

A

mRNA rel. fold change
Ctrl
Rbpj^{ΔEC}
 $p=0.013$

B

TdTomato CD31 DAPI
TdTomato CD31 DAPI

C

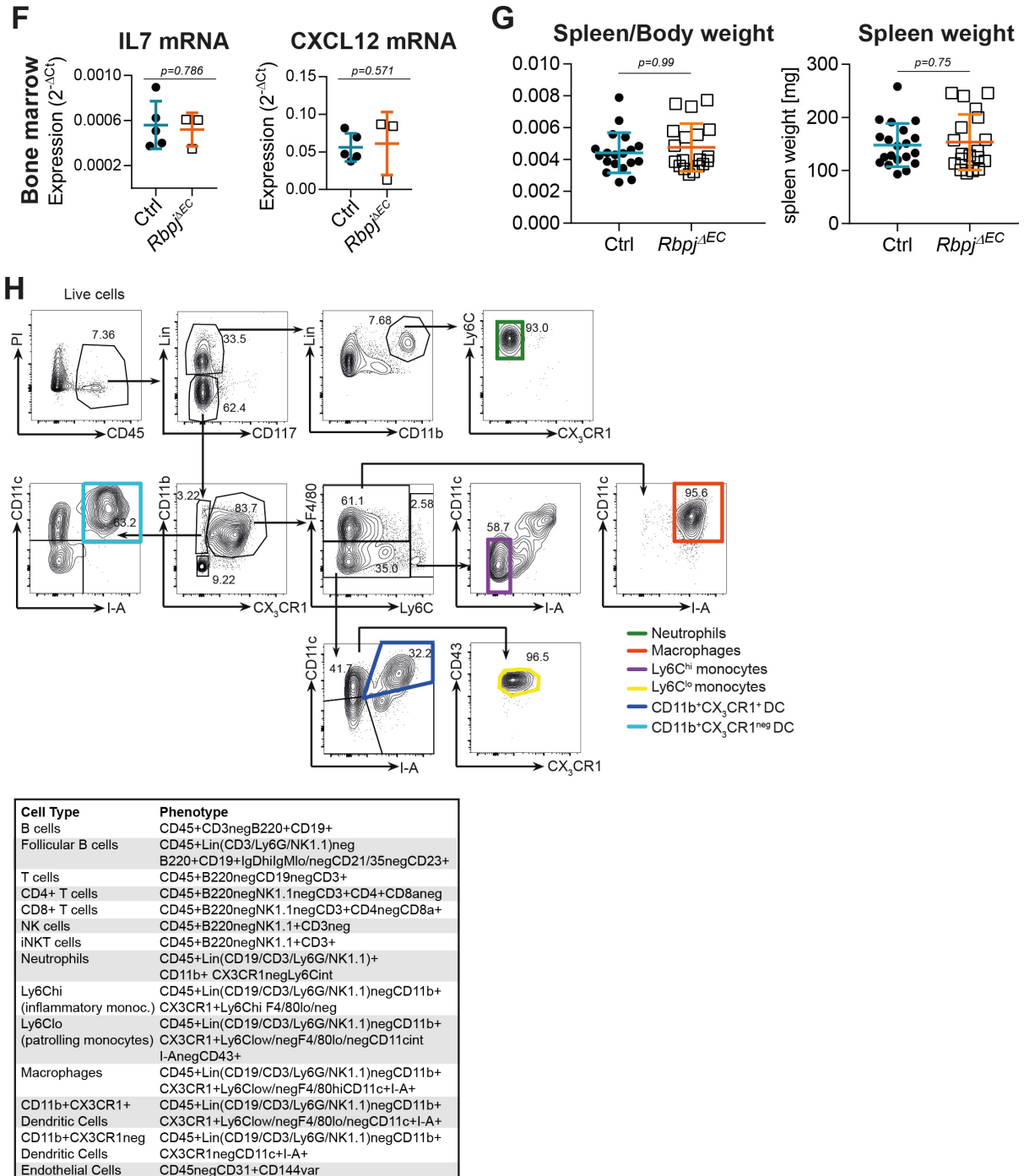
Live cells
PI
CD45
CD3
CD31
CD3
CD144
— EC
— T cells
— B cells

D

Live/Singlette/CD45⁺
T/NK/Gran
B220
CD11c
CD19
B220
CD43
CD24
IgM
PrePro B cells
CD24
IgM
Pro B cells
CD24
IgM
Immature B cells
CD24
CD23
Splenic MZ B cells
CD23
IgM
Transient B cells
CD24
CD21/35
Follicular B cells
CD23

E

Kidney
Liver
Peripheral blood
LN
Spleen
Bone marrow
% of live
Ctrl
Rbpj^{ΔEC}
 $p=0.012$
 $p=0.016$
 $p=0.005$
immB MZB Trans B IgM^{neg}IgD^{hi}CD23^{CR} pre B IgM^{neg}IgD^{hi}FoL B B220^{hi}CD19^{neg}CD24^{hi}CD43^{var} pro B PreProb

