

Table S1. Echocardiographic parameters

	CI		Sham	
	Cre+	Cre-	Cre+	Cre-
n	8	6	6	6
HR (BMP)	408.12± 37.9	453.16± 45.96	459± 18.9	418.66± 24.62
LVAW;d (Depth, mm)	0.59± 0.04	0.69± 0.04	0.7± 0.02	0.72± 0.01
LVID;d (Depth, mm)	4.17± 0.11 ^A	3.68± 0.18	3.36± 0.12	3.73± 0.02
LVPW;d (Depth, mm)	0.6± 0.03 ^A	0.75± 0.05	0.63± 0.03	0.67± 0.03
LVAW;s (Depth, mm)	0.95± 0.09	1.17± 0.1	1.16± 0.06	1.19± 0.06
LVID;s (Depth, mm)	3.04± 0.2 ^A	2.11± 0.25	1.85± 0.16	2.03± 0.13
LVPW;s (Depth, mm)	0.89± 0.07 ^A	1.18± 0.11	1.03± 0.07	1.12± 0.07
LV Vol;d (ul)	77.96± 5.03 ^A	58.83± 6.89	46.58± 4.25 ^A	59.36± 0.79
LV Vol;s (ul)	38.12± 5.77 ^A	19.08± 6.21	11.35± 2.7	13.76± 2.17
%EF	52.6± 5.23 ^A	73.57± 5.5	76.17± 4.75	76.98± 3.43
%FS	27.42± 3.35 ^A	43.13± 4.66	44.88± 4.02	45.6± 3.27
LV Mass (AW) (mg)	87.68± 5.81	89.66± 6.03	69.53± 6.1	86.85± 2.63
LV Mass (AW) Corrected (mg)	70.14± 4.65	71.72± 4.82	55.62± 4.88 ^A	69.48± 2.1

^AP < 0.05 versus Cre+, Luc line. Cre+, iTnt-Cre;Gata4fl/fl; Cre-, NTg;Gata4fl/fl.

Table S2. Primer sequences used in qRT-PCR

Gene	Forward	Reverse
<i>Gata4</i>	AAACGGAAGCCCAAGAACCTGAAT	GAGCTGGCCTGCGATGTCTGAGTG
<i>Cyclin A2</i>	GGCTGACACTCTTTCCG	CTGGTAGCAAGAATTAGAGCAT
<i>Cyclin D1</i>	TGAGAACAAGCAGACCATCC	TGAACTTCACATCTGTGGCA
<i>Cyclin D2</i>	CACCGACAACCTCTGTGAAGC	CCACTTCAGCTTACCCAACA
<i>Cdk4</i>	GGGACATCAAGGTCACCCTA	CGCTTAGAAACTGACGCATT
<i>Gdf15</i>	GAGGACTCGAACTCAGAACCAAGT	CCGGTTGACGCGGAGTAG
<i>Anf</i>	GTGTACAGTGC GG GTGTCCAA	ACCTCATCTTCTACCGGCATC
<i>Bnp</i>	ACAAGATAGACCGGATCGGA	AGCCAGGAGGTCTTCTTACA
<i>Acta</i>	AGGCGGTGCTGTCTCTCTAT	GACATTGTGGGTGACACCAT
<i>Fhl1</i>	ACTGCGTGGATTGCTACAAG	TTTACCAAACCCAGTGATGG
<i>Thbs1</i>	CCCTGATGGTAGCTGGAAAT	CTCATCGACGTCTTTGCACT
<i>Timp1</i>	ATATCCGGTACGCCTACACC	GCCCCGTGATGAGAAACTCTT
<i>Col4a3</i>	TTAAGTTCAGGCTGGTGCTG	GCATGTCTCAGCTCAGGTGT
<i>Fgf1</i>	AGCTTTCTCCCAAGAGACCA	TCATGGCGTTTGTGTCCTAT
<i>Fgf2</i>	CAACCGGTACCTTGCTATGA	TCCGTGACCGGTAAGTATTG
<i>Fgf3</i>	ACCTGGTGCCAGAGACCTT	GCAGGAAGAGAGAGGACTTTTGTG
<i>Fgf8</i>	GCTCATTGTGGAGACCGATACTT	TGGCAATTAGCTTCCCCTTCT
<i>Fgf9</i>	GCGGTGGGTTCTTATTGATT	AAATTGGCAAGTCCTCATCC
<i>Fgf12</i>	ATTCCTCAACCCTGTATCGC	ATGAGATGAGGGCTTGGTTT
<i>Fgf13</i>	TATCACCCATATTAAGCCCCATAA	AAAATTTGGCAGTCCTTCTTCCA
<i>Fgf16</i>	CCATGACTCAAGGGAGCTTT	CTATGCCAATCCTGAAGGT
<i>Fgf18</i>	AGGAAGAATCTCTATTTTTGTACATTGTGT	GTTTCAGGTCAACAGTGGAATCCTA
<i>Vegfa</i>	GAGGATGTCCTCACTCGGAT	TCTCAGACCACACTGAAGCC
<i>Vegfb</i>	AGCCACCAGAAGAAAGTGGT	GCTGGGCACTAGTTGTTTGA
<i>Vegfc</i>	CCCAAACCAGTCACAATCAG	GGTAATGTTGCTGGCAGAGA
<i>Gapdh</i>	GAAGGGCTCATGACCACAG	GATGCAGGGATGATGTTCTG

Primer sequences used in ChIP-qPCR

GATA Site on	Forward	Reverse
<i>Fgf16</i> Enhancer	CCCGGTCAACTATGAGAAGG	GCCTGTCAGTTGGAAAGCTC
<i>Fgf16</i> Control	TTTTCGCTTCTCAGACCCCTGTG	TTCTCTGGCCAAAAGAGGCTG

Primer sequences used in amplifying fragment

Fragment	Forward	Reverse
<i>Fgf16</i> Promoter	CTAGCTAGCTATGCTCATTGGTGTTCGC	CCCAAGCTTGTGCGGGCGCTCGCTTGCTC
<i>Fgf16</i> Intron	CTAGCTAGCGTAAGTTCCAACCTTCTAT	CCCAAGCTTGTCTTCTGTGAGGGTGAG
<i>Fgf16</i> Enhancer	CTAGCTAGCGAATGAGGGTTCCAGGGAC	CCCAAGCTTCTATATAAAGCTGCATGGG