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Supplemental Information

**Translatome and Transcriptome Profiling
of Hypoxic-Induced Rat Cardiomyocytes**

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Table S1. All the primers and nucleotides used in this study are listed.

Gene name	Primer sequences
BNIP3 for RNA	5'-CAAGATACCAACAGAGCTGAAAT-3' 5'-GGAAGGAAAACCTTCAGAAAG-3'
BNIP3 for RIP	5'-TGTCCCCTCAATCCCGTGTGCGCCTGGCCT-3' 5'-CTGCCGCCTCCGCGGCCCTCTCGG-3'
ADRB2 for RNA	5'-GGGCCTAGCGGTGGTGCCTTTTGGGG-3' 5'-TACCAGTGCATCTGGATAGGC-3'
ADRB2 for RIP	5'-CGCGTTCAGGCTGCAGCTGGCAGGC-3' 5'-CGGCTTTCAGTGCCAGACGCTCT-3'
NCBP3 for RNA	5'-TGAGATTTGCTACGAAAGATGACA-3' 5'-CACCACGACTCTGTCATCAGCATCCA-3'
EWSR1 for RNA	5'-GCACTGGGGCTTATGACACCACCTGCT-3' 5'-TGCATCGGGTAGCTCCCAGGA-3'
DRG2 for RNA	5'-CTCTGTGGGTAAGTCCACTTTCTTGA-3' 5'-CTCCAGCAGGGACCTCTGCACA-3'
GAPDH	5'-AGGCTGAGAATGGGAAGCTGGTCATCA-3' 5'-TAAGCAGTTGGTGGTGCAGGATGCAT-3'
Random RNA fragment	5'- CUCUCUACGGAGGAAUACUAGAGGGCUUUCUACUUCUACUUCUACUCAC-3'
Motif deleted fragment	5'- CUCUCUACGGAGGAAUACUAGAGUUCUACUUCUACUCACUUCUACUCAC-3'
Fragment_1	5'- CUCUCUACGGAGGAAUACUAGAAGCUGCCCUACUUCUACUUCUACUCAC-3'
Fragment_2	5'- CUCUCUACGGAGGAAUACUAGAAGCUUCCCUACUUCUACUUCUACUCAC-3'
Fragment_3	5'- CUCUCUACGGAGGAAUACUAGAAGAUUCCCUACUUCUACUUCUACUCAC-3'
Fragment_4	5'- CUCUCUACGGAGGAAUACUAGAAGCUUCACUACUUCUACUUCUACUCAC-3'

Table S2. The summary of all sequencing raw data in this study.

Table S3. The expression of the differential expressed genes among NC, MH and SH in RNA-seq.

Table S4. The expression of the differential expressed genes among NC, MH and SH in polyribo-seq.

Figure S1. The hypoxic-induced effects of different periods on arterial SaO₂ (A), and the activities of SOD (B) and MDA (C) in sera in each group. Data is presented as the mean \pm SEM ($n = 4$ per group). “*” the first and “^” the last significant difference ($p < 0.05$) compared with the previous group. SaO₂: oxygen saturation; SOD: superoxide dismutase; MDA: malonaldehyde; NC: normoxia control.

