## SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Fbn1<sup>C1039G/+</sup> hearts display normal cardiac function in the absence of hemodynamic stress. A. Echocardiographic quantification of cardiac dimensions and function in Fbn1<sup>+/+</sup> and Fbn1<sup>C1039G/+</sup> mice with and without valvular regurgitation at 4 and 12 months of age. EDD, end-diastolic diameter; ESD, end-systolic diameter; FS, fractional shortening; LVM, left ventricular mass. n>=14 per group. \*p<0.05, \*\*, p<0.01, \*\*\*p<0.001, 2w ANOVA, Tukey's correction. B. Representative PV loop of a 12mo Fbn1<sup>+/+</sup> (blue line, blue fill) and Fbn1<sup>C1039G/+</sup> mouse (red line, red fill) without valvular regurgitation. Summary data obtained from PV loop analysis shown in bar graphs: E<sub>es</sub>, end-systolic elastance and PRSW, preload recruitable stroke work, reflect load-independent indices of ventricular contractility. Tau, relaxation time constant reflects a load-independent index of ventricular stiffness; n=3-6 per group. C. dP/dt<sub>max</sub>, peak rate of left ventricular pressure rise, an index of contractility; dP/dt<sub>min</sub>, peak rate of left ventricular pressure decline, an index of lusitropy. Invasive blood pressure measurements taken from PV loop analysis of  $Fbn1^{+/+}$  and  $Fbn1^{C1039G/+}$  mice without valvular regurgitation at 4 and 12 months of age. n=3-6 per group. D. Gross morphometric analysis of post-natal  $Fbn1^{+/+}$ ,  $Fbn1^{C1039G/+}$ , Fbn1<sup>C1039G/C1039G</sup> mice at 8do, 6mo and 12mo age, in mice without valvular regurgitation. HW/BW, heart weight/body weight ratio; HW/TL, heart weight/tibial length ratio. n>=4 per group.

Supplemental Figure 2.  $Fbn1^{C1039G/+}$  hearts have normal  $TGF\beta$  signaling in the absence of hemodynamic stress. A-C. Representative Western blot and summary quantification for phosphorylated/total (p/t), p/tSmad2, p/tERK1/2, and GAPDH using left ventricular tissue lysates. n=4 per group. D. mRNA expression normalized to 18S and then to  $Fbn1^{+/+}$  data, assessed by real-time RT-PCR from left ventricular tissue of  $3mo\ Fbn1^{+/+}$  and

*Fbn*/*C*1039G/+ hearts without regurgitation. *Ctgf*, connective tissue growth factor. *Serpine*1, plasminogen activator inhibitor, type 1. n>=4 per group.

Supplemental Figure 3. Fbn1<sup>C1039G/+</sup> hearts develop hypertrophy and fibrosis in response to pressure overload. A. Baseline echocardiographic quantification of cardiac dimensions in 5mo Fbn1<sup>+/+</sup> and Fbn1<sup>C1039G/+</sup> mice without valvular regurgitation. EDD, end-diastolic diameter; ESD, end-systolic diameter; IVST, interventricular septum thickness; PWT, posterior wall thickness. n=4-6 per group. B. Myocyte hypertrophy, as assessed by cross-sectional area (CSA) in hematoxylin-eosin staining. Summary quantification of averaged data, >20 cells per heart. n=4 per group. C. Fibrotic area, as assessed by Masson's Trichrome stain and quantified by total number of blue pixels normalized to whole tissue area and then to Fbn1<sup>+/+</sup>:SHAM data. n=4-6 per group. D. mRNA expression of hypertrophy genes, normalized to Gapdh and then to Fbn1<sup>+/+</sup>:SHAM data, assessed by real-time RT-PCR. n=4-6 per group. Myh7, myosin heavy chain 7 (βMHC), Nppa, natriuretic peptide A (ANP), Nppb, natriuretic peptide B (BNP).
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Supplemental Figure 5. Smad2 and ERK1/2 activation are differentially increased in the myocyte and nonmyocyte compartments of failing Fbn1<sup>C1039G/+</sup> hearts. A. Representative serial sections of pSmad2 (red, top panels) and pERK1/2 (red, bottom panels) immunostaining in Fbn1<sup>C1039G/+</sup>

