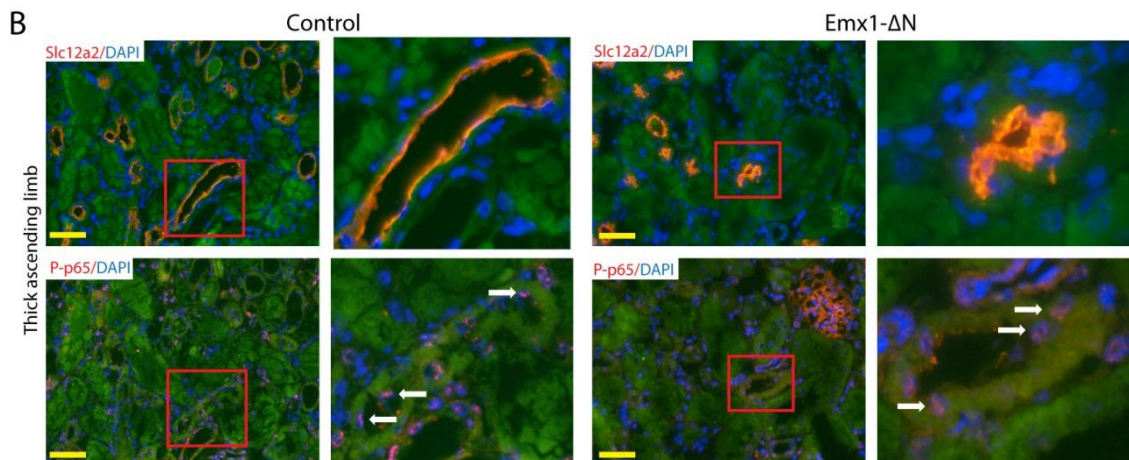
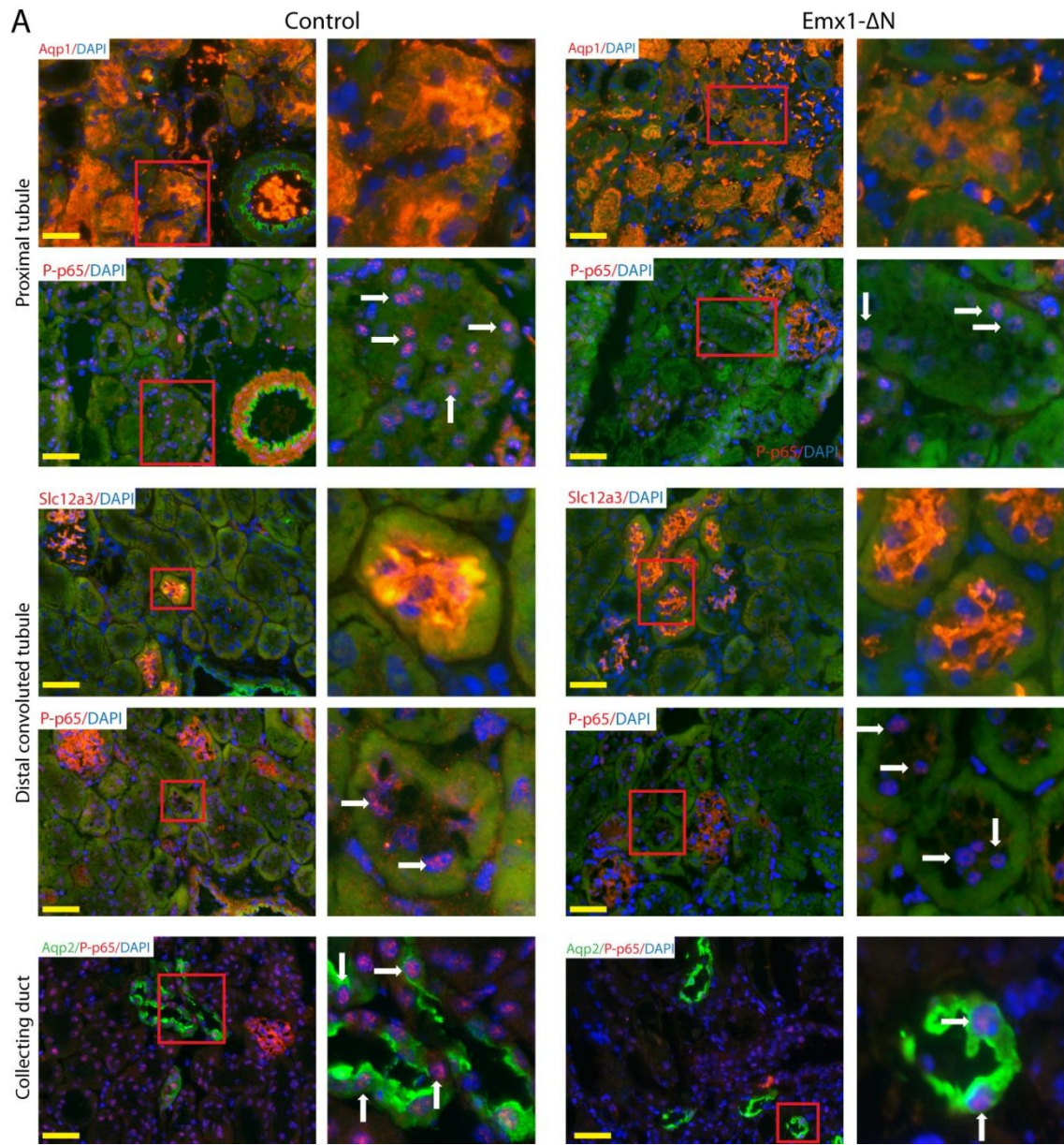
