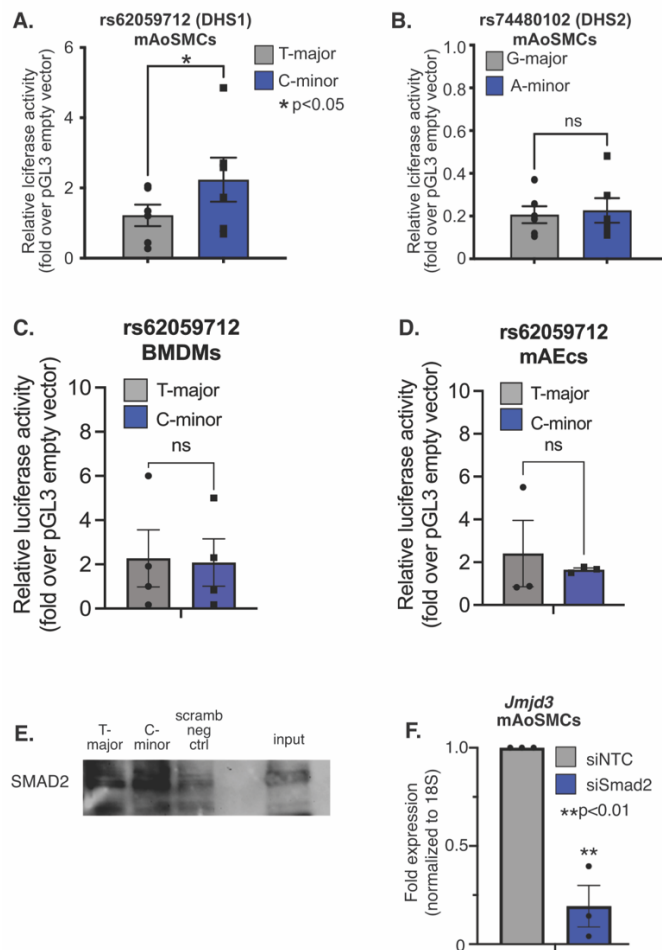


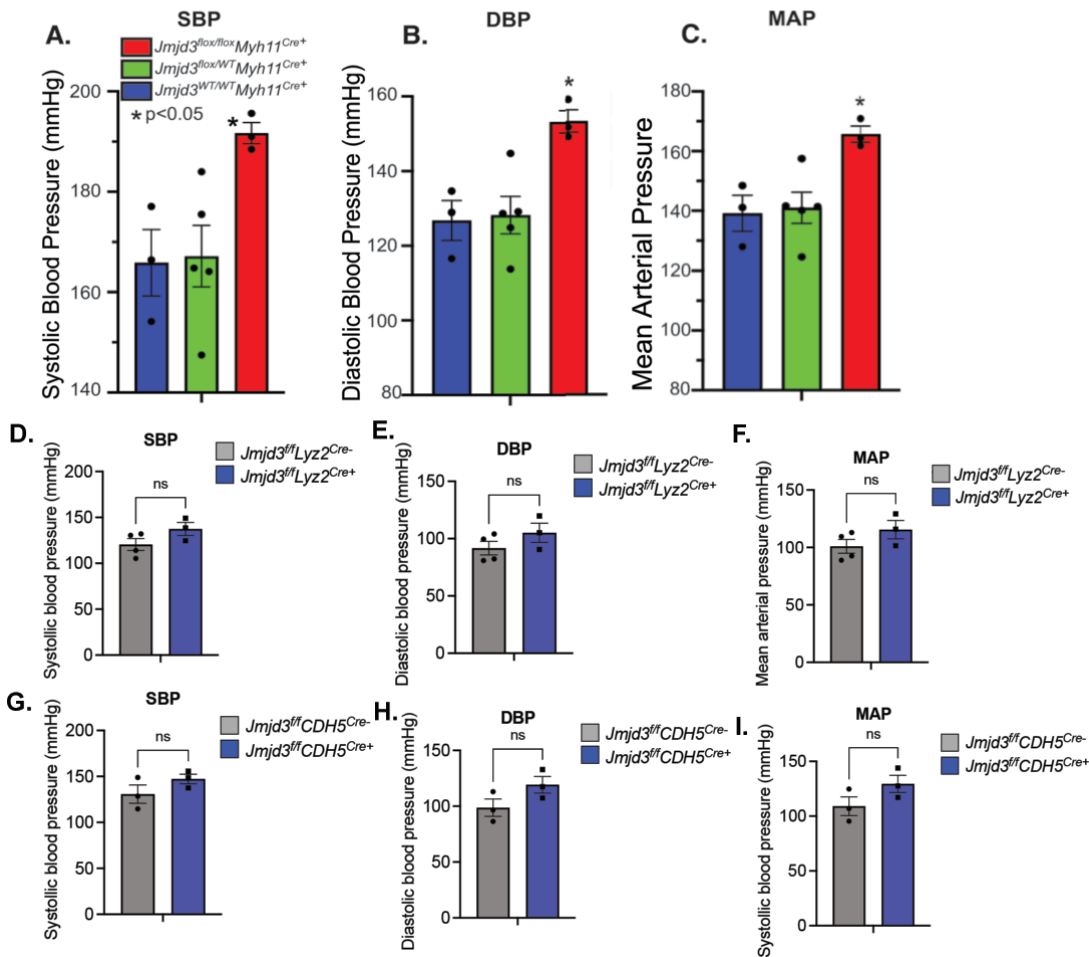
Supplemental Figures with Legends

Supplemental Figure 1



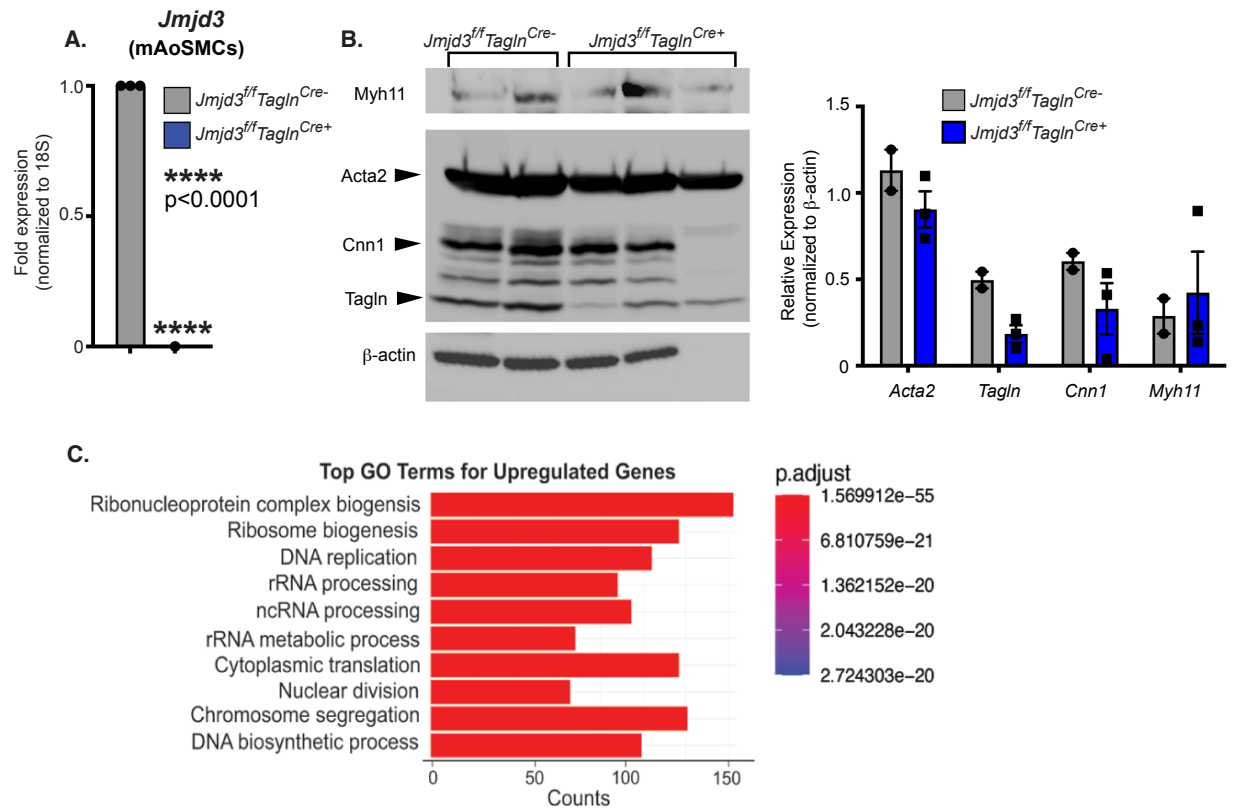
Supplemental Figure 1. A) Luciferase results of the DHS1 containing rs62059712 (T-major vs. C-minor) and B) DHS2 containing rs74480102 (G-major vs. A-minor) in cultured primary mAoSMCs. C) Luciferase results of rs62059712 T-major and C-major promoter constructs in BMDMs and (D) in mouse aortic endothelial cells (mAECs). E) Western blot of Smad2 after affinity purification using T vs. C probes corresponding to rs62059712 SNP region incubated with human aortic SMC nuclear lysate and then resolved by western blotting. F) qPCR for *Jmjd3* expression after NTC vs. Smad2 knockdown in mAoSMCs. Data are presented as the mean $\pm$ SEM, n=3 independent experiments. Experiments representative of SMCs from 4-6 mice per group. Two-tailed Student's t-test was used. *p<0.05, **p<0.01.

