

SUPPLEMENTAL MATERIALS

For

BAF60a Deficiency in Vascular Smooth Muscle Cells Prevents Abdominal Aortic Aneurysm by Reducing Inflammation and Extracellular Matrix Degradation

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Supplemental Methods

Protein Extraction and Western Blotting

Cell extracts were prepared in RIPA lysis buffer, human and mouse tissues were homogenized in T-PER™ tissue protein extraction reagent (ThermoFisher Scientific, #78510). Nuclear and cytoplasmic proteins were extracted using NE-PER™ Nuclear and Cytoplasmic Extraction Reagents (ThermoFisher Scientific, #78835) following the manufacturer's protocol. Protein extracts were resolved in SDS-PAGE gels and transferred to nitrocellulose membranes. Membranes were blocked and then incubated with primary antibodies and IRDye secondary antibodies before being scanned with the Odyssey CLx Imaging System (LI-COR Bioscience, Lincoln, NE).

siRNA mediated BAF60a knockdown

Human aortic smooth muscle cells (HASMCs) were transfected with 30 nM siBAF60a (ThermoFisher Scientific, #s13151) or non-targeting siRNA (ThermoFisher Scientific, #4390843) using Lipofectamine RNAiMAX Reagent (Invitrogen, #13778150) following the manufacturer's instructions.

Adenovirus-mediated BAF60a overexpression

Adenovirus encoding human BAF60a (AdBAF60a) and GFP (AdGFP) were used in the gain of function experiments in this study by infecting HASMCs with 20 multiplicity of infection (MOI) for 48 hours.

mRNA Isolation and Quantitative Real-time PCR Analysis

Total RNA was extracted using TRIzol Reagent (Invitrogen, #15596018) and purified using RNeasy Mini Kit (QIAGEN, #74106, Hilden, Germany). SuperScript™ III First-Strand Synthesis System (Invitrogen, #18080051) and random primers were used to reverse-transcribe RNA into cDNA. Gene expression was quantified in triplicates by quantitative real-time PCR (qPCR) using IQ SYBR Green Supermix (Bio-Rad, #1708882). qPCR primer sequences are listed in Supplemental Table V.

Co-Immunoprecipitation

VSMCs were lysed with Pierce IP Lysis Buffer (ThermoScientific, #87788) and incubated with primary antibody against p300 or normal rabbit IgG at 4°C overnight with rotation. The immunocomplexes were then precipitated with Protein A Magnetic Beads (CST, # 73778) and eluted for Western blot analysis.

Immunofluorescence Staining of Cultured Cells

Cells were cultured in Chambered Cell Culture Slides (Fisher, #08774208), fixed, blocked, and then incubated with primary antibodies against p65, followed by Alexa Fluor conjugated secondary antibody (Jackson ImmunoResearch Laboratories). Nuclei were stained with DAPI (Invitrogen, #P36935).

ELISA

ELISA was performed to measure the concentration of MCP-1 (R&D, #DCP00) and Cathepsin S (Abcam, #ab155427) in HASMCs culture supernatants following the manufacturer's instructions.

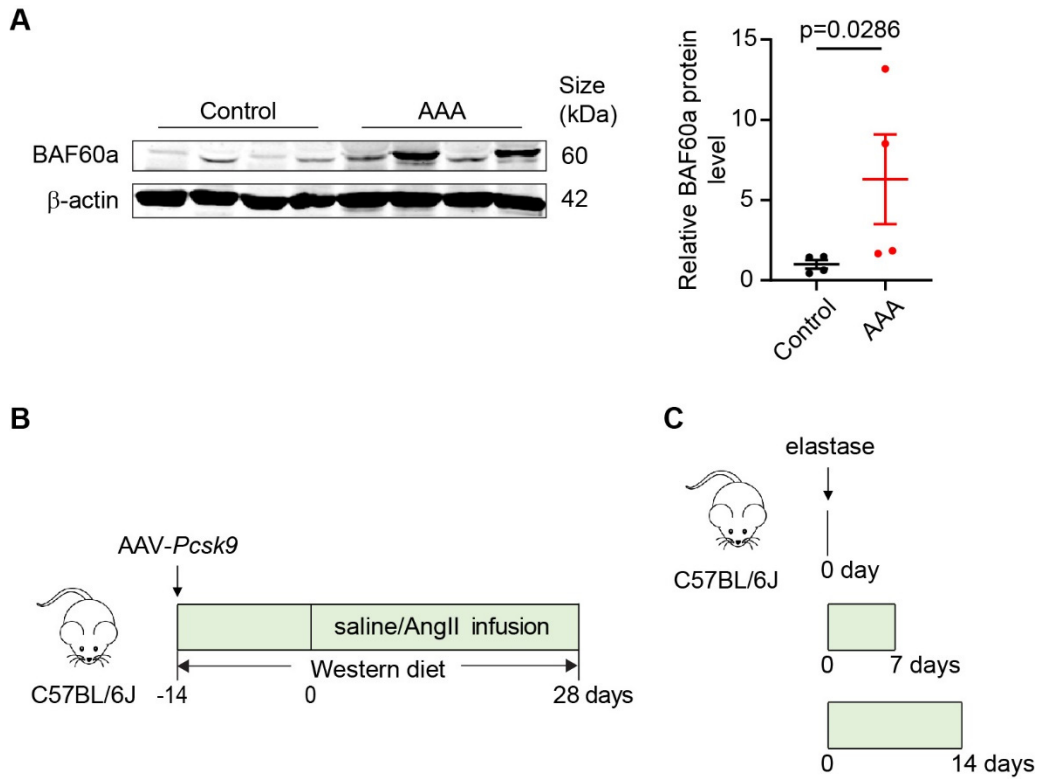
Macrophage Migration Assay

Macrophage migration assay was performed using 8.0µm transwell plates (Sigma-Aldrich #CLS3464). Briefly, HASMCs were transfected with 30 nM siBAF60a or siControl, or infected with 20MOI of AdBAF60a or AdGFP. After 48h, the cell culture medium was changed to fresh Opti-MEM I (Gibco #31985-070) with or without TNFα (20ng/ml). The medium was changed again to fresh Opti-MEM I 4 hours later and incubated for another 20 hours. The conditioned medium was collected and added to the lower chambers of the transwell plates while 2×10^5 RAW 264.7 cells starved overnight were seeded in the upper chambers. Six hours later, cells on the upper surface of the transwell insert were removed by gently scraping with a cotton swab, and the membranes were fixed and stained with 0.1% crystal violet (Sigma-Aldrich, #C0775). Images of 4 random fields per transwell were taken by microscopy and the numbers of migrated cells were determined using ImageJ software.

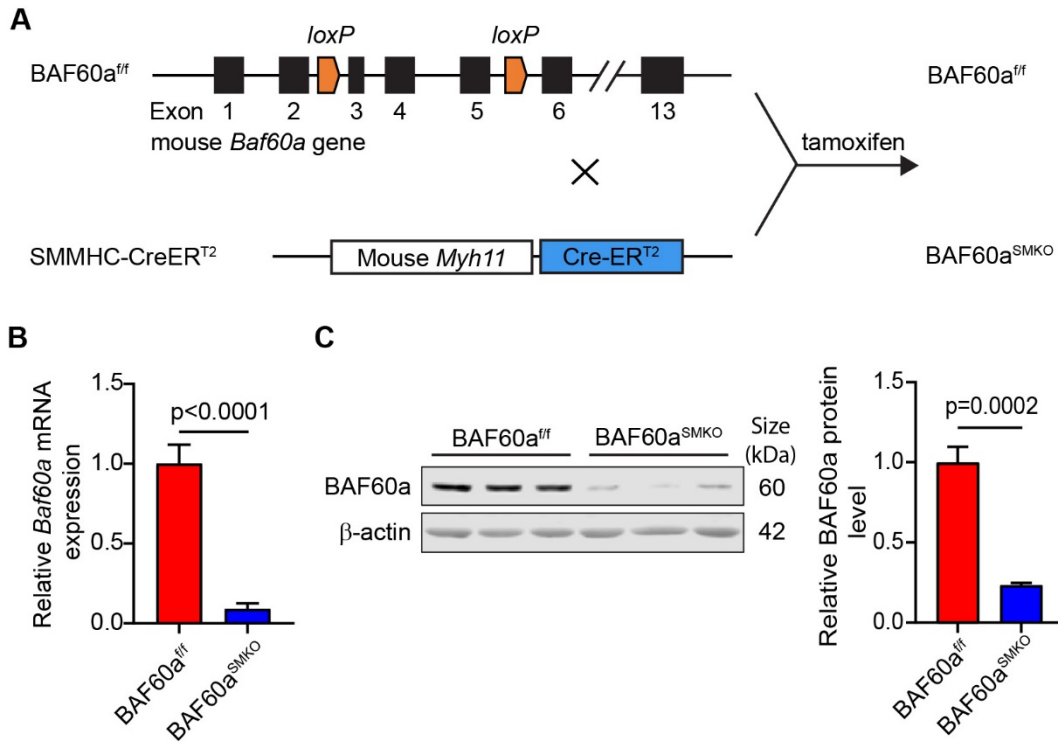
Generation of Stable Cell Lines

EcoPack2-293 cells were transfected with 20µg pMSCV-BAF60a-BirA* or pMSCV-BirA* vectors. The supernatant was collected at 24, 48 and 72 hours after transfection, and was filtered before addition to A7r5 cells. Stable transfectant selection with puromycin (Sigma-Aldrich, #P7255) started at 24 hours after infection. Upon colony formation, subclones were isolated and screened by immunofluorescence with antibodies against BAF60a and streptavidin.

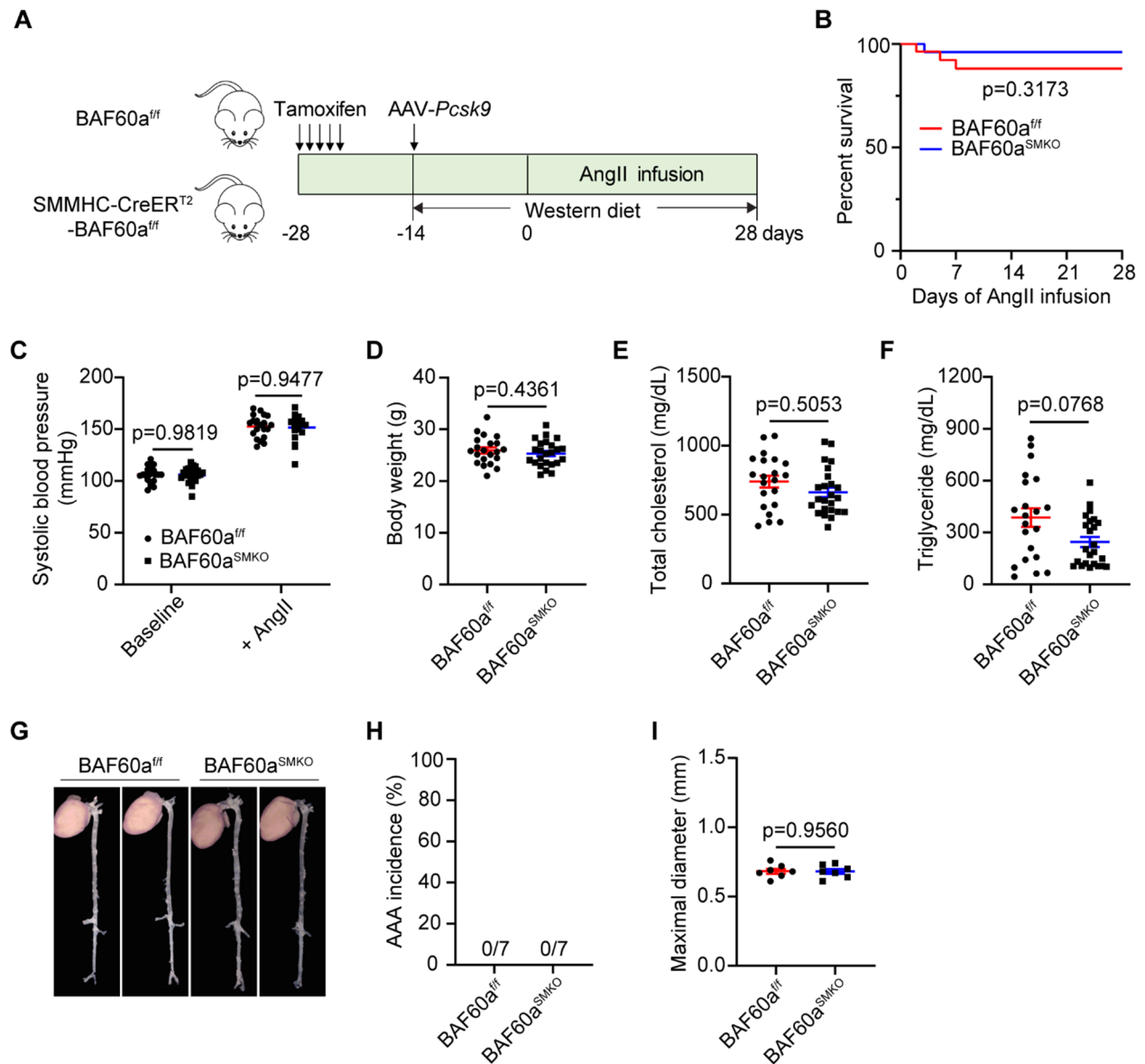
Online Figures



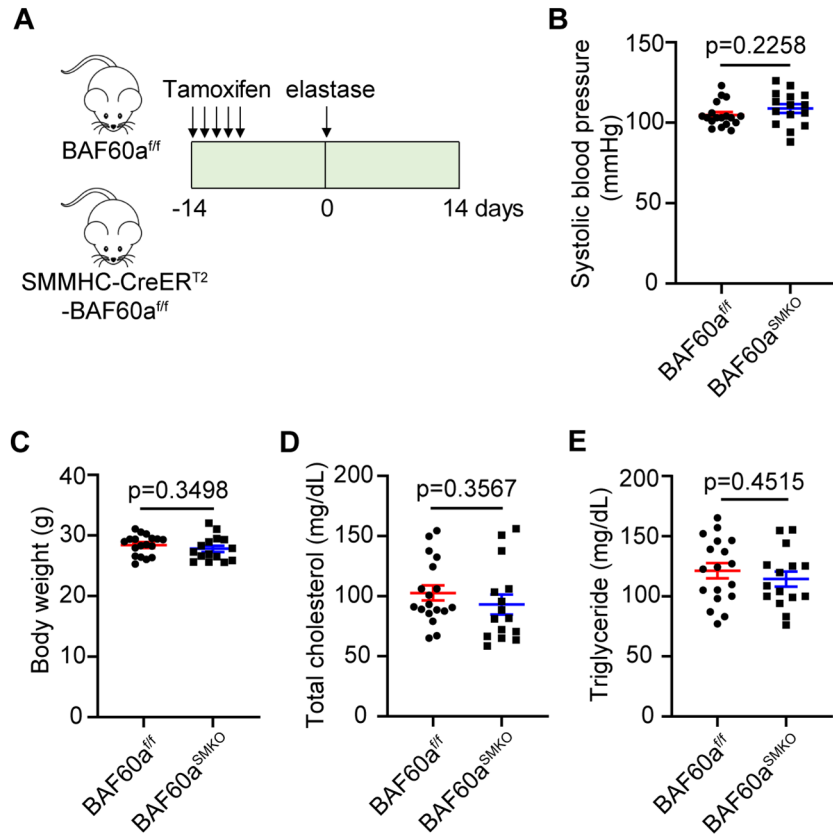
Supplemental Figure I. BAF60a expression is upregulated in human and murine AAA lesions. **A**, BAF60a protein abundance was determined by Western blotting in human AAA samples (n=4) and healthy control abdominal aortas (n=4). **B**, Schematic diagram of saline and AngII infusion in AngII-induced AAA model in C57BL/6J mice. **C**, Schematic diagram of elastase treatment for 0, 7, or 14 days in C57BL/6J mice. Data are presented as mean \pm SEM. Nonparametric Mann-Whitney test for A.



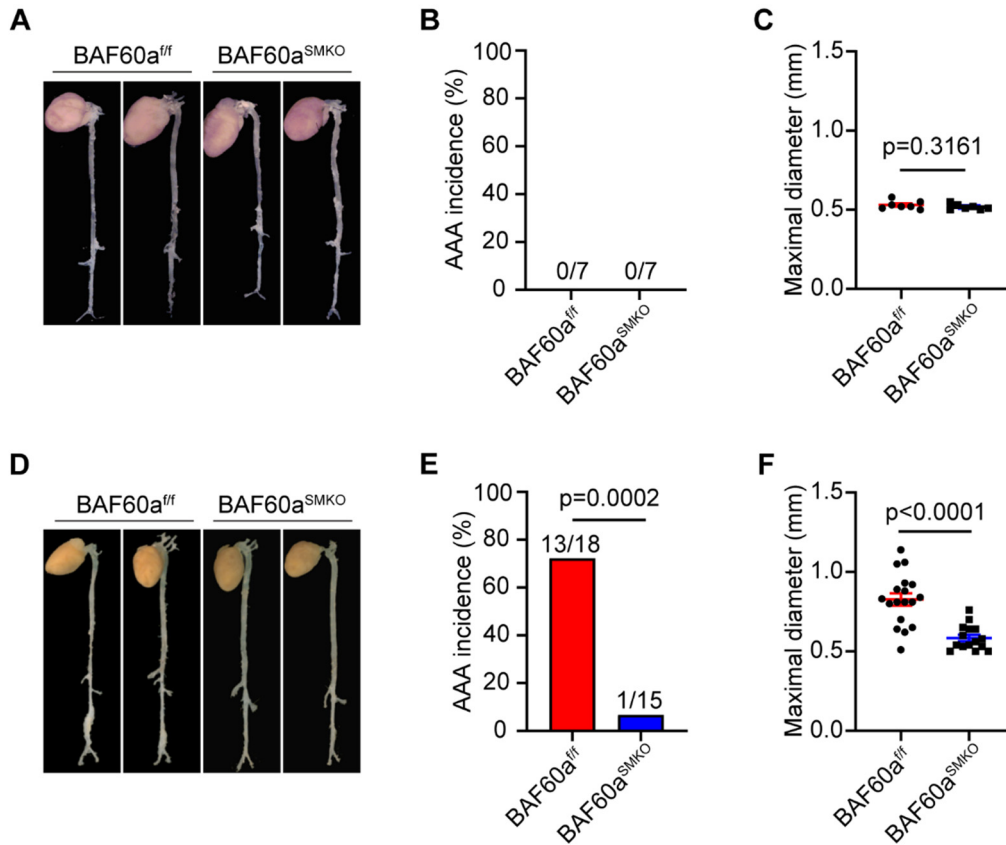
Supplemental Figure II. Generation of vascular smooth muscle cells (VSMCs) specific BAF60a conditional knockout mice. **A**, Schematic of gene targeting strategy to generate VSMC-specific BAF60a knockout mice (BAF60a^{SMKO}); tamoxifen was given consecutively for 5 days (80 mg/kg/day, i.p.). **B-C**, Relative BAF60a mRNA and protein levels were determined by qPCR (**B**) (n=5 for each group) and Western blot (**C**) (n=4 for each group) in aortas of BAF60a^{ff} and BAF60a^{SMKO} mice. Data are presented as mean±SEM. Student's t-test for B and C.



