

Supplemental Information:

Pan, et al., Prostate tumor-derived GDF11 accelerates androgen deprivation therapy-induced sarcopenia

Supplemental Methods

RNA isolation and quantitative RT-PCR. Tissues were harvested after euthanasia, snap frozen in liquid nitrogen, and stored at -80°C for mRNA expression analysis. Total RNA was extracted from pulverized QUA or tumor tissue using TRIzol (Invitrogen). Five micrograms of total RNA were reverse transcribed using pdN15 with the Superscript III reverse transcription kit (Invitrogen, Waltham, MA, USA) to generate single-strand cDNA. PCR was performed using SYBR[®] Green qPCR Master Mix (Molecular Probes, Eugene, OR, USA) in a StepOnePlus instrument (Applied Biosystems, Waltham, MA, USA). PCR primers, spanning at least one intron are listed in Supplemental Table S3. Standard curves were generated using linearized plasmids encoding the corresponding cDNAs to assure linearity of quantitation. The mean expression levels of the combination of GAPDH and eEf2 (eukaryotic elongation factor 2) were used to normalize target gene expression for total cDNA input from tumor tissue. The mean expression levels of ribosomal protein L32 were used to normalize target gene expression for total cDNA input from QUA muscle tissue. RNA from tissues from at least three mice, each reverse transcribed three times, were analyzed, and qPCR was performed in triplicate for each sample.

Mouse assessments. Total body mass absent tumor was calculated using total body mass by weighing less the mass of the tumor, estimated as 1 mg per cubic millimeter tumor volume for correlative analysis in Supplemental Fig. S3.

Supplemental Discussion

TGF β -family proteins exist largely in a latent pro-domain or inhibitor-bound form and the active, soluble dimeric TGF β -family myokines represent a small proportion of the overall protein (1, 2). Therefore, measurement of functional ligands requires that soluble active TGF β -family myokines be examined using dimer-specific assays (3). Active myostatin c-terminal dimer was measured using a specific immunoblot assay, since available ELISA assays do not discriminate this form from latent pro-domain or inhibitor-bound myostatin c-terminal dimer (4). Dimer-specific ELISA assays used for each of the activins and GDF11, and the myostatin immunoblots, demonstrated distinct patterns of induction for each catabolic myokine in muscle after castration (Fig. 3). Measurement of myostatin and GDF11 has been problematic due to protein homology (5, 6). In muscle, serum, and tumor, the patterns of myostatin and GDF11 expression were distinct (Figs. 3 and 5). Similarly, the function-neutralizing anti-GDF11 monoclonal antibody employed did not cross-react with myostatin (Supplemental Fig. S8). The observed ADT-regulation of soluble active myostatin c-terminal dimer levels and soluble GDF11 are also distinct from the ADT-unregulated and quantitatively ~100-fold higher levels of total acid-solubilized myostatin (Supplemental Fig. S9). These data strongly suggest specific measurement of the castration-induced expression level changes of the active dimers of activins, myostatin, and GDF11, and specific neutralization of circulating GDF11.

References

1. Lee SJ. Extracellular Regulation of Myostatin: A Molecular Rheostat for Muscle Mass. *Immunol Endocr Metab Agents Med Chem*. 2010;10:183-194.
2. Hill JJ, et al. The myostatin propeptide and the follistatin-related gene are inhibitory binding proteins of myostatin in normal serum. *J Biol Chem*. 2002;277(43):40735-41.
3. Rodgers BD. The Immateriality of Circulating GDF11. *Circ Res*. 2016;118(10):1472-4.
4. Anderson SB, Goldberg AL, and Whitman M. Identification of a novel pool of extracellular pro-myostatin in skeletal muscle. *J Biol Chem*. 2008;283(11):7027-35.
5. Eggerman MA, et al. GDF11 Increases with Age and Inhibits Skeletal Muscle Regeneration. *Cell Metab*. 2015;22(1):164-74.
6. Schafer MJ, et al. Quantification of GDF11 and Myostatin in Human Aging and Cardiovascular Disease. *Cell Metab*. 2016;23(6):1207-15.

Supplemental Table S1. Analysis of tumor volume correlation with physiological assessments.
Regression analysis for tumor-bearing cohort #1 of weekly measures of tumor volume versus initial pre-castration tumor volume, and grip strength and total body mass versus tumor volume at the week of assessment.

A: Post-castration tumor volumes versus initial (pre-castration) tumor volume

Relevant to supplemental Fig. S3A

Week	n	slope (% change/1000 mm ³)	Pearson Correlation ('r')	p-Value
wk2	12	-13.4	0.451	0.141
wk4	12	-16.1	0.409	0.186
wk5	12	-21.3	0.476	0.117
wk7	12	-19.5	0.386	0.215
wk8	12	-26.4	0.489	0.106
wk9	12	-22.2	0.496	0.101
wk10	12	-29.9	0.626	0.029
wk14	12	-24.5	0.472	0.121
wk16	12	-27	0.578	0.049

B: Grip strength versus tumor volume at that same week

Relevant to supplemental Fig. S3B

Week	n	slope (N/ml)	Pearson Correlation ('r')	p-Value
wk2	12	-0.032	0.164	0.610
wk4	12	-0.033	0.167	0.603
wk5	12	-0.056	0.342	0.277
wk7	12	-0.043	0.210	0.513
wk8	12	-0.047	0.173	0.590
wk9	12	-0.035	0.237	0.459
wk10	12	-0.033	0.249	0.435
wk14	12	-0.008	0.095	0.769
wk16	12	-0.011	0.130	0.686

Supplemental Table S2. Analysis of tumor volume correlation with end-point measures. Regression analysis of final measures of individual skeletal muscle mass and body composition for tumor-bearing cohort #1 versus initial pre-castration tumor volume.

A: Body composition versus tumor volume after 16 weeks castration

Relevant to supplemental Fig. S3D, S3E

	n	slope (% change/1000 mm ³)	Pearson Correlation ('r')	p-Value
%fat	12	-2.16	0.545	0.067
%fluid	12	0.52	0.065	0.841
%bone	12	0.04	0.277	0.383
%lean	12	1.7	0.599	0.040

