3	CIAO1	HOXA3
	DDIT3	CLIP1	HOXA3
	DDIT3	COL12A1	HOXA3
	DDIT3	CRYZL1	HOXA3
	DDIT3	CYP7A1	HOXA3

DDIT3	DDIT4	HOXA3
DDIT3	FAM5B	HOXA3
DDIT3	FAM96A	HOXA3
DDIT3	FAR2	HOXA3
DDIT3	FEZ1	HOXA3
DDIT3	FGF11	HOXA3
DDIT3	FZD5	HOXA3
DDIT3	GAS5	HOXA3

	DDIT3	GPBP1L1	HOXA3
	DDIT3	GRAMD1B	HOXA3
	DDIT3	HOXA11AS	HOXA3
	DDIT3	ID2	HOXA3
	DDIT3	IDH3G	HOXA3
	DDIT3	IHH	HOXA3
	DDIT3	IL2	HOXA3
	DDIT3	IL23A	HOXA3

	DDIT3	INSM1	HOXA3
	DDIT3	JMJD1B	HOXA3
	DDIT3	JMJD3	HOXA3
	DDIT3	KCNA5	HOXA3
	DDIT3	KCNJ3	HOXA3
	DDIT3	KCNK18	HOXA3
	DDIT3	KIAA1217	HOXA3
	DDIT3	KIF3C	HOXA3

DDIT3	KLF12	HOXA3
DDIT3	KRTCAP2	HOXA3
DDIT3	LAMC1	HOXA3
DDIT3	LOC100129550	HOXA3
DDIT3	LOC345630	HOXA3
DDIT3	LRRC48	HOXA3

	DDIT3	MCCD1	HOXA3
	DDIT3	MED29	HOXA3
	DDIT3	MIB1	HOXA3
	DDIT3	MOAP1	HOXA3
	DDIT3	MRPS27	HOXA3
	DDIT3	MXD3	HOXA3
	DDIT3	MYL1	HOXA3
	DDIT3	N6AMT1	HOXA3

DDIT3	NHLRC3	HOXA3
DDIT3	NTRK3	HOXA3
DDIT3	ODZ4	HOXA3
DDIT3	OR4C16	HOXA5
DDIT3	PC-3	HOXA5

	DDIT3	PHF21A	HOXA5
	DDIT3	PIP5K1B	HOXA5
	DDIT3	PLA2R1	HOXA5
	DDIT3	PPFIA3	HOXA5
	DDIT3	PRDX5	HOXA5
	DDIT3	RASSF9	HOXA5

	DDIT3	RBMS2	HOXA5
	DDIT3	RNF219	HOXA5
	DDIT3	RTP2	HOXA5
	DDIT3	SDK1	HOXA5
	DDIT3	SEBOX	HOXA5
	DDIT3	SEPHS1	HOXA5
	DDIT3	SHC3	HOXA5

	DDIT3	SLC6A2	HOXA5
	DDIT3	SNORA14B	HOXA5
	DDIT3	SNORA48	HOXA5
	DDIT3	SNORA81	HOXA5
	DDIT3	SNORD11	HOXA5
	DDIT3	SNORD74	HOXA5
	DDIT3	SNX1	HOXA5
	DDIT3	SPEG	HOXA5

	DDIT3	STEAP2	HOXA5
	DDIT3	STK40	HOXA5
	DDIT3	SYNGR4	HOXA5
	DDIT3	TAC4	HOXA5
	DDIT3	TAF8	HOXA5
	DDIT3	TBCC	HOXA5
	DDIT3	TFAP4	HOXA5
	DDIT3	THBS4	HOXA5

	DDIT3	TMEM69	HOXA5
	DDIT3	TNFRSF10B	HOXA5
	DDIT3	TNPO3	HOXA5
	DDIT3	TRIB1	HOXA5
	DDIT3	TSC2	HOXA5
	DDIT3	UTP14C	HOXA5
	DDIT3	VAT1L	HOXA5
	DDIT3	VPS53	HOXA5

DDIT3	YWHAQ	HOXA5
DDIT3	ZBTB37	HOXA5
DDIT3	ZDHHC22	HOXA5
DDIT3	ZEB2	HOXA5
DDIT3	ZHX2	HOXA5
DDIT3	ZNF219	HOXA5

DDIT3	ZNF277	HOXA5
DDIT3	ZNF385B	HOXA5
FEV	HTR1A	HOXA5
FEV	INS	HOXA5
FEV	INS2	HOXA5

FEV	SLC6A4	HOXA5
HOXA10	CDKN1A	HOXA5
HOXA10	CYBB	HOXA5
HOXA10	EMX2	HOXA5
HOXA10	ITGB3	HOXA5
HOXA10	KAT2B	HOXA5
HOXA10	KLF9	HOXA5

	HOXA10	MAFB	HOXA5
	HOXA10	MYLK	HOXA5
	HOXA10	RUNX2	HOXA5
	HOXA11	SIX2	HOXA5
	HOXA13	BMP2	HOXA5
	HOXA13	BMP4	HOXA5
	HOXA13	BMP7	HOXA5
	HOXA13	EPHA7	HOXA5

HOXA13	LMNB2	HOXA5
HOXA2	MEOX1	HOXA5
HOXA2	SIX2	HOXA5
HOXA3	AAMP	HOXA5
HOXA3	ADAMTS12	HOXA5
HOXA3	ADNP	HOXA5
HOXA3	AKTIP	HOXA5

HOXA3	ALCAM	HOXA5
HOXA3	ALDH1A3	HOXA5
HOXA3	ALX3	HOXA5
HOXA3	ANKRD28	HOXA5
HOXA3	AP1G2	HOXA5
HOXA3	ASPN	HOXA5
HOXA3	BCL2L1	HOXA5

HOXA3	C11orf67	HOXA5
HOXA3	C17orf61	HOXA5
HOXA3	C1orf43	HOXA5
HOXA3	C1QL1	HOXA5
HOXA3	C2orf63	HOXA5
HOXA3	C5orf20	HOXA5
HOXA3	C7orf33	HOXA5

HOXA3	CALM2	HOXA5
HOXA3	CCDC120	HOXA5
HOXA3	CDH3	HOXA5
HOXA3	CLDN2	HOXA5
HOXA3	CREB3L4	HOXA5
HOXA3	DDN	HOXA5
HOXA3	DENND1B	HOXA5

HOXA3	DENND2A	HOXA5
HOXA3	DIO3	HOXA5
HOXA3	DNAJC22	HOXA5
HOXA3	ELMOD3	HOXA5
HOXA3	ENOX1	HOXA5
HOXA3	EP300	HOXA5
HOXA3	EVX2	HOXA5

	HOXA3	FAM117B	HOXA5
	HOXA3	FAU	HOXA5
	HOXA3	PLBD1	HOXA5
	HOXA3	GFM2	HOXA5
	HOXA3	GJC1	HOXA5
	HOXA3	GRIK3	HOXA5
	HOXA3	GRIN2B	HOXA5

	SIX5	ATP1A1	HOXA9
	SIX5	CKM	HOXA9
	TP73	ACOT6	HOXA9
	TP73	ADA	HOXA9
	TP73	ADIG	HOXA9
	TP73	ADRBK1	HOXA9
	TP73	AEN	HOXA9
	TP73	AGPAT3	HOXA9

TP73	AGTPBP1	HOXA9
TP73	AP2A1	HOXA9
TP73	APAF1	HOXA9
TP73	APOBEC3H	HOXA9
TP73	ARAP1	HOXA9

	TP73	ARID5A	HOXA9
	TP73	ASAP1	HOXA9
	TP73	ASTN2	HOXA9
	TP73	ATP2B4	HOXA9
	TP73	ATP5F1	HOXA9
	TP73	AXIN2	HOXA9
	TP73	AXL	HOXA9
	TP73	BAX	HOXA9

	TP73	BBC3	HOXA9
	TP73	BLCAP	HOXA9
	TP73	BOP1	HOXA9
	TP73	C10orf10	HOXA9
	TP73	C10orf105	HOXA9
	TP73	C12orf77	HOXA9
	TP73	C17orf56	HOXA9
	TP73	C17orf89	HOXA9