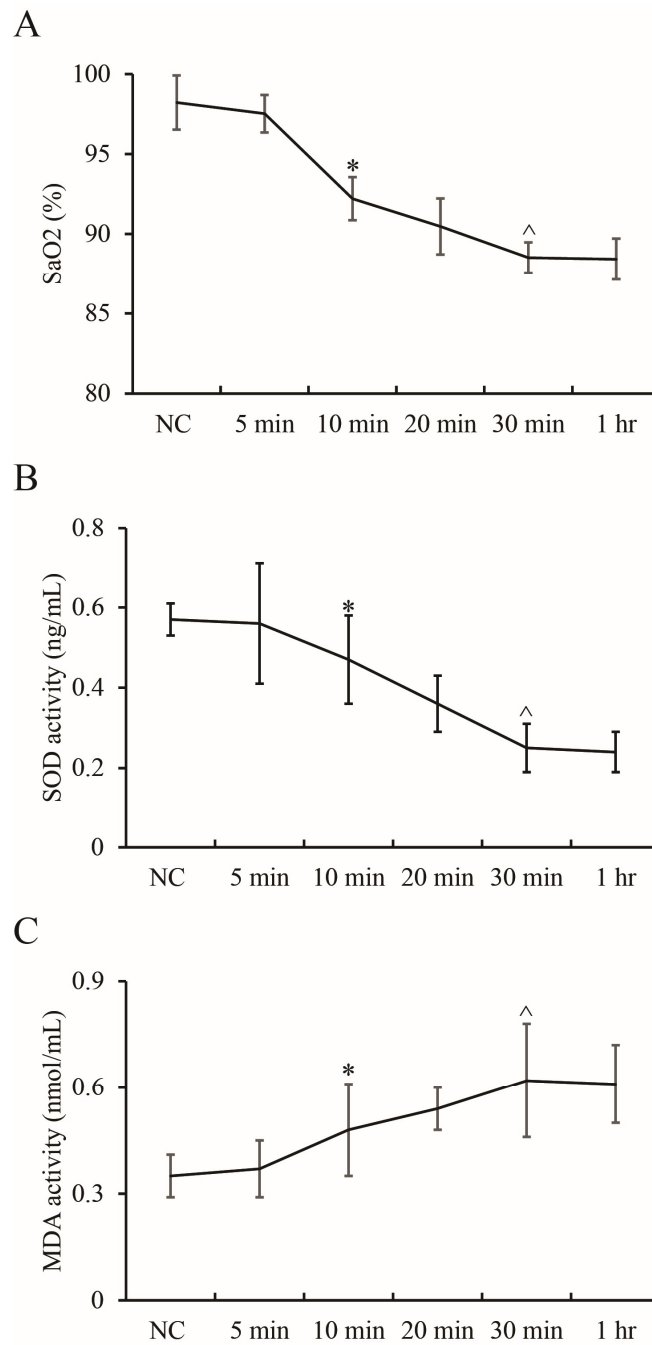


Figure S2. Validation of TTC (A) and masson (B) staining with 200X magnification in hypoxic-induced effects of left ventricular myocardial tissues. * $p < 0.05$ vs. NC group. NC: normoxia control; MH: mild hypoxia; SH: severe hypoxia.

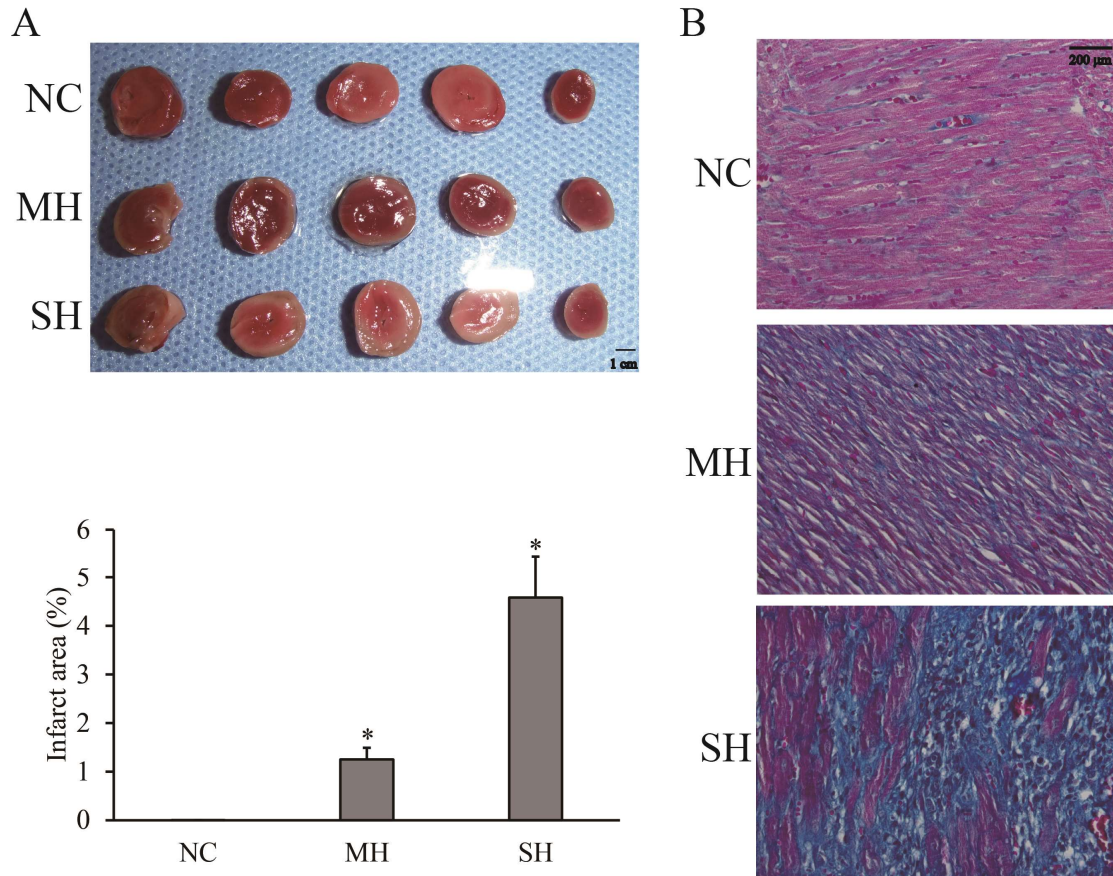


Figure S3. WB assay of HIF-1 α , VEGFA, GLUT1 and LDHA in H9C2 cells exposed to hypoxia. NC group. NC: normoxia control; MH: mild hypoxia; SH: severe hypoxia.

