Supplementary Data



Supplementary Figure 1. A summary of the comparison of the fetal gene expression among the sham surgery control groups. Total RNA was isolated from LV myocardium at 2 wk after TAC or sham surgery. Quantitative RNA dot blot analysis was utilized to assess the transcript levels of atrial natriuretic factor (ANF), β -myosin heavy chain (β -MyHC), skeletal α actin (s-Actin), α -MyHC, sarcoplasmic endoplasmic reticulum calcium ATPase 2A (SERCA), phospholamban (PLN), and GAPDH using ³²P-labeled transcript-specific oligonucleotide probes. The bound radioactive signal was captured by a phosphor-imaging screen and detected and quantified using an FX Personal Molecular Imager (BioRad). The composed RNA dot blot images are shown in Figure 2A of main text. Each dot represents an individual animal. After normalizing to the corresponding GAPDH signal, the mean intensity value of the NTG sham group was set at 100 arbitrary units (AU). The intensity signal of each individual dot was then normalized to the mean of the NTG sham. The resultant intensity of each of the 3 animals from the same group was used to derive the mean and standard deviation (error bar) and presented in subsequent panels. Compared with the NTG sham group, no changes were detected in the TG sham group but significant increases in ANF, β-MyHC, and s-Actin and decreases in PLN were detected in the KO sham group. ¶: P<0.05, *: P<0.001, vs NTG and TG; One way ANOVA.



shown in panel **A**. Each dot represents an individual animal. After normalizing to the corresponding GAPDH signal, the mean intensity value of the wild type (WT) group was arbitrarily set at 100 arbitrary units (AU). The intensity signal of each individual dot is then normalized to the mean of the WT. The resultant AU value of each of the 3 animals from the same group was used to derive the mean and standard deviation (error bar) and presented in panel **B**. Compared with the WT, *: P < 0.05, **: P < 0.001; unpaired t-test were used.

Supplementary Table 1. Baseline Characterization of CryAB TG and CryAB/HSPB2 KO

	NTG	TG	КО
Echocardiography			
Heart rate (bpm)	490±46	459±45	462±32
LVIDd (mm)	3.77±0.18	3.56±0.18	3.57±0.26
LVIDs (mm)	2.37±0.19	2.18±0.18	2.29±0.24
LVPWd (mm)	0.76±0.04	0.73±0.09	$0.92{\pm}0.04^{*}$
FS (%)	37.1±2.7	38.6±3.7	36.1±3.4
EF (%)	67.8±3.5	69.8±4.6	66.5±4.6
LV pressure			
LVSP (mmHg)	90.7±4.6	85.4±12.4	90.3±12.3
LVEDP (mmHg)	5.5±1.0	4.7±2.4	18.3±2.9*
+dP/dt _{max} (mmHg/s)	8620±1406	7742±1246	9101±1242
-dP/dt _{max} (mmHg/s)	7673±860	7888±1301	6196±1065 [†]
Gravimetry			
Body weight (BW, g)	27.5±2.5	30.4±3.3	25.3±2.2
Heart weight (HW, g)	123.7±8.4	132.5±7.8	131.7±13
HW/BW (mg/g)	4.52±0.4	4.38±0.2	5.24±0.7 [†]
Lung/BW (mg/g)	5.4±0.6	5.3±0.5	5.4±0.5
Liver/BW (mg/g)	46.0±3.0	42.6±2.2	46.2±5.0
Kidney/BW (mg/g)	13.8±0.2	14.7±0.9	14.3±1.8

Mice at 10 Weeks of Age

Compared with NTG, [†]: p<0.05; *: p<0.01.

Supplementary Table 2	Baseline	Characterization	of CryAB/HSP	B2 KO Mice at 18
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Weeks of Age

	NTG	КО	
Echocardiography	N=11	N=11	
Heart rate (bpm)	473±31	472±26	
LVIDd (mm)	3.81±0.23	3.90±0.23	
LVIDs (mm)	2.43±0.19	2.66±0.20	
LVPWd (mm)	0.75±0.08	$0.85{\pm}0.06^{*}$	
FS (%)	36.4±2.7	31.9±1.61 [*]	
EF (%)	66.7±3.5	$60.7 \pm 2.4^*$	
LV pressure	N=5	N=6	
Heart rate (bpm)	540±93	541±75	
LVSP (mmHg)	96.5±4.8	92.7±8.3	
LVEDP (mmHg)	6.5±3.0	18.8±9.2 [†]	
$+dP/dt_{max}$ (mmHg/s)	11632±2254	9041±1160	
-dP/dt _{max} (mmHg/s)	10630±1586	7878±1455 [†]	
Tau (ms)	7.3±2.3	11.7±2.6 [†]	
Gravimetry	N=8	N=10	
Body weight (BW, g)	27.2±4.2	26.6±3.9	
Heart weight (HW, g)	113.1±13.9	122.8±17.9	
HW/BW (mg/g)	4.19±0.35	$4.62 \pm 0.29^{+}$	
Lung/BW (mg/g)	5.58±0.59	5.40±0.39	

Compared with NTG, [†]: p<0.05; *: p<0.01.