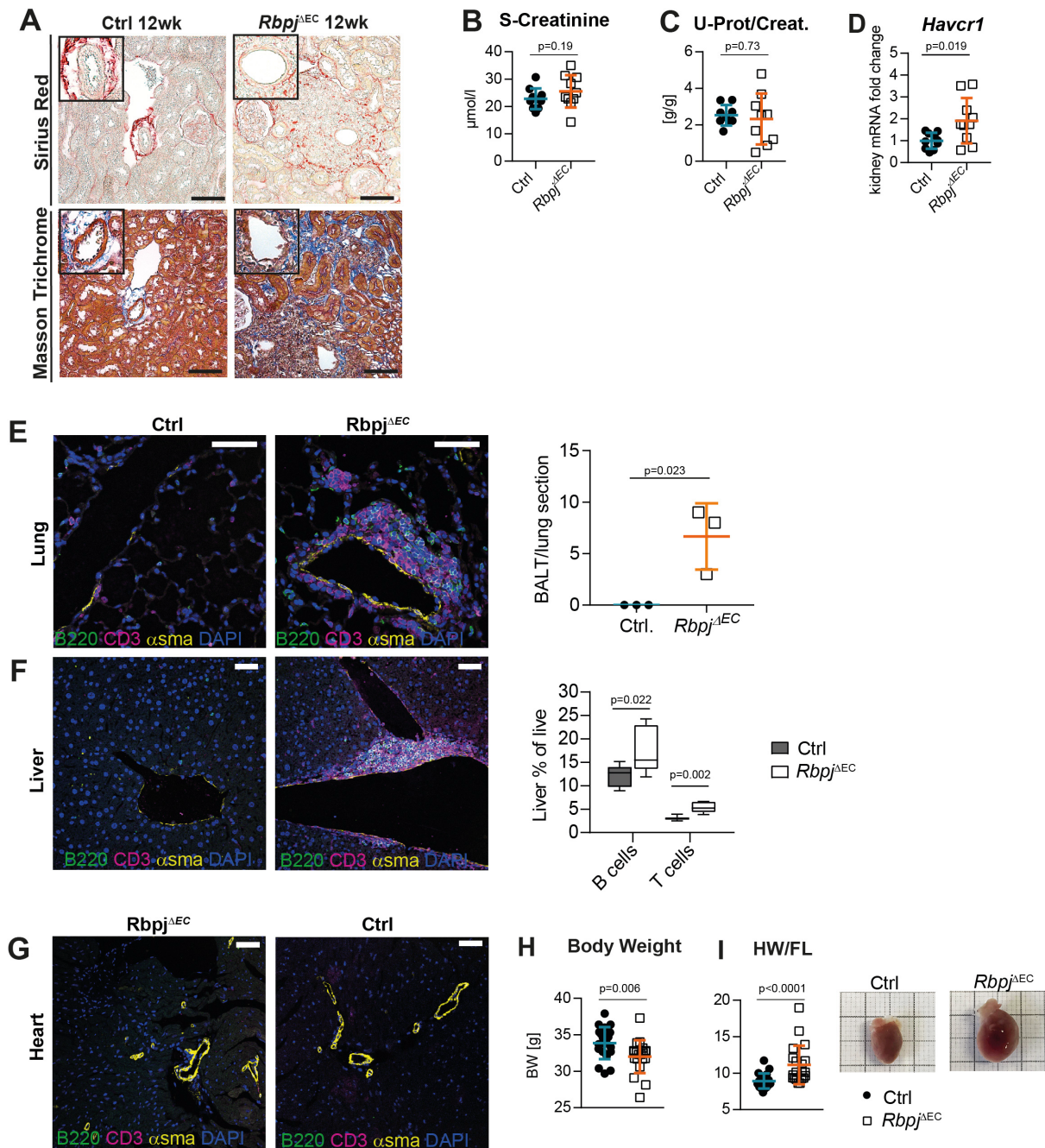


Supplementary Figure 1. Analysis of renal targeting and cell populations after endothelial-specific loss of Notch signaling

A) Recombination control: upper panel, Whole kidney mRNA expression of *Hey1*, downstream of *Rbpj*, as internal control of endothelial *Rbpj* knockdown. CTRL n=9, *Rbpj*^{AEC} n=6, * $p<0.05$ (Mann-Whitney test, two-tailed, exact $p=0.013$) Graph: Scatter dot blot with mean and SD (whiskers).

Lower panel, left side, kidney PCR for *Rbpj* deletion band (at 500bp, only upon successful deletion of exons 6 and 7). **B)** *Cdh5Cre*^{ERT2};*TdTomato*^{fl/fl} mouse model as recombination control: nuclear and cytoplasm TdTomato (yellow and middle column)

