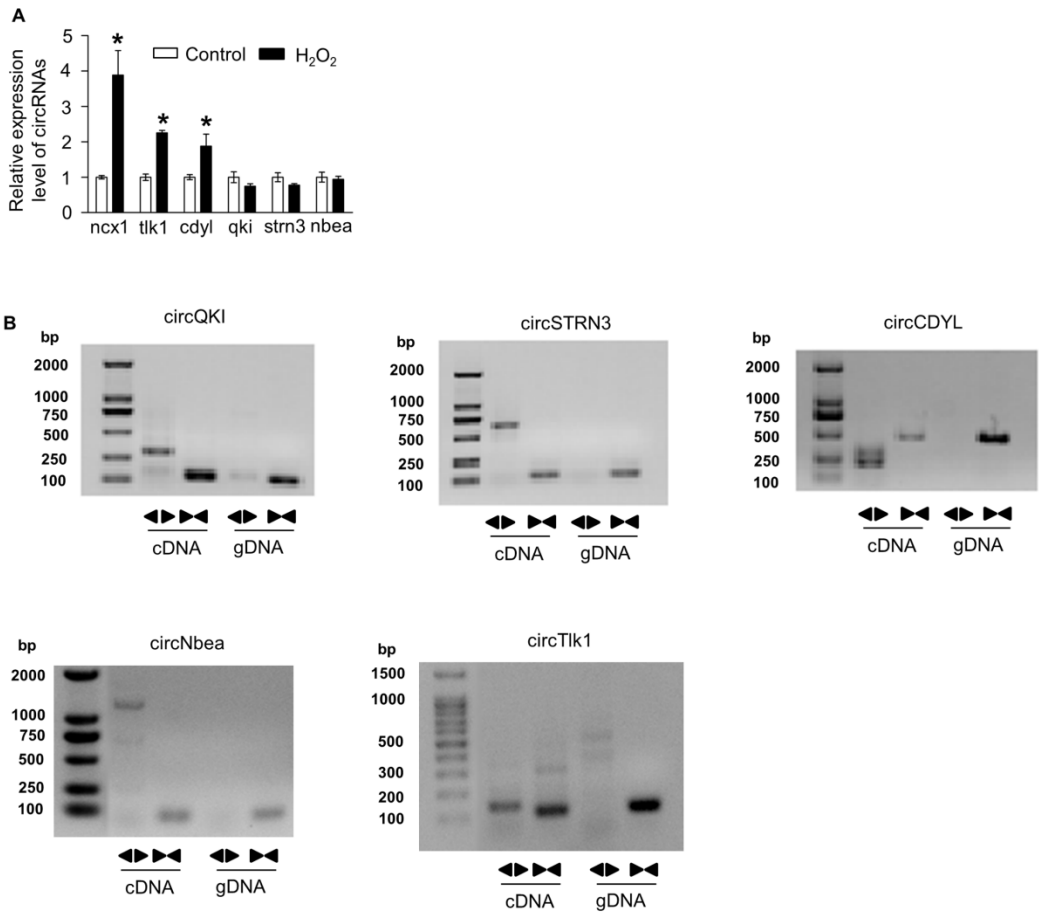
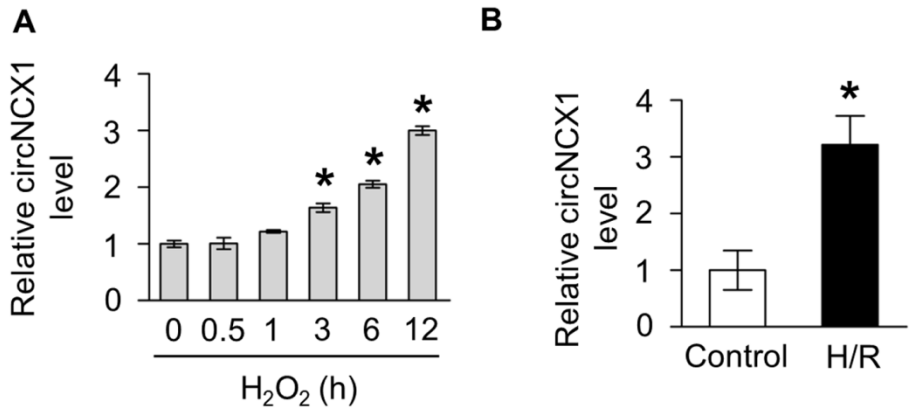


