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Supplementary Spreadsheet 1. RNAseq data in Gprc5b-cKO and control glomeruli 24h after the injection of LPS.

Supplementary Spreadsheet 2. RNAseq data in wild type glomeruli 0h and 24h after the injection of LPS.

Supplementary Figure 1. Gprc5b expression in various mouse models of glomerulopathy. (A) Microarray data extracted from previously published data sets (23-27) and an in-house data sets (db/db in 129 male mice, adriamycin nephropathy in 8-week old BALB/c male mice). In LPS-induced glomerular damage a strong up-regulation of Gprc5b is detected whereas other models do not show significant changes or no consistent induction. NPH=nephrin KO, DMS=diffuse mesangial sclerosis (Denysh-Drash syndrome), VHL=von-hippel-lindau nephropathy; OVE26=Ove26 mice overexpressing calmodulin in pancreatic β-cells, ADM=Adriamycin-induced nephropathy. (B) qPCR analysis of Gprc5b expression in glomeruli isolated from streptozotocin-induced nephropathy (STZ, 8-week old FVB male mice) shows significant up-regulation of Gprc5b.

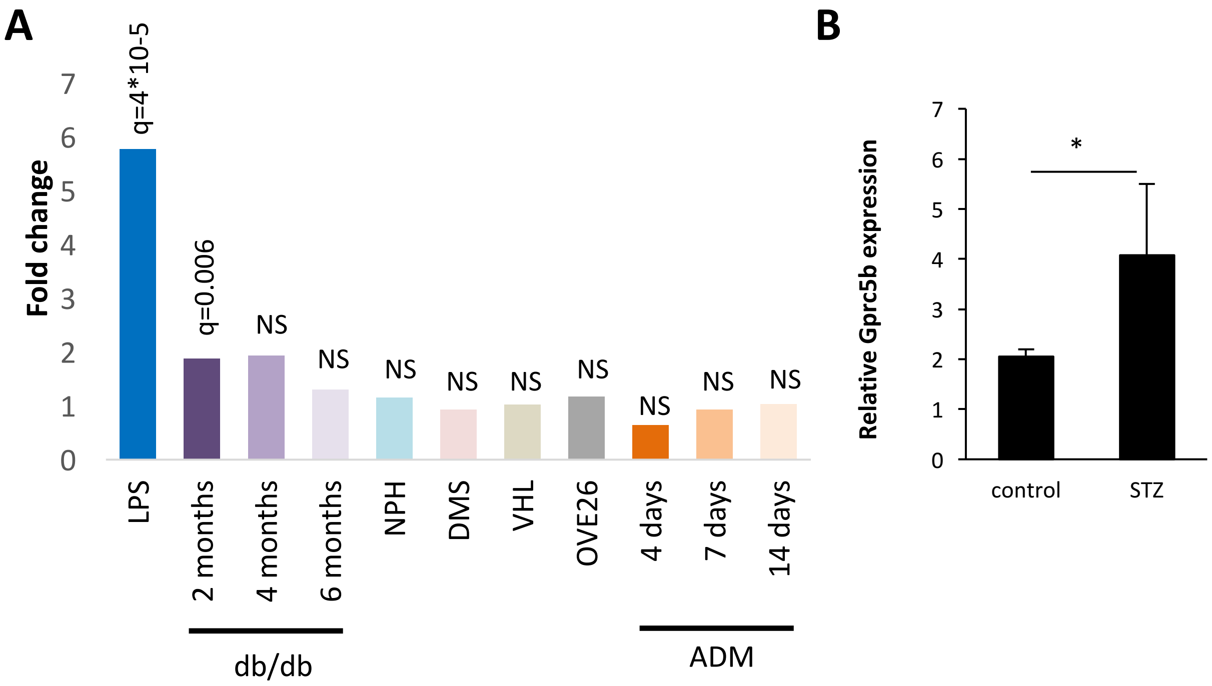
Supplementary Figure 2. Histological evaluation of kidneys 36h after LPS-injection. (A) Histological analysis (PAS staining) of kidneys 36h after the LPS injection shows apparently normal morphology in Gprc5b-cKO and control samples. (B) Both Gprc5b-cKO and control mice exhibit podocyte foot process effacement 36h after the injection, but no significant difference between groups is detected by counting numbers of slits / GBM length. Magnifications: x40 in A; Scale bar: B = 250nm.