and CD31 staining (cytoplasmatic, purple and right column) show good recombination; exemplary image, kidney sections from n=3 mice stained. Scale bars, 50µm. **C)** Flow cytometry gating strategy for Endothelial cells, B and T lymphocytes. **D)** Flow cytometry gating strategy for B cell subset and progenitor panel. **E)** Flow cytometry of B cell subpopulations in kidney, liver, blood, lymph node, spleen and bone marrow. Follicular B cells (green shade) significantly upregulated in kidney (p=0.012) and liver (p=0.016). Marginal zone B cells (red shade) slightly lower in *Rbpj^{ΔEC}* spleen (p=0.005). No other significant change between groups observed. Box plots with mean, 25-75 percentile (bounds) and min/max (whiskers). Two-tailed Mann Whitney test. **F)** Bone marrow mRNA expression of IL7 (p=0.786) and CXCL12 (p=0.571) between groups; Mann-Whitney test, two-tailed; scatter dot blot with mean and SD (whiskers), CTRL n=5, *Rbpj^{ΔEC}* n=3. **G)** Spleen weight (p=0.99) and spleen/body weight ratio (p=0.75) in Ctrl and *Rbpj^{ΔEC}*; Scatter dot blots with mean, SD (whiskers); two-tailed Mann-Whitney test; CTRL n=20, *Rbpj^{ΔEC}* n=19. **H)** Flow cytometry gating strategy for Myeloid panel. Table, list of markers used for each cell type. Source data are provided with this paper.

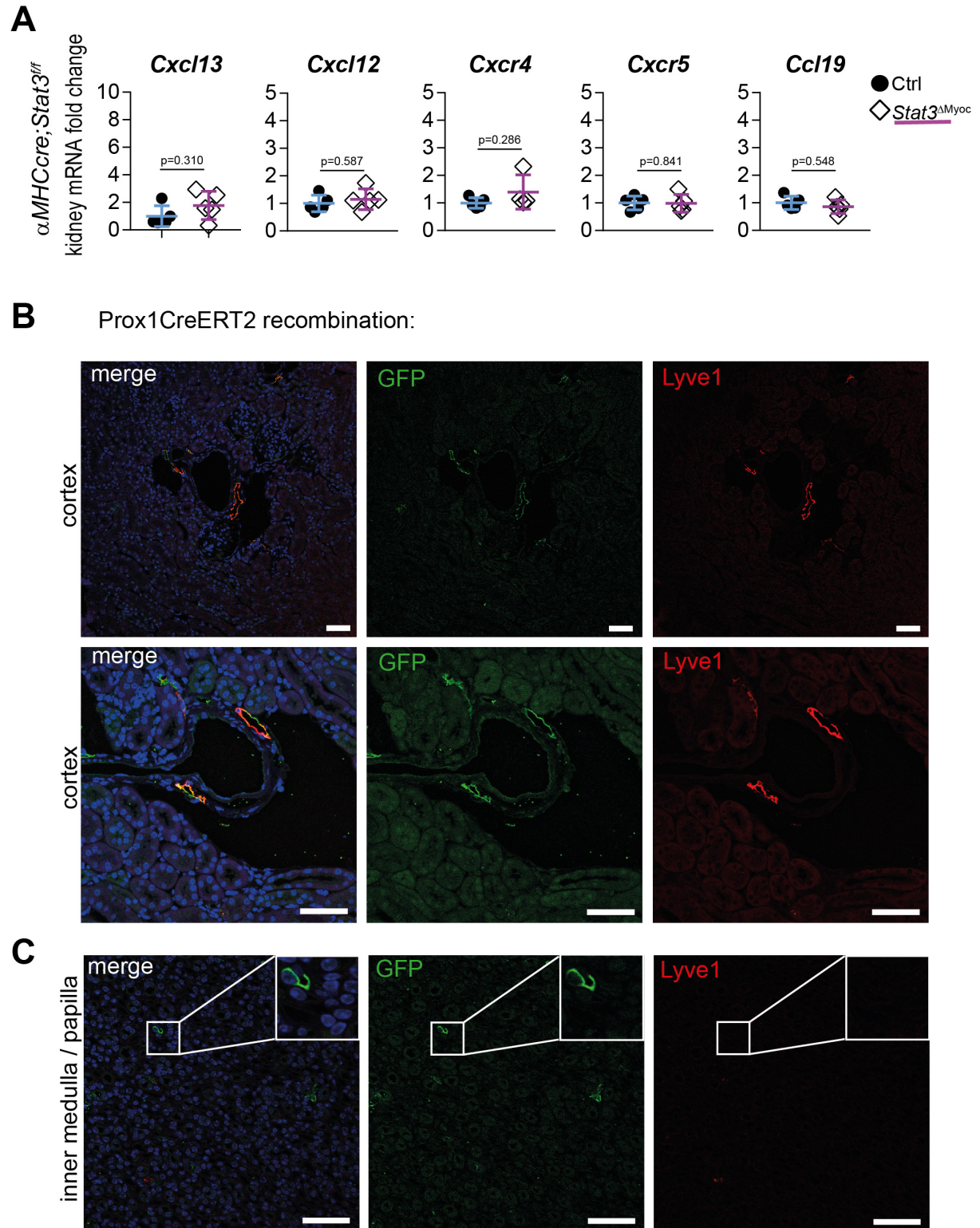


Supplementary Figure 2: Renal and cardiac parameters in Rbpj-mutant mice.

