Supplemental Methods

Generation of the BAC construct with a mutated *RBP-J*-binding site

Bacterial strain, BAC clone and plasmid. We used SW102 cells, which contain a defective λ prophage with cI857 repressor, obtained from the National Cancer Institute. The BAC clone RP2388K7 containing the renin gene was purchased from CHORI (Oakland, CA). In this clone the renin gene is centrally located, being flanked by 89kb of DNA 5' and 129kb 3'. The *RpsL*$^{+}$-*Kana* plasmid was obtained from Addgene (Cambridge, MA). This plasmid has the *RpsL*$^{+}$-*Kana* selectable markers. *RpsL* expression results in streptomycin sensitivity (*RpsL*$^{+}$), whereas the aminoglycoside phosphotransferase gene (*Aph)* expression results in kanamycin resistance (*kana*).

Two step recombineering strategy. We used dual kanamycin and streptomycin selection to make a precise modification in the BAC construct in a two-step procedure as described in Wang *et al.,* 2009.[35] First, the *RpsL*$^{+}$-*Kana* cassette was introduced into the area of interest yielding kanamycin resistant cells. Second, the *RpsL*$^{+}$-*Kana* cassette was replaced with the desired sequence yielding streptomycin resistant cells. In the control construct exon 1 of the renin gene was replaced with EGFP (Clontech Laboratories, Mountain View, CA) then the renin 3'-UTR was inserted at the 3' end of the EGFP sequence mimicking the endogenous renin gene. Primers used to PCR amplify the desired fragments contained 80 bp homologous to the target region of the BAC for recombination and 20 bp from the *RpsL*$^{+}$-*Kana* cassette. In order to obtain the recombination segment, we performed a PCR using *RpsL*+-*Kana* plasmid DNA and the primer pairs designed to the area of interest (Supplemental Table 4) using a proofreading polymerase (catalog no. 600677, Herculase II Fusion DNA polymerase, Stratagene, Santa Clara, CA) to avoid PCR errors. The PCR reaction was digested with *Dpn*I (R0176S, New England BioLabs, Inc., Ipswich, MA) to eliminate the plasmid and the PCR fragment was gel

purified using a Qiaquick Gel Extraction kit (catalog no. 28704, Qiagen, Valencia, CA). To confirm that colonies underwent the appropriate recombination to introduce the EGFP and renin 3'UTR sequences, single-colony PCRs were performed with primers flanking the region of interest and the PCR products were sequenced. To introduce the mutated *RBP-J* binding sequence the *RpsL*$^{+}$*-Kana* cassette was replaced using a synthetic 100 bp oligonucleotide containing 46 nucleotides flanking the 8 nucleotides of the mutated *RBP-J* consensus sequence. The insertion of the mutation was verified by DNA sequencing.

The recombined BAC clones were transfected into recombination incompetent cells (NEB-10-beta *E.coli, catalog* no. C3020K, New England BioLabs, Inc., Ipswich, MA) to avoid accidental recombination. BAC DNA was extracted using the NucleoBond BAC 100 kit (Macherey-Nagel Inc., Bethlehem, PA) and used for confirmation of clone integrity by restriction enzyme digestion and PCR analysis. The integrity of the whole BAC was confirmed by digesting the starting clone and the recombinants with *SpeI* (catalog no. R0133S, New England BioLabs, Inc., Ipswich, MA) and comparing the band patterns in agarose gels. Further, we amplified by PCR and sequenced amplicons from various regions of the BAC. Specifically, 240bp of the renin proximal promoter and the EGFP-renin 3'UTR sequences were confirmed as well as the ends of the BAC construct. The regulatory region upstream of renin was verified by PCR of multiple overlapping amplicons covering 1300bp of the proximal promoter, including the *RBP-J* site, and 1200 bp including the renin enhancer and surrounding sequences. After BAC integrity verification, DNA was microinjected by the University of Virginia Gene Targeting and Transgenic Facility to produce transgenic mice. To confirm that the intended mutation of the *RBP-J* binding site was present in the study mice, DNA was extracted from tails of transgenic WT-BAC and Mut-BAC mice and the region around the *RBP-J* binding site in the transgene was amplified by PCR and the amplicon was sequenced (Supplemental Figure 5).

