

Figure S1. Integrity of collected RNAs. RNA integrity and gDNA contamination test using denaturing agarose gel electrophoresis. I/R, ischemia/reperfusion.

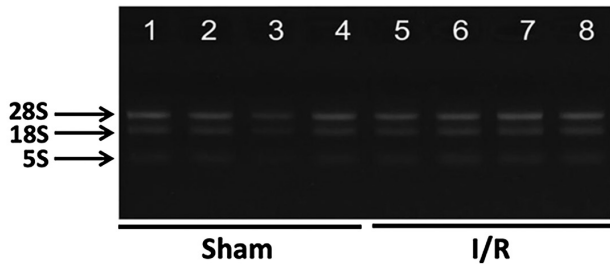


Table SI. RNA quantification and quality assurance using NanoDrop ND-1000.

Sample ID	OD 260/280 Ratio	OD 260/230 Ratio	Concentration (ng/μl)	Volume (μl)	Quantity (ng)	QC result Pass or Fail
Sham-1	2.05	2.44	1470.13	20	29402.6	Pass
Sham-2	2.03	2.46	1137.39	20	22747.8	Pass
Sham-3	2.03	2.41	784.10	20	15682.0	Pass
Sham-4	2.02	2.48	1019.80	30	30594.0	Pass
I/R-1	1.99	2.43	658.29	30	19748.7	Pass
I/R-2	2.03	2.42	965.95	30	28978.5	Pass
I/R-3	2.04	2.34	701.48	30	21044.4	Pass
I/R-4	2.02	2.46	877.75	30	26332.5	Pass

OD, optical density; I/R, ischemia/reperfusion; QC, quality control.

Table SII. Top ten up- and downregulated expressed lncRNAs in mice hearts after ischemia/reperfusion procedure.

A, Upregulated				
lncRNA	RNA length	Chromosome	Fold change	P-value
Gm11407	1,058	chr4	21.68	4.87x10 <sup>-6</sup>
AK131777	775	chr5	15.66	4.15x10 <sup>-7</sup>
AK155692	532	chr15	14.57	1.10x10 <sup>-4</sup>
1600029O15Rik	1,809	chr9	13.41	8.19x10 <sup>-6</sup>
AK012512	1,150	chr2	13.25	1.13x10 <sup>-5</sup>
Mri1	1,065	chr8	13.09	6.09x10 <sup>-6</sup>
AK198376	967	chr15	12.98	9.00x10 <sup>-7</sup>
AK134917	1,842	chr13	12.84	3.04x10 <sup>-5</sup>
AK020500	666	chr9	11.81	5.28x10 <sup>-6</sup>
Gm12403	951	chr4	11.56	1.10x10 <sup>-4</sup>
B, Downregulated				
lncRNA	RNA length	Chromosome	Fold change	P-value
Ftsj1	1,791	chrX	202.80	4.14x10 <sup>-11</sup>
Rpl7l1-ps1	725	chrX	109.49	9.82x10 <sup>-9</sup>
AK087886	1,056	chr10	95.20	1.67x10 <sup>-9</sup>
Gm14964	519	chr19	90.52	1.44x10 <sup>-6</sup>
Smim22	305	chr16	68.14	6.32x10 <sup>-9</sup>
G630055G22Rik	1,332	chr18	62.12	2.97x10 <sup>-6</sup>
XLOC_017302	522	chr4	61.42	4.31x10 <sup>-6</sup>
Amz2	1,846	chr11	57.24	9.38x10 <sup>-7</sup>
Gm12040	537	chr11	57.15	4.22x10 <sup>-6</sup>
Gm15833	957	chr1	56.50	2.23x10 <sup>-6</sup>

lncRNA, long non-coding RNA.

Table SIII. Top ten up- and downregulated expressed miRNAs in mice hearts after ischemia/reperfusion procedure.