A) Sirius red (upper panel) and Masson trichrome (lower panel) staining of Ctrl (left) and *Rbpj*^{ΔEC} kidneys (right). Insets, arterial cross section. Scale bar, 50μm. Exemplary images, kidneys from n=5 mice/group were stained. **B)** Serum creatinine, n= 10 mice/group, scatter dot blot with mean, SD (whiskers), Mann-Whitney test, two-tailed, $p=0.19$, **C)** Urine protein to creatinine ratio between groups. n= 10 mice/group, scatter dot blot with mean, SD (whiskers), Mann-Whitney test, two-tailed, $p=0.73$ **D)** Whole kidney mRNA *Havcr1* (Kim1) expression, n= 10 mice per group from 2 independent experiments, scatter dot blot with mean, SD (whiskers), $p=0.019$ (Mann-Whitney test, two-tailed).

E) Immunofluorescence costaining of B220 (green), CD3 (purple) and α sma (yellow) of Ctrl and *Rbpj^{ΔEC}* lungs. Scale bars, 50 μ m. Quantification: average number of TLS counted per lung section, each data point represents one animal (n=3 mice per group), scatter dot blot with mean, SD (whiskers), Unpaired Student's t-test, two-sided, p=0.0229, *p<0.05. **F)** Immunofluorescence costaining of B220 (green), CD3 (purple) and α sma (yellow) of Ctrl and *Rbpj^{ΔEC}* liver. Scale bars, 50 μ m. Right, quantification via flow cytometry staining, % of live. N= 5 mice per group. Mean, Box from 25.-75. Percentile, whiskers represent min/max. B-cells, p=0.022; T-cells, p=0.002, Mann-Whitney Test, two-tailed.

G) Immunofluorescence costaining of B220 (green), CD3 (purple) and α sma (yellow) of Ctrl and *Rbpj^{ΔEC}* hearts, exemplary pictures, no quantification, representative of n=5/group. Scale bar = 50 μ m. **H)** Body weight (n=20/group, p=0.0062) and **I)** heart weight to femur length ration (HW/FL), (n=20/group, p<0.0001) in 20-22 weeks old mice (12 weeks after Tamoxifen injection). H&I: Mann-Whitney test, two-tailed. Graphs: Scatter dot blot with mean and SD (whiskers). Source data are provided with this paper.

