Electronic Supplementary Material (ESI) for Molecular BioSystems.
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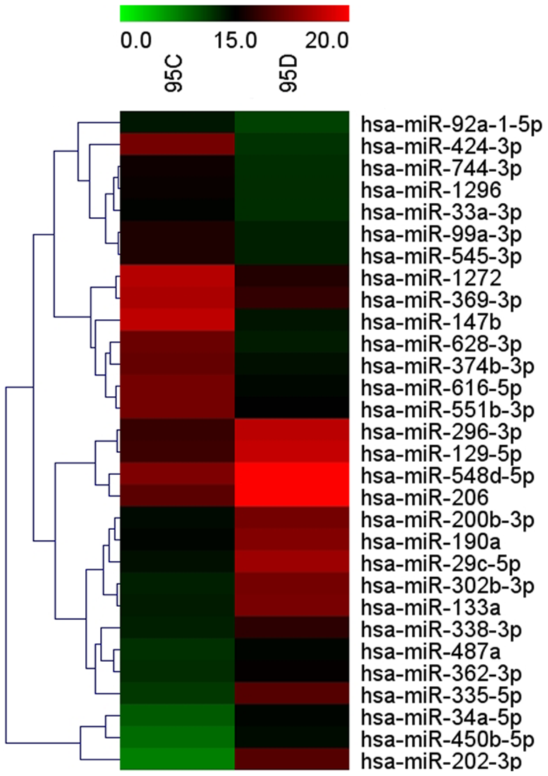
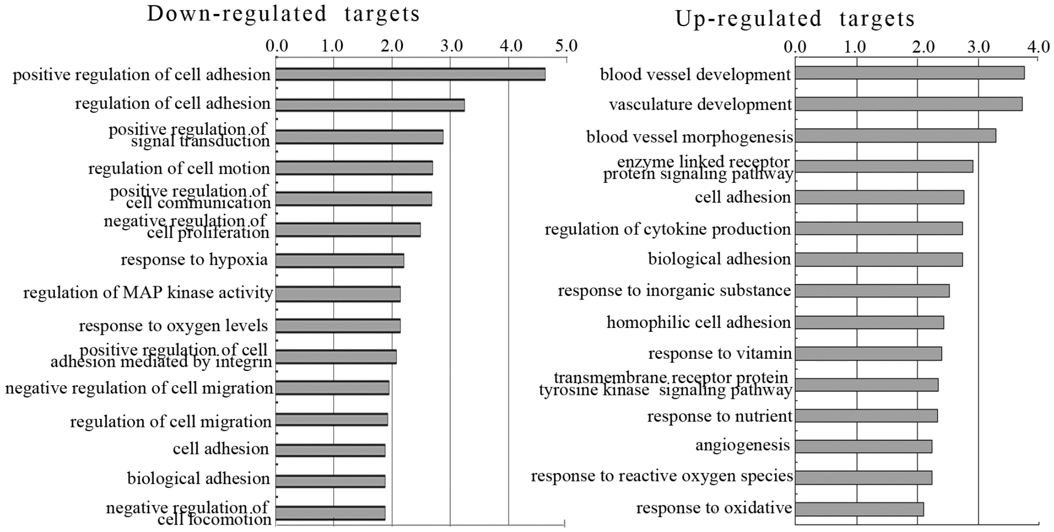
Supplementary figure 1



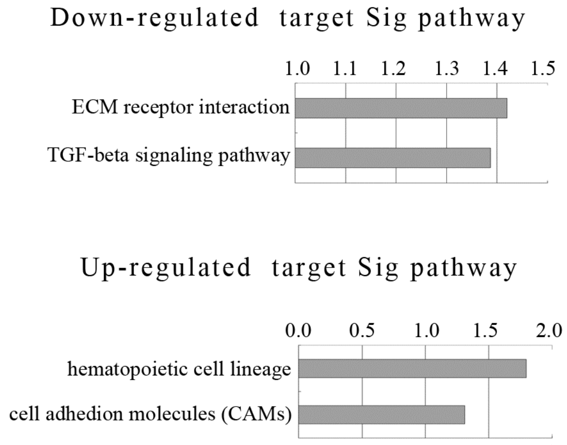
Supplementary figure.1: Differentially expressed miRNAs were divided into different groups by clustering analysis using the MeV4.9.0 software.

Supplementary figure 2



Supplementary figure.2: GO analysis identifies potential mRNA functional categories regulated by miRNAs between 95C and 95D cells. GO analysis was performed on mRNAs predicted to be targets of miRNAs, which were negatively correlated with target mRNA expression. The GO analysis was confined to the biological process category (GOTERM-BP-FAT). Only categories with a p-value smaller that 0.05 are included. The negative log of the p-value is plotted on the x-axis, and the functional categories were showed on y-axis.

