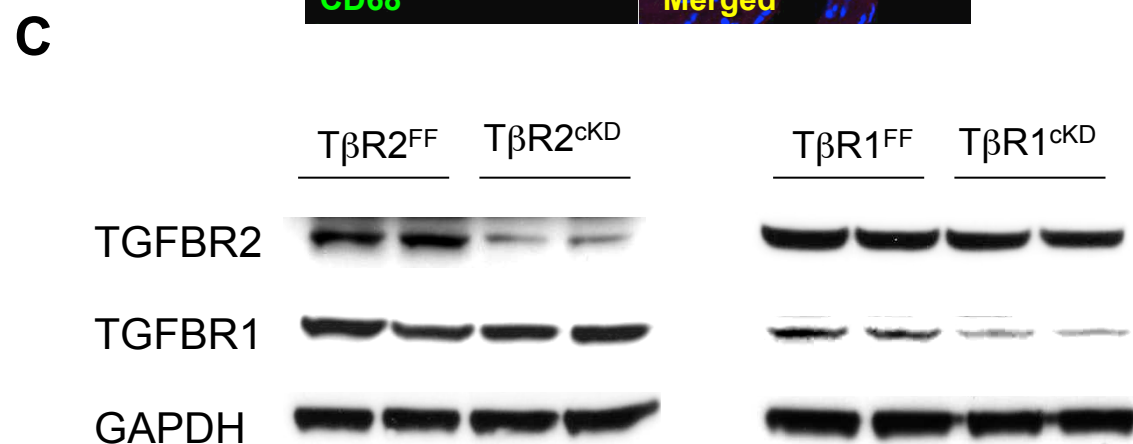
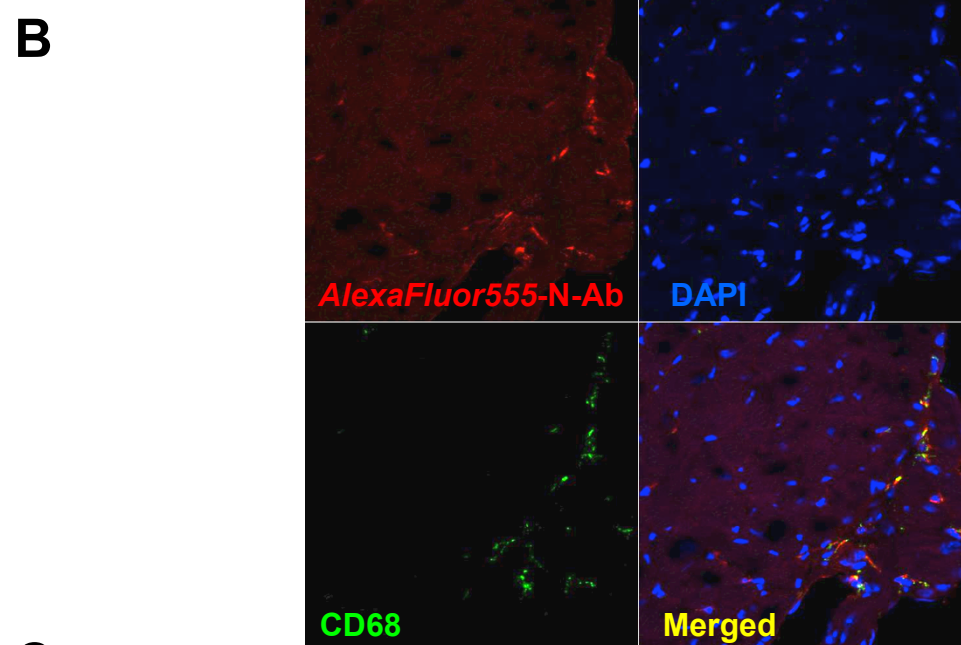