Supplemental Figure 2



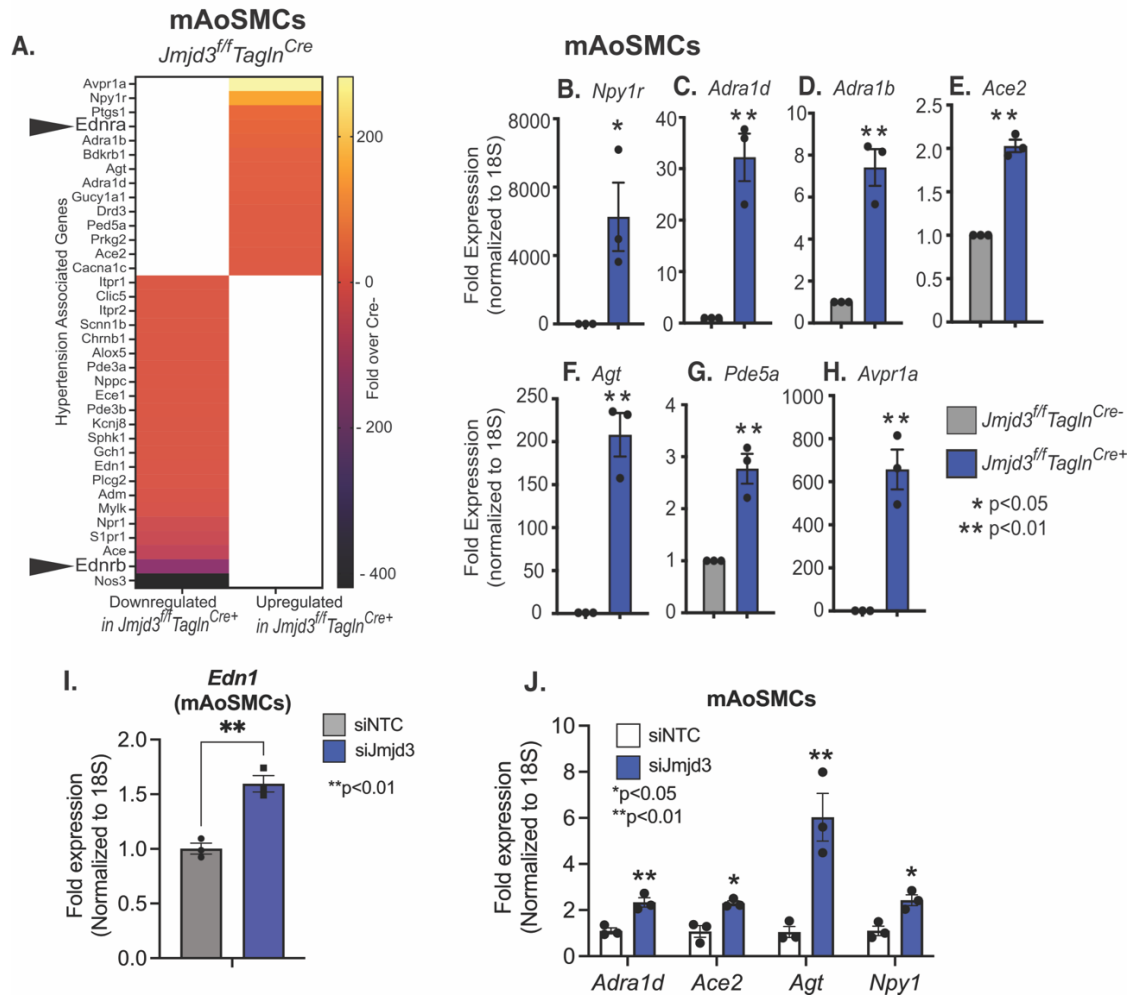
Supplemental Figure 2. A) Averages of systolic blood pressure (SBP), B) diastolic blood pressure (DBP), and C) mean arterial pressure (MAP) over 14 days in *Jmjd3^{fllox/flox}Myh11^{CreERT}* mice homozygous, heterozygous, or absent (WT) for the floxed allele injected with tamoxifen (75 mg/kg) and infused with Angiotensin II (1ug/kg/min). D) SBP, E) DBP, and F) MAP obtained by tail cuff were averaged in *Jmjd3^{fllox/flox}Lyz2^{Cre}* mice. G) SBP, H) DBP, and I) MAP were averaged in *Jmjd3^{fllox/flox}CDH5^{Cre}* mice. Data are presented as the mean $\pm$ SEM. Results are averaged from 3-6 mice per group. Two-tailed Student's t-test was used to compare blood pressures from WT vs. *Jmjd3^{fllox/flox}Myh11^{CreERT}* mice; *Jmjd3^{fllox/flox}Lyz2^{Cre}*; and *Jmjd3^{fllox/flox}CDH5^{CreERT}* mice, *p<0.05.