A, Upregulated		
miRNA	Fold change	P-value
mmu-miR-33-5p	10.17	2.93x10 <sup>-5</sup>
mmu-miR-3068-5p	5.40	8.84x10 <sup>-6</sup>
mmu-miR-329-3p	4.87	7.40x10 <sup>-4</sup>
mmu-miR-107-3p	4.65	7.46x10 <sup>-3</sup>
mmu-miR-103-3p	4.49	1.10x10 <sup>-4</sup>
mmu-miR-301a-3p	3.50	2.44x10 <sup>-2</sup>
mmu-miR-139-5p	3.48	7.08x10 <sup>-3</sup>
mmu-miR-34b-3p	3.09	5.34x10 <sup>-3</sup>
mmu-miR-325-3p	2.94	1.46x10 <sup>-3</sup>
mmu-miR-29b-3p	2.82	4.91x10 <sup>-2</sup>
B, Downregulated		
miRNA	Fold change	P-value
mmu-miR-378b/mmu-miR-378c	59.45	3.90x10 <sup>-4</sup>
mmu-miR-378a-3p	32.94	7.28x10 <sup>-3</sup>
mmu-miR-378b	21.07	4.90x10 <sup>-4</sup>
mmu-miR-143-3p	7.75	7.90x10 <sup>-4</sup>
mmu-miR-145a-5p/mmu-miR-145b	4.79	1.88x10 <sup>-2</sup>
mmu-miR-106b-5p	2.98	1.18x10 <sup>-2</sup>
mmu-miR-5624-5p	2.83	4.65x10 <sup>-3</sup>
mmu-miR-23a-3p	2.80	1.66x10 <sup>-2</sup>
mmu-miR-30e-3p	2.64	4.40x10 <sup>-4</sup>
mmu-miR-1192	2.58	4.84x10 <sup>-3</sup>

miRNA/miR, microRNA.

Table SIV. Top ten up- and downregulated expressed mRNAs in mice hearts after ischemia/reperfusion procedure.

A, Upregulated				
mRNA	RNA length	Chromosome	Fold change	P-value
Pdk4	3453	chr6	47.34	1.46x10 <sup>-7</sup>
Gm20594	334	chr6	19.66	1.64x10 <sup>-6</sup>
Xirp1	5839	chr9	18.27	3.57x10 <sup>-7</sup>
Ndufb6	534	chr4	16.88	1.75x10 <sup>-5</sup>
Acadl	1948	chr1	14.98	1.80x10 <sup>-5</sup>
Gm5595	3166	chr7	14.39	3.65x10 <sup>-5</sup>
Gm12657	978	chr4	14.07	2.45x10 <sup>-5</sup>
Sucla2	2108	chr14	13.93	8.11x10 <sup>-6</sup>
Junb	1840	chr8	13.01	4.14x10 <sup>-5</sup>
Acadm	2062	chr3	11.88	3.07x10 <sup>-5</sup>
B, Downregulated				
mRNA	RNA length	Chromosome	Fold change	P-value
Fdft1	2882	chr14	303.25	1.07x10 <sup>-10</sup>
Elovl1	1781	chr4	175.80	8.16x10 <sup>-9</sup>
Serpine1	3024	chr5	162.45	1.49x10 <sup>-9</sup>
2010002M12Rik	3365	chr19	148.82	3.36x10 <sup>-9</sup>
Mrgprg	1847	chr7	104.72	1.58x10 <sup>-8</sup>
Ifi27	1053	chr12	100.28	1.39x10 <sup>-10</sup>
Tnfaip8l2	1122	chr3	74.16	3.12x10 <sup>-6</sup>
Supt16	4491	chr14	69.27	5.85x10 <sup>-6</sup>
Stat4	2981	chr1	68.02	5.87x10 <sup>-9</sup>
Olfml1	1969	chr7	67.17	2.72x10 <sup>-6</sup>

Table SV. Functional classification of the differentially expressed genes by Gene Ontology analysis.

A, Upregulated			
Term	Count	Enrichment score	P-value
GDP binding	39	9.76	1.73x10 <sup>-10</sup>
RNA polymerase II carboxy-terminal domain kinase activity	12	3.33	4.70x10 <sup>-4</sup>
TBP-class protein binding	12	3.33	4.70x10 <sup>-4</sup>
NAD <sup>+</sup> binding	10	2.98	1.06x10 <sup>-3</sup>
Protein phosphatase type 2A regulator activity	8	2.63	2.36x10 <sup>-3</sup>
Macromolecule transmembrane transporter activity	8	2.63	2.36x10 <sup>-3</sup>
Misfolded protein binding	8	2.63	2.36x10 <sup>-3</sup>
RNA polymerase I activity	9	2.59	2.60x10 <sup>-3</sup>
Vinculin binding	9	2.59	2.60x10 <sup>-3</sup>
Angiotensin receptor binding	9	2.59	2.60x10 <sup>-3</sup>
B, Downregulated			
Term	Count	Enrichment score	P-value
Proline-rich region binding	9	3.06	8.60x10 <sup>-4</sup>
Sodium ion binding	6	2.85	1.41x10 <sup>-3</sup>
Armadillo repeat domain binding	6	2.85	1.41x10 <sup>-3</sup>
Alkali metal ion binding	8	2.75	1.78x10 <sup>-3</sup>
Peroxisome proliferator activated receptor binding	8	2.75	1.78x10 <sup>-3</sup>
G-protein $\beta$ -subunit binding	6	2.57	2.71x10 <sup>-3</sup>
C2H2 zinc finger domain binding	6	2.12	7.67x10 <sup>-3</sup>
Intracellular cyclic nucleotide activated cation channel activity	5	1.79	1.61x10 <sup>-2</sup>
High voltage-gated calcium channel activity	5	1.79	1.61x10 <sup>-2</sup>
Cyclic nucleotide-gated ion channel activity	5	1.79	1.61x10 <sup>-2</sup>

