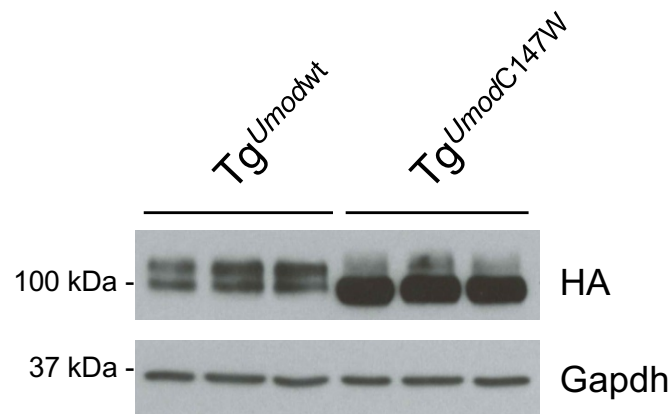


**Early involvement of cellular stress and inflammatory signals in the pathogenesis of tubulointerstitial kidney disease due to *UMOD* mutations**

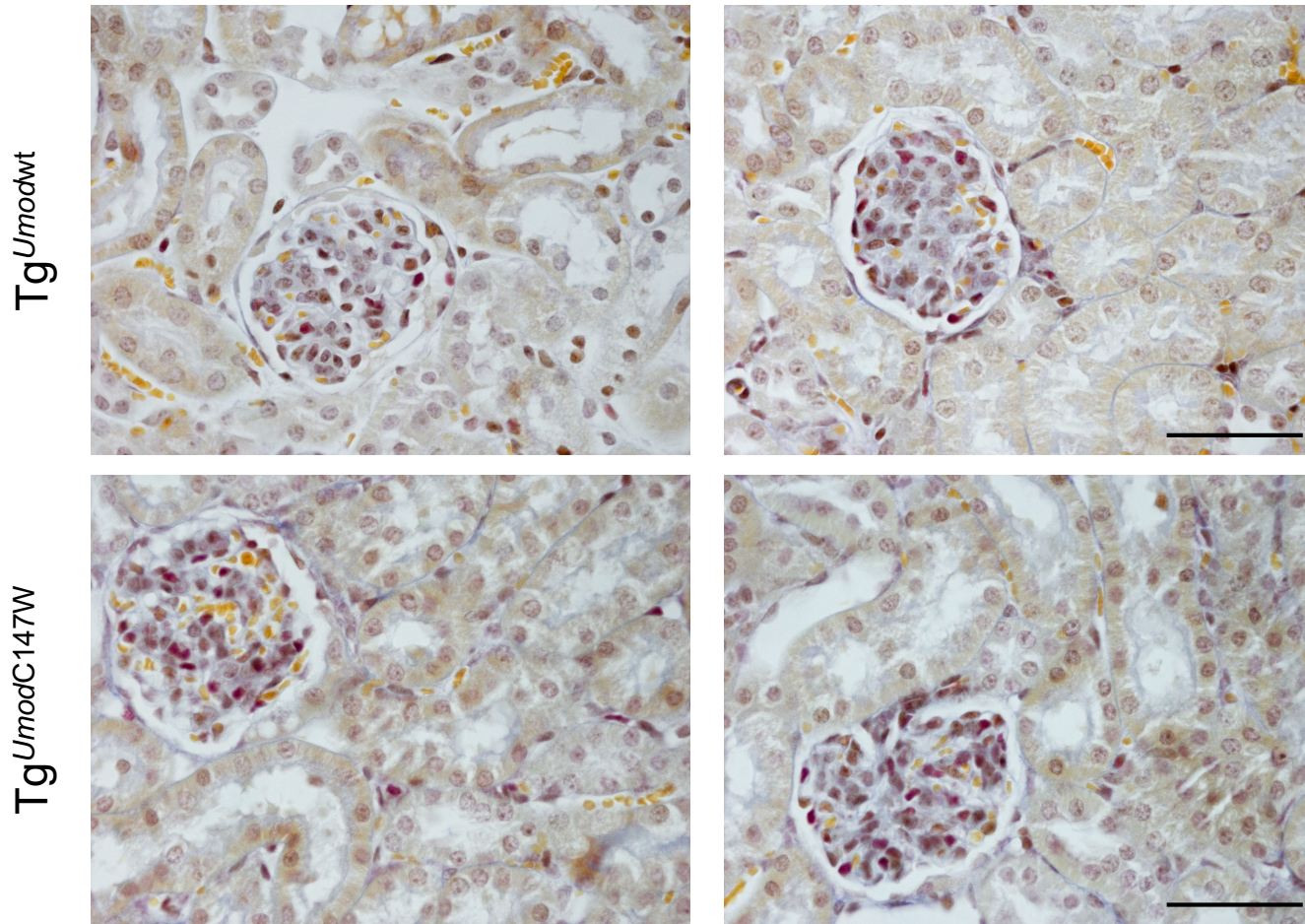
Matteo Trudu<sup>1</sup>, Celine Schaeffer<sup>1</sup>, Michela Riba<sup>2</sup>, Masami Ikehata<sup>3,4</sup>, Paola Brambilla<sup>5</sup>, Piergiorgio Messa<sup>3,4</sup>, Filippo