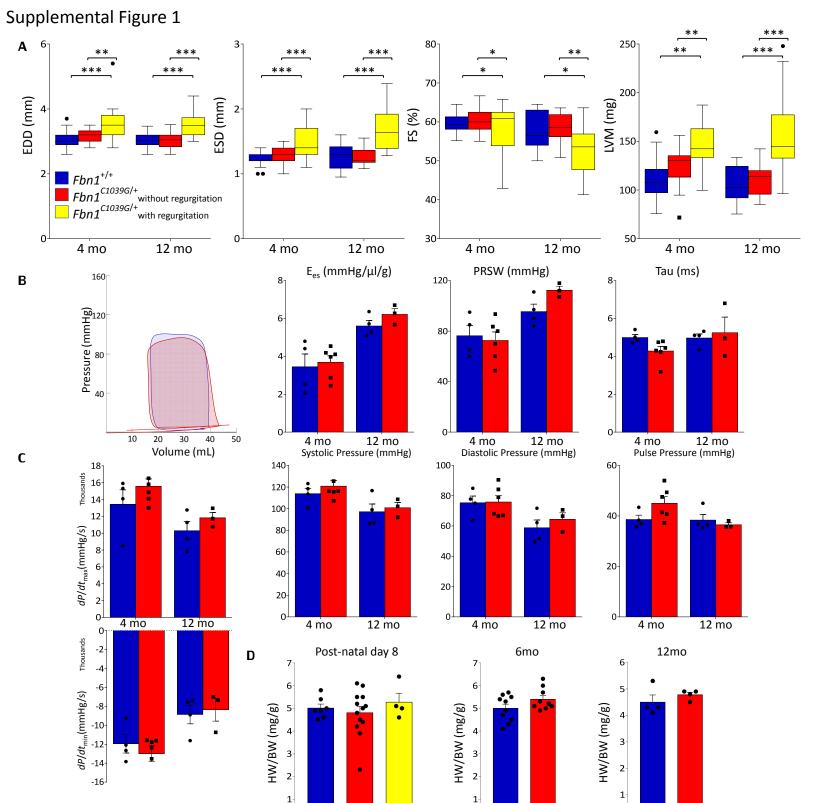
hearts subjected to 4w TAC. Far left panels, scale bar: 50  $\mu$ m. Middle and far right panels, zoom 2x. Blue, DAPI (nuclei); Green, lipofuscin (myocytes). White arrows, myocyte nuclei. Yellow arrows, nonmyocyte nuclei. B. Summary quantification of % of total pSmad2 and pERK1/2 immunofluorescence intensity localized to nonmyocyte (NM) and myocyte (M) cells per unit area. n=10-15 areas quantified. \*p<0.05, \*\*p<0.01, Student's t-test. C. Representative myocyte-enriched serial sections. Scale bar: 50  $\mu$ m. D. Representative co-immunostaining of serial sections with vimentin (yellow) and pSmad2 (left panel) and vimentin (yellow) and pERK1/2 (right panel). Scale bar: 25  $\mu$ m. Gray, lipofuscin (myocytes).

Supplemental Figure 6. *ERK1/2 activation, but not Smad2 activation, is significantly attenuated by MEK inhibition*. Immunoblot for pSmad2, pERK1/2 and GAPDH using cultured neonatal rat cardiac fibroblasts with TGF-β3 (10 ng/ml) stimulation for 15 minutes with and without treatment with MEKi, RDEA119 (100nM) or PD98059 (50μM). n=4 per group. \*\*p<0.01, \*\*\*p<0.001, 1w ANOVA, Tukey's correction.

