

Supplementary Figure

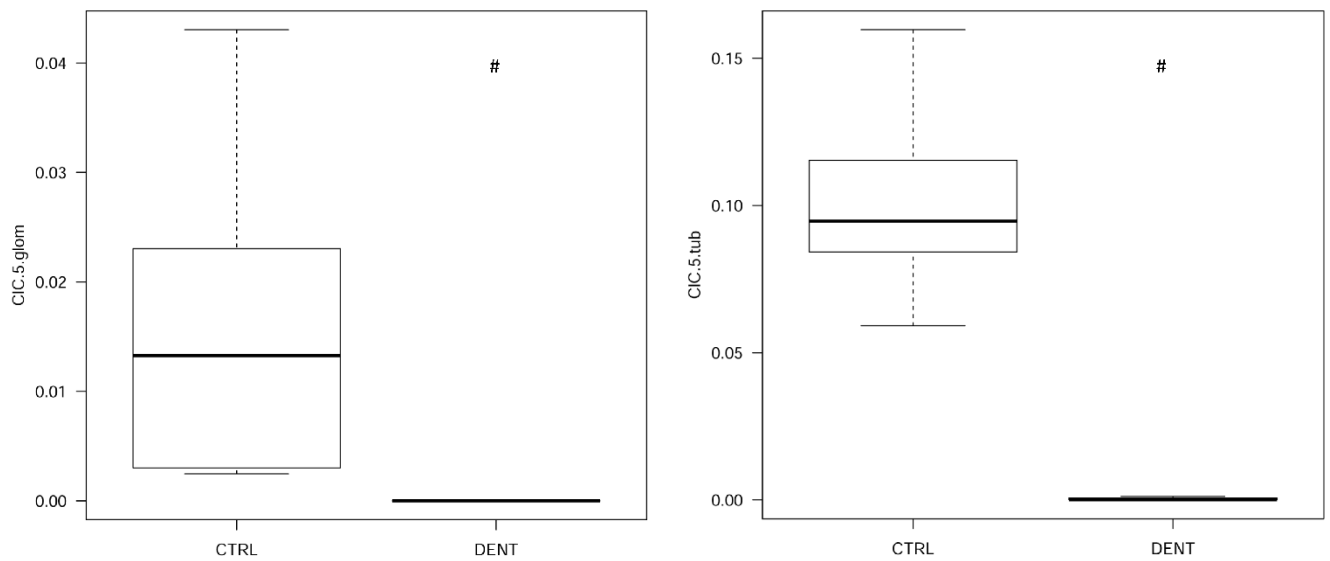


Figure S1. Morphometric evaluation of CIC-5 in CTRL and DD1 biopsies in both tubular and glomerular compartments. CIC-5 resulted down-regulated in DD1 vs CTRL (# $p < 0.01$) in both glomerular and tubular compartments. Boxplots show medians and interquartile ranges of IHC staining scores (% positive area).

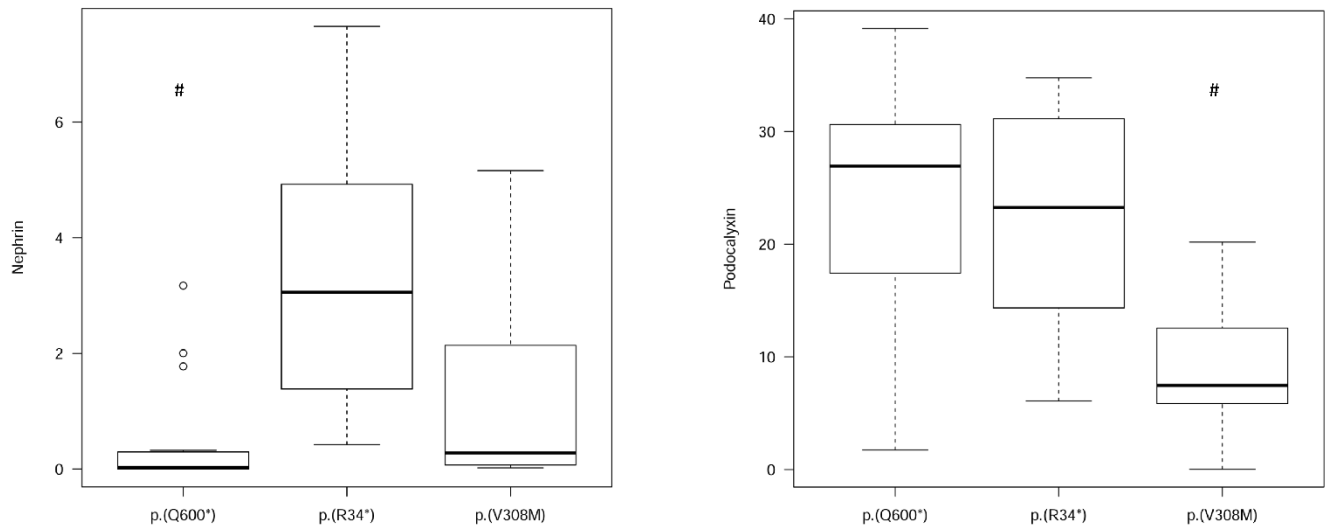


Figure S2. Morphometric evaluation of nephrin and podocalyxin in DD1 biopsies from patients carrying different *CLCN5* mutations. The patient carrying the p.(Q600*) mutation shows the highest down-regulation of Nephrin (# $p < 0.01$). The patient carrying the p.(V308M) mutation shows the highest down-regulation of Podocalyxin (# $p < 0.01$). The lowest change in both markers was seen in the patient carrying the p.(R34*) mutation. Boxplots show medians and interquartile ranges of IF staining scores (% positive area).