Supplementary Figure 3. Table of the most significantly affected pathways in Gprc5b-cKO glomeruli when compared to control glomeruli collected 24h after the LPS injection. A total of 164 significantly affected pathways was identified, here we show the 40 most significantly affected pathways ($P<0.001$ and $FDR < 0.1$).

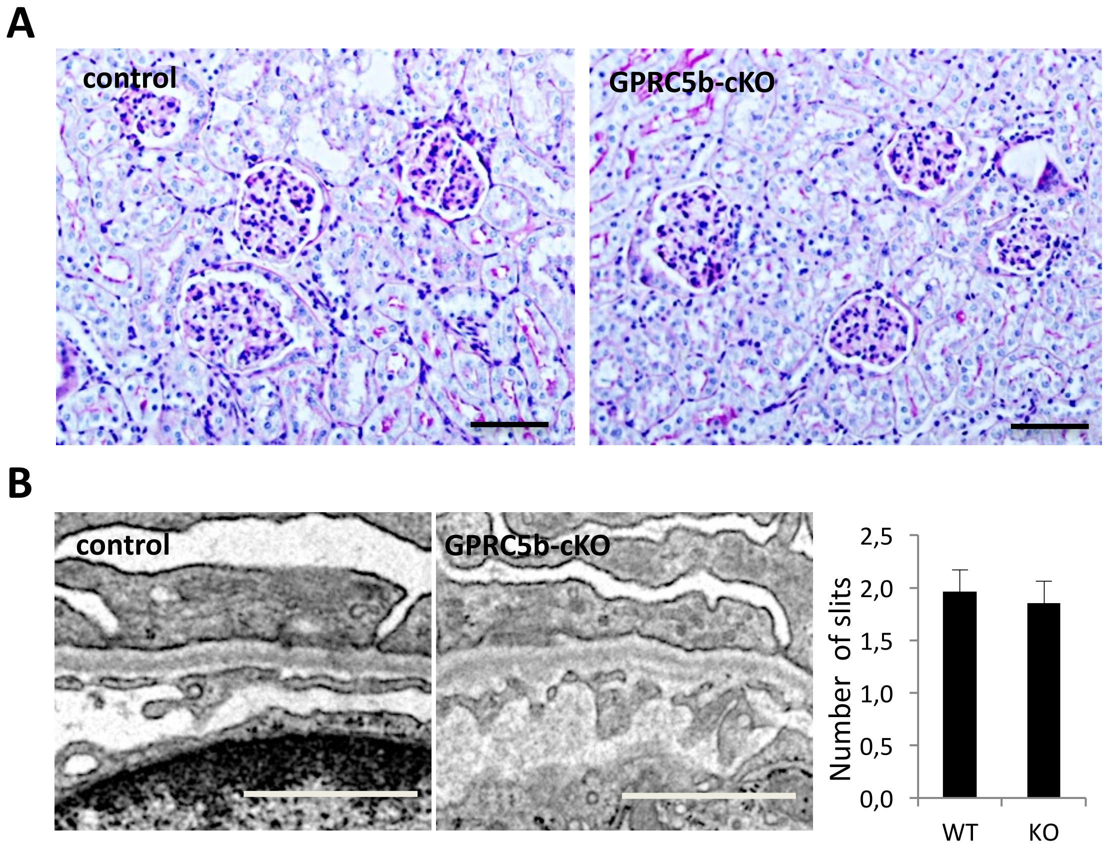
Supplementary Figure 4. Comparison of glomerular transcriptomes between 0 and 24h after LPS injection in control animals. (A) The expression of five family members of NF-κB are significantly up-regulated after 24h when compared to glomeruli collected from uninjected (0h) glomeruli as shown by RNA sequencing. (B) The expression of down-stream targets of NF-κB activation, TNF-α, IL-6, IL-1B, ICAM1, NF-κB inhibitor alpha (NF-kBIA) and NF-κB inbitor beta (NF-kBIB) are up-regulated 24h after LPS-injection. * $p<0.05$.