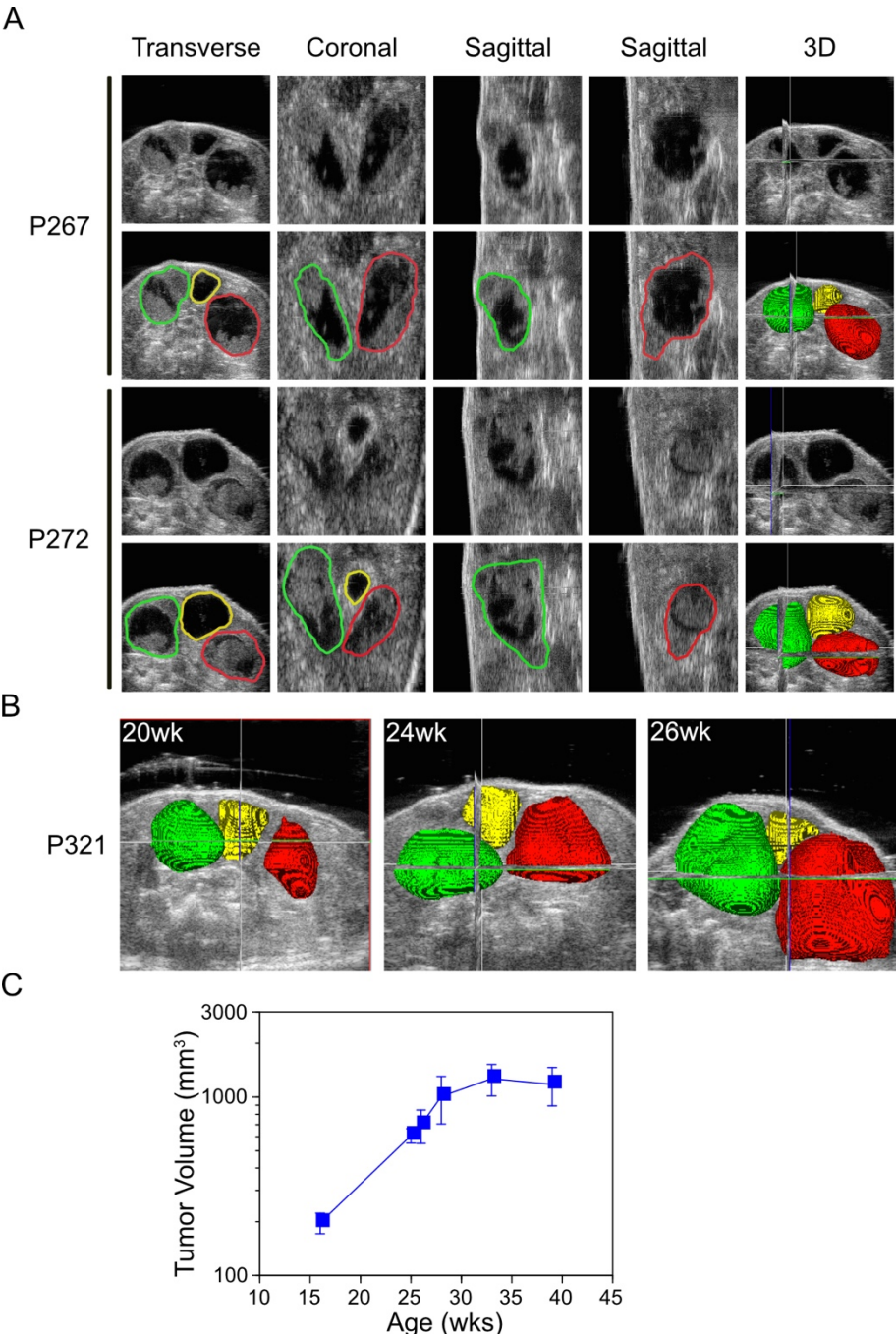
B: Muscle mass versus tumor volume after 16 weeks castration

Relevant to supplemental Fig. S3F

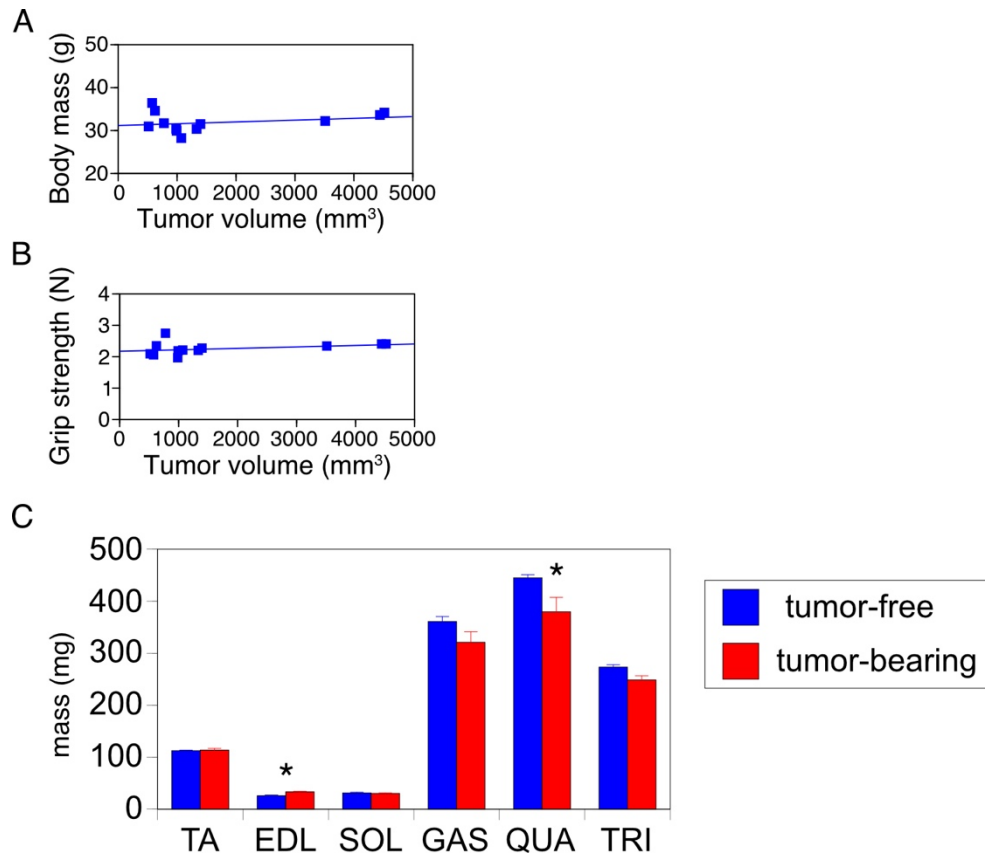
	n	slope (% change/1000 mm ³)	Pearson Correlation ('r')	p-Value
TA	12	-2.7	-0.287	0.366
EDL	12	-1.3	-0.198	0.537
SOL	12	-1.6	-0.358	0.253
GAS	12	-2.3	-0.080	0.805
QUA	12	11	0.328	0.298
TRI	12	-0.8	-0.033	0.926

Supplemental Table S3. Oligonucleotide primers used in qRT-PCR analysis. Forward and reverse primers used to quantitate the indicated gene in RT-qPCR analyses.

