Expanded View Figures

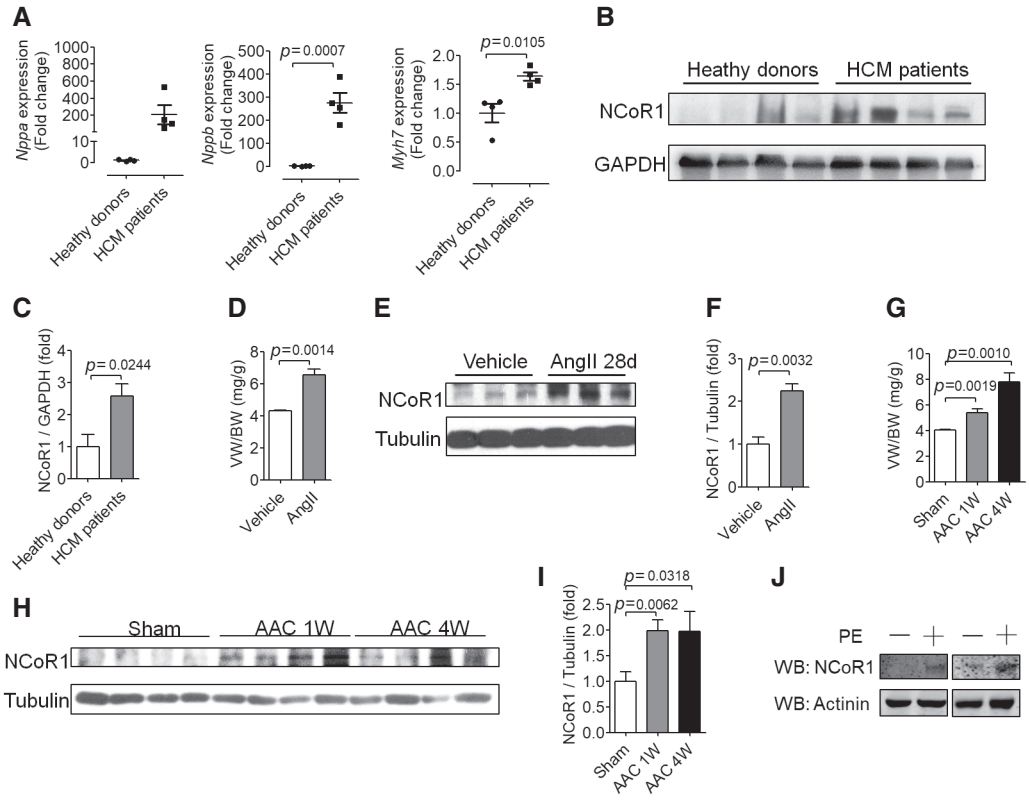

Figure EV1. The expression of nuclear receptor corepressor 1 (NCoR1) is elevated in hypertrophied hearts or cardiomyocytes.

A Quantitative reverse transcriptase polymerase chain reaction (qRT–PCR) analysis of hypertrophy-related genes in heart samples from healthy donors or hypertrophic cardiomyopathy (HCM) patients. *n* = 4:4. *Nppa*, *natriuretic peptide type A*; *Nppb*, *natriuretic peptide type B*; *Myh7*, *myosin, heavy polypeptide 7, cardiac muscle, beta*.

B Western blotting analysis of NCoR1 in heart samples from healthy donors or HCM patients.

C Quantification of (B). *n* = 4:4.

D Ventricular weight-to-body weight ratio (VW/BW) of C57BL/6 mice infused with vehicle (0.9% NaCl) or angiotensin II (AngII) for 4 weeks. *n* = 3:3.

E Western blotting analysis of NCoR1 in ventricular samples from mice shown in (D).

F Quantification of (E). *n* = 3:3.

G VW/BW of C57BL/6 mice subjected to sham operation or abdominal aortic constriction (AAC) for 1 or 4 weeks. *n* = 4:4:4.

H Western blotting analysis of NCoR1 in ventricular samples from mice shown in (G).

I Quantification of (H). *n* = 4:4:4.