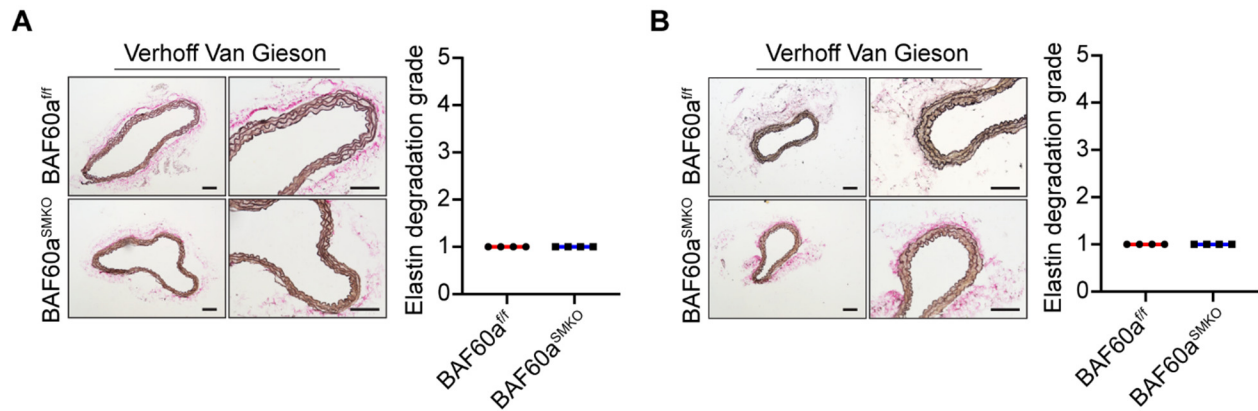
Supplemental Figure III. Experimental parameters of the AngII-induced AAA model in BAF60a^{fl/fl} and BAF60a^{SMKO} mice. **A-F**, Eight to 10 weeks old male BAF60a^{fl/fl} (n=24) and BAF60a^{SMKO} (n=25) mice were given AAV-Pcsk9 (i.p.) and Western diet to induce hypercholesterolemia followed by AngII (1,500 ng/kg/min) infusion with minipumps for 28 days. **A**, Schematic diagram indicating the process of murine AngII-induced AAA model. **B**, Survival rates indicated by Kaplan-Meier curves. **C**, Systolic blood pressure before and 28 days after AngII minipump implantation. **D-F**, Body weight (**D**), serum total cholesterol (**E**) and triglyceride levels (**F**) of BAF60a^{fl/fl} and BAF60a^{SMKO} mice infused with AngII for 28 days. **G-I**, Eight to 10 weeks old male BAF60a^{fl/fl} (n=7) and BAF60a^{SMKO} mice (n=7) were subjected to sham treatment and euthanized 28 days after surgery. **G**, Representative morphology of aortas. **H**, Incidence of AAA. **I**, Quantification of maximal external diameters of suprarenal abdominal aortas. Data are presented as mean±SEM. Mantel-Cox test for B, two-way ANOVA followed by Holm-Sidak analysis for C, and Student's t-test for D-E and I, nonparametric Mann-Whitney test for F.



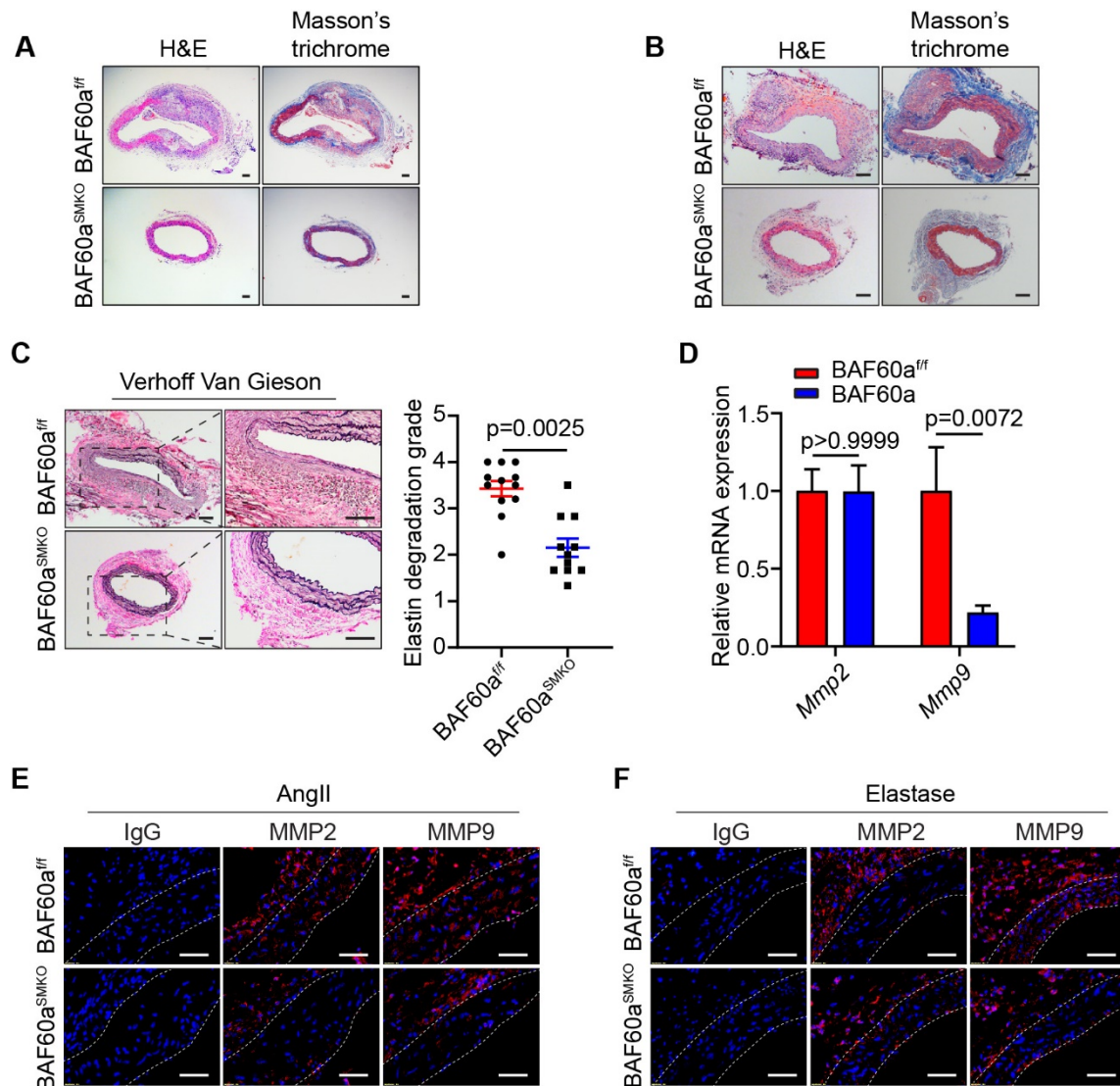
Supplemental Figure IV. Experimental parameters of the elastase-treated BAF60a^{ff} and BAF60a^{SMKO} mice. Ten to 12 weeks old male BAF60a^{ff} and BAF60a^{SMKO} mice were subjected to elastase-induced AAA by the treatment of the infrarenal abdominal aortas with 30 μ L elastase for 30 min as described in the Supplemental Methods and euthanized 14 days after elastase exposure. **A**, Schematic diagram for the elastase-induced AAA model in BAF60a^{ff} (n=18) and BAF60a^{SMKO} (n=15) mice. **B-E**, Systolic blood pressure (**B**), body weight (**C**), serum total cholesterol (**D**) and triglyceride levels (**E**) in BAF60a^{ff} and BAF60a^{SMKO} mice. Data are presented as mean \pm SEM. Student's t-test for B-E.



Supplemental Figure V. BAF60a depletion in VSMCs attenuates elastase-induced AAA in mice. **A-C**, Ten to 12 weeks old male BAF60a^{fl/fl} (n=7) and BAF60a^{SMKO} (n=7) mice were treated with heat-inactivated elastase to serve as the sham control and euthanized 14 days after surgery. **A**, Representative morphology of aortas. **B**, Incidence of AAA. **C**, Quantification of maximal external diameters of suprarenal abdominal aortas. **D-F**, In the elastase-induced AAA model, 10 to 12 weeks old male BAF60a^{fl/fl} (n=18) and BAF60a^{SMKO} (n=15) mice were treated with active elastase and euthanized 14 days after elastase exposure. **D**, Representative morphology of aortas. **E**, Incidence of AAA. **F**, Quantification of maximal external diameter of infrarenal abdominal aortas. Data are presented as mean±SEM. Student's t-test for C. Chi-squared test for E, Mann-Whitney test for F.

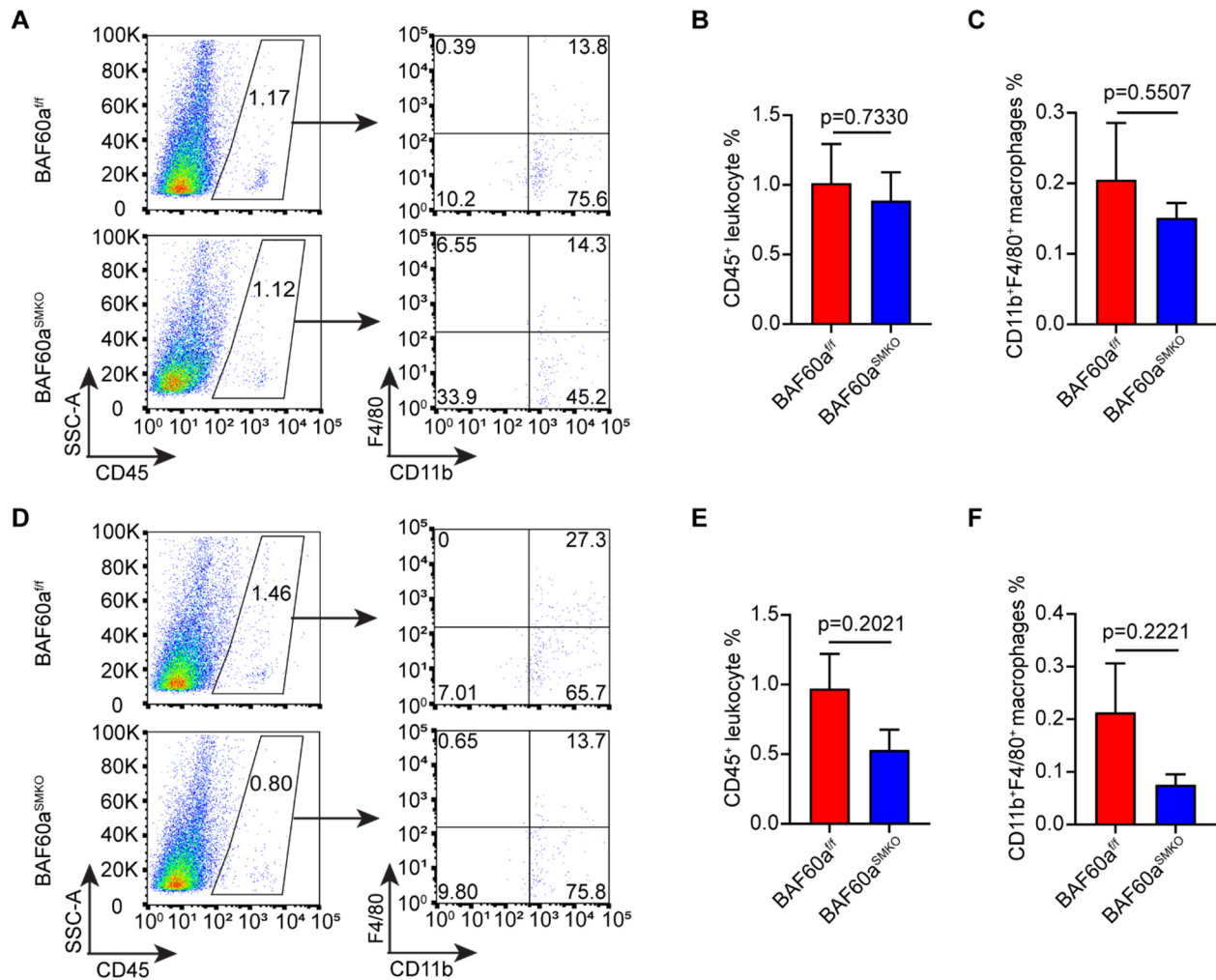


Supplemental Figure VI. BAF60a deficiency in VSMCs cannot induce aortic ECM degradation in sham control mice in both AAA models. A, Representative images of Verhoff Van Gieson staining and quantification analysis of elastin fragmentation in suprarenal abdominal aortic sections from BAF60a^{fl/fl} (n=4) and BAF60a^{SMKO} (n=4) mice 28 days after sham treatment in the AngII-induced AAA model. Scale bar=100 μ m. **B**, Representative images of Verhoff Van Gieson staining and quantification analysis of elastin fragmentation in infrarenal abdominal aortic sections from BAF60a^{fl/fl} (n=4) and BAF60a^{SMKO} (n=4) mice 14 days after heat-inactivated elastase exposure in the elastase-induced AAA model. Scale bar=100 μ m.

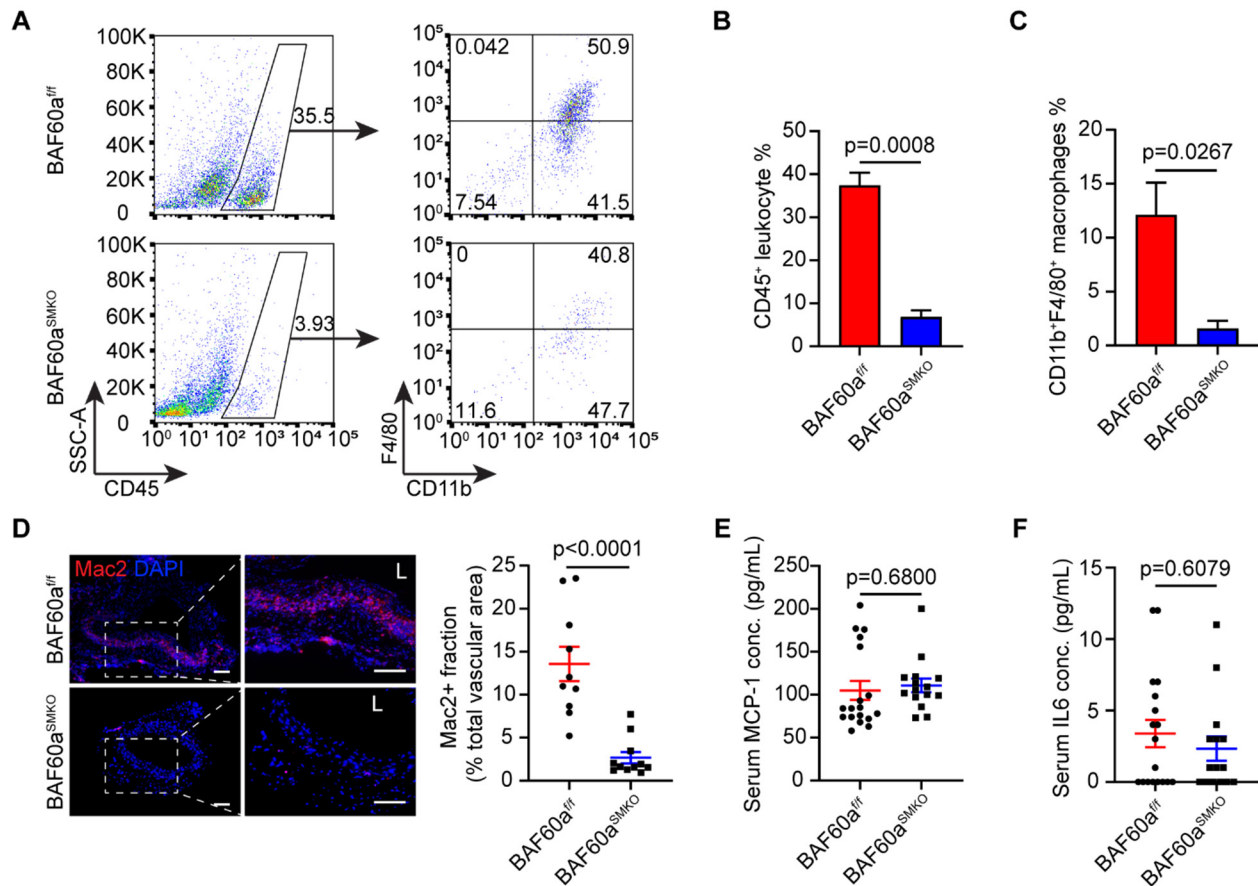


Supplemental Figure VII. BAF60a deficiency in VSMCs reduces ECM degradation in AAA lesion. **A**, Representative images of hematoxylin and eosin (H&E) and Masson's trichrome staining of the suprarenal abdominal aortic sections from BAF60a^{ff} and BAF60a^{SMKO} mice after 28 days of AngII infusion. Scale bar=100 μ m. **B**, Representative images of H&E and Masson's trichrome staining of the infrarenal abdominal aortic sections from BAF60a^{ff} and BAF60a^{SMKO} mice 14 days after elastase exposure. Scale bar=100 μ m. **C**, Representative images of Verhoff Van Gieson staining and quantification analysis of elastin fragmentation in infrarenal abdominal aortic sections from BAF60a^{ff} (n=12) and BAF60a^{SMKO} (n=11) mice 14 days after elastase treatment. Scale bar=100 μ m for whole aortic sections. **D**, Relative MMP2 and MMP9 mRNA and levels were determined by qPCR in the aortic media of BAF60a^{ff} (n=5) and BAF60a^{SMKO} (n=5) mice 28 days after AngII infusion. **E-F**, Representative immunofluorescence staining of MMP2 and MMP9 (red) in abdominal aortic sections from BAF60a^{ff} and BAF60a^{SMKO} mice subjected to AngII- (**E**) or elastase- (**F**) induced AAA model. Nuclei stained by DAPI were indicated in blue. Dotted lines depict aortic media. Lumen area is on the bottom right corner in

all pictures. Scale bar=50 μm . n=3 for each group. Data are presented as mean \pm SEM. Student's t-test for C, one-way ANOVA followed by Tukey's post hoc analysis for D.