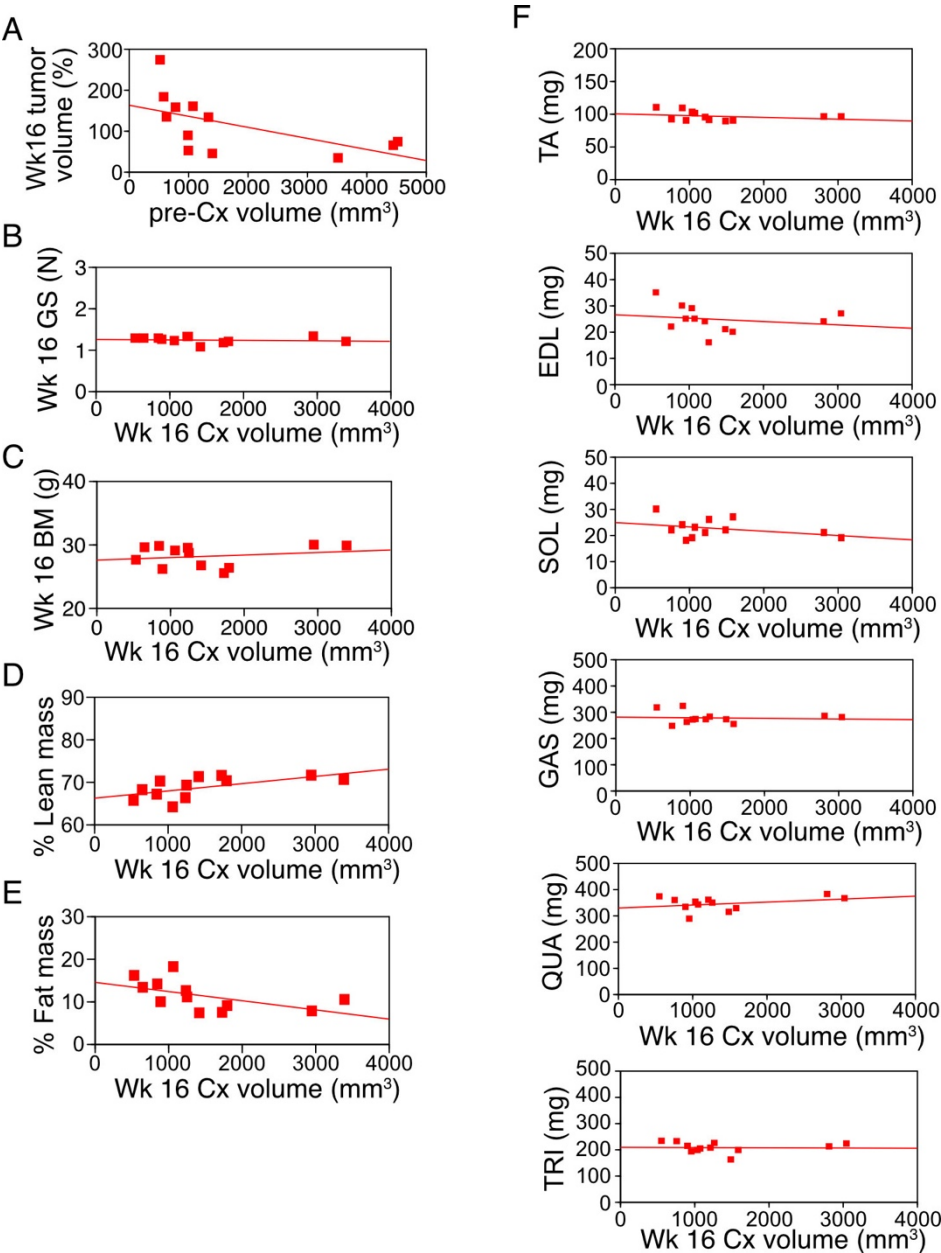
Gene	Forward primer sequence	Reverse primer sequence
B-Actin	GCAGGAGTACGATGAGTCCG	ACGCAGCTCAGTAACAGTCC
EF2	TGCCTTGCGTGTCACCGATGGA	TCAGGACGGGCTTGATGCGTTTACG
GADPH	CTTTGGCATTGTGGAAGGGC	CAGGGATGATGTTCTGGGCA
RpL32	CCTGGTCCACAATGTCAAGGA	TGGGATTGGTGACTCTGATGG
Atrogin-1	GTTCACAAAGGAAGTACGAAGG	AAGCTTTCAACAGACTGGACTTC
MuRF1	ACCTGCTGGTGGAACATC	AGGAGCAAGTAGGCACCTCA
Acvr1b	AAAGCCCTTCTACTGCCTGA	GATGATGCCGACCAGCTC
Acvr1c	GGCTGTGAAGCACGATTCTA	TCCAACCTGAACACCTTCGAG
Acvr2a	CGTTCGCCGTCTTTCTTATC	GCCCTCACAGCAACAAAAGT
Acvr2b	GTGGGAGCTCGTCTCTCG	GGTGTTCAGCCAGTGATCC
Inhibin Ba	GGAGATAGAGGACGACATTGGC	ACGCTCCACTACTGACAGGTCA
Inhibin Bb	CTCCGAGATCATCAGCTTTGCAG	GGAGCAGTTTCAGGTACAGCCA
GDF-11	TTTCGCCAGCCACAGAGCAACT	CTCTAGGACTCGAAGCTCCATG
Myostatin	AACCTTCCCAGGACCAGGAGAA	GGCTTCAAAATCGACCGTGAGG



Supplemental Figure S1. High Frequency Ultrasound imaging (HFUS) with 3D reconstruction quantitated development of PTEN prostate KO tumor. (A) Representative HFUS image slices of the genitourinary region from 2 PB-Cre4:Pten^{fl/fl} mice. Orthogonal planes (transverse, coronal and sagittal at each tumor lobe). The 3D image is an integrated reconstruction using Amira visualization. Bladder (yellow), left (green) and right (red) prostate tumor lobes. (B) Panels show Amira 3D reconstructions of HFUS images from a single PB-Cre4:Pten^{fl/fl} mouse over time. Leftmost illustrates tumor when the mouse is 20 wk (tumor volume = 215 mm³); Middle panel, at 24 wk (tumor volume = 387 mm³); Right panel at 26 wk (tumor volume = 730 mm³) Colors as in A. (C) Growth of tumor volume in mice prior to analysis in Figure 1 (n=13). The later slowing of the overall mean growth rate was due to removal from the analysis of mice bearing the fastest-growing tumors as they were entered into the experimental protocol.



Supplemental Figure S2. Tumor burden did not influence total body mass, grip strength, or individual skeletal muscle mass. (A) Individual total body mass (BM), corrected for imputed tumor mass, was not correlated with tumor volume ($R^2=0.07$, $p=0.41$). (B) Grip strength (GS) was not correlated with pre-castration tumor volume ($R^2=0.12$, $p=0.28$). (C) Mass of TA, SOL, GAS, and TRI skeletal muscles from tumor-free mice (blue) did not differ from muscles from tumor-bearing mice (red). EDL was increased in tumor bearing mice, while QUA was decreased in tumor bearing mice (* $p<0.05$), determined using one-way ANOVA with Dunnett's test.



