SUPPLEMENTAL MATERIAL

This file includes:

Supplemental Figures and Figure Legends

Supplemental Figures

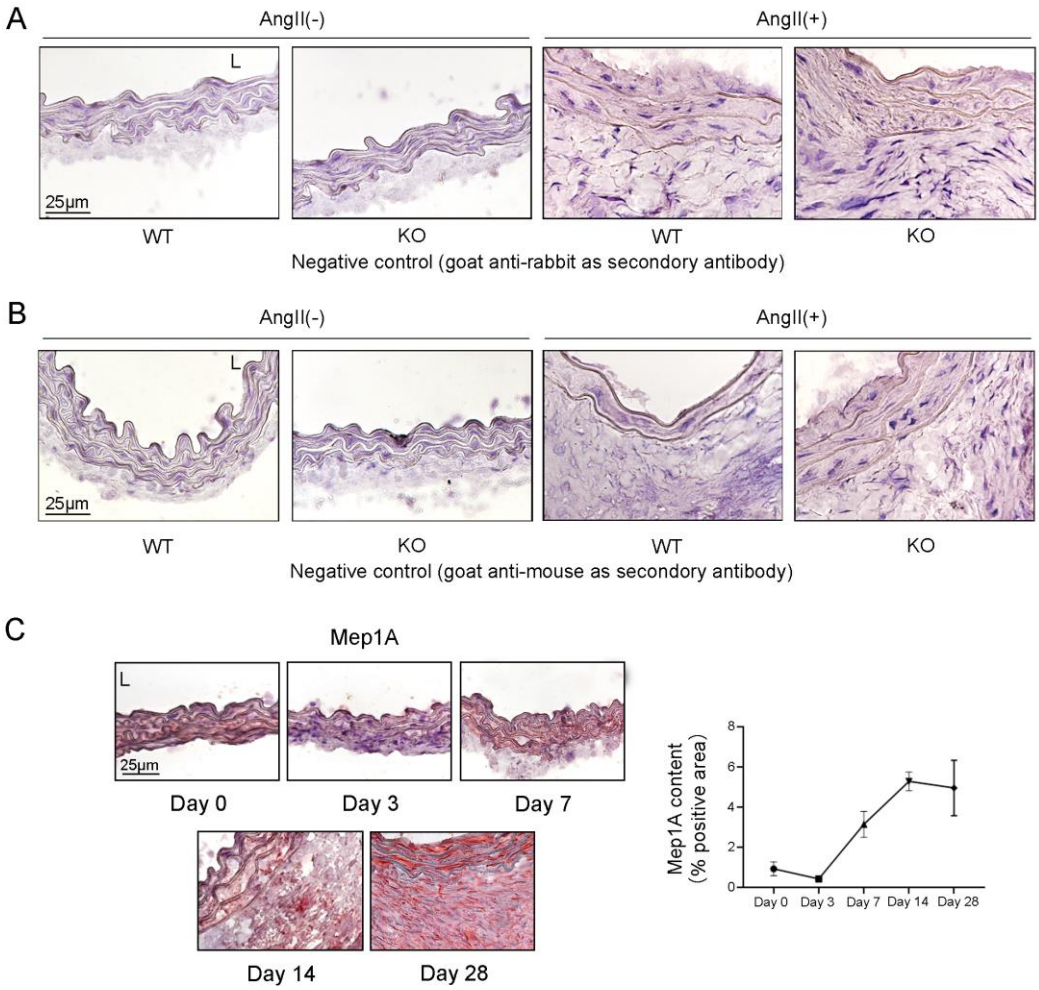

Figure S1. Immunohistochemical staining.

(A) Representative images of immunohistochemical analysis for negative control (only with goat anti-rabbit antibody as secondary antibody) of Mep1A, Mac-3, CD4, Collagen I and TNF-α in indicated mice with or without AngII infusion. (B) Representative images of immunohistochemical analysis for negative control (only with goat anti-mouse antibody as secondary antibody) of MMP2, Tryptase and major histocompatibility complex (MHC)-II in indicated mice with or without AngII infusion. (C) Representative images of immunohistochemical analysis for Mep1A in the arterial wall of the mice at different time points after AngII infusion. The graph shows the percentages of positive areas in the Mep1A immunohistochemistry staining.