J Western blotting analysis of NCoR1 in neonatal rat ventricular myocytes treated without or with phenylephrine (PE) for 24 h.

Data information: Data are presented as mean ± SEM. Student's *t*-test was used for statistical analysis.
Source data are available online for this figure.

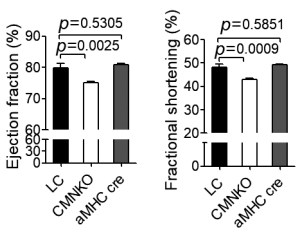

Figure EV2. αMHC-Cre did not affect cardiac function in 10-month-old mice.

Ejection fraction and fractional shortening measured by echocardiography. LC, littermate control mice; CMNKO, cardiomyocyte-specific NCoR1 knockout mice. *n* = 9:11:7. Data are presented as mean ± SEM. Student's *t*-test was used for statistical analysis.

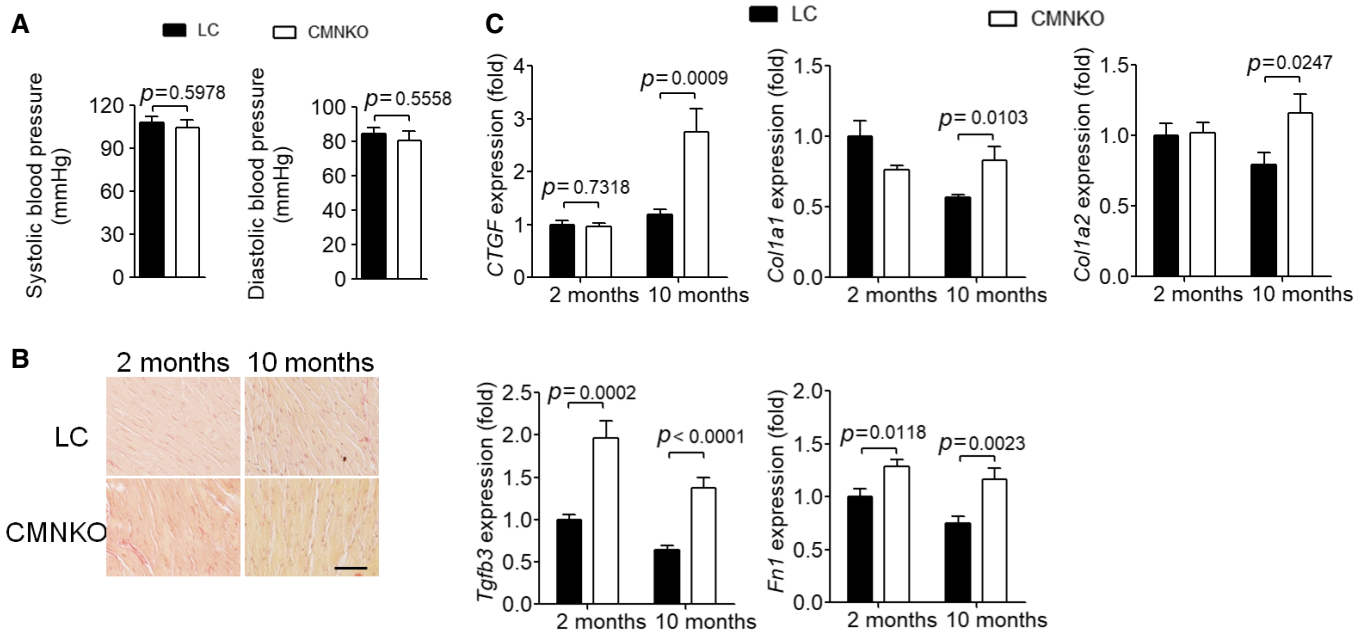

Figure EV3. NCoR1 deficiency in cardiomyocytes does not affect blood pressure or cardiac fibrosis.

A Systolic blood pressure and diastolic blood pressure were monitored using non-invasive tail-cuff system in 2-month-old mice. n = 6:6.

B Picrosirius red staining of cross sections of left ventricles of LC or CMNKO mice. Scale bar: 50 μm.