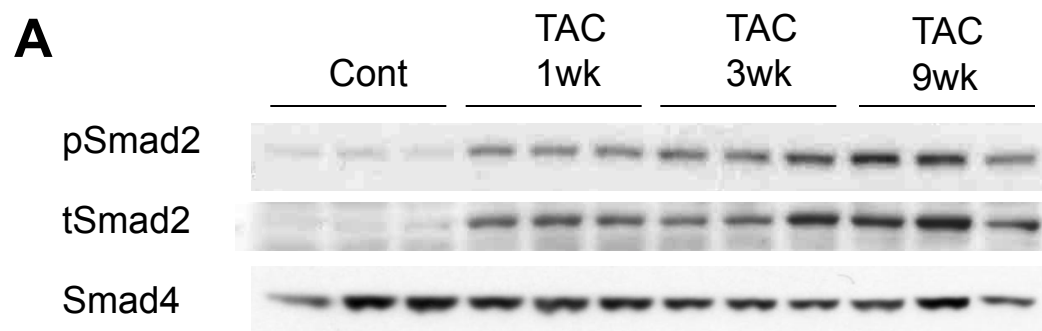
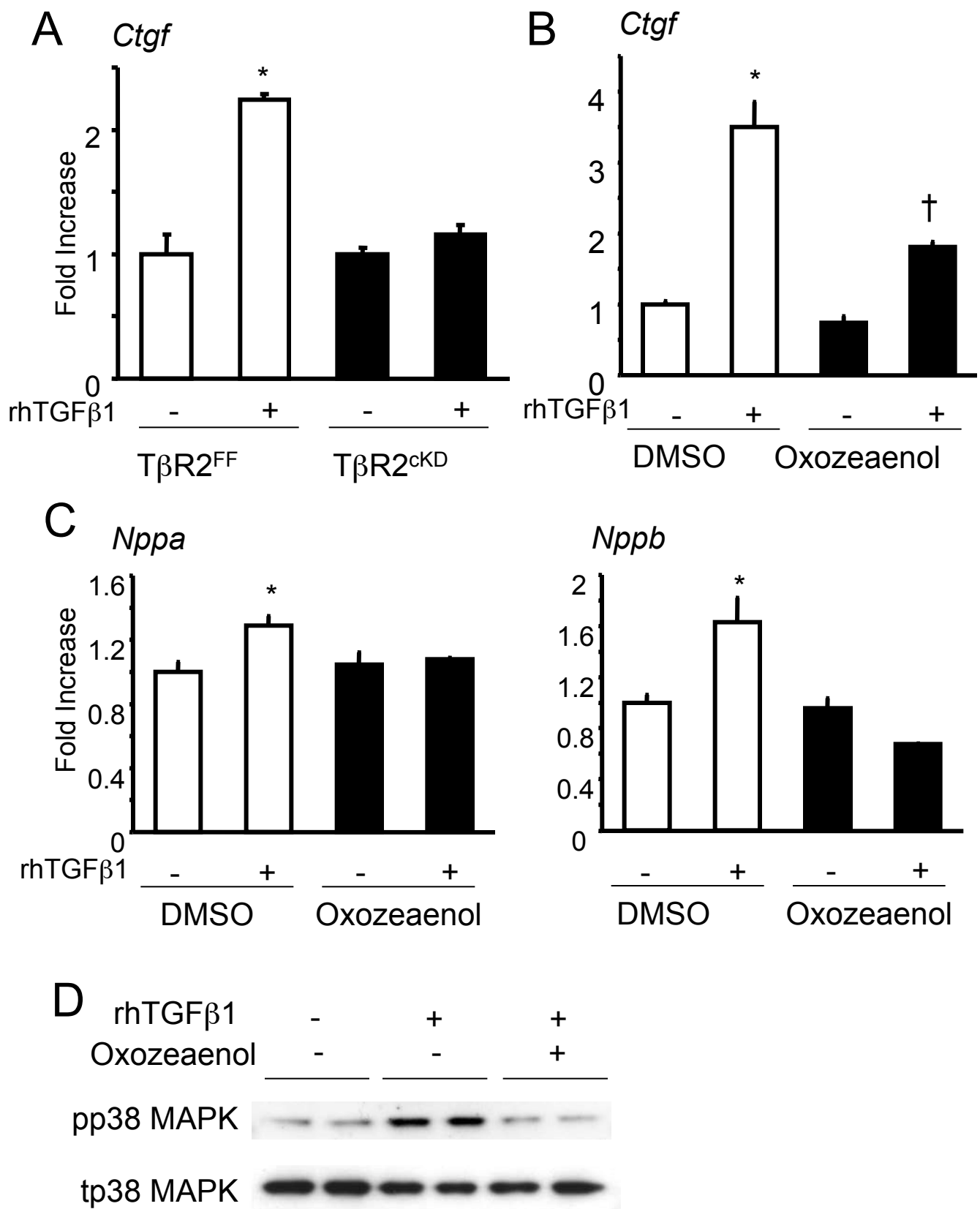