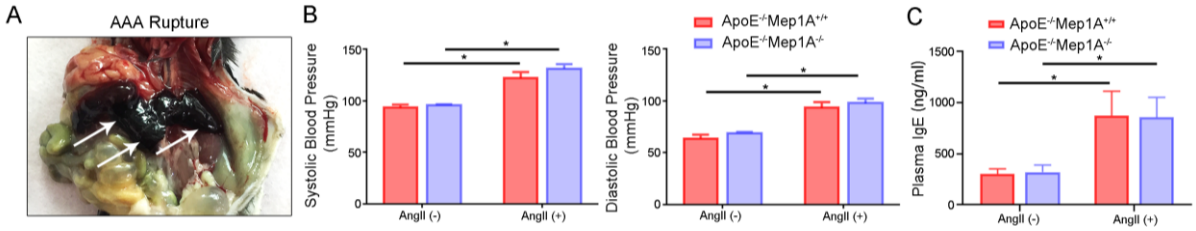

Figure S2. Phenotypic changes in animals.

(A) The picture of AAA rupture in mice. (B) Average blood pressures including systolic blood pressure and diastolic blood pressure in indicated mice with or without AngII infusion. (C) ELISA analysis of plasma IgE levels in normal and AAA mice of the indicated groups. Data represent the mean ± standard error of mean (SEM). ApoE$^{-/-}$Mep1A$^{+/+}$ mice treated with PBS (n=5), ApoE$^{-/-}$Mep1A$^{-/-}$ mice treated with PBS (n=6), ApoE$^{-/-}$Mep1A$^{+/+}$ mice treated with AngII (n=14) and ApoE$^{-/-}$Mep1A$^{-/-}$ mice treated with AngII (n=11). Two-way ANOVA was conducted to examine the statistical significance for all data. *P value <0.05 were considered statistically significant.

