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Supplemental Information

**Adeno-associated virus-mediated delivery
of anti-miR-199a tough decoys attenuates
cardiac hypertrophy by targeting *PGC-1alpha***

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Table S1. Echocardiographic assessment of each mice group.

	AAV9-EGFP	AAV9-EGFP + ISO	AAV9-anti-miR-199a TuDs + ISO
LVIDd, mm	3.22±0.16	4.06±0.26**	3.30±0.13##
LVIDs, mm	1.87±0.18	2.78±0.22**	1.90±0.18##
LVEDV, μ L	41.82±5.10	72.84±10.94**	44.25±4.36##
LVESV, μ L	10.86±2.61	29.31±5.78**	11.35±2.59##
LVEF, %	80.84±6.39	59.92±7.71**	70.05±3.19##
LVFS, %	48.58±6.43	31.69±4.96**	38.73±2.54##
number of mice	8	8	8

Abbreviation: LVIDd, left ventricular internal dimension in diastole; LVIDs, left ventricular internal dimension in systole; LVEDV, left ventricular end-diastolic volume; LVESV, left ventricular end- systolic volume; LVEF, left ventricular ejection fraction; LVFS, left ventricular fractional shortening. *: $P<0.05$, **: $P<0.01$, AAV9- EGFP+ISO vs. AAV9-EGFP; #: $P<0.05$, ## $P<0.01$, AAV9-anti-miR-199a TuDs +ISO vs. AAV9-EGFP +ISO.

Table S2. The primer sequences for RT-qPCR

Target genes	Primer sequences (5'-3')
<i>Nppa</i> (ANP)	Forward: GGGCTCCTTCTCCATCACC Reverse: CTCCAATCCTGTCAATCCTACC
<i>Nppb</i> (BNP)	Forward: CTGAAGGTGCTGTCCCAGAT Reverse: GTTCTTTTGTGAGGCCTTGG
<i>Myh7</i> (β -MHC)	Forward: CTCAGAGCTCAAGCGGGATA Reverse: CCAGCCATCTCCTCTGTCA
<i>Acta1</i>	Forward: CAAAGACAAGCTGTGCTACGTG Reverse: GATGCTGTTGTAGGTGGTCTCA
<i>Rps27a</i>	Forward: ACTCCCAAGAAGAACAAGCATA Reverse: CAGTAAGTCAGACAACACTTGC
<i>Rpl23</i>	Forward: GGATTTCCCTGGGTCTTCCG Reverse: TTCAGCCGTCCCTTGATTCC
<i>Mrps21</i>	Forward: ATAAGTCGACGACGCTACTATG Reverse: GCCATTTCCATGTTGTAGATCC
<i>Mrpl14</i>	Forward: GAATGACCCCAAAGTTTGACTC Reverse: GCTGGTCGGGATAGGTATTTTA
<i>Ndufa6</i>	Forward: CTTAATGCAGCTGGATATCACG Reverse: TTCCCTTAATGACCAGCAGAT
<i>Ndufb3</i>	Forward: CCCGAGGGCTGAGGGAT Reverse: TGCAAAGCCGCCCATG
<i>Ndufb7</i>	Forward: GCCGGACCTCGGCTTT Reverse: CTGGGCATCCATCATCTCTTG
<i>Sdhb</i>	Forward: CGCTGCCACACCATCATG Reverse: TTTCCGCAATCGCTTTCC
<i>Uqcrrh</i>	Forward: AGGACGAACGAAAGATGCTCACTG Reverse: CGGGCCTTTACACACTTCTCCAG
<i>Uqcrrq</i>	Forward: CGTTTGTAGTGGTCTACCTGAT Reverse: ATACATGGCTGGATTCTTCCTT
<i>Cox4i1</i>	Forward: TACTTCGGTGTGCCTTCGA Reverse: TGACATGGGCCACATCAG
<i>Atp5l</i>	Forward: TGCTGAAATCCCTACAGCTATT Reverse: GCACAGCTTCCTTAACTGTAAG
<i>Ppard</i>	Forward: TGGAGCTCGATGACAGTGAC Reverse: GTECTGGCTGTCAGGGTGGT
<i>Ppara</i>	Forward: ATGCCAGTACTGCCGTTTTTC Reverse: GGCCTTGACCTTGTTTCATGT
<i>Ppargc1a</i> (<i>Pgc1a</i>)	Forward: GGATATACTTTACGCAGGTCGA Reverse: CGTCTGAGTTGGTATCTAGGTC
<i>Cd36</i> (<i>Fatp</i>)	Forward: GAGCCTTCACTGTCTGTTGGAA Reverse: CTGCTACAGCCAGATTCAGAAC
<i>Cpt1b</i>	Forward: GGCACCTCTTCTGCCTTTAC