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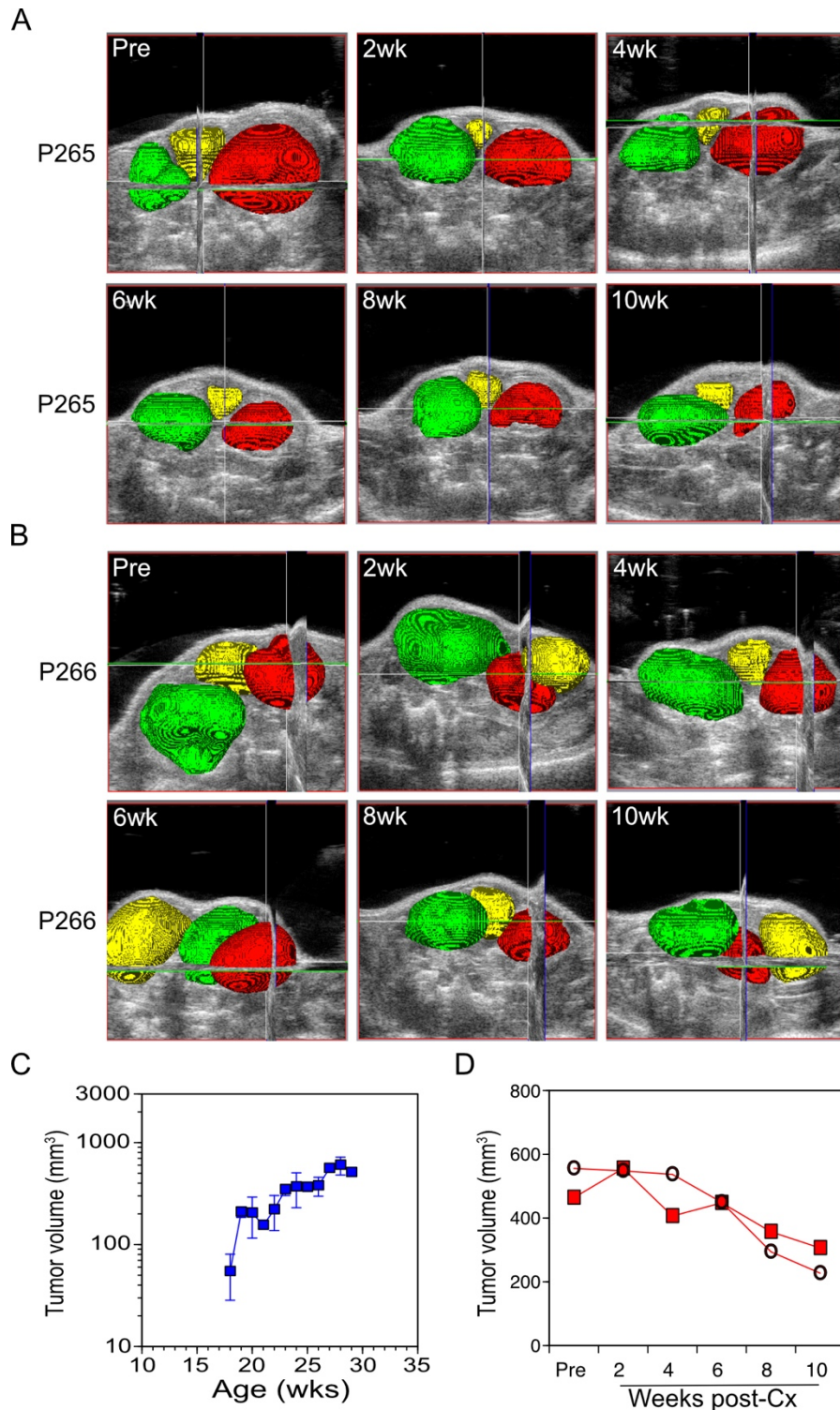
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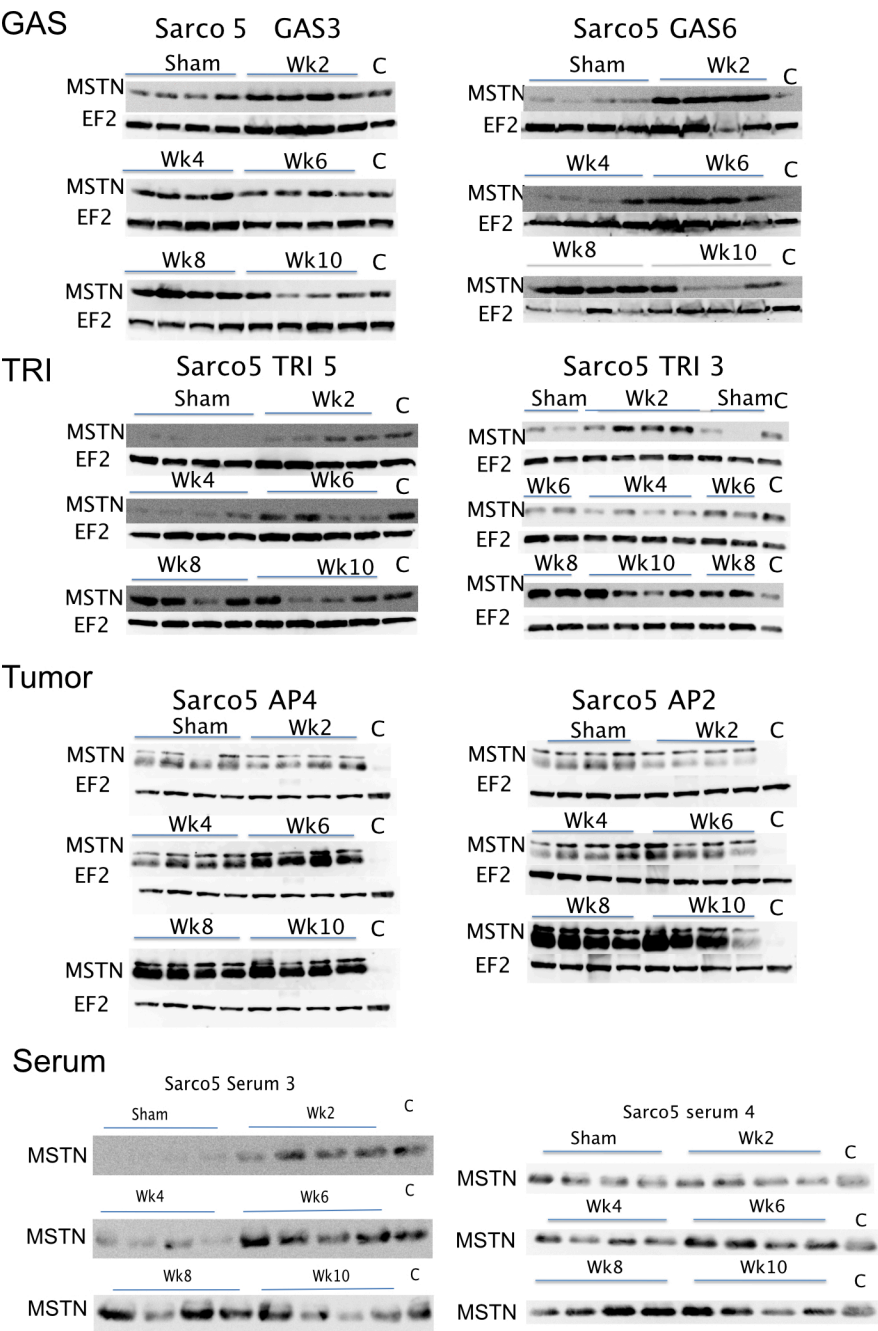
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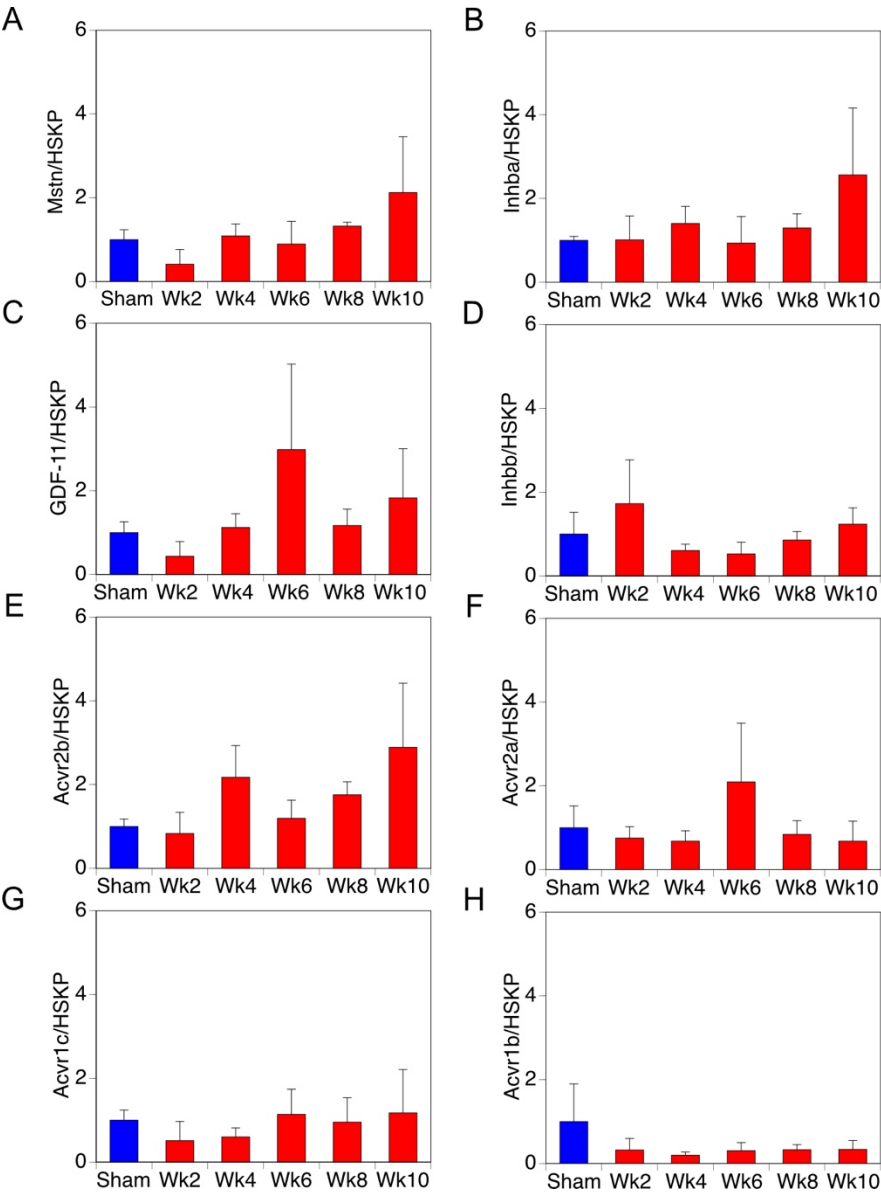
Supplemental Figure S3. Large tumors regressed more, but tumor burden did not alter grip strength, body mass, body composition, or skeletal muscle mass 16 weeks after castration. (A) Tumor regression (tumor volume as a percentage of initial volume) after 16 weeks castration (Cx) was negatively correlated (~ -25% / 1000 mm³) with pre-Cx tumor volume (p=0.049). (B) Grip strength (GS), in Newtons (N), was not correlated with tumor volume at any time up to 16 weeks after Cx. (C) Individual mean total body mass (BM), corrected for imputed tumor mass, was not correlated (R²=0.21, p=0.51) with tumor volume 16 weeks after Cx. (D) Whole-body lean mass by qNMR (including tumor) increased 1.7% per 1000 mm³ of increased tumor volume (p= 0.040) 16 weeks after Cx. (E) Whole-body fat mass by qNMR was not correlated (p= 0.067) with increased tumor volume 16 weeks after Cx. (F) Mass of individual skeletal muscles was not correlated with increased tumor volumes 16 weeks after Cx. Line indicates linear regression, n=12 for each muscle. See Supplemental Table S1 for intermediate time point (wk2-wk14) data, and Table S2 for end point data including slopes, Pearson correlations, and p-values.