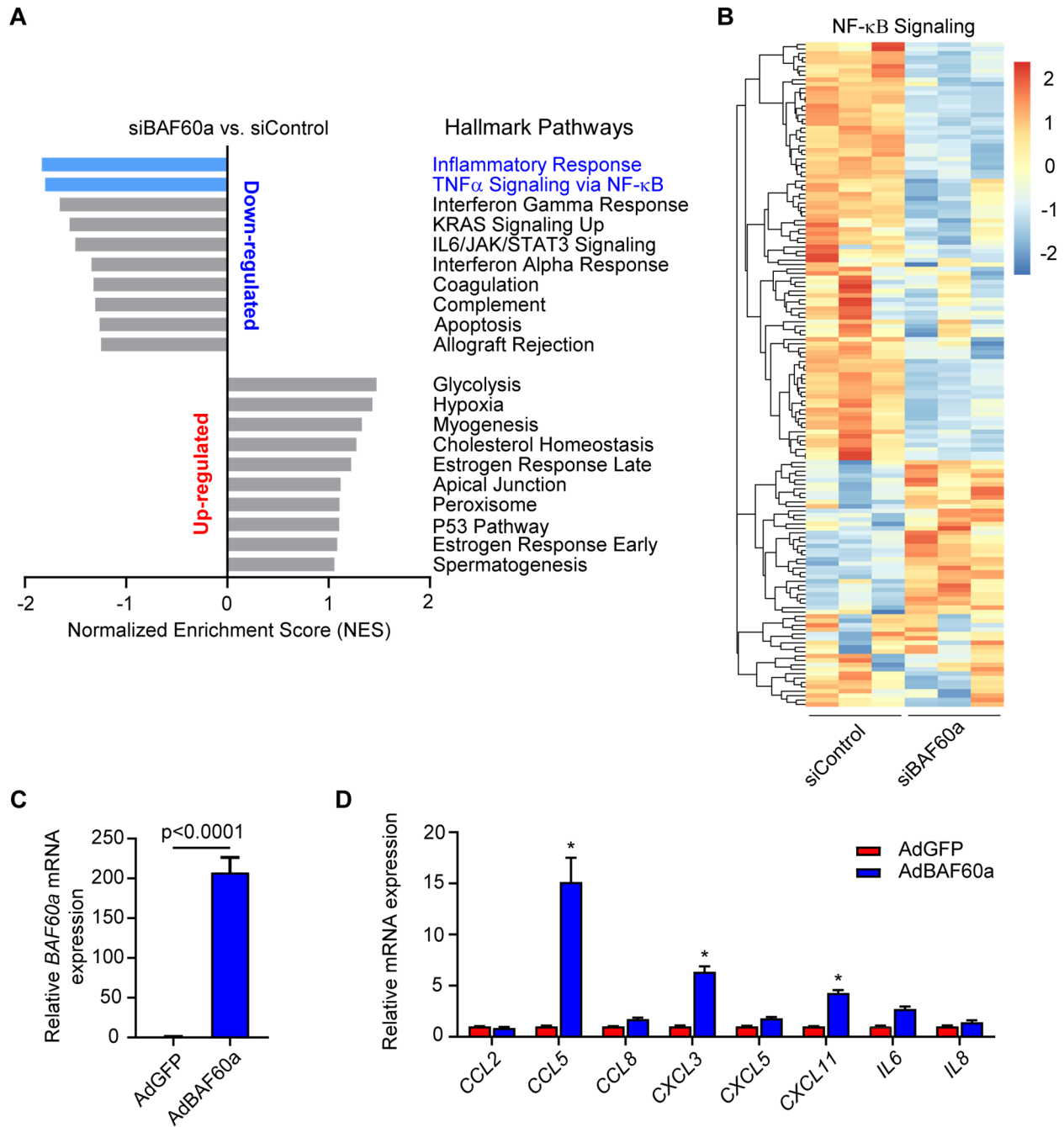


Supplemental Figure VIII. BAF60a deficiency in VSMCs does not alter the proportion of immune cells in the abdominal aorta in sham control mice. **A-C**, Single cells were isolated from suprarenal abdominal aortas of BAF60a^{fl/fl} (n=3) and BAF60a^{SMKO} (n=3) mice 28 days after sham treatment in the AngII-induced AAA model and flow cytometry analysis was performed. **A**, Representative dot plots showing the gating strategy to obtain the macrophage population (CD11b⁺F4/80⁺) from gated CD45⁺ leukocytes. **B**, Quantitative analysis of the percentage of CD45⁺ leukocytes. **C**, Quantitative analysis of the percentage of CD11b⁺F4/80⁺ macrophages. **D-F**, Single cells were isolated from infrarenal abdominal aortas of BAF60a^{fl/fl} (n=3) and BAF60a^{SMKO} (n=3) mice 14 days after heat-inactivated elastase exposure in the elastase-induced AAA model and flow cytometry analysis was performed. **D**, Representative dot plots showing the gating strategy to obtain the macrophage population (CD11b⁺F4/80⁺) from gated CD45⁺ leukocytes. **E**, Quantitative analysis of the percentage of CD45⁺ leukocytes. **F**, Quantitative analysis of the percentage of CD11b⁺F4/80⁺ macrophages. Data are presented as mean±SEM. Student's t-test for B-C and E-F.



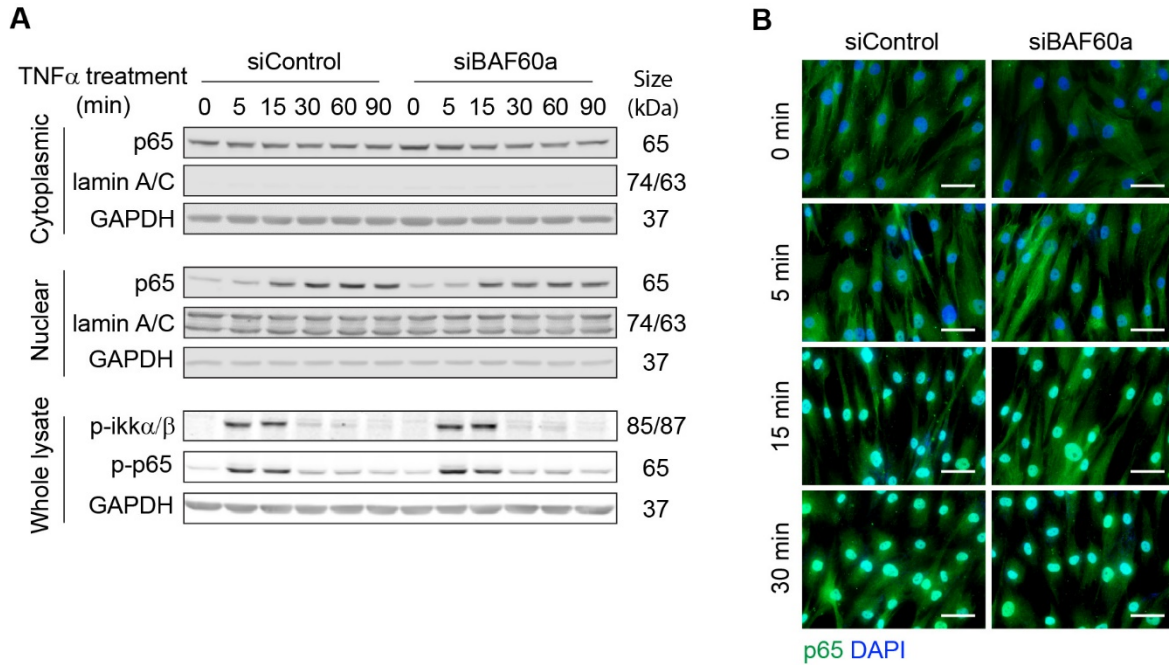
Supplemental Figure IX. BAF60a deficiency in VSMCs suppresses inflammatory

response in the elastase-induced AAA lesion. In the elastase-induced AAA model, 10 to 12 weeks old male BAF60a^{ff} (n=18) and BAF60a^{SMKO} (n=15) mice were treated with elastase and euthanized 14 days after elastase exposure. **A-C**, Single cells were isolated from abdominal aortas of BAF60a^{ff} (n=3) and BAF60a^{SMKO} (n=3) mice and flow cytometry analysis was performed. **A**, Representative dot plots showing the gating strategy to obtain the macrophage population (CD11b⁺F4/80⁺) from gated CD45⁺ leukocytes in the abdominal aortas. **B**, Quantitative analysis of the percentage of CD45⁺ leukocytes. **C**, Quantitative analysis of the percentage of CD11b⁺F4/80⁺ macrophages. **D**, Representative images of Mac2 staining and quantification analysis of Mac2⁺ fraction in infrarenal abdominal aortas from BAF60a^{ff} (n=10) and BAF60a^{SMKO} (n=11) mice. Scale bar=100 μm; L indicates lumen. **E-F**, Serum concentration of MCP-1 (BAF60a^{ff}, n=18; BAF60a^{SMKO}, n=15) (**E**) and IL-6 (BAF60a^{ff}, n=18; BAF60a^{SMKO}, n=15) (**F**) was measured by ELISA. Data are presented as mean±SEM. Student's t-test for B-F.

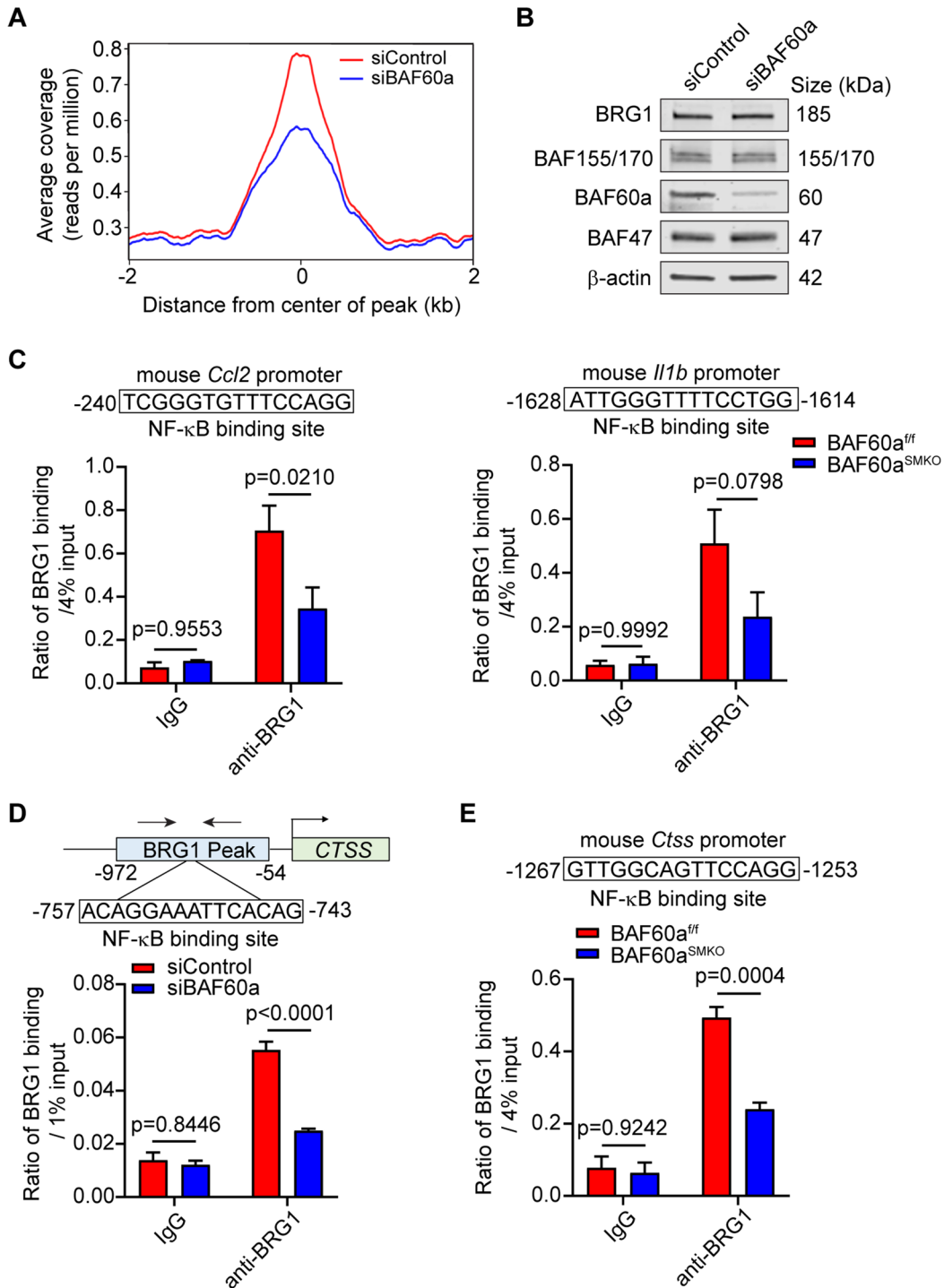


Supplemental Figure X. BAF60a regulates vascular smooth muscle cell inflammation. **A-B**, HASMCs were transfected with siControl or siBAF60a (30 nM). After 72 hours, total RNA was extracted for RNA-seq (n=3 for each group). **A**, Gene set enrichment analysis (GSEA) was performed using transcriptomic data from RNA-seq (siBAF60a vs. siControl). Bars show normalized enrichment scores (NES) of the top ten upregulated and downregulated pathways on the hallmark gene sets. **B**, Genes involved in NF- κ B signaling are shown by a heatmap. Color bar [red to blue (2 to -2) vertical bar] denotes the row-scaled transcripts per million (TPM) value, representing the Z score of gene expression across samples. **C-D**, HASMCs were infected with AdGFP or AdBAF60a (20 MOI). Total RNA was extracted after 48 hours for RNA-

seq (n=3 for each group). **C**, BAF60a mRNA expression was determined by qPCR. n=3. **D**, qPCR Validation of representative NF- κ B target genes identified by RNA-seq in 3 independent sets of samples. n=3 for each group. Data are presented as mean \pm SEM. Student's t-test for C, one-way ANOVA followed by Tukey's post hoc analysis for D.

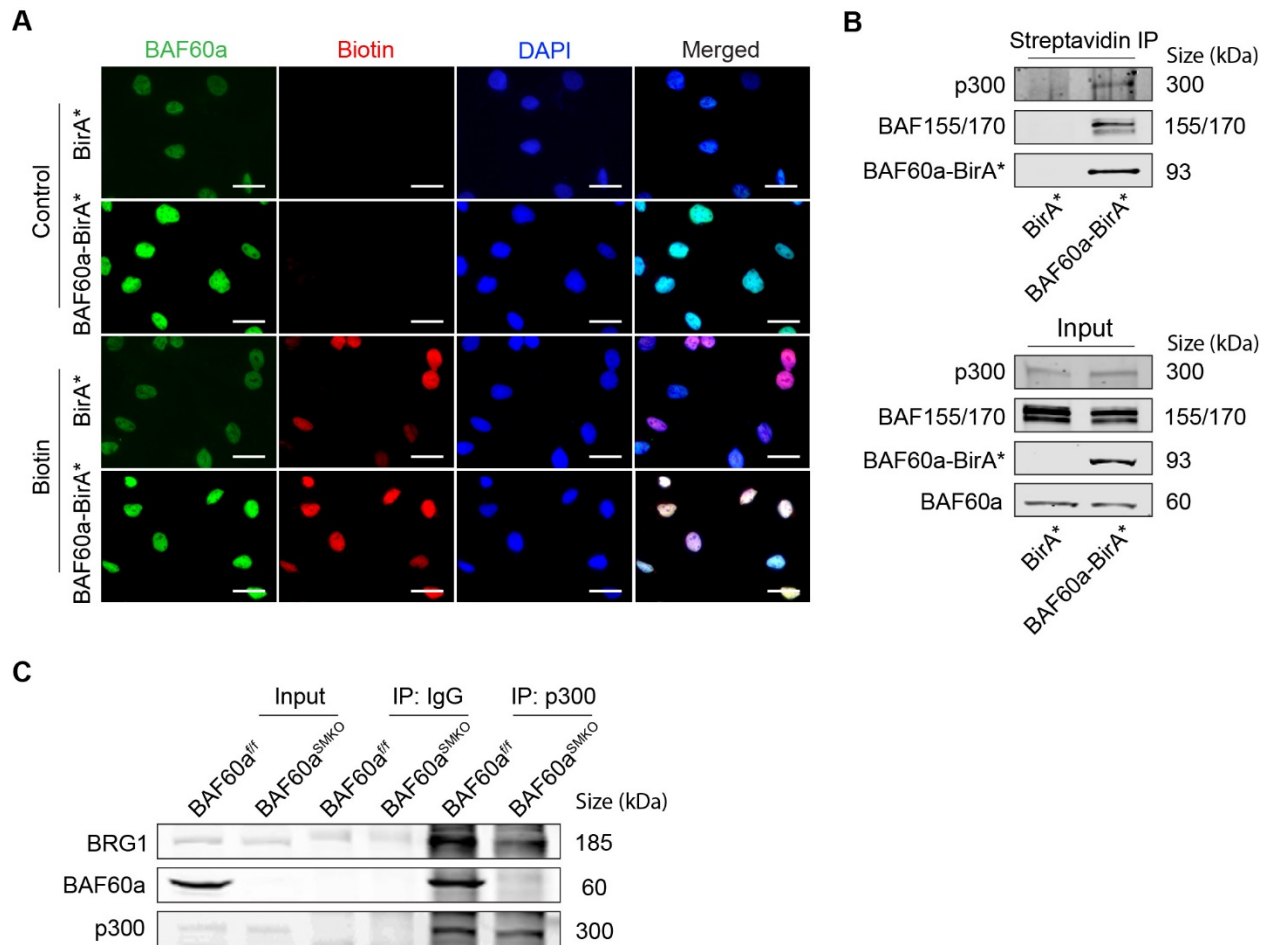


Supplemental Figure XI. BAF60a depletion in VSMCs does not alter TNF α -induced p65 nuclear translocation. HASMCs were transfected with siControl or siBAF60a (30 nM). After 72h, cells were stimulated by TNF α (20 ng/ml) for the indicated time. **A**, Representative Western blot analysis of cytoplasmic and nuclear p65 and the level of phosphorylated IKK α / β and phosphorylated p65 after TNF α (20 ng/ml) stimulation. n=3. **B**, Representative images of immunofluorescence staining of p65 (green) and DAPI (blue) in HASMCs in the same conditions. n=3. Scale bar=50 μ m.