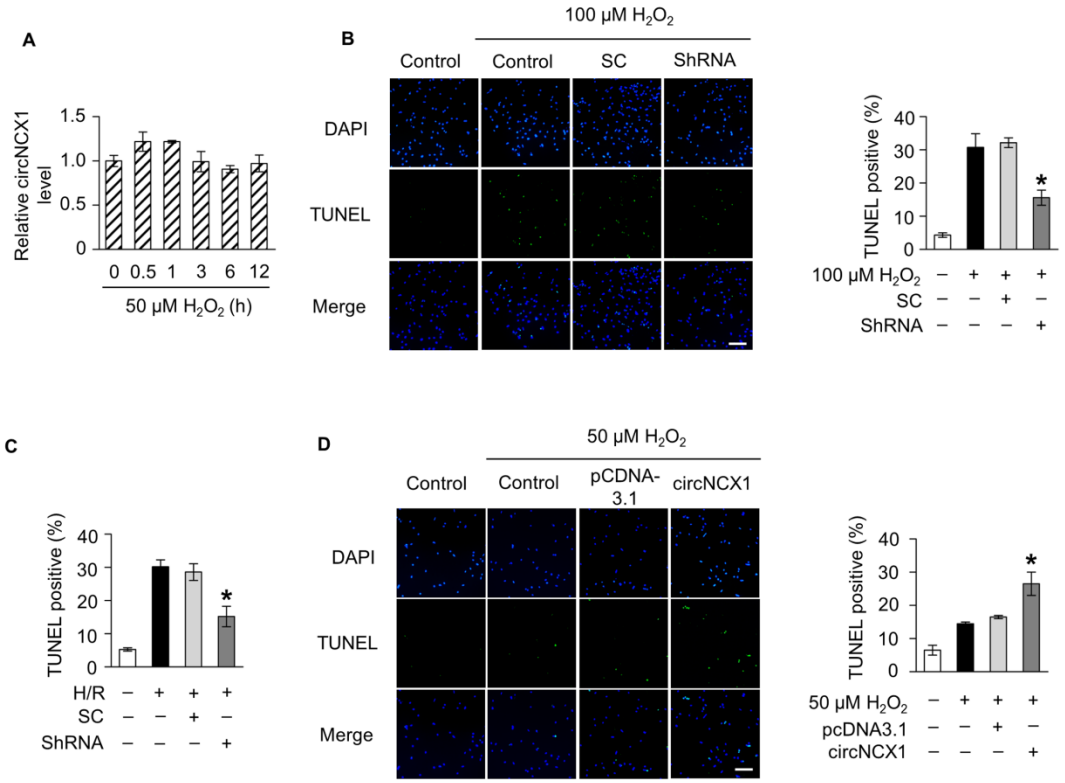
Supplementary Figure 1. (A) H9c2 cells were treated with 100 μM H_2O_2 for 12 h. Total RNAs were isolated and reverse-transcribed. The expression level of circRNAs was analyzed by qRT-PCR. GAPDH was selected as reference. *P < 0.05 versus 0 h. n=3. **(B)** The detail of verification of other circRNAs in mice myocardial tissue**.** Their head-to-tail junction parts were amplified by divergent PCR.

Supplementary Figure-2



Supplementary Figure 2. (A) Neonatal rat cardiomyocytes were treated with 100 μM H_2O_2. The expression level of circNCX1 was analyzed by qRT-PCR. *P < 0.05 versus 0 h. n=3. **(B)** Neonatal rat cardiomyocytes were treated with H/R. The expression level of circNCX1 was analyzed by qRT-PCR. *P < 0.05 versus control.