Supplemental Figure 7. *Myocyte hypertrophy in Fbn1*<sup>C1039G/+</sup>hearts is prevented with losartan and MEKi treatment. A. Representative hematoxylin-eosin staining of formalin-fixed heart sections. White dotted line delineates myocyte diameter. Scale bars: 50μm. B. Myocyte hypertrophy as assessed by wheat germ agglutinin (WGA) staining. Scale bars: 25μm. C. Summary quantification of average cross-sectional area (CSA) data, >1000 cells per heart. n=4-7 per group. D. mRNA expression of hypertrophy genes, normalized to *Gapdh* and then to *Fbn1*<sup>+/+</sup>:SHAM data, assessed by real-time RT-PCR. *Myh7*, myosin heavy chain 7 (βMHC), Myh6, myosin heavy chain 6 (αMHC), *Nppa*, natriuretic peptide *A* (ANP), *Nppb*, natriuretic peptide B (BNP). n=4-7 per group. \*p<0.05, \*\*p<0.01, \*\*\*p<0.001, 1w ANOVA, Tukey's correction.

Supplemental Figure 8. Smad2 and ERK1/2 activation are differentially increased in response to TGFβ and angiotensin II in cardiac fibroblasts. Immunoblot for pSmad2, pERK1/2 and GAPDH using cultured neonatal murine cardiac fibroblasts with TGFβ1 (5 ng/ml) or AngII (5nM) stimulation for 24 hours. Lanes were run on the same gel but were noncontiguous. n>=3 per group. \*\*p<0.01, 1w ANOVA, Tukey's correction.

Supplemental Figure 9. *Inhibition of ERK1/2 activation suppresses Smad2 activation in both* nonmyocyte and myocyte compartments. A-B. Labeling index (% positive cells) of pSmad2 or pERK1/2 immunofluorescence in the nonmyocyte and myocyte compartments. n>5 fields per group. C. Total number of nonmyocytes and myocytes normalized to Fbn1<sup>+/+</sup>:SHAM data. n=15-30 fields per group. \*p<0.05, \*\*p<0.01, \*\*\*p<0.001, 1w ANOVA, Tukey's correction. Supplemental Figure 10. TGFβ3 is predominantly expressed in the nonmyocyte compartment. A-C. Representative in situ hybridization of Tgfb3. A. Fbn1<sup>+/+</sup>:TAC vs Fbn1<sup>C1039G/+</sup>:TAC, Tgfb3, red. Left panel, scale bar: 10µm. Right panel, zoom 2x inset. Dotted line demarcates myocyte compartment. Red arrows point to examples of in situ RNA hybridization (red dots) found throughout the nonmyocyte compartment. B. Myocyte- vs nonmyocyte-enriched areas. Scale bar: 10µm. C. Tgfb3 and Vim. Left panel, Tgfb3, red, left panel and Vim, red, right panel. Dottedline outlines the cardiac myocytes. Scale bar: 10µm. D. mRNA expression of Tgfb3 and Vim normalized to *Gapdh* and then to myocyte data. n=4-6 per group. \*\*\*p<0.001, Student's t-test. Supplemental Figure 11. AngII-mediated ERK1/2 activation is differentially increased in Fbn1<sup>C1039G/+</sup> vs WT fibroblasts. Immunoblots for pSmad2, pERK1/2 and GAPDH using cultured neonatal murine cardiac fibroblasts from Fbn1<sup>C1039G/+</sup> and Fbn1<sup>+/+</sup> hearts with AngII (5nM) or TGFB3 (5 ng/ml) stimulation for 12 hours. Lanes were run on the same gel but were noncontiguous. n>=3 per group. \*\*\*p<0.001, 1w ANOVA, Tukey's correction.