TUNEL assay

To identify apoptotic cells we used the Apoptag Peroxidase In situ Apoptosis Detection kit (S7100, Millipore, Billerica, MA) in kidney sections fixed in Bouin's solution according to the manufacturer's instructions. The TUNEL assay involves addition of labeled nucleotides at DNA strand breaks by terminal deoxynucleotidyl transferase (TdT) and immunoperoxidase detection of these digoxigenin-labeled DNA strand breaks.

Supplemental Table 1

Renin expression in kidneys of *RBP-J cKO;R26R* mice

Denomination	Genotype	Age(mo)	n	JGA index	relative expression of renin mRNA
RBP-J$^{+/+}$	*RBP-J*$^{+/+}$; *Ren1*$^{dcre/+}$; R26R$^{-/+}$	1	3	43.8±2.7	100
RBP-J cKO	*RBP-J*$^{fl/fl}$; *Ren1*$^{dcre/+}$; R26R$^{-/+}$	1	5	6.1±0.9**	15.0±0.9*
RBP-J$^{+/+}$	*RBP-J*$^{+/+}$; *Ren1*$^{dcre/+}$; R26R$^{-/+}$	2	4	34.5±9.5	100
RBP-J cKO	*RBP-J*$^{fl/fl}$; *Ren1*$^{dcre/+}$; R26R$^{-/+}$	2	6	4.7±0.7**	26±0.18**

**p<0.0006 and *p<0.02 when compared to control *RBP-J*$^{+/+}$ mice, values are mean ± SEM, n = number of mice, mo=months.

Supplemental Table 2. Deletion of *RBP-J* in renin cells does not increase cell death

Denomination	Genotype	Newborn	n	Untreated adult	n	Treated adult	n
RBP-J$^{+/+}$	*RBP-J*$^{+/+}$; *Ren1*$^{dcre/+}$	5±2.2	3	9±0.9	2	31±6.1	5
RBP-J cKO	*RBP-J*$^{fl/fl}$; *Ren1*$^{dcre/+}$	6±1.6	5	3±0.3	2	33±5.9	4

Values are the percent of apoptotic cells: number of apoptotic cells/number of glomeruli X 100 expressed as mean ± SEM, Treated adult = mice treated with captopril and sodium depletion for 7 days to induce re-expression of renin, n = number of mice

Supplemental Table 3.Genes characteristic of hematopoietic marker cells significantly enriched in arterioles from *RBP-J* cKO mice

Gene symbol	Gene name	fold change	Expression	Function	Ref
LOC546230	similar to Ig heavy chain V region 102 precursor	8.74	B-lymphocytes	B immune development	[1]
Havcr1	hepatitis A virus cellular receptor 1	7.53	T helper cells	modulate immune response	[2]
Lcn2	lipocalin 2	5.25	early marker of granulocytic differentiation;expressed in several other tissue including kidney	innate immunity	[3;4]
Abp1	amiloride binding protein 1 (amine oxidase, copper-containing)	4.98	epithelium-rich and/or hematopoietic tissues	controlling the level of histamine and/or putrescine	[5]
Lyz2	lysozyme 2	4.37	myeloblasts, immature macrophages, and in both mature macrophages	bacteriolytic function	[6]
LOC641089	similar to Ig heavy chain V region BCL1 precursor	4.05	B lymphocytes	immune development and function	[7]
Il6	interleukin 6	4	T and B cells, monocytes, fibroblast, keratinocytes, endothelial cells, mesangium cells and tumor cells	differentiation of B-cells into Ig-secreting cells. Involved in lymphocyte and monocyte differentiation.	[8]
Atp4a	ATPase, H+/K+ exchanging, gastric, alpha polypeptide	3.79	gastric parietal cells	responsible for acid production in the stomach	
Ccl9	chemokine (C-C motif) ligand 9	3.74	T and B cells	induction of innate and adaptive immune responses	[9]
Fcamr	Fc receptor, IgA, IgM, high affinity	3.01	oligodendrocytes, B-cells and macrophages	roles in host immunity, allergy and autoimmunity	[10]
Timd2	T-cell immunoglobulin and mucin domain containing 2	2.93	T helper cells	regulating autoimmune inflammation	[11]
LOC672291	similar to Ig kappa chain V-V region MOPC 173	2.91	B lymphocytes	immune development and function	[12]
Cyp2d9	cytochrome P450, family 2, subfamily d, polypeptide 9	2.8	Liver, kidney and extra hepatic tissue	Male-specific; regulated by GH; sterol 16a-hydroxylase	[13]
Ccl2	chemokine (C-C motif) ligand 2	2.76	bone marrow osteoblasts, endothelial cells, stromal cells, and prostate cancer cells	recruits and activates monocytes during the inflammatory response	[14]
Bcl2a1c	B-cell leukemia/lymphoma 2 related protein A1c	2.66	B lymphocytes	may function in the response of hematopoietic cells to external signals and in maintaining endothelial survival during infection	[15]
LOC100047162	similar to immunoglobulin kappa-chain	2.65	B lymphocytes	immune development and function	[16]
Ccl5	chemokine (C-C motif) ligand 5	2.56	T cells	acts as a ligand for the chemokine receptors and directs the migration of monocytes/macrophages and T cells	[17]
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	2.56	hematopoietic cells and nonlymphoid tissues	mature cellular function in the monocytic lineage, and it may be a component of a receptor complex involved in signal transduction	[18]
S100g	S100 calcium binding protein G	2.56	uterus and interimplantation sites during early pregnancy	implicated in both intracellular and extracellular functions, including enzyme activities, immune responses, cytoskeleton dynamics, Ca^{2+} homeostasis, cell growth and cell differentiation	[19]
Cd44	CD44 antigen	2.54	expressed in epithelial, mesothelial and hematopoietic tissues	involvement in cell aggregation, signaling, cell migration, retention of pericellular matrix, and others. Co-stimulatory molecules to induce T-cells	

