

Supplemental Figure 1. Genome-wide linkage scan, using 120 single nucleotide polymorphism (SNP) markers, for blood pressure in 92 male $sGC\alpha_1^{-/-F2}$ ($sGC\alpha_1^{-/-S6} X sGC\alpha_1^{-/-B6}$) progeny. Separate plots were generated for chromosome (chr) 1 through 19 with the SNP markers used to genotype the mice plotted on the X-axis. The Y-axis represents the LOD scores. One locus (on chromosome 1) showed suggestive linkage to blood pressure.



Supplemental Figure 2. Genome-wide linkage scan, using 120 single nucleotide polymorphism (SNP) markers, for blood pressure in a separate cohort of 96 male sGC $\alpha_1^{-/-F2}$ (sGC $\alpha_1^{-/-S6}$ X sGC $\alpha_1^{-/-B6}$) progeny. Separate plots were generated for chromosome (chr) 1 through 19 with the SNP markers used to genotype the mice plotted on the X-axis. The Y-axis represents the LOD scores. One locus (on chromosome 1) showed suggestive linkage to blood pressure.



Supplemental Figure 3. Genome-wide linkage scan, using 120 single nucleotide polymorphism (SNP) markers, for blood pressure in 188 male sGC $\alpha_1^{-/-F2}$ (sGC $\alpha_1^{-/-F2}$ (sGC $\alpha_1^{-/-F2}$ x sGC $\alpha_1^{-/-F2}$) progeny (the combined linkage analysis of all 92 and 96 sGC $\alpha_1^{-/-F2}$ mice in supplemental figures 1 and 2, respectively). Separate plots were generated for chromosome (chr) 1 through 19 with the SNP markers used to genotype the mice plotted on the X-axis. The Y-axis represents the LOD scores. One locus (on chromosome 1) showed significant linkage to blood pressure. Two loci (on chromosomes 4 and 9) showed suggestive linkage to blood pressure (LODs of 3.6 and 3.9, respectively).

