Glomerular Elasticity and Gene Expression Patterns Define Two Phases of Alport Nephropathy

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Abstract.

Rationale. Early steps in glomerular injury in collagen IV nephropathies are poorly understood.

Objectives. We characterized structural, functional, and biophysical properties of glomerular capillaries and podocytes in *Col4α3*$^{-/-}$ mice and analyzed kidney cortex transcriptional profiles at various disease stages. We investigated the effects of TUDCA (suppresses ER stress) on these parameters and used human FSGS transcriptomic data to identify pathways rescued by TUDCA.

Findings. In *Col4α3*$^{-/-}$ mice, podocyte injury develops by 3 months, with maximum glomerular capillary deformability and 40% podocyte loss at 4 months. This period is followed is followed by glomerular capillary stiffening, proteinuria, reduced renal function, inflammatory infiltrates, and fibrosis. Bulk RNA sequencing at sequential time points revealed progressive increases in inflammatory and injury gene expression, including activation of the TNF pathway. Mapping Podocyte-enriched genes from FSGS patients to mice showed that TUDCA, which mitigated renal injury suppressed molecular pathways associated with podocyte stress, hypertrophy and tubulo-interstitial injury.

Conclusions. *Col4α3*$^{-/-}$ nephropathy progresses in two phases. The first is characterized by podocytopathy, increased glomerular capillary deformability and accelerated podocyte loss, and the second by increased capillary wall stiffening and renal inflammatory and profibrotic pathway activation. The response of podocytes to TUDCA treatment provides insights into signaling pathways in Alport and related nephropathies.

Introduction.

Many glomerular diseases including Alport nephropathy caused by mutations in *COL4A3,4, or 5,* focal sclerosing glomerulonephritis (FSGS), or Minimal Change Disease (MCD) begin with podocyte injury that is followed by proteinuria, hematuria, and tubulo-interstitial damage. With more prevalent genetic analysis of kidney diseases, *COL4A3,4, or 5* mutations are found in FSGS, familial IgA nephropathy, renal failure of unknown cause, and patients with hematuria as well as the classic forms of Alport syndrome with characteristic modes of inheritance(1, 2). The severity of collagen IV-associated nephropathies or Alport kidney disease ranges from kidney failure in the third or fourth decade to hematuria with GBM abnormalities on biopsy and minimal risk of kidney failure. The number of patients potentially affected by Collagen IV-associated nephropathy is unknown, but considerably greater than the number with classic Alport syndrome. The mechanisms that cause early podocyte injury and related changes in gene expression in these disorders are not fully defined, although processes responsible for progression, focusing on tubulo-interstitial fibrosis, are increasingly understood.

Podocytes accommodate traction and shear forces and contribute to a specific biophysical environment for glomerular capillaries, which depend on the podocytes' unique cytoskeletal structure for their structural integrity(3-10) In rats, 5/6th renal reduction causes glomerular capillary dilation to prevent increased shear stress(11). In acute and chronic glomerular injury models including Alport nephropathy, protamine, HIV nephropathy, ischemia and ischemia-reperfusion injury, the deformability of glomerular capillaries is increased due to podocyte injury(8, 9, 12-14). Recent intravital imaging studies show distension of glomerular capillaries and aneurisms in glomeruli from *Col4αa5*$^{-/-}$ mice at an early disease stage, indicating increased deformability and reduced structural integrity of these capillaries at a time of accelerated podocyte loss(15-17). Loss of podocytes reflects abnormal podocyte structure with reduced adhesion that may occur due to primary podocyte injury or abnormal matrix, and these two factors may be interrelated(5, 6, 8, 9). Foot process effacement may represent a compensatory mechanism to maintain podocyte attachment to the glomerulus(18).

We used the C57BL/6J *Col4α3*$^{-/-}$ mouse model of Alport syndrome, a disease of glomerular origin, to study early steps in podocyte injury. This model retains many essential characteristics of the human disease and has an 8-month time course allowing better time resolution of disease development and progression than other mouse

strains(19-21). The abnormal GBM could injure podocytes through abnormal physical properties or abnormal signaling due to chemical differences in the normal compared to the Alport GBM(6, 22). Podocytes that produce COL4α3, 4, and 5 could be injured by accumulation of the mutant or misfolded collagen molecules with activation of the unfolded protein response (UPR, ER stress) and additional cell-specific remodeling pathways (23, 24). Finally, abnormal glomerular capillary mechanics caused by disordered cytoskeletal structure could contribute to progressive podocyte injury though increased susceptibility to mechanical injury. To distinguish among these injury mechanisms, we treated one group of *Col4α3*$^{-/-}$ mice with TauroUrsoDeoxyCholic Acid (TUDCA), a compound that functions as a chemical chaperone and that protects cells from UPR/ER stress-mediated injury or death(25-28). We analyzed renal function, glomerular capillary elasticity, structure, and bulk renal RNA expression over the eight months of disease.

Results.

Increased glomerular capillary deformability precedes conventional signs of renal disease in *Col4α3*$^{-/-}$ mice. We studied the *Col4α3*$^{-/-}$ mutant in the C57/Bl6 background to characterize the course of Alport nephropathy. The mutation deletes the *Col4α3* NC1 domain so that mRNA and protein presumably representing the 7S and collagenous domains are expressed (**Figure S1**)(19-21). We compared renal function and glomerular capillary elasticity in *Col4α3*$^{-/-}$ mice and WT littermates from 2 to 8 months of age(8, 9, 29). From 4 months, creatinine increased but did not reach statistical significance until 6 months and reached a maximum value of 61 µM at 8 months(**Figure 1A**). Similarly, urine ACR increased from 0.11 at 2 months and 3.51 at 4 months to 122 at 8 months but did not reach statistical significance until 6 months(**Figure 1B**). In the WT mice, serum creatinine did not change significantly while the ACR values increased from 0.04 to 0.723.

Past work using models of acute and chronic kidney diseases, showed that glomerular capillary elasticity reflects the state of podocyte cytoskeletal structure and that with podocyte injury, capillaries develop increased deformability(8, 9, 14, 30). We measured glomerular capillary elasticity (Young's modulus, E) in the WT and *Col4α3*$^{-/-}$ mice from 2 to 8 months of age using micro-indentation (**Figure 1C**)(8, 9). The values for E for both the WT and *Col4a3*$^{-/-}$ mice were indistinguishable at 2 months (both 2.2 ± 0.2 kPa) and for the WT mice remained essentially unchanged from 2 to 8 months. However, in the *Col4α3*$^{-/-}$ mice, the E values for glomeruli began to decrease at 3 months (1.85±0.09 kPa) and reached a minimum (1.56 ± 0.3 kPa) at 4 months of age. E then increased to values significantly greater than control by 7 months, reaching a maximum at 8 months (2.7 ± 0.1 kPa). These directionally opposite changes in elasticity early and late in disease signify distinctly different structural and functional properties of glomerular capillaries(8, 9, 29, 31). The early time point at which reduced glomerular E appears, before increases in serum creatinine and with a minor increase in urine ACR, indicates that podocyte injury begins early in the course of renal disease, and is sufficiently severe to affect overall glomerular capillary mechanical properties.

To assess gene expression patterns in the *Col4α3*$^{-/-}$ kidneys compared to WT over the course of nephropathy, we performed bulk RNAseq of renal cortex at 2, 4, and 7 months. We identified 1346 Differentially Expressed Genes (DEGs) in the 4-month WT- *Col4α3*$^{-/-}$ comparison. The top 50 increased and 50 decreased genes at 4-

months from each comparison are shown in **Supplemental Tables 1-2**. The heatmaps shown in **Figure 1D and Supplemental Figure S2** display the expression of selected genes, grouped by function, from 2 to 7 months. Each column represents an individual mouse. Visually, from 2 to 4 months, gene cluster expression patterns remain relatively stable, reflecting the minimal parallel changes in renal function and histology (see below). At 7 months, changes in the remaining genes became more pronounced and statistically significant. Despite evidence of proximal tubular injury, EGF expression remained relatively stable until 7 months when it was halved. Markers of proximal tubule injury, such as HAVCR1 (Kim1) and Lcn2 (NGAL), show increased expression at each time point compared to wild-type (WT) mice, with the most significant changes occurring at 7 months. Genes involved in inflammation and fibrosis, including C3, Tnf, Tlr8, Thrombospondin, Ltbp2, Inhibin, Col1α1, Col1α2, Col3α1, and Lox (Lysyl oxidase), showed dramatic increases by 7 months, a time when kidney function was deteriorating. Similar patterns were noted for various cytokines, interleukins, and chemokines (Supplemental **Figure S2** and **Supplemental Tables S3A and S3B**). Additionally, the expression of several kidney-specific transporters, such as Slc2a5 (Glut 5), Slc26a4 (Pendrin), Slc22a7 (OAT2), Aqp4, Slc16a4 (monocarboxylic acid transporter), and Slc12a3 (NCC), decreased significantly only at 7 months. These results indicate that significant renal parenchymal injury coincides with the onset of proteinuria after the 4-month time point in this model.

By 4 months, markers of podocyte stress and injury were activated, as evidenced by a higher podocin:nephrin ratio (PNR) in *Col4α3*$^{-/-}$ mice compared to WT (2.45 vs. 1.367, $p<0.05$). This parameter, given the cell-specific expression of podocin (Nphs2) and nephrin (Nphs1) in podocytes, is a robust way to assess podocyte hypertrophic stress, injury, and stress patterns despite dilution from other more abundant cell types in the renal cortex(32).

Pathway enrichment analysis of bulk-RNA seq data comparing WT and *Col4α3*$^{-/-}$ mice at 4 months identified through the Gene Expression Omnibus (GEO) demonstrated coordinated upregulation of genes associated with extracellular matrix (ECM) organization, cell-matrix adhesion, and motility to cover the increase in glomerular capillary surface area. Biological processes enriched include ECM organization (GO:0030198), regulation of cell migration (GO:0030334), and cell-matrix adhesion (GO:0007160). Notably, inflammatory response signaling

(GO:0006954), cytokine-mediated signaling pathway (GO:0019221), and regulation of IL-8 production were enriched. The genes enriched in each signaling pathway are given in Supplementary Tables (https://drive.google.com/drive/folders/1nVBe2jZcjG1f31nIWa6CI5O0c7vqBP8e?usp=sharing). The affected cellular components include the collagen-containing ECM (GO:0062023), cell-substrate junction (GO:0030055), focal adhesion (GO:0005925), and basement membrane (GO:0005604). Enriched molecular functions include cytokine receptor activity (GO:0004896), consistent with the increased inflammatory response (GO:0006954), GTPase regulator activity (GO:0030695), actin binding (GO:0005509), and GTPase activator activity (GO:0005096). Thus, despite the relative lack of major changes observed at a low-resolution heatmap level and histology (**see Figures 3 and 6 below**), the gene enrichment pattern from cortical bulk-RNA sequencing in *Col4α3*$^{-/-}$ mice at four months was consistent with podocyte injury, hypertrophic stress, and increased ECM and basement membrane synthesis. Additionally, the transcriptomic data provides evidence of an early inflammatory response associated with this podocyte hypertrophy and injury.