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C1039G/+ C1039G/

0-

+/+

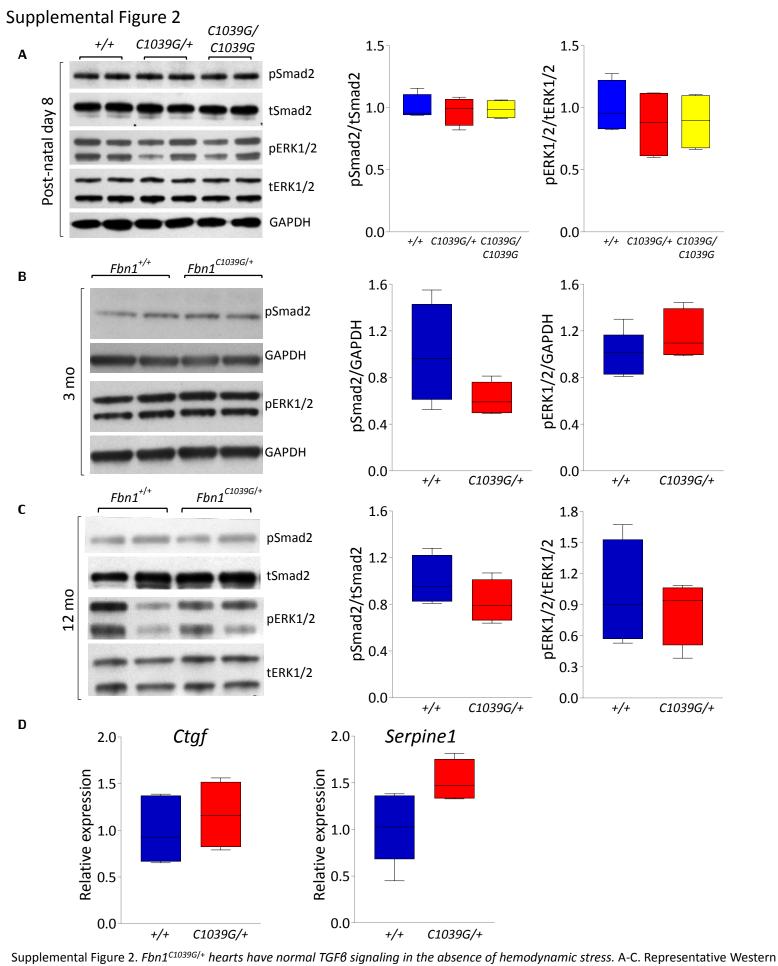
C1039G/+

+/+

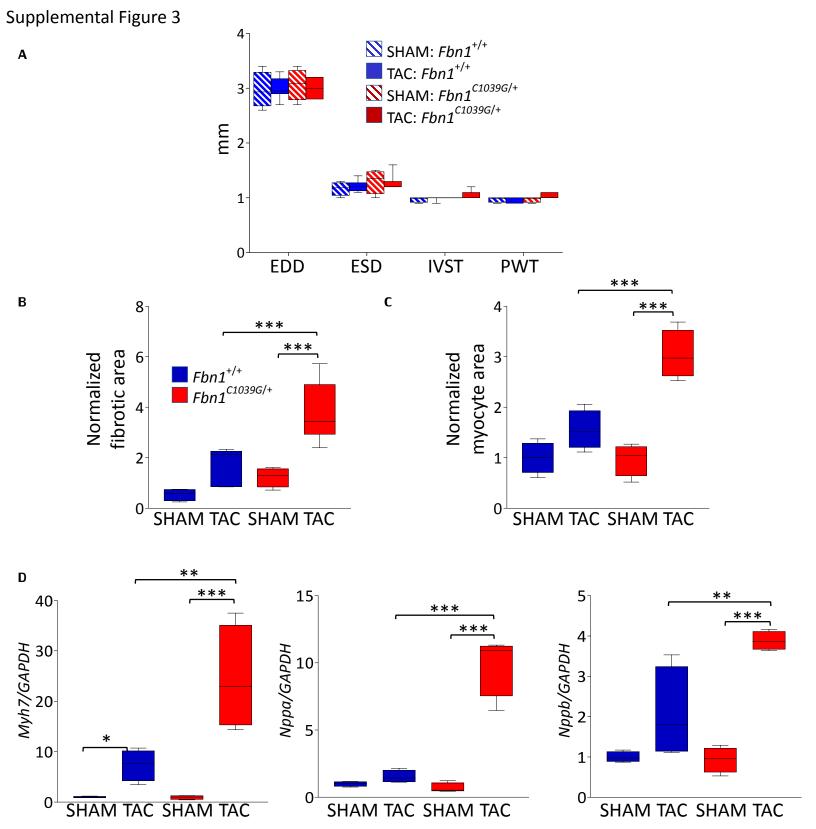
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0-