				functions	
Igk-C	immunoglobulin kappa chain, constant region	2.49	B lymphocytes and epithelial carcinoma cell lines	involved in inflammatory response and detected in various inflammatory diseases	
Cd209a	CD209a antigen	2.47	dendritic cells and in lung, spleen, lymph nodes and bone marrow	pathogen-recognition receptor. May mediate the endocytosis of pathogens	20
Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	2.4	myeloid lineage	may be involved in cell-cell interactions	21
Igk-V28	immunoglobulin kappa chain variable 28 (V28)	2.4	B lymphocytes	immune response	22
Mpeg1	macrophage expressed gene 1	2.39	macrophages	induction by CSF-1 in fetal liver macrophages	23
Rgs1	regulator of G-protein signaling 1	2.37	murine B lymphocytes	selectively regulates gut T cell trafficking and colitic potential	24
Slamf7	SLAM family member 7	2.36	spleen, lymph node, bone marrow, NK cells, B-cells and testis. Lower levels detected in thymus.	mediates NK cell activation. May play a role in lymphocyte adhesion	25
Igkv1-117	immunoglobulin kappa chain variable 1-117	2.36	B lymphocytes	immune development and function	22
Clec7a	C-type lectin domain family 7, member a	2.34	myeloid dendritic cells, monocytes, macrophages and B cells	innate immune response Enhances cytokine production in macrophages and dendritic cells	26
C3ar1	complement component 3a receptor 1	2.25	lymphoid organs	central role in inflammatory processes	27
Ccl3	chemokine (C-C motif) ligand 3	2.24	macrophages and other inflammatory cells	promotes inflammation and has been proposed to be involved in a spectrum of diseases from asthma to multiple sclerosis	28
C1qb	complement component 1, q subcomponent, beta polypeptide	2.23	macrophages and dendritic cells	recognizes antibody-bound pathogens and recognizes apoptotic debris and thus augments phagocytosis	29
C8g	complement component 8, gamma polypeptide	2.2	immune cells	anti-inflammatory and/or antimicrobial activity	
LOC100046894	similar to Igk-C protein	2.18	B lymphocytes	immune development and function	
Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	2.17	connective tissue macrophages; bone marrow-derived dendritic cells	immune responses in the skin	30
Tlr13	toll-like receptor 13	2.16	APCs as well as mucosal epithelial cells	key component of innate and adaptive immunity. Response against pathogens through recognition of molecular patterns specific to microorganisms	31
Gp49a	glycoprotein 49 A	2.15	mononuclear phagocytes, NK cells, and mast cell	may play a role in cell-cell or cell-cytokine interactions during the development of mast cells	32
Atp6v0d2	ATPase, H+ transporting, lysosomal V0 subunit D2	2.15	osteoclasts	control of bone homeostasis under normal development	33
Fbxo36	F-box protein 36	2.12	brain, germ cells, kidney, mammary gland and tumor, pituitary gland, placenta, sertoli cells, testis, uterus and spermatocytes	regulate the cell cycle, immune response, signaling cascades and developmental programs by targeting proteins, such as cyclins, for degradation by the proteasome after ubiquitination.	
C1qa	complement component 1, q subcomponent, alpha polypeptide	2.12	dendritic cells and macrophages	Proinflamatory functions and bind to Fc portion of aggregated immunoglobulins	34