TP73	C1orf144	HOXA9
TP73	C20orf196	HOXA9
TP73	C21orf49	HOXA9
TP73	C3orf17	HOXA9
TP73	CABP7	HOXA9
TP73	CCDC115	HOXA9
TP73	CCDC12	HOXA9

	TP73	CD82	HOXA9
	TP73	CDC45	HOXA9
	TP73	CDKN1A	HOXA9
	TP73	CEL	HOXA9
	TP73	CELA3A	HOXA9
	TP73	CELA3B	HOXA9
	TP73	CEMP1	HOXA9
	TP73	CEP120	HOXA9
	TP73	CHD9	HOXA9

	TP73	CKAP2	HOXA9
	TP73	COX7A2L	HOXA9
	TP73	CPEB4	HOXA9
	TP73	CROCCP3	HOXA9
	TP73	CSTF2T	HOXA9
	TP73	DCAF17	HOXA9
	TP73	DCP1B	HOXA9
	TP73	DDIT3	HOXA9

	TP73	DEAF1	HOXA9
	TP73	E2F7	HOXA9
	TP73	EIF2B2	HOXA9
	TP73	ERCC1	HOXA9
	TP73	EVPLL	HOXA9
	TP73	FAM101A	HOXA9
	TP73	FAM193A	HOXA9
	TP73	FAM73A	HOXA9
	TP73	FAU	HOXA9

TP73	FBXO15	HOXA9
TP73	FCHO2	HOXA9
TP73	FLJ35776	HOXA9
TP73	FLRT1	HOXA9
TP73	FRMD8	HOXA9
TP73	FUT6	HOXA9
TP73	GBA	HOXA9

TP73	GCFC1	HOXA9
TP73	GDF15	HOXA9
TP73	GEMIN8P4	HOXA9
TP73	GNA13	HOXA9
TP73	GNAI1	HOXA9
TP73	GOLIM4	HOXA9
TP73	GPC6	HOXA9
TP73	HCLS1	HOXA9

	TP73	HDAC5	HOXA9
	TP73	HHLA3	HOXA9
	TP73	HOPX	HOXA9
	TP73	IDH3A	HOXA9
	TP73	IFI16	HOXA9
	TP73	IKBIP	HOXA9
	TP73	IL1F10	HOXA9
	TP73	IL4R	HOXA9

TP73	ISPD	HOXA9
TP73	ITPR1	HOXA9
TP73	KCNA7	HOXA9
TP73	KIAA0195	HOXA9
TP73	KIAA0430	HOXA9
TP73	KIAA1530	HOXA9
TP73	KIAA1671	HOXA9
TP73	KLHDC7A	HOXA9
TP73	KRT5	HOXA9
TP73	KRTAP10-6	HOXA9

	TP73	LAMB4	HOXA9
	TP73	LCE1B	HOXA9
	TP73	LGALS7	HOXA9
	TP73	LOC100128531	HOXA9
	TP73	LOC100131496	HOXA9
	TP73	LOC100289092	HOXA9
	TP73	LOC100289650	HOXA9

	TP73	LOC100506054	HOXA9
	TP73	LOC100506895	HOXA9
	TP73	LOC100507389	HOXA9
	TP73	LOC154092	HOXA9
	TP73	LOC284385	HOXA9
	TP73	LOC284440	HOXA9
	TP73	LOC284837	HOXA9
	TP73	LOC391322	HOXA9
	TP73	LOC643401	HOXA9

	TP73	LOC730227	HOXA9
	TP73	MAP1LC3B2	HOXA9
	TP73	MBD6	HOXA9
	TP73	MCART3P	HOXA9
	TP73	MDM2	HOXA9
	TP73	MFSD2A	HOXA9
	TP73	MGAT1	HOXA9
	TP73	MIOS	HOXA9

	TP73	MIX1-B	HOXA9
	TP73	MRE11A	HOXA9
	TP73	MRPL11	HOXA9
	TP73	MRPL14	HOXA9
	TP73	MSGN1	HOXA9
	TP73	MTVR2	HOXA9
	TP73	MYL10	HOXA9

TP73	MYOM2	HOXA9
TP73	NDST1	HOXA9
TP73	NDUFS2	HOXA9
TP73	NDUFS8	HOXA9
TP73	NNMT	HOXA9
TP73	NRON	HOXA9
TP73	NRP1	HOXA9
TP73	NTN4	HOXA9
TP73	NWD1	HOXA9

	TP73	PADI2	HOXA9
	TP73	PAK7	HOXA9
	TP73	PANK1	HOXA9
	TP73	PARD6B	HOXA9
	TP73	PCNA	HOXA9
	TP73	PHKB	HOXA9
	TP73	PISRT1	HOXA9
	TP73	PITPNM2	HOXA9
	TP73	PLEKHG6	HOXA9
	TP73	PLK2	HOXA9

TP73	PMAIP1	HOXA9
TP73	POLDIP3	HOXA9
TP73	PPP1CA	HOXA9
TP73	PRMT10	HOXA9
TP73	PROC	HOXA9
TP73	PRPSAP1	HOXA9
TP73	PRR14	HOXA9

TP73	PSMC4	HOXA9
TP73	PTAFR	HOXA9
TP73	PTCD1	HOXA9
TP73	RAB15	HOXA9
TP73	RAB40C	HOXA9
TP73	RACGAP1	HOXA9
TP73	RANGAP1	HOXA9
TP73	RAP2B	HOXA9
TP73	RCC2	HOXA9

	TP73	REV3L	HOXA9
	TP73	RNF144B	HOXA9
	TP73	RNF187	HOXA9
	TP73	RNU11	HOXA9
	TP73	RPL32P3	HOXA9
	TP73	RPS27L	HOXA9
	TP73	RXRA	HOXA9
	TP73	S100PBP	HOXA9

	TP73	SBF1	HOXA9
	TP73	SCNN1A	HOXA9
	TP73	SCT	HOXA9
	TP73	SCYL3	HOXA9
	TP73	SDHAF1	HOXB3
	TP73	SERPINB5	HOXB3
	TP73	SERPINE1	HOXB5
	TP73	SESN1	HOXB7

	TP73	SLC12A4	HOXB7
	TP73	SLC14A1	HOXB8
	TP73	SLC1A4	HOXB9
	TP73	SLC25A45	HOXC10
	TP73	SLC46A1	HOXC11
	TP73	SNHG5	HOXC13
	TP73	SNORA77	HOXC13
	TP73	SNORD83B	HOXC13
	TP73	SNTB2	HOXC13
	TP73	SOST	HOXC8

	TP73	SP110	HOXC8
	TP73	SPRED2	HOXD10
	TP73	SSH1	HOXD10
	TP73	SYNC	HOXD13
	TP73	TBC1D10C	HOXD13
	TP73	TCTEX1D2	HOXD13
	TP73	TIMM9	HOXD13
	TP73	TM9SF4	HOXD1
	TP73	TMCO4	HOXD8

	TP73	TMED10	HOXD9
	TP73	TMEM221	HOXD9
	TP73	TMEM40	HSF4
	TP73	TMEM93	LHX2
	TP73	TOMM40L	LHX2
	TP73	TP53I3	LHX2
	TP73	TP73	LHX2
	TP73	TRAPPC3	LHX2
	TP73	TRIM32	NEUROG2

	TP73	TRPM7	NEUROG2
	TP73	TSKU	NEUROG2
	TP73	TYSND1	NEUROG2
	TP73	UBC	NEUROG2
	TP73	UTP15	NEUROG2
	TP73	VOPP1	NEUROG2
	TP73	WDR34	NEUROG2
	TP73	WISP2	NEUROG2

	TP73	YEATS2	NEUROG2
	TP73	ZFYVE16	NEUROG2
	TP73	ZMIZ2	NEUROG2
	TP73	ZNF175	NEUROG2
	TP73	ZNF25	NEUROG2
	TP73	ZNF326	NEUROG2
	TP73	ZNF683	NEUROG2
	TP73	ZNF689	NEUROG2
	NEUROG2	NDUFA9	NEUROG2