Supplementary Figure 5. Analysis of different pathways up-stream of NF-κB activation in Gprc5b-expressing cells. (A) No significant differences were detected in the levels of activation of FYN, STAT3, Smad2, ERK, AKT and caspase 3 between Gprc5b over-expressing and control cells as shown by Western blotting for activated forms of these proteins. Actin was used as a loading control. (B-C) Inhibition of EGF-activation with AG1478 does not affect the activation of P65 as detected by blotting for the phosphorylated form of the protein. (D-E) Inhibition of β-catenin pathway with IWP-2 does not affect the activation of P65 as detected by blotting for the phosphorylated form of the protein.

Supplementary figure 1



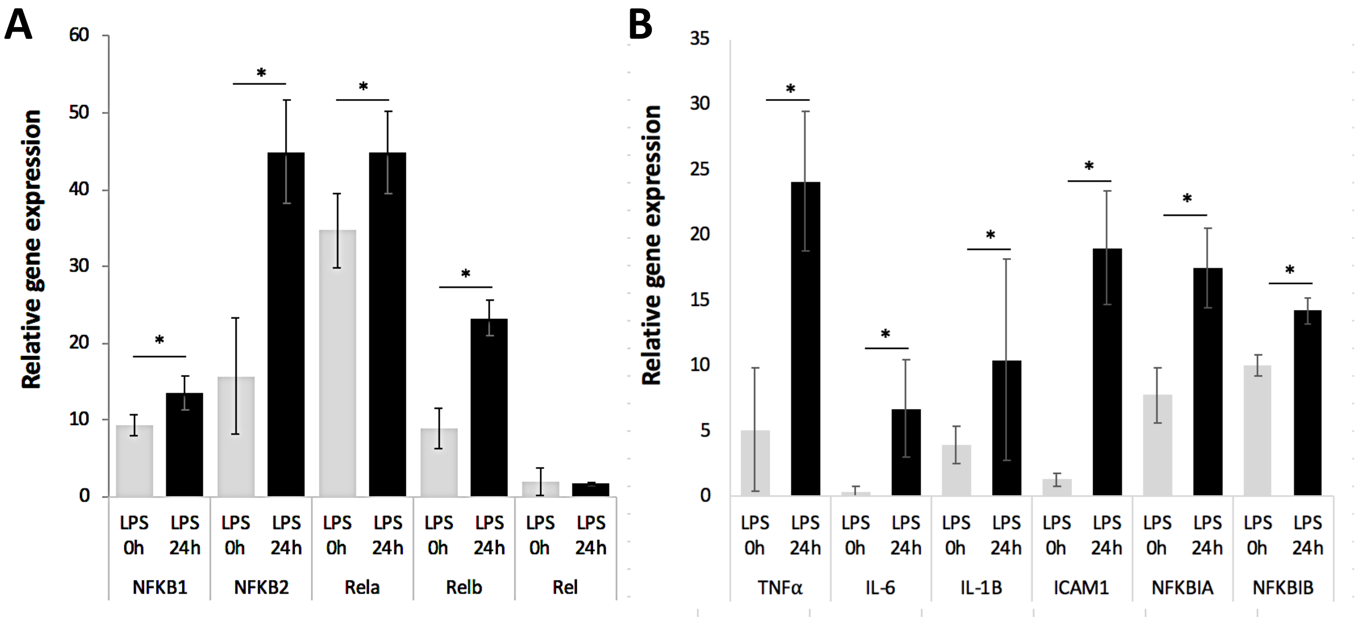
Supplementary Figure 2



Supplementary Figure 3

Pathway Ids	Descriptions	Matched genes	P values	FDR
path:mmu00030	Pentose phosphate pathway - Mus musculus	29 of 31	0.00	0.01
path:mmu00040	Pentose and glucuronate interconversions - Mus musculus	32 of 36	0.00	0.01
path:mmu00053	Ascorbate and aldarate metabolism - Mus musculus	23 of 27	0.00	0.01
path:mmu00140	Steroid hormone biosynthesis - Mus musculus	57 of 87	0.00	0.01
path:mmu00190	Oxidative phosphorylation - Mus musculus	133 of 139	0.00	0.01
path:mmu00230	Purine metabolism - Mus musculus	173 of 179	0.00	0.01
path:mmu00240	Pyrimidine metabolism - Mus musculus	102 of 104	0.00	0.01
path:mmu00562	Inositol phosphate metabolism - Mus musculus	69 of 70	0.00	0.01
path:mmu00591	Linoleic acid metabolism - Mus musculus	33 of 50	0.00	0.01
path:mmu00630	Glyoxylate and dicarboxylate metabolism - Mus musculus	29 of 30	0.00	0.01
path:mmu00640	Propanoate metabolism - Mus musculus	31 of 31	0.00	0.01