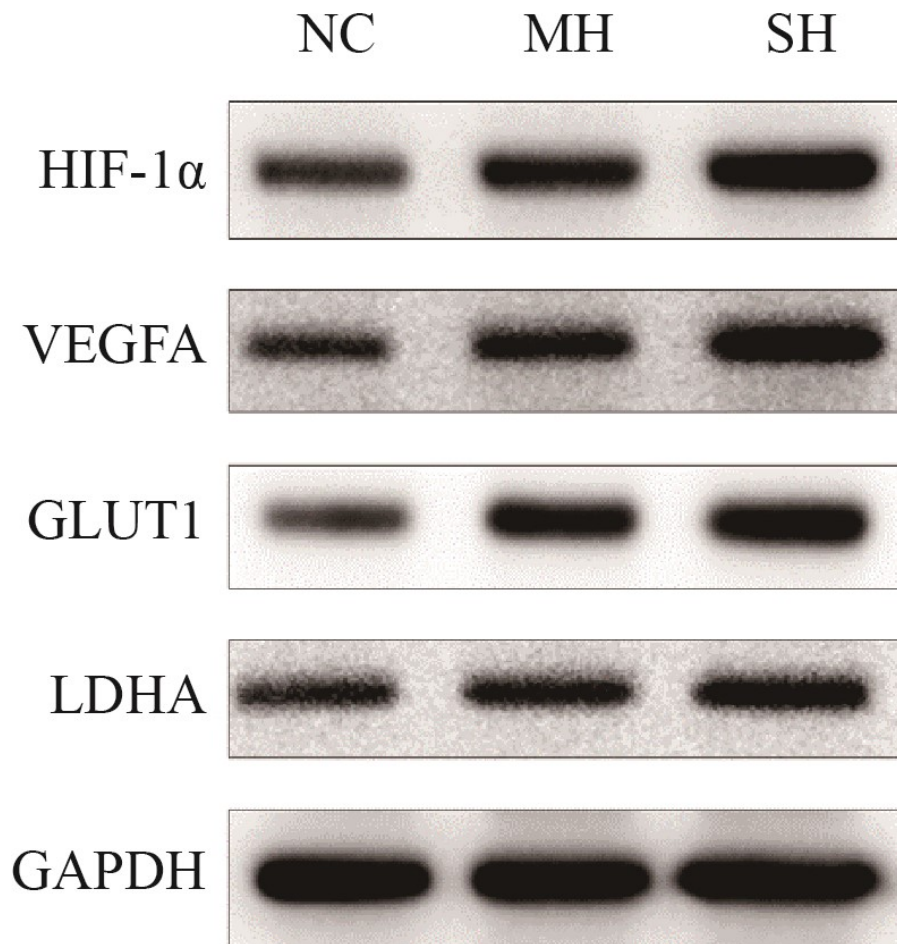


Figure S4. The Correlation analysis of the biological replications of each sequencing sample.