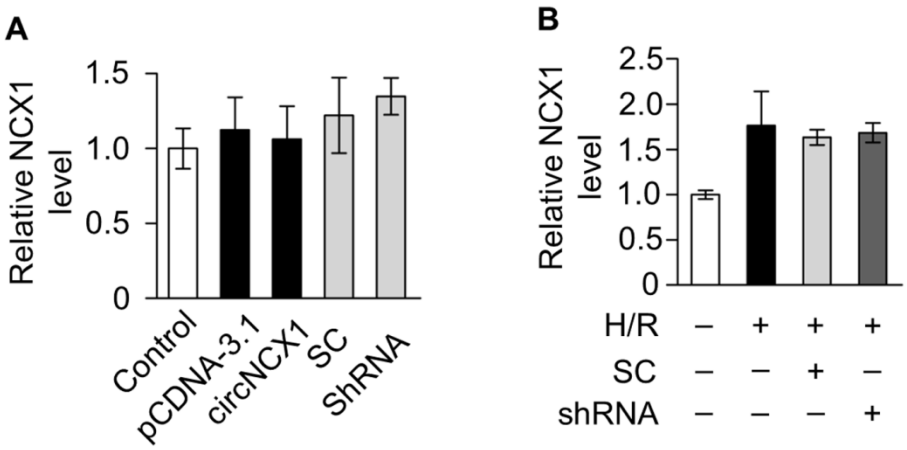
Supplementary Figure-3



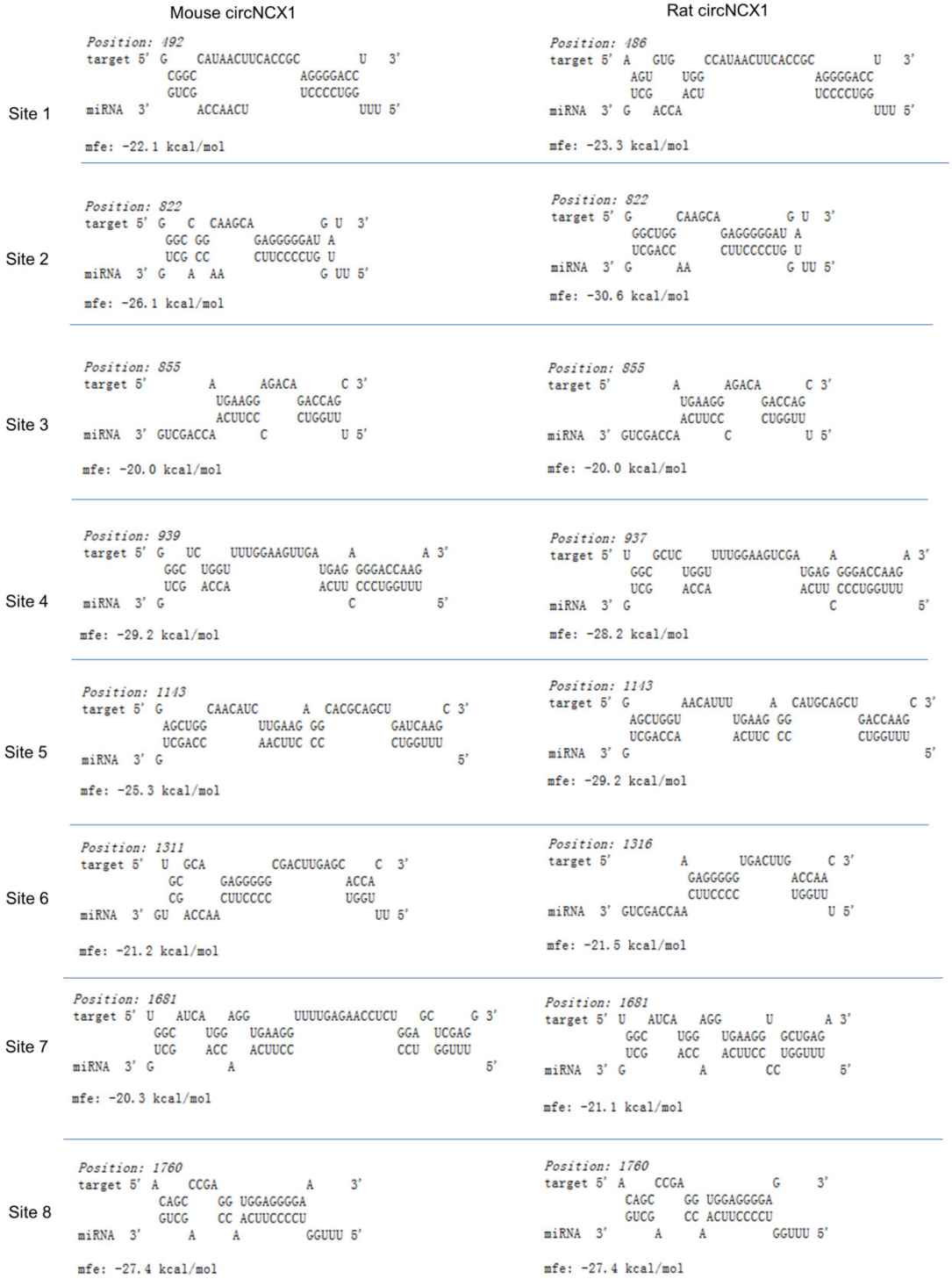
Supplementary Figure 3. (A) H9c2 cells were treated with 50 μM H_2O_2. The expression level of