	NEUROG2	NFATC2	NEUROG2
	NEUROG2	NFKBIA	NEUROG2
	NEUROG2	NFS1	NEUROG2
	NEUROG2	NHLH1	NEUROG2
	NEUROG2	NNAT	NEUROG2
	NEUROG2	NOG	NEUROG2
	NEUROG2	NPAT	NEUROG2

NEUROG2	NR2E1	NEUROG2
NEUROG2	NR4A2	NEUROG2
NEUROG2	NR4A3	NEUROG2
NEUROG2	NRGN	NEUROG2
NEUROG2	NRIP1	NEUROG2
NEUROG2	NTN3	NEUROG2
NEUROG2	NXPH4	NEUROG2

	NEUROG2	OBSCN	NEUROG2
	NEUROG2	ODZ4	NEUROG2
	NEUROG2	OIT3	NEUROG2
	NEUROG2	OPRL1	NEUROG2
	NEUROG2	PABPC1	NEUROG2
	NEUROG2	PACS1	NEUROG2

	NEUROG2	PALM2-AKAP2	NEUROG2
	NEUROG2	PARP8	NEUROG2
	NEUROG2	PAX6	NEUROG2
	NEUROG2	PAX7	NEUROG2
	NEUROG2	PC	NEUROG2
	NEUROG2	PDZRN4	NEUROG2

	NEUROG2	PEX13	NEUROG2
	NEUROG2	PHF21A	NEUROG2
	NEUROG2	PI4KAP2	NEUROG2
	NEUROG2	PIK3CA	NEUROG2
	NEUROG2	PKMYT1	NEUROG2
	NEUROG2	PLEKHA1	NEUROG2
	NEUROG2	POGZ	NEUROG2
	NEUROG2	POLK	NEUROG2

	NEUROG2	POLR3GL	NEUROG2
	NEUROG2	POU3F2	NEUROG2
	NEUROG2	POU3F3	NEUROG2
	NEUROG2	PPFIA3	NEUROG2
	NEUROG2	PPP1R9B	NEUROG2
	NEUROG2	PRKAR2A	NEUROG2
	NEUROG2	PRUNE	NEUROG2
	NEUROG2	PSKH1	NEUROG2

	NEUROG2	PSMG2	NEUROG2
	NEUROG2	PTCHD1	NEUROG2
	NEUROG2	PTPRG	NEUROG2
	NEUROG2	PTPRN	NEUROG2
	NEUROG2	QPRT	NEUROG2
	NEUROG2	RALY	NEUROG2
	NEUROG2	RAP1GAP	NEUROG2
	NEUROG2	RAPGEFL1	NEUROG2

	NEUROG2	RBKS	NEUROG2
	NEUROG2	RBMS3	NEUROG2
	NEUROG2	RBP5	NEUROG2
	NEUROG2	RCOR2	NEUROG2
	NEUROG2	ROBO2	NEUROG2
	NEUROG2	RP1L1	NEUROG2
	NEUROG2	RRBP1	NEUROG2
	NEUROG2	RTN4RL1	NEUROG2
	NEUROG2	SAP130	NEUROG2
	NEUROG2	SART3	NEUROG2

	NEUROG2	SCG2	NEUROG2
	NEUROG2	SCRT2	NEUROG2
	NEUROG2	SDCCAG3	NEUROG2
	NEUROG2	SDF4	NEUROG2
	NEUROG2	SEMA7A	NEUROG2
	NEUROG2	SEPHS1	NEUROG2
	NEUROG2	SERPINI2	NEUROG2
	NEUROG2	SESN3	NEUROG2
	NEUROG2	SFN	NEUROG2

	NEUROG2	SFRS1	NEUROG2
	NEUROG2	SGMS2	NEUROG2
	NEUROG2	SIX4	NEUROG2
	NEUROG2	SKIL	NEUROG2
	NEUROG2	SLC10A5	NEUROG2
	NEUROG2	SLC24A4	NEUROG2
	NEUROG2	SLC25A14	NEUROG2
	NEUROG2	SLC26A3	NEUROG2
	NEUROG2	SLC32A1	NEUROG2

	NEUROG2	SLC34A3	NEUROG2
	NEUROG2	SLC41A1	NEUROG2
	NEUROG2	SLC7A9	NEUROG2
	NEUROG2	SNORA48	NEUROG2
	NEUROG2	SOX14	NEUROG2
	NEUROG2	SP5	NEUROG2
	NEUROG2	SPRY4	NEUROG2
	NEUROG2	SSBP3	NEUROG2
	NEUROG2	SSH2	NEUROG2
	NEUROG2	ST8SIA1	NEUROG2
	NEUROG2	STC1	NEUROG2

	NEUROG2	SULT4A1	NEUROG2
	NEUROG2	SYAP1	NEUROG2
	NEUROG2	SYNGAP1	NEUROG2
	NEUROG2	TAL1	NEUROG2
	NEUROG2	TCF23	NEUROG2
	NEUROG2	TCF4	NEUROG2
	NEUROG2	TCF7L2	NEUROG2
	NEUROG2	TD1	NEUROG2

	NEUROG2	TESSP1	NEUROG2
	NEUROG2	TFAP2B	NEUROG2
	NEUROG2	THAP2	NEUROG2
	NEUROG2	TIGD6	NEUROG2
	NEUROG2	TLE3	NEUROG2
	NEUROG2	TLL1	NEUROG2
	NEUROG2	TLN1	NEUROG2
	NEUROG2	TLX2	NEUROG2

NEUROG2	TMED2	NEUROG2
NEUROG2	TMEM154	NEUROG2
NEUROG2	TMEM198	NEUROG2
NEUROG2	TMEM80	NEUROG2
NEUROG2	TMEM93	NEUROG2
NEUROG2	TMPRSS3	NEUROG2
NEUROG2	TRIM46	NEUROG2

	NEUROG2	TRIM8	NEUROG2
	NEUROG2	TRIP12	NEUROG2
	NEUROG2	TSEN54	NEUROG2
	NEUROG2	UBE2G1	NEUROG2
	NEUROG2	USP25	NEUROG2
	NEUROG2	VGF	NEUROG2
	NEUROG2	VIL1	NEUROG2
	NEUROG2	VKORC1L1	NEUROG2
	NEUROG2	VWA1	NEUROG2

	NEUROG2	WAPAL	NEUROG2
	NEUROG2	WBSCR17	NEUROG2
	NEUROG2	WFIKKN2	NEUROG2
	NEUROG2	WNT10B	NEUROG2
	NEUROG2	WNT2	NEUROG2
	NEUROG2	WNT3	NEUROG2
	NEUROG2	XCL1	NEUROG2
	NEUROG2	XCL2	NEUROG2
	NEUROG2	ZBED3	NEUROG2
	NEUROG2	ZBTB7B	NEUROG2

NEUROG2	ZC3H6	NEUROG2
NEUROG2	ZDHHC14	NEUROG2
NEUROG2	ZFP91	NEUROG2
NEUROG2	ZFP91-CNTF	NEUROG2
NEUROG2	ZFR	NEUROG2
NEUROG2	ZFYVE27	NEUROG2

	NEUROG2	ZIC2	NEUROG2
	NEUROG2	ZNF232	NEUROG2
	NEUROG2	ZNF319	NEUROG2
	NEUROG2	ZNF397OS	NEUROG2
	NEUROG2	ZNF469	NEUROG2
	NEUROG2	ZNF503	NEUROG2
	NEUROG2	ZNF652	NEUROG2
	NEUROG2	ZNF710	NEUROG2

	NEUROG2	ZNF827	NEUROG2
	NEUROG2	ZNF835	NEUROG2
	NEUROG2	ZSWIM6	NEUROG2
	NEUROG2	LOC100144603	NEUROG2
	NEUROG2	LOC220930	NEUROG2
	NEUROG2	LOC286016	NEUROG2
	NEUROG2	LOC338651	NEUROG2
	NEUROG2	LOC492311	NEUROG2
	NEUROG2	LRG1	NEUROG2

NEUROG2	LRGUK	NEUROG2
NEUROG2	LRP4	NEUROG2
NEUROG2	LYST	NEUROG2
NEUROG2	MAP1A	NEUROG2
NEUROG2	MAP3K11	NEUROG2
NEUROG2	MAP4K4	NEUROG2
NEUROG2	MDGA2	NEUROG2

