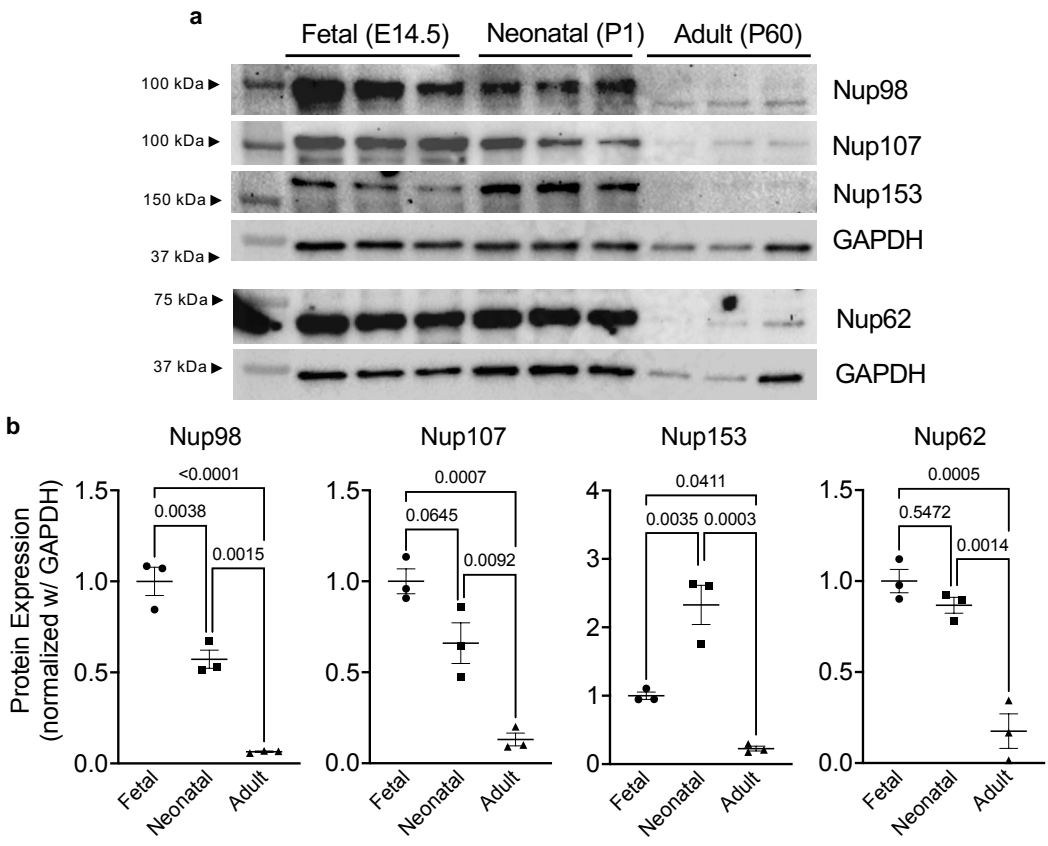
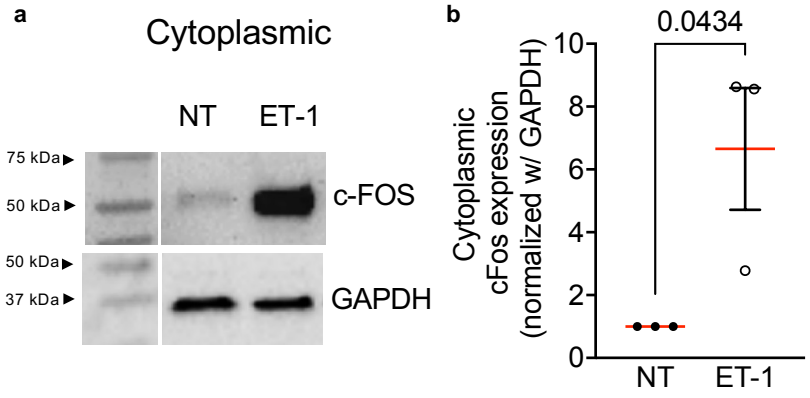
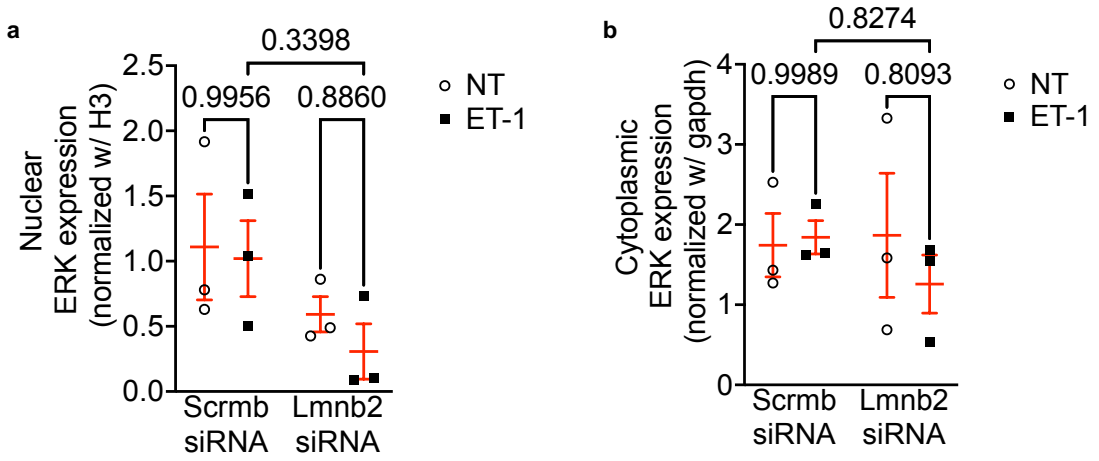


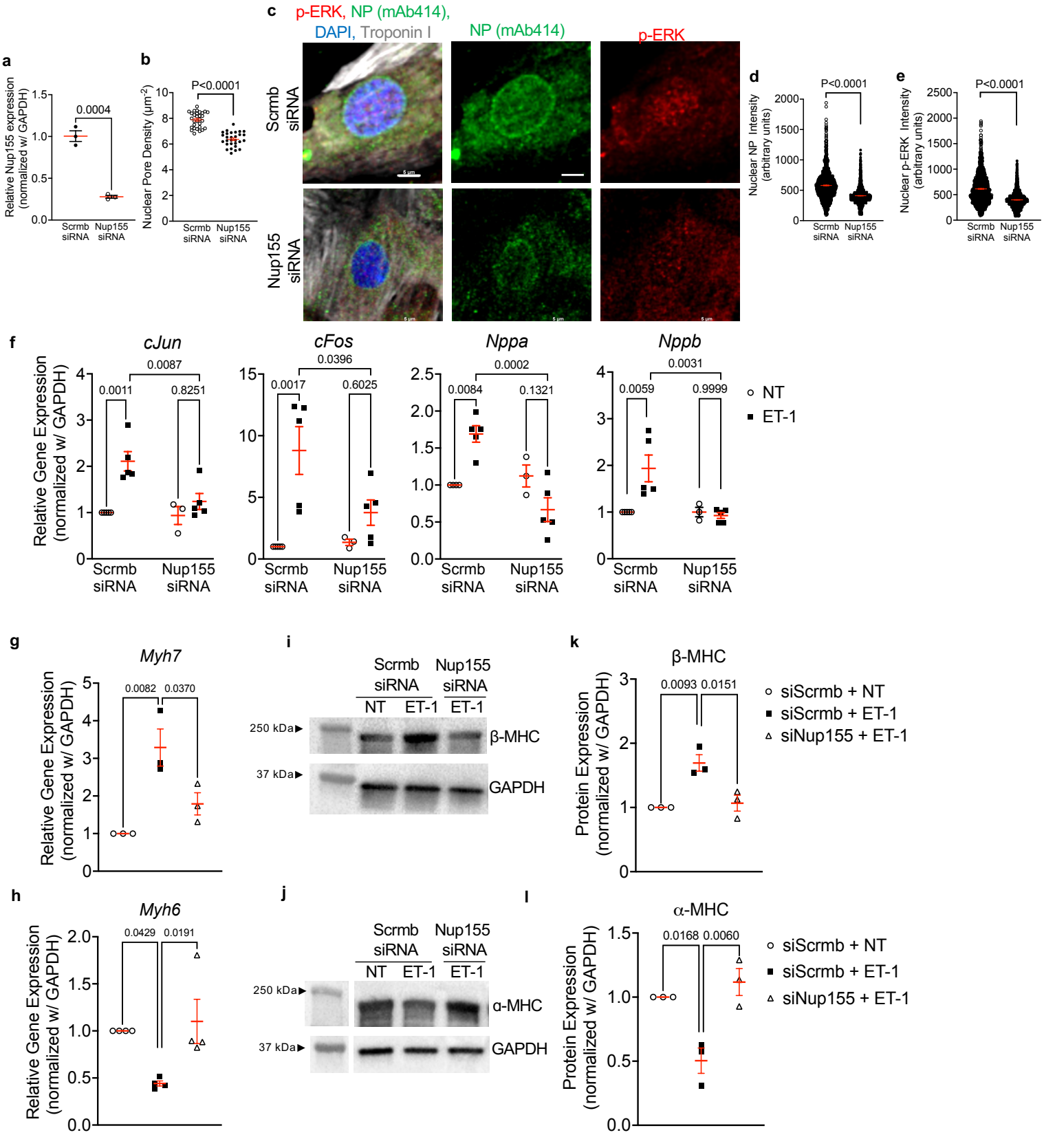
Supplemental Figure S1. Representative Western blots and summary data of protein expression of selected nucleoporins (Nup) in rat cardiomyocytes at indicated developmental stages. Corresponding to Figure 1. GAPDH was served as loading control.



Supplemental Figure S2. c-FOS expression is upregulated by ET-1 stimulation in the cytoplasmic fraction. Corresponding to Figure 5. Representative Western blots and summary data of level of c-FOS in the cytoplasmic fraction of neonatal rat cardiomyocytes in the presence and absence of ET-1 (100 nM for 30 mins). NT: no treatment. GAPDH served as loading control.



Supplemental Figure S3. Quantification of Western blots of total ERK in nuclear and cytoplasmic fractions. Corresponding to Figure 4j. Neonatal rat ventricular cardiomyocytes (NRVM) control (Scrmb = scrambled) and Lmnb2 knockdown (Lmnb2 siRNA), both at baseline (No treatment: NT) and stimulation with ET-1 (100 nM, 30 min). Histone H3 served as loading control for nuclear fraction, and GAPDH served as loading control for cytoplasmic fraction. Representative blots are shown in **Fig. 4j**. No significant difference among groups were detected.



Supplemental Figure S4. Decreasing nuclear pore (NP) numbers by suppressing *Nup155* expression reduces nuclear import of ERK and expression of stress genes in neonatal rat ventricular myocytes. Corresponding to Figure 4. (**a**) *Nup155* mRNA level was effectively decreased by *Nup155* siRNA in NRVMs. Real-time PCR quantified *Nup155* mRNA, normalized to *GAPDH*, and graphed as percent of scrambled siRNA. (**b**) NPs were detected with mAb414 and visualized with confocal microscopy. Quantification shows that *Nup155* knockdown decreases NP area density in nuclei of NRVMs. Each symbol represents one nucleus. Two independent experiments with n=30 for scrambled siRNA; n=29 for *Nup155* siRNA. (**c**) Immunofluorescence microscopy shows *Nup155* siRNA knockdown decreases NP and p-ERK intensity in nuclear envelope of NRVMs. Scale bar 5 μm. (**c, d**) Quantitative analysis of photomicrographs shows lower NP (**d**) and nuclear p-ERK (**e**) with *Nup155* knockdown. Each symbol represents one cardiomyocyte nucleus (3 independent experiments). (**f-h**) RT-PCR shows that *Nup155* siRNA reduces ET-1-stimulated (100 nM) stress gene and hypertrophic gene (*Myh7, Myh6)* mRNA levels. (**i, j**) Representative Western blots of β-MHC and α-MHC stimulated with ET-1 (100 nM, 24 hrs) in the presence and absence of *Nup155* siRNA. Results from one of three independent experiments shown. (**k, l**) Corresponding quantifications of Western blots. Statistical tests: t-test (**a,b, d, e**), ANOVA (**f-h, k, l**).