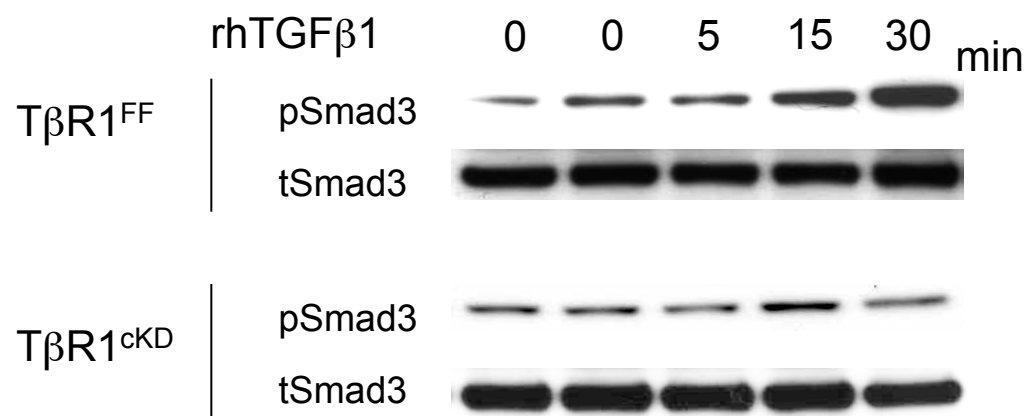


Supplemental Figure 1

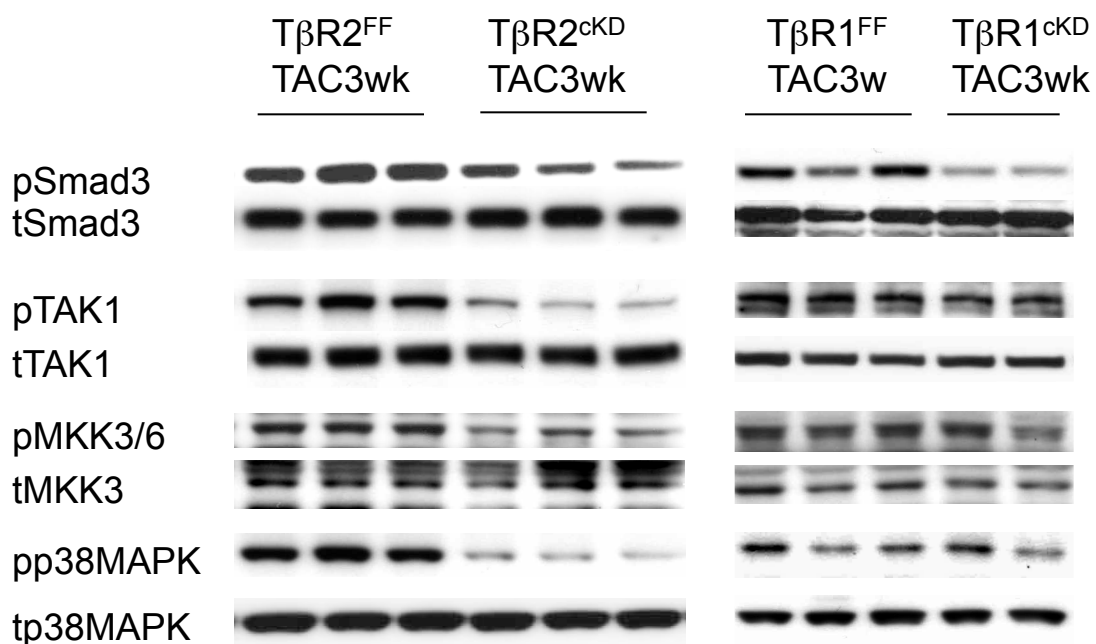


Supplemental Figure 2

A



B



Supplemental Figure 3

Supplemental Table 1: Hemodynamic parameters and indices derived from PV loop analysis with N-Ab study at TAC-9wk