C qRT–PCR analysis of fibrosis-related genes in left ventricles of LC or CMNKO mice. n = 9:9:11:8. CTGF indicates connective tissue growth factor precursor; Fn1, fibronectin 1; TGFβ3, transforming growth factor β 3; Col1a1, collagen, type I, alpha 1; Col1a2, collagen, type I, alpha 2.

Data information: Data are presented as mean ± SEM. Student's t-test was used for statistical analysis.

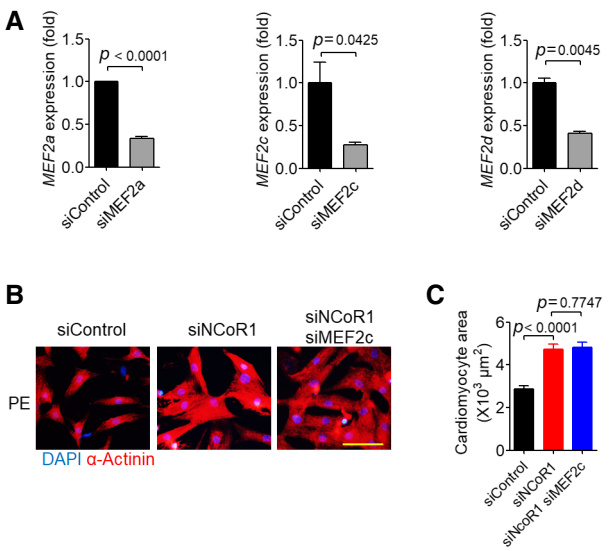

Figure EV4. MEF2c does not mediate the effects of NCoR1 on PE-induced cardiomyocyte hypertrophy.

A Knockdown efficiency of MEF2a, MEF2c, and MEF2d in NRVMs. siControl indicates control siRNA; siMEF2a indicates MEF2a siRNA; siMEF2c, MEF2c siRNA; siMEF2d, MEF2d siRNA. n = 3.

B Representative immunofluorescence staining of α-Actinin in NRVMs transfected with siRNA for 48 h and then treated with PE for another 48 h. Scale bar: 50 μm.

C Quantification of the surface area of α-Actinin-positive NRVMs with or without knockdown of NCoR1 and/or MEF2c. A total of 30 NRVMs were randomly chosen from three replicate coverslips for each group and used for statistical analysis.

Data information: Data represent three independent experiments. Data are presented as mean ± SEM. Student's t-test was used for statistical analysis.

Figure EV5. NCoR1 affects subcellular translocation of HDACs but does not directly interact with them in NRVMs.

A Representative immunofluorescence staining of HDAC4-GFP in NRVMs. Cells were infected by HDAC4-GFP adenovirus and then control lentivirus (Control) or NCoR1-flag lentivirus (NCoR1-OV), and subsequently treated with vehicle (H_2O) or PE. Scale bar: 20 μm.

B Quantification of cytosolic accumulation of HDAC4-GFP. $n = 5$.

C Representative immunofluorescence staining of HDAC5-GFP in NRVMs. Cells were infected by HDAC5-GFP adenovirus and then control lentivirus (Control) or NCoR1-flag lentivirus (NCoR1-OV), and subsequently treated with vehicle or PE. Scale bar: 20 μm.

D Quantification of cytosolic accumulation of HDAC5-GFP. $n = 5$.

E Co-IP analysis detecting interactions between NCoR1 and HDAC4, HDAC5 or HDAC9 in NRVMs. Cells were infected with NCoR1-flag lentivirus and then HDAC4 adenovirus, HDAC5-GFP adenovirus, or HDAC9 adenovirus.

F Co-IP analysis showing interactions between NCoR1, MEF2a, and HDAC4 in ventricular samples.

G Co-IP analysis detecting interactions between NCoR1, MEF2a, and HDAC5 in NRVMs. Cells were infected with NCoR1-flag lentivirus and then MEF2a-HA lentivirus and HDAC5-GFP adenovirus.