Supplemental Figure XII. BAF60a is required for SWI/SNF complex recruitment to the promoters of NF-κB target genes. **A**, Global occupancy of BRG1 ± 2 kb surrounding the peak center from BRG1 ChIP-seq for HASMCs transfected with siControl or siBAF60a (30 nM) for 72h. **B**, Protein abundance of the SWI/SNF core subunits and BAF60a was determined by Western blot in whole lysates of HASMCs transfected with siControl or siBAF60a (30 nM) for

72h. n=3. **C**, BRG1 binding to the NF- κ B binding site located in the mouse *Ccl2* (left panel) and *I11b* (right panel) promoters was detected by CHIP assay in primary aortic smooth muscle cells isolated from abdominal aortas of BAF60a^{fl/fl} and BAF60a^{SMKO} mice. n=3. **D**, BRG1 binding on the NF- κ B binding site located in the *CTSS* promoter was detected by CHIP assay in HASMCs transfected with 30 nM siControl or siBAF60a for 72h. n=3. **E**, BRG1 binding to the NF- κ B binding site located in the mouse *Ctss* promoter was detected by CHIP assay in primary aortic smooth muscle cells isolated from abdominal aortas of BAF60a^{fl/fl} and BAF60a^{SMKO} mice. n=3. Data are presented as mean \pm SEM. Two-way-ANOVA followed by Holm-Sidak post hoc analysis for C-E.



Supplemental Figure XIII. BAF60a-BirA* identified p300 as a BAF60a-interacting protein.

A, A7r5 cells stably expressing BirA* or BAF60a-BirA* fusion protein were treated with or without biotin (50 μ M) for 24h. BAF60a (green) and biotinylated protein (red fluorescence-labeled streptavidin) were detected by immunofluorescence staining. Nuclei stained by DAPI are indicated in blue. $n=3$. Scale bar=50 μ m. **B**, A7r5 cells stably expressing BirA* or BAF60a-BirA* fusion protein were treated with biotin (50 μ M) for 24h, and biotin-labeled proteins were immunoprecipitated by streptavidin. p300 was detected by Western blot. BAF170 and BAF155 were used as positive controls. $n=3$. **C**, Physical interaction between p300 and BRG1 was detected by Co-IP assay using a p300 antibody, with IgG as the negative control, in primary aortic smooth muscle cells isolated from abdominal aortas of BAF60a^{ff} and BAF60a^{SMKO} mice. $n=3$.

Supplemental table I Human AAA patients' information

Sample #	Sex	Age (y)	Race	Description	Antiplatelet drug	Anti-hypertensive drugs	Blood lipid reducing drugs	qPCR	Western blot
1	M	65	Caucasian	Abdominal aortic aneurysm	yes	Beta-Adrenergic Blocking Agents, Calcium Channel Blockers	Statins, Fibrin Acid Derivatives	yes	
2	M	61	Caucasian	Abdominal aortic aneurysm	N/A	N/A	Statins, Fibrin Acid Derivatives	yes	yes
3	M	60	Caucasian	Abdominal aortic aneurysm	yes	Angiotensin-Converting Enzyme Inhibitors, Beta-Adrenergic Blocking Agents, Diuretics	Statins, Fibrin Acid Derivatives	yes	
4	M	65	Caucasian	Abdominal aortic aneurysm	yes	Calcium Channel Blockers	Statins, Fibrin Acid Derivatives	yes	
5	M	66	Caucasian	Abdominal aortic aneurysm	yes	Angiotensin-Converting Enzyme Inhibitors, Beta-Adrenergic Blocking Agents	Statins, Fibrin Acid Derivatives		yes
6	M	72	Caucasian	Abdominal aortic aneurysm	yes	Beta-Adrenergic Blocking Agents	N/A	yes	
7	M	65	Caucasian	Abdominal aortic aneurysm	yes	Beta-Adrenergic Blocking Agents	Statins, Fibrin Acid Derivatives	yes	
8	F	58	Caucasian	Abdominal aortic aneurysm	yes	Angiotensin-Converting Enzyme Inhibitors, Beta-Adrenergic Blocking Agents, Diuretics	Statins, Fibrin Acid Derivatives	yes	yes
9	M	50	African American	Abdominal aortic aneurysm	N/A	N/A	N/A	yes	yes
10	M	31	Caucasian	Abdominal aortic aneurysm	N/A	N/A	N/A	yes	
11	M	71	American Indian or Alaska Native/Caucasian	Abdominal aortic aneurysm	N/A	N/A	N/A	yes	

12	M	37	Caucasian	Heart transplant donor	N/A	N/A	N/A	yes	
13	F	39	Caucasian	Heart transplant donor	yes	Diuretics	Statins, Fibrin Acid Derivatives	yes	yes
14	F	26	African American	Heart transplant donor	N/A	Diuretics	N/A	yes	
15	M	54	Caucasian	Heart transplant donor	N/A	N/A	N/A	yes	yes
16	M	59	Caucasian	Heart transplant donor	N/A	N/A	N/A	yes	
17	F	64	Caucasian	Heart transplant donor	yes	Calcium Channel Blockers	Statins, Fibrin Acid Derivatives	yes	
18	M	61	Caucasian	Heart transplant donor	yes	N/A	N/A	yes	
19	M	69	Caucasian	Heart transplant donor	N/A	N/A	N/A	yes	
20	M	65	Caucasian	Heart transplant donor	yes	N/A	N/A		yes
21	M	68	Caucasian	Heart transplant donor	N/A	Angiotensin-2 Receptor Antagonists, Beta-Adrenergic Blocking Agents, Diuretics	N/A	yes	yes
22	F	55	Caucasian	Heart transplant donor	yes	Diuretics	N/A	yes	

Supplemental Table II. Characteristics of the BAF60a^{fl/fl} and BAF60a^{SMKO} mice subjected to the AngII-induced AAA model at the 28 days' endpoint

Group	BAF60a ^{fl/fl}	BAF60a ^{SMKO}
Number of mice	24	25
Number of ruptures	3	1
Number of AAA	12	2
Maximal Diameter of AA (mm)	1.41±0.09	1.05±0.05
SBP baseline (mmHg)	106±2	106±1
SBP + AngII (mmHg)	152±2	152±2
Body weight (g)	25.9±0.6	25.3±0.5
TC (mg/dL)	740±43	662±35
TG (mg/dL)	387±54	245±29

Data are presented as mean±SEM. AAA, abdominal aortic aneurysm; AA, abdominal aorta; SBP, systolic blood pressure; TC, total cholesterol; TG, triglycerides.

Supplemental Table III. Characteristics of the BAF60a^{ff} and BAF60a^{SMKO} mice 14 days after elastase exposure

Group	BAF60a ^{ff}	BAF60a ^{SMKO}
Number of mice	18	15
Number of AAA	13	1
Maximal Diameter of AA (mm)	0.83±0.04	0.58±0.02
SBP (mmHg)	105±2	109±3
Body weight (g)	28.4±0.4	27.1±0.5
TC (mg/dL)	105±6	93±8
TG (mg/dL)	121±6	114±6

Data are presented as mean±SEM. AAA, abdominal aortic aneurysm; AA, abdominal aorta; SBP, systolic blood pressure; TC, total cholesterol; TG, triglycerides.

Supplemental Table IV: GSEA report for the RNA-seq data on HASMCs transfected with siBAF60a vs. siControl

Supplemental Table IVa: Gene sets enriched in HASMCs transfected with siControl

Name	Size	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val	Rank at Max	Leading Edge
Hallmark_Inflammatory Response	197	-0.5248261	-1.8330	0	0.0014	0.001	4345	tags=39%, list=12%, signal=44%
Hallmark_TNF α Signaling via NF κ B	198	-0.5190536	-1.7997944	0	7.14E-04	0.001	4432	tags=49%, list=13%, signal=56%
Hallmark_Interferon Gamma Response	197	-0.477279	-1.6564283	0	0.0058	0.008	4394	tags=35%, list=12%, signal=39%
Hallmark_KRAS Signaling Up	194	-0.4546483	-1.5589495	0	0.0151	0.025	1808	tags=26%, list=5%, signal=27%
Hallmark_IL6/JAK/STAT3 Signaling	87	-0.4899177	-1.5033814	0.0048	0.0208	0.042	2276	tags=29%, list=6%, signal=31%
Hallmark_Interferon Alpha Response	93	-0.4231654	-1.3420421	0.0146	0.0813	0.194	4380	tags=34%, list=12%, signal=39%
Hallmark_Coagulation	136	-0.3978205	-1.3213208	0.0061	0.0860	0.228	4312	tags=26%, list=12%, signal=30%
Hallmark_Complement	195	-0.3772207	-1.3050694	0	0.0900	0.266	4528	tags=27%, list=13%, signal=31%
Hallmark_Apoptosis	159	-0.3710751	-1.2615163	0.0154	0.1136	0.358	5380	tags=38%, list=15%, signal=44%
Hallmark_Allograft Rejection	199	-0.3584006	-1.2464709	0.0081	0.1181	0.403	3521	tags=23%, list=10%, signal=26%
Hallmark_Xenobiotic Metabolism	198	-0.3413361	-1.1839731	0.0161	0.1815	0.588	3594	tags=26%, list=10%, signal=29%
Hallmark_Apical Surface	43	-0.3939157	-1.0938723	0.2872	0.3512	0.847	5240	tags=40%, list=15%, signal=46%
Hallmark_Unfolded Protein Response	140	-0.3225256	-1.0713874	0.2289	0.3875	0.903	5659	tags=36%, list=16%, signal=42%
Hallmark_Angiogenesis	109	-0.3346617	-1.0513581	0.3164	0.4133	0.93	4683	tags=29%, list=13%, signal=34%
Hallmark_UV Response DN	36	-0.3959701	-1.047586	0.3597	0.3964	0.936	3402	tags=33%, list=10%, signal=37%
Hallmark_mTORC1 Signaling	197	-0.2987588	-1.0410534	0.2946	0.3914	0.939	3750	tags=28%, list=11%, signal=31%

Hallmark_Androgen Response	97	-0.3194047	-1.0193276	0.3915	0.4375	0.967	2764	tags=24%, list=8%, signal=26%
Hallmark_Protein Secretion	194	-0.2717993	-0.934126	0.7414	0.7389	1	5533	tags=30%, list=16%, signal=35%
Hallmark_G2M Checkpoint	96	-0.2869166	-0.9136794	0.7581	0.7736	1	3967	tags=27%, list=11%, signal=30%
Hallmark_Notch Signaling	32	-0.2999279	-0.7913953	0.8721	0.9615	1	4252	tags=34%, list=12%, signal=39%

ES: enrichment score

NES: normalized enrichment score

NOM p -val: nominal p -value

FDR q -val: p -value adjusted for the False Discovery Rate

FWER p -val: p -value adjusted for the Familywise Error Rate

Supplemental Table IV: GSEA report for the RNA-seq data on HASMCs transfected with siBAF60a vs. siControl

Supplemental Table IVb: Gene sets enriched in HASMCs transfected with siBAF60a

Name	Size	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val	Rank at Max	Leading Edge
Hallmark_Glycolysis	198	0.5024	1.4587	0	0.1552	0.194	5372	tags=34%, list=15%, signal=40%
Hallmark_Hypoxia	194	0.4921	1.4428	0	0.0989	0.237	5801	tags=39%, list=16%, signal=47%
Hallmark_Myogenesis	199	0.4522	1.3279	0.0151	0.2879	0.706	5891	tags=31%, list=17%, signal=37%
Hallmark_Cholesterol Homeostasis	73	0.4817	1.2810	0.0683	0.3674	0.872	7154	tags=41%, list=20%, signal=51%
Hallmark_Estrogen Response Late	198	0.4222	1.2282	0.0652	0.5142	0.98	5666	tags=32%, list=16%, signal=38%
Hallmark_Apical Junction	194	0.3834	1.1290	0.1799	1	1	5432	tags=29%, list=15%, signal=35%
Hallmark_Peroxisome	103	0.4046	1.1129	0.2484	1	1	4591	tags=25%, list=13%, signal=29%
Hallmark_P53 Pathway	195	0.3773	1.1069	0.2209	0.9204	1	7129	tags=39%, list=20%, signal=49%
Hallmark_Estrogen Response Early	197	0.3739	1.0933	0.2576	0.9001	1	5865	tags=31%, list=17%, signal=37%
Hallmark_Spermatogenesis	133	0.3733	1.0549	0.3436	1	1	5927	tags=27%, list=17%, signal=32%
Hallmark_Myc Targets V1	197	0.3579	1.0421	0.3589	1	1	8628	tags=41%, list=24%, signal=54%
Hallmark_E2f Targets	196	0.3526	1.0279	0.4045	1	1	8336	tags=40%, list=24%, signal=52%
Hallmark_Myc Targets V2	58	0.3935	1.0107	0.4394	1	1	8057	tags=40%, list=23%, signal=51%
Hallmark_Fatty Acid Metabolism	156	0.3513	1.0084	0.4350	0.9661	1	4956	tags=22%, list=14%, signal=25%
Hallmark_UV Response Up	154	0.3426	0.9887	0.4889	0.9939	1	7809	tags=38%, list=22%, signal=48%
Hallmark_Heme Metabolism	194	0.3296	0.9629	0.5836	1	1	4322	tags=23%, list=12%, signal=26%

Hallmark_Bile Acid Metabolism	112	0.3388	0.9394	0.5888	1	1	7294	tags=33%, list=21%, signal=41%
Hallmark_Mitotic Spindle	197	0.3193	0.9263	0.6636	1	1	8200	tags=39%, list=23%, signal=50%
Hallmark_Epithelial Mesenchymal Transition	197	0.3065	0.9051	0.6958	1	1	4956	tags=23%, list=14%, signal=26%
Hallmark_PI3K/AKT/mTOR Signaling	104	0.3291	0.8918	0.6949	1	1	6878	tags=33%, list=19%, signal=40%
Hallmark_IL2/STAT5 Signaling	195	0.3001	0.8825	0.7733	1	1	6978	tags=33%, list=20%, signal=41%
Hallmark_Hedgehog Signaling	35	0.3691	0.8725	0.6790	1	1	3768	tags=26%, list=11%, signal=29%
Hallmark_KRAS Signaling DN	190	0.2978	0.8647	0.8104	1	1	7793	tags=28%, list=22%, signal=36%
Hallmark_Pancreas Beta Cells	40	0.3528	0.8510	0.7479	1	1	3947	tags=23%, list=11%, signal=25%
Hallmark_DNA Repair	141	0.2951	0.8398	0.8372	1	1	7896	tags=34%, list=22%, signal=44%
Hallmark_Reactive Oxygen Species Pathway	45	0.3408	0.8353	0.7702	0.9749	1	3502	tags=24%, list=10%, signal=27%
Hallmark_Adipogenesis	190	0.2655	0.7778	0.9595	1	1	7775	tags=31%, list=22%, signal=40%
Hallmark_TGFβ Signaling	54	0.2920	0.7397	0.9230	1	1	7337	tags=33%, list=21%, signal=42%
Hallmark_Wnt/β-catenin Signaling	42	0.3022	0.7343	0.9080	1	1	9697	tags=45%, list=27%, signal=62%
Hallmark_Oxidative Phosphorylation	183	0.2344	0.6764	1	0.9948	1	9507	tags=34%, list=27%, signal=47%