Evidence for unfolded protein pathway activation in *Col4α3*$^{-/-}$ podocytes. Podocytes determine the elastic properties of glomerular capillaries and produce and secrete the Col4α3,4,5 heterotrimer for the GBM(8, 9, 33). With loss-of-function mutations in any one of these proteins, podocytes must contend with inadequately processed collagen(23, 34, 35). Cells compensate for excess or misfolded protein by upregulating pathways that can improve folding and/or protein degradation including Bip (HSPA5), Xbp1s (Xbp1) and CHOP (DDIT3). We imaged WT and *Col4α3*$^{-/-}$ mouse cortex with confocal microscopy and found increased Bip expression in glomerular podocytes (**Figure 2A**). The levels of Bip and Xbp1s, protein and mRNA are increased in conditionally immortalized *Col4α3*$^{-/-}$ podocytes compared to their WT counterparts (**Figure 2B**). Cultured WT podocytes increase expression of Bip, Xbp1s, and CHOP in response to Tunicamycin, an agent that induces UPR, and the expression is reduced in a dose-dependent manner by treatment with TUDCA(25, 26, 28) (**Figure 2D**). Three genes related to UPR activation were differentially expressed in the *Col4α3*$^{-/-}$ - *Col4α3*$^{-/-}$-T comparison, Xbp1 (increased 1.85 X), Dnajb9 (increased 1.50 X), and Eef1akmt3 (decreased to 0.38 X). For these reasons and expanded ER in *Col4α3*$^{-/-}$ glomerular podocytes (see **Figures 7 and Supplemental 5**), we propose that an early step in podocyte injury could be UPR activation with disruption of normal protein processing and degradation.

TUDCA treatment slows progression of renal disease in *Col4α3$^{-/-}$* mice. Although ER stress activation due to Col IV misfolding was found in cell culture systems, a mouse model, and human skin fibroblasts from Alport patients, protection from renal disease by inhibition of ER stress has not been demonstrated *in vivo*(23, 24). We tested the possibility that collagen misfolding is the basis for podocyte injury in the *Col4α3$^{-/-}$* mice by suppressing ER stress with TUDCA. *Col4α3$^{-/-}$* mice were fed 0.8% TUDCA-incorporated into mouse chow from weaning, 21 - 25 days old, 3 – 4 months before they developed proteinuria, continuously until sacrifice(36). We compared the effects of TUDCA in *Col4α3$^{-/-}$* mice (*Col4α3$^{-/-}$*-T) to *Col4α3$^{-/-}$* and WT mice measuring serum creatinine (**Figure 3A**), urine ACR (**Figure 3B**), and the Young's modulus (E) of glomeruli (**Figure 3C**) at 4 and 7 months, the nadir and peak of glomerular E (**Figure 1C**). At 4 months, serum creatinine and urine ACR values were similar among the WT, *Col4α3$^{-/-}$*, and TUDCA-treated *Col4α3$^{-/-}$* (*Col4α3$^{-/-}$*-T) groups (**Figure 3**, left top two panels). However, at 7 months, when average serum creatinine and ACR in the Col4α3$^{-/-}$ mice were respectively 55±7 µm and 90±11, values for creatinine and ACR in the Col4α3$^{-/-}$-T mice were respectively, 33±3.9 µm and 40±8.6. At 4 months, the value for E in the WT mice was 2.1±0.04 kPa, 1.56±0.05 kPa for the *Col4α3$^{-/-}$* mice, and 2.0±1.0 kPa in the *Col4α3$^{-/-}$*-T mice (**Figure 3C**). At 7 months, E for WT glomeruli was 2.1±0.06 kPa, and for the *Col4α3$^{-/-}$* glomeruli it was 2.70±0.05 kPa, while the value for the *Col4α3$^{-/-}$*-T glomeruli was 1.9±0.04 kPa, comparable to WT. These results demonstrate that TUDCA preserves the elastic properties of *Col4α3$^{-/-}$* glomeruli, indicative of normalized podocyte cytoskeletal structure, reduces the severity of glomerular and renal injury in the *Col4α3$^{-/-}$*-T mice, and implicates UPR activation in glomerular capillary injury.

TUDCA treatment preserves *Col4α3$^{-/-}$* kidney structure. Chronic kidney disease is marked by progressive fibrosis and loss of renal function. Our physiologic measurements at 7 months, late-stage disease, (**Figure 3A-C**) showed preserved renal function in the *Col4α3$^{-/-}$*-T mice implying preserved glomerular and renal structure. Low magnification kidney sections from 4-month mouse kidneys stained with PAS or Picrosirius Red (PSR) show that sections from WT, *Col4α3$^{-/-}$*, and *Col4α3$^{-/-}$*-T mice are indistinguishable (**Supplemental Figure S3, also see Figure 6**), indicating that at the 4-month time point, overall renal injury is minimal. At seven months (**Figure 3D**), the extent of injury in the *Col4α3$^{-/-}$* kidneys is evident with the PAS-stained *Col4α3$^{-/-}$* kidneys showing disrupted renal architecture, fibrosis, and inflammatory cell infiltrates. In the kidneys of *Col4α3$^{-/-}$*-T mice, these features

are present, but to a significantly lesser extent. The glomeruli from the *Col4α3*$^{-/-}$ mice are sclerotic and have excess, irregular PSR staining. Although glomeruli from the *Col4α3*$^{-/-}$-T mice are not normal, their structure is relatively preserved compared to the untreated *Col4α3*$^{-/-}$ glomeruli.

We measured the expression of genes associated with renal injury and fibrosis at 7 months using qRT-PCR of RNA samples from renal cortex in WT, *Col4α3*$^{-/-}$, and *Col4α3*$^{-/-}$-T mice (**Table 1**). In *Col4α3*$^{-/-}$ mice, expression of Col1α1, Col1α2, Col3α1, lysyl oxidase (LOX), lysyl oxidase like 2 (Loxyl2), TGF-β1, CxCl1, Ccl2, Ccr2, CN1 (Cyr61), a gene involved in development and wound healing and repair, TNFα, and IGF2, a gene involved in hypertrophy, all increased compared to WT. In the *Col4α3*$^{-/-}$-T mice, the mRNA expression for these genes was reduced to levels intermediate between those in WT and untreated *Col4α3*$^{-/-}$ mice. The reduction of TNF-α by half by TUDCA is notable because of the role of that pathway in other renal diseases(37). EGF mRNA, a marker for renal tubular health, decreased significantly in the *Col4α3*$^{-/-}$ mice compared to WT, but in *Col4α3*$^{-/-}$-T mice, was expressed at an intermediate level, significantly higher than in *Col4α3*$^{-/-}$ mice. These results demonstrate that TUDCA, initiated early in the course of disease, reduces glomerular injury and proteinuria, slows progression of nephropathy in *Col4α3*$^{-/-}$ mice in part by reducing cytokine and chemokine production and fibrosis, and that significant differences between the WT and Col4α3$^{-/-}$ mice are only evident after 4 months when they are associated with proteinuria, glomerular capillary stiffening and progressive renal injury.

TUDCA reduces podocyte loss from *Col4α3*$^{-/-}$ mouse glomeruli. Glomerular capillaries become deformable at 3 months, before increases in creatinine or urine ACR, indicating that podocyte injury begins at or before that point. Alport patients lose podocytes in the urine at an accelerated rate, and podocytes can be detected in their urine before significant proteinuria develops(16, 17)**.** To identify an early time point for podocyte injury, we compared glomerular podocyte density in WT, *Col4α3*$^{-/-}$, and *Col4α3*$^{-/-}$-T mice at 2, 3, and 4 months using WT1 staining as a podocyte marker (**Figure 5**)(38). At 2 months, podocyte density was similar among all three groups (Podocytes/10^6 μm^3 ± SD, WT 296±44, *Col4α3*$^{-/-}$ 276±39, and *Col4α3*$^{-/-}$-T 262±45). At 3 months, when increased glomerular deformability was detectable in the *Col4α3*$^{-/-}$ glomeruli, podocyte density remained unchanged in the three groups and comparable to the values for 2-month glomeruli (Podocytes/10^6 μm^3 ± SD, WT 285±35, Col4α3$^{-/-}$ 270±40, and Col4α3$^{-/-}$+T 299±32). However, at 4 months, when glomerular E in the *Col4α3*$^{-/-}$ mice was at its

nadir, 1.56 kPa, podocyte density (Podocytes/10^6 μm^3 ± SD) in the *Col4α3*$^{-/-}$ mice was reduced to 162±37 compared to WT 276±48, or 60% of WT. TUDCA treatment protected glomeruli from podocyte loss (Podocytes/10^6 μm^3 ± SD) *Col4α3*$^{-/-}$-T 246±40). This reduction in podocyte loss from the glomeruli in *Col4α3*$^{-/-}$-T mice was accompanied by a lower PNR compared to Col4α3$^{-/-}$ mice(39).

Early glomerular capillary deformability corresponds to reduced podocyte adhesion. We expected that podocyte injury should be detectable at 3 months as decreased podocyte adhesion because that is the earliest detectable change in capillary elasticity, and *Col4α3*$^{-/-}$ podocyte numbers are preserved. WT and *Col4α3*$^{-/-}$ glomeruli had similar patterns of synaptopodin and nephrin staining indicating preserved structure at that level(**Supplemental Figure S4**). We measured podocyte adhesion in 3-month-old mice as urinary podocyte loss *in vivo* following volume loading. Mice were injected with 0.5N saline (80 µl/g IP), and urine was collected over two hours(40). Urinary podocytes were quantified by immunoblot of urine for nephrin normalized for creatinine (**Figure 5A, B**), and counting WT-1 positive cells in urine sediment (**Figure 5C**). With volume loading, urinary nephrin increased four-fold over WT in the *Col4α3*$^{-/-}$ samples. TUDCA treatment reduced urine nephrin by approximately half. Urinary podocyte loss increased in *Col4α3*$^{-/-}$ mice compared to WT (**Figure 5C**). These observations were consistent in 3 different experiments, where although the number of total podocytes lost in the urine varied from mouse to mouse, only the *Col4α3*$^{-/-}$ mice had multiple WT-1 positive cells in their urine. TUDCA protects against reduced podocyte adhesion at early stages of nephropathy.

TUDCA protects glomerular capillary and podocyte structure. Light microscopic images of glomeruli from 4-month-old *Col4α3*$^{-/-}$ mice show generally preserved structure, but the glomeruli are hypertrophic compared to the WT mice and have multiple dilated capillaries (**Figure 6, top row**). Additionally, focal lesions are present, but there is little evidence of tubulo-interstitial damage. The *Col4α3*$^{-/-}$-T glomeruli show evidence of focal lesions and capillary dilation, but considerably less than the *Col4α3*$^{-/-}$ glomeruli and have no evidence of hypertrophy. At 7 months, the patterns described above persist but in the *Col4α3*$^{-/-}$ mice are more severe with more glomerulosclerosis, focal glomerular lesions, and significant tubulo-interstitial injury and inflammation. The *Col4α3*$^{-/-}$-T kidneys show less glomerular and tubulo-interstitial injury compared to the *Col4α3*$^{-/-}$ kidneys, but injury progressed from the 4-month time point (**Supplemental Table S4**).

