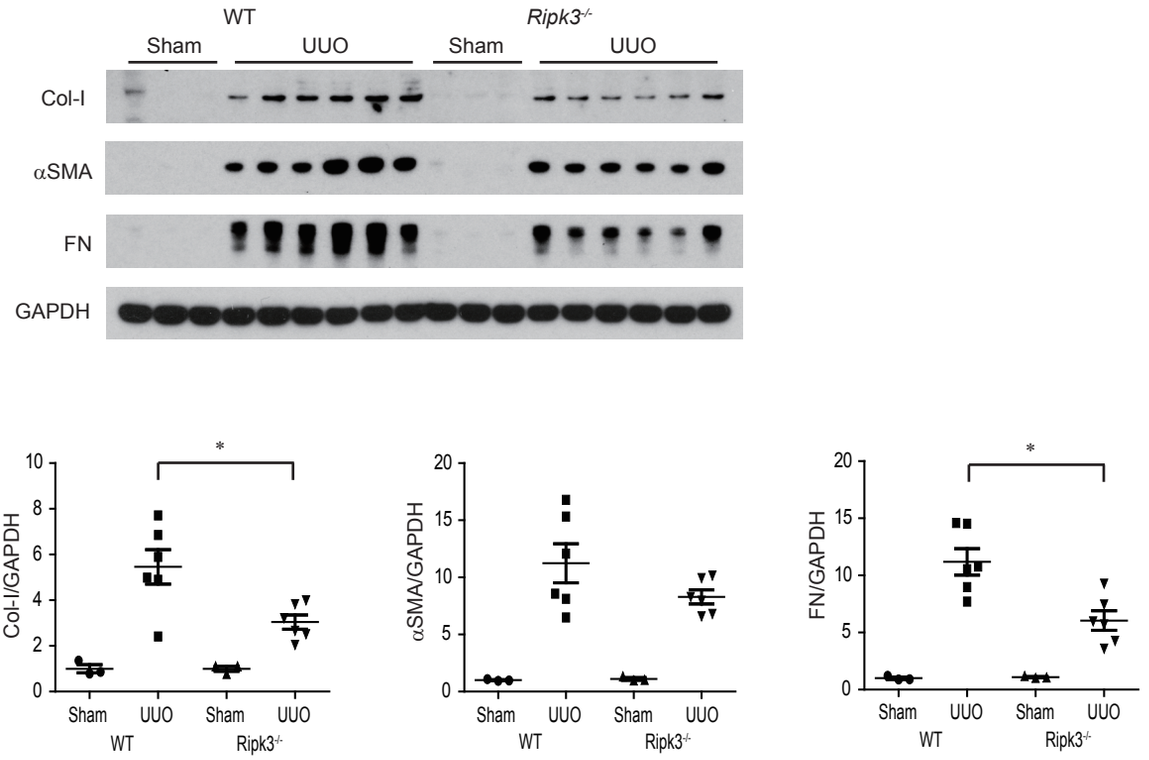
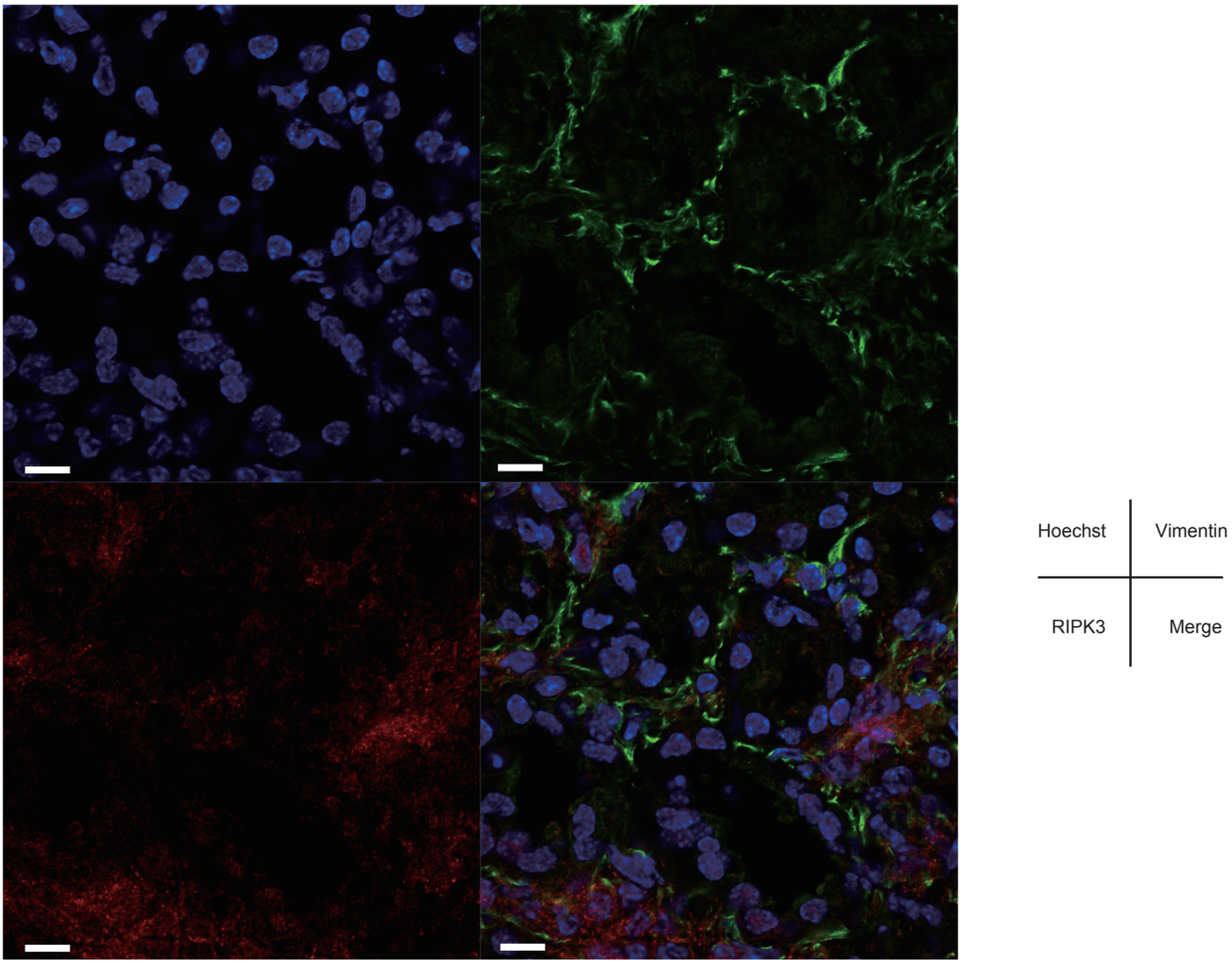
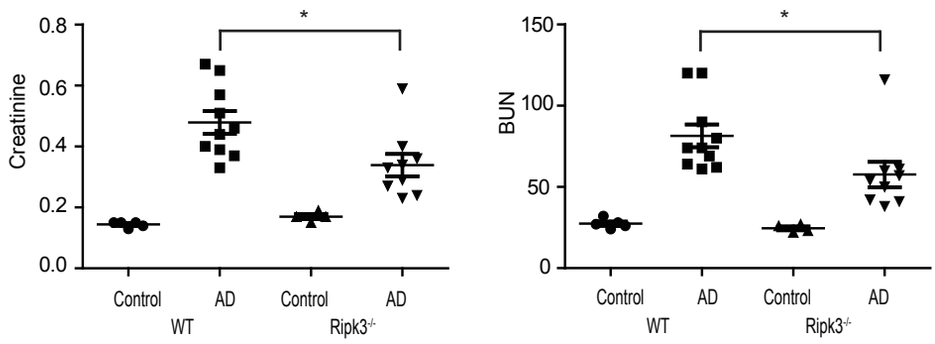