Supplemental Table V: RNA-seq analysis of the NF- κ B target genes in HASMCs

Supplemental Table Va: RNA-seq analysis of the NF- κ B target genes in HASMCs transfected with siControl or siBAF60a

gene_ensembl_id	gene_name	base Mean	TPM_siC ontrol_1	TPM_siC ontrol_2	TPM_siC ontrol_3	TPM_siB AF60a_1	TPM_siB AF60a_2	TPM_siB AF60a_3	log2Fold Change	lfcSE	stat	p value	p adj
ENSG00000165029	ABCA1	4208.461	24.205	18.523	20.134	14.155	12.458	13.756	-0.666	0.1083	-6.151	7.71E-10	2.66E-08
ENSG00000081051	AFP	32.14958	4.4089	5.1093	4.8704	3.9484	4.2027	3.7569	-0.3321	0.232	-1.431	0.15229	0.34373
ENSG00000153207	AHCTF1	2762.14	29.655	27.375	25.339	23.886	25.826	27.844	-0.2452	0.0939	-2.61	0.00904	0.04378
ENSG00000187134	AKR1C1	46466.94	1070.6	1017.3	1061	617.51	639.04	601.02	-0.8044	0.108	-7.449	9.37E-14	5.68E-12
ENSG00000242110	AMACR	409.9856	3.7828	3.9132	4.4801	2.4686	2.5231	2.772	-0.6483	0.1312	-4.941	7.8E-07	1.5E-05
ENSG00000154188	ANGPT1	1164.308	6.7709	8.1133	5.8026	9.9746	9.2248	10.671	0.42934	0.1269	3.382	0.00072	0.00562
ENSG00000101246	ARFRP1	1192.079	50.079	53.711	41.726	55.456	53.62	51.763	0.14727	0.1727	0.853	0.39376	0.62167
ENSG00000198363	ASPH	19116.21	758.24	840.81	693.72	450.87	508.69	468.05	-0.7349	0.0862	-8.529	1.48E-17	1.35E-15
ENSG00000130707	ASS1	5023.933	321.46	279.12	315.53	339.29	306.52	332.55	0.06195	0.0908	0.682	0.49517	0.70617
ENSG00000166710	B2M	114363.9	9459.3	10388	9521.8	8561	9990.5	9313.8	-0.1663	0.062	-2.68	0.00735	0.03737
ENSG00000087088	BAX	3216.073	254.37	236.21	271.28	261.89	263.41	278.71	0.05288	0.0807	0.655	0.5124	0.72075
ENSG00000140379	BCL2A1	55.90206	4.9334	5.2774	3.7608	1.5904	2.2633	3.1628	-1.3731	0.3496	-3.928	8.6E-05	0.00093
ENSG00000171552	BCL2L1	2655.182	18.162	18.105	19.323	24.779	28.279	24.394	0.38214	0.0861	4.436	9.2E-06	0.00014
ENSG00000100739	BDKRB1	788.5608	30.671	26.906	27.374	26.106	28.282	26.034	-0.1293	0.0816	-1.585	0.11297	0.2823
ENSG00000176697	BDNF	1516.868	4.5615	4.157	4.2975	5.3219	5.3973	6.7627	0.17502	0.1738	1.007	0.31392	0.5425
ENSG00000182492	BGN	44931.2	371.67	326.93	373.19	370.31	335.22	361.97	-0.023	0.078	-0.295	0.76787	0.88571
ENSG00000125378	BMP4	684.2205	4.309	4.2132	5.2152	7.8772	9.5677	9.7276	0.97263	0.2142	4.541	5.6E-06	8.8E-05
ENSG00000176171	BNIP3	4453.834	42.053	50.395	44.531	71.068	75.758	63.76	0.62835	0.1026	6.122	9.24E-10	3.13E-08
ENSG00000105974	CAV1	9984.462	126.58	121.35	123.16	96.331	90.378	90.598	-0.4287	0.0722	-5.936	2.92E-09	9.26E-08
ENSG00000108691	CCL2	6380.218	570.44	556.63	558.29	226.79	228.38	273.47	-1.3086	0.0959	-13.65	2.01E-42	1.27E-39
ENSG00000115009	CCL20	45.92178	13.781	17.268	14.103	4.1487	4.5235	7.0235	-1.7819	0.2911	-6.121	9.29E-10	3.15E-08
ENSG00000271503	CCL5	73.46322	15.262	16.27	16.102	6.6668	9.1856	6.2968	-1.1548	0.133	-8.685	3.78E-18	3.62E-16
ENSG00000108688	CCL7	109.1916	84.524	93.49	75.292	30.037	33.817	39.711	-1.2332	0.1352	-9.12	7.49E-20	8.83E-18
ENSG00000108700	CCL8	42.20367	28.901	28.543	26.671	8.7385	8.7427	8.5772	-1.7042	0.1714	-9.941	2.76E-23	4.46E-21
ENSG00000110092	CCND1	23974.1	238.78	192.19	214.86	179.29	163.04	191.93	-0.4291	0.1656	-2.59	0.00958	0.04595
ENSG00000120217	CD274	130.3621	9.9148	11.298	8.6132	5.259	5.0866	4.2276	-1.118	0.1565	-7.143	9.15E-13	4.93E-11
ENSG00000004468	CD38	76.90484	23.315	21.775	18.894	10.513	8.7196	9.9822	-1.1261	0.2113	-5.329	9.89E-08	2.3E-06
ENSG00000101017	CD40	256.7601	5.3183	5.4857	5.2896	4.2334	4.0953	3.7486	-0.4702	0.1493	-3.149	0.00164	0.01111
ENSG00000026508	CD44	11653.6	915.2	942.59	846.71	669.23	680.41	702.62	-0.4644	0.0476	-9.763	1.62E-22	2.46E-20
ENSG00000124762	CDKN1A	47916.69	287.38	283	303.06	246.64	240.29	221.87	-0.2965	0.0844	-3.514	0.00044	0.00376
ENSG00000221869	CEBPD	4289.938	26.569	30.076	30.845	27.693	30.514	24.366	-0.0866	0.1125	-0.77	0.44152	0.66237

ENSG0000003402	CFLAR	2867.429	45.782	52.772	44.427	38.957	43.763	39.763	-0.2963	0.0894	-3.313	0.00092	0.00694
ENSG00000133048	CHI3L1	26.0331	2.8629	2.4551	1.9567	1.2284	1.2992	2.0853	-0.5618	0.2484	-2.261	0.02373	0.09257
ENSG00000164692	COL1A2	808162.1	5085.6	4848.6	5000	5005.1	4822.1	4840	-0.0383	0.0666	-0.575	0.56511	0.75751
ENSG00000107175	CREB3	2944.384	44.145	40.512	42.843	38.762	36.308	41.762	-0.1692	0.0791	-2.14	0.03232	0.11646
ENSG00000184371	CSF1	1311.846	31.92	29.924	29.356	23.67	21.969	20.771	-0.6024	0.1349	-4.467	7.9E-06	0.00012
ENSG00000108342	CSF3	206.6006	31.779	30.411	34.909	7.0175	7.6376	15.812	-2.0664	0.5936	-3.481	0.0005	0.00414
ENSG00000164733	CTSB	50530.65	859.37	742.27	822.48	776.77	750.84	765.95	-0.1245	0.0657	-1.893	0.05829	0.17815
ENSG00000163739	CXCL1	7266.801	967.93	939.81	934.76	690.46	770.81	965.74	-0.3888	0.1735	-2.241	0.02501	0.09643
ENSG00000169245	CXCL10	312.3122	195.19	233.24	180.79	135.8	149.44	135.5	-0.5816	0.1553	-3.746	0.00018	0.00178
ENSG00000169248	CXCL11	40.10742	35.961	35.769	33.404	12.682	17.79	12.145	-1.364	0.1634	-8.349	6.91E-17	5.97E-15
ENSG00000163734	CXCL3	799.9816	191.23	210.45	194.28	70.329	71.34	85.559	-1.3776	0.1168	-11.79	4.35E-32	1.84E-29
ENSG00000163735	CXCL5	1508.181	203.45	237.04	192.63	87.634	107.44	123.07	-0.9732	0.1246	-7.81	5.73E-15	4.09E-13
ENSG00000124875	CXCL6	7403.422	712.77	784.73	765.81	413.48	471.81	467	-0.7562	0.1133	-6.676	2.46E-11	1.10E-09
ENSG00000169429	CXCL8	11448.79	513.94	522.67	481.82	209.84	240.14	398.96	-1.1211	0.4233	-2.649	0.00808	0.0402
ENSG00000132912	DCTN4	3965.462	32.316	27.49	28.175	26.396	24.652	24.916	-0.3485	0.0865	-4.03	5.6E-05	0.00065
ENSG00000211448	DIO2	17385.73	73.345	62.685	65.6	38.656	42.996	61.897	-0.7666	0.3205	-2.392	0.01677	0.07127
ENSG00000188641	DPYD	3966.34	8.7166	8.0883	7.8865	8.9773	9.9593	8.5773	0.10435	0.111	0.94	0.3473	0.57713
ENSG00000120129	DUSP1	1174.954	12.151	10.685	11.43	8.0818	8.5796	10.993	-0.5778	0.2316	-2.495	0.0126	0.0571
ENSG00000146648	EGFR	6854.809	14.663	14.265	13.731	11.775	11.009	11.615	-0.3281	0.0685	-4.79	1.7E-06	3E-05
ENSG00000120738	EGR1	2503.573	3.6516	3.0947	2.7989	2.9332	2.748	2.8657	-0.1717	0.1572	-1.093	0.27448	0.49955
ENSG00000111674	ENO2	2148.539	35.887	44.336	47.957	77.128	70.907	63.032	0.65141	0.1133	5.751	8.90E-09	2.5E-07
ENSG00000070404	FSTL3	1786.831	7.4895	6.4259	8.104	10.44	11.506	11.711	0.43746	0.139	3.147	0.00165	0.01117
ENSG00000167996	FTH1	239320.5	12873	13412	12995	11358	11949	10884	-0.2117	0.0814	-2.599	0.00935	0.04496
ENSG00000160211	G6PD	8457.087	120.58	111.13	142.22	105.31	102.67	102.08	-0.2983	0.0984	-3.031	0.00244	0.01543
ENSG00000099860	GADD45B	662.403	23.982	22.633	32.374	25.414	19.57	15.269	-0.5056	0.1962	-2.577	0.00997	0.04729
ENSG00000117228	GBP1	2964.156	75.107	81.912	64.923	62.995	67.995	66.458	-0.2497	0.1089	-2.293	0.02187	0.08701
ENSG00000001084	GCLC	1394.256	49.898	48.5	43.266	28.161	32.258	36.269	-0.6417	0.1336	-4.801	1.6E-06	2.8E-05
ENSG00000023909	GCLM	2243.257	55.027	60.006	56.239	70.037	78.915	66.139	0.30109	0.1443	2.086	0.03698	0.12833
ENSG00000114353	GNAI2	15914.39	107.63	96.692	105.51	121.59	108.9	117.04	0.10446	0.0682	1.532	0.1256	0.30283
ENSG00000084207	GSTP1	9154.413	486.67	401.4	423.01	721.19	588.79	722.79	0.62769	0.1036	6.059	1.37E-09	4.49E-08
ENSG00000019991	HGF	19063.77	57.714	58.923	54.368	59.022	65.394	65.125	0.06524	0.0749	0.871	0.38397	0.61239
ENSG00000100644	HIF1A	39209.65	412.45	421.38	372.01	387.39	419.81	440.25	-0.1453	0.1033	-1.407	0.15948	0.35414
ENSG00000205581	HMGNI	2156.672	97.69	104.13	88.098	28.038	33.596	30.383	-1.7367	0.0975	-17.82	5.18E-71	5.62E-68
ENSG00000100292	HMOX1	3620.209	110.42	104.8	115.86	230.23	210.18	186.88	0.9622	0.1457	6.606	3.96E-11	1.68E-09
ENSG00000232357	HSD17B8	117.0889	1.6782	1.6882	2.2023	1.1121	0.905	1.1937	-0.6839	0.2685	-2.548	0.01085	0.05058
ENSG00000160888	IER2	1413.369	6.6349	6.8412	6.7135	7.2687	6.5693	7.0837	-0.0622	0.0929	-0.669	0.50323	0.71279
ENSG00000137331	IER3	2020.457	33.159	30.786	26.01	31.299	36.484	33.685	-0.0252	0.1909	-0.132	0.89515	0.95101

ENSG00000137959	IFI44L	14684.03	194.13	217.17	191.96	186.05	204.48	176.33	-0.1176	0.097	-1.212	0.22536	0.44099
ENSG00000115008	IL1A	221.843	5.9995	7.325	5.7355	2.3738	2.9997	4.3182	-1.1577	0.2444	-4.738	2.2E-06	3.8E-05
ENSG00000125538	IL1B	867.0515	22.684	19.781	19.918	10.613	8.1291	15.95	-1.0313	0.4615	-2.235	0.02543	0.09753
ENSG00000136689	IL1RN	4.485481	1.3428	1.5886	1.8582	0.6814	0.5836	0.9742	-1.2168	0.3054	-3.985	6.8E-05	0.00077
ENSG00000137033	IL33	19176.52	95.353	91.218	85.835	45.581	51.698	76.026	-1.081	0.3863	-2.799	0.00513	0.02823
ENSG00000136244	IL6	7981.845	1005.4	920.99	942.63	450.24	444.63	681.61	-1.0232	0.2798	-3.656	0.00026	0.00238
ENSG00000125347	IRF1	1764.448	29.58	28.713	26.699	22.523	22.636	22.167	-0.4025	0.0722	-5.575	2.47E-08	6.6E-07
ENSG00000168310	IRF2	1570.984	59.687	62.83	53.347	55.669	56.824	59.3	-0.0378	0.0918	-0.411	0.68074	0.83347
ENSG00000185507	IRF7	595.9928	23.298	25.076	26.014	36.335	34.002	26.306	0.33057	0.1364	2.423	0.01539	0.06661
ENSG00000171223	JUNB	4238.344	16.28	17.875	17.421	15.056	17.859	15.044	-0.1851	0.084	-2.204	0.0275	0.10309
ENSG00000172037	LAMB2	19484.23	546.26	479.2	571.69	612.11	615.7	591.97	0.15539	0.0747	2.079	0.03761	0.12997
ENSG00000101670	LIPG	966.9517	22.451	21.726	21.28	14.543	14.96	19.491	-0.4822	0.1231	-3.917	9E-05	0.00097
ENSG00000110492	MDK	11467.43	219.15	212.77	225.26	247.86	229.54	235.39	0.11709	0.0877	1.335	0.18186	0.38532
ENSG00000196611	MMP1	144075.8	1024.6	1056.5	974.5	756.83	797.44	937.23	-0.452	0.1224	-3.694	0.00022	0.0021
ENSG00000149968	MMP3	248.4587	73.056	75.186	68.724	31.682	45.925	61.201	-0.9973	0.4092	-2.437	0.01481	0.06459
ENSG00000100985	MMP9	0.389481	0.0056	0	0	0	0	0	-1.0573	3.5258	-0.3	0.76427	NA
ENSG00000157601	MX1	30682.87	1214.4	1359.8	1191	1340.6	1474.1	1280.6	0.08785	0.1139	0.772	0.44034	0.66159
ENSG00000136997	MYC	2281.403	27.67	29.465	30.53	22.976	21.885	18.912	-0.3907	0.1231	-3.174	0.0015	0.01041
ENSG00000109320	NFKB1	3099.801	17.626	19.018	19.728	17.382	18.361	17.679	-0.1276	0.0825	-1.547	0.12189	0.29737
ENSG00000077150	NFKB2	604.7963	5.7012	7.9419	8.2491	5.4339	6.5593	4.9531	-0.567	0.2106	-2.692	0.00711	0.03645
ENSG00000100906	NFKBIA	5156.267	420.97	440.18	452.01	315.94	324.2	303.14	-0.5302	0.0716	-7.404	1.32E-13	7.83E-12
ENSG00000144802	NFKBIZ	6311.337	61.968	61.681	64.187	46.466	46.503	50.402	-0.4884	0.1128	-4.328	1.5E-05	0.00021
ENSG00000181019	NQO1	9735.703	244.09	252.23	242.51	201.12	204.2	180.96	-0.3731	0.0928	-4.022	5.8E-05	0.00067
ENSG00000113580	NR3C1	10010.13	41.899	40.555	39.47	36.266	36.721	36.082	-0.1716	0.0612	-2.803	0.00507	0.02796
ENSG00000163545	NUAK2	299.2818	2.1201	2.0603	2.1989	1.5846	1.4108	1.6436	-0.4241	0.131	-3.238	0.0012	0.00863
ENSG00000125618	PAX8	43.3861	3.409	2.763	3.3348	2.0966	2.529	1.5579	-0.5281	0.2496	-2.116	0.03437	0.12138
ENSG00000205268	PDE7A	602.678	2.8342	2.5994	2.4125	2.9988	3.3703	3.5247	0.18543	0.1199	1.546	0.12211	0.29747
ENSG00000181195	PENK	109.9003	8.6845	8.1586	10.719	6.9244	6.5481	7.4327	-0.3684	0.1626	-2.265	0.0235	0.09194
ENSG00000151665	PIGF	505.7534	14.318	13.433	13.944	11.922	13.899	13.564	-0.1569	0.1167	-1.345	0.17878	0.38149
ENSG00000121879	PIK3CA	1929.034	10.261	10.626	9.8595	9.3465	9.4451	8.5491	0.04967	0.1812	0.274	0.78397	0.89465
ENSG00000137193	PIM1	1340.825	5.4811	4.9285	5.9941	9.1267	7.7186	6.8491	0.54516	0.1639	3.326	0.00088	0.00666
ENSG00000173846	PLK3	1218.008	13.183	10.211	12.479	14.573	14.612	17.634	0.24146	0.1645	1.467	0.14225	0.32953
ENSG00000011485	PPP5C	2095.164	40.285	43.857	43.08	41.304	44.354	47.236	-0.0739	0.0878	-0.841	0.40027	0.62804
ENSG00000072062	PRKACA	4864.75	33.944	30.05	33.346	32.874	30.713	35.407	-0.0472	0.0785	-0.601	0.5477	0.74636
ENSG00000163932	PRKCD	930.9193	5.1282	5.1881	5.2748	5.0007	5.396	5.7397	-0.0138	0.0892	-0.155	0.87704	0.94305
ENSG00000240508	PSMB9	639.17	37.454	36.468	38.27	30.147	29.507	26.015	-0.297	0.1053	-2.82	0.0048	0.02676
ENSG00000092010	PSME1	5681.536	235.77	269.22	238.37	219.88	216.66	218.76	0.1231	0.0559	2.204	0.02756	0.10323