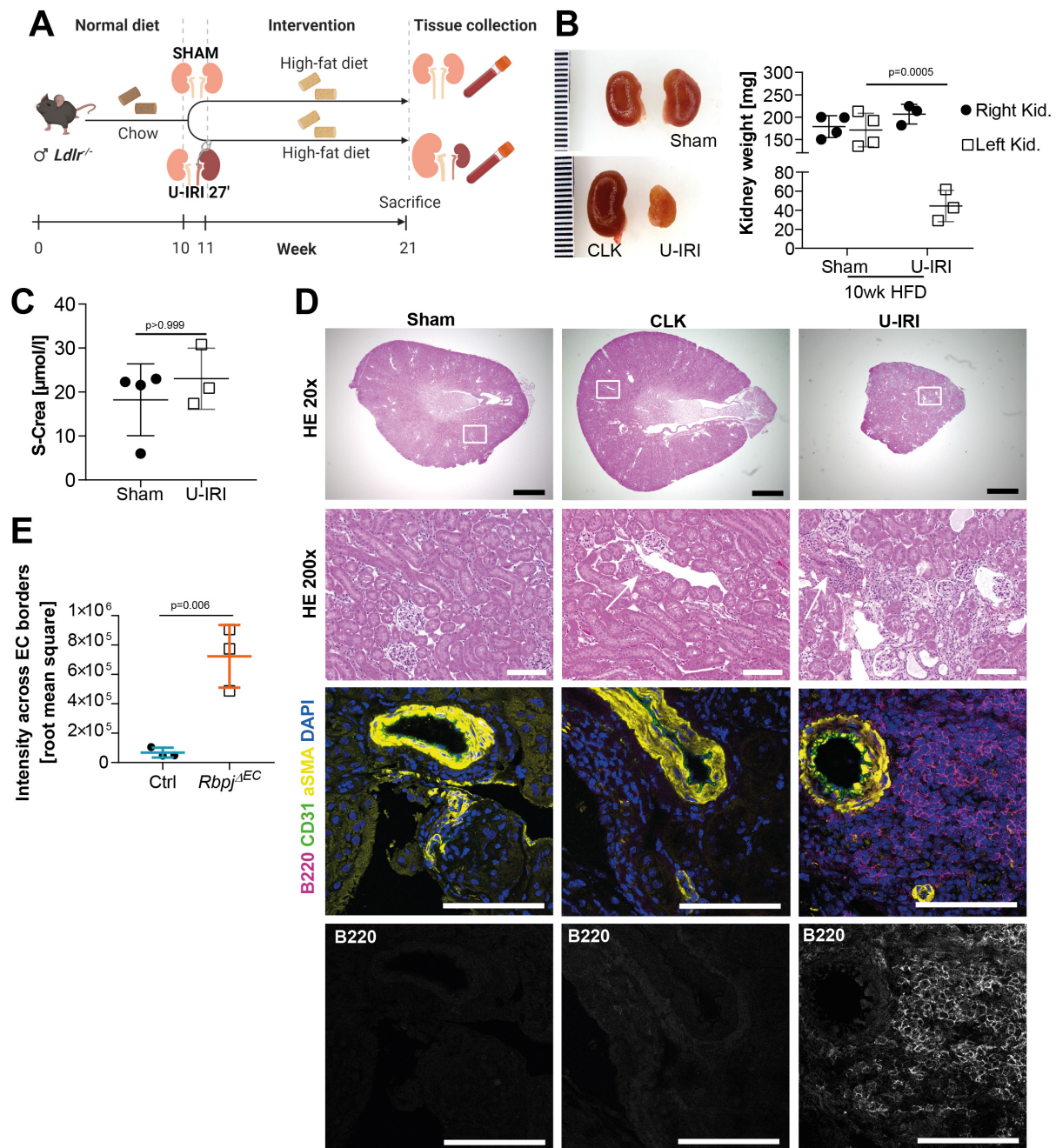


Supplementary Figure 3: Gene / transgene expression in Stat3 Δ Myoc and Prox1Cre^{ERT2} recombination control kidneys

A) Kidney mRNA expression of Cxcl13 (p=0.310), Cxcl12 (p=0.587), Cxcr4 (p=0.286), Cxcr5 (p=0.841) and Ccl19 (p=0.548) in Stat3 Δ Myoc vs. Control. N=5/group. Scatter dot

plots with mean and SD (whiskers), two-tailed Mann Whitney test. Experiment repeated 2x with similar results. Source data are provided with this paper.

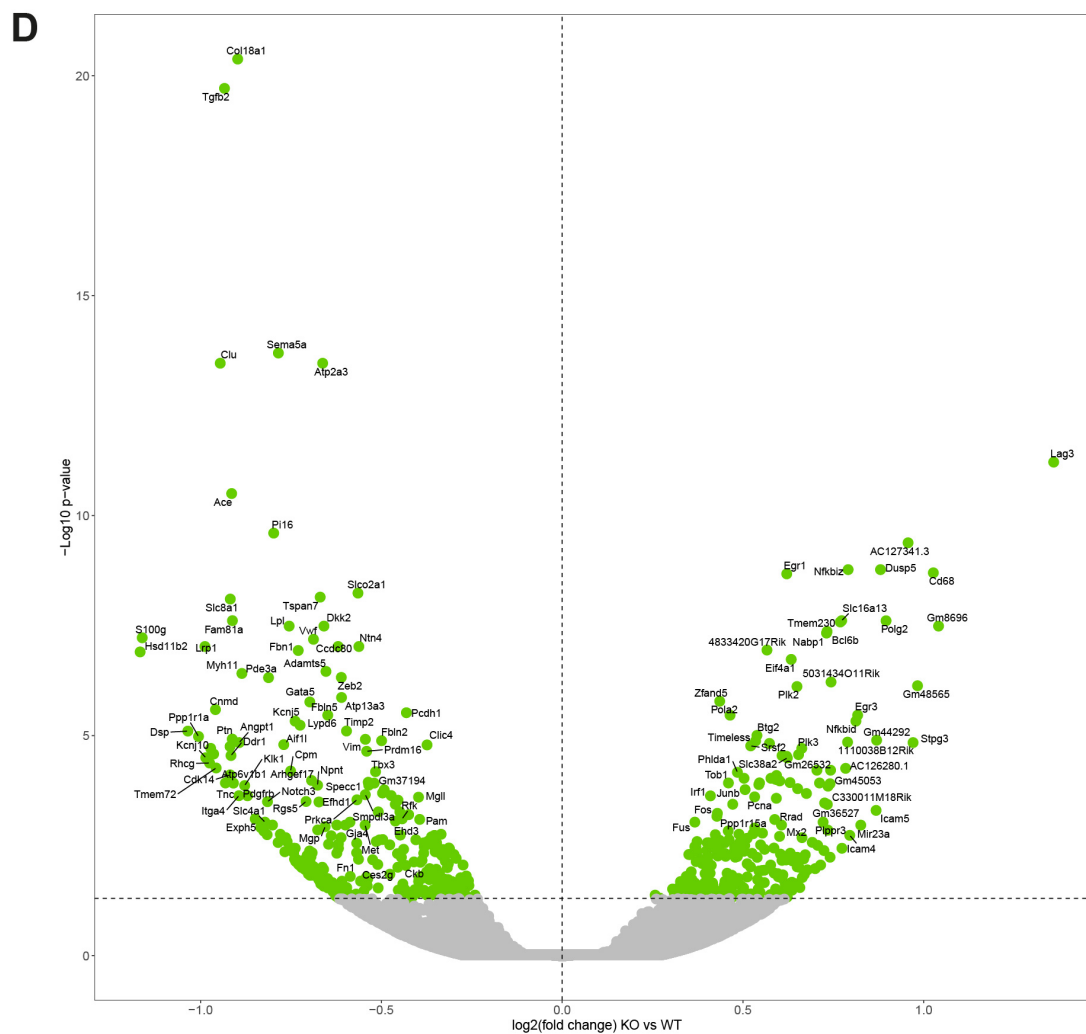
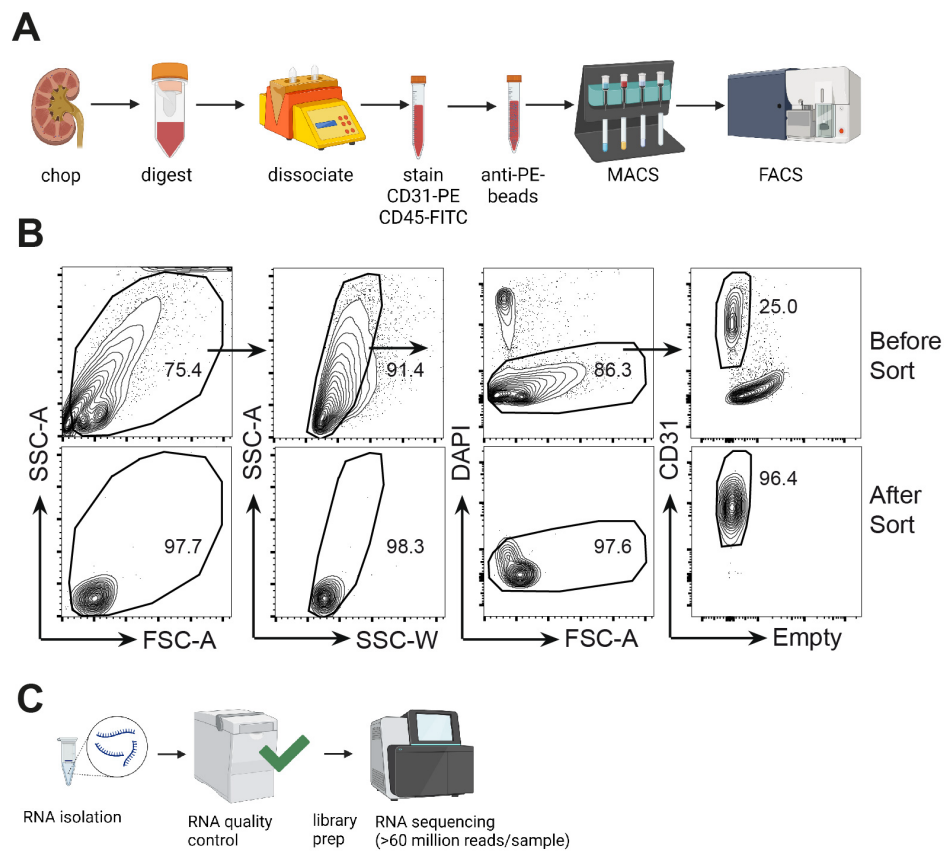
B and **C**: Recombination control of *Prox1Cre^{ERT2}* expression in adult mouse kidney (*Prox1Cre^{ERT2};mTmG* mouse model). Prox1-GFP in green, Lyve1-costaining in red. Exemplary pictures, several sections on different levels of the kidney were stained from n=2 mice. **A**) cortex area; **B**) inner medulla/papilla area. All scale bars 50µm.



