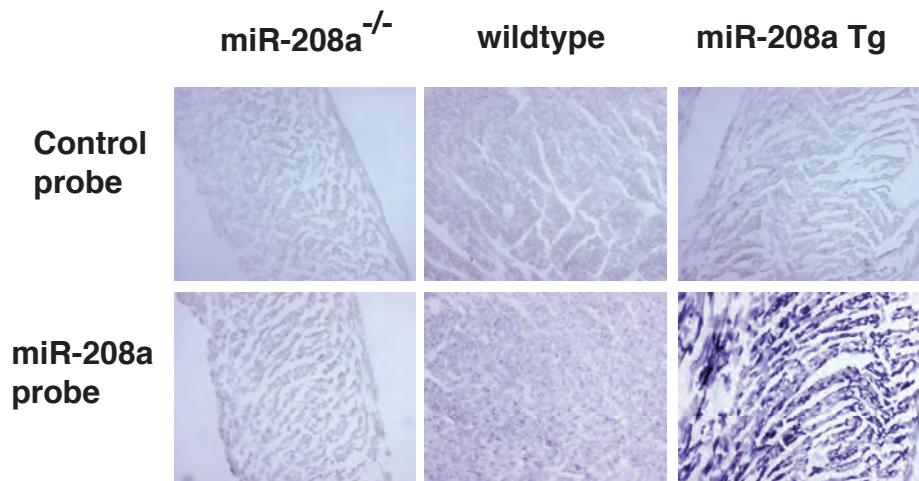


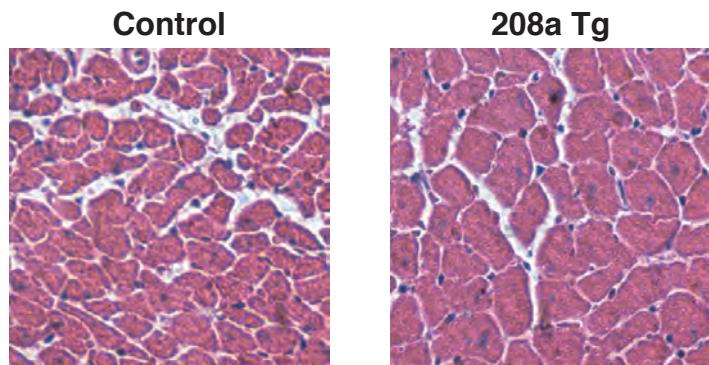
Callis et al, Supplemental Figure 1



Supplemental Figure 1

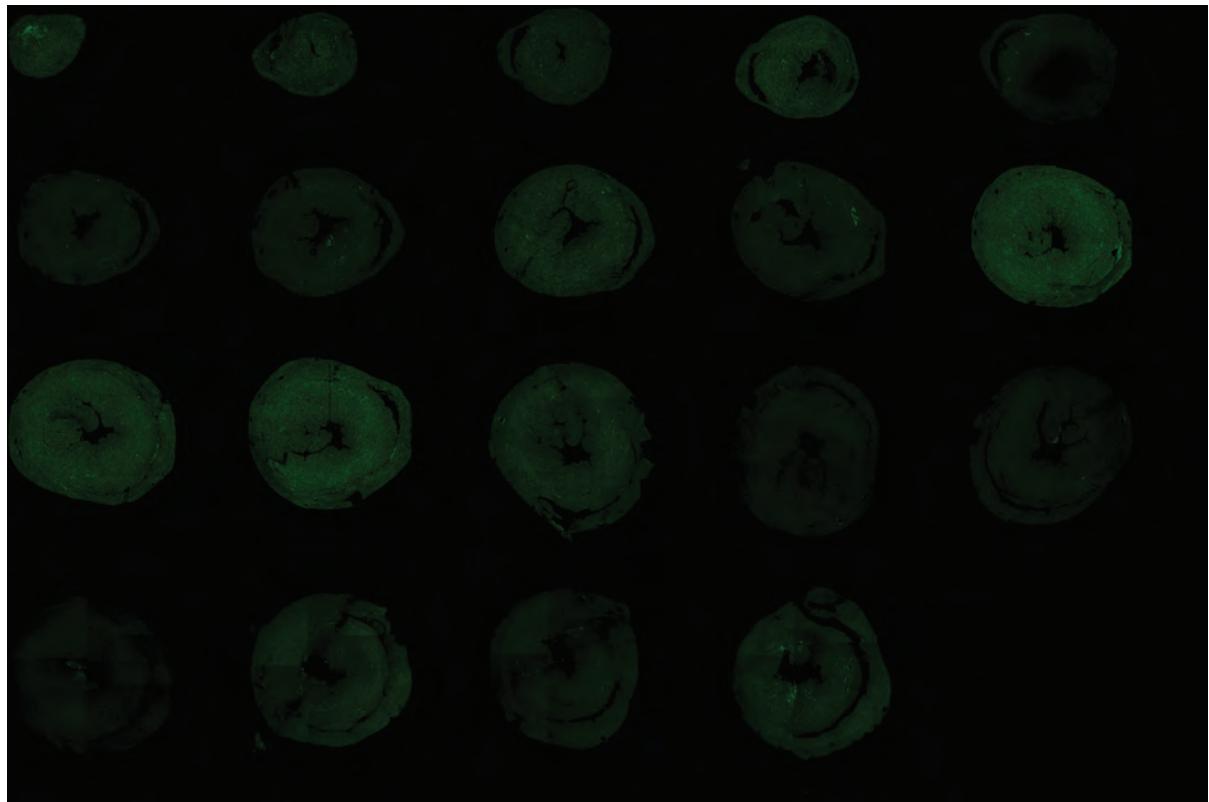
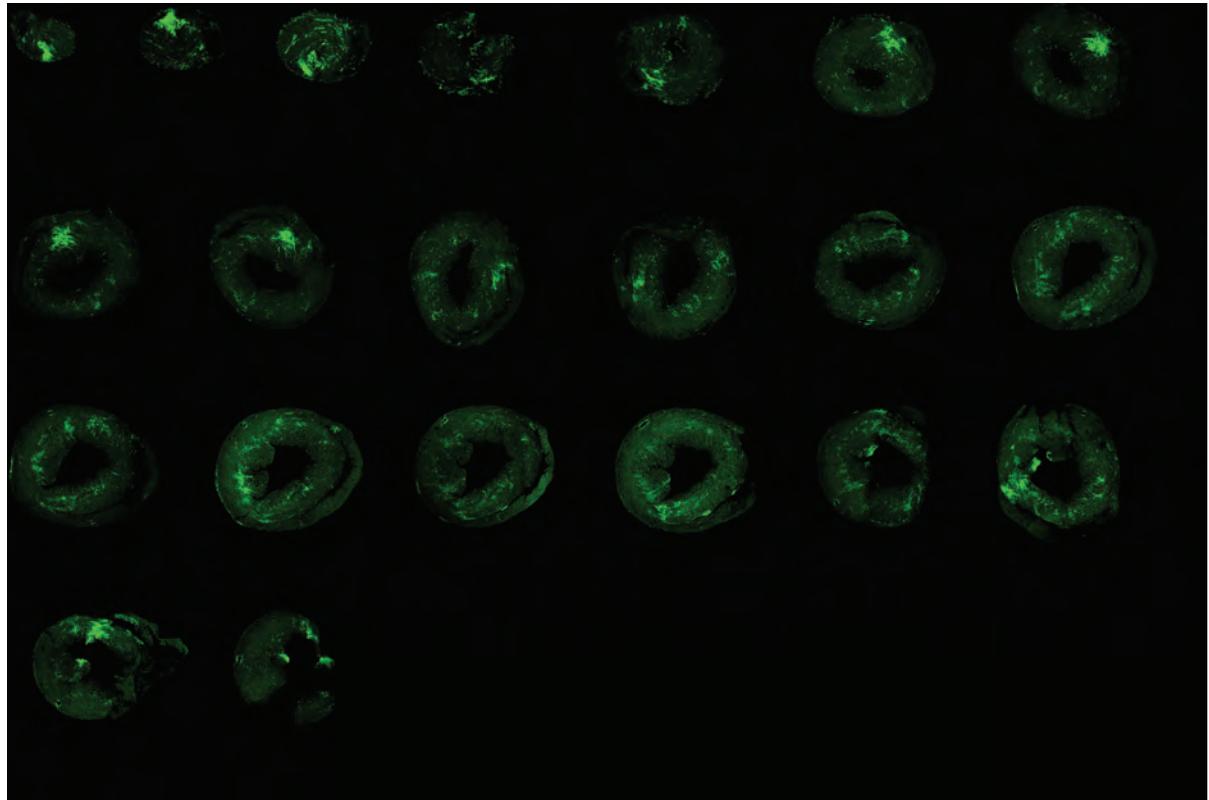
Representative images of adult miR-208a^{-/-}, wildtype, and miR-208a Tg mouse hearts hybridized with LNA miR-208a probes or scrambled control probes. miR-208 signal was completely absent from miR-208a^{-/-} hearts and uniformly upregulated in miR-208a Tg hearts relative to wildtype hearts.