We used transmission electron microscopy (TEM) to compare podocyte and GBM structures in our three groups of mice at 4 and 7 months (**Figure 7**). At 4 months, the glomeruli from the *Col4α3*$^{-/-}$ mice show regions of irregular GBM structure with thin and thick regions. The podocyte foot processes are normal in some regions but also show evidence of effacement and widening in other regions. Some podocyte cell bodies appear hypertrophic, exhibiting vacuolization, and have expanded ER indicative of ER stress, and microvillus formation (**Supplemental Figure S5, Supplemental Table S5**. In the *Col4α3*$^{-/-}$-T glomeruli, these pathologic findings are present, but less severe than in the *Col4α3*$^{-/-}$ mice. By 7 months, the pathologic changes in the *Col4α3*$^{-/-}$ GBMs and podocytes are more advanced with evidence of substantial glomerulosclerosis. The *Col4α3*$^{-/-}$-T glomeruli have characteristics intermediate between the WT and *Col4α3*$^{-/-}$ glomeruli. The pathologic findings are quantified in **Supplemental Table S5**.

Human FSGS Gene Signature Mapping to Mouse RNA-seq data. Podocytes form a small fraction of the kidney cell population, making early gene changes reflective of podocyte injury difficult to detect. To address this problem, we employed a novel approach by mapping Glomerular disease Associated Proteinuria (GAP) genes from human FSGS patients to the mouse RNA-seq data, further expanding our understanding of the podocyte transcriptional responses. We used the NEPTUNE FSGS database because of the large number of samples and depth of the analysis. Unbiased Independent Component Analysis (ICA) of the mouse RNA-seq data identified a gene cluster (N=327 genes) enriched in podocyte genes. Sixty of these genes were perturbed by TUDCA treatment in the *Col4α3*$^{-/-}$ mice, showing expression patterns directionally opposite or of lesser magnitude compared to those observed in untreated *Col4α3*$^{-/-}$ mice (**Supplemental Figures S6 and S7, Supplemental** Table S6).

In *Col4α3*$^{-/-}$ compared to *Col4α3*$^{-/-}$-T mice, Gene Ontology analysis revealed enrichment for molecular functions including phosphatidylinositol transfer (GO:0008526), filamin binding (GO:0031005), and inhibitors of metalloendopeptidase activity (GO:0008191). Enriched biological processes included podocyte development (GO:0072015), cell migration (GO:0030334), and podocyte differentiation (GO:0072112). Cellular components enriched gene groups included collagen-containing extracellular matrix (GO:0062023), basement membrane

(GO:0005604), and microvillous formation (GO:0031528). This pattern is similar to the enrichment observed between *Col4α3*$^{-/-}$ and WT animals. The drive to increase ECM and basement membrane synthesis was evident, alongside increased expression of inhibitors of metalloendopeptidase activity, presumably to prevent the degradation of existing and newly synthesized ECM. Additionally, there was increased expression of genes associated with epithelial to mesenchymal transition (GO:0010717), indicating ongoing podocyte injury. This ongoing injury was further supported by decreased expression of transcripts associated with glycerophospholipid and lipid synthesis, suggesting that cells were reducing energy-consuming biosynthetic activities to support growth. TUDCA treatment that rescued the Alport phenotype had lower enrichment for the genes listed above.

To further validate the significance of these findings, we applied this gene set to a previously published report of a rapidly progressing Svj126 *Col4α3*$^{-/-}$ Alport model and an intermediate progression model, F1 hybrid Svj126 X Bl6 *Col4α3*$^{-/-}$ mice(41). In these mice, therapy with anti-miR-21 and ACE inhibitors (ACEi) rescued the mice from renal disease progression and reversed the disease-associated direction of change for most of these genes (49 in anti-miR-21 and 38 in ACEi of 60 respectively) (**Supplemental Figure S8**). This result indicates that this smaller set of podocyte-enriched genes is causally related to the development of the Alport nephropathy phenotype in these model systems.

To test whether the molecular signatures associated with glomerular disease progression is relevant to functional outcomes in humans we performed a cross-species comparison. We identified genes associated with proteinuria in 7-month *Col4α3*$^{-/-}$ mice and then mapped these genes to human RNA-seq data from a recently published NEPTUNE cohort which included patients with FSGS and Minimal Change Disease (MCD)(37). The rationale for choosing the 7-month timepoint was its phenotypic match to a disease state representative of what is seen in pediatric and adult nephrology clinics. An ICA using the 7-month RNA-seq data from *Col4α3*$^{-/-}$ mice identified a set of 253 genes in a module (IC6) associated with proteinuria ($p<0.05$) (**Supplemental Figure S6**). The proteinuria-associated genes in our *Col4α3*$^{-/-}$ model were strongly enriched in top 10% of overexpressed genes from micro-dissected glomerular bulk-RNA seq data of FSGS patients comparing nephrotic with sub-nephrotic range proteinuria in the NEPTUNE cohort ($p=1.22E-6$; $q=5.11E4$, Odds Ratio: 2.6(37).

Supplemental Table S7 shows RT-PCR validation of expression of selected genes (Lif, Krt19, C3, FosB, Vcan, and Egr1) from the NEPTUNE cohort in the 7 Month *Col4α3*$^{-/-}$ mouse data. Not only did these genes change in the same direction in the *Col4α3*$^{-/-}$ mouse data, but the increases were suppressed by TUDCA. The paper by Mariani et al showed increased expression of TNF-α signaling pathway markers in patients with FSGS and MCD who progressed(37). Among these, TIMP1 and CCL2 (MCP-1) mRNAs were increased in renal biopsy tissue in parallel with the urine proteins. At 7 months, these mRNAs in the *Col4α3*$^{-/-}$ mice are also increased (Ccl2 9.2 X, TIMP1 20.8 X, and TNF-α 2.91 X over WT with several other TNF-α-responsive genes in a pattern similar to the NEPTUNE population **Table 2**(37). At 7 months, TUDCA suppressed TNF-α expression by 50% (**Table 1**). However, TNF-α, like many other genes associated with inflammation was not significantly increased or not differentially expressed at 2 and 4 months (**Table 2A, 2B, Supplementary Tables 3A, 3B**). These results indicate that not only does the Alport nephropathy mouse model express genes associated with proteinuria in human renal biopsies of patients with glomerular disease, but that genes that have pathologic roles in glomerular disease are shared between these two datasets. Additionally, in the *Col4α3*$^{-/-}$ mice, the magnitude of the change correlates with the stage of the disease.

Discussion.

We followed the course of nephropathy in *Col4α3*$^{-/-}$ mice (C57Bl6 strain) from 2 to 8 months of age to identify mechanisms of renal injury at early time points. We assessed renal function and structure including glomerular capillary and podocyte structure, function, elastic properties, and gene expression. We have three principal findings. First, in *Col4α3*$^{-/-}$ mice, Alport nephropathy has two distinct phases. In the first phase, from birth through 4 months, podocyte injury and loss occur in the absence of significant proteinuria, reduced renal function, tubulo-interstitial injury, or inflammatory responses. Podocyte stress, hypertrophy, and injury pathways are activated. This phase may represent reversible disease. The second phase, from 4 to 7 months following loss of approximately 40% of podocytes, is characterized by increasing rigidity of glomerular capillaries, progressive proteinuria and tubulo-interstitial fibrosis with activation of genes associated with progressive glomerulosclerosis, and tubulo-interstitial fibrosis with decreasing expression of differentiated genes related to renal transport. The expression of many inflammatory mediators, including TNF, increases significantly during this time. This second phase may represent irreversible disease.

The second major finding is that TUDCA, an agent that reduces the consequences of UPR activation, significantly slowed the progression of renal disease in *Col4α3*$^{-/-}$ mice by ameliorating podocyte injury, stress, and loss beginning at 3 months and resulting in a 50% reduction in serum creatinine, 65% reduction in urine ACR, and near normalization of glomerular capillary E at 7 months. This effect of TUDCA is the first demonstration that interfering with UPR activation suppresses the Alport renal disease phenotype and implicates the UPR pathway in the pathogenesis of the disease.

Third, we found that TUDCA treatment of *Col4α3*$^{-/-}$ mice reversed the direction of change or blunted the magnitude of change in expression of 60 of the 327 podocyte enriched genes identified in the NEPTUNE cohort. The expression patterns of many of these TUDCA-responsive podocyte-enriched genes was also reversed in another model of Alport nephropathy using a different mouse strain, Svj129 X Bl6 Fi hybrid, and two distinct treatments (ACEi and anti-miR-21)(41). Furthermore, in 7-month *Col4α3*$^{-/-}$ mice, we identify a gene expression pattern characteristic of TNF-α activation that is also found in a NEPTUNE cohort of FSGS and MCD patients, that is also suppressed by TUDCA treatment(37). These data indicate that the human podocyte injury-enriched

gene set we identified is mechanistically related to podocyte injury and progression in currently available Alport model systems.

This last finding is relevant to human disease since a logical next step would be to test whether TNF inhibitors could be used to mitigate the inflammation and thus scarring in Alport model systems followed by human studies. A phase IIa trial with Adalibumab, an FDA-approved anti-TNF monoclonal antibody, was initiated in 2019 to determine if it could reduce urinary levels of TIMP1 and MCP-1 (CCL2) in children and adults with biopsy-proven FSGS and MCD (clinical-trials.gov/NCT04009668). The trial was completed in October, 2023, but results are not available. If successful, this approach could identify a new treatment for selected patients with high TNF levels that may include patients with Alport nephropathy. Our results suggest that anti-TNF therapy could slow disease progression but might not affect the primary disease process. Investigating other genes from this dataset such as C3, TLR8, or IL-1 may be informative.

In glomerular disease, podocyte injury, hypertrophy in response to podocyte loss, or other hypertrophic stimuli can increase capillary deformability and may represent a podocyte-specific remodeling program(8, 9, 14, 42-44). Increased podocyte and capillary deformability are early steps in injury, probably predispose to mechanical trauma, and accelerate glomerular failure, consistent with the beneficial effect of ACEi/ARB therapy(41, 44, 45). Our finding of increased capillary deformability in the *Col4α3*$^{-/-}$ mouse model is supported by studies of Gyarmati et al, who found dilated glomerular capillaries with aneurisms and thrombi in early-stage *Col4α5*$^{-/-}$ mice (C57/Bl6 background)(15). Hypertrophy is sufficient to increase the deformability of podocytes and glomerular capillaries. Cortes et al perfused glomeruli from control and remnant rat kidneys with hypertrophic glomeruli at progressively increasing pressures over the physiologic range and found a value for E for control glomeruli, 2.3 kPa that is similar to ours, 2.2 kPa. The remnant kidney glomerular E decreased by 40% to 1.4 kPa, a value similar to 1.56 kPa seen in our 4-month-old *Col4α3*$^{-/-}$ mice (9, 42). These results indicate that the GBM in early Alport nephropathy is not rigid, does not determine the distensibility of glomerular capillaries, and that podocyte structure is more likely to have the dominant effect. In this setting, even normal blood pressure is likely to injure podocytes and hypertension would be even more damaging(39). Decreased glomerular E could be a valuable therapeutic target.