	Sham N=8	TAC+C-Ab N=5	TAC+N-Ab N=3
<i>Parameter</i>			
HR (/min)	533±11	486±9	514±15
LVPmax (mmHg)	105±3.8	174±3.8*	164±3.6*
EDP (mmHg)	6.0±0.6	8.3±1.8	6.0±0.8
EDV (μL)	29.3±2.2	51.0±3.4*	75.7±13.4*†
ESV (μL)	7.9±1.3	32.6±2.9*	60.6±12.5*†
CO (mL/min)	11.4±0.6	8.8±0.5*	7.7±0.4*
Ea (mmHg/μL)	4.5±0.3	9.4±1.0*	10.7±0.9*
EF (%)	74.5±3.2	36.3±2.3*	20.7±2.5*†
<i>Systolic indexes</i>			
Ees	8.4±0.7	6.8±1.6	6.5±2.2
PRSW	92.9±4.0	103.6±11.5*	76.3±10.0
dP/dt _{max} (mmHg/sec)	12951±701	9359±695	9627±308
PWR _{Max} /EDV (mmHg/μL)	37.4±2.1	24.5±1.4*	14.4±1.9*†
<i>Diastolic indexes</i>			
-dP/dt _{min} (mmHg/sec)	-9555±694	-9709±674	-8078±290
Tau (msec)	4.2±0.24	5.1±0.26	6.7±0.5*†
PFR/EDV (/sec)	30.6±2.4	16.0±3.0*	9.4±1.3*

HR, heart rate; ESP, end-systolic pressure; EDP, end-diastolic pressure; EDV, end-diastolic volume; ESV, end-systolic volume; CO, cardiac output; Ea, arterial elastance; Ees, end-systolic elastance; PRSW, preload recruitable stroke work; EF, ejection fraction; dP/dt_{max}, peak rate of pressure rise; PWR_{max}/EDV, peak LV power normalized to end-diastolic volume; -dP/dt_{min}, peak rate of pressure decline; Tau (S), relaxation time constant calculated by Suga method; PFR/EDV, peak filling rate/end-diastolic volume, * p<0.05 vs sham, †p<0.05 vs TAC+C-Ab, 1-way ANOVA

Supplemental Table 2 : Hemodynamic parameters and indices derived from PV loop analysis with T β R2, T β R1 knockdown studies at TAC-9wk

	MCM N=5	T β R2 ^{FF} N=4	T β R2 ^{CKD} N=6	T β R1 ^{FF} N=4	T β R1 ^{CKD} N=4
<i>Parameter</i>					
HR (/min)	484±19	525±31	556±17*	578±14	585±36*
LVPmax (mmHg)	158.0±1.9	176.5±8.7	160.2±4.2	155.0±3.2	147.6±7.4
EDP (mmHg)	5.3±1.0	3.3±0.7	6.2±0.9	4.8±3.2	4.5±2.0
EDV (μL)	61.9±8.3	72.0±8.0	35.8±7.1*†	54.5±10.2	39.9±13.9
ESV (μL)	40.8±9.9	50.4±4.3	14.7±5.8*†	41.7±11.5	24.8±14.1
CO (mL/min)	10.2±1.4	10.9±1.6	11.7±1.0	7.35±0.7	8.6±1.0
Ea (mmHg/μL)	7.5±1.2	8.5±4.4	7.4±0.4	11.8±1.4	9.5±1.4
EF (%)	37.6±7.3	29.0±2.9	66.4±6.6*	29.5±10.9	54.7±16.3
<i>Systolic indexes</i>					
Ees	6.7±1.8	8.4±3.9	22.1±6.1	9.3±4.7	15.6±6.5
PRSW	108.0±19.0	104.6±14.8	166.7±8.5*†	81.3±20.8	103.7±21.2
dP/dt _{max} (mmHg/sec)	9492±685	10274±552	14553±887*†	10989±863	10880±704
PWR _{Max} /EDV (mmHg/μL)	26.9±5.5	18.8±1.4	52.9±6.2*	23.2±8.7	39.5±14.1
<i>Diastolic indexes</i>					
-dP/dt _{min} (mmHg/sec)	-8131±911	-9456±745	-11066±1012	-9874±739	-9556±847
Tau (G) (msec)	11.9±1.4	10.8±0.9	8.6±0.8	11.1±0.7	9.5±0.7
PFR/EDV (/sec)	17.3±2.7	18.4±2.0	37.6±5.9*	17.5±3.4	36.0±10.7

