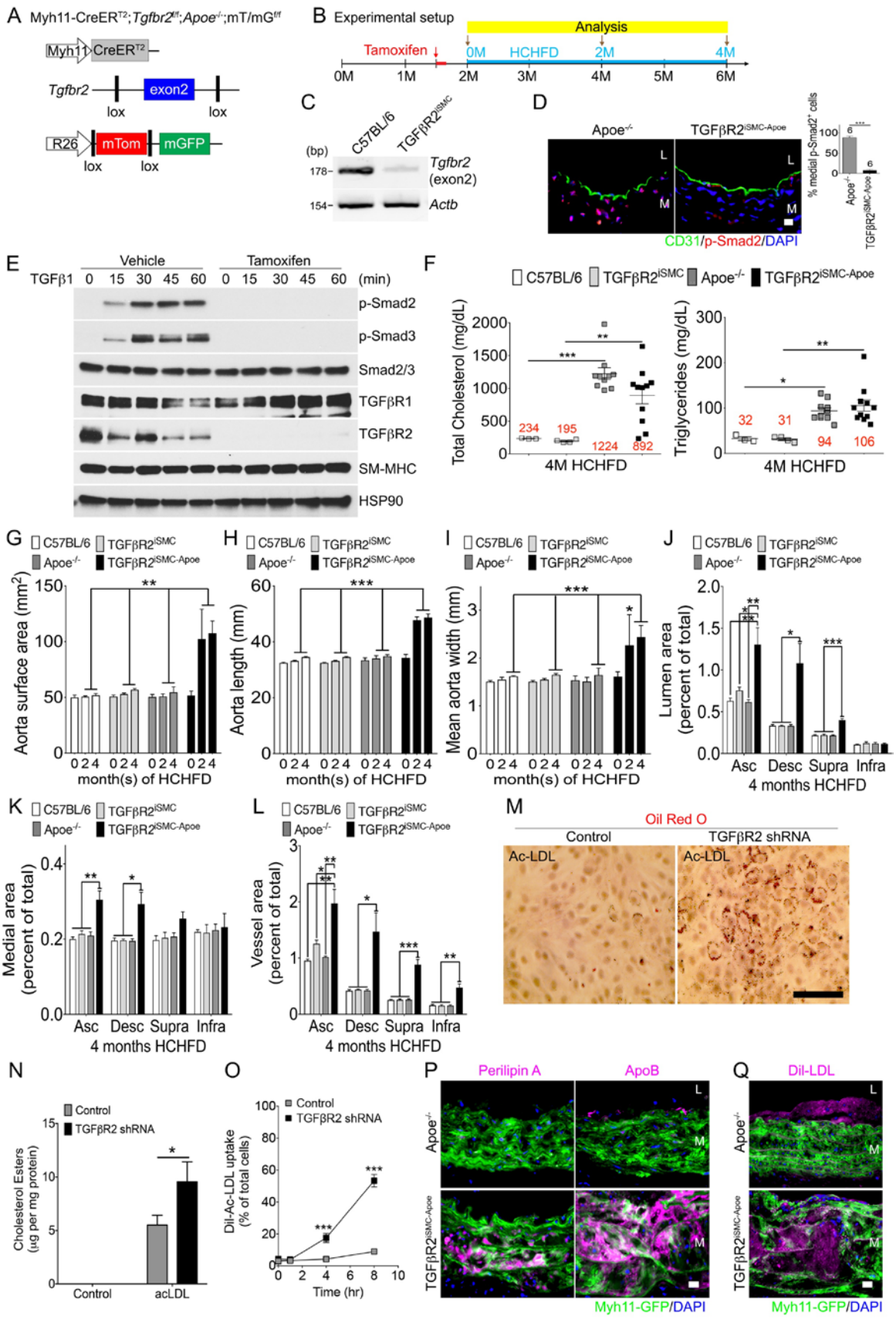
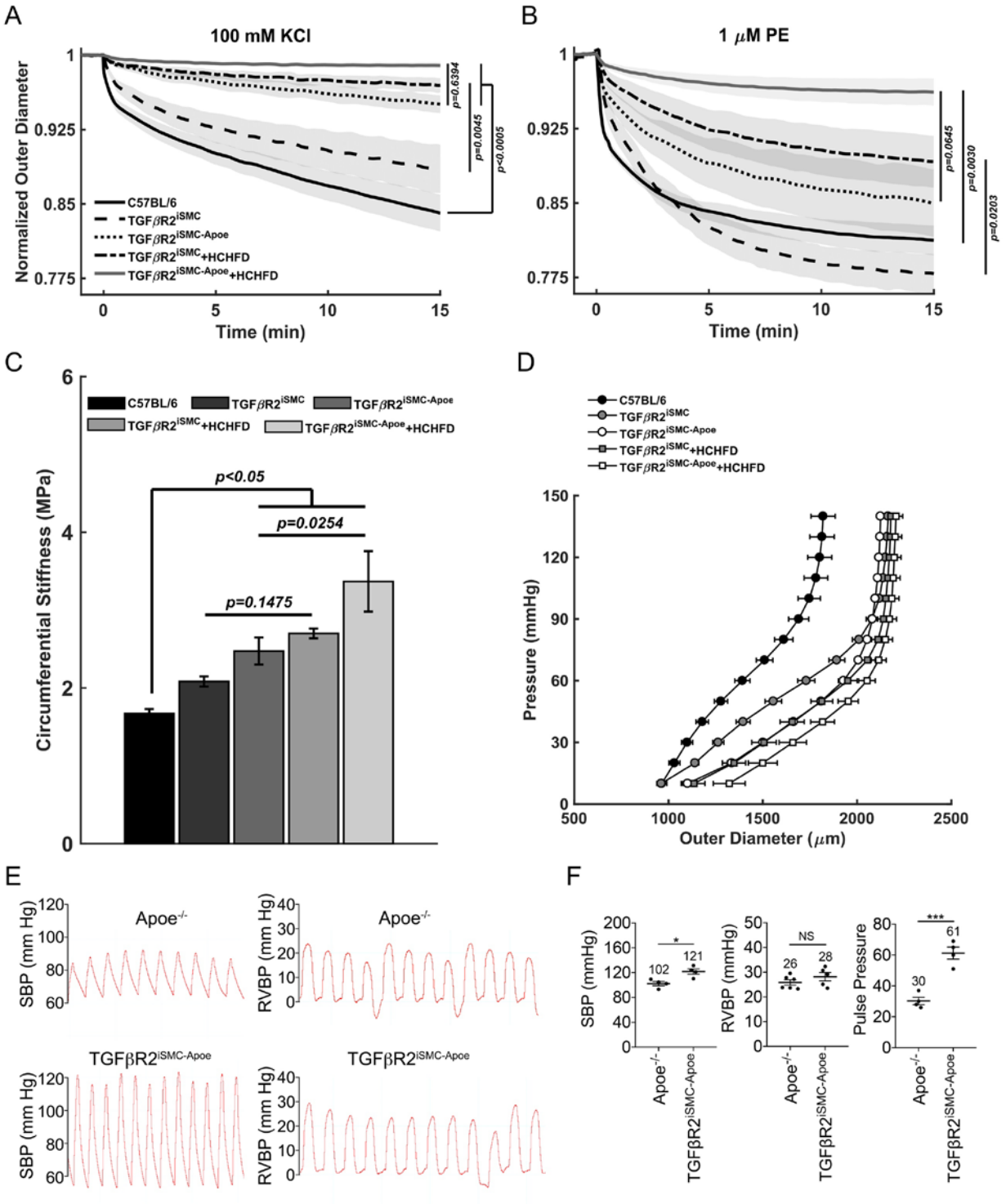