ENSG00000100911	PSME2	4957.698	235.77	269.22	238.37	219.88	216.66	218.76	-0.2685	0.0602	-4.462	8.1E-06	0.00012
ENSG00000284792	PTEN	2914.126	55.953	72.374	52.654	54.936	59.276	49.258	0.09887	0.1052	0.94	0.34718	0.57708
ENSG00000148344	PTGES	1119.289	28.805	28.978	28.13	14.973	16.44	22.056	-0.7644	0.1467	-5.209	1.9E-07	4.2E-06
ENSG00000124212	PTGIS	40278.13	36.9	35.424	38.495	59.649	55.235	48.942	0.56426	0.1238	4.557	5.2E-06	8.2E-05
ENSG00000073756	PTGS2	6602.426	59.489	62.358	50.258	28.662	31.208	57.444	-0.9463	0.5064	-1.869	0.06167	0.18554
ENSG00000087494	PTHLH	171.7922	6.7677	6.0686	5.3625	3.8145	2.4992	4.4807	-1.2016	0.3726	-3.225	0.00126	0.00898
ENSG00000196396	PTPN1	2439.5	13.757	13.638	13.564	12.62	12.785	13.116	-0.1673	0.0528	-3.171	0.00152	0.01048
ENSG00000163629	PTPN13	3902.703	6.6724	6.9435	7.5762	7.8825	11.607	11.856	0.5565	0.1321	4.213	2.5E-05	0.00033
ENSG00000103490	PYCARD	691.27	5.9867	6.8887	8.3941	10.919	10.618	10.888	0.5801	0.1757	3.302	0.00096	0.00718
ENSG00000162521	RBBP4	4217.928	50.099	60.046	52.283	51.764	50.224	50.226	-0.087	0.0896	-0.971	0.33131	0.56099
ENSG00000173039	RELA	3421.807	135.5	186.41	144.66	161.12	187.23	121.06	0.09544	0.1647	0.579	0.56229	0.75544
ENSG00000104856	RELB	976.8408	7.9245	8.5195	6.8063	7.117	5.588	8.1144	-0.217	0.1704	-1.273	0.20296	0.41273
ENSG00000009413	REV3L	5791.711	59.726	61.693	54.053	50.116	58.817	51.596	-0.1816	0.0942	-1.927	0.05403	0.16846
ENSG00000104312	RIPK2	1772.162	20.869	22.599	19.769	15.246	16.909	16.981	-0.4565	0.0842	-5.42	5.96E-08	1.5E-06
ENSG00000196154	S100A4	8444.56	87.481	67.861	87.605	114.8	102.96	137.47	0.35918	0.1508	2.381	0.01726	0.07261
ENSG00000197956	S100A6	43535.37	1010	894.91	1036.4	1258.1	1136.7	1329.4	0.26897	0.0897	2.998	0.00272	0.0169
ENSG00000130066	SAT1	13963.76	386.8	447.16	392.98	290.06	309.48	348.55	-0.5528	0.1272	-4.348	1.4E-05	0.00019
ENSG00000196136	SERPINA3	682.5698	10.531	9.231	10.277	10.299	9.1077	9.8182	-0.0012	0.1384	-0.009	0.99294	0.99727
ENSG00000021355	SERPINB1	1251.455	33.167	37.537	29.359	50.309	56.485	42.399	0.40931	0.1256	3.26	0.00112	0.00814
ENSG00000106366	SERPINE1	32056.27	555.39	536.76	529.21	249.74	245.99	299.85	-1.07	0.1181	-9.062	1.28E-19	1.47E-17
ENSG00000135919	SERPINE2	72012.2	3087.9	2954.4	2931.8	2711.2	2697.2	3053.5	-0.1815	0.0852	-2.129	0.03324	0.11874
ENSG00000145604	SKP2	395.4459	7.5409	7.7076	7.7448	6.851	5.0107	4.7658	-0.4614	0.1655	-2.788	0.00531	0.02898
ENSG00000110911	SLC11A2	3689.193	78.504	77.499	72.744	61.837	63.901	75.356	-0.2793	0.0951	-2.936	0.00333	0.0198
ENSG00000155380	SLC16A1	5495.062	30.738	34.884	30.447	43.521	43.227	39.306	0.40305	0.0962	4.189	2.8E-05	0.00036
ENSG00000168003	SLC3A2	6047.854	575.73	532.38	533.42	411.19	414.37	402.06	-0.4213	0.0706	-5.97	2.37E-09	7.57E-08
ENSG00000124216	SNAI1	1141.099	3.7721	3.4943	4.1006	3.6654	3.7183	3.4263	-0.1811	0.176	-1.029	0.30325	0.53126
ENSG00000111728	ST8SIA1	184.465	1.1441	1.2952	1.1193	1.9822	1.8341	1.6481	0.7195	0.2038	3.53	0.00041	0.00358
ENSG00000126561	STAT5A	683.4394	5.8824	5.6799	6.4949	6.2949	6.0604	6.2045	0.00497	0.1006	0.049	0.96057	0.98102
ENSG00000156502	SUPV3L1	950.7204	32.643	32.525	30.714	28.104	28.19	24.728	-0.3274	0.0759	-4.315	1.6E-05	0.00022
ENSG00000168394	TAP1	2486.759	72.212	69.223	71.631	64.048	59.004	61.065	-0.2777	0.056	-4.961	7E-07	1.4E-05
ENSG00000236490	TAPBP	2561.25	36.389	37.354	39.895	49.864	45.347	42.143	-0.1481	0.1041	-1.422	0.1549	0.3476
ENSG00000105967	TFEC	5.35072	0.6572	0.8015	0.7341	0.2984	0.272	0.1715	-1.8433	0.4194	-4.395	1.1E-05	0.00016
ENSG00000137801	THBS1	27699.25	110.39	112.25	105.71	92.387	94.389	97.787	-0.2555	0.0843	-3.031	0.00244	0.01543
ENSG00000186340	THBS2	34675.45	203.29	172.72	193.87	258.86	240.03	245.17	0.34693	0.0761	4.557	5.2E-06	8.2E-05
ENSG00000041982	TNC	38265.62	314.5	314.79	326.3	380.92	385.35	511.8	0.37565	0.117	3.21	0.00133	0.00938
ENSG00000230108	TNF	11.43641	0.0656	0.0164	0.0921	0.0182	0.0609	0	NA	NA	NA	NA	NA
ENSG00000185215	TNFAIP2	12840.35	264.2	286.09	305.69	156.71	139.11	153.54	-0.9284	0.0847	-10.96	5.97E-28	1.49E-25

ENSG00000118503	TNFAIP3	5808.19	72.8	77.913	72.903	47.757	50.803	55.482	-0.6594	0.0926	-7.124	1.05E-12	5.60E-11
ENSG00000121858	TNFSF10	2005.559	98.681	102.57	89.328	70.379	70.572	56.422	-0.5567	0.2012	-2.767	0.00566	0.03041
ENSG00000102524	TNFSF13B	585.8452	86.066	89.897	83.128	77.934	84.09	67.141	-0.218	0.1409	-1.547	0.12193	0.29737
ENSG00000181634	TNFSF15	102.9641	0.4199	0.3959	0.4157	0.2264	0.237	0.2219	-0.885	0.1719	-5.148	2.6E-07	5.6E-06
ENSG00000050730	TNIP3	11.41582	3.8513	5.5199	4.4812	0.9097	1.0282	0.6591	-2.3379	0.223	-10.48	1.02E-25	2.04E-23
ENSG00000141510	TP53	2881.632	117.36	134.1	132.62	157.03	157.79	156.92	0.32566	0.2451	1.329	0.18388	0.38802
ENSG00000056558	TRAF1	600.1565	1.2242	1.2519	1.1548	1.141	1.1484	1.1335	-0.216	0.1136	-1.901	0.05727	0.17586
ENSG00000124731	TREM1	5.677793	9.0865	8.2976	8.3201	3.8542	4.7299	5.4343	-1.0071	0.2329	-4.324	1.5E-05	0.00021
ENSG00000130725	UBE2M	2259.242	99.588	91.898	113.81	118.92	103.79	108.59	0.0841	0.1061	0.792	0.42821	0.65092
ENSG00000162692	VCAM1	6258.808	38.011	42.514	38.524	42.393	42.691	35.333	0.0265	0.2144	0.124	0.90162	0.9541
ENSG00000150630	VEGFC	1530.309	21.076	22.752	20.996	18.651	21.949	20.88	-0.1596	0.0811	-1.967	0.04921	0.15755
ENSG00000026025	VIM	172218.1	727.66	747.19	728.32	750.45	754.11	744.25	-0.0307	0.0328	-0.938	0.3481	0.57779
ENSG00000100811	YY1	4640.467	49.931	48.101	44.17	45.454	46.431	41.248	-0.2383	0.0838	-2.844	0.00445	0.02515

Supplemental Table V: RNA-seq analysis of the NF- κ B target genes in HASMCs

Supplemental Table Vb: RNA-seq analysis of the NF- κ B target genes in HASMCs infected with AdGFP or AdBAF60a

gene_ensembl_id	gene_name	baseMean	TPM_ AdGFP _1	TPM_ AdGFP _2	TPM_ AdGFP _3	TPM_ AdBAF 60a 1	TPM_ AdBAF 60a 2	TPM_ AdBAF 60a 3	log2Fold Change	lfcSE	stat	p value	p adj
ENSG00000165029	ABCA1	1389.0658	6.2671	7.5542	7.244	7.8698	8	7.1179	0.152508	0.11265	1.3538	0.1758	0.32869
ENSG00000081051	AFP	8.7728116	0.6985	0.4481	0.8077	0.9952	1.757	1.8566	1.268497	0.72854	1.74115	0.08166	0.18292
ENSG00000153207	AHCTF1	1598.0733	13.009	14.794	15.907	11.048	9.899	10.469	-0.4479	0.10227	-4.37938	1.2E-05	7.7E-05
ENSG00000187134	AKR1C1	20008.196	1189.5	1224.5	1204.4	969.67	967.4	938.19	-0.30458	0.03772	-8.07568	6.7E-16	1.2E-14
ENSG00000242110	AMACR	458.75977	12.715	14.086	12.024	16.648	18.67	18.642	0.498514	0.11144	4.47324	7.7E-06	5.1E-05
ENSG00000154188	ANGPT1	736.62927	10.13	11.425	11.586	15.762	16.683	15.51	0.558202	0.0981	5.69035	1.3E-08	1.3E-07
ENSG00000101246	ARFRP1	1808.0742	58.491	56.842	55.516	65.925	62.298	64.174	0.198934	0.08511	2.3373	0.01942	0.05648
ENSG00000198363	ASPH	18567.756	357.73	359.78	355.5	379.65	378.49	371.27	0.101011	0.03266	3.09266	0.00198	0.00796
ENSG00000130707	ASS1	627.57019	16.448	15.904	16.084	34.199	31.212	29.99	1.007795	0.09844	10.2377	1.3E-24	4.1E-23
ENSG00000166710	B2M	16981.93	1156.9	1170.2	1178.4	2474.1	2276.9	2027.8	0.978141	0.0785	12.4606	1.2E-35	5.7E-34
ENSG00000087088	BAX	386.92328	64.752	46.268	70.085	46.384	61.136	41.074	-0.25987	0.23424	-1.10943	0.26724	0.44442
ENSG00000140379	BCL2A1	38.342681	2.0121	3.0566	2.0806	3.2479	3.7093	4.0763	0.639373	0.43061	1.48479	0.1376	0.27437
ENSG00000171552	BCL2L1	2058.1623	42.914	44.949	42.341	66.509	69.594	66.5	0.663574	0.0557	11.9136	1E-32	4.3E-31
ENSG00000100739	BDKRB1	29.04623	1.6014	0.3704	1.7159	0.5042	5.0458	1.63	0.972356	1.06168	0.91587	0.35974	0.5439
ENSG00000176697	BDNF	1151.1479	19.484	19.961	19.224	15.306	15.359	13.282	-0.38997	0.07588	-5.1391	2.8E-07	2.3E-06
ENSG00000182492	BGN	31159.278	582.47	598.44	573.7	784.54	808.08	825.3	0.489741	0.04335	11.2974	1.4E-29	5E-28
ENSG00000125378	BMP4	224.74895	7.0713	7.4271	7.4878	8.0855	6.7951	7.2518	0.040702	0.14352	0.2836	0.77672	0.87659
ENSG00000176171	BNIP3	5703.6581	117.45	118.97	112.85	198.64	233.25	189.27	0.857219	0.07376	11.6214	3.2E-31	1.3E-29
ENSG00000105974	CAV1	4902.3049	150.63	145.52	154.65	126.69	128.61	118.7	-0.24214	0.04878	-4.96409	6.9E-07	5.4E-06
ENSG00000108691	CCL2	531.42124	128.13	123.81	123.35	41.378	39.373	36.505	-1.64932	0.10395	-15.8672	1.1E-56	9.6E-55
ENSG00000115009	CCL20	5.1130612	1.534	0.1192	0.761	1.0845	1.3896	0.6311	0.565579	1.05065	0.53831	0.59036	0.74807
ENSG00000271503	CCL5	80.393134	2.5447	1.6308	2.9987	5.3644	2.9029	4.3659	0.867255	0.3187	2.7212	0.0065	0.02239
ENSG00000108688	CCL7	3.3370157	0	0	0.4497	0.0983	0.4053	0.2434	0.765265	1.49715	0.51115	0.60925	0.76223
ENSG00000108700	CCL8	0.9898256	0	0	0	0.0452	0	0.1668	2.586505	2.45151	1.05506	0.2914	NA
ENSG00000110092	CCND1	48253.66	791.58	812.78	792.43	605.7	563.03	574.03	-0.43277	0.08534	-5.07111	4E-07	3.2E-06
ENSG00000120217	CD274	77.429235	0.4728	2.0268	1.5531	3.6402	2.3641	1.3941	0.923199	0.49681	1.85826	0.06313	0.14954
ENSG00000004468	CD38	4.7282032	0	0.0239	0	0.1024	0.3767	0.1498	3.927011	1.3813	2.84298	0.00447	0.01614
ENSG00000101017	CD40	104.21128	2.7306	3.0322	2.1049	5.708	5.7304	6.9784	1.251284	0.23683	5.28342	1.3E-07	1.1E-06
ENSG00000026508	CD44	6752.0615	503.91	516.86	533.37	476.41	477.02	434.77	-0.13573	0.07484	-1.81347	0.06976	0.16176
ENSG00000124762	CDKN1A	16768.799	315.82	311.18	307.98	496.15	530.99	532.21	0.765052	0.04447	17.2024	2.5E-66	2.8E-64

ENSG00000221869	CEBPD	408.74109	7.9614	7.8769	7.9144	11.506	12.671	10.614	0.577433	0.12021	4.80359	1.6E-06	1.2E-05
ENSG00000003402	CFLAR	1388.1735	21.127	21.724	21.218	23.147	20.781	23.971	0.110709	0.11208	0.98776	0.32327	0.50746
ENSG00000133048	CHI3L1	1.9768057	0	0	0.035	0.0492	0.505	0.0606	3.683096	2.03675	1.80832	0.07056	0.16311
ENSG00000164692	COL1A2	341255.43	2948.5	3053.5	2843.2	4155.4	3786.3	4054.1	0.466406	0.05281	8.83211	1E-18	2.3E-17
ENSG00000107175	CREB3	3063.9895	85.242	82.296	81.387	110.98	111.19	110.68	0.44714	0.05207	8.58713	8.9E-18	1.9E-16
ENSG00000184371	CSF1	71.576553	8.5443	7.4915	2.4526	4.1903	11.269	6.7888	0.28328	0.47143	0.6009	0.54791	0.71372
ENSG00000108342	CSF3	12.424773	0.4553	0.2669	0.2971	0.5286	0.4672	0.2565	0.358687	0.66102	0.54263	0.58739	0.74577
ENSG00000164733	CTSB	23061.937	760.3	805.65	762.22	879.82	895.75	883.15	0.218702	0.05	4.37432	1.2E-05	7.8E-05
ENSG00000163739	CXCL1	243.48916	17.924	18.314	20.501	19.728	19.977	21.728	0.141989	0.17175	0.82671	0.4084	0.59155
ENSG00000169245	CXCL10	8.7114562	0	0	0.0754	1.2884	1.2781	1.0548	5.486829	1.33572	4.10776	4E-05	0.00023
ENSG00000169248	CXCL11	9.677618	0	0	0.1164	1.7438	1.0942	1.0184	5.05401	1.25079	4.04065	5.3E-05	0.00031
ENSG00000163734	CXCL3	28.003646	0.404	0.656	1.9835	2.6889	3.1199	2.749	1.531652	0.5404	2.83432	0.00459	0.01652
ENSG00000163735	CXCL5	38.86437	1.6785	1.5775	1.9309	0.6761	1.2074	0.9109	-0.87747	0.34764	-2.52407	0.0116	0.03672
ENSG00000124875	CXCL6	261.37569	18.434	17.468	18.294	9.6165	8.9829	8.0106	-0.99641	0.14679	-6.7879	1.1E-11	1.5E-10
ENSG00000169429	CXCL8	1877.1695	164.66	165.13	167.9	72.594	76.72	72.113	-1.14153	0.11023	-10.3556	3.9E-25	1.2E-23
ENSG00000132912	DCTN4	2450.6178	42.143	42.664	45.295	47.907	48.949	46.241	0.164326	0.05803	2.83152	0.00463	0.01665
ENSG00000211448	DIO2	6589.7128	205.86	193.44	217.13	167.08	185.36	172.87	-0.2036	0.10272	-1.98205	0.04747	0.11872
ENSG00000188641	DPYD	857.00089	14.823	15.135	15.004	17.466	15.664	17.4	0.19634	0.117	1.6781	0.09333	0.20303
ENSG00000120129	DUSP1	573.50239	5.3238	5.962	5.1779	14.262	10.956	10.798	1.156533	0.14057	8.22743	1.9E-16	3.7E-15
ENSG00000146648	EGFR	3259.253	28.902	31.595	29.71	20.568	18.613	19.197	-0.6002	0.06493	-9.24449	2.4E-20	5.8E-19
ENSG00000120738	EGR1	590.10731	0.9602	0.8238	1.029	16.421	12.107	13.203	3.928139	0.19441	20.2049	8.9E-91	1.8E-88
ENSG00000111674	ENO2	3712.581	64.221	62.023	65.33	95.341	103.99	108.53	0.711819	0.06422	11.084	1.5E-28	5.4E-27
ENSG00000070404	FSTL3	6436.327	109.86	111.2	103.89	156.2	160.23	156.13	0.56698	0.04748	11.9405	7.3E-33	3.1E-31
ENSG00000167996	FTH1	29253.421	3485.6	3368	3405.5	3845.7	4131.4	3886.1	0.236533	0.04153	5.69565	1.2E-08	1.2E-07
ENSG00000160211	G6PD	8697.5759	218.06	223.55	222.18	264.69	266.5	276.5	0.310315	0.05787	5.36249	8.2E-08	7.2E-07
ENSG00000099860	GADD45B	1239.0464	34.48	35.601	34.468	46.37	47.034	49.76	0.479687	0.06879	6.97274	3.1E-12	4.4E-11
ENSG00000117228	GBP1	1065.8699	3.6049	3.3225	2.7354	40.015	34.14	30.557	3.467774	0.14977	23.1545	1E-118	6E-116
ENSG00000001084	GCLC	953.62309	20.483	19.051	18.914	18.515	18.708	20.775	0.015651	0.11545	0.13556	0.89217	0.9442
ENSG00000023909	GCLM	1433.4634	30.266	30.844	29.169	28.174	29.745	27.572	-0.0517	0.06557	-0.7885	0.43041	0.61241
ENSG00000114353	GNAI2	1189.2566	69.916	72.221	73.453	70.478	72.04	72.389	0.022631	0.11999	0.1886	0.85041	0.92063
ENSG00000084207	GSTP1	9737.9234	1078.5	1119	1048.4	1058	1047.9	1071.4	-0.00383	0.04403	-0.08707	0.93062	0.9635
ENSG00000019991	HGF	12145.442	294.64	331.39	340.15	268.44	252.34	260.81	-0.27811	0.06024	-4.61636	3.9E-06	2.7E-05
ENSG00000100644	HIF1A	13331.731	275.95	259.26	270.19	260.13	268.65	236.47	-0.04706	0.05617	-0.83785	0.40211	0.58506
ENSG00000205581	HMGN1	5042.3694	353.78	330.23	305.13	292.66	313.02	301.5	-0.09826	0.08022	-1.22497	0.22059	0.38812
ENSG00000100292	HMOX1	7864.1074	171.65	182.48	169.27	227.18	253.93	233.93	0.476836	0.06331	7.53126	5E-14	8.2E-13
ENSG00000232357	HSD17B8	61.777708	5.3829	3.7237	4.4049	5.2586	4.9806	3.9299	0.102046	0.33706	0.30275	0.76208	0.86712