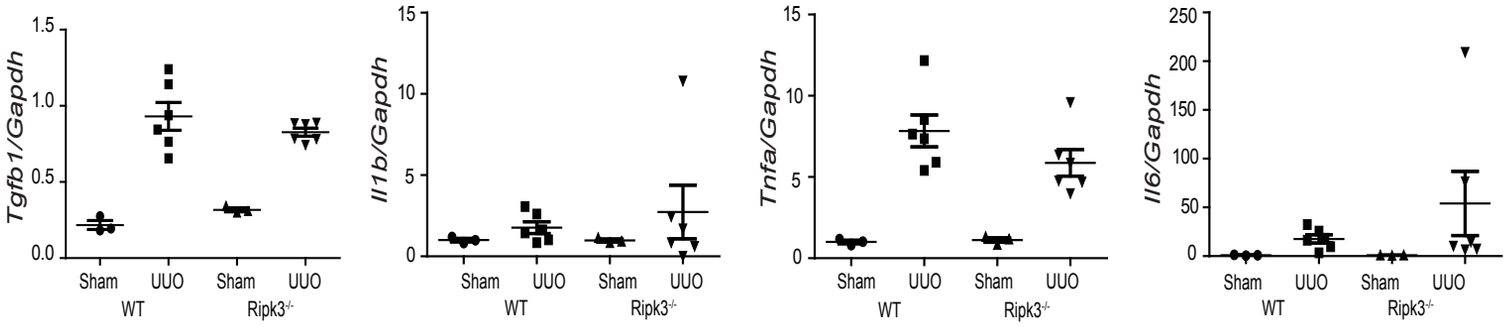
Supplemental Figure 1. Western blot analysis at 13 days after UUO or sham surgery. WT or *Ripk3*$^{-/-}$ mice were subjected to sham operation or UUO and kidneys were harvested at 13 d after surgery. Kidney tissue lysates were subjected to Western blot analysis for α–smooth muscle actin (αSMA), Type-I collagen (Col-I), and fibronectin (FN). GAPDH was the standard. (n = 6 for UUO, n = 3 for Sham) Dot plots are densitometric analysis of Western blot data (mean ± s.e.m). *P<0.05 compared with WT UUO mice by ANOVA with Newman-Keuls post-hoc test.