Data information: Data represent three independent experiments. Data are presented as mean ± SEM. Two-way ANOVA followed by Bonferroni post-tests was used for statistical analysis.
Source data are available online for this figure.

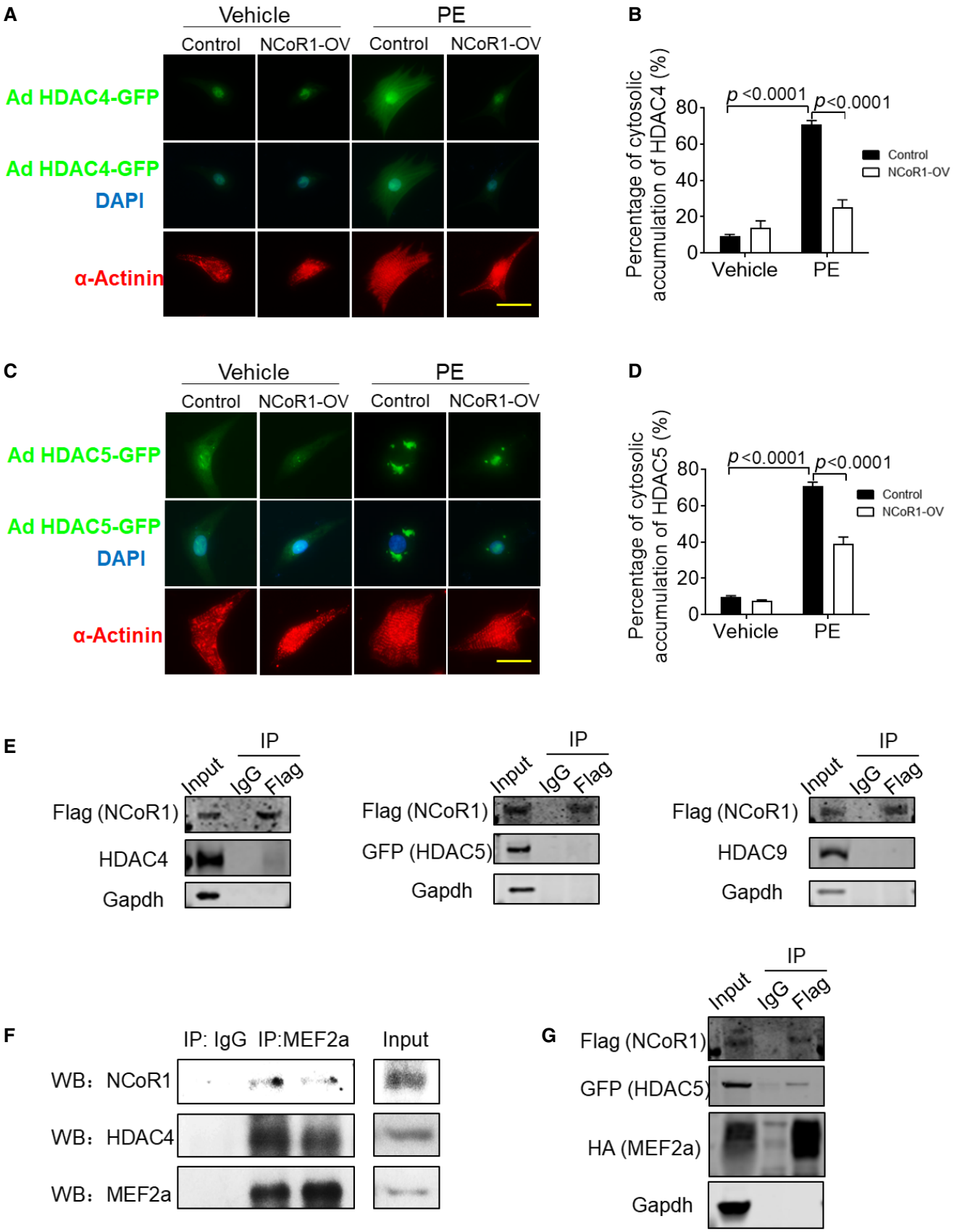

Figure EV5.