Prame	preferentially expressed antigen in melanoma	2.12	testis, many melanomas and cancer cells including leukemic cells and T cells	expressed in a variety of cancer cells including leukemic cells	35
Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.11	cerebellar Purkinje cells on postsynaptic dendritic spines	is essential for the efficient removal of glutamate from extracellular fluids	36
Pilra	paired immunoglobin-like type 2 receptor alpha	2.1	immune system cells, t	novel regulator of the innate and adaptive immune systems	37
H2-Aa	histocompatibility 2, class II antigen A, alpha	2.08	B-cells	essential for antigen-specific immune responses	38
Cxcl2	chemokine (C-X-C motif) ligand 2	2.08	bone marrow stroma and tissue	role during ontogeny of the hematopoietic system	39
Tyrobp	TYRO protein tyrosine kinase binding protein	2.07	adult nervous system and nonneural tissues such as kidney, ovary, and testis, and hematopoietic cell lines	anticoagulant actions	40
H2-Eb1	histocompatibility 2, class II antigen E beta	2.06	APC	immune response	41
Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4	2.04	monocytes, macrophages, dendritic cells, lung, NK cells and B-cells	involved in the down-regulation of the immune response and the development of tolerance	42
C1qc	complement component 1, q subcomponent, C chain	2.04	macrophages and denditric cells	clearance of immune complexes and apoptotic cell and modulation of cytokine expression	43
Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	2.04	germ cells	essential for spermatogenesis	44
Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	2.03	lymphoid tissue	immune response	45
Cd72	CD72 antigen	2.03	B-cells and a subset of T-cells	plays a role in B-cell proliferation and differentiation	46
Fn1	fibronectin 1	2.02	hepatic stellate cells	involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape	47
IghmAC38.205.12	Ig mu chain V region AC38 205.12	2.02	B lymphocytes	immune development and function	
Hmcn1	hemicentin 1	2.01	germ cells	role in cytokinesis	48
Fcgr2b	Fc receptor, IgG, low affinity IIb	2.01	cells of hematopoietic origin	involved in phagocytosis of antigen-antibody complexes and modulation of antibody production by B-cells	49
H2-Dma	histocompatibility 2, class II, locus DMa	2.01	APCs	regulates interactions of leukocytes	50
H2-Ab1	histocompatibility 2, class II antigen A, beta 1	2.01	APCs	regulates interactions of leukocytes	

APC; antigen presenting cells, NK; natural killer, CSF-1; colony-stimulating factor-1

