

1 Manuscript number: JASN-2020-04-0523

2 **SUPPLEMENTARY INFORMATION**

3  
4 **Only hyperuricemia with crystalluria but not asymptomatic hyperuricemia drives chronic**  
5 **kidney disease**

6  
7 Markus Sellmayr, Moritz Roman Hernandez Petzsche, Qiuyue Ma, Nils Krüger, Helen Liapis,  
8 Andreas Brink, Barbara Lenz, Maria Lucia Angelotti, Viviane Gnemmi, Christoph Kuppe, Hyojin  
9 Kim, Eric M.J. Bindels, Ferenc Tajti, Julio Saez-Rodriguez, Maciej Lech, Rafael Kramann, Paola  
10 Romagnani, Hans-Joachim Anders, Stefanie Steiger

11  
12  
13 Table of content

14 1. Supplementary Methods .....	2
15 1.1 Human microarray gene expression data of different CKD entities .....	2
16 2. Supplementary Figures.....	3
17 2.1 Supplementary Figure 1 .....	3
18 2.2 Supplementary Figure 2 .....	5
19 2.3 Supplementary Figure 3 .....	6
20 2.4 Supplementary Figure 4 .....	8
21 3. Supplementary Movies.....	10
22 3.1 Supplementary Movie 1 .....	10
23 3.2 Supplementary Movie 2 .....	10
24 4. Supplementary Tables .....	11
25 4.1 Supplementary Table 1. Murine primer sequences .....	11
26 5. References .....	12

27  
28

29 **1. Supplementary Methods**

30 **1.1 Human microarray gene expression data of different chronic kidney disease entities**

31 We searched in Nephroseq ([www.nephroseq.org](http://www.nephroseq.org)) and Gene Expression Omnibus (GEO) <sup>3</sup>,  
32 <sup>4</sup>, and identified five studies – GSE20602 <sup>5</sup>, GSE32591 <sup>6</sup>, GSE37460 <sup>6</sup>, GSE47183 <sup>7,8</sup>, GSE50469  
33 <sup>9</sup> – with human microarray gene expression data for different CKD entities: lupus nephritis  
34 (LN), rapidly progressive glomerulonephritis (RPGN), membranous glomerulonephritis (MGN),  
35 IgA nephropathy (IgAN), hypertensive nephropathy (HN), diabetic nephropathy (DN), focal  
36 segmental glomerulosclerosis (FSGS), and minimal change disease (MCD), as well as healthy  
37 tissue from kidney tumor nephrectomy (TN) as control, as previously described <sup>10</sup>. In one  
38 dataset, patients were labeled as an overlap of FSGS and MCD (FSGS-MCD). The data were  
39 imported in R (R version 3.3.2), processed and normalized involving quality controls <sup>10</sup>.  
40 Heatmaps were generated to demonstrate the normalized expression of the inflammatory  
41 genes of interest across all CKD entities and the hierarchical clustering of the arrays based on  
42 the gene expression Spearman's correlation coefficients.