	NEUROG2	MEG3	NEUROG2
	NEUROG2	MEOX2	NEUROG2
	NEUROG2	MEX3B	NEUROG2
	NEUROG2	MGAT1	NEUROG2
	NEUROG2	CCSER1	NEUROG2
	NEUROG2	MID1IP1	NEUROG2
	NEUROG2	MLLT10	NEUROG2
	NEUROG2	MN1	NEUROG2
	NEUROG2	MOV10	NEUROG2

	NEUROG2	MRPL48	NEUROG2
	NEUROG2	MSC	NEUROG2
	NEUROG2	MSRB3	NEUROG2
	NEUROG2	MSX1	NEUROG2
	NEUROG2	NAALADL2	NEUROG2
	NEUROG2	NCDN	NEUROG2
	NEUROG2	NDUFA4L2	
targets of miRNAs which targted by differently methylated TFs			
		hypermethylated TF	TF target miRNA

	DDIT3	hsa-miR-195
	DDIT3	hsa-miR-195
	DDIT3	hsa-miR-195
	DDIT3	hsa-miR-195

	DDIT3	hsa-miR-195
	DDIT3	hsa-miR-195
	DDIT3	hsa-miR-195
	DDIT3	hsa-miR-195

DDIT3	hsa-miR-195
DDIT3	hsa-miR-195
DDIT3	hsa-miR-195

DDIT3	hsa-miR-195
DDIT3	hsa-miR-195
DDIT3	hsa-miR-195
DDIT3	hsa-miR-195

DDIT3	hsa-miR-195
DDIT3	hsa-miR-195
DDIT3	hsa-miR-28
DDIT3	hsa-miR-28

DDIT3	hsa-miR-28
DDIT3	hsa-miR-28
DDIT3	hsa-miR-28

DDIT3	hsa-miR-28
DDIT3	hsa-miR-28
DDIT3	hsa-miR-28
DDIT3	hsa-miR-497

DDIT3	hsa-miR-497
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195

NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195
NEUROG2	hsa-miR-195

NEUROG2	hsa-miR-497
NEUROG2	hsa-miR-497

Table S4. DNA methylation status of three categories of intragenic miRNAs harboring differentially methylated regions (DMRs) and their host genes. The three categories of miRNAs are host-methylated miRNAs, miRNA-methylated and host-miRNA-methylated miRNAs. MiRNAs filled with the same color means locating in the same miRNA cluster.

Host-methylated miRNAs

miRNA	chr	strand	methy_start	methy_end	methy_len	hyper/hypo	CpG_start	CpG_end	overlap	host gene
hsa-miR-425	chr3	-	-3469	-3370	99	hypo	NO			DALRD3
hsa-miR-191	chr3	-	-2994	-2895	99	hypo	NO			DALRD3
hsa-miR-378	chr5	+	-2632(149089949)	-2333(149090248)	299	hyper	149089763	149091943	299	PPARGC1B
hsa-miR-449a	chr5	-	-7337	-7138	199	hyper	NO			CDC20B
			-7689	-7488	201	hyper	NO			
hsa-miR-449b	chr5	-	-7217	-7018	199	hyper	NO			CDC20B
			-7569	-7368	201	hyper	NO			
hsa-miR-580	chr5	-	-6515	-6316	199	hyper	NO			LMBRD2
hsa-miR-93	chr7	-	-10181	-9966	215	hypo	NO			MCM7
hsa-miR-106b	chr7	-	-9954	-9739	215	hypo	NO			MCM7
hsa-miR-25	chr7	-	-10385	-10170	215	hypo	NO			MCM7
hsa-miR-490	chr7	+	-34153(136204301)	-31904(136206550)	2249	hyper	136204394	136206734	2156	CHRM2
hsa-miR-126	chr9	+	-21948	-20399	1549	hypo	NO			EGFL7
			-19748	-19199	549	hypo	NO			
			-13946(138670929)	-13097(138671778)	849	hypo	138671075	138671380	305	
hsa-miR-608	chr10	+	-5746(102718986)	-5376(102719356)	370	hyper	102719289	102719700	67	SEMA4G
hsa-miR-210	chr11	-	3551	3800	249	hypo	NO			MIR210HG
hsa-miR-675	chr11	-	-11018	-8969	2049	hypo	NO			H19
			-8268	-7969	299	hypo	NO			
			-8968(1983605)	-8269(1982906)	699	hypo	1983309	1983592	283	
hsa-miR-616	chr12	-	-3258	-3159	99	hyper	NO			DDIT3
hsa-miR-92a-1	chr13	+	-3587(90797982)	-2438(90799131)	1149	hyper	90797542	90799442	1149	MIR17HG

hsa-miR-19a	chr13	+	-3164(90797982)	-2015(90799131)	1149	hyper	90797542	90799442	1149	MIR17HG
hsa-miR-19b-1	chr13	+	-3465(90797982)	-2316(90799131)	1149	hyper	90797542	90799442	1149	MIR17HG
hsa-miR-17	chr13	+	-2878(90797982)	-1729(90799131)	1149	hyper	90797542	90799442	1149	MIR17HG
hsa-miR-20a	chr13	+	-3338(90797982)	-2189(90799131)	1149	hyper	90797542	90799442	1149	MIR17HG
hsa-miR-18a	chr13	+	-3024(90797982)	-1875(90799131)	1149	hyper	90797542	90799442	1149	MIR17HG
hsa-miR-621	chr13	+	-22239	-22090	149	hypo		NO		SLC25A15
hsa-miR-626	chr15	+	-39819	-39720	99	hypo		NO		MGA
			-35016	-34861	155	hypo		NO		
hsa-miR-497	chr17	-	-9245	-8296	949	hyper		NO		MIR497HG
			-4894(6866959)	-4495(6866560)	399	hyper	6866124	6868251	399	
hsa-miR-195	chr17	-	-9566	-8617	949	hyper		NO		MIR497HG
			-5215(6866959)	-4816(6866560)	399	hyper	6866124	6868251	399	
hsa-miR-22	chr17	-	-4354	-4155	199	hyper		NO		MIR22HG
			-5154	-4605	549	hyper		NO		
			-9970	-9571	399	hyper		NO		
			-11570(1575601)	-11021(1575052)	549	hyper	1574495	1576647	549	
			-7720	-7264	456	hypo		NO		
hsa-miR-33b	chr17	-	3064(17654906)	3163(17654874)	99	hyper	17653636	17655181	99	SREBF1
hsa-miR-301a	chr17	-	-14223	-13874	349	hypo		NO		SKA2
hsa-miR-638	chr19	+	-3327	-2278	1049	hypo		NO		DNM2
			-4477	-3528	949	hypo		NO		
hsa-miR-7-3	chr19	+	-4754	-3804	950	hypo		NO		MIR7-3HG
hsa-miR-637	chr19	-	-9293(3921803)	-8441(3920951)	852	hypo	3921536	3921746	210	DAPK3
hsa-miR-1-1	chr20	+	-9075	-8976	99	hypo		NO		C20orf166
hsa-miR-647	chr20	-	-14343(62058866)	-13940(62058463)	403	hyper	62057363	62058662	199	UCKL1
hsa-miR-545	chrX	-	-6765	-6515	250	hypo		NO		FTX
hsa-miR-374a	chrX	-	-6617	-6367	250	hypo		NO		FTX

miRNA-methylated miRNAs

miRNA	chr	strand	methy_start	methy_end	methy_len	hyper/hypo	CpG_start	CpG_end	overlap	host gene
hsa-miR-553	chr1	+	4946	5045	99	hyper		NO		RTCA
			5196	5303	107	hyper		NO		
hsa-miR-933	chr2	-	1415	1516	101	hyper		NO		ATF2
hsa-let-7g	chr3	-	-1057	-908	149	hypo		NO		WDR82
			3146	4095	949	hyper		NO		
hsa-miR-15b	chr3	+	4235	4534	299	hyper		NO		SMC4
			4585	4787	202	hyper		NO		
hsa-miR-16-2	chr3	+	4078	4377	299	hyper		NO		SMC4
			4428	4630	202	hyper		NO		
hsa-miR-567	chr3	+	1794	1843	49	hyper		NO		C3orf52
			2408	2797	389	hyper		NO		
hsa-miR-885	chr3	-	-34261	-34112	149	hypo		NO		ATP2B2
			-33071	-32512	559	hypo		NO		
			-31261	-30612	649	hypo		NO		
			-29261	-29212	49	hypo		NO		
			-25761	-25662	99	hypo		NO		
			-16960	-16461	499	hypo		NO		
			-7460	-7011	449	hypo		NO		
			1540	1589	49	hypo		NO		
			8943	9992	1049	hypo		NO		
hsa-miR-95	chr4	-	-50301	-49852	449	hypo		NO		ABLIM2
			-46999	-46300	699	hypo		NO		
			-46008	-45850	158	hypo		NO		
			-43599	-41600	1999	hypo		NO		
			-37599	-36838	761	hypo		NO		
			-34072	-33723	349	hypo		NO		

