

**Supplementary Figure S1. Identification of BK**  $\alpha$  knockout rats (A) PCR products of genomic DNA distinguish wild type, heterozygote and homozygous knockout rats. (B) The expressions of BK  $\alpha$  in blood vessels of WT and BK  $\alpha^{-/-}$  rats were detected by western blot analysis. *n*=4 per group.



Supplementary Figure S2. Representative gross morphology and statistical diagrams of body weight of WT and BK  $\alpha^{-/-}$  rats. (A) Representative gross morphology of WT and BK  $\alpha^{-/-}$  rats. (B) Representative statistical diagrams of body weight of WT and BK  $\alpha^{-/-}$  rats. Data are shown as the mean  $\pm$  SD. n=5 per group. \*\*\*\**P*<0.0001.



Supplementary Figure S3. Heart rate and blood pressure in BK  $\alpha^{-/-}$  and WT rats Representative statistical diagrams of (A) the heart rate, (B) diastolic blood pressure, (C) mean arterial pressure, (D) systolic blood pressure in BK  $\alpha^{-/-}$  and WT rats. Data are shown as the mean  $\pm$  SD. *n*=5 per group. \**P* < 0.05, \*\*\**P* < 0.001.



Supplementary Figure S4. The concentration of inflammatory factors in the plasma of BK  $\alpha^{-/-}$  and wild-type rats Representative statistical diagrams of (A) IL-6, (B) TNF- $\alpha$  in the plasma of BK  $\alpha^{-/-}$  and WT rats. Data are shown as the mean  $\pm$  SD. *n*=6 per group. \**P* < 0.05.



Supplementary Figure S5. Expression of BK  $\alpha$  after NC siRNA or BK  $\alpha$  siRNA transfection in HUASMCs Representative blots and statistical diagrams of the expression of BK  $\alpha$  determined by (A) qPCR and (B,C) western blot analysis after BK  $\alpha$  knockdown. Data are shown as the mean  $\pm$  SD. *n*=3 per group. \*\**P*<0.01, \*\*\**P*<0.001.



Supplementary Figure S6. Expression of CTRP7 after NC siRNA or CTRP7 siRNA transfection in HUASMCs Representative blots and statistical diagrams of the expression of CTRP7 determined by (A) qPCR and (B,C) western blot analysis in HUASMCs after CTRP7 knockdown. Data are shown as the mean  $\pm$  SD. n = 3 per group, \*\**P* < 0.01, \*\*\**P* < 0.001, \*\*\**P* < 0.001.



Supplementary Figure S7. The mRNA expression of MMP2 and MMP9 in HUASMCs after CTRP7 knockdown Representative statistical diagrams of the mRNA expression of (A) *MMP9* and (B) *MMP2* determined by qPCR in HUASMCs after CTRP7 knockdown. Data are shown as the mean  $\pm$  SD. *n*=3 per group. \*\*\**P*<0.001, \*\*\*\**P* < 0.0001.

Rat_	Fold change	Human_	Fold change	P value	Q value
gene name	(rat)	gene name	(human)	(human)	(rat)
PLCE1	-1.586821795	PLCE1	-1.14	0.0197	0.022356975
KCAMA1	-3.52035339	KCAMA1	-1.9	0.00404	0.000000000
HSPB7	2.302307596	HSPB7	-3.03	0.00192	0.004153660
POSTN	2.084065827	POSTN	-1.3	0.0168	0.006251043
CTRP7	-1.511678631	CTRP7	-1.25	0.00237	0.006730873
STK38L	2.220607698	STK38L	-1.85	0.00024	0.000031700
KBTBD8	2.132939253	KBTBD8	0.555	0.00723	0.042030716
TGFBI	-1.750901486	TGFBI	0.94	0.0154	0.047071719
MYOZ2	3.903020707	MYOZ2	-0.619	0.0133	0.037833822
FZD1	-1.518835336	FZD1	-1.64	0.00487	0.000022300

Supplementary Table S1. The overlapped target genes of differentially expressed genes from the transcriptome (fold change>1.5) and the dataset GSE 7084