Despite evidence of UPR activation in cultured podocytes, glomeruli from Alport mouse models, and skin fibroblasts from men with Alport syndrome, showing a benefit of UPR suppression on the course of Alport nephropathy has been difficult (Pers. Comm Jeff Miner)(23, 24). Several factors may contribute to this situation. First, podocyte injury probably begins with expression of the disrupted *Col4α3,4,5* heterotrimer before or near birth, long before clinical evidence of disease, and accelerates with birth and post-natal renal perfusion(33, 46). Our intervention began early in the course of disease, at the time of weaning, 4 weeks after birth and 8 weeks before the earliest detectable evidence of podocyte injury. TUDCA treatment preserved podocyte numbers, reduced glomerular hypertrophy, and led to a 50% reduction in serum creatinine, 65% reduction in urine ACR, and preservation for glomerular capillary E. If interventions start with the onset of "clinical" evidence of renal disease, 4 – 6 months in the Bl6 model, sufficient injury is present that the rate of loss of renal function may not be slowed. Similarly, in models that progress more rapidly such as the SvJ strain or with severe mutations such as the *Col4α5* G5X mutation, proteinuria and renal failure occur earlier, compressing the course of disease, and interventions that occur relatively late in the disease course with more severe preexisting pathology may have limited ability benefit(20, 47). Nevertheless, Rubel et al initiated ACEI therapy at 4 weeks and anti miR-21 therapy at 6 weeks, a later stage of disease than in our studies, and found comparable benefit(41). The magnitude and nature of the effect of anti miR-21 and synergistic effects of ACEI treatment may be responsible for the success of their approach(41).

A recent randomized controlled trial of anti miR-21 in adult Alport patients was stopped for lack of effect(48). The patients began treatment with a mean eGFR value of approximately 55 ml/min/1.73 m^2/yr, an eGFR slope of ˜8 ml/min/1.73 m^2/yr, and mean UACR value of 2681. Proteinuria did not change with treatment. These patients had disease that is probably equivalent to our 6-month-old mice with significant loss of GFR, podocyte loss, glomerular hypertrophy, and established tubulo-interstitial fibrosis and inflammation. The patients in this trial may have had no benefit because of their advanced kidney disease.

TUDCA suppresses the effects of UPR activation, and in these studies preserves glomerular and renal function. Although UPR activation in podocytes appears to be an early step in Alport nephropathy, it probably initiates distinct, later processes involved in progression and different processes in other cell types. Thus, disease progression and each cell type could have their own disease trajectory that could be altered with other external noxious stimuli. This idea lends itself to targeting therapies to processes such as endothelial injury and fibrosis driven by IL-11 which we see increased at 7 months and is important for disease progression(15, 49). These beneficial effects of TUDCA may derive from improved podocyte function with reduced proteinuria as suggested by preserved podocyte numbers and our transcriptomic analysis, but TUDCA may have additional effects including suppression of innate immunity and tubulo-interstitial inflammation(27, 50-52). UPR activation with mitochondrial injury initiates the UPR which in turn can activate the integrated stress response (ISR) that includes the innate immune pathway(53, 54). In our data, many RNAs associated with these processes were suppressed by TUDCA but whether that is a primary effect or secondary to improved podocyte function, possibly as a result or reduced proteinuria, is unclear(52). The connections between initial injury and progression pathways remain to be defined, and future single cell studies should begin to resolve these questions.

We identified a subset of podocyte enriched genes from the NEPTUNE FSGS population that corresponds to a similar set of Alport nephropathy genes in *Col4α3*$^{-/-}$ mice that respond to TUDCA (**Supplemental Figure S7 and Table S6**). This set of TUDCA responsive genes was also found in the study by Rubel et al in Svj/129 F1 mice that respond to combined treatment with ACEi and anti-miR-21 (**Supplemental Figure S8**)(41). The similarity of these gene subsets, their relationship to glomerular diseases, and response to different interventions demonstrates that these gene sets not only reflect disease behavior in mouse models of Alport nephropathy but are also relevant to human podocytopathies including Alport nephropathy and FSGS. This pattern of gene expression may represent an early, but general response to podocyte injury so it may have relevance to other diseases with podocyte injury, particularly FSGS and IgA Nephropathy with *Col4α3,4,5* mutations and heterozygous states(2). To the extent that UPR activation is a component of other podocyte and glomerular diseases, these gene sets may be relevant to developing treatments. Podocyte injury, an early potentially reversible step and later downstream renal injury could be mitigated by TUDCA or by targeting its downstream signaling pathways if initiated early before disease is established and irreversible.

Methods.

Reagents. Fluorescent antibodies were purchased from Invitrogen. *Antibodies for immunofluorescence* **-** Col4α3: (Rat) Clone H31 97076), Chondrex, Inc.; Col4α3: (Rabbit) MBS2026491, BioSource; Bip: ab21685, Abcam; WT-1: sc-7385, Santa Cruz; Synaptopodin: sc-21537, Santa Cruz; Nephrin: AF3169, R&D Systems. *Antibodies for immunoblotting* - Bip: ab21685, Abcam; Xbp1s: sc-7160, Cell signaling, and 24868-1-AP, Proteintech; Chop: (D46F1), #5554, Cell Signaling; GAPDH: XP, #5174S, Cell signaling; β-actin – #AM4302 Invitrogen.

Mouse breeding and treatment. Col4α3$^{-/-}$ mice in the C57Bl/6J background were obtained from Jeff Miner(20). Genotyping was performed by Transnetyx. Homozygous males were bred with heterozygous females to obtain Col4α3$^{-/-}$ and Col4α3$^{+/+}$ mice. KO mice were fed 0.8% TauroUrsoDeoxyCholic Acid, 3α,7β-Dihydroxy-5β-cholanoyltaurine (TUDCA) incorporated into mouse chow from the time of weaning (25-28 days old) until sacrifice (25, 26, 28, 36). TUDCA (98% purity) was from Chemimpex and was incorporated into standard mouse chow by Teklad. WT littermates served as controls. Serum and urine creatinine levels were measured by UTSW O'Brien Kidney Research Center Physiology Core using capillary electrophoresis. Urine albumin-to-creatinine ratios were calculated to assess the severity of albuminuria. Urine albumin concentrations were measured using a Mouse Albumin ELISA Kit (Immunology Consultants Laboratory, Inc)(8, 29).

Podocyte adhesion was measured in vivo by injecting 0.5N saline (80 µl/g IP) and collecting urine over two hours(40). An aliquot of urine was normalized for creatinine and immunoblotted for nephrin. Another aliquot was centrifuged, the sediment attached to a slide and stained for DAPI and WT-1.

Podocyte cell line development and culture. Podocyte cell lines were derived from WT and Col4α3$^{-/-}$ primary podocyte outgrowths from glomeruli isolated from adult mice (12-16 weeks of age). Glomeruli were maintained in DMEM with 0.1% FBS at room temperature and seeded onto collagen I-coated dishes for 4-6 days to allow primary glomerular cell outgrowth. Primary podocytes were then trypsinized, filtered with 20 µm cell strainer, and re-plated for experiments or immortalization. Primary podocytes were conditionally immortalized by infection with a lentivirus expressing the temperature sensitive SV40 T antigen tsA58. Lentivirus was produced from

pLenti-SV40-T-tsA58 (abm cat# LV629) as previously described (55) using the VSV envelope from pMD2.G (Addgene cat#12259, gift from Didier Trono) and the packaging plasmid pCMV delta R8.2 (Addgene cat # 12263, gift from Didier Trono). Primary glomerular outgrowths were infected for 48 hours followed by selection with puromycin (2ug/ml). Conditionally immortalized mouse podocytes were cultured in RPMI 1640 with 10% FBS. Cells cultures were expanded at 33°C and for experiments, differentiated at 37°C for 7-10 days as previously described (56).

Animal Studies. Animal research was performed in accordance with the UT Southwestern Medical Center Animal IACUC guidelines. The research study protocol (number 2014-0078) was approved by the UT Southwestern Medical Center Animal IACUC (NIH OLAW Assurance Number A3472-01). UT Southwestern Medical Center is fully accredited by the American Association for the Assessment and Accreditation of Laboratory Care, International (AAALAC).

Kidney total RNA sample preparation for RNAseq. Kidneys from each group of mice were removed and 20 mg of cortex was processed for RNA purification. All samples were stored with RNA later in -80 °C and thawed for RNA purification. Total RNA was purified using Direct-Zol™ RNA Miniprep Plus (Zymo research) and the concentration was measured with DS-11 FX+ (Denovix). Final RNA samples were submitted for sequencing to Next Generation Sequencing Core of UTSW. Sequence analysis and results were performed by the University of Michigan Nephrotic Syndrome Study Network (NEPTUNE).

Quantitative RT-PCR. Total RNAs were purified from each group of mouse cortex part using Direct-Zol™ RNA Miniprep Plus (Zymo research) and used for reverse transcription by SuperScript III First-Strand Synthesis System (Invitrogen). Quantitative PCR was carried out with specific primers using SYBR™ Green PCR Master Mix (Applied Biosystems) and StepOnePlus™ Real-Time PCR System (Applied Biosystems). For quantitative analysis, the samples were normalized to GAPDH (Glyceraldehyde 3-phosphate dehydrogenase) gene expression using the ΔΔCT value method. Primer sequences for specific genes are shown in **Table 3**.

Measurement of glomerular elasticity. Glomeruli were isolated using differential sieving as previously described(8). The elastic moduli of glomeruli isolated from 3–8-month-old mice were measured using a microindentation(8, 9, 57). Briefly, the microtensiometer probe (Kibron, Inc, Helsinki) was mounted on a 3-D

micromanipulator with 160 nm step size (Eppendorf, Inc) attached to a Leica inverted microscope. A glass slide containing a dilute sample of glomeruli was imaged and the probe was brought into contact with the surface of a single glomerulus. Calibration was performed as described(8, 57).

Light microscopy of renal tissue. Formalin-fixed, paraffin-embedded kidney tissue was sectioned at 3 µm, and sections were stained with periodic acid-Schiff or picrosirius red stains. Stained tissue sections were examined, and digital images were collected under brightfield microscopy with an Olympus BX-80 microscope equipped with a Q-Imaging Retiga 2000R imaging system.

Immunofluorescence staining. Treated glomeruli were spun down at 5,000g for 5 min, resuspended and fixed in 4% paraformaldehyde for 30 minutes, and then washed 3x in PBS. Washed glomeruli were resuspended in PBS, 100 µl pipetted onto a slide, and attached to a coverslip overnight at 4˚C. The slide was rinsed in PBS to remove unattached glomeruli and further fixed with 4% paraformaldehyde for 1 hour at room temperature. Attached and fixed glomeruli on coverslips were then washed 3x in PBS, blocked with SEA BLOCK Blocking Buffer (PIERCE) for 40 minutes, then permeabilized with 0.5% Triton X-100 in PBS for 10 minutes. Glomeruli on coverslips were then stained using standard procedures, and imaging was performed using a Zeiss LSM 880 confocal microscope.

Confocal microscopy. Confocal imaging was performed in the Cell Biology and Imaging Core in the O'Brien Kidney Research Core, on a Zeiss LSM880 with Airyscan laser scanning microscope equipped with Plan-Apochromat 10x/0.3 NA, 20x/0.8 NA, 25x/0.8 NA and 63×/1.40 NA oil-immersion objective (ZEISS, Oberkochen, Germany). Fluorescence images were acquired using ZEN black 2.3 software with a 20x/0.8 NA or 63x/1.40 NA objective and Zeiss Immersion Oil 518F was used for the 63x/1.40 NA objective. Experiments were performed at constant room temperature. Images or regions of interest (ROIs) were further processed with ZEN 2.6 (blue edition) software.