			-31072	-29973	1099	hypo	NO			
			-27872	-27773	99	hypo	NO			
			-26363	-25162	1211	hypo	NO			
			-23577	-22978	599	hypo	NO			
			-21877	-21278	599	hypo	NO			
			-20127	-19678	449	hypo	NO			
			-18127	-17978	149	hypo	NO			
			-16275	-15876	399	hypo	NO			
			-15125	-14826	299	hypo	NO			
			-10025	-9926	99	hypo	NO			
			-7726	-6676	1050	hypo	NO			
			-5625	-5526	99	hypo	NO			
			4496	6288	1792	hypo	NO			
hsa-miR-218-2	chr5	-	-36009	-35910	99	hypo	NO			SLIT3
			-7259	-7161	98	hypo	NO			
			-5359	-5171	188	hypo	NO			
			3691	3790	99	hypo	NO			
hsa-miR-874	chr5	-	8923	9022	99	hypo	NO			KLHL3
			-44583	-44334	249	hypo	NO			
hsa-miR-581	chr5	-	8373	8483	110	hypo	NO			ARL15
			9534	9633	99	hypo	NO			
hsa-miR-873	chr9	-	7788	8648	860	hypo	NO			LINGO2
hsa-miR-346	chr10	-	-31066	-29717	1349	hypo	NO			GRID1
			251	400	149	hypo	NO			
			2101	2200	99	hyper	NO			
			1351(88013174)	2100(88012425)	749	hyper	88012620	88013259	554	
hsa-miR-609	chr10	-	1646	2895	1249	hypo	NO			WDR96
			8046	8308	262	hypo	NO			

hsa-miR-483	chr11	-	-9014	-8315	699	hypo		NO		IGF2
			251	350	99	hypo		NO		
hsa-miR-1228	chr12	+	-37614	-37115	499	hyper		NO		LRP1
			-36549	-36355	194	hyper		NO		
			4586	4785	199	hyper		NO		
			5436	5535	99	hyper		NO		
			18286	18385	99	hyper		NO		
hsa-miR-629	chr15	-	4997	5246	249	hyper		NO		TLE3
hsa-miR-1233	chr15	-	392	491	99	hypo		NO		GOLGA8B
			-708	291	999	hypo		NO		
			-2659	-1559	1100	hypo		NO		
hsa-miR-211	chr15	-	-39544	-39453	91	hypo		NO		TRPM1
			-26330	-26131	199	hypo		NO		
			1568	1666	98	hypo		NO		
hsa-miR-152	chr17	-	1513	1762	249	hypo		NO		COPZ2
			2713	3106	393	hypo		NO		
hsa-miR-634	chr17	+	6591	6996	405	hyper		NO		PRKCA
hsa-miR-640	chr19	+	-36023	-35924	99	hypo		NO		GATAD2A
			-23096	-22897	199	hyper		NO		
			-9063	-8614	449	hyper		NO		
			-8063	-7914	149	hypo		NO		
			7817	8266	449	hyper		NO		
hsa-miR-1227	chr19	-	150	599	449	hypo		NO		PLEKHJ1
			-1850(2186749)	-1601(2186998)	249	hypo	2186681	2188102	249	
hsa-miR-644	chr20	+	7879	9539	1660	hypo		NO		ITCH
			9732	11128	1396	hyper		NO		
hsa-miR-941-1	chr20	+	-20850	-20401	449	hyper		NO		DNAJC5
			-7794	-7601	193	hypo		NO		

			-1841	-1692	149	hypo		NO		
			3759	4058	299	hypo		NO		
			6576	7528	952	hyper		NO		
hsa-miR-941-2	chr20	+	-21157	-20708	449	hyper		NO		DNAJC5
			-8101	-7908	193	hypo		NO		
			-2148	-1999	149	hypo		NO		
			3452	3751	299	hypo		NO		
			6269	7221	952	hyper		NO		
hsa-miR-941-3	chr20	+	-21269	-20820	449	hyper		NO		DNAJC5
			-8213	-8020	193	hypo		NO		
			-2260	-2111	149	hypo		NO		
			3340	3639	299	hypo		NO		
			6157	7109	952	hyper		NO		
hsa-miR-502	chrX	+	9623	10872	1249	hypo		NO		CLCN5
hsa-miR-98	chrX	-	8237	8286	49	hyper		NO		HUWE1
hsa-let-7f-2	chrX	-	9170	9219	49	hyper		NO		HUWE1

Host-miRNA-methylated miRNAs

miRNA	chr	strand	methy_start	methy_end	methy_len	hyper/hypo	CpG_start	CpG_end	overlap	host gene
hsa-miR-9-1	chr1	-	-17205(154674050)	-14939(154671784)	2266	hyper	154671784	154672974	1190	C1orf61
			-14938	-14556	382	hyper		NO		
			-1300(154658145)	549(154656296)	1849	hyper	154657027	154658205	1118	
			8503	9376	873	hypo		NO		
hsa-miR-137	chr1	-	-7798(98292113)	-6849(98291164)	949	hyper	98291589	98292571	524	MIR137HG
			302(98284013)	504(98283811)	202	hyper	98283554	98284298	202	
hsa-miR-1231	chr1	+	-6572	-6221	351	hypo		NO		NAV1
			-2527	-2378	149	hypo		NO		
hsa-miR-555	chr1	-	-36170	-35212	958	hypo		NO		ASH1L

hsa-miR-921	chr1	-	-17491	-17442	49	hypo		NO		FAM78B
			-14419	-13979	440	hyper		NO		
			-12207(164402866)	-10223(164400882)	1984	hyper	164400882	164403072	1984	
			-6907	-6758	149	hypo		NO		
			-51401(3518615)	-49652(3516866)	1749	hyper	3517479	3517938	459	
			-40351	-39952	399	hypo		NO		
hsa-miR-551a	chr1	-	-37601(3504815)	-33002(3500216)	4599	hypo	3501569	3501978	409	MEGF6
			-36601	-34952	1649	hypo		NO		
			-13801	-13502	299	hypo		NO		
			-6701	-6602	99	hypo		NO		
hsa-miR-765	chr1	-	7627	7726	99	hypo		NO		ARHGEF11
			11577	15076	3499	hypo		NO		
			-1195	-996	199	hyper		NO		
hsa-miR-149	chr2	+	-29802	-29353	449	hypo		NO		GPC1
			-3502(241040589)	-53(241044038)	3449	hyper	241040549	241042271	117	
			1898	1997	99	hypo		NO		
			3898	3997	99	hyper		NO		
			4198	5047	849	hyper		NO		
hsa-miR-559	chr2	+	-18658	-17909	749	hypo		NO		EPCAM
			-15858	-14809	1049	hypo		NO		
			-11658	-11459	199	hypo		NO		
			-6964	-6315	649	hypo		NO		
hsa-miR-562	chr2	+	-38488	-38089	399	hypo		NO		DIS3L2
			-37238	-37039	199	hypo		NO		
			-18682	-17533	1149	hypo		NO		
hsa-miR-153-1	chr2	-	-15571(219882737)	-14572(219881738)	999	hyper	219882114	219882527	413	PTPRN
			-14571	-14472	99	hyper		NO		