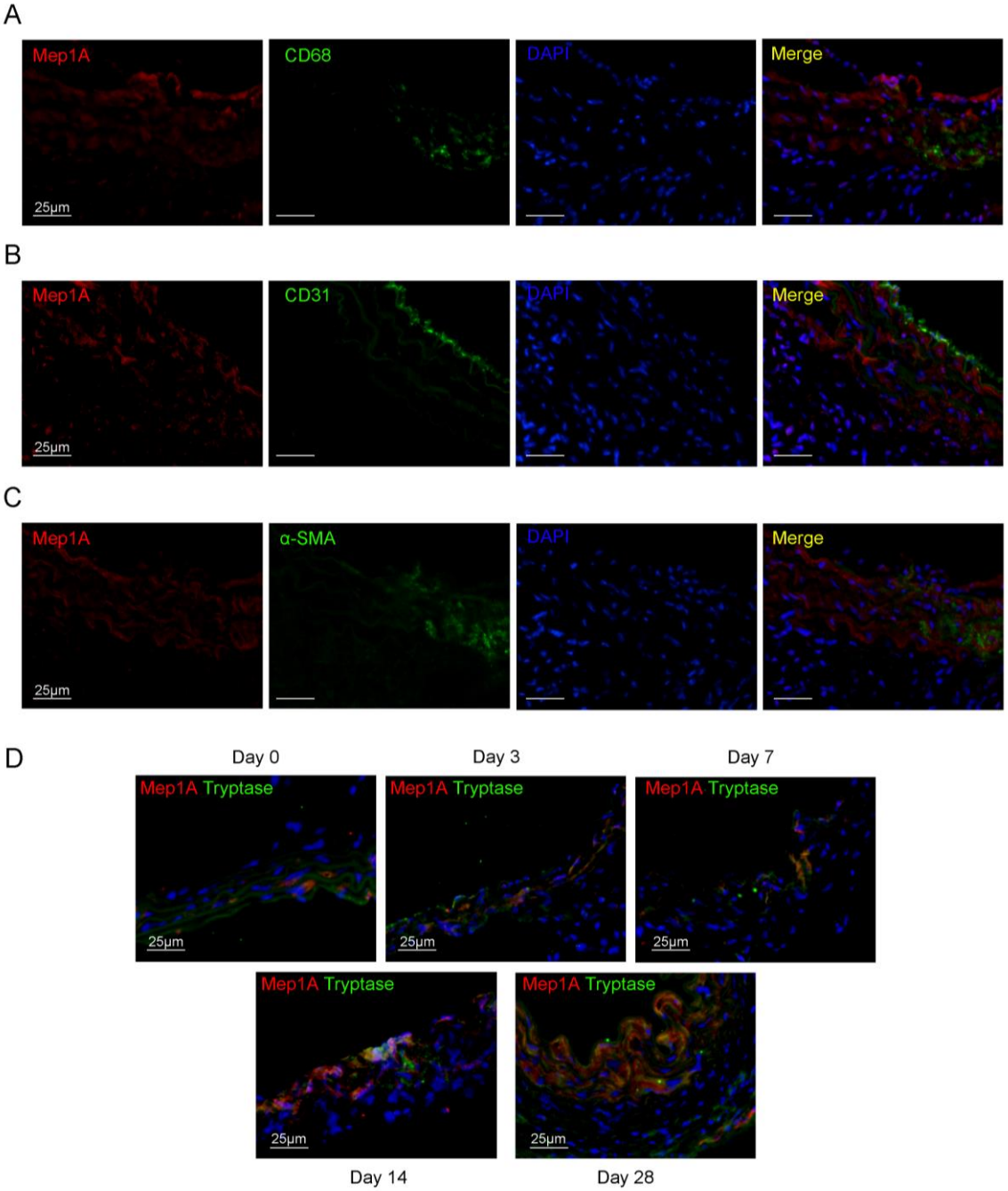

Figure S3. Immunofluorescence staining of Mep1A and different cell markers.

(A) Immunofluorescence staining of Mep1A and CD68 (macrophage marker). Mep1A: red, CD68: green, DAPI: blue. (B) Immunofluorescence staining of Mep1A and CD31 (endothelial cell marker). Mep1A: red, CD31: green, DAPI: blue. (C) Immunofluorescence staining of Mep1A and α-SMA (smooth muscle cells marker). Mep1A: red, α-SMA: green, DAPI: blue. (D) Immunofluorescence staining of Mep1A and Tryptase (mast cell marker) with different time points. Mep1A: red, Tryptase: green, DAPI: blue.

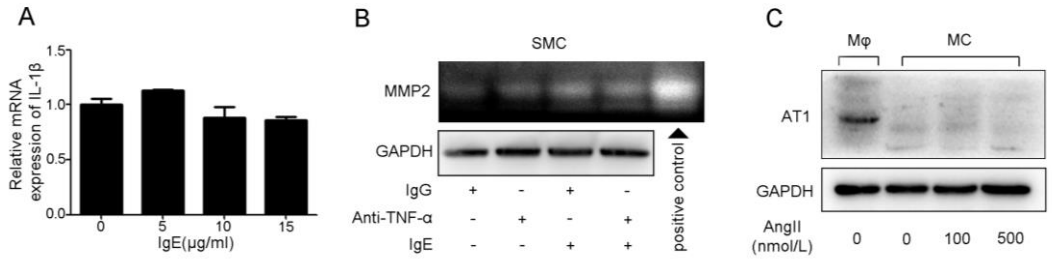

Figure S4. Cellular mechanism.

(A) RT-PCR analysis of IL-1β expression in MCs treated with IgE in different doses as indicated. (B) Gelatin zymography to detect MMP2 activity in SMCs treated with the indicated supernatant. (positive control: Recombinant protein MMP2) (C) Immunoblot to detect the expression of angiotensin II type 1 receptor (AT1) in macrophages (Mφ) and MCs after treated with AngII in the indicated doses. Data represent mean ± SEM of five independent experiments. One-way ANOVA was conducted to examine the statistical significance for A. **P* value <0.05 was considered statistically significant.