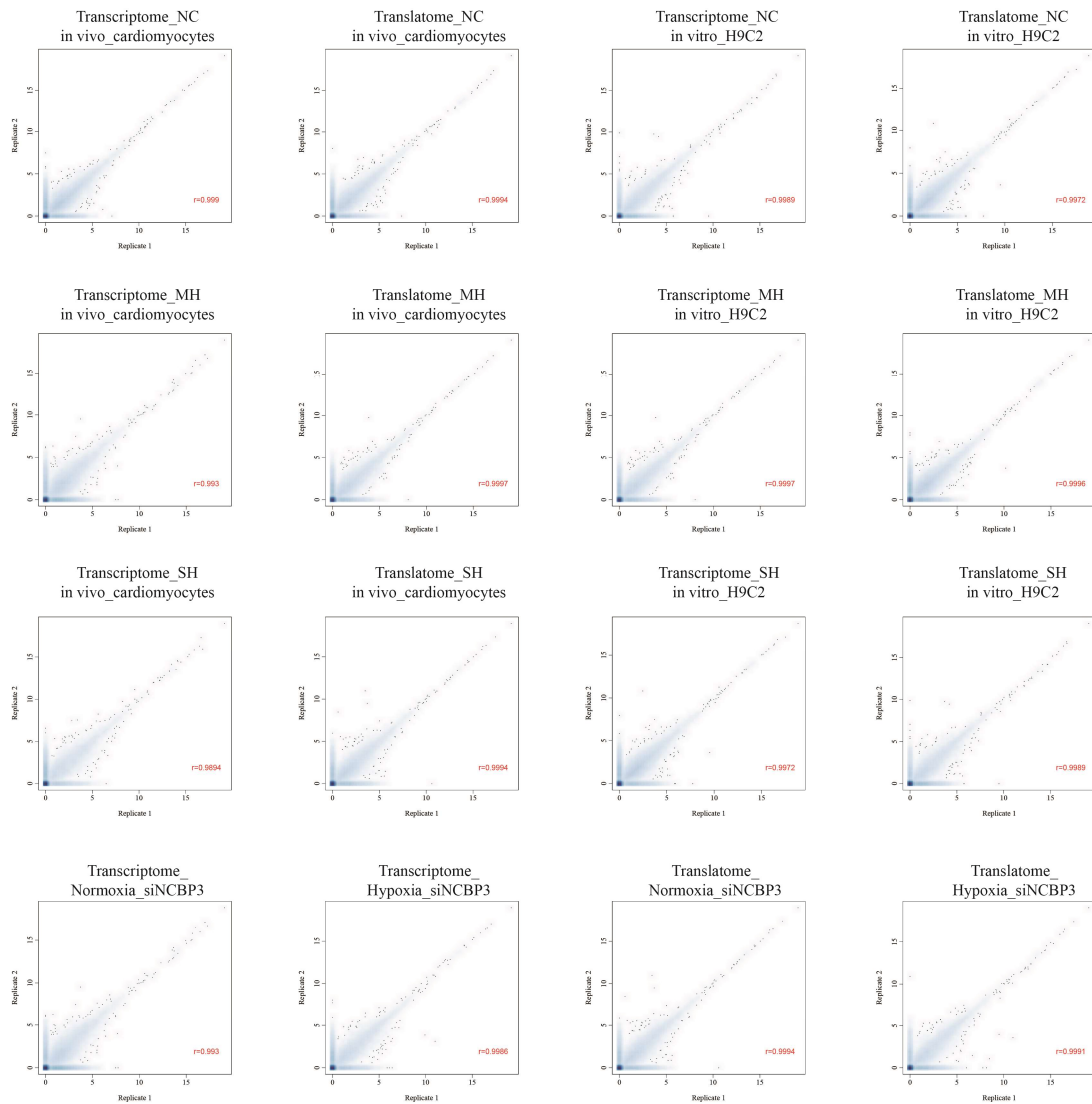


Figure S5. The alignment view of wild type and mutant 5'UTR of BNIP3 (A) and ADRB2 (B). The differences between wild type (top) and mutant (below) sequences are indicated by red frame.

A

Score	Expect	Identities	Gaps	Strand
187 bits(101)	4e-53	116/123(94%)	2/123(1%)	Plus/Plus
Query 1	TGTCCCCTCAATCCCGTGTGCGCTGGCCTCAGAGCTGAGCGGGCGCA-AGCTGCC-CTGCT	58		
Sbjct 1	TGTCCCCTCAATCCCGTGTGCGCTGGCCTCAGAGCTGAGCGGGCGCCAGGACCATCTGCT	60		
Query 59	ACCTCTCAGTGGTCACTTCCCAGGCCGTGTCGCAGTTGGGCTCCGGCTCCTTTGCGGAGCC	118		
Sbjct 61	ACCTCTCAGTGGTCACTTCCCAGGCCGTGTCGCAGTTGGGCTCCGGCTCCTTTGCGGAGCC	120		
Query 119	ACC 121			
Sbjct 121	ACC 123			

B

Score	Expect	Identities	Gaps	Strand
329 bits(178)	2e-95	193/200(97%)	1/200(0%)	Plus/Plus
Query 1	C CGGTT CAGGCTGCAGCTGGCAGGCATCGCGAGCCCGGAGCACCCACGAGCTCAGTGTGC	60		
Sbjct 1	C CGGTT CAGGCTGCAGCTGGCAGGCATCGCGAGCCCGGAGCACCCACGAGCTCAGTGTGC	60		
Query 61	AGGACGCGCCCCAGCACAGCCACCTACGGTCTCTGAATGAAGCTTC-CAGGAGTCCGCC	119		
Sbjct 61	AGGACGCGCCCCAGCACAGCCACCTACGGTCTCTGAATGTTGAGACGAAGGAGTCCGCC	120		
Query 120	CCCGACGGCTGCGCCCATCGGAGGTGCACCCGCTGAGAGCGTCTGGGCACTGAAAGCC	179		
Sbjct 121	CCCGACGGCTGCGCCCATCGGAGGTGCACCCGCTGAGAGCGTCTGGGCACTGAAAGCC	180		
Query 180	GGTGGCTCACCTGCCGGCC 199			
Sbjct 181	GGTGGCTCACCTGCCGGCC 200			