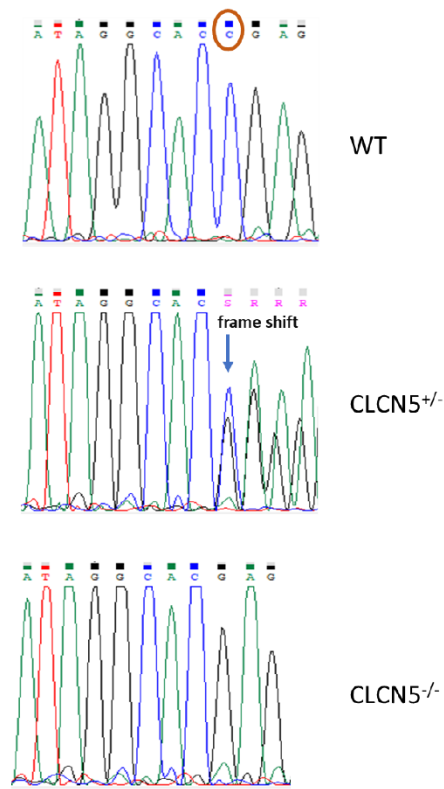


Figure S3. *CLCN5* gene editing in podocyte cells by CRISPR-Cas9 technology. Representative image of Sanger sequencing of PCR products of exon 2 from WT, *CLCN5*^{+/-} and *CLCN5*^{-/-} clones. The c.100delC mutation is shown.

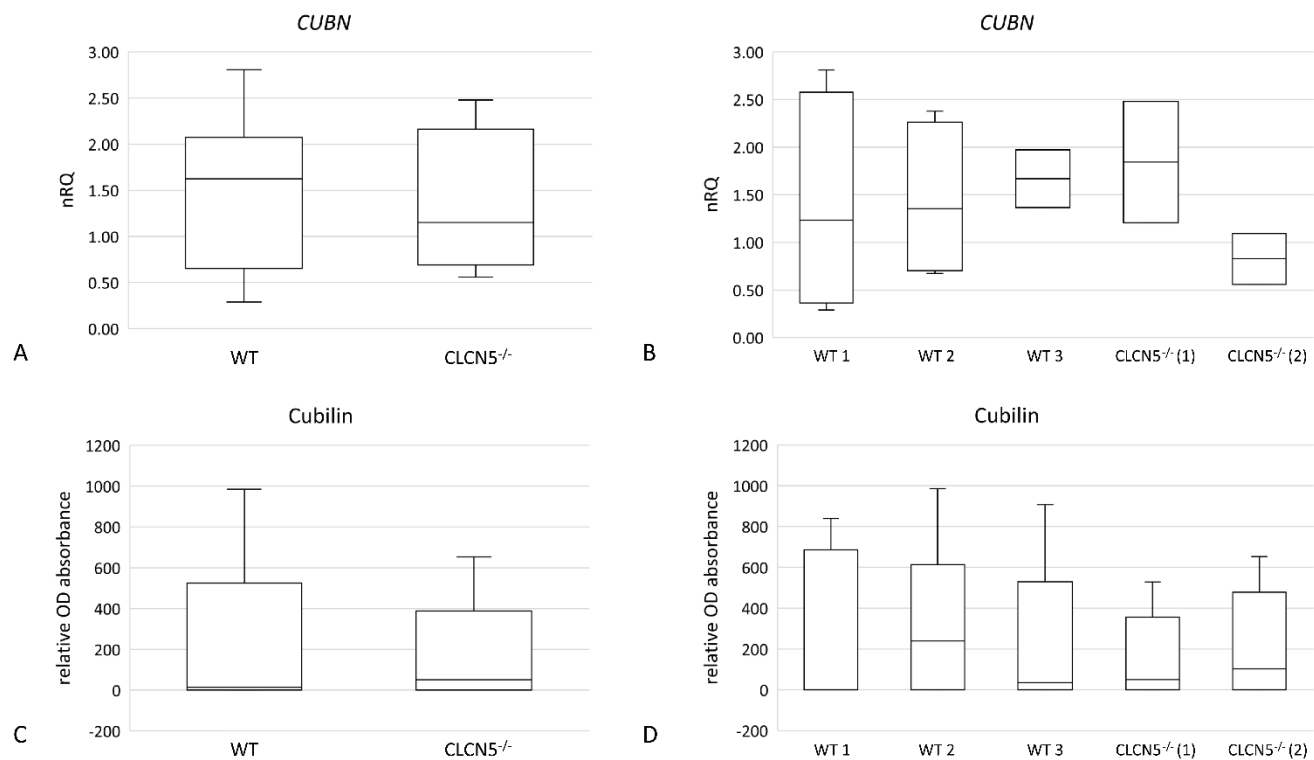


Figure S4. Cubilin gene (*CUBN*) and protein expression in WT and *CLCN5*^{-/-} clones. Boxplots show medians and interquartile ranges of (A-B) relative mRNA, as determined by qRT-PCR, and (C-D) protein expression, as determined by ICW. p-values were obtained with the Mann-Whitney U test. Results are from two independent experiments performed in triplicate. Abbreviations: nRQ: normalized relative quantity; OD, optical density.