A
Myh11-CreER^{T2};*Tgfbr2*$^{f/f}$;*Apoe*$^{-/-}$;mT/mG$^{f/f}$
Myh11
CreER^{T2}
Tgfbr2
exon2
lox
lox
R26
mTom
mGFP
lox
lox
B
Experimental setup
Analysis
Tamoxifen
0M
HCHFD
2M
4M
0M
1M
2M
3M
4M
5M
6M
C
C57BL/6
TGFβR2^{iSMC}
(bp)
178
154
Tgfbr2
(exon2)
Actb
D
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
L
M
CD31/p-Smad2/DAPI
% medial p-Smad2$^+$ cells
100
50
0
6
6
***
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
E
Vehicle
Tamoxifen
TGFβ1
0 15 30 45 60 0 15 30 45 60 (min)
p-Smad2
p-Smad3
Smad2/3
TGFβR1
TGFβR2
SM-MHC
HSP90
F
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Total Cholesterol (mg/dL)
2000
1500
1000
500
0
234
195
1224
892
4M HCHFD
Triglycerides (mg/dL)
300
200
100
0
32
31
94
106
4M HCHFD
G
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Aorta surface area (mm^2)
150
100
50
0
0 2 4 0 2 4 0 2 4 0 2 4
month(s) of HCHFD
H
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Aorta length (mm)
60
40
20
0
0 2 4 0 2 4 0 2 4 0 2 4
month(s) of HCHFD
I
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Mean aorta width (mm)
3
2
1
0
0 2 4 0 2 4 0 2 4 0 2 4
month(s) of HCHFD
J
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Lumen area (percent of total)
2.0
1.5
1.0
0.5
0.0
Asc Desc Supra Infra
4 months HCHFD
K
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Medial area (percent of total)
0.4
0.2
0.0
Asc Desc Supra Infra
4 months HCHFD
L
C57BL/6
TGFβR2^{iSMC}
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
Vessel area (percent of total)
3
2
1
0
Asc Desc Supra Infra
4 months HCHFD
M
Oil Red O
Control
TGFβR2 shRNA
Ac-LDL
Ac-LDL
N
Control
TGFβR2 shRNA
Cholesterol Esters (μg per mg protein)
15
10
5
0
Control
acLDL
O
Control
TGFβR2 shRNA
DiI-Ac-LDL uptake (% of total cells)
100
80
60
40
20
0
0 2 4 6 8 10
Time (hr)
P
Perilipin A
ApoB
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
L
M
Myh11-GFP/DAPI
Q
DiI-LDL
Apoe$^{-/-}$
TGFβR2$^{iSMC-Apoe}$
L
M
Myh11-GFP/DAPI

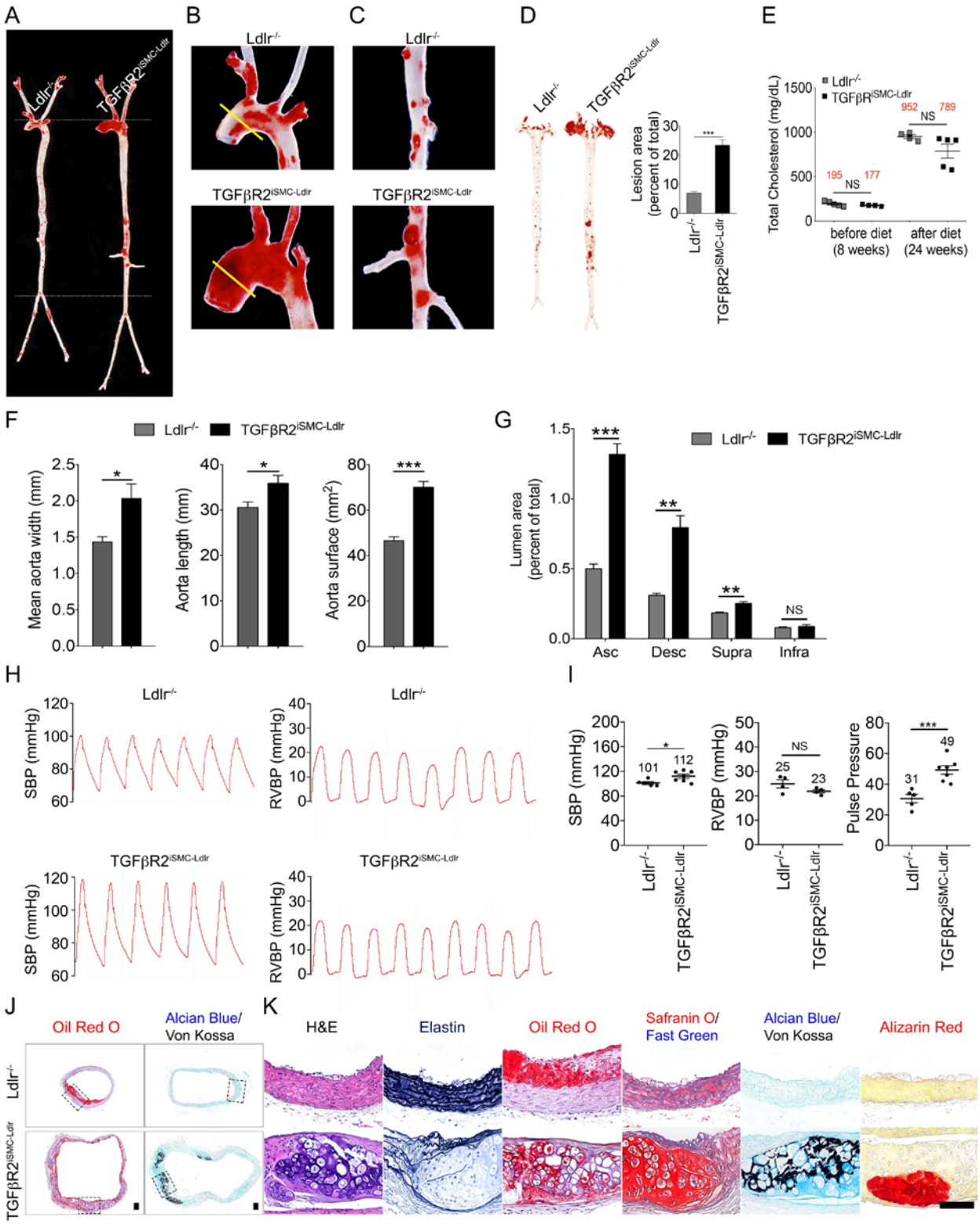
Supplementary Figure 1. Related to Figure 2. Generation and characterization of *Apoe*$^{-/-}$ mice with smooth muscle cell-specific *Tgfbr2* ablation.