ENSG00000160888	IER2	1513.1988	17.038	15.481	14.128	44.811	42.865	46.317	1.551762	0.08584	18.0778	4.8E-73	6.2E-71
ENSG00000137331	IER3	0	0	0	0	0	0	0	NA	NA	NA	NA	NA
ENSG00000137959	IFI44L	1460.2709	2.2444	1.587	2.1785	105.08	83.43	75.817	5.513229	0.19891	27.7174	4E-169	4E-166
ENSG00000115008	IL1A	143.20119	6.0877	5.8039	6.6055	3.8899	3.6204	3.5571	-0.71079	0.19166	-3.70853	0.00021	0.00107
ENSG00000125538	IL1B	546.61126	31.228	29.226	31.477	16.641	15.485	16.062	-0.90179	0.10139	-8.89419	5.9E-19	1.3E-17
ENSG00000136689	IL1RN	5.6243113	0.1822	0.1902	0.4182	0.3279	0.2237	0.2864	0.197185	0.9004	0.219	0.82665	0.90708
ENSG00000137033	IL33	10494.893	366.87	383.93	392.66	283.07	293.83	277.46	-0.39316	0.06911	-5.68876	1.3E-08	1.3E-07
ENSG00000136244	IL6	122.9191	6.8902	6.8933	9.7254	6.5282	4.9929	7.0707	-0.30647	0.2531	-1.21088	0.22594	0.39487
ENSG00000125347	IRF1	590.9118	8.5774	10.124	12.135	25.58	29.7	27.79	1.458107	0.12299	11.8553	2E-32	8.5E-31
ENSG00000168310	IRF2	362.92882	10.768	11.541	13.394	15.156	13.896	11.136	0.197189	0.16265	1.21238	0.22537	0.39412
ENSG00000185507	IRF7	9.3110113	0	0	0.7274	1.2975	2.1255	1.296	2.876699	1.04267	2.75897	0.0058	0.02025
ENSG00000171223	JUNB	2871.4216	37.737	40.406	38.474	88.241	90.672	90.427	1.232672	0.0499	24.7018	1E-134	7E-132
ENSG00000172037	LAMB2	17504.585	283.44	250.41	243.79	278.23	275.57	272.59	0.114	0.07364	1.5481	0.1216	0.25037
ENSG00000101670	LIPG	823.61248	29.36	26.006	25.651	14.423	13.677	13.162	-0.94346	0.09521	-9.90878	3.8E-23	1.1E-21
ENSG00000110492	MDK	4171.9433	290.4	287.72	263.32	451.03	469.05	451.4	0.731606	0.05738	12.7492	3.1E-37	1.6E-35
ENSG00000196611	MMP1	70762.221	3301.4	3168	3277.7	1991.3	1875.1	1989.9	-0.70811	0.05504	-12.8656	7E-38	3.6E-36
ENSG00000149968	MMP3	140.73842	4.3028	3.9739	4.4855	4.0578	4.667	3.7938	-0.00099	0.19192	-0.00518	0.99587	0.99941
ENSG00000100984	MMP9	3.5605512	0	0	0	0.0502	0.1644	0.1648	4.874823	1.67385	2.91235	0.00359	0.01331
ENSG00000157601	MX1	8602.536	1.5187	1.42	2.93	510.7	427.3	342.71	7.791903	0.34604	22.5171	3E-112	1E-109
ENSG00000136997	MYC	391.24849	5.6986	5.5495	7.0581	9.9581	9.6456	10.018	0.730226	0.12812	5.69943	1.2E-08	1.2E-07
ENSG00000109320	NFKB1	731.35277	12.866	13.618	12.815	11.375	9.7366	10.761	-0.27356	0.0868	-3.15146	0.00162	0.00667
ENSG00000077150	NFKB2	407.88653	14.613	12.657	15.694	15.496	16.495	17.256	0.225709	0.12112	1.86347	0.0624	0.14812
ENSG00000100906	NFKBIA	952.63829	34.228	39.138	42.851	41.69	39.155	42.336	0.111435	0.10043	1.10961	0.26717	0.44434
ENSG00000144802	NFKBIZ	412.75178	10.398	8.5763	13.49	8.0151	7.6638	7.7826	-0.43753	0.16516	-2.64919	0.00807	0.02695
ENSG00000181019	NQO1	7248.8847	354.23	341.77	348.29	593.16	579.61	573.92	0.769949	0.0384	20.052	1.9E-89	3.9E-87
ENSG00000113580	NR3C1	3867.9372	54.916	52.456	53.169	42.224	39.755	40.814	-0.35943	0.0789	-4.55527	5.2E-06	3.6E-05
ENSG00000163545	NUAK2	49.304308	0.1854	0.3634	0.3693	0.6947	0.9158	0.8972	1.431696	0.35045	4.0853	4.4E-05	0.00026
ENSG00000125618	PAX8	52.993704	1.4751	0.924	1.4871	1.2862	1.0176	0.9457	-0.20328	0.33192	-0.61243	0.54025	0.70717
ENSG00000205268	PDE7A	287.96648	7.8333	7.1635	7.1794	5.9834	7.0239	5.2934	-0.25179	0.17531	-1.43621	0.15094	0.29355
ENSG00000181195	PENK	544.99558	26.491	28.956	30.184	38.966	39.648	39.427	0.488499	0.10002	4.88384	1E-06	7.9E-06
ENSG00000151665	PIGF	116.2769	17.171	11.099	14.222	7.8312	11.444	12.295	-0.39849	0.25527	-1.56104	0.11851	0.24548
ENSG00000121879	PIK3CA	1291.424	25.33	16.809	23.32	20.367	18.784	16.688	-0.20202	0.17962	-1.12469	0.26072	0.43706
ENSG00000137193	PIM1	453.90715	18.177	13.668	17.727	8.0494	6.0883	6.678	-1.2219	0.15495	-7.88593	3.1E-15	5.5E-14
ENSG00000173846	PLK3	659.41911	8.4133	7.5315	8.9952	19.486	17.396	22.788	1.288699	0.1322	9.7483	1.9E-22	5.1E-21
ENSG00000011485	PPP5C	2363.0851	79.382	82.431	79.52	58.085	58.312	58.673	-0.43632	0.05425	-8.0433	8.7E-16	1.6E-14
ENSG00000072062	PRKACA	5146.1222	121.94	130.48	122.82	140.78	135.7	147.28	0.202521	0.06245	3.2431	0.00118	0.00505

ENSG00000163932	PRKCD	945.29839	20.002	17.666	19.395	25.732	24.278	25.022	0.425484	0.09555	4.45288	8.5E-06	5.6E-05
ENSG00000240508	PSMB9	63.624604	0	1.1323	1.6678	15.421	14.571	11.71	3.86758	0.48711	7.93991	2E-15	3.6E-14
ENSG00000092010	PSME1	110.87596	8.5207	7.5722	8.0458	10.089	12.388	8.2868	0.373479	0.24667	1.51406	0.13001	0.26307
ENSG00000100911	PSME2	2693.8483	102.93	96.564	96.864	422.14	327.85	352.07	1.922439	0.09277	20.7222	2.2E-95	5E-93
ENSG00000284792	PTEN	1012.285	11.72	10.638	11.627	14.573	11.357	11.306	0.158983	0.12632	1.25854	0.2082	0.37255
ENSG00000148344	PTGES	674.08316	16.626	16.746	16.633	23.836	21.102	22.734	0.465504	0.09573	4.86243	1.2E-06	8.7E-06
ENSG00000124212	PTGIS	8944.6332	106.23	116.76	108.74	83.293	88.839	80.972	-0.36351	0.05483	-6.6297	3.4E-11	4.3E-10
ENSG00000073756	PTGS2	3876.2237	77.448	77.172	88.303	62.732	53.458	61.141	-0.42575	0.07299	-5.83322	5.4E-09	5.6E-08
ENSG00000087494	PTHLH	1067.7761	51.138	51.84	46.902	47.783	45.069	44.851	-0.09443	0.08217	-1.14911	0.25051	0.42488
ENSG00000196396	PTPN1	2200.1551	28.255	28.671	29.368	34.569	32.809	34.844	0.272426	0.05342	5.09945	3.4E-07	2.8E-06
ENSG00000163629	PTPN13	1824.6558	10.232	11.896	12.964	21.955	14.584	21.844	0.761578	0.14016	5.43351	5.5E-08	5E-07
ENSG00000103490	PYCARD	279.00798	28.853	24.943	24.698	23.505	26.806	20.133	-0.12934	0.17797	-0.72676	0.46737	0.64671
ENSG00000162521	RBBP4	1743.1594	72.209	74.857	70.542	67.584	73.702	68.99	-0.02375	0.07079	-0.33541	0.73731	0.85182
ENSG00000173039	RELA	2890.6013	66.049	65.228	65.713	67.97	65.003	67.744	0.054909	0.05768	0.95193	0.34113	0.52604
ENSG00000104856	RELB	27.911318	0.1245	0.3942	0.7984	1.6776	1.6315	0.4058	1.420886	0.76543	1.85633	0.06341	0.15007
ENSG00000009413	REV3L	913.40337	8.7909	11.444	11.445	9.6757	9.9735	9.3788	-0.09976	0.10646	-0.93703	0.34874	0.53364
ENSG00000104312	RIPK2	1152.8854	36.014	32.927	37.337	37.962	42.001	40.96	0.214021	0.09707	2.20476	0.02747	0.07566
ENSG00000196154	S100A4	1633.1426	343.8	351.59	374.32	308.63	312.21	306.42	-0.1791	0.0592	-3.02567	0.00248	0.00967
ENSG00000197956	S100A6	22003.078	3142.1	3014.1	3143	3053.8	2899.7	2941.6	-0.03711	0.05091	-0.7288	0.46612	0.64529
ENSG00000130066	SAT1	4729.4465	479.56	504.55	507.56	276.77	294.9	292.71	-0.76071	0.04816	-15.7958	3.3E-56	3E-54
ENSG00000196136	SERPINA3	39.249156	0.9481	0.9694	1.209	1.9643	1.4221	2.1003	0.837444	0.35743	2.34299	0.01913	0.05584
ENSG00000021355	SERPINB1	525.63697	13.983	13.503	11.692	20.898	20.3	19.758	0.666752	0.14244	4.68104	2.9E-06	2.1E-05
ENSG00000106366	SERPINE1	76776.767	1138.8	1174.3	1141	1324.6	1323.2	1314.1	0.224966	0.0261	8.61916	6.7E-18	1.4E-16
ENSG00000135919	SERPINE2	25381.532	733.03	777.05	770.32	723.06	753.9	703.96	-0.03719	0.03848	-0.96653	0.33378	0.51817
ENSG00000145604	SKP2	79.827006	3.1498	3.8709	4.1096	3.7628	3.0636	3.6926	-0.05011	0.25476	-0.19671	0.84405	0.91788
ENSG00000110911	SLC11A2	704.20877	16.575	15.058	17.806	14.359	14.083	13.535	-0.20605	0.09066	-2.27276	0.02304	0.06509
ENSG00000155380	SLC16A1	3192.1825	43.21	42.223	43.355	60.555	69.755	58.286	0.576617	0.07217	7.99017	1.3E-15	2.4E-14
ENSG00000168003	SLC3A2	1388.0107	111.18	78.389	71.92	128.78	116.42	95.69	0.407676	0.17442	2.33726	0.01943	0.05648
ENSG00000124216	SNAI1	2103.8371	48.668	52.864	46.128	70.1	69.191	70.39	0.5316	0.06261	8.49101	2E-17	4.2E-16
ENSG00000111728	ST8SIA1	19.50298	0.0603	0.0636	0.0565	0.981	0.4311	0.6483	3.515235	0.5728	6.1369	8.4E-10	9.3E-09
ENSG00000126561	STAT5A	143.58417	2.2019	1.7922	2.9124	2.3616	2.7105	3.2676	0.313205	0.23131	1.35403	0.17573	0.32863
ENSG00000156502	SUPV3L1	461.39334	15.053	13.568	11.869	13.928	12.948	17.668	0.164012	0.15078	1.08778	0.27669	0.45473
ENSG00000168394	TAP1	5.9353157	11.101	11.698	12.49	117.23	97.559	87.121	2.032563	3.53946	0.57426	0.56579	0.7278
ENSG00000236490	TAPBP	2213.2794	25.253	26.625	25.766	38.539	39.419	40.978	0.641802	0.05646	11.3673	6.1E-30	2.3E-28
ENSG00000105967	TFEC	1.1831527	0.0171	0.0343	0	0	0.0139	0.1272	0.584369	2.47675	0.23594	0.81348	NA
ENSG00000137801	THBS1	2387.5689	21.849	20.801	22.955	14.158	12.308	14.223	-0.66024	0.07425	-8.8922	6E-19	1.4E-17

ENSG00000186340	THBS2	18913.236	185.44	194.04	193.86	178.38	176.8	171.25	-0.09596	0.04102	-2.33958	0.01931	0.05624
ENSG00000041982	TNC	9668.7766	45.114	48.507	49.512	75.01	65.389	67.551	0.566356	0.0545	10.3926	2.7E-25	8.4E-24
ENSG00000230108	TNF	0.1174592	0	0	0.0529	0	0	0	-1.19589	4.08046	-0.29308	0.76946	NA
ENSG00000185215	TNFAIP2	1630.671	15.918	15.833	16.452	46.771	41.543	45.512	1.501514	0.07308	20.5452	8.5E-94	1.9E-91
ENSG00000118503	TNFAIP3	780.13524	9.9744	9.174	9.5546	12.323	12.576	11.313	0.364229	0.13774	2.64431	0.00819	0.02727
ENSG00000121858	TNFSF10	98.097633	0.0912	0.154	0.2104	11.053	9.0975	7.6322	5.945945	0.516	11.523	1E-30	3.9E-29
ENSG00000102524	TNFSF13B	161.63355	2.2304	2.2335	4.3657	12.834	10.814	9.8561	1.979165	0.3022	6.54928	5.8E-11	7.3E-10
ENSG00000181634	TNFSF15	17.244827	0.1519	0.1759	0.0919	0.1795	0.1117	0.1548	0.128663	0.51465	0.25	0.80258	0.89265
ENSG00000050730	TNIP3	4.9503539	0.1326	0.0879	0	0.0571	0.6286	0.4129	2.167276	1.20908	1.7925	0.07305	0.16759
ENSG00000141510	TP53	1103.8967	41.184	35.623	36.381	36.54	33.299	32.753	-0.11228	0.10309	-1.08911	0.27611	0.45436
ENSG00000056558	TRAF1	282.18951	3.5293	3.3806	3.4694	2.6933	2.3945	2.804	-0.36389	0.13358	-2.72416	0.00645	0.02219
ENSG00000124731	TREM1	116.39879	4.0237	4.503	4.5356	8.9645	9.2272	9.8145	1.127159	0.20722	5.43953	5.3E-08	4.9E-07
ENSG00000130725	UBE2M	3768.6848	153.46	151.02	149.56	166.12	163.51	152.2	0.112906	0.05463	2.06684	0.03875	0.10079
ENSG00000162692	VCAM1	75.612291	0.8692	1.0769	1.452	2.9802	2.416	2.5377	1.247872	0.29899	4.17366	3E-05	0.00018
ENSG00000150630	VEGFC	3643.5074	88.184	94.471	91.422	110.06	106.52	100.52	0.237237	0.05621	4.22037	2.4E-05	0.00015
ENSG00000026025	VIM	180887.09	6599.8	6676.2	6760.5	5062.2	5357.7	5274.3	-0.32509	0.05331	-6.09782	1.1E-09	1.2E-08
ENSG00000100811	YY1	2558.363	31.687	33.077	30.224	34.97	33.076	36.056	0.158983	0.06172	2.57601	0.00999	0.03235

Supplemental Table VI: GSEA report for RNA-seq data on HASMCs infected with AdBAF60a vs. AdGFP

Online Table VIa: Gene sets enriched in HASMCs infected with AdGFP

Name	Size	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val	Rank at Max	Leading Edge
Hallmark_Mitotic Spindle	198	-0.6706	-1.2981	0	0.4006	0.154	3548	tags=44%, list=10%, signal=49%
Hallmark_Spermatogenesis	133	-0.4845	-1.2796	0	0.2452	0.207	3545	tags=29%, list=10%, signal=32%
Hallmark_DNA Repair	149	-0.5793	-1.2277	0	0.2533	0.505	6249	tags=52%, list=17%, signal=63%
Hallmark_Myc Targets V2	58	-0.6258	-1.2114	0	0.2097	0.505	6699	tags=60%, list=19%, signal=74%
Hallmark_G2M Checkpoint	195	-0.8044	-1.1819	0	0.2157	0.698	2560	tags=64%, list=7%, signal=69%
Hallmark_Myc Targets V1	196	-0.6955	-1.1679	0	0.1978	0.698	6631	tags=66%, list=18%, signal=80%
Hallmark_E2f Targets	198	-0.8602	-1.1590	0	0.1838	0.742	2556	tags=75%, list=7%, signal=80%
Hallmark_TGFβ Signaling	53	-0.3933	-1.0874	0.1882	0.2495	0.888	4658	tags=38%, list=13%, signal=43%
Hallmark_Oxidative Phosphorylation	200	-0.3595	-1.0841	0.1008	0.2338	0.888	8200	tags=54%, list=23%, signal=69%
Hallmark_Protein Secretion	96	-0.3105	-0.9882	0.4187	0.4640	1	7399	tags=36%, list=21%, signal=46%