circNCX1 was analyzed by qRT-PCR. n=3. **(B)** Neonatal rat cardiomyocytes were transfected with shRNA vector and treated by 100 μM H_2O_2 for 12h. Cell apoptosis was analyzed by TUNEL assay. Scale bars, 50 μm. *P < 0.05 versus SC. n=3. **(C)** Neonatal rat cardiomyocytes were transfected with shRNA vector and treated with H/R. Cell apoptosis was analyzed by TUNEL assay. *P < 0.05 versus SC. n=3. **(D)** Neonatal rat cardiomyocytes were transfected with circNCX1 expression vector and treated with 50 μM H_2O_2 for 12 h. Cell apoptosis was analyzed by TUNEL assay. *P < 0.05 versus pCDNA 3.1. n=3.

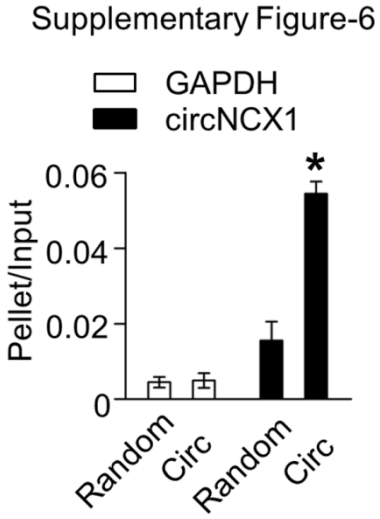
Supplementary Figure-4



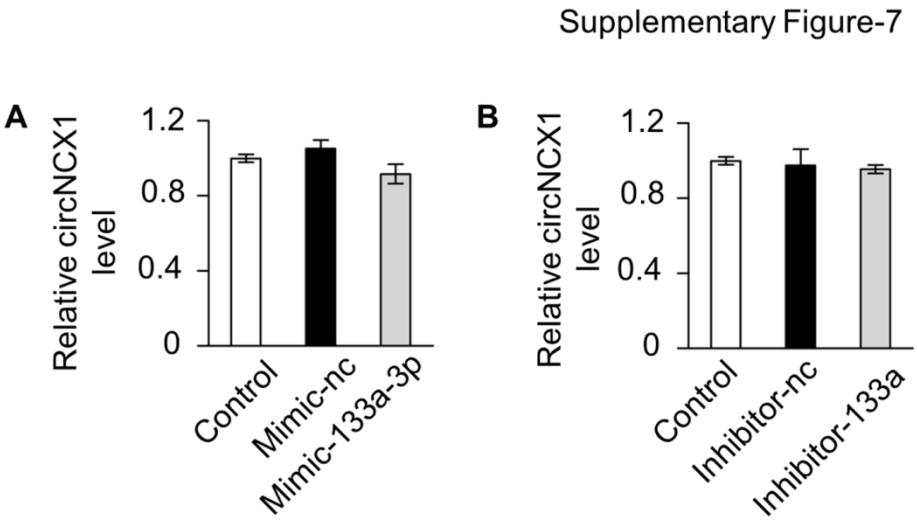
Supplementary Figure 4. (A) H9c2 cells were transfected with shRNA vector or circNCX1 expression vector. The expression levels of NCX1 mRNAs was analyzed by qRT-PCR. n=3. **(B)** H9c2 cells were transfected with shRNA vector and treated with H/R. The expression levels of NCX1 mRNAs was analyzed by qRT-PCR. n=3.



Supplementary Figure 5. Detail of the putative miR-133a-3p binding sites in mouse and rat circNCX1 sequences.

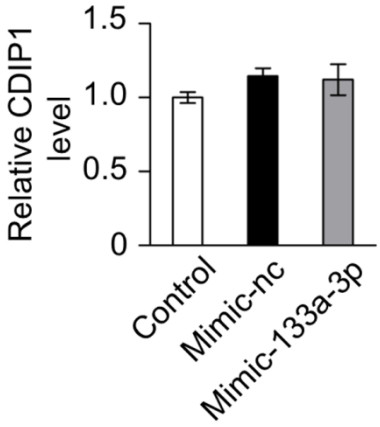


Supplementary Figure 6. Lysates of H9c2 cells were incubated with probe-coated beads. The captured RNAs were purified. The level of captured circNCX1 was analyzed by qRT-PCR. GAPDH mRNA was selected as a negative control. Pellet/Input was calculated. *P < 0.05 versus Random. n=3.