Supplemental Table 4. Primers used for recombineering

Gene		Sequences	Size (bp)
GFP	F	5'GAAGGAGAGCAAAAGGTAAGAG3'	860
	R	5'GCCGATGGGGGTGTTCTG3'	
RpsL^{+}-*Kana* cassette for *Renin* site	F	5'GTGATACATGGTGTGTATAAAAGAAGGCTCAGGGGGTCTG GGCTACACAGCTCTTAGAAAGCCTTGGCTGAACCAGCCGGA ATTGCCAGCTGGGG3'(underline is KANA homology)	1480
	R	5'atagacagctgagggcgttagtaagatgccagttcctgtaccctgccacccccttctctgc ccaagttacTCAGAAGAACTCGTCAAGAAGGCGATAGAA	
EGFP for *RpsL*$^{+}$-*Kana* cassette	F	5'GTGATACATGGTGTGTATAAAAGAAGGCTCAGGGGGTCTG GGCTACACAGCTCTTAGAAAGCCTTGGCTGAACCAGATGGT GAGCAAGGGCGAGGA 3'(underline is GFP homology)	875
	R	5'gatccaacgtatagacagctgagggcgttagtaagatgccagttcctgtaccctgccac cccttctctgcccaagttacTTACTTGTACAGCTCGTC 3'	
3' UTR insertion			
KANA	F	5'AGCGCGATCCATGGTCCTGCTGGAGTTCGTGACCGCCGC CGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAACCGG AATTGCCAGCTGGGG 3'	1481
	R	5'atagacagctgagggcgttagtaagatgccagttcctgtaccctgccacccccttctctgc ccaagttacTCAGAAGAACTCGTCAAGAAGGCGATAGAA 3'	
3'UTR	F	5'AGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCG CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGGC CCTCTGCCACCCAGTAA 3'	339
	R	5'atccaacgtatagacagctgagggcgttagtaagatgccagttcctgtaccctgccacc ccttctctgcccaagttacGGCTTTAAACATGAAATCTTT 3'	
RpsL^{+}-*Kana* cassette for *RBP-J* site	F	5' TTCCTCATTAGACTCTGTCTAAGCTAGAGGTTGCGGGGCCA GGCCAAACAGGGACTCTAGAGTCATTGGGCTCAGCCACCCC CGGAATTGCCAGCTGGGG 3'	1494
	R	5'GAGACCAAGCTAGGTAGGTATAGGATAAGCAGGACCTGGT CACAGAGCAGAGTGGTGGCAGGCATGGGGGTCAGAAGAAC TCGTCAAGAAGGCGATAGAA 3'	
Mutated *RBP-J* oligo	F	5'ATAAGCAGGACCTGGTCACAGAGCAGAGTGGTGGCAGGC ATGGGGG**CT**TG**AA**AAGGGTGGCTGAGCCCAATGACTCTAGA GTCCCTGTTTGGCCTGGCCC 3'	100
	R	5'GGGCCAGGCCAAACAGGGACTCTAGAGTCATTGGGCTCA GCCACCCTT**TT**CA**AG**CCCCCATGCCTGCCACCACTCTGCTC TGTGACCAGGTCCTGCTTAT 3'	
RBP-J	F	5'CAGTTCCTCATTAGACTCTG3'	177
	R	5'ATCTTAGCCTGTGAGACC3'	

Targeting the RBP-J site. To replace the *RBP-J* site with the *RpsL*$^{+}$*-Kana* cassette we used the primers labeled as *RpsL*$^{+}$*-Kana* cassette for the *RBP-J* site. The mutated bases are in bold and underlined in the 'Mutated *RBP-J*' oligonucleotides.