Callis et al, Supplemental Figure 2



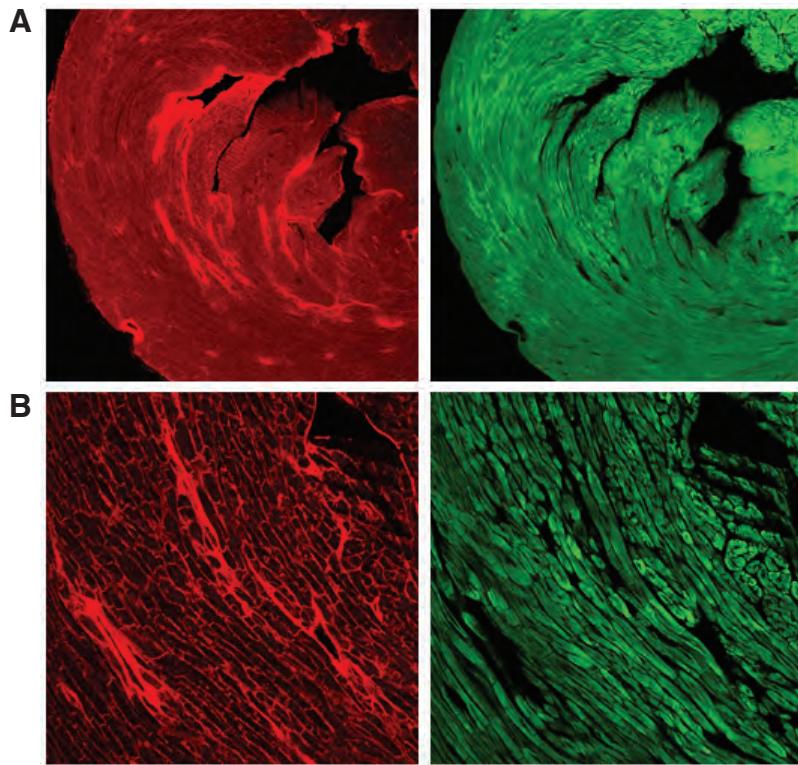
Supplemental Figure 2

Microscopic view of H&E stained histological sections from control and miR-208a Tg hearts.

Control; YFP- β MHC**miR-208a Tg; YFP- β MHC****Supplemental Figure 3**

Confocal microscopy for YFP detection on serial coronal sections from control; YFP- β MHC and miR-208a Tg; YFP- β MHC hearts (from left to right, top to bottom: apex to the top of the ventricles).

Callis et al, Supplemental Figure 4

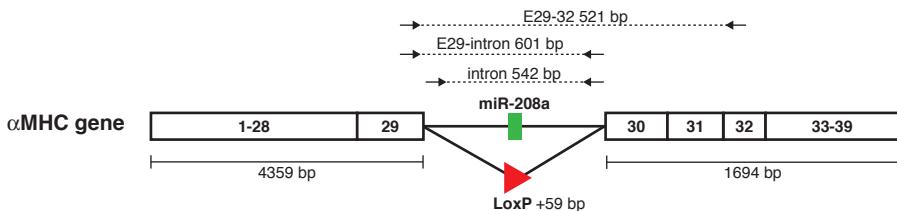


Supplemental Figure 4

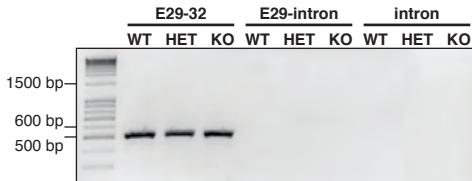
(A) Representative confocal fluorescent image of coronal section from an adult YFP- β MHC; miR-208a Tg heart treated with PTU for 6 weeks. PTU resulted in uniform YFP- β MHC (green) expression throughout the myocardium, consistent with inhibition of thyroid hormone signaling. Wheat germ agglutinin-TRITC staining in red. (B) PTU-treated YFP- β MHC; miR-208a Tg heart imaged with a 20x objective for YFP- β MHC (green) expression and wheat germ agglutinin-TRITC staining (red).

Callis et al, Supplemental Figure 5

A



B



Supplemental Figure 5

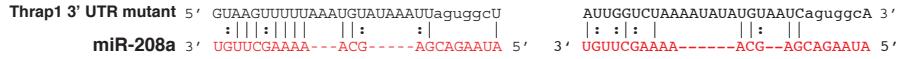
Splicing of αMHC transcript containing mutant miR-208a allele is undisturbed. **(A)** Diagram of αMHC gene showing the proper splicing pattern of the intron that encodes the miR-208a allele or a mutant allele that carries a loxP site instead. Location of primers and regions amplified marked by arrows and dashed lines. **(B)** Results of PCR analysis using genomic DNA from wildtype (WT), miR-208^{+/−} (Het) or miR-208^{−/−} (KO) animals and the primer sets as marked.