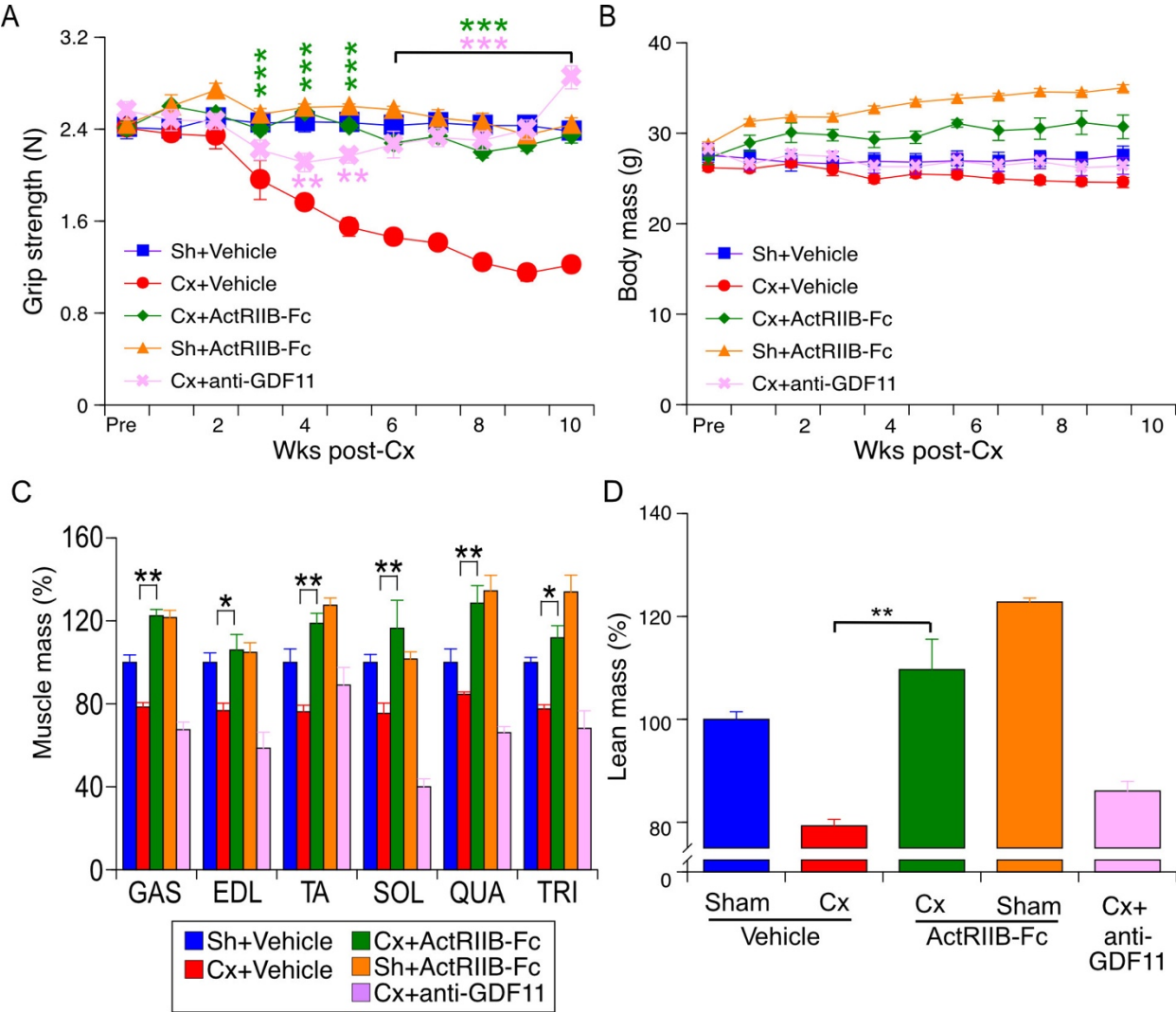
Supplemental Figure S4. High Frequency Ultrasound imaging with 3D reconstruction quantitated regression of PTEN prostate KO tumor. (A) Panels show Amira 3D reconstructions of HFUS images of prostate tumor from a single PB-Cre4:Pten^{fl/fl} mouse imaged prior to castration (pre) and every two weeks for 10 weeks after castration. Bladder (yellow), left (green) and right (red) prostate tumor lobes. (B) As in A. for a second tumor-bearing mouse. (C) Growth of tumor volume in mice prior to castration (n=12). (D) Quantitation of the tumor volumes of the mice depicted in each panel of A. (P265, open circles) and B. (P266, solid squares).