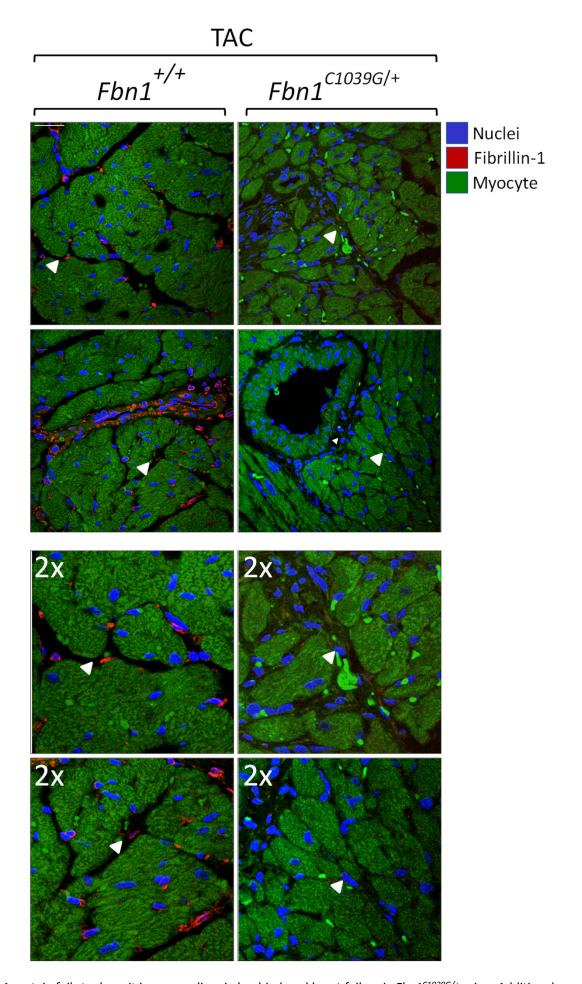
+/+



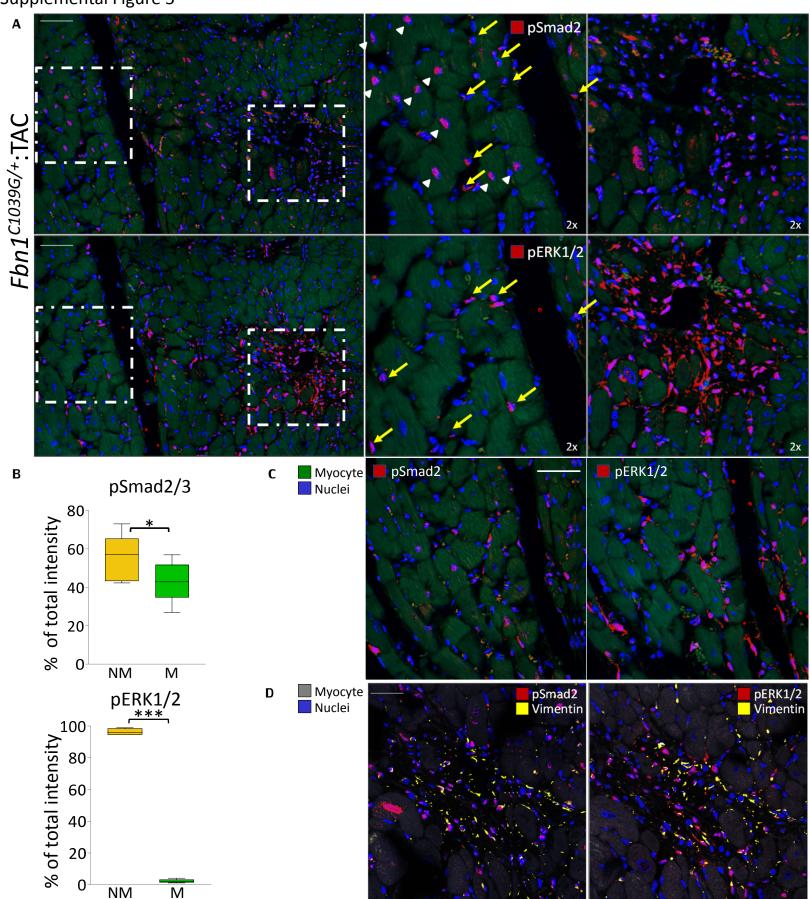
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