(A) Scheme of the Myh11-CreER^{T2} transgene, *Tgfbr2* floxed alleles, and R26-mTmG reporter constructs. (B) Scheme of Tamoxifen injection (1 mg/day i.p. for 5 days starting at 6 weeks old) and high cholesterol high fat diet (HCHFD) feeding. (C) PCR for Tgfbr2 exon 2 mRNA expression using medial layers of mouse ascending aorta without adventitia. (D) Representative images of p-Smad2 immunofluorescence staining of *Apoe*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Apoe}$ aorta. Endothelial cells are visualized by CD31 (green). L: lumen. M: Media. Nuclei were stained with DAPI (blue). N= 6 mice/group. Scale bar: 10 μm. (E) Aortic smooth muscle cells were isolated from vehicles or tamoxifen treated mice and were treated with TGFβ1 (0.5 ng/ml) for the indicated times and downstream signaling was analyzed by immunoblotting. Blots are representative of 3 independent experiments. (F) Total cholesterol and triglycerides levels from C57BL/6, TGFβR2^{iSMC}, *Apoe*$^{-/-}$, and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months on a HCHFD (*p<0.05; **p<0.01; ***p<0.001; unpaired two-tailed Student's t test). N=3 for C57BL/6 mice; N=4 for TGFβR2^{iSMC} mice; N=10 for *Apoe*$^{-/-}$ mice; and N=11 for TGFβR2$^{iSMC\text{-}Apoe}$ mice. (G-I) Aorta surface area, aorta length, and width in C57BL/6, TGFβR2^{iSMC}, *Apoe*$^{-/-}$, and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 0, 2, 4 months on a high cholesterol high fat diet (HCHFD). All data shown as mean ± SEM (*p<0.05; ***p<0.01; ***p<0.001; unpaired two-tailed Student's t test) (for each time point N=3 for C57BL/6 mice; N=3 for TGFβR2^{iSMC} mice; N=11 for *Apoe*$^{-/-}$ mice; and N=11 for TGFβR2$^{iSMC\text{-}Apoe}$ mice). (J-L) Lumen, media, and vessel areas of ascending (Asc), descending (Desc), suprarenal (Supra), and infrarenal (Infra) aortas in 24-week-old mice after 4 months of HCHFD. All data shown as mean ± SEM (*p<0.05; ***p<0.01; ***p<0.001; unpaired two-tailed Student's t test) (N=3 for C57BL/6 mice; N=3 for TGFβR2^{iSMC} mice; N=11 for *Apoe*$^{-/-}$ mice; and N=11 for TGFβR2$^{iSMC\text{-}Apoe}$ mice). (M) Representative pictures from control and TGFβR2 knockdown HASMCs incubated with Ac-LDL (100 μg/ml) for 72 hrs and stained with Oil Red O. Nuclei were counterstained with haematoxylin. Images are representative of three independent experiments. Scale bar: 100 μm. (N) Control and TGFβR2 knockdown HASMCs were incubated with or without Ac-LDL (100 μg/ml) for 72 hrs. Quantification of cholesterol esters in control and TGFβR2 knockdown HASMCs. Data represent the mean ± SEM and are representative of three experiments in duplicate. (*p<0.05; unpaired two-tailed Student's t test). (O) Cells were treated with control and TGFβR2 shRNA for 4 days and incubated with Dil-Ac-LDL (100 μg/ml) in low LDL media (LPDS) for 0, 1, 4, 8 hrs at 37°C. At the end of labeling period, cells were rinsed with probe-free media and analyzed by FACS. Data represent the mean ± SEM and are representative of three experiments in duplicate. (***p<0.001; unpaired two-tailed Student's t test). (P) Immunohistochemical staining of Perilipin A (lipid droplet) and ApoB (major very-low-density lipoprotein component) in the ascending aortas of *Apoe*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 1 month of high cholesterol high fat diet (N=3 mice/group). L: lumen. M: Media. Nuclei were counterstained with DAPI (blue). Scale bar: 16 μm. (Q) Cross-section images of ascending aorta from *Apoe*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Apoe}$ mice 18 hrs after intravenous injection with DiI-LDL (300 μg). Immunofluorescence analysis of DiI-LDL infiltration (N=3 mice/group). I: Intima. L: lumen. M: Media. Nuclei were counterstained with DAPI (blue). Scale bar: 16 μm.



Supplementary Figure 2. Related to Figure 2. Active, passive biomechanical analysis, and blood pressure measurement of C57BL/6, TGFβR2^{iSMC}, *Apoe*$^{-/-}$, and TGFβR2$^{iSMC\text{-}Apoe}$ mice ascending aortas.
(A,B) Time-course of changes in outer diameter of the ascending aorta following *ex vivo* exposure to (A) potassium chloride (KCl) or (B) phenylephrine (PE), with diameter normalized to the group-specific value prior to agonist exposure (time < 0 min). Transmural pressure was maintained at 90 mmHg and axial stretch at group-specific *in vivo* values λ_z^{iv}. Lines denote group means and shaded regions denote ± SEM. Between-group *p* values are shown for C57BL/6 vs. all mutant groups as well as for mutants on normal vs. high cholesterol high fat diet (HCHFD).