			-14471(219881637)	-14322(219881488)	149	hyper	219881265	219881515	27	
			-5171	-5022	149	hypo	NO			
			2928	3428	500	hypo	NO			
			4279	4378	99	hypo	NO			
hsa-miR-566	chr3	+	-27908	-27709	199	hypo	NO			SEMA3F
			-24308	-23859	449	hypo	NO			
			-22408	-22309	99	hypo	NO			
			-17658(50168105)	-17358(50168405)	300	hyper	50166975	50168134	29	
			-13957	-11958	1999	hypo	NO			
			-207	92	299	hypo	NO			
			3993	4142	149	hypo	NO			
			8498	8797	299	hypo	NO			
hsa-miR-425	chr3	-	-3469	-3370	99	hypo	NO			DALRD3
			-1819(49034490)	-1670(49034341)	149	hyper	49033329	49034990	149	
			377(49032294)	2030(49030641)	1653	hypo	49030218	49031321	680	
hsa-miR-191	chr3	-	-2994	-2895	99	hypo	NO			DALRD3
			-1344(49034490)	-1195(49034341)	149	hyper	49033329	49034990	149	
			852(49032294)	2505(49030641)	1653	hypo	49030218	49031321	680	
hsa-miR-922	chr3	-	-39414	-39365	49	hypo	NO			KIAA0226
			-35217	-35059	158	hyper	NO			
			-16916	-16567	349	hyper	NO			
hsa-miR-569	chr3	-	-19556	-19196	360	hyper	NO			TNIK
hsa-miR-1224	chr3	+	-12058(185429829)	-10400(185431487)	1658	hyper	185429731	185431492	1658	VWA5B2
			-8549	-8150	399	hypo	NO			
			-7699	-7600	99	hypo	NO			
hsa-miR-1226	chr3	+	-50438	-49689	749	hypo	NO			DHX30
			-37143	-37047	96	hypo	NO			

			-35083	-34934	149	hypo	NO			
			-28610	-28161	449	hyper	NO			
hsa-miR-575	chr4	-	-45357(83938964)	-45058(83938665)	299	hyper	83938033	83939265	299	SCD5
			-44807(83938414)	-44208(83937815)	599	hyper	83938033	83939265	381	
hsa-miR-576	chr4	+	-43258	-43108	150	hypo	NO			SEC24B
hsa-miR-943	chr4	-	-27640	-27391	249	hypo	NO			NELFA
			-23157(1981159)	-23008(1981010)	149	hyper	1979512	1981157	147	
			3458	3557	99	hyper	NO			
hsa-miR-571	chr4	+	-13212(320734)	-11813(322133)	1399	hyper	320162	322068	1334	ZNF141
			-18818	-18660	158	hypo	NO			
			-11812	-11163	649	hyper	NO			
			-2352	-2253	99	hypo	NO			
			795	1044	249	hypo	NO			
hsa-miR-143	chr5	+	-26024	-25975	49	hypo	NO			MIR143HG
			-12623	-11274	1349	hypo	NO			
hsa-miR-145	chr5	+	-27752	-27703	49	hypo	NO			MIR143HG
			-14351	-13002	1349	hypo	NO			
hsa-miR-103-1	chr5	-	-9585	-9432	153	hyper	NO			PANK3
hsa-miR-580	chr5	-	9381	9672	291	hyper	NO			LMBRD2
			-6515	-6316	199	hyper	NO			
hsa-miR-887	chr5	+	-42803	-42254	549	hypo	NO			FBXL7
			-23792	-22643	1149	hypo	NO			
			-7586	-7337	249	hypo	NO			
			-7336(15980955)	-6837(15981454)	499	hypo	15981088	15981518	366	
			49	1348	1299	hypo	NO			
hsa-miR-1229	chr5	-	-14416	-14317	99	hyper	NO			MGAT4B
			-11466	-11367	99	hypo	NO			

			-3705(179161657)	-3406(179161358)	299	hyper	179160889	179161609	251	
			2339(179155613)	2638(179155314)	199	hyper	179155214	179156431	299	
hsa-miR-9-2	chr5	-	-18928(88017441)	-17670(88016183)	1258	hyper	88016634	88017028	394	LINC00461
			-13419(88011932)	-12854(88011367)	565	hyper	88011850	88012302	82	
			-12212(88010725)	-10854(88009307)	1358	hyper	88009707	88010050	343	
			-9107(88007620)	-5607(88004120)	3500	hyper	88005716	88007826	1853	
			6151(87991213)	7300(87992362)	1149	hyper	87991394	87991620	226	
hsa-miR-874	chr5	-	-44583	-44384	199	hypo		NO		KLHL3
			-44383	-44334	49	hypo		NO		
hsa-miR-340	chr5	-	-12346	-12247	99	hyper		NO		RNF130
			-1563	-1467	96	hyper		NO		
			-207	-106	101	hyper		NO		
hsa-miR-585	chr5	-	-38578	-38029	549	hyper		NO		SLIT3
			-37278(168660554)	-36229(168659505)	1049	hyper	168660007	168660853	547	
			-27378	-27279	99	hypo		NO		
			-26228	-26129	99	hypo		NO		
			-12678	-12529	149	hypo		NO		
hsa-miR-877	chr6	+	-9598	-9499	99	hyper		NO		ABCF1
			-9343	-9149	194	hyper		NO		
			3088	4037	949	hypo		NO		
hsa-miR-548b	chr6	-	-12711	-12462	249	hypo		NO		FAM184A
			-9054(119441061)	-8955(119440962)	99	hyper	119440790	119441922	99	
hsa-miR-1236	chr6	-	-8098	-7999	99	hyper		NO		NELFE
			754	953	199	hypo		NO		
			1704	3053	1349	hyper		NO		
hsa-miR-595	chr7	-	-30561	-29712	849	hypo		NO		PTPRN2
			-27861	-27412	449	hypo		NO		

			-25361	-25262	99	hypo		NO		
			-22411	-21712	699	hypo		NO		
			-18461	-18362	99	hypo		NO		
			-14861	-12310	2551	hypo		NO		
			-10459	-10310	149	hypo		NO		
			-8249	-7650	599	hypo		NO		
			-6354	-6150	204	hypo		NO		
			-1849	1350	3199	hypo		NO		
			2701	2800	99	hypo		NO		
			3901	5150	1249	hypo		NO		
			5301(158012965)	6550(158011716)	1249	hypo	158011731	158011933	202	
hsa-miR-592	chr7	-	-34508	-32659	1849	hypo		NO		GRM8
			-44466	-44367	99	hyper		NO		
			-43816	-43717	99	hyper		NO		
hsa-miR-591	chr7	-	-24360	-24156	204	hyper		NO		SLC25A13
			-10258	-10147	111	hyper		NO		
			-8896	-8597	299	hyper		NO		
			-62698	-62211	487	hypo		NO		
			-45055(1074243)	-42206(1071394)	2849	hyper	1071785	1072500	715	
			-41655	-37704	3951	hyper		NO		
			-26003	-25404	599	hyper		NO		
hsa-miR-339	chr7	-	-20259	-19854	405	hyper		NO		C7orf50
			-19753(1048941)	-18004(1047192)	1749	hypo	1047361	1047595	234	
			-17803	-17054	749	hypo		NO		
			-17053(1046241)	-12892(1042080)	4161	hyper	1042453	1042654	201	
			-6491	-5842	649	hypo		NO		
hsa-miR-590	chr7	+	-25394	-24542	852	hypo		NO		EIF4H