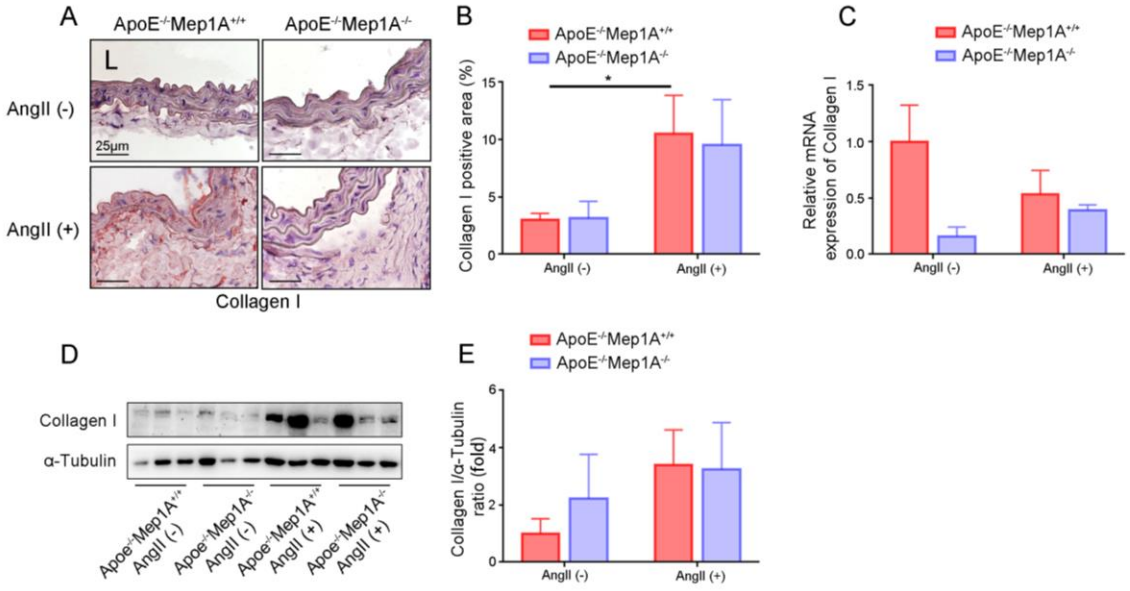

Figure S5. Expression of Collagen I in aorta.

(A) Representative images of immunohistochemical analysis for Collagen I in the arterial wall of the mice. (B) Percentages of positive Collagen I staining in different groups respectively. (C) RT-PCR analysis of Collagen I in indicated mice. (D) Representative image of immunoblot to detect the expression of Collagen I in mice arterial wall. (E) Quantification of Collagen I expression by immunoblot. Data represent mean ± SEM. ApoE$^{-/-}$Mep1A$^{+/+}$ mice treated with PBS (n=5), ApoE$^{-/-}$Mep1A$^{-/-}$ mice treated with PBS (n=6), ApoE$^{-/-}$Mep1A$^{+/+}$ mice treated with AngII (n=5) and ApoE$^{-/-}$Mep1A$^{-/-}$ mice treated with AngII (n=6). Two-way ANOVA was conducted to examine the statistical significance for all data from experimental AAAs. *P value <0.05 was considered statistically significant. L: lumen.

Supplemental Tables

Table S1. Clinical information of samples

	Control (n=7)	AAA patients (n=6)	p
Sex: Male[C]	85.71% (6/7)	100% (6/6)	0.335
Age(yrs)[T]			
Mean	68.86± 20.69	49.00± 19.28	0.117
Median	82	55	
Range	42-92	15-65	
Hypertension[C]	14.29% (1/7)	33.33% (2/6)	0.416
Diabetes[C]	14.29% (1/7)	0% (0/6)	0.335
Smoking[C]	0% (0/7)	33.33% (2/6)	0.097
Alcohol[C]	14.29% (1/7)	16.67% (1/6)	0.906

C Chi-Square Tests; T t-test *p<0.05

Table S2. RT-PCR Primers

Primer name	Primer sequence (5'-3')
hMep1A Forward	TGACAGCACAGGCAATGTTCGC
hMep1A Reverse	GTCGCCTTTTGTGCCCTGGAAA
hMep1B Forward	ATGCTGACTGGCAACGGGTTTC
hMep1B Reverse	CAGCGTTCTACTTTCCAGCACTG
mMep1A Forward	CTGATACCAGGAACAGGATGTCC
mMep1A Reverse	CATAGACTCCCACCTTGGATGG
mMep1B Forward	GGTTTCACAGGTTCTCAGTGGC
mMep1B Reverse	CAGTCTGCTCTCCAACATCGCC
rMep1A Forward	TTCCAGCAGAAGCGTGATAC
rMep1A Reverse	TACGTTCACACAGGTGCCTT
mTNF-α Forward	GGTGCCTATGTCTCAGCCTCTT
mTNF-α Reverse	GCCATAGAACTGATGAGAGGGAG
rTNF-α Forward	ACTGAACTTCGGGGTGATCG
rTNF-α Reverse	GCTTGGTGGTTTGCTACGAC
mMMP2 Forward	CAAGGATGGACTCCTGGCACAT
mMMP2 Reverse	TACTCGCCATCAGCGTTCCCAT
mCollagen I Forward	CCTCAGGGTATTGCTGGACAAC
mCollagen I Reverse	CAGAAGGACCTTGTTTGCCAGG
rIL-1β Forward	TGGACCTTCCAGGATGAGGACA
rIL-1β Reverse	GTTCATCTCGGAGCCTGTAGTG
mGAPDH Forward	CATCACTGCCACCCAGAAGACTG
mGAPDH Reverse	ATGCCAGTGAGCTTCCCGTTCAG
hGAPDH Forward	GTCTCCTCTGACTTCAACAGCG
hGAPDH Reverse	ACCACCCTGTTGCTGTAGCCAA