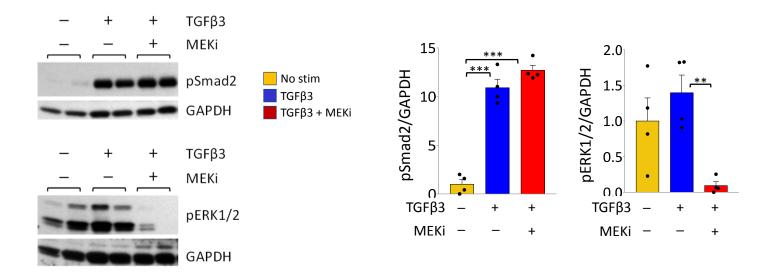


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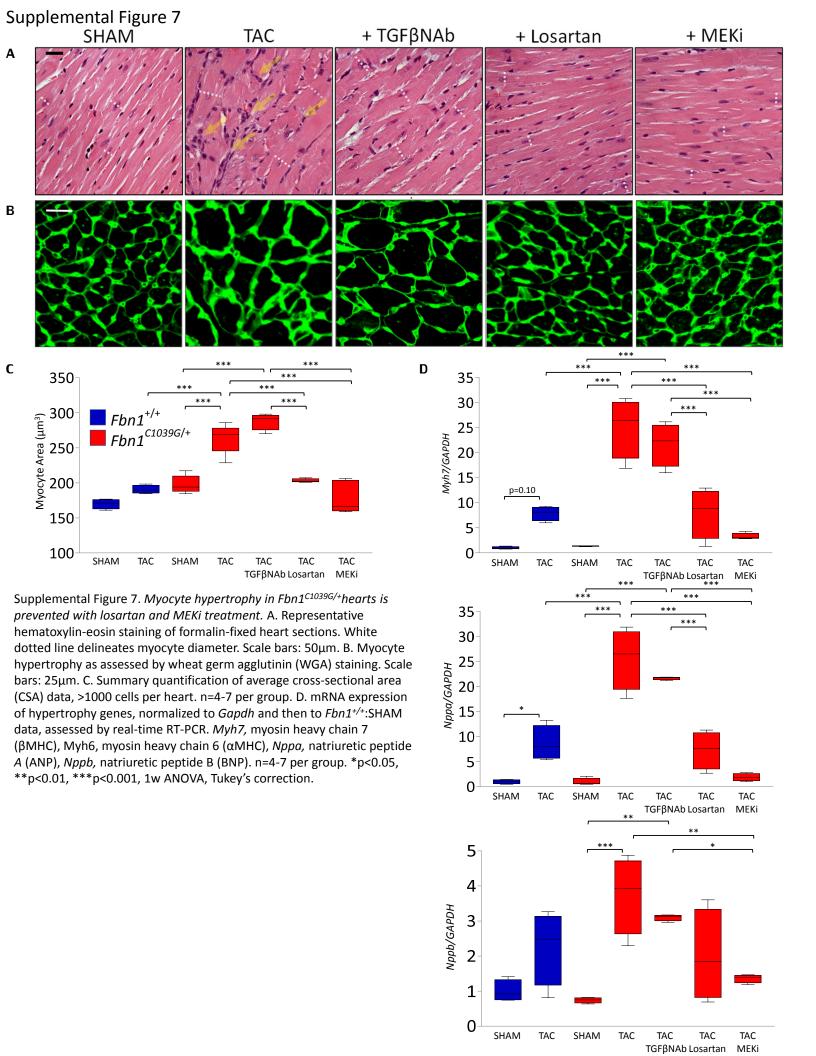