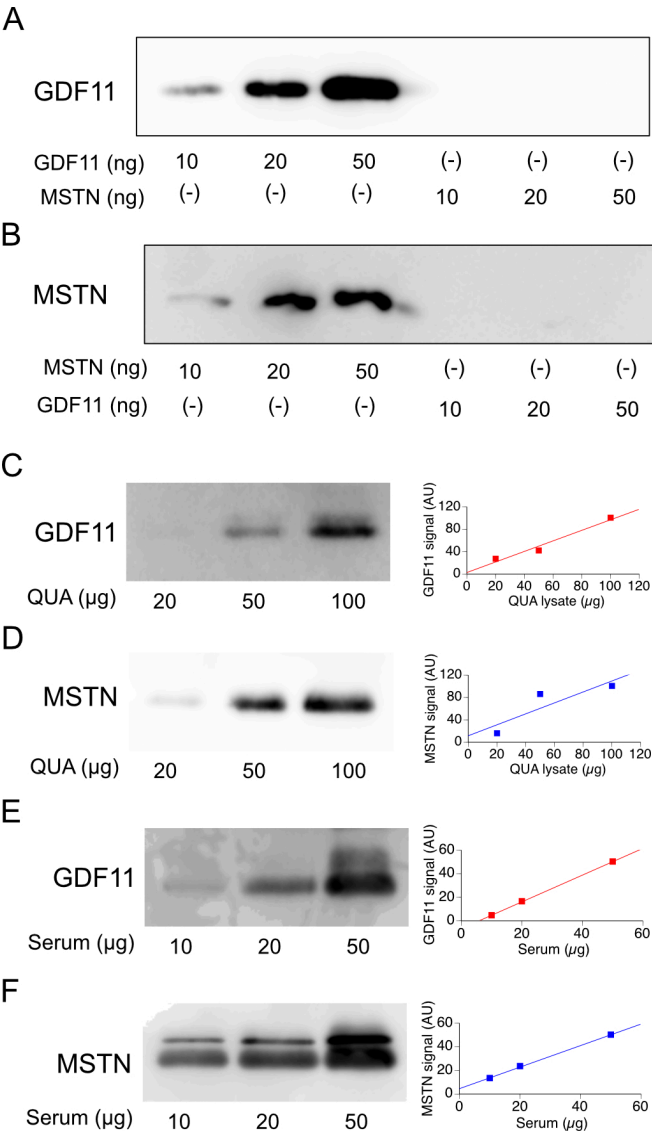
Supplemental Figure S5. Second and third replicates of immunoblots for myostatin quantitation in Figures 3 and 5. Images of the additional immunoblots of myostatin (MSTN), including eukaryotic elongation factor 2 (EF2) expression in prostate tumor tissue from sets of 4 mice, castrated for the indicated times or sham-castrated. Lanes of immunoblots marked “C” contain identical control sample for inter-blot comparison.