Supplemental References

Supplemental Table 3

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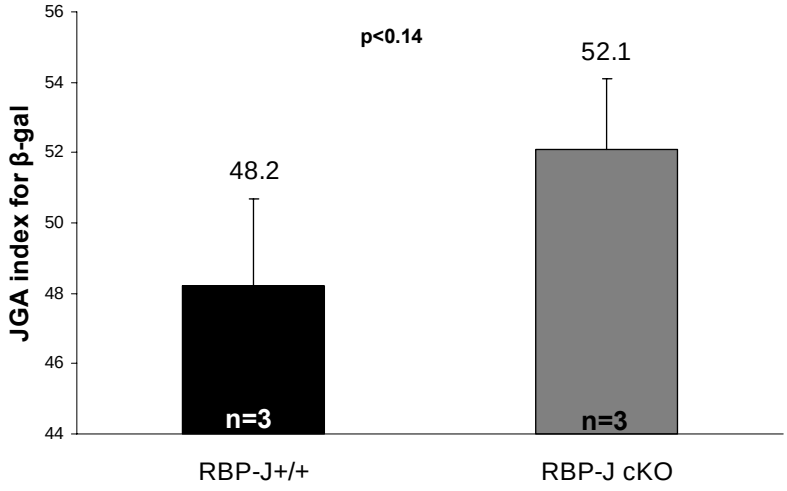
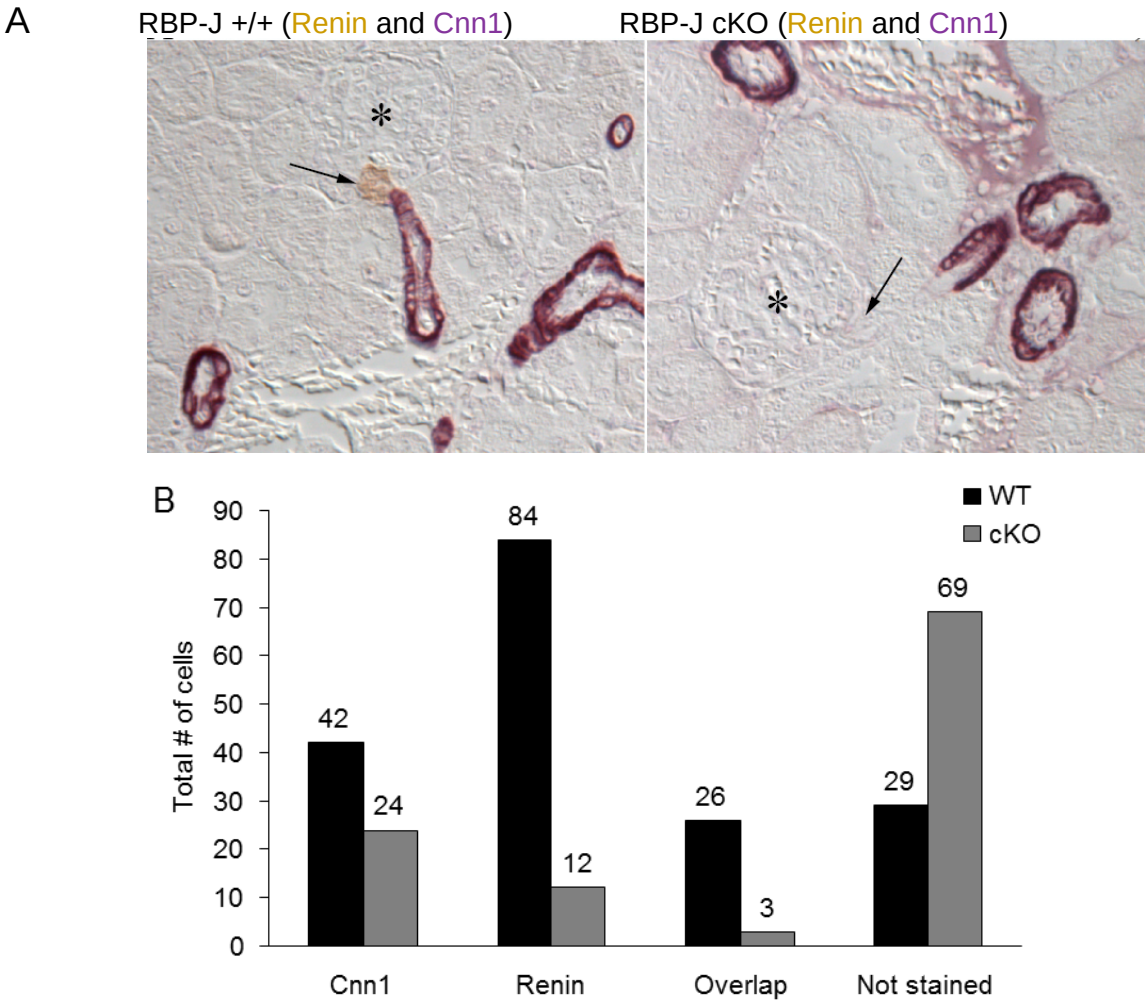
Supplemental Figure 1