Supplemental Figure 3



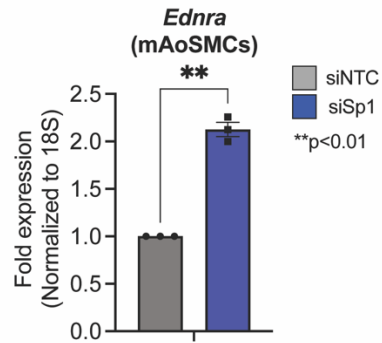
Supplemental Figure 3. A) qPCR of *Jmjd3* expression in SMCs isolated from *Jmjd3*^{flox/flox} *Tagln*^{Cre} mice. B) Western blot of aortas isolated from *Jmjd3*^{flox/flox} *Tagln*^{Cre} mice probed for SMC markers with accompanying densitometry results to right. C) Bar graph of gene ontology (GO) analysis for top 10 upregulated genes in *Jmjd3*^{flox/flox} *Tagln*^{Cre+} SMCs from RNA-seq results. Gene pathways listed on y-axis and number of gene counts for each pathway are listed on x-axis. Data are presented as the mean ± SEM, n=3 independent experiments, n=4-6 mice per group. Two-tailed Student's t-test, ****p<0.0001.

Supplemental Figure 4



Supplemental Figure 4. A) Superarray heatmap comparing differentially expressed hypertension-associated genes in mAoSMCs from *Jmjd3^{fl/fl}Tagln^{Cre+}* mice compared to *Jmjd3^{fl/fl}Tagln^{Cre-}* mice. Data presented as fold over gene expression values in *Jmjd3^{fl/fl}Tagln^{Cre-}* SMCs. *Ednra* and *Ednrb* designated with arrowheads. B) Validation qPCR for several of hypertension genes in A) including *Npy1r* (B), *Adra1d* (C), *Adra1b* (D), *Ace2* (E), *Agt* (F), *Pde5a* (G), and *Avpr1a* (H). I) qPCR for endothelin-1 (*Edn1*) in mAoSMCs treated with siRNA to *Jmjd3* or siNTC and then serum starved for 16 hours. J) qPCR for *Adra1*, *Ace2*, *Agt*, and *Npy1* in mAoSMCs treated with siRNA to *Jmjd3* or siNTC. Data are presented as the mean $\pm$ SEM, n=3 independent experiments. Results represent data from SMCs from 4-6 mice per group. Two-tailed Student's t-test, *p<0.05, **p<0.01.