Martinelli-Boneschi<sup>5</sup>, Maria Pia Rastaldi<sup>3</sup>, Luca Rampoldi<sup>1\*</sup>

***SUPPLEMENTARY INFORMATION***

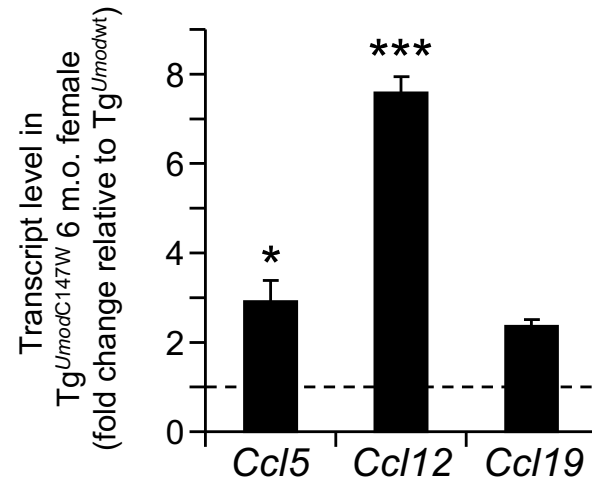
***Supplementary Figures 1-6, Supplementary Table 1***



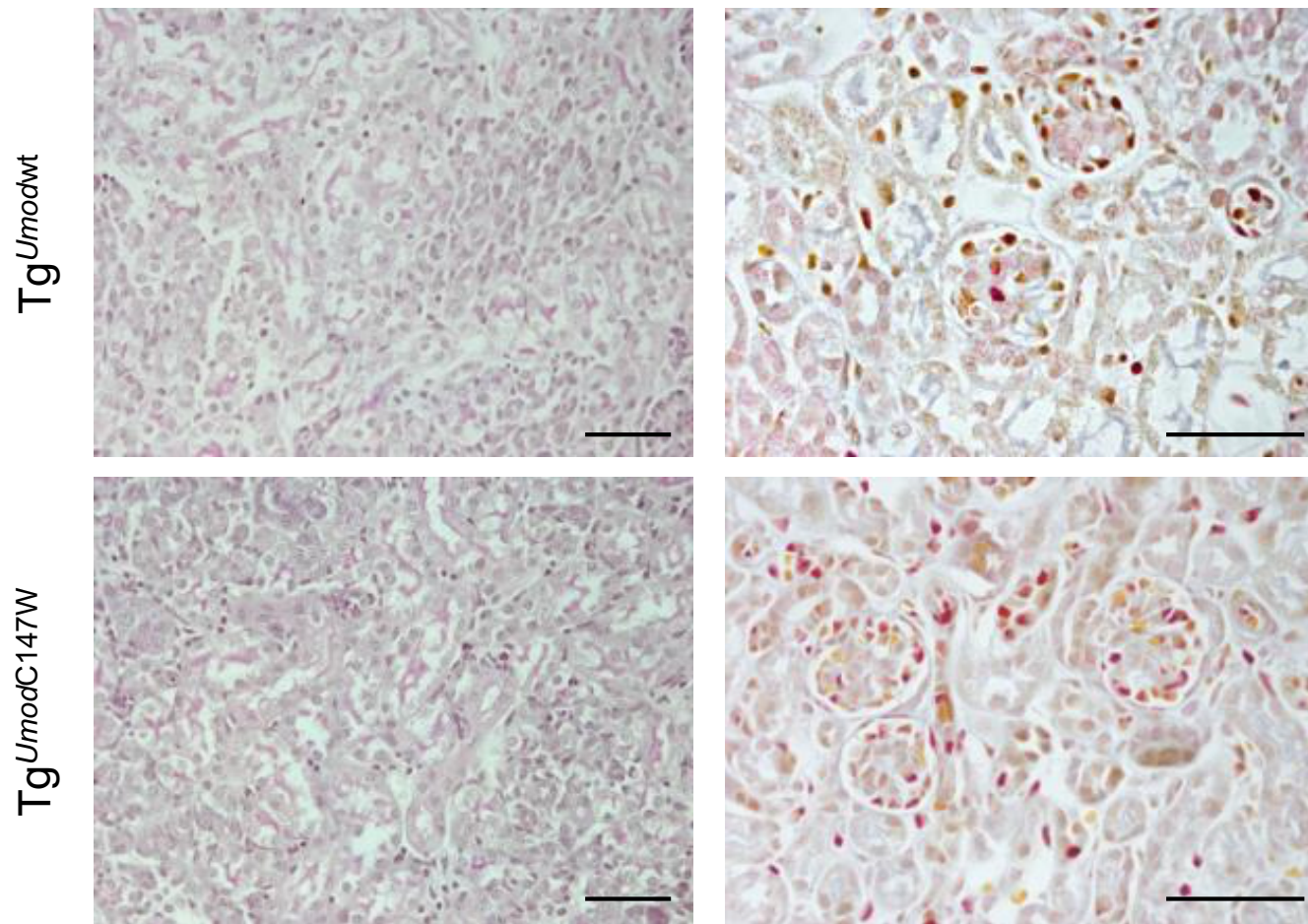
**Supplementary Figure 1.** Western blot analysis showing expression of HA-tagged transgenic uromodulin in kidneys of 1 month-old  $Tg^{Umodwt}$  and  $Tg^{UmodC147W}$  mice. The figure shows cropped blot images (full blots are reported in **Supplementary Figure 6**). Mutant uromodulin is strongly retained in the ER, as demonstrated by the accumulation of the lower molecular weight isoform, corresponding to uromodulin ER precursor. Gapdh was used as loading control.



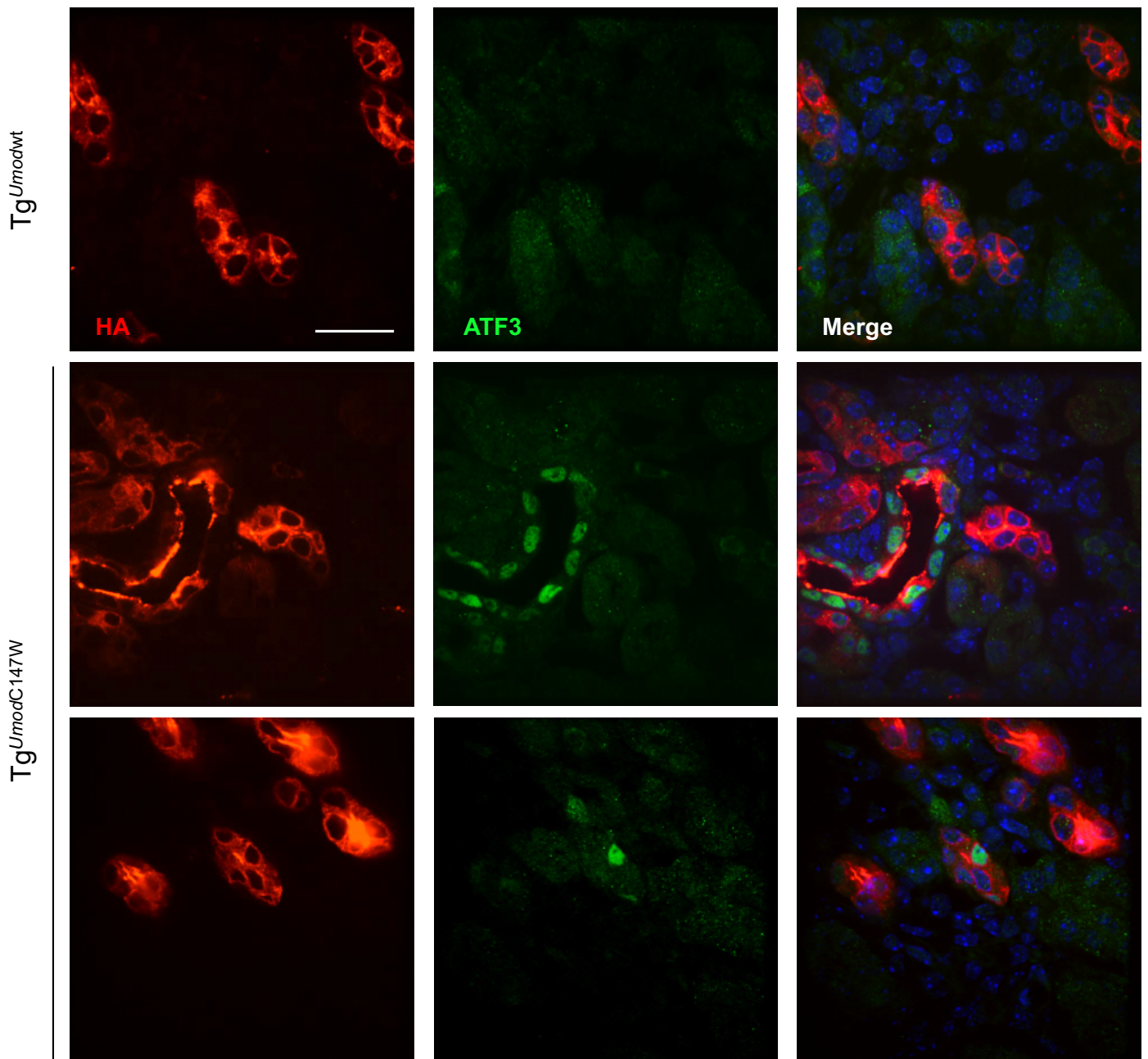
**Supplementary Figure 2.** Representative histological images of glomeruli in kidneys of 1 month-old  $Tg^{UmodC147W}$  and  $Tg^{Umodwt}$  (AFOG; scale bar 50  $\mu$ m). Quantification of mesangial hypercellularity, mesangial matrix expansion and focal/segmental glomerulosclerosis showed no difference between  $Tg^{UmodC147W}$  and  $Tg^{Umodwt}$  mice (data not shown, n = 9  $Tg^{Umodwt}$  and 6  $Tg^{UmodC147W}$ ).



