

Table SI. Primer sequences for reverse transcription-quantitative PCR.

Genes	Direction	Sequences (5'-3')
RUNX1(R)	Forward	GCCACCTACCATAGAGCCAT
	Reverse	AGTGGAGTGGTTCAAGGAGG
RUNX1(M)	Forward	GATGGCACTCTGGTCACCG
	Reverse	GCCGCTCGGAAAAGGACAA
GAPDH(R)	Forward	AACGACCCCTTCATTGACCT
	Reverse	CCCCATTTGATGTTAGCGGG
GAPDH(M)	Forward	AGGTCGGTGTGAACGGATTTG
	Reverse	TGTAGACCATGTAGTTGAGGTCA
MSTN(R)	Forward	GAGGACAGTGAGAGAGAGGC
	Reverse	TCTGGACGTCGTACTGATCG
PELI3(R)	Forward	TCGTGCATCCTCTCTTCTCC
	Reverse	ATGAGATGCTATGCTGGCCT
TOX(R)	Forward	TTTATCCACCTCCAGCCCAG
	Reverse	CAGAGAGTGGTCAGGGAGTG
PBLD1(R)	Forward	TACCCGAAACTCCTGGTCC
	Reverse	GAGAACGGTGTGTGCAGATC
DRD2(R)	Forward	AAACCCGGACCTCCCTTAAG
	Reverse	AGAGGACTGGTGGGATGTTG
TNIP3(R)	Forward	CAGGATGCCTTGACAATCGG
	Reverse	TGGAGGAAGCTGGTTGAGAG
KCNA2(R)	Forward	CGGGAGGATGAAGGCTACAT
	Reverse	CTCGTTCTCATCCCGGAAGA
CNTN2(R)	Forward	CGGAGACCTACGCACTAGTT
	Reverse	CCTTGGAGTTCTCTGCCTCA
FMOD(R)	Forward	TACGAGACCTCCGACCCTTA
	Reverse	AGCGATCTGGTTGTTCTGGA
KCNJ3(R)	Forward	ATCAAGATGTCCCAGCCCAA
	Reverse	AGGTGTCTGCCGAGATTGA
GBP6(R)	Forward	CGGCCAACACATGACAAAGA
	Reverse	GAGTTGTCACCGCATCATCC

ZFP970(R)	Forward	ACGAAGCAGTCATCTCGGAA
	Reverse	TTTGGAGAGGACCGCTTTGT
miR-142-3p	Forward	TGTAGTGTTCCTACTT
	Reverse	GTGCAGGGTCCGAGGT
U6	Forward	CTCGCTTCGGCACATA
	Reverse	CGAATTTGCGTGTCATCCT

R, rat; M, mouse; RUNX1, runt-related transcription factor 1; MSTN, growth/differentiation factor 8; PELI3, E3 ubiquitin-protein ligase pellino homolog 3; TOX, thymocyte selection-associated high mobility group box protein; PBLD1, phenazine biosynthesis-like domain-containing protein 1; DRD2, dopamine receptor D2; TNIP3, TNFAIP3-interacting protein 3; KCNA2, potassium voltage-gated channel subfamily A member 2; CNTN2, contactin-2; FMOD, fibromodulin; KCNJ3, G protein-activated inward rectifier potassium channel 1; GBP6, guanylate-binding protein 6; ZFP970, zinc finger protein 970; miR, microRNA.

Table SII. Differentially expressed miRNAs ($\log_2FC > 2$ or < -2 with a q value of no more than 0.05). MIRI + emodin mice versus MIRI mice.