43

44

45

46

47

48

49

50

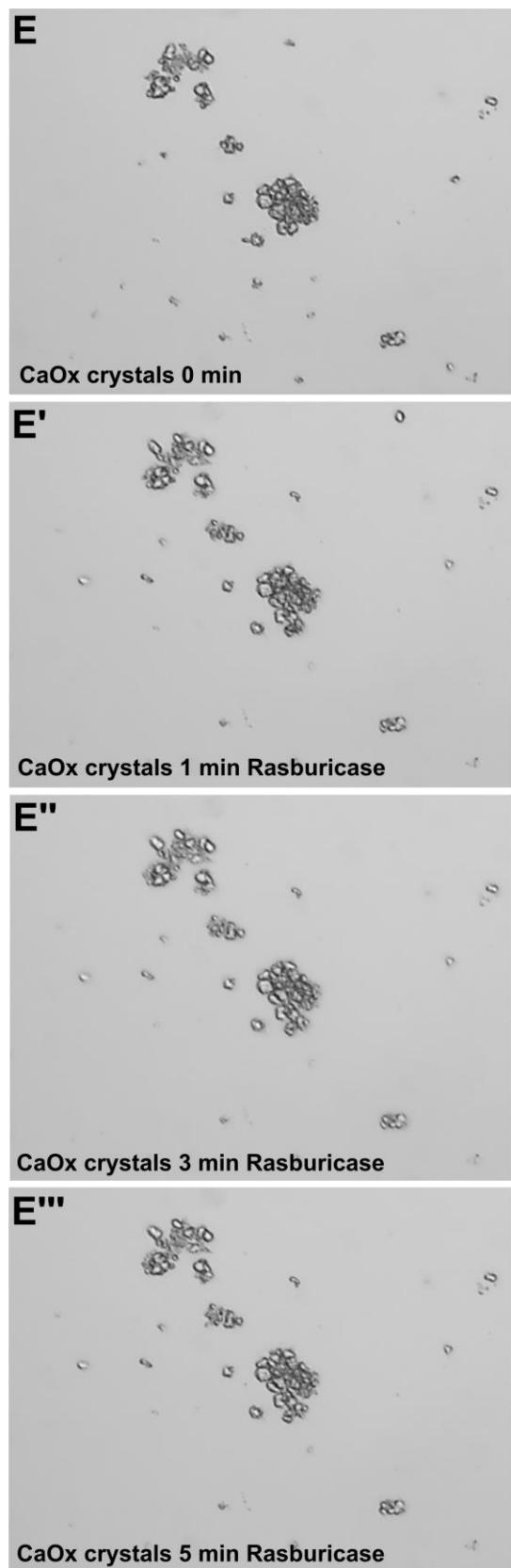
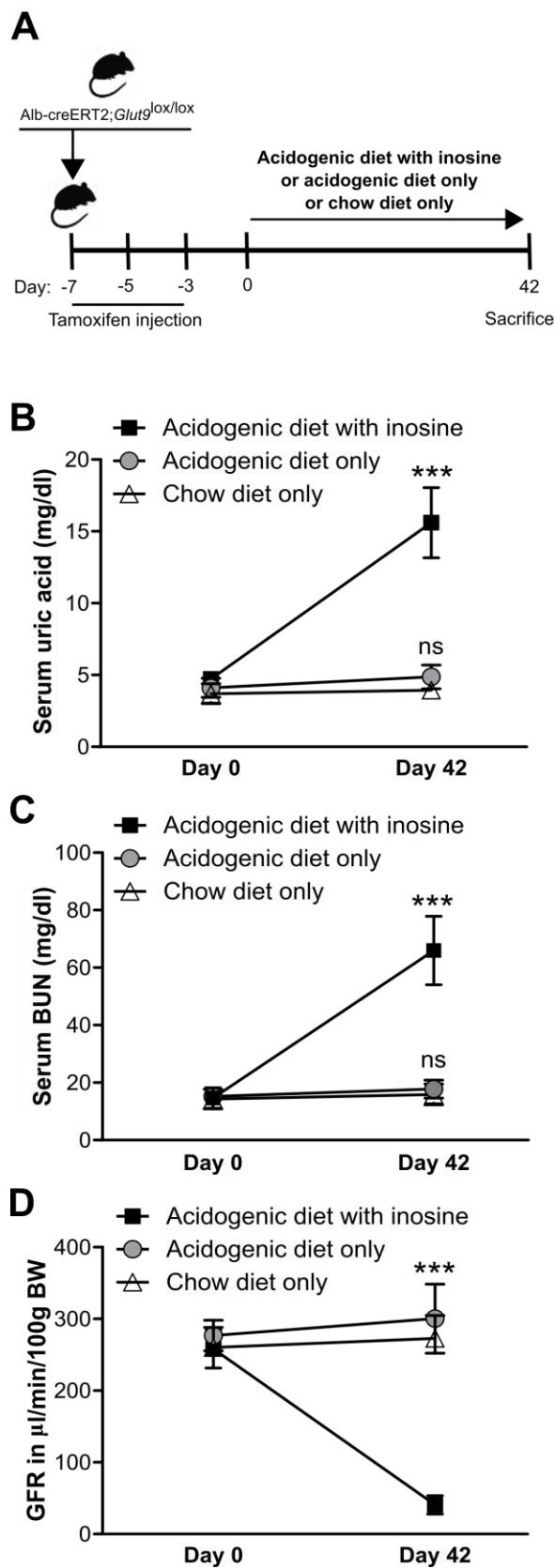
51

52

53

54 **2. Supplementary Figures**

55 **2.1 Supplementary Figure 1**



57 **Supplementary Figure 1. Only an acidogenic diet with inosine causes impairment in kidney**  
58 **function but not acidogenic and chow diet without inosine. (A - D)** Alb-creERT2;*Glut9*<sup>lox/lox</sup>  
59 mice were injected with tamoxifen and then placed either on an acidogenic diet with inosine,  
60 an acidogenic diet only or standard chow diet only for up to 42 day (A). Serum uric acid (B),  
61 blood urea nitrogen (BUN) (C) and GFR (D) were measured on day 0 and 42 (n = 5 mice per  
62 group). (E – E'') Urinary calcium oxalate (CaOx) crystals from mice with chronic oxalate  
63 nephropathy did not dissolve upon rasburicase treatment after 5 minutes. Magnification:  
64 x400. Data are mean ± SD. \*\*\* p<0.001; ns, not significant by one-way ANOVA.