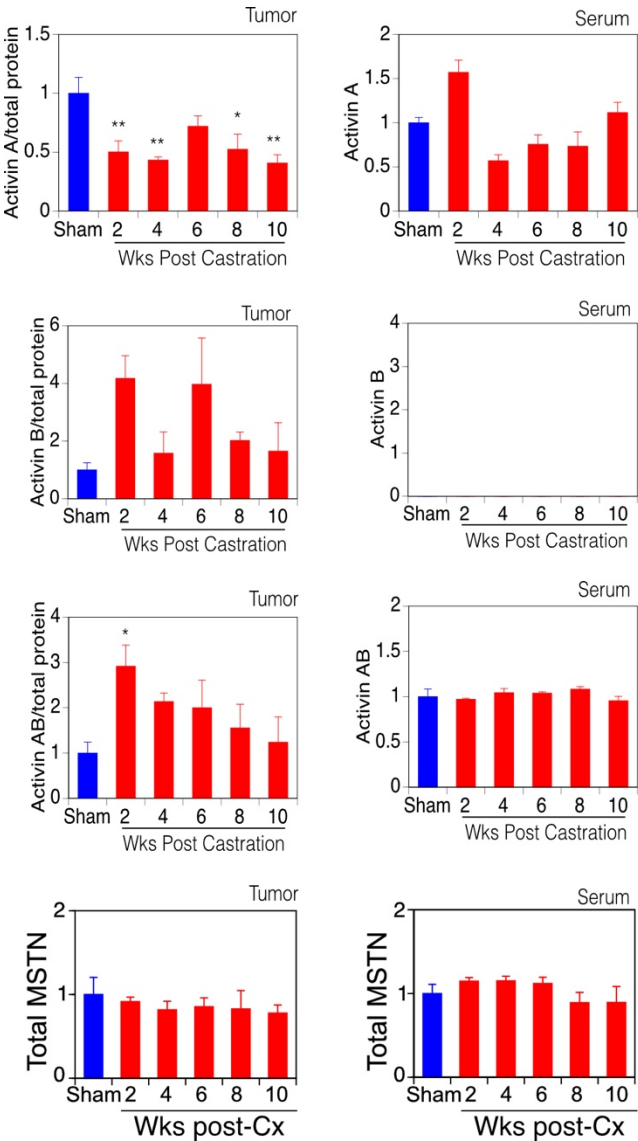
Supplemental Figure S6. Quantitation of TGFβ-family myokine related mRNAs in muscle. Expression of the indicated ligand and receptor mRNAs (A-H) from QUA muscle tissue of PTEN prostate KO mice sacrificed at the indicated number of weeks after castration. Expression of each gene was normalized to control (HSKP), and subsequently to the sham castrate expression levels, from 4 mice at each time, measured 3 times.



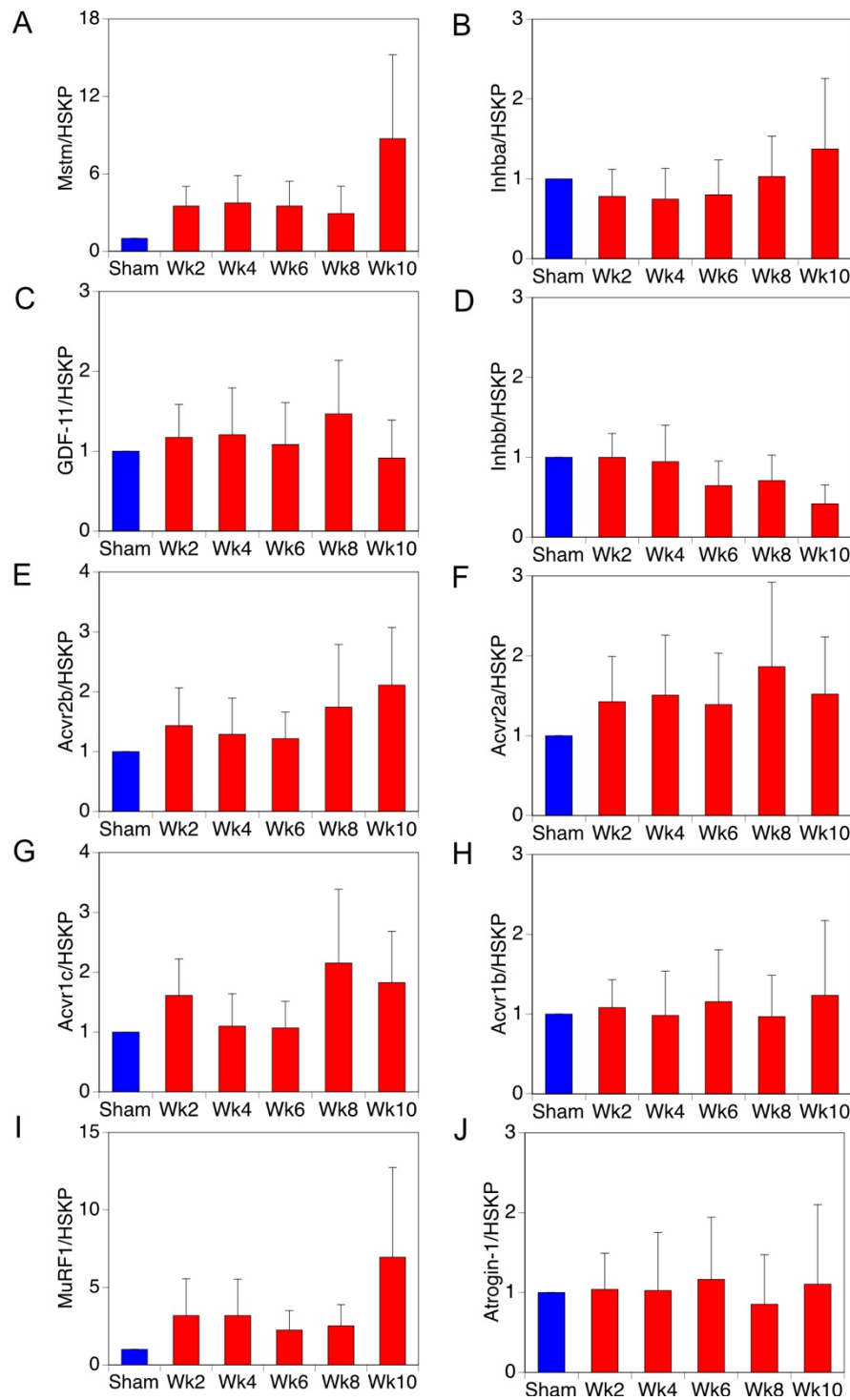
Supplemental Figure S7. Additional data for TGFβ-family myokine ligand blockade treated cohorts of Fig. 4, including Sham-castrated/ActRIIB-Fc treated cohort and Total body mass. (A) Grip strength after castration or sham-castration of mice treated with PBS, ActRIIB-Fc, or anti-GDF11 antibody. In addition to the indicated comparisons (green and purple asterisks), mice castrated and vehicle treated were also different ($p < 0.001$) from either sham castrated group from three weeks after castration. **(B)** Total body mass. **(C)** Individual skeletal muscle mass after 10 weeks castration by dissection and weighing. **(D)** Lean body mass by qNMR, as % of sham-castrated. Not indicated: Castration induced a significant reduction of each muscle mass and lean body mass ($p < 0.05$, blue versus red columns). ActRIIB-Fc treated groups were not different from each other. Mean (lines or columns), SEM (bars). $n = 3-5/\text{group}$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ for ActRIIB-Fc treated castrated (or anti-GDF11 treated castrated) versus vehicle treated castrated mice determined using two-way ANOVA with Tukey's HSD test.