Callis et al, Supplemental Figure 6

A

	Thrap1 3' UTR Site 1	Thrap1 3' UTR Site 2
Mouse	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Human	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Rat	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Dog	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Cow	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Chicken	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Zebrafish	GUAGUUUUAAAUGUAUAAAUGCUUGAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
Xenopus	GUAGUUUUAAAUGUAUAAAUGCUUAU	AUUGGUCUAAAAAUAGUAUACGCUUAA
	*****	*****

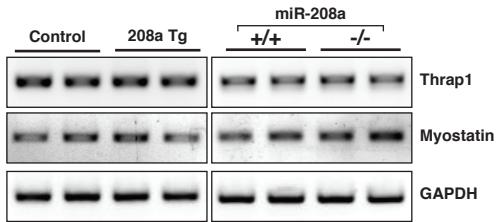
B



C

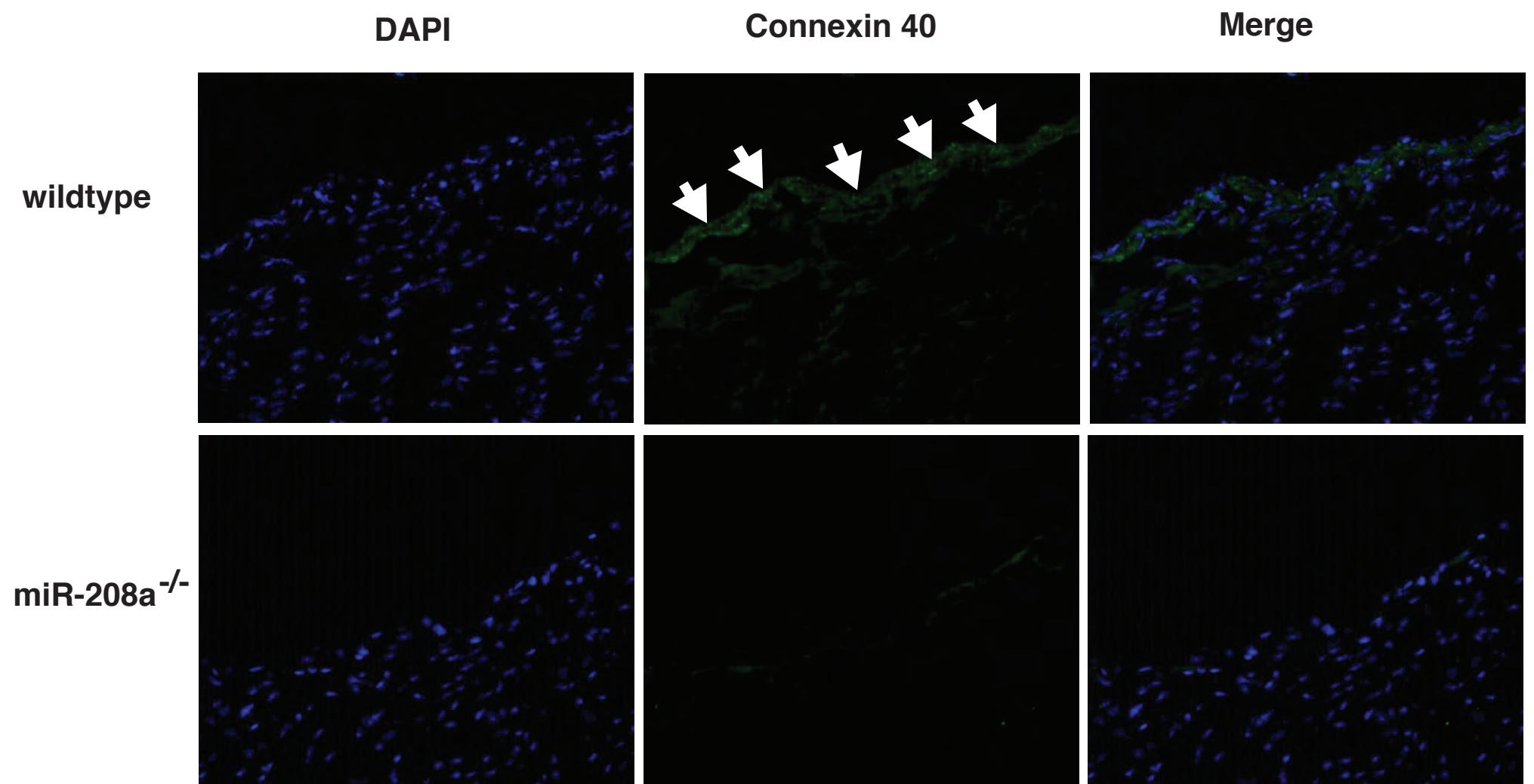
	Myostatin 3' UTR Site
Mouse	AGCAGAUUCAAAUAGGGCUUAA
Human	AGCAGAUAAAAGGGCUUAA
Rat	AGCAGAUUCAAAUAGGGCUUAA
Dog	AGCAGAUAAAAGGGCUUAA
Cow	AGUUGAUAAAAGGGCUUAA