	Reverse: TTTGGGTCAAACATGCAGAT
<i>Acox1</i>	Forward: GGGAGTGCTACGGGTTACATG
	Reverse: CCGATATCCCCAACAGTGATG
<i>Acadm</i>	Forward: GATGCATCACCCCTCGTGTAAC
	Reverse: AAGCCCTTTTCCCCTGAA
<i>Acadvl</i>	Forward: TTACATGCTGAGTGCCAACATG
	Reverse: CGCCTCCGAGCAAAAGATT
<i>Esrra(ERRα)</i>	Forward: GGCACAAGGAGGAGGAGGATGG
	Reverse: AGGCAGAGGCGTTTGGGTAGAG
<i>Gsk3b</i>	Forward: TGGTAGCATGAAAGTTAGCAGA
	Reverse: CTCTCGGTTCTTAAATCGCTTG
<i>Slc2a1(Glut1)</i>	Forward: GAAGAAGGTCACCATCTTGGAG
	Reverse: CGAAGATGCTCGTTGAGTAGTA
<i>Slc2a4(Glut4)</i>	Forward: TATTCAACCAGCATCTTCGAGT
	Reverse: GTCCAGCTCGTTCTACTAAGAG
<i>Hk1</i>	Forward: AGTGGAAGCCAGCTTTTTGA
	Reverse: TTCAGCAGCTTGACCACATC
<i>Gapdh</i>	Forward: TGTGTCCGTCGTGGATCTGA
	Reverse: CCTGCTTCACCACCTTCTTGA

Abbreviation: Nppa, natriuretic peptide type A; Nppb, natriuretic peptide type B; Myh7, myosin heavy chain 7; Acta1, actin alpha 1, skeletal muscle; Rps27a, ribosomal protein S27A; Rpl23, ribosomal protein L23; Mrps21, mitochondrial ribosomal protein S21; Mrpl14, mitochondrial ribosomal protein L14; Ndufa6, NADH:ubiquinone oxidoreductase subunit A6; Ndufb3, NADH:ubiquinone oxidoreductase subunit B3; Ndufb7, NADH:ubiquinone oxidoreductase subunit B7; Sdhb, succinate dehydrogenase complex, subunit B, iron sulfur (Ip); Uqcrh, ubiquinol-cytochrome c reductase hinge protein; Uqcrcq, ubiquinol-cytochrome c reductase, complex III subunit VII; Cox4i1, cytochrome c oxidase subunit 4I1; Atp5l, ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit G; Ppard, peroxisome proliferator activated receptor delta; Ppara, peroxisome proliferator activated receptor alpha; Ppargc1a, peroxisome proliferative activated receptor, gamma, coactivator 1 alpha; Cd36, also known as fatty acid translocase (FAT); Acox1, acyl-Coenzyme A oxidase 1, palmitoyl; Acadm, acyl-Coenzyme A dehydrogenase, medium chain; Acadvl, acyl-Coenzyme A dehydrogenase, very long chain; Slc2a1, solute carrier family 2 member 1, also known as glucose transporter 1 (Glut1); Slc2a4, solute carrier family 2 member 4, also known as glucose transporter 4 (Glut4); Hk1, hexokinase 1; Gapdh, glyceraldehyde-3-phosphate dehydrogenase; Esrra, estrogen related receptor alpha; Gsk3b, glycogen synthase kinase 3 beta.