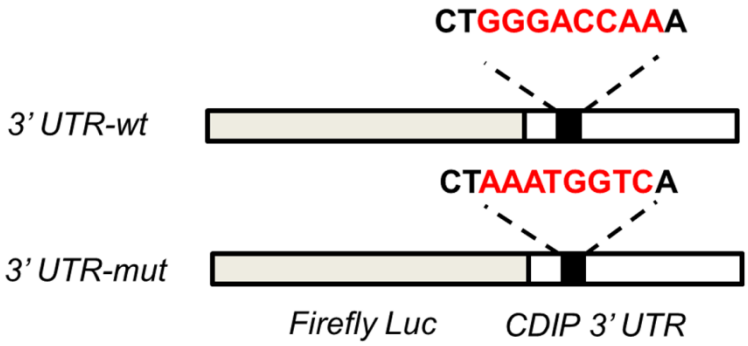
Supplementary Figure 7. H9c2 cells were transfected with miR-133a-3p mimics **(A)** or miR-133a-3p inhibitor **(B)**. The expression level of circNCX1 was analyzed by qRT-PCR. n=3.

Supplementary Figure-8



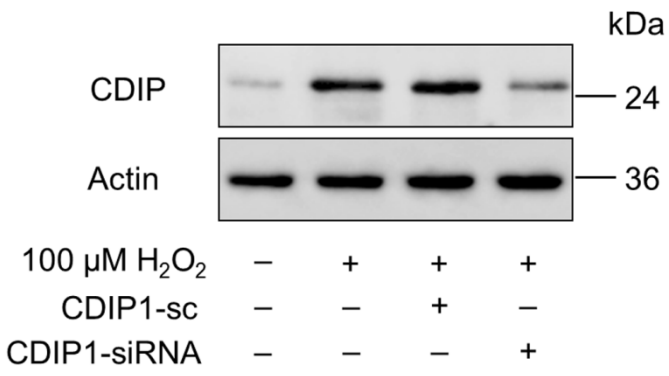
Supplementary Figure 8. H9c2 cells were transfected with miR-133a-3p mimics or control mimics. CDIP1 mRNA level was analyzed by qRT-PCR. n=3

Supplementary Figure-9



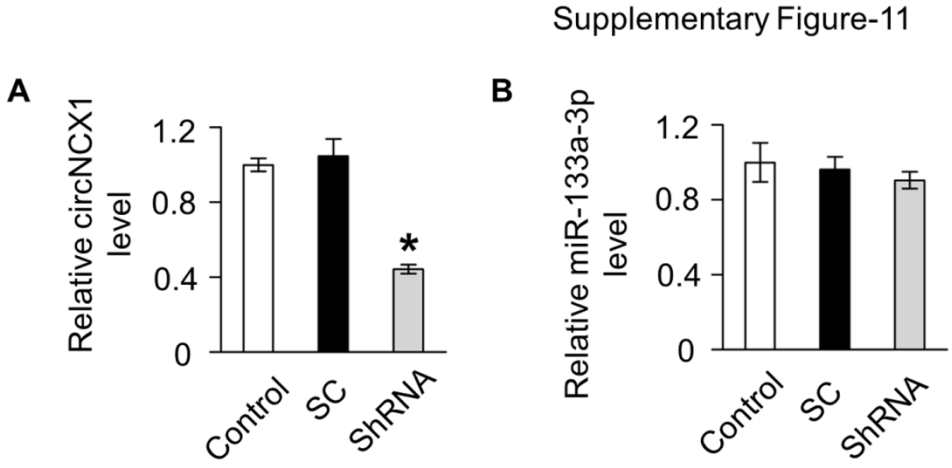
Supplementary Figure 9. Detail of the mutation of CDIP1 3' UTR.

Supplementary Figure-10



Supplementary Figure 10. H9c2 cells were transfected with CDIP1 siRNA or control oligo. Cells

were treated with 100 μM H_2O_2 for 12 h. CDIP1 level was analyzed by western-blot.



Supplementary Figure 11. Mice hearts were infected by adenovirus harbored shRNA. The expression level of circNCX1 **(A)** or miR-133a-3p **(B)** in mice hearts was analyzed by qRT-PCR. n=3. *P < 0.05 versus SC.