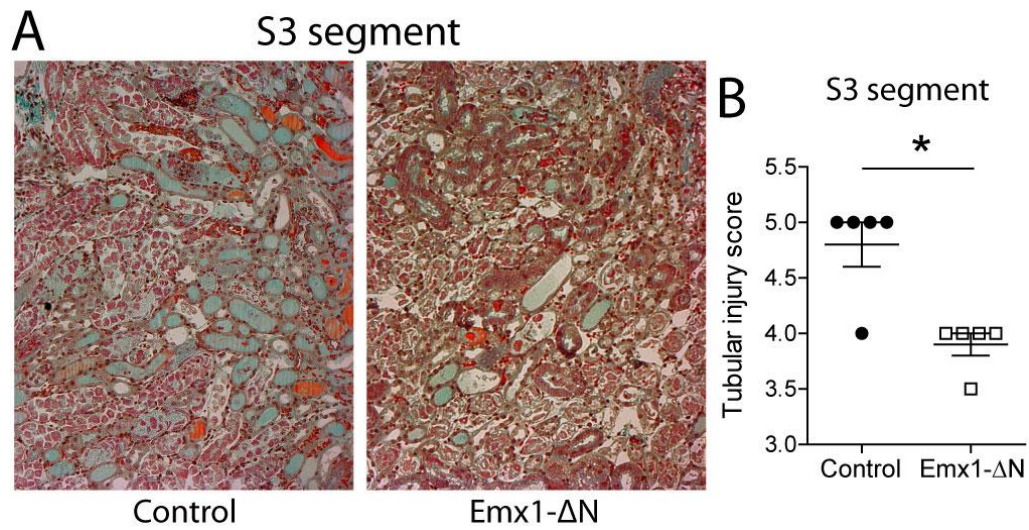