1	GGAGTCTG	10 GACAGCCTA	20 ACATGACTGA ACATGACTGA	30 .TGGCCACAG <i>I</i> .TGGCCACAG <i>I</i>	40 AATTATGGAGC	50 50 TGGGTCCTTG TGGGTCCTTG	60 GCCAGAAAAC GCCAGAAAAC	70 AGGCTGCCTT	80 TCATGGTCCC	90 ACAGGCCCT	+ 100 GGGGTAATAAA GGGGTAATAAA	110 ATCAAAGCAG	120 A <mark>G</mark> CCTGTGAT# ATCCTGTGAT#	130 ACATGGTGTGI ACATGGTGTGI	+ 140 ГАТААААGААG ГАТААААGААG	+ 150 GCTC Renin- GCTC Renin-
1.	AGGGGGTC: AGGGGGTC:	-+ 160 IGGGCTAC2 IGGGCTAC2	170 ACAGCTCTTA ACAGCTCTTA	180 GAAAGCCTTC GAAAGCCTTC	190 GGCTGAACCAG GGCTGAACCAG	+ 200 ATGGACAG <mark>A</mark> A ATGGACAG <mark>G</mark> A	210 AGGAGGATGCC AGGAGGATGCC	220 TCTCTGGGCA	230 CTCTTGTTGC CTCTTGTTGC	240 TCTGGAGTCO TCTGGAGTCO	250 CTTGCACCTTC CTTGCACCTTC	260 CAGTCTCCCA CAGTCTCCCA	270 ACACGCACCGO ACACGCACCGO	280 CTACCTTTGAA CTACCTTTGAA	290 Acgaatccc <mark>g</mark> c Acgaatccc <mark>a</mark> c	+ 300 TCAA Renin - TCAA Renin -
L	GAAAATGCO GAAAATGCO	-+ 310 C <mark>T</mark> TCTGTC(C <mark>C</mark> TCTGTC(320 CGGGAAATCC CGGGAAATCC	330 TGGAGGAGCO TGGAGGAGCO	340 GGGGAGTGGAC GGGGAGTGGAC	350 ATGACCAGGC ATGACCAGGC	360 TCAGTGCTGA TCAGTGCTGA	370 A <mark>T</mark> GGGGCGTA A <mark>A</mark> GGGGCGTA	+ 380 TTCACAAAGA TTCACAAAGA	390 GGCCTTCCT GGCCTTCCT	400 IGA <mark>C</mark> CAATCTI IGA <mark>T</mark> CAATCTI	410 FACCTCCCCCC FACCTCCCCCC	420 GTGGTCCTCAC GTGGTCCTCAC	430 CCAACTACCTO CCAACTACCTO	440 GAATACCCAGT. GAATACCCAGT.	450 ACTA Renin ACTA Renin
L	CGGCGAGAS	460 TTGGCATCO TTGGCATCO	470 GGTACCCCAC GGTACCCCAC	480 CCCAGACCTI	490 CCAAAGTCATC CCAAAGTCATC	500 TTTGACACGG TTTGACACGG	510 GTTC <mark>A</mark> GCCAA GTTC <mark>G</mark> GCCAA	520 CCTCTGGGTG CCTCTGGGTG	530 CCCTCCACCA CCCTCCACCA	540 AGTGCAGCCO AGTGCAGCCO	550 5CCTCTACCT1 GCCTCTACCT1	560 FGCTTGTGGGA	570 570 ATTCACAGCCI	580 580 CTATGAGTCO CTATGAGTCO	590 CTCTGACTCCT CTCTGACTCCT	+ 600 CCAG Renin CCAG Renin
1	CTACATGGA CTACATGGA	-+ 610 AGAACGGG AGAACGGG	620 FCCGACTTCA FCCGACTTCA	630 CCATCCACTA CCATCCACTA	640 640 ACGGATCAGG <mark>G</mark> ACGGATCAGG <mark>A</mark>	650 AGAGTCAAAG AGAGTCAAAG	660 GG <mark>T</mark> TTCCTCAG GG <mark>C</mark> TTCCTCAG	670 CCAGGAC <mark>TC</mark> G CCAGGAC <mark>TC</mark> G	680 GTGACTGTGG GTGACTGTGG	690 GTGGAATCAG GTGGAATCAG	700 CTGTGACACAG CTGTGACACAG	710 GACCTTTGGAG GACCTTTGGAG	720 GAGGTCACCGA GAGGTCACCGA	730 AGCTGCCCCTC AGCTGCCCCTC	740 GATCCCTTTCA GATCCCTTTCA	+ 750 TGCT Renin TGCT Renin
	GGCCAAGT GGCCAAGT	760 TTGACGGTO TTGACGGTO	770 GT <mark>T</mark> CTAGGCA GT <mark>C</mark> CTAGGCA	780 TGGGCTTTCC TGGGCTTTCC	790 CGCTCAGGCC TGCTCAGGCC	800 GTTGGCGGGG GTTGGCGGGG	810 STTACCCCTGT GTTACCCCTGT	820 CTTTGACCAC	830 ATTCTCTCCC ATTCTCTCCC	840 AGGGGGTGC AGGGGGTGC	850 BAAGGAGGA <i>F</i> T <mark>A</mark> AAGGAGGA <i>F</i>	860 AGTGTTCTCTC AGTGTTCTCTCTC	870 GTCTACTACAA GTCTACTACAA	880 ACAGGGGTTCO ACAGGGGTTCO	890 CCACCTGCTGG CCACCTGCTGG	+ 900 GGGG Renin GGGG Renin
-	CGAGGTGG CGAGGTGG	910 9CTAGGAG IGCTAGGAG	920 GG <mark>T</mark> AG <mark>C</mark> GACC GG <mark>C</mark> AG <mark>T</mark> GACC	930 CGCAGCATTA CGCAGCATTA	940 TCAAGGCAAT A <mark>C</mark> CAAGGCAAT	950 950 TTTCACTATG	960 960 TGAGCATCAG	970 CAAGACTGAC CAAGACTGAC	980 TCCTGGCAGA TCCTGGCAGA	990 TCACGATGAA TCACGATGAA	1000 AGGGGGGTGTCI AGGGGGGTGTCI	1010 IGTGGGGTCT IGTGGGGTCT	1020 FCCACCCTGCT	1030 FATGTGAAGAA FATGTGAAGAA	1040 AGGCTGTGCGG AGGCTGTGCGG	+ 1050 TAGT Renin TAGT Renin
-	GGTGGACAG GGTGGACAG	1060 CTGGTTCA CTGGTTCA	1070 FCCTTTATCT FCCTTTATCT	1080 CGGCTCCTAC CGGCTCCTAC	1090 CGAGCTCCCTG CGAGCTCCCTG	+ 1100 AAGTTGATCA AAGTTGATCA	1110 MIGCAAGCCCT	1120 GGGAGCCAAG GGGAGCCAAG	+ 1130 GAGAAGAGAA GAGAAGAGAA	1140 TAGA <mark>A</mark> GAAT <i>i</i> TAGA <mark>T</mark> GAAT <i>i</i>	1150 ATGTTGTGAAC ATGTTGTGAAC	1160 CTGTAGCCAGO CTGTAGCCAGO	1170 GTGCCCACCCI GTGCCCACCCI	1180 FCCCCGACATT	1190 TTCCTTTGACC	+ 1200 TGGG Renin TGGG Renin
	AGGCAGGG	-+ 1210 CCTACACAG CCTACACAG	1220 TCAGCAGTA	1230 CGGACTACGI	1240 IGCTACAGTAT IGCTACAGTAT	+ 1250 CCC <mark>A</mark> ACAGGA CCC <mark>T</mark> ACAGGA	1260 AGAGACAAGCT AGAGACAAGCT	1270 GTGCACACTG	1280 GCTCTCCATG GCTCTCCATG	1290 CCATGGACA CCATGGACA	1300 ICCCACCACCO ICCCACCACCO	1310 CACTGGGCCTC	1320 GTCTGGGTCCI GTCTGGGTCCI	1330 IGGGTGCCACO IGGGTGCCACO	1340 CTTCATCCGCA CTTCATCCGCA	+ 1350 AGTT Renin AGTT Renin
	CTATACAGA	-+ 1360 AGTTTGAT(AGTTTGAT(1370 CGGCATAACA CGGCATAACA	1380 ATCGCATTGO ATCGCATTGO	1390 GATTCGCCTTG GATTCGCCTTG	+ 1400 GCCCGCTAAG GCCCGCTAAG	1410 GCCCTCTGCC GCCCTCTGCC	1420 ACCCAGTAAC ACCCAGTAAC	+ 1430 CCTAGGCCAA CCTAGGCCAA	1440 GCCAAGCTGO GCCAAGCTGO	1450 GCA <mark>G</mark> TCCTGGO GCA <mark>C</mark> TCCTGGO	1460 GGGCCATTTT GGGCCATTTT	1470 GTCTGGCTTTG	1480 GTCCCCAACAI	1490 IAGGGACACTG IAGGGACACTG	+ 1500 GACA Renin GACA Renin
L	CAGAGACCO	-+ 1510 CTAACGAG	1520 1570	1530 TTCACCTGC	1540 ACTCACCCTTC	+ 1550 CCTGCTTTAA	1560 Mggaaaaa <mark>t</mark> cg	+ 1570 AATAAAGATT	+ 1580 TCATGTTTAA	+ 1590 AGCCTG						Renin