Electron microscopy. Tissue samples were fixed with 2.5% (v/v) glutaraldehyde in 0.1M sodium cacodylate buffer (pH7.4). After three rinses with 0.1 M sodium cacodylate buffer, samples were embedded in 3% agarose and sliced into small blocks (1mm^3), rinsed with the same buffer three times and post-fixed with 1% osmium

tetroxide and 0.8 % potassium ferricyanide in 0.1 M sodium cacodylate buffer for one and a half hours at room temperature. Samples were rinsed with water and then block stained with 4% uranyl acetate in 50% ethanol for two hours. They were then dehydrated with increasing concentration of ethanol, transitioned into propylene oxide, infiltrated with Embed-812 resin, and polymerized in a 60°C oven overnight. Blocks were sectioned with a diamond knife (Diatome) on a Leica Ultracut 7 ultramicrotome (Leica Microsystems) and collected onto copper grids, post stained with 2% aqueous uranyl acetate and lead citrate. Images were acquired on a JEM-1400 Plus transmission electron microscope equipped with a LaB_6 source operated at 120 kV using an AMT-BioSprint 16M CCD camera.

Bulk RNA sequencing. One hundred ng RNA was used for each library that was prepared using Illumina TruSeq RNA Library Prep Kit v2 (RS-122-2001) according to Manufacturer's protocol. Illumina UMI barcodes were used to multiplex the libraries as per the Manufacturer's instructions. The quality and quantity of each sequencing final library were assessed using Agilent 2100 BioAnalyzer system (Agilent, CA, USA). A total of 10 nM picogreen measured library were pooled for 1.3pM loading on the sequencer and sequenced on the Illumina NexSeq platform in PE75 (75 bp paired end) run with the NextSeq reagent kit v2.5 for 75 cycles. Approximately 30-40 Million sequencing reads were generated per sample for the transcriptome analysis.

Paired end demultiplexed fastq files were generated using bcl2fastq2 (Illumina, v2.17), from NextSeq550 v2.5 reagent's bcl files. Initial quality control was performed using FastQC v0.11.8 and multiqc v1.7. Fastq files were imported batch wise, trimmed for adapter sequences followed by quality trimming using CLC Genomics Workbench (CLC Bio, v23.0.3). The imported high-quality reads were mapped against gene regions and transcripts annotated by ENSEMBL v99 hg38 using the RNA-seq Analysis tool v2.7 (CLC Genomics Workbench), only matches to the reverse strand of the genes were accepted (using the strand-specific reverse option).

Gene expression QC, quantification, and DEG analysis. Fastq reads were aligned to the mouse genome (GENCODE Version M27) followed by a multi-step quality control process, which included assessments at the read, mapping, and dataset levels according to RNA sequencing quality control methods previously outlined

(58). Gene-level expression quantification utilized HTSeq, and the resulting count data were normalized using voom. Differential gene expression analysis was performed in R using the Limma package (59). The Benjamini & Hochberg method for controlling the false discovery rate was applied as a correction factor for the adjusted p-value. Statistically significant differentially expressed genes (DEGs) were determined based on an adjusted p-value threshold of less than 0.05. All heatmaps were created using the ComplexHeatmap R package (60).

The Podocin:Nephrin ratio (PNR), a term introduced by Roger C. Wiggins, serves as a crucial marker for assessing podocyte hypertrophic stress by examining the differential mRNA expression of Podocin (NPHS2) and Nephrin (NPHS1). Under hypertrophic stress, podocytes exhibit an increase in NPHS2 and NPHS1 mRNA, with a disproportionately higher rise in NPHS2. This ratio has been shown to correlate with podocyte density, podocyte detachment, proteinuria, progressive glomerulosclerosis, and end-stage kidney disease (ESKD)(32). Elevated PNR indicates reduced podocyte density and increased detachment, both of which contribute to proteinuria and glomerulosclerosis, ultimately progressing to ESKD. Nishizono et al. provided robust evidence supporting the association between PNR and these pathological conditions and treatment effects, underscoring its potential as a diagnostic and prognostic tool in kidney disease(61).

Integration of podocyte-specific enriched genes from NEPTUNE FSGS patients projected onto mouse models. We identified 77 patients from the NEPTUNE cohort with a diagnosis of FSGS. Molecular data in the form of microdissected bulk RNA-seq was available for analysis and was utilized for this study. An Independent Component Analysis was performed to identify clusters of co-expressed genes in an unsupervised way. ICA is a matrix decomposition method that separates multifactorial signals into additive subcomponents. Each component could be driven by latent factors such as disease, cell type, and even noise. 25 optimal modules were extracted using Python package stabilized-ica-2.0. Optimal module number was determined as described(62). We identified one module enriched for podocyte-specific genes. Because Alport nephropathy, like FSGS, is a primary podocytopathy, we utilized this module as being reflective of podocyte injury (**Supplemental Figure S9**). Furthermore, we reasoned that because injury patterns are likely to be conserved

across disease types and species, identifying the presence of these genes and their differential expression across all the time points (2, 4, and 7 months) will offer a temporal perspective on how these human data enriched podocyte genes change over time. Their alteration with TUDCA therapy will provide clues to temporal changes in these genes and therapeutic potential with TUDCA or signals downstream of TUDCA.

Identification of mouse genes correlating with proteinuria in the mouse models: To identify and link gene modules with metadata information we performed an Independent Component Analysis (ICA) using the Stabilized-ica Python package (version 2.0.0) available at https://github.com/ncaptier/stabilized-ica. This analysis was applied to gene expression data, excluding the TUDCA effect group. Subsequently, the ICA component mixing matrix was correlated with metadata, revealing a significant correlation between IC6 and UACR (p-value < 0.05). The genes contributing to IC6 were identified using an arbitrary threshold value of 3 deviations from the mean of the distribution. A network analysis was then conducted on the resulting set of 253 genes (see **Supplemental Figure S2**).

Determining whether mouse genes associated with proteinuria are associated with Nephrotic Range Proteinuria in Humans: The above set of 253 genes associated with proteinuria in mice was then applied as a concept in Nephroseq version 4. The entry of these concept genes allows to identify the enrichment of this gene set in other glomerular disease and other CKD datasets. Specifically, we determined whether this set of mouse genes when applied to their human orthologs are enriched in cohorts with nephrotic range proteinuria. For the purpose of this analysis, we used FSGS patients from the recent paper by Mariani et al to determine whether this set of genes was significantly enriched in nephrotic range versus non-nephrotic range proteinuria.

Author contributions

JY and ZL conducted experiments, JY, ZL, OA, and IM acquired data, JY, ZL, MA, CAA, OA, IM, SE, MK, JMH, VN, ASN, ANC, and RTM analyzed data, LAB and PAJ provided critical methods and reagents, ASN, ANC and RTM wrote the manuscript, all authors contributed to editing the manuscript.

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Figures

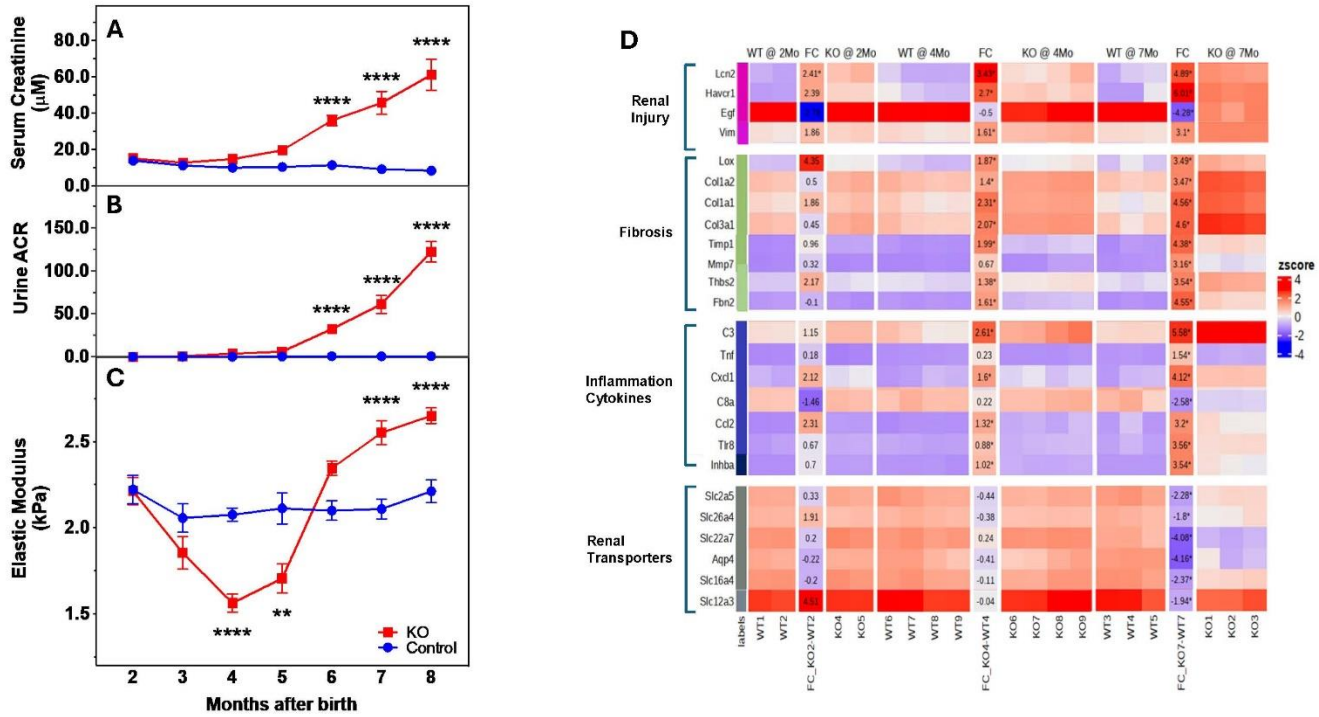

Figure 1. Measurement of serum creatinine (**A**), urine ACR (**B**), and glomerular elastic modulus (E, Young's modulus) (**C**) in *Col4α3*$^{-/-}$ (KO, red) mice over the course of renal disease compared to wildtype or heterozygote controls (Control, blue). Beginning two months after birth, serum creatinine (µM) and urine ACR (mg/g) were measured monthly through eight months. Glomerular E (kPa) was measured in mice sacrificed at indicated time point using microindentation of isolated glomeruli. Each point in graphs shows average E values from 4 - 12 different mice. Average glomerular E for each mouse was calculated from 6-10 glomeruli. Significance was determined by 2-way ANOVA using Graphpad; **P<0.01, ****P<0.0001. **(D)** Differentially expressed genes in KO kidneys at 2, 4, and 7 months compared to age-matched WT. N=2 per group at 2 months, 4 per group at 4 months, and 3 per group at 7 months.