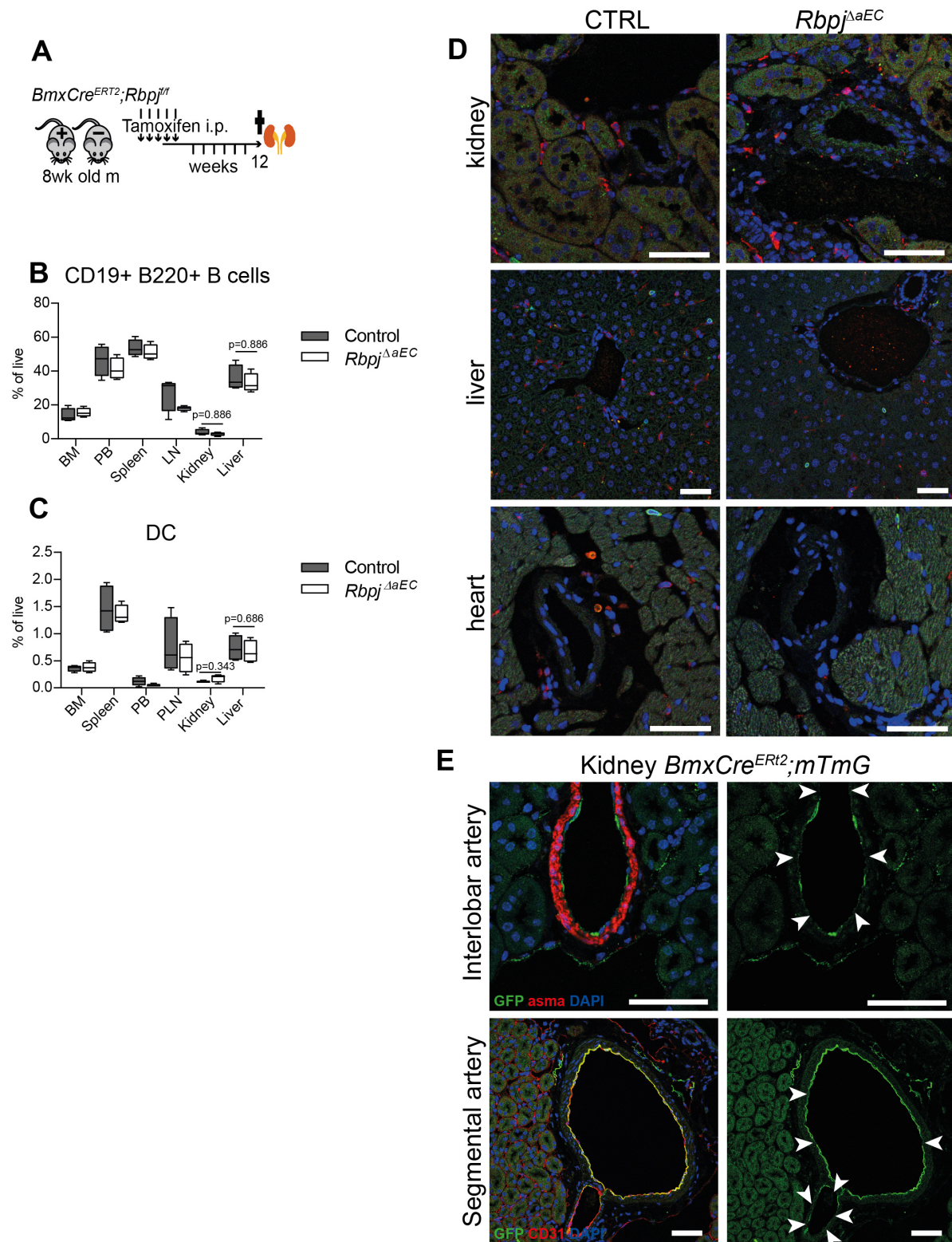
Supplementary Figure 4: Inflammatory kidney damage model using unilateral IRI and high fat diet. **A)** Sketch of experimental protocol. 4A-D, n=4 Ctrl, n=3 U-IRI. **B)** Kidneys of Sham and U-IRI mice, mm-scale on left. Right panel, kidney weight in mg. Scatter dot plot with mean and SD (whiskers), *** $p=0.0005$, Multiple T tests, Two-stage linear step-up procedure of Benjamini, Krieger and Yekutieli, with $Q = 1\%$. **C)** serum creatinine, scatter dot blot, mean, SD (whiskers). $P=0.99$, two-tailed Mann Whitney test. **D)** HE (upper panels; arrow, arterial lumen) and B220 CD31 αSMA immunofluorescence costaining (third panel, lowest panel B220 channel only) in