Supplemental Figure 4. Alignment of the cDNA sequences of renin1-d (the S6 allele, upper strand) and renin1-c (the B6 allele, lower strand). The 21 residues that differ between the 2 strains are highlighted in yellow.

	+	+	+	+	+	+	+	+	+	+
	10	20	30	40	50	60	70	80	90	100
1	MDRRRMPLWALLLLWS	PCTFSLPTR	TATFERIPLKF	MPSVREILE	ERGVDMTRLSA	E <mark>W</mark> GVFTKRPS	SL <mark>T</mark> NLTSPVVI	LTNYLNTQYYC	GEIGIGTPPQ	TFKVI Renin-1c
1	MDRRRMPLWALLLLWS	PCTFSLPTR	[ATFERIPLK]	MPSVREILE	ERGVDMTRLSA	LE <mark>R</mark> GVFTKRPS	SL <mark>I</mark> NLTSPVVI	LTNYLNTQYYO	GEIGIGTPPQ	FKVI Renin-1d
	+	+	+	+	+	+	+	+	+	+
	110	120	130	140	150	160	170	180	190	200
101	FDTGSANLWVPSTKCS	SRLYLACGIHS	SLYESSDSSSY	MENGSDFTI	HYGSGRVKGFI	JSQD <mark>S</mark> VTVGGI	LTVTQTFGEVI	TELPLIPFMLA	AKFDGVLGMGI	FPAQA Renin-1c
101	FDTGSANLWVPSTKCS	SRLYLACGIHS	SLYESSDSSSY	MENGSDFTI	HYGSGRVKGFI	JSQD <mark>V</mark> VTVGGI	LTVTQTFGEVI	TELPLIPFMLA	AKFDGVLGMGI	FPAQA Renin-1d
	+	+	+	+	+	+	+	+	+	+
	210	220	230	240	250	260	270	280	290	300
201	VGGVTPVFDHILSQGV	LKEEVFSVY	YNRGSHLLGGE	EVVLGGSDPQI	HYQGNFHYVSI	SKTDSWQITN	AKGVSVGSSTI	LCEEGCAVV	/DTGSSFISAI	PTSSL Renin-1c
201	VGGVTPVFDHILSQGV	LKEEVFSVY	YNRGSHLLGGE	EVVLGGSDPQI	HYQGNFHYVSI	SKTDSWQITN	AKGVSVGSSTI	LCEEGCAVV	/DTGSSFISAI	PTSSL Renin-1d
	+	+	+	+	+	+	+	+	+	+
201	310	320	330	340	350	360	370	380	390	400
301 201	KLIMQALGAKEKRIEE	YVVNCSQVP'	L'LPDISFDLGO	GRAYTLSSTD:	(VLQYP <mark>N</mark> RRDF	LCTLALHAMI	DIPPPTGPVW	LGATEIRKEY	TEFDRHNNR.	IGFAL Renin-Ic
301	KLIMQALGAKEKRI <mark>D</mark> E	YVVNCSQVP.	L'L'ADISEDLGO	RATTLSSTD	u vlqi p <mark>i</mark> rrdf	LCTLALHAMI	DIPPPTGPVWV	LGATEIRKEI	TEFDRHNNR.	IGFAL Renin-Id
401	AR									Renin-1c
401	AR									Renin-1d