Supplementary figure 3



Supplementary figure.3: miRNAs target genes were involved in many cellular pathways. (A) Significant pathways targeted by upregulated miRNAs, and (B) Significant pathways by downregulated miRNAs. The vertical axis is the pathway category, and the horizontal axis is the negative log of the p-value.

Supplementary table1：4 pairs of synthesized MET shRNA and NC oligonucleotide inserts

No	Sequence
sh-MET1	S: 5′-CACCGCAGTGAATTAGTTCGCTACGTTCAAGAGACGTAGCGAACTAATTCACTGCTTTTTTG-3′
	A: 5′-GATCCAAAAAAGCAGTGAATTAGTTCGCTACGTCTCTTGAACGTAGCGAACTAATTCACTGC-3′
sh-MET2	S: 5′-CACCGCACAAAGCAAGCCAGATTCTTTCAAGAGAAGAATCTGGCTTGCTTTGTGCTTTTTTG-3′
	A: 5′-GATCCAAAAAAGCACAAAGCAAGCCAGATTCTTCTCTTGAAAGAATCTGGCTTGCTTTGTGC-3′
sh-MET3	S: 5′-CACCGCTGGTGGCACTTTACTTACTTTCAAGAGAAGTAAGTAAAGTGCCACCAGCTTTTTTG-3′
	A: 5′-GATCCAAAAAAGCTGGTGGCACTTTACTTACTTCTCTTGAAAGTAAGTAAAGTGCCACCAGC-3′
sh-MET4	S: 5′-CACCGCTGGTGTTGTCTCAATATCATTCAAGAGATGATATTGAGACAACACCAGCTTTTTTG-3′
	A: 5′-GATCCAAAAAAGCTGGTGTTGTCTCAATATCATCTCTTGAATGATATTGAGACAACACCAGC-3′
NC	S: 5′- CACCGTTCTCCGAACGTGTCACGTCAAGAGATTACGTGACACGTTCGGAGAATTTTTTG-3′
	A: 5′- GATCCAAAAAATTCTCCGAACGTGTCACGTAATCTCTTGACGTGACACGTTCGGAGAAC-3′

Supplementary table2： The RT and PCR primers of six key miRNAs used in qRT–PCR analysis.

NO	primer	(5' to 3')
miR-424-3p	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACATAGCA
	PCR primer	F: CGGCAAAACGTGAGGCG R: CAGTGCAGGGTCCGAGGTAT
miR-450b-5p	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTATTCA
	PCR primer	F: CAGCGTTTTGCAATATGTTCC R: CAGTGCAGGGTCCGAGGTA
miR-335-5p	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACATTT
	PCR primer	F: CCGCCGTCAAGAGCAATAAC R: CAGTGCAGGGTCCGAGGTA
miR-34a-5p	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACAACC
	PCR primer	F: GGCGGTGGCAGTGTCTTAG R: CAGTGCAGGGTCCGAGGTAT
miR-302b-3p	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCTACTA
	PCR primer	F: GGCGGCTAAGTGCTTCCAT R: CAGTGCAGGGTCCGAGGTAT
miR-206	RT primer	CTCAGCGGCTGTCGTGGACTGCGCGCTGCCGCTGAGCCACACAC
	PCR primer	F: GGCGGTGGAATGTAAGGAAG R: GGCTGTCGTGGACTGCG

Supplementary Table 3 Differential expression of miRNAs in strain 95D and 95C

miRBase_human_18th	Fold Change (95D vs.95C)	miRBase_human_18th	Fold Change (95D vs. 95C)
miR-424-3p	37.473	miR-487a	0.181
miR-147b	31.455	miR-548d-5p	0.174
miR-628-3p	13.054	miR-338-3p	0.161
miR-744-3p	7.885	miR-296-3p	0.160
miR-1272	7.367	miR-362-3p	0.154
miR-374b-3p	7.298	miR-129-5p	0.151
miR-1296	6.588	miR-200b-3p	0.138
miR-616-5p	6.313	miR-190a	0.134
miR-33a-3p	5.468	miR-206	0.083
miR-92a-1-5p	5.410	miR-29c-5p	0.066
miR-99a-3p	5.399	miR-302b-3p	0.061
miR-545-3p	5.207	miR-133a	0.060
miR-369-3p	5.116	miR-34a-5p	0.031
miR-551b-3p	5.107	miR-335-5p	0.031
		miR-450b-5p	0.021
		miR-202-3p	0.002