Contractile response to PE is significantly impaired in the TGFβR2^{iSMC} group with a HCHFD compared to those on a normal diet. Though change in normalized diameter was not different between TGFβR2$^{iSMC\text{-}Apoe}$ on a normal diet and HCHFD, differences manifested when comparing contractile induced reductions in circumferential wall stress ($p = 0.0291$). N=5 for C57BL/6 mice; N=5 for TGFβR2^{iSMC} mice; N=4 for TGFβR2$^{iSMC\text{-}Apoe}$ mice; N=5 for TGFβR2^{iSMC} mice fed with HCHFD; and N=4 for TGFβR2$^{iSMC\text{-}Apoe}$ mice fed with HCHFD. (C) Circumferential material stiffness increases with lipid challenge in the TGFβR2$^{iSMC\text{-}Apoe}$ group alone. Data are represented as mean ± SEM. Significance was considered when $p < 0.05$. N=5 for C57BL/6 mice; N=5 for TGFβR2^{iSMC} mice; N=4 for TGFβR2$^{iSMC\text{-}Apoe}$ mice; N=5 for TGFβR2^{iSMC} mice fed with HCHFD; and N=4 for TGFβR2$^{iSMC\text{-}Apoe}$ mice fed with HCHFD. (D) Pressure-diameter data from fixed-length cyclic pressurization testing at λ_z^{iv}. The pressure-diameter behavior of the TGFβR2$^{iSMC\text{-}Apoe}$ + HCHFD group (white squares) loses the characteristic "S"-shape, suggesting that the elastic fibers contribute less. N=5 for C57BL/6 mice; N=5 for TGFβR2^{iSMC} mice; N=4 for TGFβR2$^{iSMC\text{-}Apoe}$ mice; N=5 for TGFβR2^{iSMC} mice fed with HCHFD; and N=4 for TGFβR2$^{iSMC\text{-}Apoe}$ mice fed with HCHFD. (E) Representative record of SBP and RVBP in *Apoe*$^{-/-}$and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months of HCHFD. N=4 mice/group. (F) Summarized data (mean ± SEM) showing the peak value of SBP, RVBP and pulse pressure.

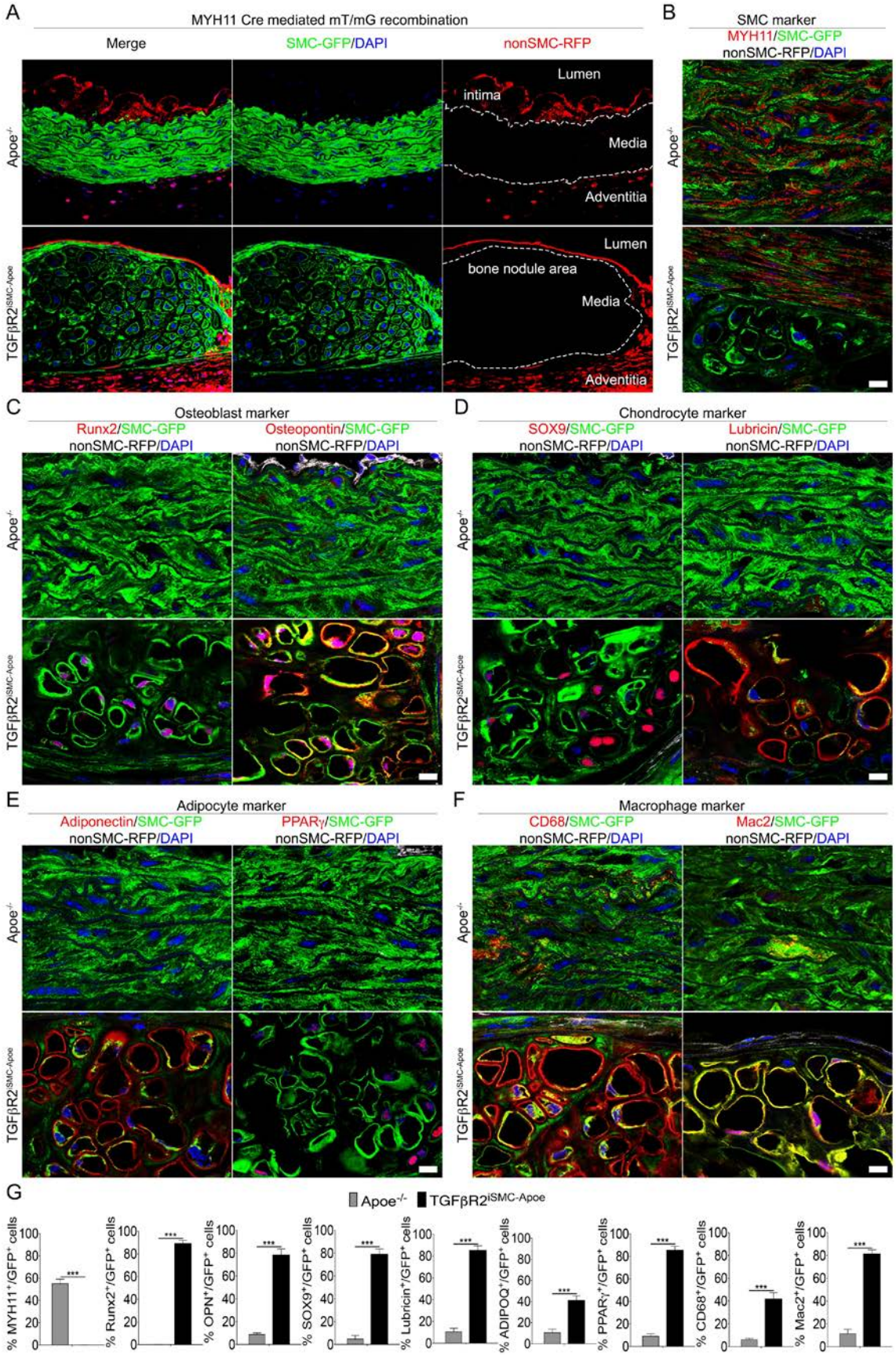


Supplementary Figure 3. Related to Figure 2 and Figure 3. Smooth muscle cell *Tgfbr2* knockout in *Ldlr*$^{-/-}$ background accelerates aneurysm formation and atherosclerosis plaque development.