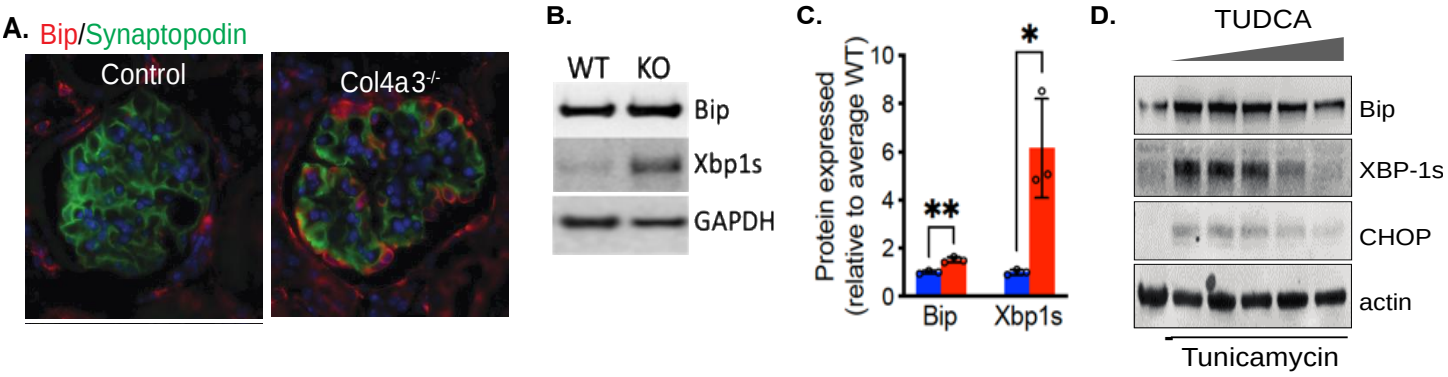

Figure 2. Evidence of UPR activation in glomeruli and podocytes from *Col4α3*$^{-/-}$ mice. A) Immunofluorescence images of Bip and Synaptopodin staining in 4-month T and *Col4α3*$^{-/-}$ mouse glomeruli, **B)** Blots of UPR markers in podocyte cell lines under basal conditions derived from WT and *Col4α3*$^{-/-}$ (KO) mice. The cells were maintained under standard conditions, harvested in RIPA buffer at 7% confluence, and the crude extract was immunoblotted with antibodies against Bip, Xbp1s, and GAPDH. The conditionally immortalized WT and *Col4α3*$^{-/-}$ cells were developed from primary cultures of 3-month WT and Col4α3$^{-/-}$ glomeruli. **C)** Comparison of Bip and Xbp1s protein expression from B (N=3, normalized to WT). **D)** Efficacy of TUDCA for blocking tunicamycin-induced of UPR marker expression in WT podocytes. Podocytes were treated with tunicamycin 1 μg/ml and then increasing concentrations of TUDCA from 1 - 4 mM for four hours.

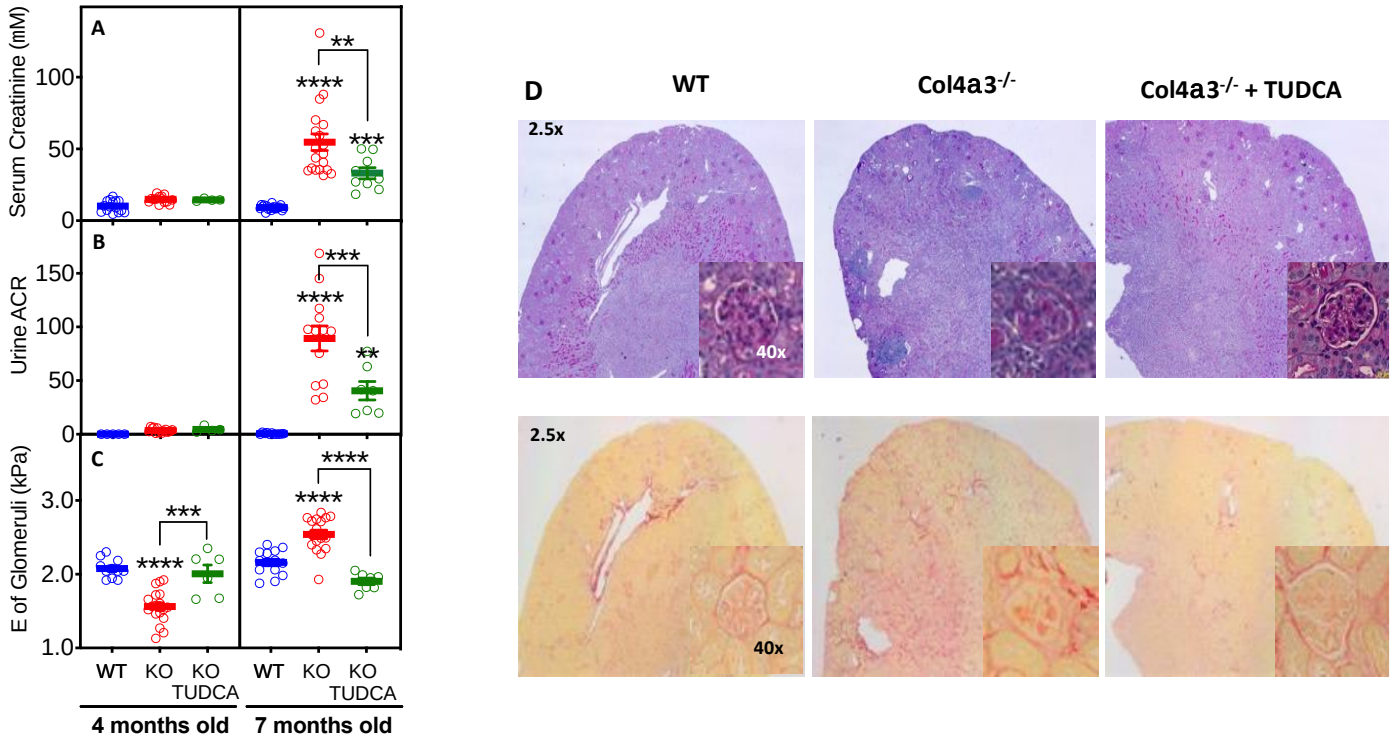

Figure 3. TUDCA treatment slows progression of renal disease and moderates the changes in E in Col4α3$^{-/-}$ mice. Col4α3$^{-/-}$ (KO) mice were treated from weaning (approximately 4 weeks), with 0.8% TUDCA mouse chow (KO TUDCA) until sacrifice. At 4 and 7 months of age, serum creatinine (µM) (**2A**), urine ACR (**2B**), and glomerular elastic modulus (E, kPa) (**2C**) was measured in WT (Blue), KO (Red) and TUDCA treated KO animals (Green). In A and B, each circle represents measurement from one mouse, and in C, each circle represents E measured from an average of 6-10 individual glomeruli from a single mouse. Significance was determined by ANOVA and multiple comparisons test using GraphPad; **P<0.01, ***P<0.001, ****P<0.0001. **2D.** Comparison of kidney cortex from WT, *Col4α3*$^{-/-}$ (KO), and TUDCA treated *Col4α3*$^{-/-}$ (KO) animals. Top row, sections from 7-month mice are stained with PAS and bottom row sections from 7-month mice are stained with picrosirius red. Insets in each panel show representative glomeruli from each condition.

Fibrosis	WT (N)	KO (N)	KO-TUDCA (N)
Col1α1	1 (4)	55.5 ± 13 (3)	26.2± 6.2 (4)
Col1α2	1 (4)	29.6 ± 7.3 (5)	13.9 ± 3.2 (4)
Col3α1	1 (4)	74.1 ± 31.9 (5)	31.9 ± 2.4 (4)
Lox	1 (4)	29.7 ± 7.4 (3)	13..3 ± 7.6 (4)
Loxl2	1 (4)	21.5 ± 7.1 (3)	6.7 ± 3.1 (4)
Cytokines			
TGF-β1	1 (4)	4.8 ± 0.8 (4)	3.0 ± 0.7 (4)
TNF-α	1 (4)	30.3 ± 7.9 (3)	14.3 ± 3.0 (4)
IGF-1	1 (4)	9.81 ± 2.23 (4)	5.93 ± 1.72 (4)
Chemokines/Receptors			
Cxcl1	1 (4)	45.0 ± 11.4 (4)	20.9 ± 2.11 (3)
Ccl2	1 (4)	41.5 ± 9.3 (4)	34.6 ± 5.68 (4)
Ccr2	1 (4)	15.0 ± 3.45 (5)	4.04 ± 1.57 (3)
Injury Markers			
EGF	1 (4)	0.20 ± 0.1 (5)	0.7 ± 0.2 (4)
Ccn1 (Cyr61)	1 (4)	4.46 ± 0.6 (3)	2.0 ± 1.0 (4)

Table 1. Summary of qRT-PCR of selected fibrosis, cytokine, chemokine, or injury-related genes in 7-month *Col4α3*$^{-/-}$ mice without (KO) and with (KO-TUDCA) TUDCA treatment, compared to age-matched WT littermates. All values in KO and KO-TUDCA groups represent fold change from WT ± SD, and were significantly different from Control, as determined by ANOVA. The number of samples in each group is shown in parentheses after the values (N).