miRNA	$\log_2FC$	q-value
mmu-miR-466c-3p	10.38	1.69×10^{-3}
mmu-miR-133b-3p	2.90	4.63×10^{-2}
mmu-miR-1247-5p	2.84	1.63×10^{-2}
mmu-miR-328-3p	2.60	5.77×10^{-3}
mmu-miR-29b-3p	2.56	1.75×10^{-5}
mmu-miR-1843a-3p	2.30	5.00×10^{-3}
mmu-miR-181a-2-3p	2.24	1.63×10^{-2}
mmu-miR-30c-2-3p	2.06	2.34×10^{-2}
mmu-miR-29a-3p	2.06	9.25×10^{-3}
mmu-miR-338-3p	2.05	4.71×10^{-3}
mmu-miR-671-5p	2.04	7.19×10^{-3}
mmu-miR-29c-3p	2.00	2.21×10^{-3}
mmu-miR-143-3p	-2.02	1.20×10^{-3}
mmu-miR-100-5p	-2.27	2.07×10^{-3}
mmu-miR-361-3p	-2.29	1.61×10^{-2}
mmu-miR-279-3p	-2.40	2.38×10^{-2}
mmu-miR-1843b-3p	-2.47	1.22×10^{-3}
mmu-miR-101-5p	-2.63	4.05×10^{-2}
mmu-miR-2-5p	-2.82	1.15×10^{-2}
mmu-miR-6538	-2.86	4.62×10^{-5}
mmu-miR-142-3p	-3.02	5.17×10^{-5}
mmu-miR-669p-5p	-3.21	3.87×10^{-2}
mmu-miR-186-5p	-3.21	4.36×10^{-5}
mmu-miR-327-5p	-3.36	2.71×10^{-2}
mmu-miR-3470a	-3.70	5.17×10^{-5}
mmu-miR-5099	-3.82	1.05×10^{-4}
mmu-miR-72-3p	-4.03	6.07×10^{-4}
mmu-miR-5121	-4.11	1.66×10^{-2}
mmu-miR-3470b	-4.45	1.42×10^{-5}

mmu-miR-24-5p	-4.47	3.96×10^{-8}
mmu-miR-74-5p	-4.47	2.07×10^{-3}
mmu-miR-112-3p	-4.82	2.93×10^{-7}
mmu-miR-365-5p	-6.13	3.41×10^{-10}
mmu-miR-61-3p	-6.79	1.07×10^{-7}

miRNA/miR, microRNA; MIRI, myocardial ischemia/reperfusion injury.

Table SIII. A total of four pairs of matched differentially expressed regulatory networks between TFs and miRNAs.

mRNA/TF	log ₂ FC	q-value	miRNA	log ₂ FC	q-value
REST	-1.07	4.33×10 ⁻³	mmu-mir-29b	2.56	1.75×10 ⁻⁵
STAT1	1.11	1.54×10 ⁻⁶	mmu-mir-143	-2.02	1.20×10 ⁻³
RUNX1	-2.4	1.36×10 ⁻⁵	mmu-mir-142	-3.02	5.17×10 ⁻⁵
CEBPB	-1.13	1.79×10 ⁻²	mmu-mir-142	-3.02	5.17×10 ⁻⁵

REST, RE1-silencing transcription factor; STAT1, signal transducer and activator of transcription 1; RUNX1, runt-related transcription factor 1; CEBPB, CCAAT/enhancer-binding protein β; TF, transcription factor; miRNA/miR, microRNA.

Table SIV. Overlapped 12 potential genes between subset one and subset two.

Gene symbol	log ₂ FC	q-value
MSTN	2.42	4.86×10^{-2}
PELI3	2.35	3.66×10^{-2}
TOX	2.00	1.80×10^{-2}
KCNA2	2.07	1.09×10^{-2}
TNIP3	2.35	3.28×10^{-3}
PBLD1	2.78	3.19×10^{-3}
DRD2	2.13	1.11×10^{-3}
CNTN2	2.41	2.55×10^{-4}
FMOD	3.81	1.51×10^{-5}
KCNJ3	2.60	2.24×10^{-6}
GBP6	2.70	2.80×10^{-7}
ZFP970	2.22	2.38×10^{-11}

MSTN, growth/differentiation factor 8; PELI3, E3 ubiquitin-protein ligase pellino homolog 3; TOX, thymocyte selection-associated high mobility group box protein; PBLD1, phenazine biosynthesis-like domain-containing protein 1; DRD2, dopamine receptor D2; TNIP3, TNFAIP3-interacting protein 3; KCNA2, potassium voltage-gated channel subfamily A member 2; CNTN2, contactin-2; FMOD, fibromodulin; KCNJ3, G protein-activated inward rectifier potassium channel 1; GBP6, guanylate-binding protein 6; ZFP970, zinc finger protein 970.