(A-C) Representative photomicrographs of Oil-Red-O stained whole aorta (A), aortic arch (B) or abdominal aorta (C) of *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC-Ldlr}$ mice after 4 months of high cholesterol high fat diet (HCHFD). N=3 mice/group.

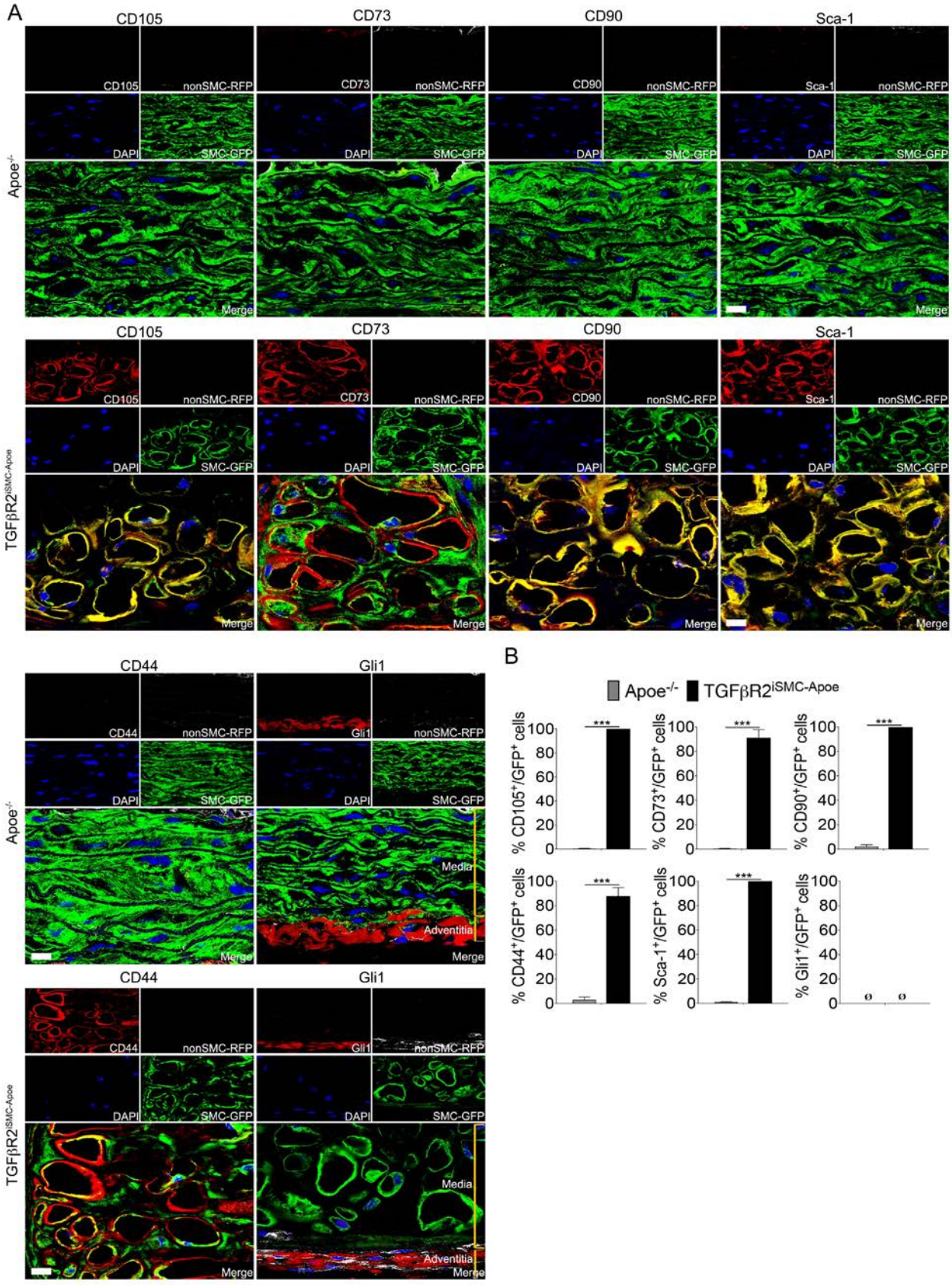
(D) (left) Microphotographs of en face aortas from *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC-Ldlr}$ mice after 4 months of HCHFD

stained with Oil-Red-O. (right) Lesion area quantification: % lesion area refers to Oil-Red-O stained as a % of the total aortic surface. All data shown as mean ± SEM (Ø: not detected; ***p<0.001; unpaired two-tailed Student's t test) (N=10 mice/group). (E) Total cholesterol levels from *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Ldlr}$ mice after 4 months on a HCHFD (NS: not significant; unpaired two-tailed Student's t test). N=4 mice/group. (F) Aorta surface area, aorta length, and width in *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Ldlr}$ mice after 4 months on a high cholesterol high fat diet (HCHFD). All data shown as mean ± SEM (*p<0.05; ***p<0.001; unpaired two-tailed Student's t test) (N=10 mice/group). (G) Lumen areas of ascending (Asc), descending (Desc), suprarenal (Supra), and infrarenal (Infra) aortas in 24-week-old mice after 4 months of HCHFD. All data shown as mean ± SEM (NS: not significant; **p<0.01; ***p<0.001; unpaired two-tailed Student's t test) (N=10 mice/group). (H) Representative record of SBP and RVBP in *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Ldlr}$ mice. (I) Summarized data (mean ± SEM) showing the peak value of SBP, RVBP and pulse pressure. For SBP and pulse pressure measurement N=5 for *Ldlr*$^{-/-}$ mice; and N=7 for TGFβR2$^{iSMC\text{-}Ldlr}$ mice; for RVBP measurement N=4 mice/group. (J) Histologic analysis of mouse ascending aortas dissected from 24-week-old *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Ldlr}$ mice after 4 months of high cholesterol high fat diet (HCHFD). Representative low-magnification images of Oil-Red-O and Alcian Blue (cartilage)/Von Kossa (bone) stained mouse ascending aortas. N=6 mice/group. Scale bar: 200 μm. (K) Representative images of H&E, Elastin, Oil-Red-O, Safranin O (cartilage)/Fast Green, Alcian Blue (cartilage)/Von Kossa (bone), and Alizarin Red (calcium)-stained mouse ascending aortas from *Ldlr*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Ldlr}$ mice (N=6 mice/group). Scale bar: 50 μm.