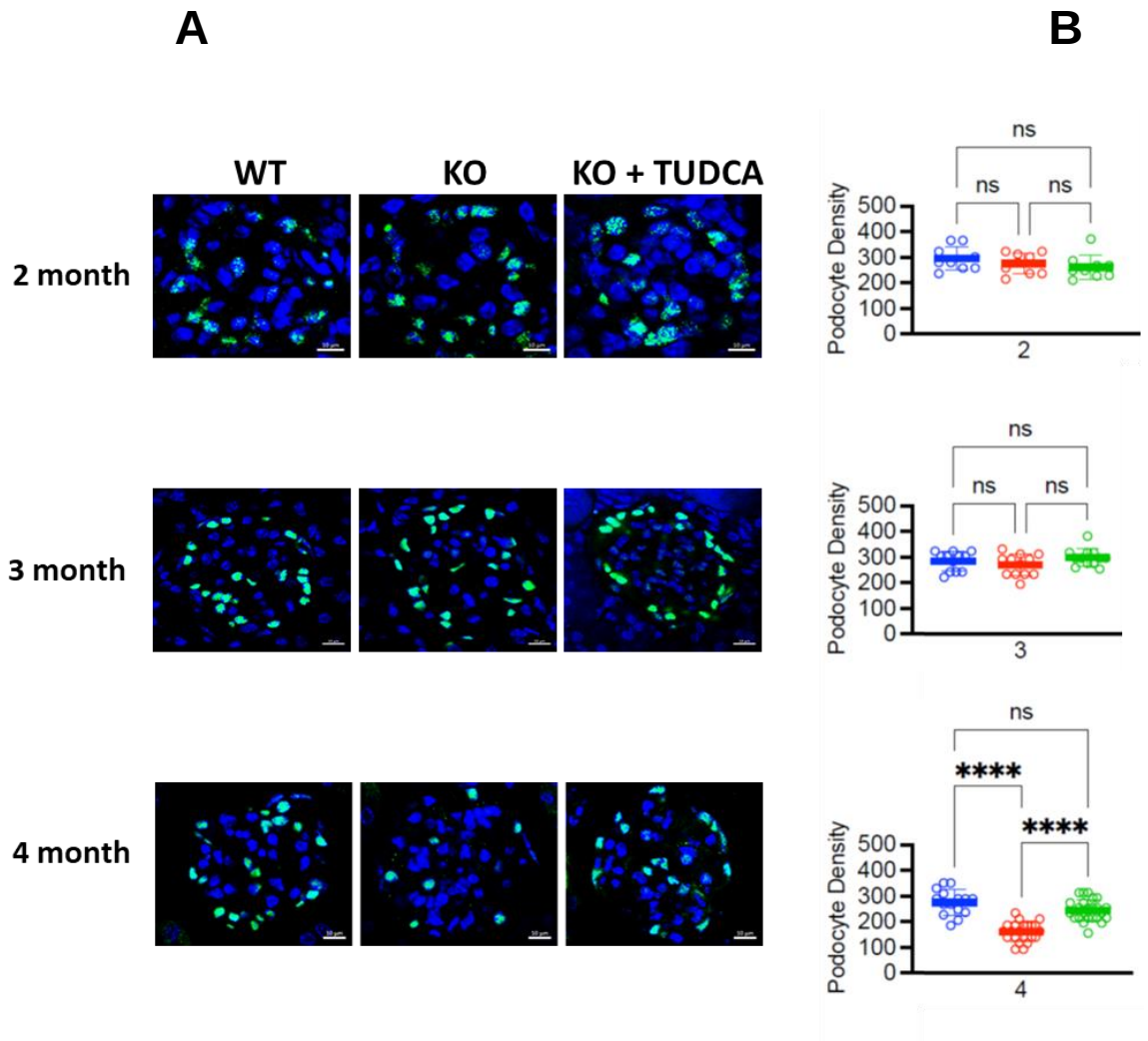

Figure 4. TUDCA reduces podocyte loss from *Col4α3*$^{-/-}$ mouse glomeruli. A) Representative glomeruli in kidney sections from WT, *Col4α3*$^{-/-}$ (KO), and TUDCA-treated *Col4α3*$^{-/-}$ (KO+TUDCA) mice from 2, 3, and 4-month-old mice were stained for WT-1 and DAPI. Scale bar: 10 µm. **B)** Summary of podocyte density analysis. WT – Blue, *Col4α3*$^{-/-}$ - Red, and *Col4α3*$^{-/-}$ - T Green. The number of WT-1 and DAPI-positive nuclei in 20 glomeruli from 3 mice were counted and used for podocyte density calculations. Each dot represents the number of WT-1 positive nuclei in a single glomerulus. Data are shown as mean ± SEM and significance was determined by ordinary one-way ANOVA, followed by Dunnett's multiple comparisons test; ****P<0.0001. At 2 months - Podocytes/10^6 µm^3 ± SD, WT 296±44, *Col4α3*$^{-/-}$ 276±39, and *Col4α3*$^{-/-}$+T 262±45). At 3 months - Podocytes/10^6 µm^3 ± SD, WT 285±35, *Col4α3*$^{-/-}$ 270±40, and *Col4α3*$^{-/-}$+T 299±32). At 4 months, Podocytes/10^6 µm^3 ± SD, WT 276±48, *Col4α3*$^{-/-}$ 162±37, and *Col4α3*$^{-/-}$+T 246±40).

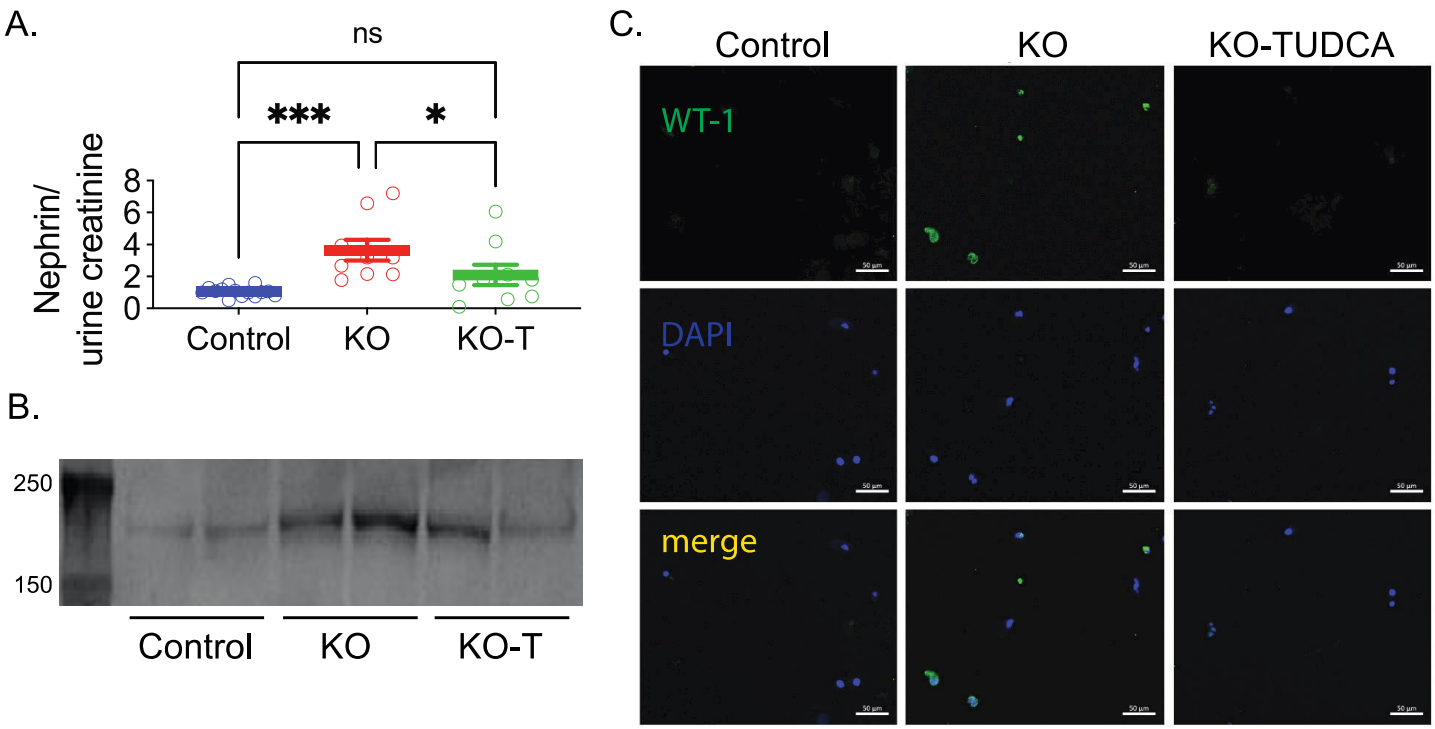

Figure 5. Glomerular capillary deformability and podocytes adhesion. WT (Control), *Col4α3*$^{-/-}$ (KO), and *Col4α3*$^{-/-}$ -T (KO-TUDCA) mice were injected (IP) with approximately 1 ml of saline, and urine was collected over the subsequent two hours. The urine samples were normalized for creatinine, immunoblotted for nephrin, and quantitated with densitometry. The pellet was stained for WT-1 and DAPI. **A**) shows aggregate data for all samples groups expressed as nephrin/creatinine (arbitrary densitometry units for nephrin) for each sample group. WT – Blue, *Col4α3*$^{-/-}$ - Red, and *Col4α3*$^{-/-}$ - T Green. Each point represents a sample from a single mouse, bar indicates mean ± SEM. Significance was determined by ordinary one-way ANOVA, followed by Tukey's multiple comparisons test; *P<0.05, ***P<0.001. **B**) Representative urine nephrin immunoblot with duplicate samples, loading normalized with creatinine. **C**) representative urine sediment samples stained for WT-1 and DAPI.

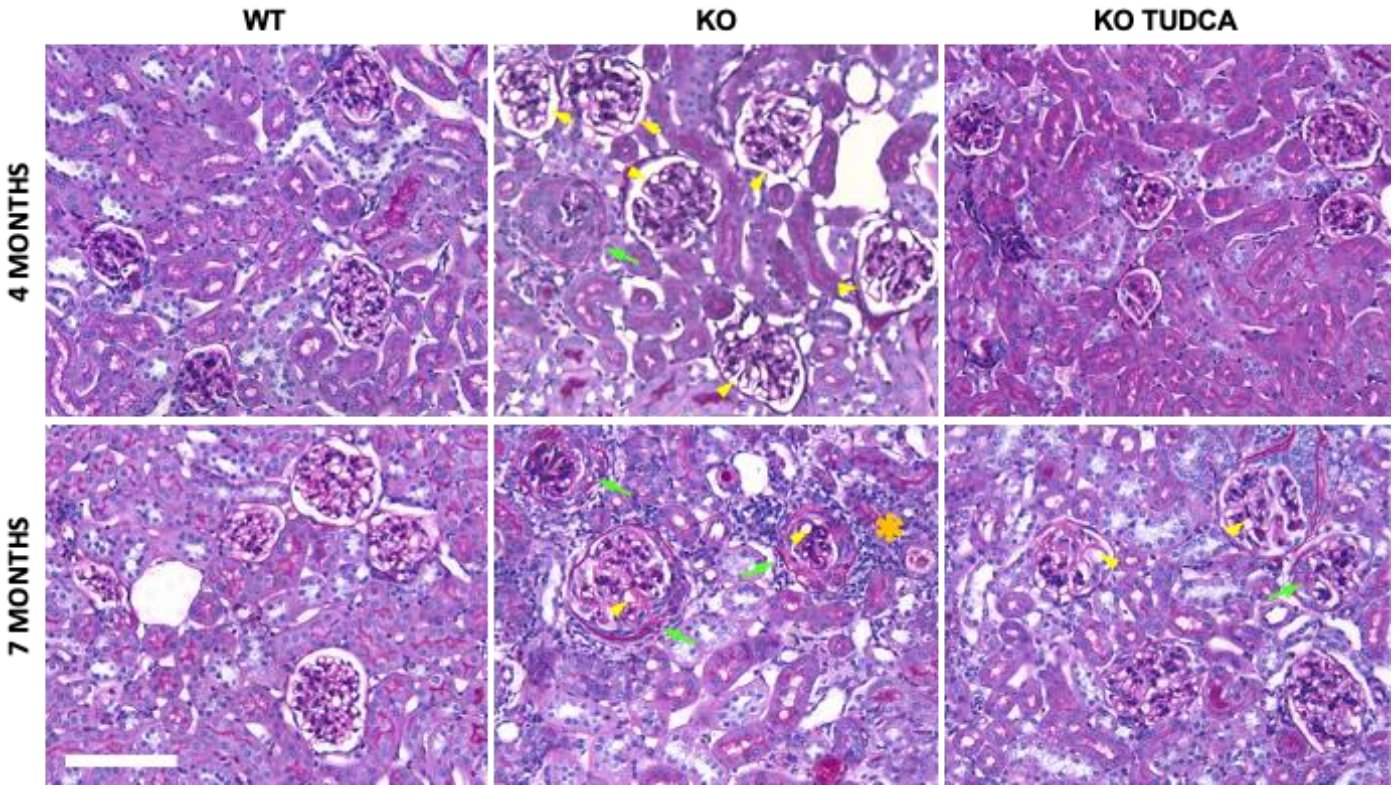

Figure 6. Brightfield photomicrographs of PAS-stained kidney sections from 4 month- (top row) and 7-month-old WT mice, *Col4α3*$^{-/-}$ (KO), and TUDCA-treated *Col4α3*$^{-/-}$ (KO TUDCA) mice. The 4-month KO image shows glomerular enlargement and focal proliferative glomerular lesions (green arrow), and distension of glomerular capillary lumens (yellow arrowheads) that are not observed in Control (top left) or the TUDCA treated KO mice (top right). The 7-month KO mice (bottom center) show more extensive glomerular proliferative lesion development (green arrows), with proliferation composed predominantly of epithelial cells filling Bowman's space, along with patchy areas of tubular atrophy and interstitial fibrosis and chronic inflammation (orange asterisk). The section from the 7-month TUDCA-treated mice show evidence of glomerular injury with PAS stain; bar = 200 µm for all images.