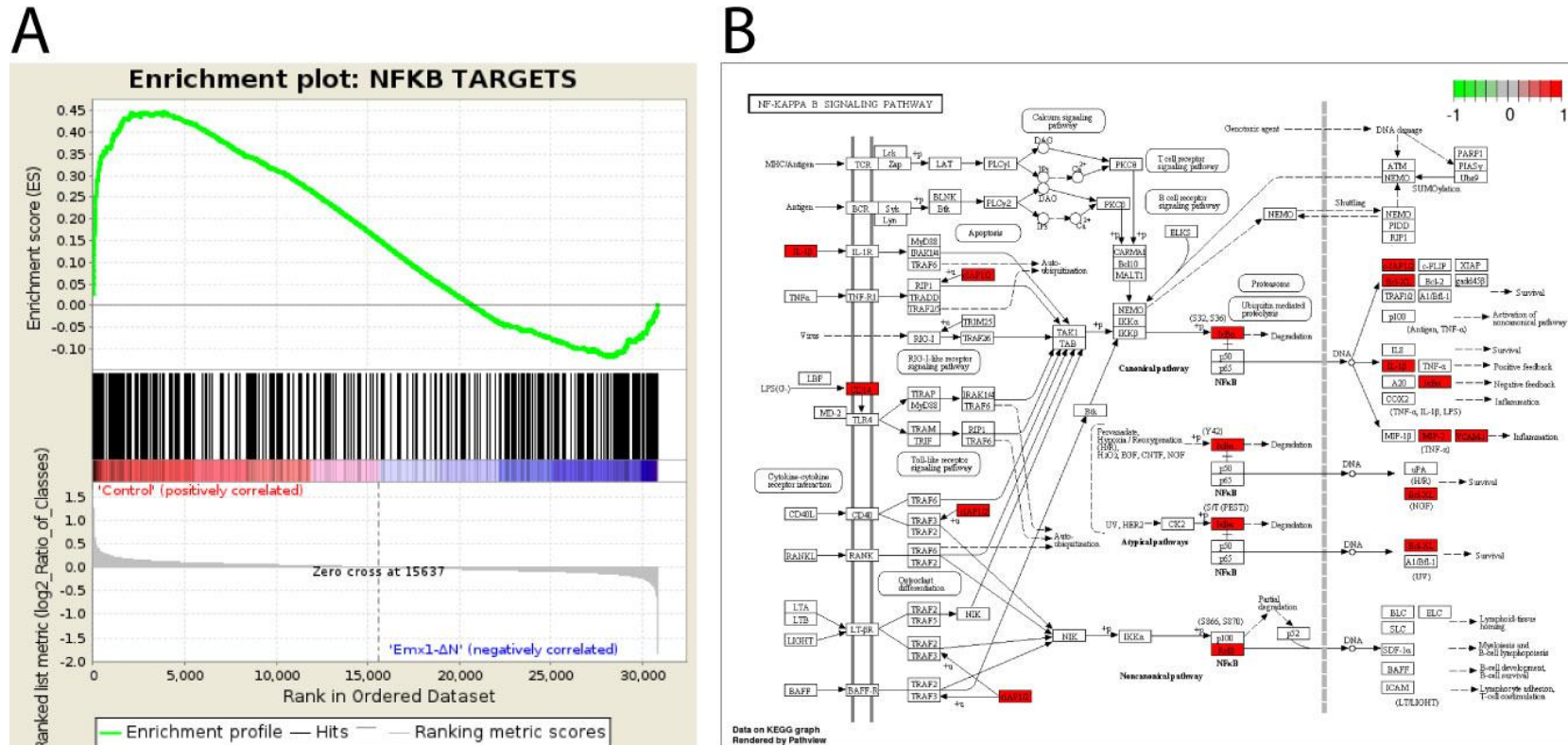
Supplemental Figure 1. (A) Analysis of renal tubular Cre activity in *Emx1-Cre/Rosa 26 reporter (R26R)* mice, which display *Emx1-Cre*-mediated activation of β -galactosidase. (B) Full membrane of Western blot for $I\kappa B\alpha$ protein expression. Kidney tissue lysates of *Emx1-ΔN* mice display the truncated $I\kappa B\alpha\Delta N$ fragment, while controls (wildtype (WT), *Emx1-Cre* and *loxP-I\kappa B\alpha\Delta N*) do not. Kidney tissue lysates of *I\kappa B\alpha\Delta N^{ubi}* mice, which constitutively express $I\kappa B\alpha\Delta N$ in all cells, served as positive control. (C) Representative cortical and medullar images of *Emx1-ΔN* and control mice after anti-P-p65 antibody staining 24 hours post ischemic AKI. Yellow bar represents 50 μ m.