TBP, TATA-binding protein; C2H2, Cys2His2-like fold group.

Table SVI. Functional classification of the differentially expressed genes by pathway analysis.

A, Upregulated			
Term	Count	Enrichment score	P-value
Alzheimer's disease	178	7.63	1.64x10 <sup>-7</sup>
Sphingolipid signaling pathway	124	6.78	5.35x10 <sup>-7</sup>
Protein processing in endoplasmic reticulum	169	6.27	2.36x10 <sup>-6</sup>
Non-alcoholic fatty liver disease	158	5.63	6.05x10 <sup>-6</sup>
Parkinson's disease	152	5.22	6.82x10 <sup>-6</sup>
Ribosome	148	5.17	6.93x10 <sup>-6</sup>
Carbon metabolism	118	5.16	7.19x10 <sup>-6</sup>
Biosynthesis of antibiotics	219	5.14	1.11x10 <sup>-5</sup>
mRNA surveillance pathway	96	4.96	1.83x10 <sup>-5</sup>
Citrate cycle	32	4.74	9.91x10 <sup>-7</sup>
B, Downregulated			
Term	Count	Enrichment score	P-value
Endocytosis	234	6.00	7.50x10 <sup>-4</sup>
Bacterial invasion of epithelial cells	78	3.13	1.27x10 <sup>-3</sup>
Type II diabetes mellitus	50	2.90	1.64x10 <sup>-3</sup>
Oxytocin signaling pathway	159	2.79	2.00x10 <sup>-3</sup>
Arrhythmogenic right ventricular cardiomyopathy	74	2.70	2.45x10 <sup>-3</sup>
Nicotine addiction	40	2.61	2.57x10 <sup>-3</sup>
Morphine addiction	94	2.59	4.33x10 <sup>-3</sup>
Amphetamine addiction	69	2.36	4.58x10 <sup>-3</sup>
Transcriptional misregulation in cancer	178	2.34	7.22x10 <sup>-3</sup>
Ras signaling pathway	230	2.14	1.64x10 <sup>-7</sup>

Table SVII. Highest degree list of miRNAs, mRNAs and lncRNAs in myocardial ischemia/reperfusion injury via competing endogenous RNA analysis.

A, miRNA	
Gene	Degree
mmu-miR-330-3p	67
mmu-miR-107-3p	61
mmu-miR-103-3p	60
mmu-miR-125a-5p	56
mmu-miR-125b-5p	55
mmu-miR-669h-3p	45
mmu-miR-1224-3p	35
mmu-miR-190a-5p	32
mmu-miR-330-3p	31
mmu-miR-3084-3p	31
B, mRNAs	
Gene	Degree
Plxna4	7
Twf1	7
Plcx2	7
Eif5	7
Cfl2	7
Vamp1	7
Gpr146	6
Ap3d1	6
Zfp711	6
Antxr2	6
C, lncRNAs	
Gene	Degree
Rpl711-ps1	12

1600029O15Rik	12
Gm11407	11
Gm12040	9
AK155692	2

miRNA/miR, microRNA; lncRNA, long non-coding RNA; Plxna4, plexin A4; Twf1, twinfilin actin binding protein 1; Plcx2, phosphatidylinositol specific phospholipase C X domain containing 2; Eif5, eukaryotic translation initiation factor 5; Cfl2, cofilin 2; Vamp1, vesicle associated membrane protein 1; Gpr146, G protein-coupled receptor 146; Ap3d1, adaptor related protein complex 3 subunit  $\delta$  1; Zfp711, zinc finger protein 711; Antxr2, ANTXR cell adhesion molecule 2.