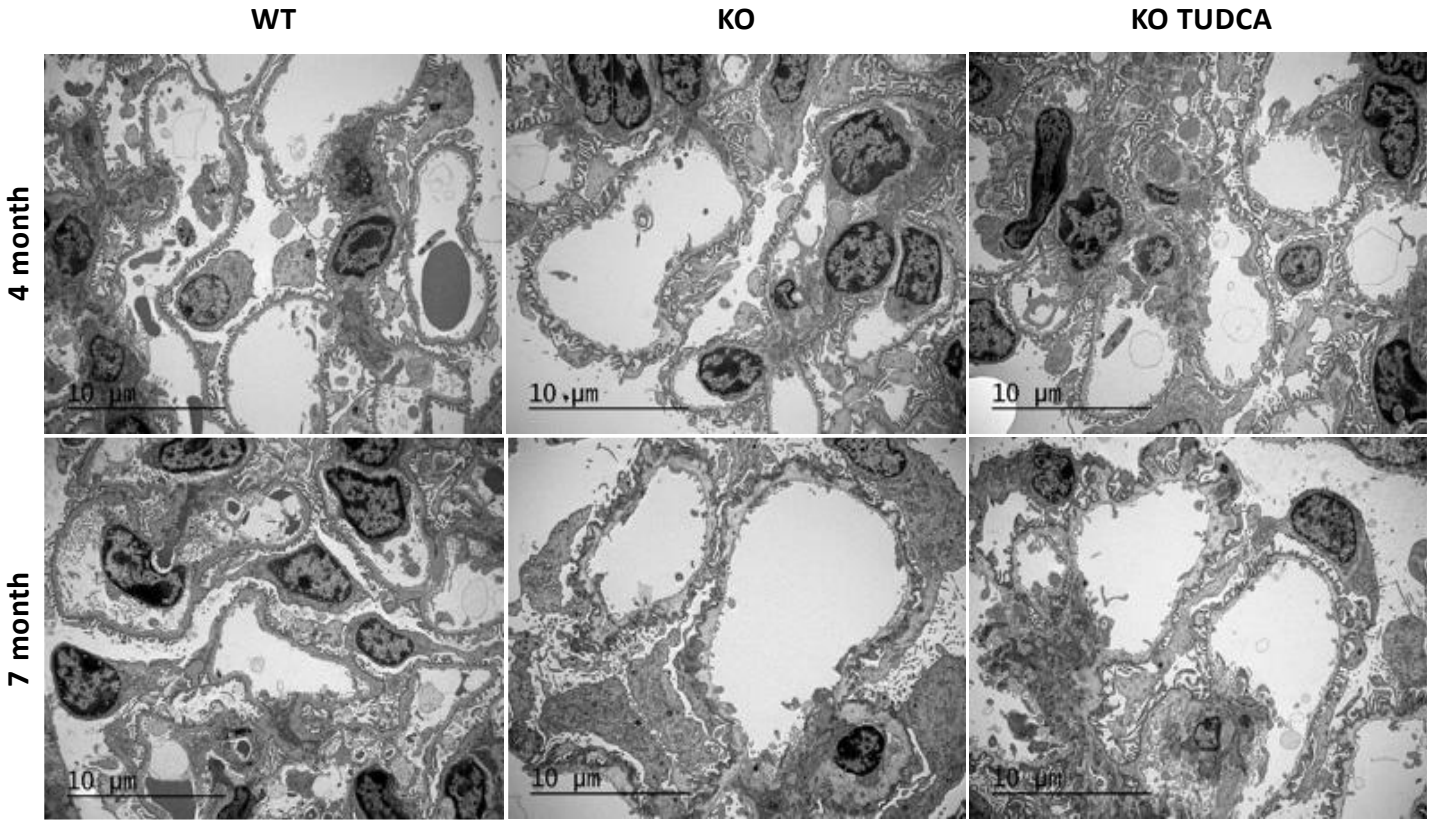

Figure 7. Transmission Electron micrographs of mouse kidneys, showing glomerular changes at 4 (top row) and 7 (bottom row) months in WT, *Col4α3*$^{-/-}$ (KO), and TUDCA-treated *Col4α3*$^{-/-}$ (KO TUDCA) mice. At 4 months, glomeruli of KO mice (top center) and KO TUDCA mice (top right) reveal features of segmental podocyte injury, including mild segmental podocyte foot process effacement, more extensive but segmental foot process irregularity, and mild microvillous change. These podocyte changes are concurrent with segmentally prominent "knob-like" subepithelial basement redundancy, characteristic of the *Col4α3*$^{-/-}$ mouse model. WT mice (top left) show none of these changes. At 7 months (bottom row), KO mice (bottom center) reveal more severe and widespread podocyte injury, demonstrated by extensive podocyte foot process effacement and irregularity, cellular hypertrophy, and microvillous change. There are also comparable glomerular basement membrane changes including extensive subepithelial basement redundancy and segmental "basket weave", and segmental glomerular capillary loop dilation. In contrast, KO TUDCA mice (bottom right) show podocyte and glomerular basement membrane changes that are similar in nature to those of the KO mice but are less extensive and more segmental. None of these changes are seen in Control mice (bottom left). All images are the same magnification – scale bar = 10 µm.

A

Gene	2 Mo	4 Mo	7 Mo
CCL2	NS	2.5	9.2
CCL4	ND	ND	ND
CCL5	NS	ND	2.81
CCL11	2.6	ND	ND
CCL22	NS	ND	4.03
CXCL1	3.34	3.03	17.4
CXCL10	ND	ND	1.57
IL1RN	NS	ND	6.73
IL-7	NS	ND	1.77
MMP2	1.62	2.64	13.4
MMP9	NS	ND	2.07
TIMP1	2.13	3.97	20.8
TIMP2	NS	1.77	4.2
Rela	1.35	1.26	1.79
NFKBIA	NS	ND	2.33
Jun	NS	ND	2.67
Osm	NS	ND	1.42
Smarca4	NS	1.17	1.52
Kras	NS	ND	1.7

B

Gene	2 Mo	4 Mo	7 Mo
CCL2	NS	2.5	9.2
CCL4	ND	ND	ND
CCL5	NS	ND	2.81
CCL11	2.6	ND	ND
CCL22	NS	ND	4.03
CXCL1	3.34	3.03	17.4
CXCL10	ND	ND	1.57
IL1RN	NS	ND	6.73
IL-7	NS	ND	1.77
MMP2	1.62	2.64	13.4
MMP9	NS	ND	2.07
TIMP1	2.13	3.97	20.8
TIMP2	NS	1.77	4.2

Table 2. Upstream activators (A) and downstream TNF pathway markers (B) from the NEPTUNE dataset characterizing FSGS and MCD outcome. In A, the upstream activators were identified in the poor prognosis cluster representing disease progression, and the genes in B were identified in the same NEPTUNE population in renal parenchyma and as urine proteins and represent down-stream targets of TNF. The values represent DEGs from the *Col4α3*$^{-/-}$ mice at 2, 4, or 7 months and are expressed as fold-increase over respective age-matched WT and are FCLog 10. All values are significant ($p<0.05$) or shown as NS - not significant, or ND - Not Differentially Expressed.

C3 forward: 5'-CGCAACGAACAGGTGGAGATCA, reverse: 5'-CTGGAAGTAGCGATTCTTGGCG-3'

Ccl2 forward: 5'-GCTACAAGAGGATCACCAGCAG-3', reverse: 5'-GTCTGGACCCATTCCTTCTTGG-3'

Ccr2 forward: 5'-GCTGTGTTTGCCTCTCTACCAG-3', reverse: 5'-CAAGTAGAGGCAGGATCAGGCT-3'

Cxcl1 forward: 5'-TCCAGAGCTTGAAGGTGTTGCC-3', reverse: 5'-AACCAAGGGAGCTTCAGGGTCA-3'

Col1α1 forward: 5'-GGAGAGAGCATGACCGATGG-3', reverse: 5'-AAGTTCCGGTGTGACTCGTG-3'

Col1α2 forward: 5'-GCTGGTGTAATGGGTCCTCC-3', reverse: 5'-ATCCGATGTTGCCAGCTTCA-3'

Col3α1 forward: 5'-AGGCTGAAGGAAACAGCAA-3', Col3α1 reverse: 5'-TAGTCTCATTGCTTGCGTG-3'

Col4a3 forward: 5'-CAAAGGCATCAGGGGAATAACT-3' (aa-88, N-terminal region, 7S domain), 5'-ATTAGTGGCAGAGCTCTCG-3' (NC-1 domain), reverse: 5'-ACCCTTAGATCCGTTGCATCC-3'

Col4a4 forward: 5'-TTTGGACAGGGTACAGCTTG, reverse: 5'-TAGTGGCACACTTGGTGGAT

Col4a5 forward: 5'-CTGGAAGAATGGGTCCAGAT, reverse: 5'-GTTCCTTTGAAACCTGGGAA

Cyr61 forward: 5'-GTGAAGTGCGTCCTTGTGGACA-3', reverse: 5'-CTTGACACTGGAGCATCCTGCA-3'

EGF forward: 5'-ATCTGACTTCATGGAGACA-3', reverse: 5'-AACTGGCTCTGTCTGCCGT-3'

Egr1 forward: 5'-AGCGAACAACCCTATGAGCACC-3', reverse: 5'-ATGGGAGGCAACCGAGTCGTTT-3'

FosB forward: 5'-ACCTGTCTTCGGTGGACTCCTT-3', reverse: 5'-TGGCTGGTTGTGATTGCGGTGA-3'

GAPDH forward: 5'-CCATGGAGAAGGCTGGGG-3', reverse: 5'-CAAAGTTGTCATGGATGACC-3'

Lif forward: 5'-TCAACTGGCACAGCTCAATGGC-3', reverse: 5'-GGAAGTCTGTCATGTTAGGCGC-3'

LOX forward: 5'-CCGGTTACTTCCAGTACGGT-3', reverse: 5'-ATCCGCCCTATATGCTGAAC-3'

LOXL2 forward: 5'-GGAAAGCCTACAAGCCAGAG-3', reverse: 5'-GCAGATACCAGGTCCCACTT-3'

TNFα forward: 5'-ACGTCGTAGCAAACCACCA-3', reverse: 5'-TTGTCCCTTGAAGAAAACCT-3'

TGFβ-1 forward: 5'-CAGTGGCTGAACCAAGGAG-3', reverse: 5'-ATCCCGTTGATTCCAGGTG-3'

Vcan forward: 5'-GGACCAAGTTCCACCCTGACAT-3', reverse: 5'-CTTCACTGCAAGGTTCCTCTTCT-3'

Table 3. PCR Primer Sequences - Methods