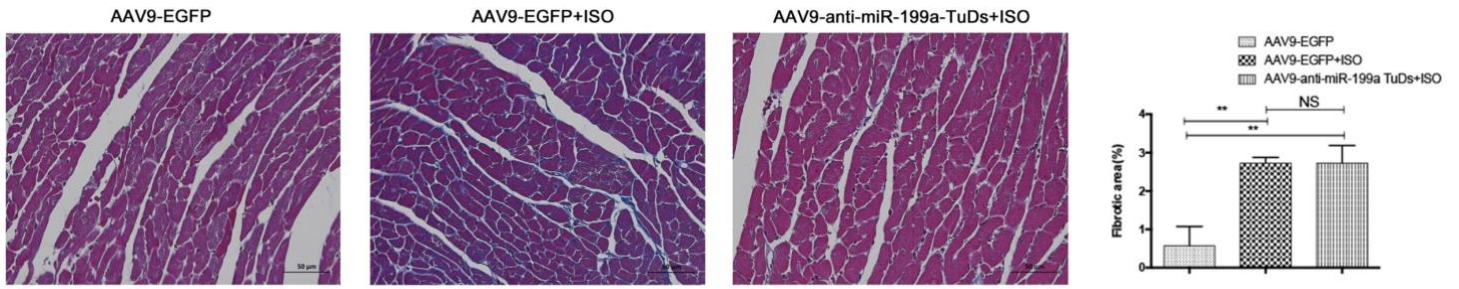


Figure S1. Masson staining of cardiac fibrosis of cardiomyocyte in each group. Bars, 50 μ m. Fibrosis ratio is calculated by the ratio of the blue-stained interstitial fibrotic areas and the red-stained whole cardiomyocyte area. *: $P < 0.05$, **: $P < 0.01$, NS, not significant.

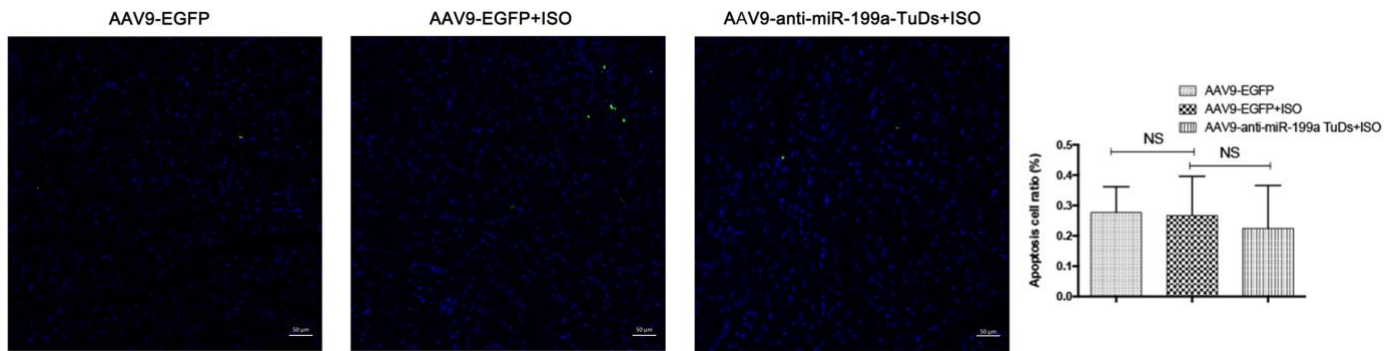


Figure S2. TUNEL detection of apoptosis of cardiomyocyte in each group. Blue, DAPI staining of nuclei; Green, cell apoptosis detected by TUNEL kit. Bars, 50 μ m. Apoptosis cell ratio is calculated by the ratio of TUNEL positive cells and DAPI cells. TUNEL, terminal deoxynucleotidyl transferase-mediated nick-end labeling; NS, not significant.

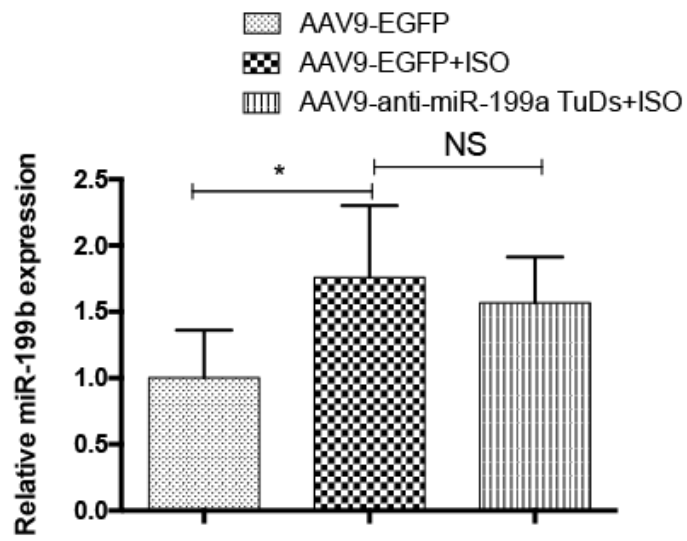


Figure S3. miR-199b expression level detected by real-time PCR. * $P < 0.05$.