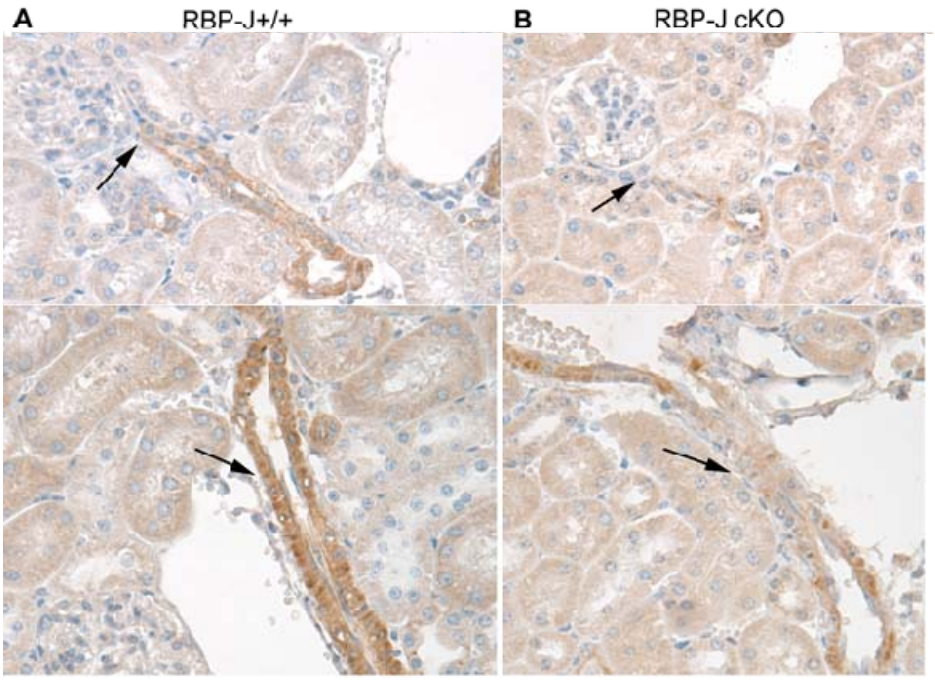
Supplemental Figure 1. Deletion of *RBP-J* does not affect the number of LacZ-positive JGAs. Kidneys from *RBP-J*$^{+/+}$; *Ren1*$^{dcre/+}$; *R26R*$^{-/+}$ (RBP-J +/+) control and *RBP-J*$^{fl/fl}$; *Ren1*$^{dcre/+}$; *R26R*$^{-/+}$ (RBP-J cKO) mice were subjected to the X-gal reaction to label the LacZ positive cells. In 2 month old mice the percentage of JGAs containing LacZ-positive cells was not significantly different between control (n=3) and mutant mice (n=3). Values are means ± SEM.

Supplemental Figure 2



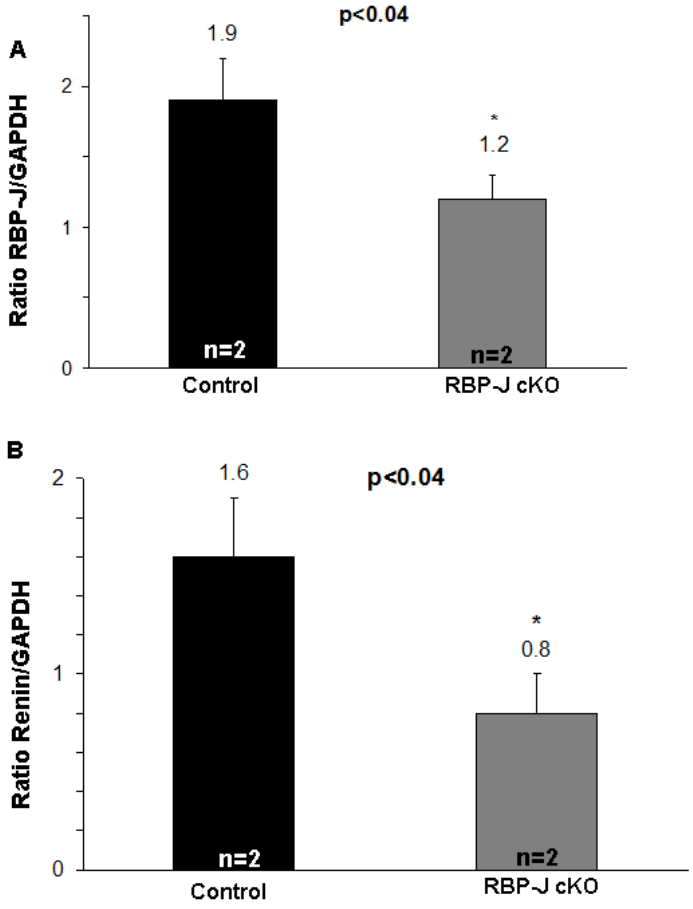
Supplemental Figure 2. Expression of renin and Cnn 1 in *RBP-J cKO* mice. Double staining for renin and Cnn1 in *RBP-J* cKO mice at 2 months of age. (A) *RBP-J cKO* mice have few or no renin positive (brown) cells in the JGAs and less Cnn1 (purple) expression. (B) Quantification of double staining for renin and Cnn1 using the categories described for Figure 3. RBP-J *cKO* mice had a significant increase in the number of unstained cells and a decrease in the number of Cnn1 only, renin only and overlap cells. A total of 110 JGAs were counted in the controls (n=2) and 76 JGAs in the *RBP-J cKO* (n=2). Asterisks mark glomeruli.