Online Table VIb: Gene sets enriched in HASMCs infected with AdBAF60a

Name	Size	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val	Rank at Max	Leading Edge
Hallmark_Notch Signaling	32	0.5978	1.5103	0	0.0530	0	2200	tags=25%, list=6%, signal=27%
Hallmark_PI3K/AKT/mTOR Signaling	105	0.4362	1.4290	0	0.0530	0.053	4600	tags=26%, list=13%, signal=29%
Hallmark_KRAS Signaling Down	198	0.5904	1.4012	0	0.0530	0.053	3487	tags=27%, list=10%, signal=29%
Hallmark_Unfolded Protein Response	110	0.5102	1.3920	0	0.0530	0.053	3413	tags=29%, list=10%, signal=32%
Hallmark_Fatty Acid Metabolism	156	0.4672	1.3874	0	0.0530	0.053	5655	tags=31%, list=16%, signal=36%
Hallmark_IL2/STAT5 Signaling	199	0.5297	1.3862	0	0.0530	0.053	3511	tags=32%, list=10%, signal=35%
Hallmark_Allograft Rejection	195	0.5609	1.3741	0	0.0530	0.053	4327	tags=27%, list=12%, signal=31%
Hallmark_Interferon Gamma Response	197	0.8059	1.3657	0	0.0677	0.097	2065	tags=50%, list=6%, signal=53%
Hallmark_Inflammatory Response	200	0.6097	1.3619	0	0.0660	0.097	3510	tags=32%, list=10%, signal=35%
Hallmark_P53 Pathway	195	0.6065	1.3609	0	0.0647	0.097	4092	tags=38%, list=11%, signal=43%
Hallmark_Apical Junction	200	0.4738	1.3596	0	0.0637	0.097	5719	tags=36%, list=16%, signal=43%
Hallmark_Myogenesis	198	0.6840	1.3567	0	0.0628	0.097	3969	tags=40%, list=11%, signal=45%
Hallmark_UV Response Up	156	0.6337	1.3545	0	0.0620	0.097	4787	tags=44%, list=13%, signal=51%
Hallmark_Complement	200	0.5773	1.3429	0	0.0614	0.097	5800	tags=40%, list=16%, signal=47%
Hallmark_Cholesterol Homeostasis	73	0.5106	1.3429	0	0.0608	0.097	3904	tags=33%, list=11%, signal=37%

Hallmark_TNF α Signaling via NF κ B	199	0.6520	1.3411	0	0.0603	0.097	2791	tags=41%, list=8%, signal=44%
Hallmark_KRAS Signaling Up	199	0.5227	1.3330	0	0.0599	0.097	5515	tags=38%, list=15%, signal=45%
Hallmark_IL6/JAK/STAT3 Signaling	86	0.6382	1.3328	0	0.0595	0.097	3700	tags=38%, list=10%, signal=43%
Hallmark_Reactive Oxygen Species Pathway	48	0.4444	1.3255	0	0.0592	0.097	6672	tags=33%, list=19%, signal=41%
Hallmark_Apoptosis	160	0.6086	1.3207	0	0.0589	0.097	4313	tags=46%, list=12%, signal=52%
Hallmark_Angiogenesis	36	0.6169	1.3122	0	0.0586	0.097	2022	tags=31%, list=6%, signal=32%
Hallmark_Adipogenesis	198	0.4555	1.3075	0	0.0614	0.152	6336	tags=36%, list=18%, signal=44%
Hallmark_Xenobiotic Metabolism	198	0.5680	1.3043	0	0.0610	0.152	4978	tags=38%, list=14%, signal=44%
Hallmark_Estrogen Response Early	199	0.4911	1.2997	0	0.0607	0.152	2063	tags=24%, list=6%, signal=25%
Hallmark_Coagulation	138	0.5916	1.2976	0	0.0604	0.152	4691	tags=39%, list=13%, signal=45%
Hallmark_Hedgehog Signaling	36	0.5052	1.2923	0	0.0601	0.152	1556	tags=22%, list=4%, signal=23%
Hallmark_Glycolysis	197	0.4757	1.2834	0	0.0671	0.201	3888	tags=30%, list=11%, signal=34%
Hallmark_Hypoxia	200	0.5531	1.2686	0	0.0771	0.295	4827	tags=45%, list=13%, signal=52%
Hallmark_Apical Surface	44	0.5068	1.2648	0	0.0762	0.295	2484	tags=27%, list=7%, signal=29%
Hallmark_Estrogen Response Late	199	0.5123	1.2568	0	0.0809	0.387	3791	tags=33%, list=11%, signal=37%
Hallmark_Heme Metabolism	193	0.4080	1.2419	0	0.0881	0.491	4410	tags=26%, list=12%, signal=29%
Hallmark_Epithelial Mesenchymal Transition	199	0.4770	1.2403	0.0949	0.0870	0.491	5331	tags=39%, list=15%, signal=46%
Hallmark_mTORC1 Signaling	196	0.5043	1.2355	0	0.0859	0.491	4560	tags=36%, list=13%, signal=41%
Hallmark_Wnt/ β -catenin Signaling	42	0.4722	1.2160	0.1052	0.0923	0.491	3441	tags=24%, list=10%, signal=26%
Hallmark_Interferon Alpha Response	96	0.9028	1.2136	0	0.0968	0.491	2247	tags=77%, list=6%, signal=82%
Hallmark_Bile Acid Metabolism	112	0.3978	1.1853	0	0.1094	0.706	7329	tags=41%, list=20%, signal=51%
Hallmark_UV Response DN	143	0.3665	1.0733	0.2343	0.2503	0.909	4991	tags=27%, list=14%, signal=32%
Hallmark_Androgen Response	98	0.3276	0.9741	0.4019	0.5519	1	5096	tags=30%, list=14%, signal=34%
Hallmark_Peroxisome	104	0.3124	0.9687	0.3866	0.5575	1	6884	tags=35%, list=19%, signal=43%
Hallmark_Pancreas Beta Cells	40	0.3794	0.9657	0.3855	0.5519	1	7406	tags=33%, list=21%, signal=41%

Supplemental Table VII: Gene expression profile of differentially expressed cathepsins from BAF60a knockdown or overexpressing HASMCs

Supplemental Table VIIa: Gene expression profile of differentially expressed cathepsins from BAF60a knockdown HASMCs

gene_ensembl_id	gene_name	baseMean	TPM_siControl_1	TPM_siControl_2	TPM_siControl_3	TPM_siBAF60a_1	TPM_siBAF60a_2	TPM_siBAF60a_3	log2FoldChange	lfcSE	stat	p value	p adj
ENSG00000256043	CTSO	2802.61	28.981	30.6715	26.8006	3.87282	4.37445	4.49655	-2.8012	0.08597	-32.585	6.72E-233	5.1E-229
ENSG00000163131	CTSS	1359.87	178.545	184.721	155.547	74.7809	101.422	95.109	-1.0797	0.10796	-10.001	1.511E-23	2.5E-21
ENSG00000109861	CTSC	8504.95	241.658	261.658	251.688	161.788	158.171	161.071	-0.7508	0.05207	-14.419	3.936E-47	2.99E-44
ENSG00000135047	CTSL	5415.16	350.564	381.74	321.974	234.349	308.819	271.153	-0.4251	0.09976	-4.261	2.036E-05	0.000273

Differentially expressed genes are defined as >1.3-fold change in expression level, false discovery rate (FDR) <0.05 and adjusted p value <0.05.

Supplemental Table VIIb: Gene expression profile of differentially expressed cathepsins from BAF60a overexpressing HASMCs

gene_ensembl_id	gene_name	baseMean	TPM_AdGFP_1	TPM_AdGFP_2	TPM_AdGFP_3	TPM_AdBAF60a_1	TPM_AdBAF60a_2	TPM_AdBAF60a_3	log2FoldChange	lfcSE	stat	p value	p adj
ENSG00000163131	CTSS	86.4095	2.24835	2.58374	0.93908	5.63182	4.83678	4.49993	1.42994	0.36606	3.90629	9.373E-05	0.000514
ENSG00000143387	CTSK	2182.48	71.52	79.884	77.9657	101.218	96.5673	99.332	0.39991	0.06137	6.516	7.221E-11	9.02E-10
ENSG00000117984	CTSD	15882.9	349.85	350.883	352.36	434.033	466.691	446.442	0.38239	0.04907	7.79205	6.593E-15	1.15E-13
ENSG00000109861	CTSC	6103.42	299.753	302.66	324.214	223.055	229.416	232.399	-0.409	0.04472	-9.1454	5.942E-20	1.43E-18

Differentially expressed genes are defined as >1.3-fold change in expression level, false discovery rate (FDR) <0.05 and adjusted p value <0.05.

Supplemental Table VIII. Sequences of the primers used for real-time PCR

Name	Forward primer Sequence	Reverse primer Sequence
human <i>BAF60a</i>	TCAGTCCCGCAAGAGACCT	CCAGTTCACGAATCCTTTGAGG
mouse <i>Baf60a</i>	GGCGGTCCAAAATCGAAATC	ACCAGTTCCCGAATCCTTTG
human <i>CTSS</i>	GCAGTGGCACAGTTGCATAA	AGCACCACAAGAACCCATGT
mouse <i>Ctss</i>	CCATTGGGATCTCTGGAAGAAAA	TCATGCCCACTTGGTAGGTAT
mouse <i>Mmp2</i>	TGGGGGAGATTCTCACTTTG	CATCACTGCGACCAGTGTCT
mouse <i>Mmp9</i>	CGTCGTGATCCCCACTTACT	AACACACAGGGTTTGCCTTC
human <i>CCL2</i>	CAGCCAGATGCAATCAATGCC	TGGAATCCTGAACCCACTTCT
human <i>CCL5</i>	CTGCTTTGCCTACATTGCC	CTTGTTCAGCCGGGAGTCAT
human <i>CCL7</i>	AGAAGGACCACCAGTAGCCA	CCACTTCTGTGTGGGGTCAG
human <i>CCL8</i>	TCATGCTGAAGCTCACACCC	GTCCCTGAGGGCTGAAAGTG
human <i>IL6</i>	ACTCACCTCTTCAGAACGAATTG	CCATCTTTGGAAGGTTTCAGGTTG
human <i>IL1A</i>	TGGTAGTAGCAACCAACGGGA	ACTTTGATTGAGGGCGTCATTC
human <i>IL1B</i>	AGCTACGAATCTCCGACCAC	CGTTATCCCATGTGTCTGAAGAA
human <i>IL8</i>	TGGACCCCAAGGAAAACCTGG	TTTGCTTGAAGTTTCACTGGC
human <i>IL33</i>	AGAACACAGCAAGCAAAGCC	GGGCAAACCTCTTTGGCCTTC
human <i>CXCL3</i>	CGCCCAAACCGAAGTCATAG	GCTCCCCTTGTTTCAGTATCTTTT
human <i>CXCL5</i>	AGCTGCGTTGCGTTTGTTTAC	TGGCGAACACTTGCAGATTAC
human <i>CXCL11</i>	GACGCTGTCTTTGCATAGGC	GGATTTAGGCATCGTTGTCCTTT
human <i>VCAM1</i>	CGAACCCAAACAAAGGCAGA	ACAGGATTTTCGGAGCAGGA
human <i>HMOX1</i>	CGTTCCTGCTCAACATCCAG	TGAGTGTAAGGACCCATCGG
human <i>IRF4</i>	AGCATAAGGTCTGCCGAAGC	CTCTGGGTAGGGGAACAGGA
human <i>TNF</i>	CCTCTCTCTAATCAGCCCTCTG	GAGGACCTGGGAGTAGATGAG
human <i>ACTB</i>	GTCATTCCAAATATGAGATGCGT	GCTATCACCTCCCCTGTGTG
mouse <i>Actb</i>	GGCTGTATTCCCCTCCATCG	CCAGTTGGTAACAATGCCATGT
human <i>CTSS</i> ChIP	CAAAGCACGACTCCGTCTCG	ATGAGGTTGAGGATCTTTTCACAC
mouse <i>Ccl2</i> ChIP	TCCAACCCACAGTTTCTCTC	GAATCCGCTGAGTAAGTGCA
mouse <i>Cxcl6</i> ChIP	TTCTTTCCACACTGCCCCCT	TGCATTTCATCCCCTCCCGACT
mouse <i>Il1b</i> ChIP	CAGGAATGGAGGGCTATCT	GCTTGAACCTCTGATAGCCAC
mouse <i>Ctss</i> ChIP	CTGGGAAATGGGAGCATAAATG	AGGTGAGGAACTCCTGTTTC

Major Resources Table

Animals (in vivo studies)

Species	Vendor or Source	Background Strain	Sex	Persistent ID / URL
C57BL/6J mice	Jackson Laboratory	C57BL/6	Male	000664 - C57BL/6J
BAF60a ^{ff} mice	Dr. Jiandie Lin at the University of Michigan	C57BL/6	Male and female	
SMMHC-CreER ^{T2} mice	Jackson Laboratory	C57BL/6	Male	019079 - B6.FVB-Tg(Myh11-cre/ERT2)1Soff/J
Smooth muscle cell specific BAF60a knockout (BAF60a ^{SMKO}) mice	Generated by crossbreeding BAF60a ^{ff} mice with SMMHC-CreER ^{T2} mice	C57BL/6	Male	

Antibodies

Target antigen	Vendor or Source	Catalog #	Working concentration	Lot # (preferred but not required)	Persistent ID / URL
BAF60a	BD Biosciences	611728	0.25µg/mL for Western blot	7271976	BAF60a-BD Biosciences-611728
BAF60a	Abcam	ab245222	0.497 µg/mL for Western blot 4.97 µg/mL for immunostaining	GR3314163-2	smarcd1-abcam-ab245222
BRG1	Abcam	ab110641	0.2 µg/mL for Western blot 4 µg/mL for Chromatin IP	GR3208604-17	BRG1-abcam-ab110641
Cathepsin S	Abcam	ab92780	1 µg/mL for Western blot	GR78357-1	cathepsin S-abcam-ab92780
SM22α	Abcam	ab10135	2.5 µg/mL for immunostaining	GR224121-4	TAGLN-abcam-ab10135
Mac2	eBioscience	14-5301-82	3.3 µg/mL for immunostaining		Galectin-3-eBioscience-14-5301-82
MMP2	ABclonal	A11144	8.9 µg/mL for immunostaining	0207280101	MMP2-ABclonal-A11144
MMP9	ABclonal	A2095	8 µg/mL for immunostaining	11151690301	MMP9-ABclonal-A2095

BAF155	Cell Signaling Technology	11956	0.4 µg/mL for Western blot	2	BAF155-CST-11956
BAF170	Cell Signaling Technology	12760	0.4 µg/mL for Western blot	1	BAF170-CST-12760
BAF47	Cell Signaling Technology	91735	0.4 µg/mL for Western blot	1	BAF47-CST-91735
p65	Cell Signaling Technology	8242	0.2 µg/mL for Western blot; 2 µg/mL for immunostaining 4 µg/mL for Chromatin IP	9	nf-kb-p65-CST-8242
p-p65	Cell Signaling Technology	3033	0.2 µg/mL for Western blot	16	phospho-nf-kb-p65-ser536-CST-3033
p-IKKα/β	Cell Signaling Technology	2697	0.4 µg/mL for Western blot	19	phospho-ikkb-ser176-180-CST-2697
p300	Cell Signaling Technology	54062	0.4 µg/mL for Western blot 4 µg/mL for co-IP		p300-d2x6n-CST-54062
p300	Cell Signaling Technology	70088	0.4 µg/mL for Western blot 4 µg/mL for co-IP	1	p300-d1m7c-CST-70088
lamin A/C	Cell Signaling Technology	2032	0.4 µg/mL for Western blot	4	lamin-a-c-CST-2032
β-actin	Cell Signaling Technology	3700	0.01 µg/mL for Western blot	17	b-actin-CST-3700
GAPDH	Santa Cruz Biotechnology	sc-365062	0.1 µg/mL for Western blot	G2618	scbt-GAPDH-G-9
Alexa Fluor® 680 AffiniPure Goat Anti-Mouse IgG, light chain specific antibody	Jackson ImmunoResearch	115-625-174	0.075 µg/mL for Western blot	138707	jacksonimmuno-115-625-174
Alexa Fluor® 488 Streptavidin Conjugate antibody	Jackson ImmunoResearch	016-540-084	1 µg/mL for immunostaining	138322	jacksonimmuno-016-540-084
Alexa Fluor® 488-AffiniPure Donkey Anti-Mouse IgG (H+L)	Jackson ImmunoResearch	715-545-151	1 µg/mL for immunostaining	125268	jacksonimmuno-715-545-151

Alexa Fluor® 647 AffiniPure Donkey Anti-Rat IgG (H+L)	Jackson ImmunoResearch	712-605-153	1 µg/mL for immunostaining	123725	jacksonimmuno-712-605-153
Alexa Fluor® 488-AffiniPure Donkey Anti-Rabbit IgG (H+L)	Jackson ImmunoResearch	711-545-152	1 µg/mL for immunostaining	139168	jacksonimmuno-711-545-152
CD16/CD32	eBioscience	14-0161-85	0.5 µg/test for flow cytometry		CD16-CD32-14-0161-85
Rat IgG2b kappa Isotype Control, PE	eBioscience	12-4031-82	0.2 µg/test for flow cytometry		Rat-IgG2b-kappa-PE-12-4031-82
Rat IgG2b kappa Isotype Control, eFluor 450	eBioscience	48-4031-82	0.2 µg/test for flow cytometry		Rat-IgG2b-kappa-eFluor 450-48-4031-82
Rat IgG2b kappa Isotype Control, APC	eBioscience	17-4321-81	0.2 µg/test for flow cytometry		Rat-IgG2b-kappa-APC-17-4321-81
CD45, eFluor 450	eBioscience	48-0451-82	0.2 µg/test for flow cytometry		CD45-eFluor 450-48-0451-82
F4/80, APC	eBioscience	17-4801-82	0.2 µg/test for flow cytometry		F4-80-APC-17-4801-82
CD11b, PE	Tonbo Biosciences	50-0112	0.2 µg/test for flow cytometry		CD11b-PE-50-0112

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Cultured Cells

Name	Vendor or Source	Sex (F, M, or unknown)	Persistent ID / URL
Human aortic smooth muscle cells	Lonza	M	AoSMC-Lonza-CC2571
A7r5 cells	ATCC	unknown	A7r5-atcc-CRL-1444
RAW 264.7	ATCC	unknown	RAW264.7-atcc-TIB-71
EcoPack2-293 cells	Takara	unknown	EcoPack2-293 cells