hsa-miR-196b	chr7	-	-20066	-19967	99	hypo	NO			HOXA10-HOXA9
			3441	3640	199	hyper	NO			
			-7130	-6881	249	hyper	NO			
			-2730	-2081	649	hyper	NO			
			-226(27175933)	6223(27169484)	6449	hyper	27175396	27176141	2897	
			8572(27166186)	9521(27167135)	949	hyper	27166186	27167485	949	
hsa-miR-589	chr7	-	-25234	-24085	1149	hypo	NO			FBXL18
			-21683	-20734	949	hypo	NO			
			-16533	-15654	879	hypo	NO			
			-14603	-12183	2420	hypo	NO			
			-11482	-11033	449	hypo	NO			
			-10732	-9881	851	hypo	NO			
			12619	12718	99	hypo	NO			
hsa-miR-153-2	chr7	-	-33512	-33463	49	hypo	NO			PTPRN2
			-9121	-9022	99	hypo	NO			
hsa-miR-593	chr7	+	-51481(127457668)	-48284(127460865)	3197	hyper	127458394	127460089	1695	SND1
			-48283	-48190	93	hyper	NO			
			-10086	-9337	749	hyper	NO			
hsa-miR-335	chr7	+	-5867	-5768	99	hyper	NO			MEST
			-5667(129917521)	-4018(129919170)	1649	hyper	129917975	129920347	1195	
			-3467(129919721)	-2614(129920574)	853	hyper	129917975	129920347	626	
			-2613	-2318	295	hyper	NO			
hsa-miR-1234	chr8	-	-11685	-11086	599	hypo	NO			CPSF1
			-9635(145606002)	-9286(145605653)	349	hyper	145605198	145606030	349	
			-6635	-6086	549	hyper	NO			
			-2821	-2272	549	hyper	NO			
hsa-miR-939	chr8	-	-17799	-17200	599	hypo	NO			CPSF1

			-15749(145606002)	-15400(145605653)	349	hyper	145605198	145606030	349	
			-12749	-12200	549	hyper		NO		
			-8935	-8386	549	hyper		NO		
hsa-miR-486	chr8	-	-1468	-1369	99	hypo		NO		ANK1
			787	1086	299	hypo		NO		
hsa-miR-598	chr8	-	-41667	-40518	1149	hypo		NO		XKR6
			-25035(10955257)	-23986(10954208)	1049	hyper	10954072	10954507	299	
			-17835	-16986	849	hypo		NO		
			-16435	-16236	199	hypo		NO		
			-13135	-12986	149	hypo		NO		
			-4810	-3961	849	hypo		NO		
			1787	2003	216	hypo		NO		
hsa-miR-151	chr8	-	-24504	-24299	205	hyper		NO		PTK2
			-23648	-23249	399	hyper		NO		
			-15871	-15471	400	hypo		NO		
hsa-miR-661	chr8	-	-9932	-9833	99	hypo		NO		PLEC
			-4732	-4583	149	hypo		NO		
			-4182	-3033	1149	hypo		NO		
hsa-miR-548d-1	chr8	-	-41271	-41172	99	hypo		NO		ATAD2
			-40921	-40622	299	hypo		NO		
hsa-miR-876	chr9	-	-17461	-17359	102	hypo		NO		LINGO2
			-17358	-16601	757	hypo		NO		
hsa-miR-601	chr9	-	-31879	-31680	199	hyper		NO		DENND1A
			-31038	-30930	108	hyper		NO		
			8728	8827	99	hypo		NO		
hsa-miR-31	chr9	-	-47633(21549817)	-47484(21549668)	149	hyper	21549133	21549816	148	MIR31HG
			-24931	-24777	154	hypo		NO		

hsa-miR-101-2	chr9	+	-30476	-29925	551	hyper	NO	RCL1
			-22876	-22677	199	hyper	NO	
			-14676	-14577	99	hyper	NO	
			-14476	-13527	949	hyper	NO	
			2514	2963	449	hyper	NO	
hsa-miR-7-1	chr9	-	-5532	-5433	99	hyper	NO	HNRNPK
hsa-miR-455	chr9	+	-43853	-43288	565	hypo	NO	COL27A1
			-39303	-38304	999	hyper	NO	
			-22951	-22802	149	hyper	NO	
			1906	2205	299	hyper	NO	
hsa-miR-23b	chr9	+	-11177	-11081	96	hyper	NO	C9orf3
			-1380	-677	703	hyper	NO	
hsa-miR-24-1	chr9	+	-11990	-11894	96	hyper	NO	C9orf3
			-2193	-1490	703	hyper	NO	
hsa-miR-27b	chr9	+	-11414	-11318	96	hyper	NO	C9orf3
			-1617	-914	703	hyper	NO	
hsa-miR-511-2	chr10	+	-12443	-12344	99	hypo	NO	MRC1
hsa-miR-938	chr10	-	-29977	-29879	98	hypo	NO	SVIL
			-26527	-26428	99	hyper	NO	
			-23425	-23326	99	hyper	NO	
			-8395	-8046	349	hypo	NO	
hsa-miR-604	chr10	-	-35043	-34194	849	hypo	NO	SVIL
			-16682	-16483	199	hyper	NO	
hsa-miR-603	chr10	+	-48267	-48218	49	hyper	NO	KIAA1217
			-17189	-16540	649	hypo	NO	
			-13689	-13038	651	hypo	NO	
hsa-miR-605	chr10	+	-18674	-18325	349	hypo	NO	PRKG1

hsa-miR-326	chr11	-	-18950	-18766	184	hypo	NO			ARRB1
			-11861	-11762	99	hypo	NO			
			-11111	-10912	199	hypo	NO			
			3320	3821	501	hypo	NO			
			3972	4071	99	hypo	NO			
			9749	9898	149	hypo	NO			
hsa-miR-1237	chr11	+	-9646(63883004)	-9447(63883203)	199	hyper	63883006	63883536	197	RPS6KA4
			-3696	-3489	207	hypo	NO			
hsa-miR-139	chr11	-	-46860	-46011	849	hypo	NO			PDE2A
			-41764	-41311	453	hypo	NO			
			-40668	-40061	607	hypo	NO			
			-34810	-34011	799	hypo	NO			
			-26058	-25959	99	hypo	NO			
			-8108	-8009	99	hypo	NO			
			-4558	-3659	899	hypo	NO			
			-558	1391	1949	hypo	NO			
hsa-miR-708	chr11	-	-39353(78830154)	-34604(78825405)	4749	hyper	78826006	78829848	3842	TENM4
hsa-miR-148b	chr12	+	-19615	-19466	149	hypo	NO			COPZ1
			-11046	-10384	662	hypo	NO			
			-2934	-2385	549	hypo	NO			
hsa-miR-1228	chr12	+	-37614	-36355	1259	hyper	NO			LRP1
			-16882	-14415	2467	hyper	NO			
			-8314	-7315	999	hyper	NO			
			4586	4785	199	hyper	NO			
			5436	5535	99	hyper	NO			
			18286	18385	99	hyper	NO			
hsa-miR-619	chr12	-	-30171	-29372	799	hypo	NO			SSH1

			-21069	-20870	199	hyper		NO		
			-20869(107775780)	-20420(107775331)	449	hyper	107775334	107775715	381	
			-13764	-13465	299	hypo		NO		
			-13214	-13115	99	hypo		NO		
			-4664	-4470	194	hypo		NO		
hsa-miR-548c	chr12	+	-20673	-20474	199	hypo		NO		RASSF3
			-18372	-17821	551	hypo		NO		
			1312	1461	149	hypo		NO		
hsa-miR-26a-2	chr12	-	-31128	-31030	98	hypo		NO		CTDSP2
			-28523	-27974	549	hyper		NO		
			-21597(56526339)	-21198(56525940)	399	hyper	56525107	56527313	399	
			-5897	-4548	1349	hyper		NO		
hsa-miR-615	chr12	+	-19711(52694290)	-19062(52694939)	649	hyper	52694693	52694980	246	HOXC5
			-15276(52698725)	-13927(52700074)	1349	hyper	52699257	52699613	356	
			-4775(52709226)	-2226(52711775)	2549	hyper	52710877	52711440	563	
			-453(52713548)	1404(52715405)	1857	hyper	52713292	52714976	1428	
hsa-miR-623	chr13	+	-42572	-42478	94	hyper		NO		UBAC2
			-12319	-12130	189	hypo		NO		
			-1479	-1280	199	hyper		NO		
			-1179	-730	449	hyper		NO		
hsa-miR-770	chr14	+	-28156(100360324)	-23607(100364873)	4549	hyper	100363180	100364186	666	MEG3
			-21156	-21007	149	hypo		NO		
			-20356	-19186	1170	hypo		NO		
			-15285	-14581	704	hypo		NO		
			-12885	-12486	399	hypo		NO		
			-10985	-9736	1249	hypo		NO		
			-6785	-6185	600	hypo		NO		