Supplemental Figure 3



Supplemental Figure 3. Deletion of *RBP-J* affects *Crip1* expression. Immunostaining for Crip1 in *RBP-J* +/+ and *RBP-J cKO* mice at 2 months of age shows that: (A) Crip1 is expressed in the JGA and afferent arterioles (upper) and in interlobular arteries (lower) in *RBP-J* +/+ kidney. (B) In the *RBP-J cKO* mice there is an overall decrease in Crip1 expression in the JGA, in afferent arterioles and in interlobular arteries. Arrows in upper panels, JGA; in lower panels, interlobular artery

Supplemental Figure 4



Supplemental Figure 4. Semiquantitative PCR for *RBP-J* and renin in isolated arterioles. (A) In the *RBP-J cKO* there is 1.5-fold decrease in *RBP-J* mRNA and (B) a 2-fold decrease in renin mRNA when compared to controls. Values are means ± SEM *, p<0.05

Supplemental Figure 5. Sequence of the renin promoter surrounding the mutated RBP-J binding site in Mut-BAC mice. To ensure that only intended recombination occurred at the RBP-J binding site after generation of the transgenic mice, we extracted DNA from tails of transgenic WT-BAC and Mut-BAC mice and sequenced the region upstream of the RBP-J site to the GFP insertion. The diagram shows a textual representation of the pairwise alignment of the region flanking the RBP-J DNA binding site from the Mut-BAC mice and the endogenous renin gene. In the endogenous renin gene (query), the RBP-J consensus sequence is 5'-TGTGGGAA-3' marked in yellow while in the Mut-BAC it is in purple (Sbjct). Results shows that Mut-BAC mice had the intended four nucleotides mutated and that the flanking region of the RBP-J binding site of the Mut-BAC matches perfectly with the endogenous renin gene.

Blast WT versus Mut BAC

Score = 1411 bits (764), Expect = 0.0
Identities = 780/787 (99%), Gaps = 3/787 (0%)
Strand=Plus/Plus

```
Query  9    TTATCTAATCTCCCCCAG-AGGCCTCCCAGCATTTCCAGCTGCCAGACCACCCAGTGCCT  67
            ||||||  |||||||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  10   TTATCT-ATCTCCCCCAGAAGGCCTCCCAGCATTTCCAGCTGCCAGACCACCCAGTGCCT  68

Query  68   TCCCCTGCTGTCTGCCCGCCCAGTCTCTCTGAGCTCTGGTGAGTCTCGCCCACCTCCTTT  127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  69   TCCCCTGCTGTCTGCCCGCCCAGTCTCTCTGAGCTCTGGTGAGTCTCGCCCACCTCCTTT  128

Query  128  ATTTCCCCACGCCAGGTGCCCAACAAGGCCCATGGCAGGGCAGCTCTGATAAATCTTAGC  187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  188  CTGTGAGACCAAGCTAGGTAGGTATAGGATAAGCAGGACCTGGTCACAGAGCAGAGTGGT  247
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Sbjct  189  CTGTGAGACCAAGCTAGGTAGGTATAGGATAAGCAGGACCTGGTCACAGAGCAGAGTGGT  248

Query  248  GGCAGGCATGGGGGTGTGGGAAGGGTGGCTGAGCCCAATGACTCTAGAGTCCCTGTTTGG  307
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Query  308  CCTGGCCCCGCAACCTCTAGCTTAGACAGAGTCTAATGAGGAACTGTGCTGTTCAAGCAT  367
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