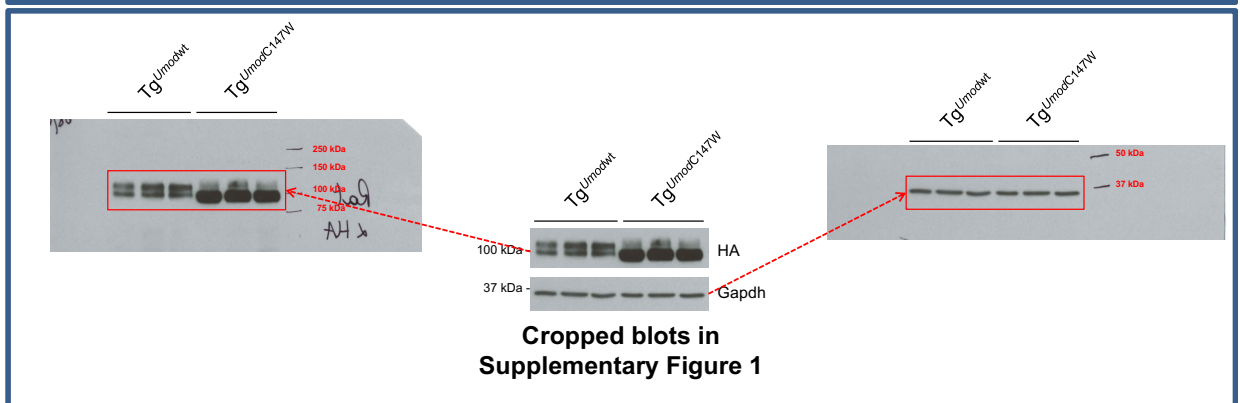
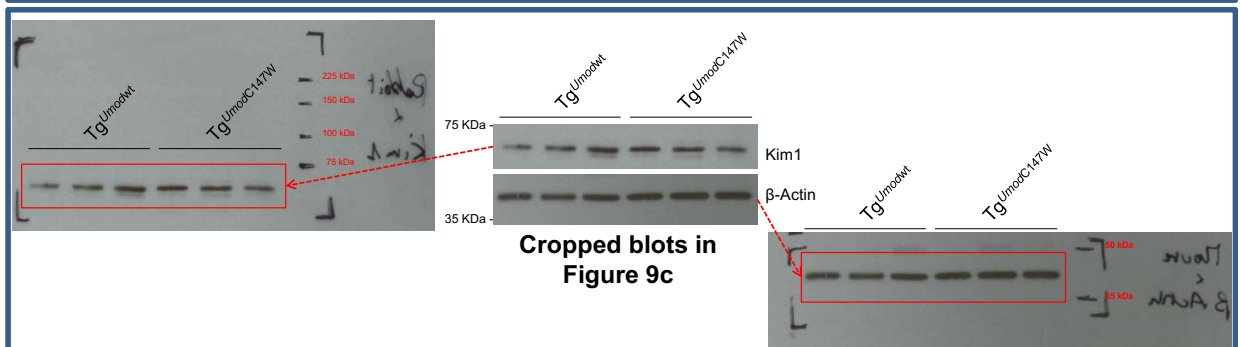
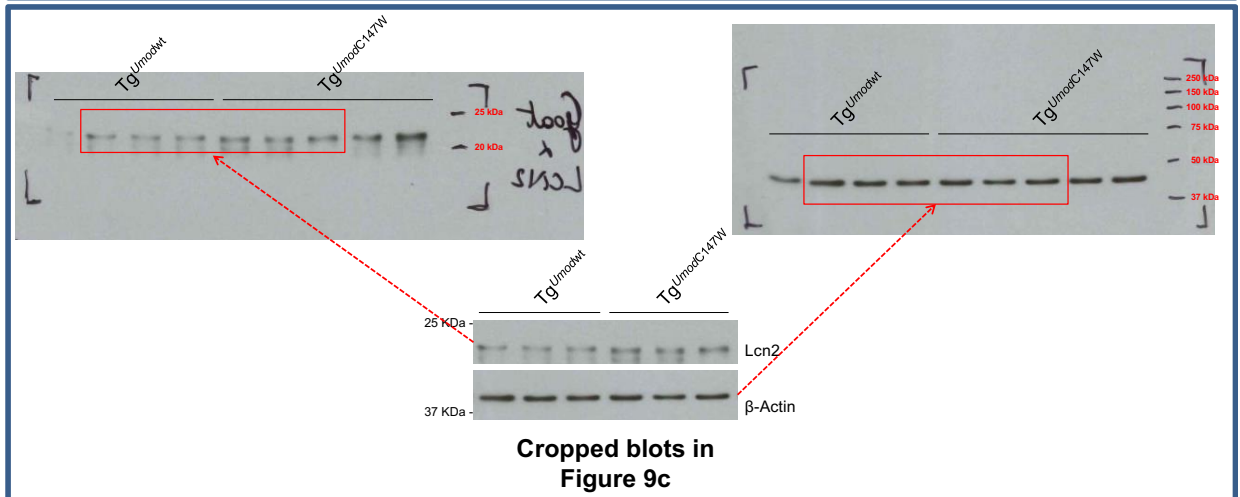
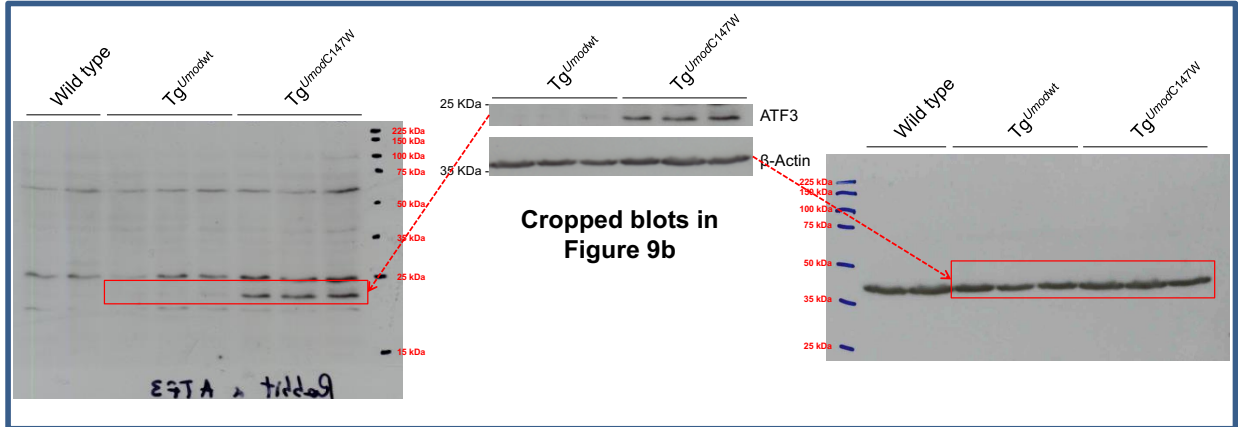
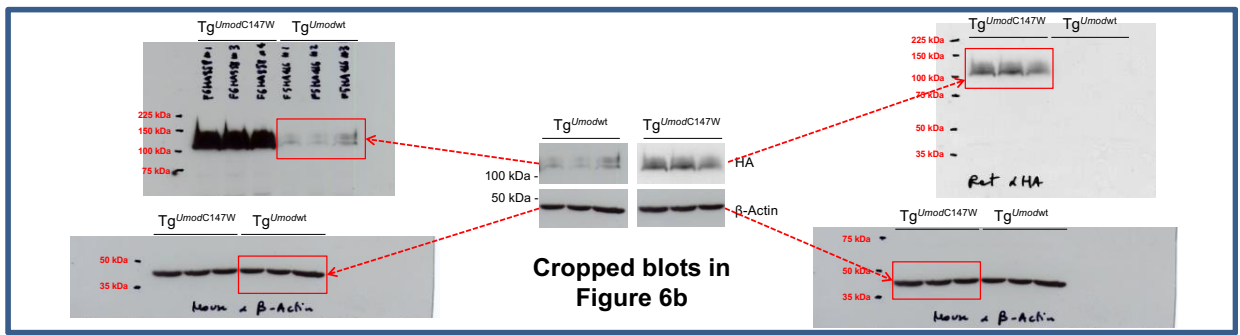
**Supplementary Figure 3.** Analysis by real-time RT-qPCR of the expression of selected chemokines in 6 month-old  $Tg^{UmodC147W}$  mice relative to age- and sex-matched  $Tg^{Umodwt}$  (n = 5/group). Data are expressed as mean  $\pm$  s.e.m. \* $P$  < 0.05; \*\*\* $P$  < 0.001 (unpaired  $t$ -test).



**Supplementary Figure 4.** Representative histological images of tubular architecture and glomeruli in kidneys of  $Tg^{UmodC147W}$  and  $Tg^{Umodwt}$  mice at p8 (PAS, left panels, and AFOG, right panels; scale bar 50  $\mu$ m). Quantification of tubular casts, tubular damage, interstitial inflammation, interstitial fibrosis, mesangial hypercellularity, mesangial matrix expansion and focal/segmental glomerulosclerosis showed no difference between  $Tg^{UmodC147W}$  and  $Tg^{Umodwt}$  mice (data not shown, n = 4/group).