			-3983	-3884	99	hyper		NO		
			-870	-671	199	hypo		NO		
			180	479	299	hypo		NO		
			2730	5979	3249	hypo		NO		
			7430	8579	1149	hypo		NO		
			9630	9679	49	hypo		NO		
hsa-miR-342	chr14	+	-43502	-42503	999	hyper		NO		EVL
			-7965	-7416	549	hypo		NO		
			-2415	-2266	149	hypo		NO		
			4796	5454	658	hypo		NO		
			8946	9145	199	hypo		NO		
hsa-miR-625	chr14	+	-48103	-47754	349	hypo		NO		FUT8
hsa-miR-208b	chr14	-	-14738	-13989	749	hypo		NO		MYH7
			-2138(22959250)	-1872(22958984)	266	hypo	22958984	22959248	264	
			-1871	-1189	682	hypo		NO		
			259	1555	1296	hypo		NO		
			4262	5311	1049	hypo		NO		
			6562	7561	999	hypo		NO		
hsa-miR-208a	chr14	-	-22835	-21836	999	hypo		NO		MYH6
			-16585	-16386	199	hypo		NO		
			-14935	-13886	1049	hypo		NO		
			-9340	-9086	254	hypo		NO		
			-1919(22929634)	-1270(22928985)	649	hypo	22929196	22929460	264	
			-1269	1030	2299	hypo		NO		
hsa-miR-626	chr15	+	-39819	-39620	199	hypo		NO		MGA
			-35016	-34861	155	hypo		NO		
			-18043	-17094	949	hypo		NO		

hsa-miR-211	chr15	-	-39544	-38241	1303	hypo		NO		TRPM1
			-26330	-26131	199	hypo		NO		
			-23873	-23774	99	hyper		NO		
			-12873	-12424	449	hypo		NO		
			1568	3017	1449	hypo		NO		
hsa-miR-1233	chr15	-	-2659	-1759	900	hypo		NO		GOLGA8B
hsa-miR-628	chr15	-	-42583	-42484	99	hypo		NO		DYX1C1-CCPG1
hsa-miR-190	chr15	+	-49820	-49773	47	hypo		NO		TLN2
			-48922	-48823	99	hypo		NO		
			-29294	-29095	199	hypo		NO		
hsa-miR-1225	chr16	-	-38986	-38887	99	hypo		NO		PKD1
			-37186(2117472)	-36437(2116723)	749	hypo	2117129	2117330	201	
			-18179(2098465)	-5264(2085550)	12915	hyper	2097863	2102140	1017	
hsa-miR-140	chr16	+	-35140	-35021	119	hypo		NO		WWP2
			-9473	-9274	199	hyper		NO		
			7927	8626	699	hyper		NO		
hsa-miR-338	chr17	-	-16566	-15967	599	hypo		NO		AATK
hsa-miR-657	chr17	-	-17142	-16543	599	hypo		NO		AATK
hsa-miR-454	chr17	-	-27572	-27223	349	hypo		NO		SKA2
			-889	-790	99	hypo		NO		
			8166	8219	53	hypo		NO		
hsa-miR-635	chr17	-	-19700	-19538	162	hyper		NO		WIPI1
			-8687	-8392	295	hypo		NO		
			-4332	-4233	99	hyper		NO		
			302	601	299	hyper		NO		
			2307	2706	399	hypo		NO		
			4555	5006	451	hypo		NO		

hsa-miR-330	chr19	-	-6779	-6480	299	hyper		NO		EML2
			-3676	-3627	49	hyper		NO		
			1048	1197	149	hypo		NO		
			7183	7282	99	hypo		NO		
			14583	14982	399	hypo		NO		
hsa-miR-642	chr19	+	-15456	-11525	3931	hypo		NO		GIPR
			-9224	-9125	99	hypo		NO		
			-5474	-5375	99	hypo		NO		
			2926(50872952)	3225(50873251)	299	hyper	50873060	50873295	191	
			3226(50873252)	3375(50873401)	149	hyper	50873060	50873295	43	
			5026	5125	99	hypo		NO		
hsa-miR-935	chr19	+	-23465	-23016	449	hyper		NO		CACNG8
			-19751	-19236	515	hyper		NO		
			-16135	-15436	699	hypo		NO		
			-11975	-11476	499	hypo		NO		
			-8471	-8364	107	hypo		NO		
hsa-miR-643	chr19	+	-4454	-3955	499	hypo		NO		ZNF766
hsa-miR-641	chr19	-	-11502	-11403	99	hypo		NO		AKT2
			-10852	-10653	199	hypo		NO		
			-8902	-8503	399	hypo		NO		
			1732	2281	549	hyper		NO		
			5032	5081	49	hyper		NO		
hsa-miR-1238	chr19	+	-13215	-11066	2149	hypo		NO		ATG4D
			-8215(10515583)	-8066(10515732)	149	hyper	10515228	10516042	149	
			-7015	-6716	299	hyper		NO		
			-3897	-2748	1149	hypo		NO		
			-1347	-593	754	hypo		NO		

hsa-miR-499	chr20	+	-32947	-31736	1211	hypo	NO			MYH7B
			-22909	-22710	199	hypo	NO			
			-17909	-17160	749	hypo	NO			
			-13591	-12542	1049	hypo	NO			
hsa-miR-663	chr20	-	-1721(26138635)	-1413(26138327)	308	hyper	26136638	26138348	21	LOC284801
			-1312(26138226)	276(26136638)	1588	hyper	26136638	26138348	1588	
			277	537	260	hyper	NO			
hsa-miR-646	chr20	+	-11495	-11346	149	hypo	NO			LOC284757
			6106	6155	49	hypo	NO			
hsa-miR-647	chr20	-	-14343(62058866)	-13940(62058463)	403	hyper	62057363	62058662	199	UCKL1
			1912(62042611)	2561(62041962)	649	hyper	62042182	62043000	429	
			2562	2661	99	hyper	NO			
hsa-miR-103-2	chr20	+	-30086	-29937	149	hypo	NO			PANK2
			-28236(3817905)	-28037(3818104)	199	hyper	3817453	3818570	199	
			-18154	-17792	362	hypo	NO			
hsa-miR-133a-2	chr20	+	-19681	-19582	99	hypo	NO			C20orf166
			5269	6218	949	hypo	NO			
hsa-miR-125b-2	chr21	+	-1701	-1344	357	hypo	NO			LINC00478
hsa-miR-155	chr21	+	-12468(25855695)	-11669(25856494)	799	hyper	25856294	25856676	200	MIR155HG
			-11211	-11017	194	hyper	NO			
hsa-let-7a-3	chr22	+	-11936	-11687	249	hypo	NO			MIRLET7BHG
hsa-let-7b	chr22	+	-12873	-12624	249	hypo	NO			MIRLET7BHG
hsa-miR-33a	chr22	+	-31798	-31649	149	hyper	NO			SREBF2
			-29169	-29070	99	hyper	NO			
			-24937	-24582	355	hyper	NO			
hsa-miR-648	chr22	-	-19979(16863706)	-19880(16863607)	99	hyper	16863191	16864500	99	MICAL3
hsa-miR-185	chr22	+	-2770	-1825	945	hypo	NO			TANGO2

hsa-miR-503	chrX	-	4628	4925	297	hypo	NO			MGC16121
			8493	8692	199	hypo	NO			
			-5521(133513615)	-4815(133512909)	706	hyper	133510840	133513129	220	
			-377	-278	99	hyper	NO			
			573(133507521)	1523(133506571)	950	hyper	133506261	133506867	296	
			1674(133506420)	2073(133506021)	399	hyper	133506261	133506867	159	
hsa-miR-766	chrX	-	-45886(118710725)	-45587(118710426)	299	hypo	118710480	118711759	245	SEPT6
			-35356	-35257	99	hypo	NO			
			-32806	-32557	249	hypo	NO			
			-31506	-31257	249	hypo	NO			
			-9947	-9848	99	hypo	NO			