Supplemental Figure S8. Anti-GDF11 and anti-MSTN antibodies are sensitive and specific. (A) Immunoblot using anti-GDF11 (R&D #MAB19851) of an SDS-PAGE gel containing the indicated quantity of purified GDF11 and MSTN. (B) Immunoblot using anti-MSTN antibody (R&D #788-G8) of an SDS-PAGE gel containing the indicated quantity of purified MSTN and GDF11. (C) Immunoblot of GDF11 active dimer expression in the indicated quantity of mouse quadriceps (QUA) muscle extract. Right, quantitation of GDF11 active dimer expression versus total protein, $R^2 = 0.96$. (D) Immunoblot of MSTN active dimer expression in mouse quadriceps (QUA) muscle extract. Right, quantitation of MSTN active dimer expression versus total protein, $R^2 = 0.76$. E, Immunoblot of GDF11 active dimer expression in the indicated quantity of serum. Right, quantitation of GDF11 active dimer expression versus total protein, $R^2 = 0.99$. (F) Immunoblot of MSTN active dimer expression in the indicated quantity of serum. Right, quantitation of MSTN active dimer expression versus total protein, $R^2 = 0.99$.

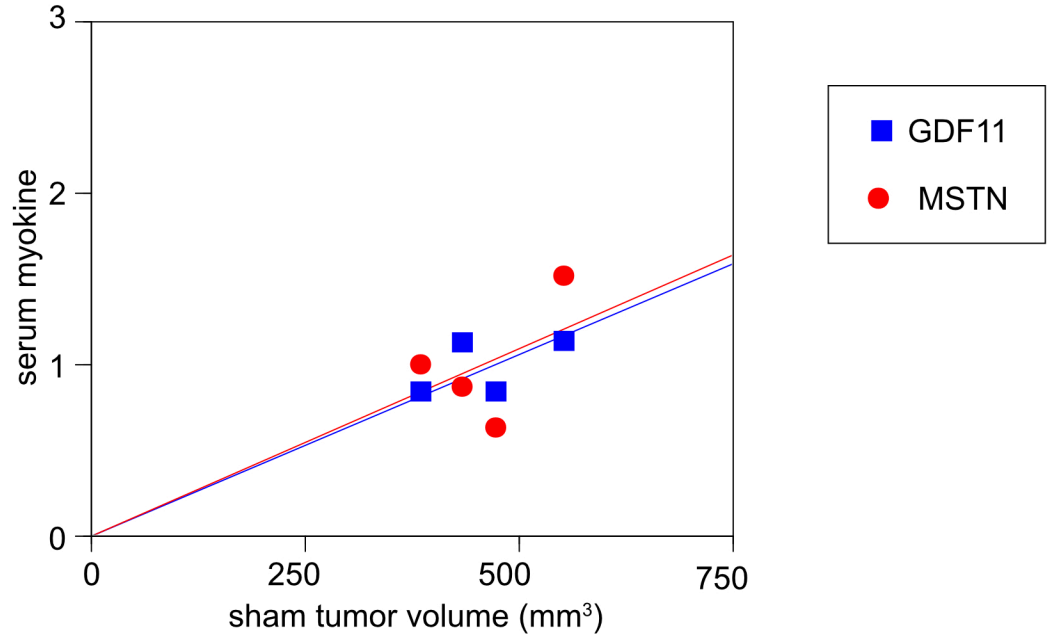


Supplemental Figure S9. Activins and total myostatin in tumor and serum after castration. ELISA determined levels of soluble, active activin A, Activin B, and Activin AB proteins, and total acid-solubilized myostatin (MSTN) in tumor and serum at the indicated time after castration. Activin B was not detected in serum. Mean protein levels after castration were normalized to sham-castrate group, from 4 mice at each time, measured 3 times.

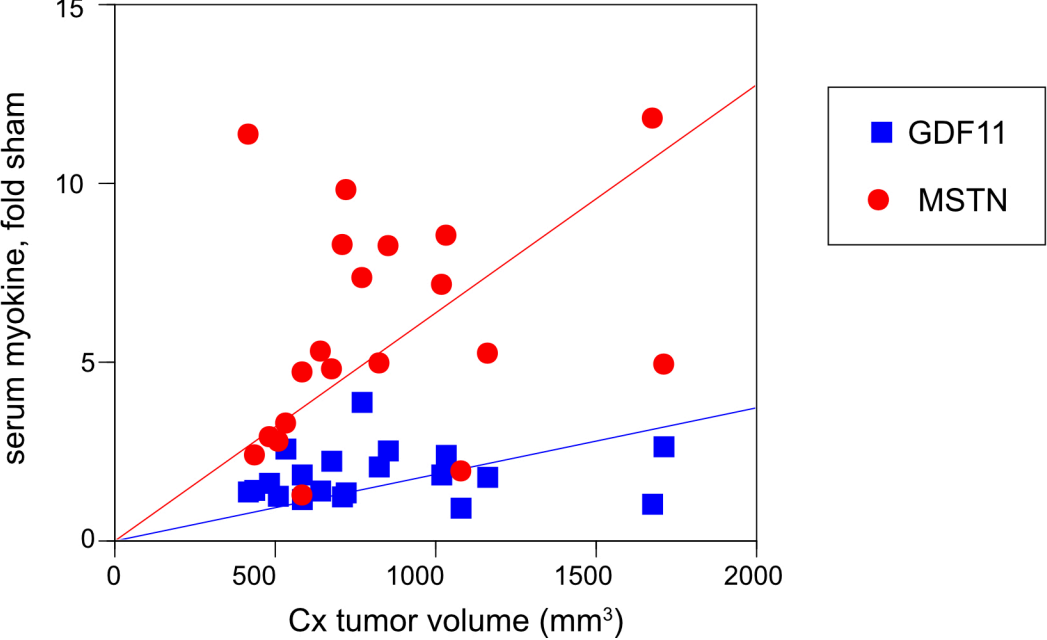


Supplemental Figure S10. Quantitation of catabolic TGFβ-family myokine-related mRNAs in tumor. Expression of the indicated myokine associated mRNAs (A-J) from tumor tissue of PTEN prostate KO mice sacrificed at the indicated number of weeks after castration. Expression of each gene was normalized to control (HSKP) gene expression levels, and subsequently to the sham castrate expression levels, from 4 mice at each time, measured 3 times.

A



B



Supplemental Figure S11. Tumor volume predicted circulating GDF11 and myostatin protein levels. ELISA determined soluble GDF11 levels or immunoblot determined soluble active myostatin levels plotted by tumor volume (A) Myokines in serum of sham castrated animals in cohort #2 (n=4). Correlation for GDF11 $R^2=0.98$, $p=0.018$, MSTN $R^2=0.93$, $p=0.065$. (B) Myokines in serum at week of harvest for castrated (Cx) animals in cohort #2 (n=20). Correlation for GDF11 $R^2=0.75$, $p<0.001$, MSTN $R^2=0.76$, $p<0.001$.