A
MYH11 Cre mediated mT/mG recombination
Merge
SMC-GFP/DAPI
nonSMC-RFP
Lumen
intima
Media
Adventitia
Lumen
bone nodule area
Media
Adventitia
Apoe-/-
TGFβR2iSMC-Apoe
B
SMC marker
MYH11/SMC-GFP
nonSMC-RFP/DAPI
C
Osteoblast marker
Runx2/SMC-GFP
nonSMC-RFP/DAPI
Osteopontin/SMC-GFP
nonSMC-RFP/DAPI
D
Chondrocyte marker
SOX9/SMC-GFP
nonSMC-RFP/DAPI
Lubricin/SMC-GFP
nonSMC-RFP/DAPI
E
Adipocyte marker
Adiponectin/SMC-GFP
nonSMC-RFP/DAPI
PPARγ/SMC-GFP
nonSMC-RFP/DAPI
F
Macrophage marker
CD68/SMC-GFP
nonSMC-RFP/DAPI
Mac2/SMC-GFP
nonSMC-RFP/DAPI
G
Apoe-/-
TGFβR2iSMC-Apoe
% MYH11+/GFP+ cells
% Runx2+/GFP+ cells
% OPN+/GFP+ cells
% SOX9+/GFP+ cells
% Lubricin+/GFP+ cells
% ADIPOQ+/GFP+ cells
% PPARγ+/GFP+ cells
% CD68+/GFP+ cells
% Mac2+/GFP+ cells
***

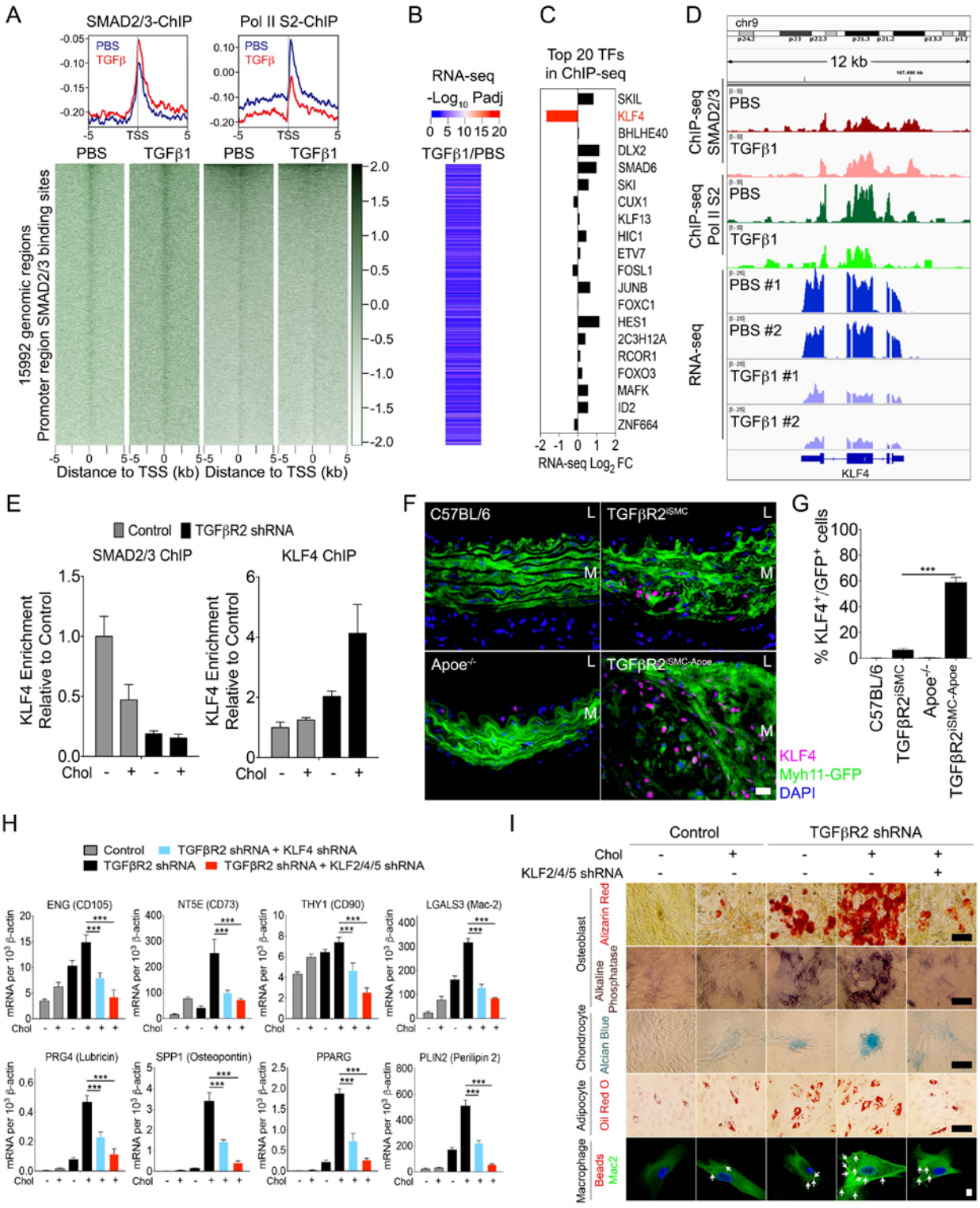
Supplementary Figure 4. Related to Figure 3 and Figure 4. SMCs express smooth muscle cell, chondrocyte, adipocyte, osteoblast, and macrophage lineage markers in TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months of high cholesterol high fat diet.

(A) Z-stack confocal images of ascending aorta cross sections showing tamoxifen-dependent loss of RFP (red) and induction of GFP (green) expression by vessel wall cells selectively within the media, but not the neointima or adventitia, with DAPI-labeled nuclei (blue) in overlays (bar=10 μm). Please note: only GFP$^+$ cell but not RFP$^+$ cells in the bone nodule area. N=4 mice/group. (B) Immunohistochemical staining of smooth muscle cell lineage-specific marker (MYH11) in the ascending aortas of *Apoe*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months of high cholesterol high fat diet using SP8 confocal microscope. (C-F) Immunohistochemical staining of lineage-specific markers (Osteoblast, Chondrocyte, Adipocyte, and Macrophage) in the ascending aortas of *Apoe*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months of high cholesterol high fat diet using SP8 confocal microscope (N=6 mice/group). Scale bar: 10 μm. (G) Quantification of the number of ascending aortic media smooth muscle cells expressing GFP (MYH11$^+$) and SMC, adipocyte, osteoblast, chondrocyte, and macrophage lineage markers (***$p<0.001$; unpaired two-tailed Student's t test). N=6 mice/group.


