

Supplemental Figure 1. Renin lineage cells contribute to arteriolar hypertrophy in a polyclonal way. Kidney tissues from  $Ren1^{\circ}KO;Ren1^{\circ}-Cre;Confetti$  and control mice. Masson's Trichrome staining, immunohistochemistry for  $\alpha$ -SMA showed the progression of the renal disease with aging. Frozen sections showed that the policlonality was maintained during the disease progression. Scale bars, 50 µm.  $\alpha$ -SMA; alpha-smooth muscle actin,  $Ren1^{\circ}KO; Ren1^{\circ}$  gene knockout.



**Supplemental Figure 2. Transcriptome of** *Renin<sup>null</sup>* **cells with the Fluidigm C1 system.** (**A**) The UMAP with all the cells after normalization. (**B**) Feature plots and ridge plots for *Ren1*, *Akr1b7*, and *YFP*. (**C**) ISH for *Ren1* and *Akr1b7* mRNA. *Akr1b7* positive cells were increased in kidneys from *Ren1<sup>c</sup>KO* mice. Scale bars, 50 µm. (**D**) Ridge plots of smooth muscle genes (*Acta2*, *Mhy11*, *TagIn*, and *Cnn1*). ISH; *in situ* hybridization, *Ren1<sup>c</sup>KO*; *Ren1<sup>c</sup>* gene knockout, UMAP; Uniform Manifold Approximation and Projection, WT; wild-type.



Supplemental Figure 3. Vascular abnormality in *Ren1<sup>c</sup>KO* mice at different time points. PAS staining and immunohistochemistry for  $\alpha$ -SMA in *Ren1<sup>c</sup>KO* mouse kidneys and their controls at P1, P5, P14, P30, and 2 months of age. The afferent arteriolar hypertrophy was significantly detected in *Ren1<sup>c</sup>KO* mice starting at P14. Scale bars, 50 µm.  $\alpha$ -SMA;  $\alpha$ -smooth muscle actin, *Ren1<sup>c</sup>KO*; *Ren1<sup>c</sup>* gene knockout, WT; wild-type.



**Supplemental Figure 4. Labeling** *Renin<sup>null</sup>* **cells and other vascular SMCs.** (**A**) Kidney sections from  $Ren1^{c+/-};Myh11-CreER^{T2};tdTomato;Ren1^{c}-YFP$  mouse and  $Ren1^{c-}$  /-; $Myh11-CreER^{T2};tdTomato;Ren1^{c}-YFP$  mouse. Vascular SMCs were labeled with tdTomato, and WT renin cells and  $Renin^{null}$  cells were labeled with YFP. The merged pictures also show nuclear staining by Hoechst and differential interference contrast microscopy. Scale bars, 50 µm. (**B**) FACS results of  $Ren1^{c-/-};Myh11-CreER^{T2};tdTomato;Ren1^{c}-YFP$  mouse kidney. Of the isolated cells, 19% were the  $Renin^{null}$  cells (16.0% and 3.0% were tdTomato<sup>+</sup>;YFP<sup>+</sup> and were tdTomato<sup>-</sup>;YFP<sup>+</sup>, respectively), and 81.0% were other tdTomato<sup>+</sup>;YFP<sup>-</sup> vascular SMCs. FACS; fluorescence-activated cell sorting,  $Ren1^{c}KO$ ;  $Ren1^{c}$  gene knockout, SMCs; smooth muscle cells.



Supplemental Figure 5. scRNA-seq of cAMP pathway and mechanotransduction related genes. (A) Heatmap of the cAMP pathway genes from scRNA-seq of WT renin cells and *Renin<sup>null</sup>* cells (C1 system). (B) Violin plots of the major cAMP pathway-related genes by C1 scRNAseq. (C, D) Heatmap of the cAMP pathway genes from scRNA-seq of *Ren1<sup>c</sup>KO;SMMHC-CreER<sup>T2</sup>;tdTomato;Ren1<sup>c</sup>-YFP* mice (Chromium System). (E) Feature plots of UMAP for *Akr1b7*, *Itgb1*, and *Lmna* in scRNA-seq of Chromium System. *Ren1<sup>c</sup>KO*; *Ren1<sup>c</sup>* gene knockout, scRNA-seq; single-cell-RNA sequencing, UMAP; Uniform Manifold Approximation and Projection, WT; wild-type.



**Supplemental Figure 6. The phenotype of the** *Ren1<sup>c</sup>KO;Itgb1cKO* mouse. (A, B) Body sizes were not different between *Ren1<sup>c</sup>KO* control and *Ren1<sup>c</sup>KO;Itgb1cKO* mice. There was no significant difference in body weight (A; male  $n \ge 6$ , female  $n \ge 5$ ) and kidney/body weight rate (B;  $n \ge 11$ ) (Student's t-test). (C, D) Blood tests did not differ in *Ren1<sup>c</sup>KO* control and *Ren1<sup>c</sup>KO;Itgb1cKO* mice. There was no significant difference in BUN (C;  $n \ge 11$ ) and hematocrit (D;  $n \ge 9$ ) (Student's t-test). All data are reported as means  $\pm$  standard deviation. Black triangles show male samples, and purple dots show female samples. BUN; blood urea nitrogen, *Itgb1cKO*; deletion of the *Itgb1* gene in cells of the renin lineage, *Ren1<sup>c</sup>KO*; *Ren1<sup>c</sup>* gene knockout.



Supplemental Figure 7. Phenotypes of the BPN/3 and BPH/2 mice with and without long-term inhibition of RAS. (A) Body sizes were not different between with and without long-term usage of captopril in both BPN/3 and BPH/2 mice ( $n \ge 5$ , two-way ANOVA followed by Tukey's multiple comparison test). (B) Kidney/body weight rates were decreased by long-term usage of captopril in BPN/3 mice, but not in BPH/2 mice ( $n \ge 6$ , two-way ANOVA followed by Tukey's multiple comparison test). All data are reported as means ± standard deviation. Black triangles show male samples, and purple dots show female samples. \*P < 0.05, \*\*P < 0.01.



**Supplemental Figure 8. The background of the human samples.** (**A**) The creatinine clearance of patients with long-term usage of RASi (n=6) was not significantly different from patients with nephrosclerosis without RASi (n=6) (One-way ANOVA followed by Tukey's multiple comparisons test). (**B**) The urinary protein of patients with long-term usage of RASi (n=6) was not significantly different from patients with nephrosclerosis without RASi (n=6) (One-way ANOVA followed by Tukey's multiple comparisons test). (**B**) The urinary protein of patients with nephrosclerosis without RASi (n=6) (One-way ANOVA followed by Tukey's multiple comparisons test). (**C**) Blood pressure was not different between patients with long-term usage of RASi (n=6), healthy controls (n=4), and patients with nephrosclerosis without RASi (n=6) (One-way ANOVA followed by Tukey's multiple comparisons test). All data are reported as means ± standard deviation. Black triangles show male samples, and purple dots show female samples. \*P<0.05, \*\*P<0.01. RASi; renin-angiotensin system inhibitor.