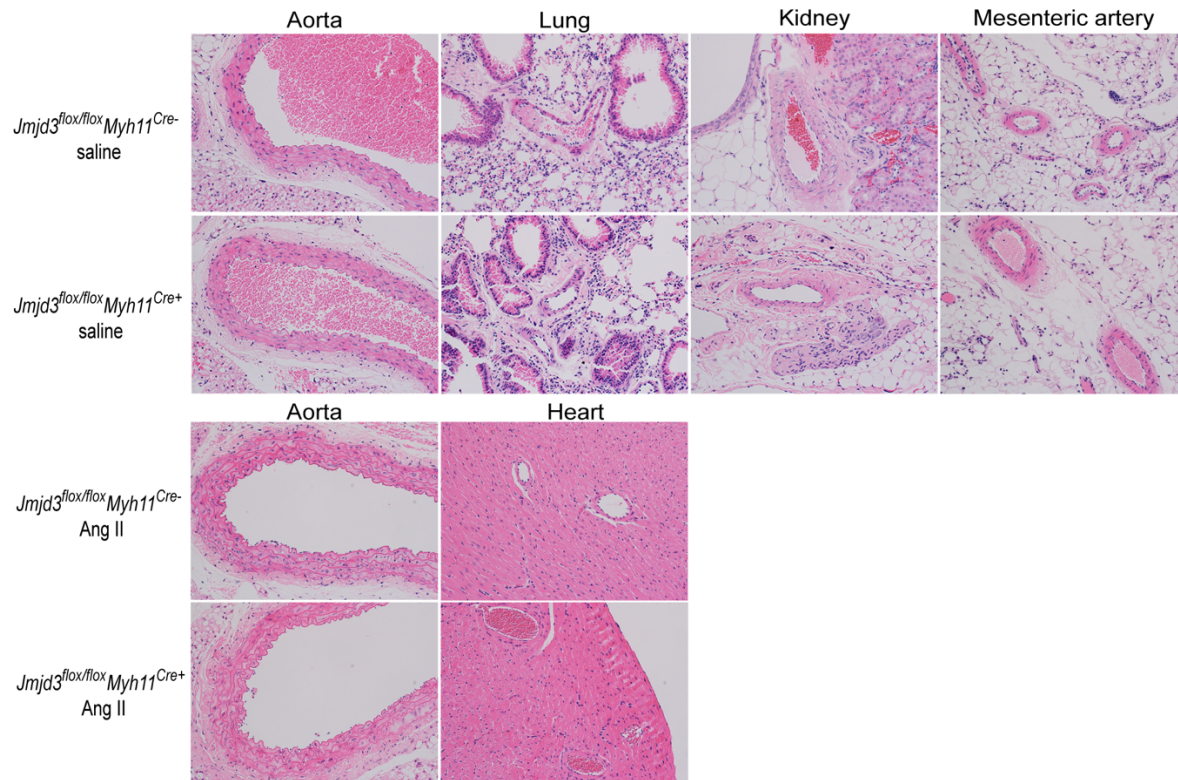
Supplemental Figure 5



Supplemental Figure 5. qPCR for *Ednra* expression after NTC vs. Sp1 knockdown in mAoSMCs.

Data are presented as the mean $\pm$ SEM, n=3 independent experiments. Data were first analyzed for normal distribution, and if data passed the normality test, a two-tailed Student's *t* test was used, **p<0.01.

Supplemental Figure 6



Supplemental Figure 6. H&E stained sections from multiple vascular containing tissues including aorta, lung, kidney, and mesenteric artery isolated from *Jmjd3^{flox/flox}Myh11^{CreERT}* under basal (saline-treated) conditions. Aorta and heart from *Jmjd3^{flox/flox}Myh11^{CreERT}* mice treated with Ang II are also depicted.