Supplemental Figure 2. Immunofluorescence staining for RIPK3 (red), Vimentin (green), and Hoechst (Blue) in the kidney of WT mice 7 days after UUO surgery. Single channel and merged staining as indicated. Scale bars, 10 μm.



Supplemental Figure 3. Renal function at 7 days after adenine diet. WT or *Ripk3*$^{-/-}$ mice were subjected to control or 0.2% adenine diet (AD) and serum was harvested at 7 d. Serum creatinine and BUN were measured (mean ± s.e.m). **P*<0.05 compared with WT AD-fed mice by ANOVA with Newman-Keuls post-hoc test. WT control diet (n=5), WT AD (n=10), *Ripk3*$^{-/-}$ Control diet (n=4), *Ripk3*$^{-/-}$ AD (n=9).



Supplemental Figure 4. Cytokine expression at 3 days after UUO. WT and *Ripk3*$^{-/-}$ mice were subjected to UUO or sham surgery and kidneys were harvested after 3 d. Expression of *Tgfb1*, *Il1b*, *Tnfa*, and *Il6* mRNA was analyzed by qRT-PCR. *Gapdh* was the standard. Values represent mean ± s.e.m (*n*=6 for UUO, *n*=3 for Sham).

Supplemental Table 1. Patient characteristics.

Subject number	Age	Gender	History	Serum Creatinine	Diagnosis
1	51	Male	Clear Cell Renal Carcinoma, HTN	1.3	Normal kidney tissue margins (nephrectomies for renal carcinoma)
2	72	Male	Clear Cell Renal Carcinoma, HTN	1.3	Normal kidney tissue margins (nephrectomies for renal carcinoma)
3	61	Female	Clear Cell Renal Carcinoma, HTN	1.4	Normal kidney tissue margins (nephrectomies for renal carcinoma)
4	57	Male	Unclassified kidney tumor	1.5	Normal kidney tissue margins (nephrectomies for renal carcinoma)
5	78	Male	Clear Cell Renal Carcinoma, HTN	1.5	Normal kidney tissue margins (nephrectomies for renal carcinoma)
6	48	Male	RT	2.05	Acute tubular injury
7	39	Male	RT Prograf	1.51	Acute tubular injury
8	47	Male	SLE, LRT, RT Prograf	7.63	Acute tubular injury
9	68	Female	RT	3.33	Acute tubular injury , ATN
10	48	Female	HTN, LURT DGF	2.09	Acute tubular injury , ATN
11	72	Male	DM, HTN, DDRT	5.56	DM nephropathy with extensive TIF
12	57	Female	DM, DDRT	3.52	DM nephropathy with widespread TIF
13	50	Male	DM, DDRT	1.53	DM nephropathy with extensive TIF
14	68	Female	DM, uncontrolled, DDRT	2.84	DM nephropathy with moderate TIF
15	64	Male	HTN, DM, PVD RT	2.92	DM nephropathy with extensive TIF
16	85	Male	ESRD unknown etiology, CAD, DDRT	1.13	DM nephropathy with minimal TIF (Donor had DM)

RT: renal transplantation, LURT: living unrelated renal transplantaion, LRT: living related donor renal transplantaion, DM: diabetes mellitus, HTN: hypertension, CAD: coronary artery disease, SLE: systemic lupus erythematosus, DGF: delayed graft function , ATN: acute tubular necrosis, TIF: tubular interstitial fibrosis, DDRT: deceased-donor renal Transplant , PVD: peripheral vascular disease, ESRD: end-stage renal disease

Supplemental Table 2. Primers used for qRT-PCR.

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
mRIPK3	CTCCGTGCCTTGACCTACTG	AACCATAGCCTTCACCTCCC
mCol1a1	AGCTTTGTGGATACGCGGAC	TAGGCACGAAGTTACTGCAAG
mActa2	GCTGGTGATGATGCTCCCA	GCCCATTCCAACCATTACTCC
mTGFb1	AACTATTGCTTCAGCTCCAGAGAGA	AGTTGGATGGTAGCCCTTG
mIl1b	CAACCAACAAGTGATATTCTCCAT	GATCCACACTCTCCAGCTGCA
mTnfa	GCGGTGCCTATGTCTCAG	GCCATTTGGGAACTTCTCATC
mIl6	ACAACCACGGCCTTCCCTACTT	CACGATTTCCCAGAGAACATGTG
mGAPDH	TCAACAGCAACTCCCACTCTTCCA	ACCCTGTTGCTGTAGCCGTATTCA
hRIPK3	AATTCGTGGCTGCGCCTAGAAG	TCGTGCAGGTAAAACATCCCA
hGAPDH	ACCAAATCCGTTGACTCCGAC	CTCCTGTTCGACAGTCAGCC