Sham, contralateral kidney and U-IRI kidney. Representative images of n=4 Sham mice and n=3 CLK/U-IRI kidneys. Scale bars: Black bar, 1mm; white bars 100 μ m.

E) Referring to figure 4: Quantification of PNAd staining on kidney endothelium; root mean square of greyscale intensity values across EC borders. Scatter dot plot with mean and SD (whiskers). n=3 mice/group, p=0.0063. Source data are provided with this paper.



Supplementary Figure 5: RNA seq cell-isolation strategy and analysis. **A)** Sketch of EC single cell isolation and enrichment protocol, A, C created with biorender.com. **B)** CD31⁺ cell purity after MACS-Sorting (upper panel, input) and after FACS-sorting (lower panel) **C)** From single EC to RNAseq: 2ng of RNA were used for library preparation with the w 'SMARTer Stranded Total RNA-Seq Kit v2 – Pico Input Mammalian' (Takara). Generated libraries were barcoded by dual indexing approach and were finally amplified with 12 cycles of PCR. **D)** Volcano plot showing in green the genes significantly up- or downregulated in *Rbpj*^{ΔEC} EC ("KO") as compared to control EC ("WT"), at a threshold of adj. p-value < 0.05 (See methods section and supplementary data file 1,4.)



Supplementary Figure 6: Arterial EC-specific deletion of *Rbpj*.

A) Experimental outline analogous to Fig. 1A. **B)** Flow cytometry of B lymphocytes across bone marrow, blood, spleen, lymph node, kidney and liver from *BmxCre^{ERT2};Rbpj^{fl/fl}* mice and Cre-negative littermates. N=4 mice/group. **C)** Flow cytometry of dendritic cells across the same organ panel. N=4 mice/group. B and C: box plots with mean (line), 25-75% (box) and min/max (whiskers). Two-tailed Mann

Whitney test. Source data are provided with this paper. **D)** Immunofluorescence staining of B220 (green) and CD3 (red) in Ctrl and BMX-cre mediated Rbpj knockout, representative images, n= 4 mice/group. **E)** *BMX-Cre^{ERT2};mTmG* recombination control induced in adult age; rehydrated paraffin sections. Several kidney sections from different areas stained from n=2 mice. Green, GFP visualized via anti-GFP-Antibody, shows Cre-mediated recombination. Other channels as indicated. White arrow heads point to non-recombined endothelial cells. All scale bars in D and E, 50µm.

Supplementary Table 1: List of antibodies used for flow cytometry.