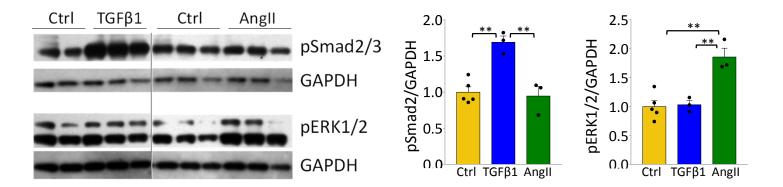
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## Supplemental Figure 6

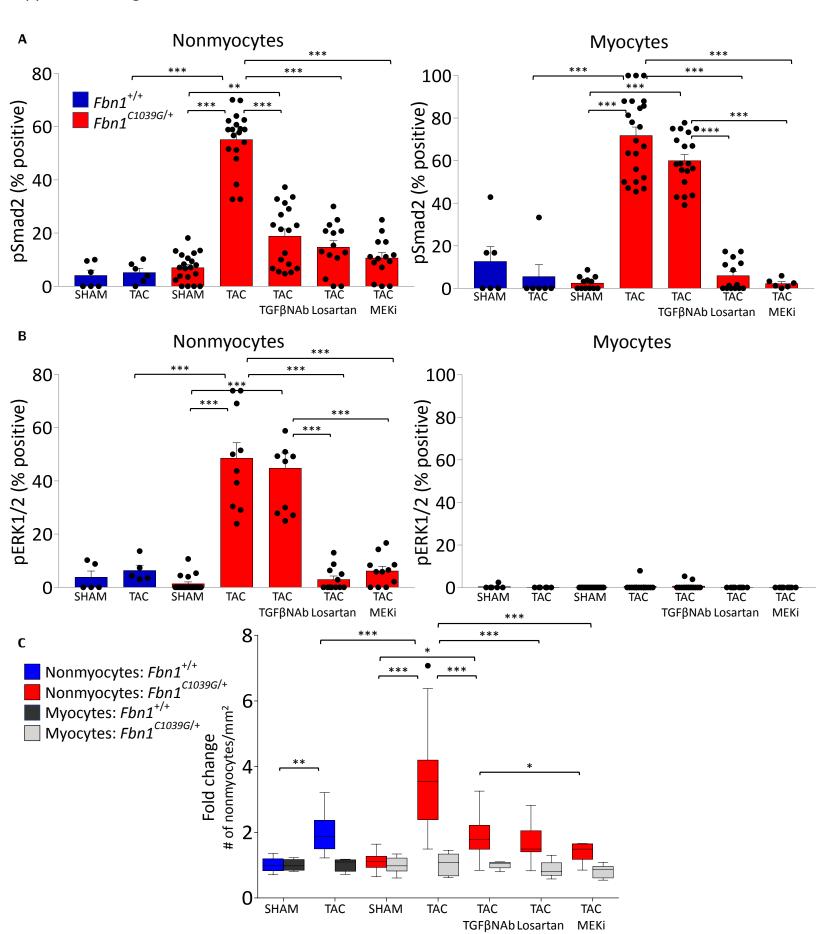


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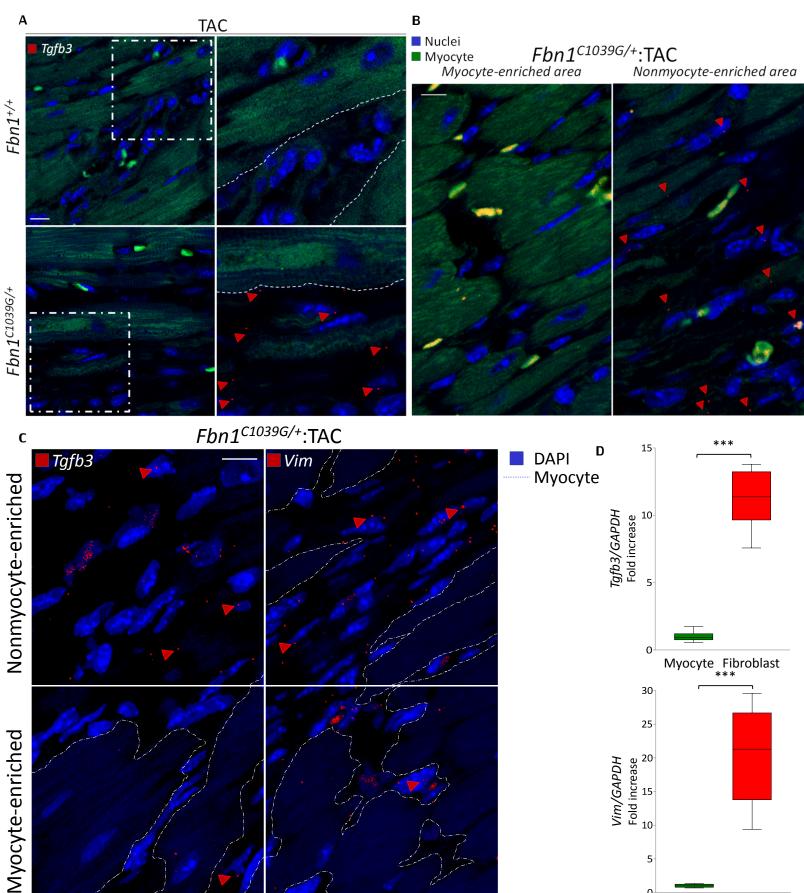