Supplementary Table 4 Differential expression of genes in strain 95D and 95C

Gene Symbol	fold(95D/95C)	regulation	Gene Symbol	fold(95D/95C)	regulation
MME	25.002	up	XCL2	0.499	down
TNC	11.027	up	GABBR2	0.499	down
LPHN2	7.001	up	RTBDN	0.490	down
ASB5	6.965	up	SULF2	0.490	down
LOX	6.325	up	RIPK4	0.486	down
DNER	6.222	up	FXYD6	0.483	down
S100A16	6.135	up	CKMT1B	0.477	down
PVRL3	4.787	up	CKMT1B	0.477	down
ZEB2	4.538	up	C12orf59	0.473	down
SLC4A4	4.323	up	CITED2	0.471	down
4-Mar	4.080	up	ARAP2	0.468	down
AJAP1	4.009	up	JUP	0.462	down
ZFPM2	3.974	up	PRAC	0.458	down
HLA-DRA	3.945	up	MECOM	0.456	down
ADAM12	3.938	up	LOC643955	0.451	down
LOC151760	3.909	up	IGLON5	0.449	down
SPP1	3.851	up	EIF4E3	0.447	down
GJA1	3.690	up	ZNF608	0.444	down
ANPEP	3.632	up	TC2N	0.443	down
PTPRK	3.501	up	TRNAK36P	0.437	down
DSEL	3.482	up	THBS2	0.424	down
FGF5	3.471	up	DMKN	0.414	down
STK17A	3.436	up	PIEZO2	0.412	down
VEPH1	3.411	up	CD24	0.408	down
IL13RA2	3.363	up	ADAMTSL3	0.407	down
B3GALT1	3.321	up	MYO1D	0.403	down
TXNIP	3.291	up	TGFB2	0.402	down
SNORA36A	3.271	up	TSPYL5	0.398	down
F2RL2	3.096	up	OLFM1	0.390	down
HLA-DRA	3.025	up	GPC3	0.383	down
NDRG1	2.981	up	PACRG	0.365	down
HLA-DRA	2.963	up	MC5R	0.358	down
NETO1	2.948	up	APOE	0.356	down
EREG	2.939	up	CDH11	0.349	down
B3GNT5	2.926	up	RGS4	0.349	down
EPAS1	2.822	up	ANKRD20A5P	0.349	down
EYA4	2.804	up	KLHL4	0.346	down
SRPX2	2.798	up	ODZ1	0.341	down
FAM198B	2.787	up	GYG2	0.337	down
PRICKLE2	2.781	up	PDE10A	0.335	down

PLA2G4A	2.764	up	SEPP1	0.335	down
Gene Symbol	**fold(95D/95C)**	**regulation**	**Gene Symbol**	**fold(95D/95C)**	**regulation**
PTPRG	2.761	up	PLK2	0.333	down
BCHE	2.738	up	CPQ	0.332	down
SGK1	2.733	up	PDE8B	0.330	down
DSC2	2.655	up	PRICKLE1	0.314	down
TMEFF2	2.652	up	MXRA5	0.310	down
HSPB8	2.648	up	RPS6KA6	0.309	down
PLAU	2.586	up	KRT18	0.303	down
IL7	2.566	up	GABRB3	0.245	down
PTPRZ1	2.539	up	MIR622	0.244	down
CDR1	2.444	up	EDIL3	0.244	down
TSPAN13	2.438	up	SEMA3A	0.239	down
LURAP1L	2.419	up	GPC4	0.234	down
TRPS1	2.382	up	PIEZO2	0.216	down
SHC3	2.376	up	OLR1	0.212	down
GLIPR1	2.375	up	SLC16A7	0.187	down
KYNU	2.366	up	RGS5	0.177	down
ANTXR2	2.362	up	THBS1	0.172	down
CD68	2.358	up	FSTL5	0.156	down
EPHA5	2.343	up	SDC2	0.141	down
MCTP1	2.301	up	SLITRK6	0.133	down
GFPT2	2.282	up	KRT8	0.092	down
MET	2.280	up			
CXCL2	2.275	up			
MAN1A1	2.266	up			
RN5S331	2.258	up			
BCL2A1	2.257	up			
CDCP1	2.236	up			
GEM	2.234	up			
CRLF2	2.233	up			
DSC3	2.220	up			
SNORD58A	2.220	up			
SLITRK3	2.213	up			
LDOC1	2.189	up			
STC1	2.188	up			
RNF128	2.166	up			
RNY1P5	2.159	up			
IL18	2.155	up			
TRIM16	2.153	up			
SERPINE1	2.153	up			
CXorf57	2.150	up			
STMN2	2.149	up			
CDH2	2.142	up			

ADAMTS18	2.139	up
Gene Symbol	**fold(95D/95C)**	**regulation**
SRGN	2.116	up
TLR6	2.096	up
ARRDC3	2.084	up
RAB27B	2.077	up
RGMB	2.074	up
IER3	2.072	up
FAT4	2.070	up
OCIAD2	2.069	up
KLF7	2.061	up
ALCAM	2.042	up
TMEM158	2.037	up
PAQR5	2.023	up