D



Supplemental Figure 6

(A) Target sites for miR-208a in the 3' UTR of Thrap1 show a high level of cross-species sequence conservation. (B) Alignment of miR-208a with mutated Thrap1 target sites. Lower case lettering indicates mutant nucleotides. (C) Target site for miR-208a in the 3' UTR of myostatin shows a high level of cross species sequence conservation. (D) RT-PCR analysis for Thrap1 and myostatin transcript levels in hearts from 4 month-old miR-208a Tg versus control animals and miR-208a-/- versus wild type (+/+) animals. GAPDH serves as loading control.



Supplemental Figure 7 Immunohistochemistry of connexin 40 in ventricle septums of 3 month old wildtype and miR-208a knockout hearts. DAPI labels nuclei. Arrowheads indicate the expression of connexin 40 in the heart of wildtype mouse.

Callis et al, Supplemental Figure 8

A

GATA4 Target Site

miR-208a	3'	TGTTCGAAAAACGAGCAGAATA	5'
		:	
Mouse	5'	CAACCCGTTAACATTGTCTTAA	3'
Human		AAACCTGTTAACATTGTCTTAA	
Rat		CAACCCGTTAACATTGTCTTAA	
Dog		AAACCTGTTAACATTGTCTTAA	
		***** *****	

Supplemental Figure 8

(A) Alignment of miR-208a with conserved target site in the 3' UTR of GATA4.

Supplemental Table 1

Echocardiography of dimensions and function of 7 month-old miR-208a transgenic mice

	Control			miR-208a Tg		
	n = 5			n = 5		
BW (g)	28.7	±	1.58	33.7	±	2.97
LV mass (mg)	104	±	4.10	169	±	10.1***
LV mass/BW (mg/g)	3.67	±	0.24	5.60	±	0.22**
HR (bpm)	666	±	15.1	672	±	18.7
IVSTD (mm)	0.89	±	0.03	1.16	±	0.10**
IVSTS (mm)	1.42	±	0.08	1.79	±	0.10**
PWTD (mm)	0.89	±	0.02	1.17	±	0.09**
PWTS (mm)	1.39	±	0.06	1.55	±	0.11
LVEDD (mm)	3.2	±	0.04	3.4	±	0.11*
LVESD (mm)	1.62	±	0.04	1.9	±	0.10**
FS%	49.5	±	0.71	41.495	±	0.33***

Transthoracic echocardiography on unanesthetized mice. Data are mean ± SEM. BW, body weight; LV, left ventricular; HR, heart rate; IVSTD, interventricular septal thickness in diastole; IVSTS, interventricular septal thickness in systole; PWTD, posterior wall thickness in diastole; PWTS, posterior wall thickness in systole; LVEDD, LV end-diastolic dimension; LVESD, LV end-systolic dimension. LV mass index was calculated as (external LV diameter in diastole³ – LV end-diastolic dimension³) x 1.055. Fractional shortening (FS) was calculated as (LV end-diastolic dimension – LV end-systolic dimension)/LV end-diastolic. *, P < 0.01; **, P < 0.001; ***, P < 0.0001.

Supplemental Table 2
Summary of 1-month and 6-month Surface ECG Findings

	HR (bpm)	PR (ms)	QRS (ms)	QT (ms)	QTc (ms)
1-month					
Control (n=6)	453 ± 26	34 ± 1	9 ± 1	51 ± 1	44 ± 1
208a Tg (n=7)	405 ± 27	49 ± 3**	11 ± 1	53 ± 1	43 ± 2
6-month					
Control (n=6)	425 ± 25	40 ± 2	10 ± 1	54 ± 2	45 ± 2
208a Tg (n=7)	436 ± 15	51 ± 3*	11 ± 1	59 ± 2	50 ± 2

HR, heart rate; bpm, beats per minute; ms, milliseconds; *, $P < 0.05$; **, $P < 0.001$.