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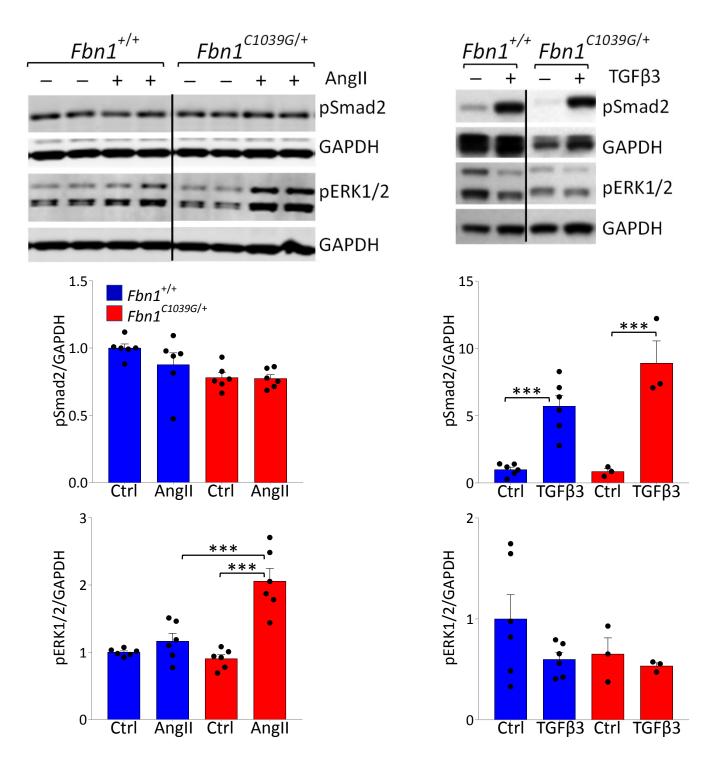


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Myocyte Fibroblast



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