path:mmu00830	Retinol metabolism - Mus musculus	63 of 89	0.00	0.01
path:mmu00980	Metabolism of xenobiotics by cytochrome P450 - Mus musculus	58 of 65	0.00	0.01
path:mmu00983	Drug metabolism - other enzymes - Mus musculus	45 of 51	0.00	0.01
path:mmu03008	Ribosome biogenesis in eukaryotes - Mus musculus	78 of 83	0.00	0.01
path:mmu03010	Ribosome - Mus musculus	136 of 148	0.00	0.01
path:mmu03013	RNA transport - Mus musculus	156 of 170	0.00	0.01
path:mmu03015	mRNA surveillance pathway - Mus musculus	88 of 96	0.00	0.01
path:mmu03018	RNA degradation - Mus musculus	73 of 83	0.00	0.01
path:mmu03020	RNA polymerase - Mus musculus	30 of 30	0.00	0.01
path:mmu03030	DNA replication - Mus musculus	35 of 35	0.00	0.01
path:mmu03040	Spliceosome - Mus musculus	129 of 135	0.00	0.01
path:mmu03050	Proteasome - Mus musculus	45 of 45	0.00	0.01
path:mmu03060	Protein export - Mus musculus	27 of 31	0.00	0.01
path:mmu03410	Base excision repair - Mus musculus	35 of 35	0.00	0.01
path:mmu04060	Cytokine-cytokine receptor interaction - Mus musculus	232 of 265	0.00	0.01
path:mmu04062	Chemokine signaling pathway - Mus musculus	186 of 198	0.00	0.01
path:mmu04064	NF-kappa B signaling pathway - Mus musculus	94 of 104	0.00	0.01
path:mmu04080	Neuroactive ligand-receptor interaction - Mus musculus	207 of 285	0.00	0.01
path:mmu04110	Cell cycle - Mus musculus	123 of 125	0.00	0.01
path:mmu04120	Ubiquitin mediated proteolysis - Mus musculus	139 of 145	0.00	0.01
path:mmu04141	Protein processing in endoplasmic reticulum - Mus musculus	162 of 167	0.00	0.01
path:mmu04142	Lysosome - Mus musculus	119 of 124	0.00	0.01
path:mmu04144	Endocytosis - Mus musculus	272 of 294	0.00	0.01

Supplementary Figure 4



Supplementary figure 5