Supplemental Figure 5. Alignment of the amino acid sequences of renin1-d (the S6 allele, upper strand) and renin1-c (the B6 allele, lower strand). The 5 amino acids that differ between the 2 strains are highlighted in yellow.



Supplemental Figure 6. Adrenal CYP11B2 expression is higher in sGC $\alpha_1^{-r,S6}$ than in WT^{S6} mice . mRNAs encoding the cytochrome P450, family 11, subfamily b, polypeptide 2 (CYP11B2 or aldosterone synthase) were measured via quantitative RT-PCR in adrenal glands of male WT and sGC α_1^{-r} mice on the S6 or B6 genetic background. N=8-11/ group. Adrenal expression level of CYP11B2 was higher in sGC $\alpha_1^{-r,S6}$ than in WT^{S6} mice. *P<0.01 vs WT^{S6}.



Supplemental Figure 7. Spironolactone does not affect blood pressure in WT^{B6} or sGC $\alpha_1^{-/-B6}$ mice. Mean arterial blood pressure (MAP) measured invasively in anesthetized male WT and sGC $\alpha_1^{-/-}$ mice on the B6 background, treated with vehicle (n=5 and 3, respectively) or spironolactone (n=5 and 6, respectively). P=NS for WT vehicle vs WT Spironolactone and for sGC $\alpha_1^{-/-}$ vehicle vs sGC $\alpha_1^{-/-}$ spironolactone (*t* test).



Supplemental Figure 8. Losartan decreases blood pressure more in sGC α_1^{-l-S6} mice than in WT^{S6} mice. Decrease in mean arterial blood pressure (MAP) measured invasively in anesthetized male WT and sGC α_1^{-l-} mice on the S6 background, treated intravenously with 0.1 mg/kg Losartan (n=4 and 5, respectively). Repeated measures Anova *P< 0.001.



Supplemental Figure 9. The strain-specific hypertension in sGC $\alpha_1^{-/-}$ mice is associated with greater impairment of vascular reactivity in sGC $\alpha_1^{-/-S6}$ mice than in sGC $\alpha_1^{-/-B6}$ mice. Acetylcholine-induced relaxation was studied in phenylephrine-precontracted mesenteric arteries from male wild-type (WT, closed symbols, full line) and sGC $\alpha_1^{-/-}$ mice on the B6 (circles) or S6 (squares) genetic background. Acetylcholine-induced vascular relaxation was impaired to a greater extent in sGC $\alpha_1^{-/-S6}$ than in sGC $\alpha_1^{-/-B6}$ mice. N= 3, 5, and 6 for sGC $\alpha_1^{-/-S6}$, sGC $\alpha_1^{-/-B6}$, and WT^{B6}, respectively. *P<0.05 vs sGC $\alpha_1^{-/-S6}$, \dagger P<0.05 vs sGC $\alpha_1^{-/-S6}$ and sGC $\alpha_1^{-/-B6}$.



Supplemental Figure 10. Schematic representation, generated via e!Ensembl of *Mus musculus* chromosome 1 (Mmus Chr.1), *Rattus norvegicus* chromosome 13 (Rnor Chr.13), and *Homo sapiens* chromosome 1 (Hsap Chr.1). The red boxes in the top panel represent part of the syntenic region containing the renin locus and are magnified in the multi-species view in the bottom panel. Black ovals highlight the location of the renin gene in the murine, human, and rat genome.



Supplemental Figure 11. Alignment of the amino acid sequences of mouse renin1-c (the B6 allele, upper strand) and human renin-1 (lower strand). Amino acids that differ between murine renin1-c and human renin-1 are highlighted in yellow. The amino acids that differ between B6 and S6 (see **Supplemental Figure 5**) are highlighted in red.