**Supplementary Figure 5.** Expression of Atf3 in the kidneys of p8 transgenic mice. Immunofluorescence analysis reveals that Atf3 is specifically detected in nuclei of TAL segments in kidneys of *Tg<sup>UmodC147W</sup>* mice (scale bar 15  $\mu$ m).



**Supplementary Figure 6.** Full image of blots shown as cropped images in **Figure 6b**, **Figure 9b**, **Figure 9c**, **Supplementary Figure 1**. The red boxes indicate the cropped images.

**Supplementary Table 1.** List of primers used for SYBR Green real-time RT-qPCR.

<b>Target gene</b>	<b>Forward primer (5'-3')</b>	<b>Reverse primer (5'-3')</b>
<i>Ccl5</i>	GTGCCCACGTCAAGGAGTATT	CCCACCTTCTTCTCTGGGTTGG
<i>Ccl12</i>	CATCAGTCCTCAGGTATTGGCTGGA	CTTGGGGTCAGCACAGATCTCCTT
<i>Ccl19</i>	CTGGCCTTCAGCCTGCTGGT	TGCGATCCACCCAGGGCTGG
<i>Tgfb1</i>	CCCGCGTGCTAATGGTGGACC	TGCACGGGACAGCAATGGGG
<i>Vim</i>	GGATCAGCTCACCAACGACA	GGTCAAGACGTGCCAGAGAA
<i>Col6a1</i>	ACCGACTGCGCCATTAAGAA	GTCGGTCACCACGATCAAGT
<i>Acta2</i>	GCTACGAACTGCCTGACGG	GCTGTTATAGGTGGTTTCGTGGA
<i>Acox3</i>	GCTCACTTCACAAGCCCTCT	TAGCAAACAAGCCAGCGGTA
<i>Ehhadh</i>	GCCATAGTGATCTGTGGAGCA	ACCACTGGCTTCTGGTATCG
<i>Cyp4b1</i>	CCAGCTCAGCAAGCCAGTAA	GTGGGTCAAAGACCTCTGGG
<i>Col1a1</i>	CTGACGCATGGCCAAGAAGA	ATACCTCGGGTTTCCACGTC
<i>Ntn4</i>	AGGATTTTCTGCCCTCCGAC	ATGGGAGCCTTTGTCTGTGG
<i>Panx1</i>	GCTCATCTCGCTGGCCTTCGC	AATCCACAAAGGCAGCCTGTCGC
<i>Slc13a3</i>	TATGGTGAATGAGCTGGAGA	GGCAAACGTGCAGAACAAGAT
<i>Slc25a17</i>	GCCTCTGTGCTGTCCTACG	ACCTGAAGCCGAAGTCTAGC
<i>Cd5</i>	CCCTTGCCAATTCGATGGGA	GGGCTGGAAATCAGAGCAGA
<i>Cd19</i>	ACCAGTTGGCAGGATGATGG	GCTGAGGAGCTGCATAGAGG
<i>Ptprc</i>	GGAGACCAGGAAGTCTGTGC	GTTCTGGGCTCCTTCCTCTT
<i>Cd68</i>	CTGACAAGGGACACTTCGGG	AGGCCAATGATGAGAGGCAG
<i>Fut4</i>	GAGGTGGGTGTGGATGAACT	GTTGGATCGCTCCTGGAATA
<i>Lcn2</i>	TCCCCCTGCAGCCAGACTTCC	AGTAGCGACAGCCCTGGTCCTG
<i>Havcr1</i>	TTGGCATCTGCATCGCAGCCC	GGGAATGCACAACCGCTGCGT
<i>Atf3</i>	CAGAAGTCAGTGCGACCGCC	TCGCCGCCTCCTTTTCTCTCA
<i>Hprt1</i>	ACATTGTGGCCCTCTGTGTG	TTATGTCCCCCGTTGACTGA