Antibody	Clone	Label		Company	Cat. #
CD32/16	93	Unlabeled	1:200	Biolegend	101319
CD45	30-F11	AF700	1:400	Biolegend	103128
F4/80	BM8	APC	1:100	Biolegend	123116
CX3CR1	SA011F11	PE	1:200	Biolegend	149005
CD115	AFS98	AF488	1:200	Biolegend	135511
CD117	2B8	APC-Cy7	1:100	Biolegend	105803
CD19	6D5	Bio	1:400	Biolegend	115504
CD19	6D5	PE-Cy7	1:400	Biolegend	115519
B220	RA3-6B2	Bio	1:400	Biolegend	103203
B220	RA3-6B2	BV650	1:400	Biolegend	103241
CD3	17A2	Bio	1:200	Biolegend	100243
CD3	17A2	Pacific Blue	1:200	Biolegend	100213
Ter119	Ter119	Bio	1:400	Biolegend	116203
NK1.1	PK136	Bio	1:200	Biolegend	108704
NK1.1	PK136	PE	1:200	Biolegend	108707
Ly6G	1A8	Bio	1:400	Biolegend	127603
CD11b	M1/70	Pacific Blue	1:400	Biolegend	101224
Ly6C	HK1.4	PE-Cy7	1:1400	Biolegend	128018
I-A/I-E	M5/114.15.2	BV510	1:400	Biolegend	107635
CD11c	N418	BV605	1:400	Biolegend	117334
CD31	390	FITC	1:100	Serotec	MCA1364F
CD21/35	7E9	APC-Cy7	1:400	Biolegend	123417
CD23	B3B4	Pacific Blue	1:200	Biolegend	101615
IgM	RMM-1	PE	1:100	Biolegend	406507
IgD	11-26c.2a	AF647	1:400	Biolegend	405707
CD4	GK1.5	APC-Cy7	1:200	Biolegend	100413
CD8a	53-6.7	BV650	1:400	Biolegend	100741
CD43	S7	PerCP-Cy5.5	1:400	BD Pharmingen	562865
CD43	S11	PerCP-Cy5.5	1:400	Biolegend	143219
CD144	11D4.1	PE	1:100	BD Pharmingen	562243
Streptavidin		PE-Dazzle 594	1:400	Biolegend	405247

Supplementary Table 2: List and sequences of primer pairs used for QPCR.

Gene name	Forward-Primer	Reverse-Primer
<i>Rps9</i>	GGA TTT CTT GGA GAG GCG GC	ACC TGC TTG CGG ACC CTA AT
<i>Havcr1 (Kim1)</i>	ATG AAT CAG ATT CAA GTC TTC	TCT GGT TTG TGA GTC CAT GTG
<i>Cxcl13</i>	TGA GGC TCA GCA CAG CAA	ATG GGC TTC CAG AAT ACC G
<i>Cxcl12</i>	CCA AAC TGT GCC CTT CAG AT	ATT TCG GGT CAA TGC ACA CT
<i>Cxcr4</i>	TGG AAC CGA TCA GTG TGA GT	GGG CAG GAA GAT CCT ATT GA
<i>Cxcr5</i>	GTG ACC TCT CTC GGC TTC TG	AGA CTA CTC TTG CGC CAG TTG
<i>Hey1</i>	GCG CGG ACG AGA ATG GAA AC	GGC GCT TCT CGA TGA TGC CT
<i>Dll1</i>	TCC GAT TCC CCT TCG GCT TC	TGG GTT TTC TGT TGC GAG GT
<i>Dll4</i>	GGC CGG GAA CCT TCT CAC TC	TTT CCT GGC GAA GTC TCT GGC
<i>Il7</i>	TCT GCT GCC TGT CAC ATC ATC	GGA CAT TGA ATT CTT CAC TGA TAT TCA
<i>Jagged1</i>	CAA ATG AGT GCG AGG CCA AAC CTT	AGC CAG GAA GGC AAT CAC AGT AGT
<i>Notch1</i>	AGT GTC AGA GGC CAG CAA GAA GAA	TGA TTG TCG TCC ATC AGA GCA CCA
<i>EphrinB2</i>	TTC TGC TGG ATC AGC CAG GAA TCA	ACC TGG ATT TGG CTT CAC AAA GGG
<i>Vcam1</i>	TCT TAC CTG TGC GCT GTG AC	ACT GGA TCT TCA GGG AAT GAG T
<i>Madcam</i>	TGT CAG ACA CAG GCA CTC CT	AAG GAA CTC CGG GGA CAC
<i>Sell</i>	CCA TGG AAC TCA CTG TTG GA	AAA TCT GTG TAA TTT TGC TTG CAG
<i>Selp</i>	AAT GCC CCT TGA ACC CTC AC	GAC CGG GTT TCT TAA GGG GT
<i>Rankl</i>	GGA TGA AAC AAG CCT TTC AGG	ACA TCC AAC CAT GAG CCT TC
<i>Ccl21</i>	TCC AAG GGC TGC AAG AGA	TGA AGT TCG TGG GGG ATC T
<i>Baff</i>	CAG GGA CCA GAG GAA ACA GA	TTT CTG AGG TTC ATT CCA TTA TCA
<i>Ap1nr</i>	GTG CTC TGG ACC GTG TTT C	CAC CAC AAA GGT CAA GTC AGC
<i>Nppa</i>	GCC GGT AGA AGA TGA GGT CA	GGG CTC CAA TCC TGT CAA TC