A
CD105
CD73
CD90
Sca-1
CD105
nonSMC-RFP
CD73
nonSMC-RFP
CD90
nonSMC-RFP
Sca-1
nonSMC-RFP
DAPI
SMC-GFP
DAPI
SMC-GFP
DAPI
SMC-GFP
DAPI
SMC-GFP
Apoe-/-
Merge
Merge
Merge
Merge
TGFβR2iSMC-Apoe
CD44
Gli1
CD44
nonSMC-RFP
Gli1
nonSMC-RFP
Media
Adventitia
Merge
Merge
B
Apoe-/-
TGFβR2iSMC-Apoe
% CD105+/GFP+ cells
% CD73+/GFP+ cells
% CD90+/GFP+ cells
% CD44+/GFP+ cells
% Sca-1+/GFP+ cells
% Gli1+/GFP+ cells
***
ø

Supplementary Figure 5. Related to Figure 4. Smooth muscle cells express stem cell markers in TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months of high cholesterol high fat diet,

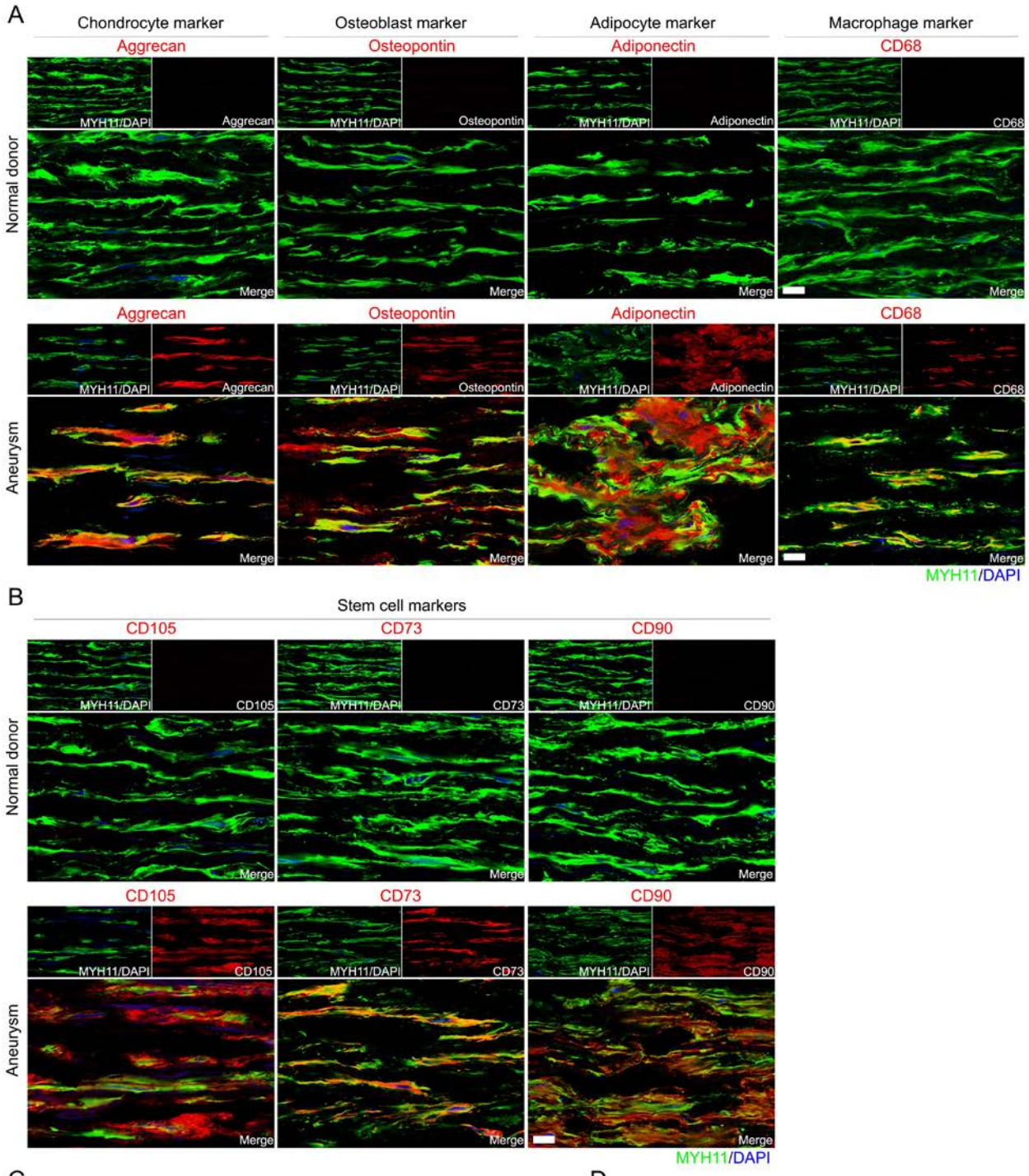
(A) Immunohistochemical staining of stem cell markers (CD105, CD73, CD90, Sca-1, CD44, Gli1) in the ascending aortas of *Apoe*$^{-/-}$ and TGFβR2$^{iSMC\text{-}Apoe}$ mice after 4 months of high cholesterol high fat diet using SP8 confocal microscope. N=6 mice/group. Scale bar: 10 μm. (B) Quantification of the number of ascending aortic media smooth muscle cells expressing GFP (MYH11^{+}) and stem cell markers (Ø: not detected; unpaired two-tailed Student's t test). See also Figure 4.



Supplementary Figure 6. Related to Figure 7. KLF4 is the key regulator controlling TGFβ inhibition and Cholesterol responsive SMC transition.