Supplemental Figure 2. Analysis of renal tubular P-p65 expression in ischemic-injured kidneys of control and *Emx1-ΔN* mice by immunostaining using antibodies against (A) P-p65, aquaporin-1 (Aqp1), sodium-chloride symporter (Slc12a3), aquaporin-2 (Aqp2) and (B) P-p65 and sodium-potassium-chloride cotransporter 2 (Slc12a2) to verify NF-κB activity in the different tubular segments after ischemic injury. Red squares mark equivalent tubular sections represented on adjacent sections. Green is autofluorescent if other not stated. White arrows point to S276 P-p65 staining. Yellow bar represents 50 μm.



Supplemental Figure 3. (A) Representative images of Masson's trichrome stain of control and *Emx1-ΔN* kidneys in the S3 segment 24 hours after ischemic AKI (x400). (B) Semi-quantification of the tubular injury. $n_{\text{control}}=5$, $n_{\text{Emx1-}\Delta\text{N}}=5$, * $P<0.05$, Student's t-test.



Supplemental Figure 4. (A) Gene set enrichment analysis on microarray data from kidney samples of *Emx1-ΔN* and control mice 24 hours after induction of ischemia. All genes were sorted according to their fold change (control/*Emx1-ΔN*). We then used a set of known NF-κB targets from <http://www.bu.edu/nf-kb/gene-resources/target-genes/> as a target set. As can be seen from the green plot, known NF-κB targets show a significant enrichment in genes that are down-regulated in *Emx1-ΔN* mice when compared to controls (FDR<0.01). (B) Visualization of differentially expressed genes in the NF-κB signaling pathway from Kyoto Encyclopedia of Genes and Genomes (KEGG) using the R package Pathview. The respective genes are highlighted according to their absolute fold change (control/*Emx1-ΔN*) as indicated by the color bar.

Supplemental Table 3. Serum and urine parameters of *Emx1-ΔN* and littermate control mice. n.a.= not applicable.

Serum parameter	Unit	Control		Emx1-ΔN		P-value
		Mean	SD	Mean	SD	
Sodium	mmol/L	148.00	4.00	147.43	3.41	0.82
Potassium	mmol/L	6.80	0.53	6.44	0.86	0.53
Chloride	mmol/L	111.67	1.15	110.57	1.99	0.41
Ionized Calcium	mmol/L	1.06	0.15	1.03	0.13	0.76
Total Carbon Dioxide	mmol/L	22.00	4.36	24.57	2.88	0.29
Glucose	mg/dL	176.33	20.31	170.14	17.57	0.64
Urea Nitrogen	mg/dL	10.23	2.66	8.90	0.82	0.24
Creatinine	umol/L	<18	n.a.	<18	n.a.	n.a.
Hematocrit	% PCV	39.67	3.21	41.00	4.40	0.65
Hemoglobin	g/dL	13.47	1.12	13.96	1.49	0.63
Anion Gap	mmol/L	22.00	1.00	19.71	1.50	0.07

Urine parameter	Unit	Control		Emx1-ΔN		P-value
		Mean	SD	Mean	SD	
Sodium	μmol/g/day	5.19	2.18	5.70	0.46	0.70
Creatinine	μmol/g/day	0.11	0.03	0.11	0.03	0.86
Osmolarity	mOsm/kg	1049.00	168.58	1106.33	82.31	0.60

Supplemental Table 4. Primer sequences for quantitative real-time PCR.

Gene	Forward	Probe	Reverse
18s	5'-ACATCCAAGGAAGGCAGCAG-3'	5'-FAM-CGCGCAAATTACCCACTCCCGAC-TAMRA-3'	5'-TTTTCGTCACTACCTCCCCG-3'
NFKBIA	5'-CTGCACACCCCAGCATCTC-3'	5'-FAM-ACTCCGTCCTGCAGGCCACCAA-TAMRA-3'	5'-CAGACACGTGTGGCCATTGT-3'
NGAL	5'-TGATCCCTGCCCCATCTCT-3'	5'-FAM-TCACTGTCCCCCTGCAGCCAGA-TAMRA-3'	5'-GGAAGTATCGCTCCGGAA-3'
CD14	5-CAGCCCTCTGTCCCCTCAA-3	-	5-TCTCCATCCCCGCGTTAC-3
S100A8	5'-TCACCATGCCCTCTACAAGA-3'	-	5'-CCAATTCTCTGAACAAGTTTTTCG-3'
S100A9	5'-TCAGACAAATGGTGAAGCA-3'	-	5'-GTCCAGGTCCTCCATGATGT-3'
IL1B	5'-AGAAGAGCCCATCCTCTGTGACTCATGG-3'	5'-FAM-AGAAGAGCCCATCCTCTGTGACTCATGG-TAMRA-3'	5'-CACACACCAGCAGGTTATCATCA-3'
IL6	5'- TGTCTCGAGCCCACCAGG-3'	5'-FAM-CGAAAGTCAACTCCATCTGCCCTTCAGG-TAMRA-3'	5'- TGCGGAGAGAACTTCATAGCTG-3'
CXCL1	5'-CTGCACCCAAACCGAAGTC-3'	-	5'- AGCTTCAGGGTCAAGGCAAG-3'
CXCL2	5'-GGGCGGTCAAAAAGTTTGC-3'	5'-FAM-TTGACCCTGAAGCCCCCTGGT-TAMRA-3'	5'-TGTTCAAGTATCTTTGGATGATTTTCTG-3'
VEGFA	5'-CTGTAACGATGAAGCCCTGGAG-3'	-	5'-TGGTGAGGTTTGGATCCGCAT-3'