Abbreviations as in Table 1. * p<0.05 vs MCM, †p<0.05 vs T β R2^{FF}, 1-way ANOVA

Supplemental Table 3 : Summary of genes identified as significantly changed in myocyte-T β RII knockdown heart with TAC. Comparison is between 9wk-TAC T β R2^{CKD} (n=4) and MCM or T β R2^{FF} controls (n=6).

Gene	Description	Fold Difference	P
<i>Up-regulated in myocyte-TβR2 knockdown</i>			
<i>Bmp7</i>	Bone morphogenetic protein 7	4.4154	0.000064
<i>Tgfb3</i>	Transforming growth factor, beta receptor III	1.9767	0.004121
<i>Jun</i>	Jun oncogene	1.5743	0.031677
<i>Tsc22d1</i>	TSC22 domain family, member 1	1.556	0.018822
<i>Bmp2</i>	Bone morphogenetic protein 2	1.459	0.015009
<i>Down-regulated in myocyte-TβR2 knockdown</i>			
<i>Il6</i>	Interleukin 6	0.0691	0.034336
<i>Ltb2</i>	Latent transforming growth factor beta binding protein 2	0.0957	0.021253
<i>Col3a1</i>	Collagen, type III, alpha 1	0.1075	0.008139
<i>Col1a2</i>	Collagen, type I, alpha 2	0.1281	0.002377
<i>Myc</i>	Myelocytomatosis oncogene	0.1282	0.033906
<i>Cdkn2b</i>	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0.1832	0.007873
<i>Inhba</i>	Inhibin beta-A	0.2145	0.009288
<i>Smad1</i>	MAD homolog 1 (Drosophila)	0.2573	0.015857
<i>Tgfb1</i>	Transforming growth factor, beta induced	0.258	0.027156
<i>Tgfb2</i>	Transforming growth factor, beta 2	0.2636	0.02561
<i>Col1a1</i>	Collagen, type I, alpha 1	0.2684	0.005023
<i>Gdf6</i>	Growth differentiation factor 6	0.2761	0.016347
<i>Runx1</i>	Runt related transcription factor 1	0.2989	0.004426
<i>Acvr1</i>	Activin A receptor, type 1	0.3523	0.036733
<i>Itgb7</i>	Integrin beta 7	0.4295	0.008822
<i>Serpine1</i>	Serine (or cysteine) peptidase inhibitor, clade E, member 1	0.4703	0.024798
<i>Tgfb1</i>	Transforming growth factor, beta 1	0.5399	0.021768
<i>Ltb4</i>	Latent transforming growth factor beta binding protein 4	0.5969	0.013737
<i>Bmpr2</i>	Bone morphogenic protein receptor, type II (serine/ threonine kinase)	0.7398	0.021766

Supplemental Table 4 : Summary of genes identified as significantly changed in myocyte-T β R1 knockdown heart with TAC. Comparison is TAC: T β R1^{CKD} (n=4) versus MCM or T β R1^{FF} only controls (n=6).

Gene	Description	Fold Difference	P
<i>Up-regulated in myocyte-TβR1 knockdown</i>			
<i>Lefty1</i>	Left right determination factor 1	1.6021	0.035148
<i>Pdgfb</i>	Platelet derived growth factor, B polypeptide	1.4455	0.004625
<i>Down-regulated in myocyte-TβR1 knockdown</i>			
<i>Gdf6</i>	Growth differentiation factor 6	0.2829	0.035711