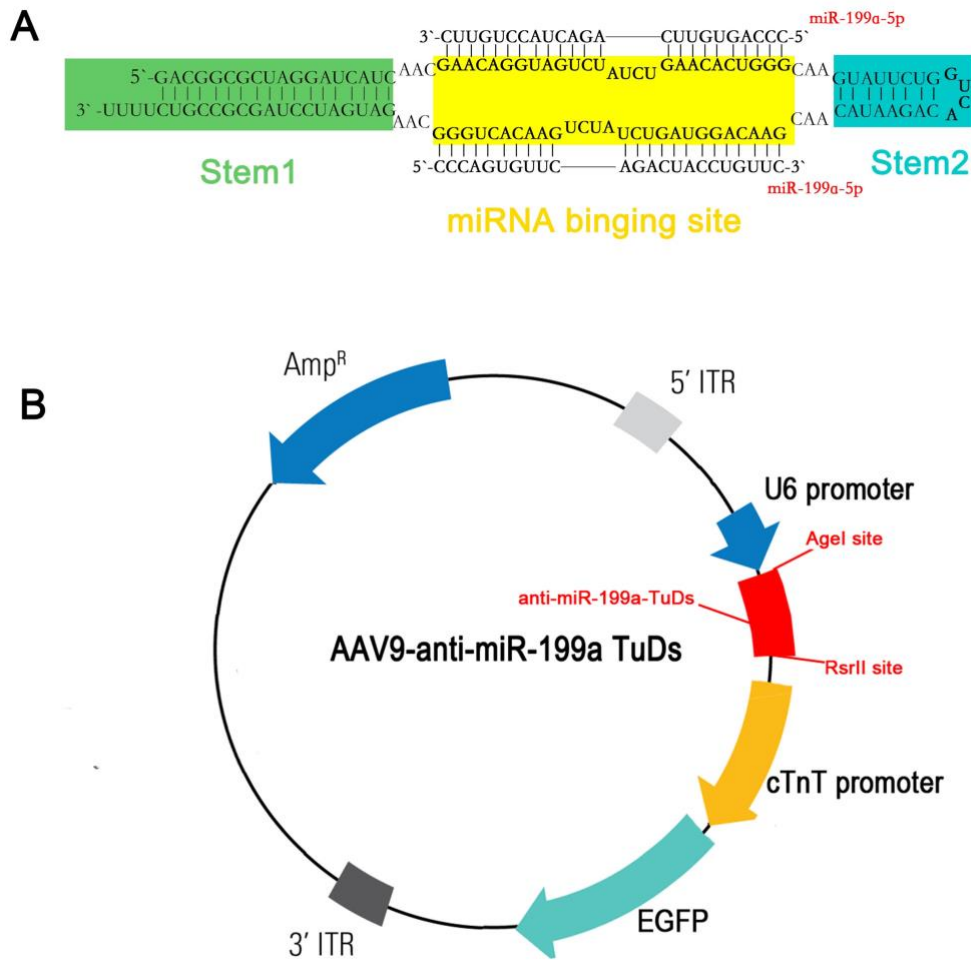


Figure S4. Schematic diagram of AAV9-anti-miR-199a TuDs plasmid. (A) the harpin structure of anti-miR-199a TuDs insert contains two single-stranded miR-199a-5p binding sites (yellow sequences) and two double-stranded stems (green and blue sequences). (B) AAV9-anti-miR-199a TuDs plasmid harbors the U6 promoter and the chicken cardiac TNT promoter, to generate anti-miR-199a TuDs and EGFP, respectively. ITR, inverted terminal repeat. TuDs, tough decoys.