(A) Enrichment of genomic signals on 15,992 genes identified from running differential expression analysis for bulk RNA-Seq comparison of TGFβ treated vs. control groups. (Upper) Genome-wide occupancy of SMAD2/3 and Pol2-Ser2p at strong SMAD2/3 peaks in control (blue) and TGFβ treated (red) SMCs. The average signal within 5 kb genomic regions flanking the center of TSS is shown. (Lower) Heatmaps of SMAD2/3 ChIP-seq and Pol2-Ser2p

read counts for targets annotated TSS regions in the strong-binding group in control and TGFβ treated SMCs. Promoters are sorted in order of their SMAD2/3 intensity values. (B) Gene expression of upregulated and downregulated genes in response to TGFβ treatment. (C) Top 20 up and down-regulated differentially expressed transcription factors from ChIP-seq list. (D) Genomic coverage tracks depicting binding profile of SMAD2/3 and Pol2-Ser2p in KLF4 locus in control and TGFβ treated SMCs. RNA-seq analyses were also included with two biological repeats. Coverage tracks were normalized based on the number of reads. (E) Enrichment levels of SMAD2/3 and KLF4 by ChIP-qPCR at KLF4 locus in control and TGFβR2 KD SMCs in the presence or absence of CD-cholesterol. Data represent mean ± SEM of technical triplicates. Enrichment is shown as ChIP-to-input ratio normalized to the enrichment at the non-bound regions. (F) Histological analysis of KLF4 expression in mouse ascending aortas after 4 month of high cholesterol high fat diet. Nuclei were stained with DAPI (blue). Scale bar: 16 μm. (G) Quantification of the number of ascending aortic media smooth muscle cells expressing GFP (green) and KLF4 (magenta) (***$p<0.001$; unpaired two-tailed Student's t test). (N=6 for C57BL/6 mice; N=6 for TGFβR2^{iSMC} mice; N=8 for *Apoe*$^{-/-}$ mice; and N=8 for TGFβR2$^{iSMC\text{-}Apoe}$ mice). (H) Expression of MSC markers (ENG, NT5E, THY1) and osteoblast (SPP1), chondrocyte (PRG4), adipocyte (PPARG, PLIN2) and macrophage (LGALS3) markers in control, TGFβR2 KD, TGFβR2/KLF4 KD, and TGFβR2/KLF2/KLF4/KLF5 KD SMCs with or without CD-cholesterol. Data represent the mean ± SEM and are representative of three experiments in duplicate. (I) Control, TGFβR2 KD, and TGFβR2/KLF2/KLF4/KLF5 KD SMCs with or without CD-cholesterol cells possess in vitro trilineage differentiation capacity toward osteoblast (Alizarin Red, Alkaline Phosphatase), chondrocyte (Alcian Blue), adipocyte (Oil Red O), and macrophage beads uptake activity. Scale bar: 100 μm for trilineage differentiation images. Scale bar: 8 μm for macrophage beads uptake images. Experiments were repeated three times.


A
Chondrocyte marker
Osteoblast marker
Adipocyte marker
Macrophage marker
Aggrecan
Osteopontin
Adiponectin
CD68
Normal donor
Aneurysm
MYH11/DAPI
Merge
MYH11/DAPI
B
Stem cell markers
CD105
CD73
CD90
MYH11/DAPI
C
Normal donor
Aneurysm
% Aggrecan+MYH11+ cells
% OPN+MYH11+ cells
% ADIPOQ+MYH11+ cells
% CD68+MYH11+ cells
D
% CD105+MYH11+ cells
% CD73+MYH11+ cells
% CD90+MYH11+ cells
***

Supplementary Figure 7. Related to Figure 1 and Figure 4. Smooth muscle cell express mesenchymal stem cell, bone, cartilage, and adipocyte lineage markers in older patients with aneurysm.
(A-B) Histological analysis of human ascending aortas with lineage markers (Aggrecan, Osteopontin, Adiponectin, CD68) and stem cell markers (CD105, CD73, CD90) from normal donors (N=6) and aneurysm patients (N=6). Nuclei were stained with DAPI (blue). Scale bar: 16 μm. (C-D) Quantification of the number of ascending aortic media smooth muscle cells expressing MYH11 (green) and lineage and stem cell markers (Ø: not detected; ***$p<0.001$; unpaired two-tailed Student's t test). See also Figure 1 and Figure 4.

Table S3. List of Primers used for qRT-PCR. Related to: Quantitative Reverse Transcription PCR" in the STAR Methods.

Gene Symbol	QIAGEN Catalog Number	RefSeq Accession	Reference Positions	Band Size (bp)
ACTB	PPH00073G	NM_001101	730	174
Actb	F: CCAGTTGGTAACAATGCCATGT R: GGCTGTATTCCCCTCCATCG			
ENG	PPH01140G	NM_000118	1381	116
KLF2	PPH02566A	NM_016270	1128	164
KLF4	PPH18388A	NM_004235	2002	151
KLF4 (specific)	F: CTTATAACTTCCTTCGCTACAGCC R: GCCGAGTTTGTTGATTTAGCTG			
KLF4 (non-specific)	F: ACAGAGTCTCCCTATATTGACCA R: AGGTAGCTCACAACTATAATGCCA			
KLF5	PPH00434A	NM_001730	996	191
LGALS3	PPH01754G	NM_002306	581	62
NR1H3	PPH01276C	NM_005693	1504	76
NT5E	PPH12908E	NM_002526	3559	63
PLIN2	PPH02583A	NM_001122	1213	142
PPARG	PPH02291G	NM_015869	1287	93
PRG4	PPH06096E	NM_005807	3453	131
SPP1	PPH00582E	NM_000582	892	88
Tgfbr2 (exon2)	F: GACCATCCATCCACTGAAACATTTTAAC R: GACTTCATGCGGCTTCTCACAG			
THY1	PPH02406G	NM_006288	1759	134
		TaqMan Assay ID		**Band Size (bp)**
Cd44		Mm01277161_m1		63
Col2a1		Mm01309565_m1		66
Eng		Mm00468252_m1		77
Klf2		Mm00500486_g1		75
Klf4		Mm00516104_m1		77
Klf5		Mm00456521_m1		140
Lgals3		Mm00802901_m1		108
Ly6a		Mm00726565_s1		92
Myh11		Mm00443013_m1		92
Nt5e		Mm00501910_m1		77
Plin1		Mm00558672_m1		89
Pparg		Mm00440940_m1		63
Prg4		Mm01284582_m1		63
Runx2		Mm00501584_m1		91
Sox9		Mm00448840_m1		101
Spp1		Mm00436767_m1		114
Thy1		Mm00493681_m1		68