65

66

67

68

69

70

71

72

73

74

75

76

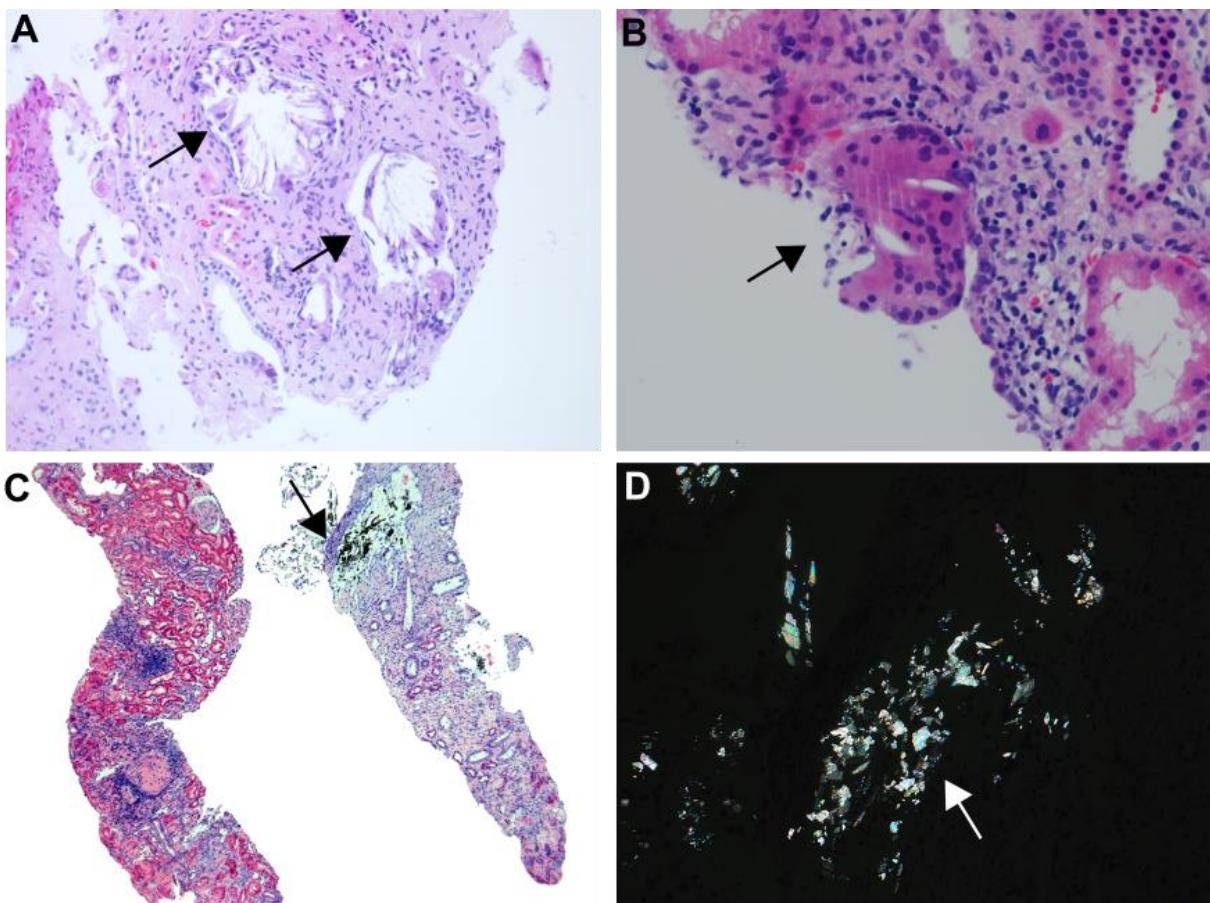
77

78

79

80

81 **2.2 Supplementary Figure 2**



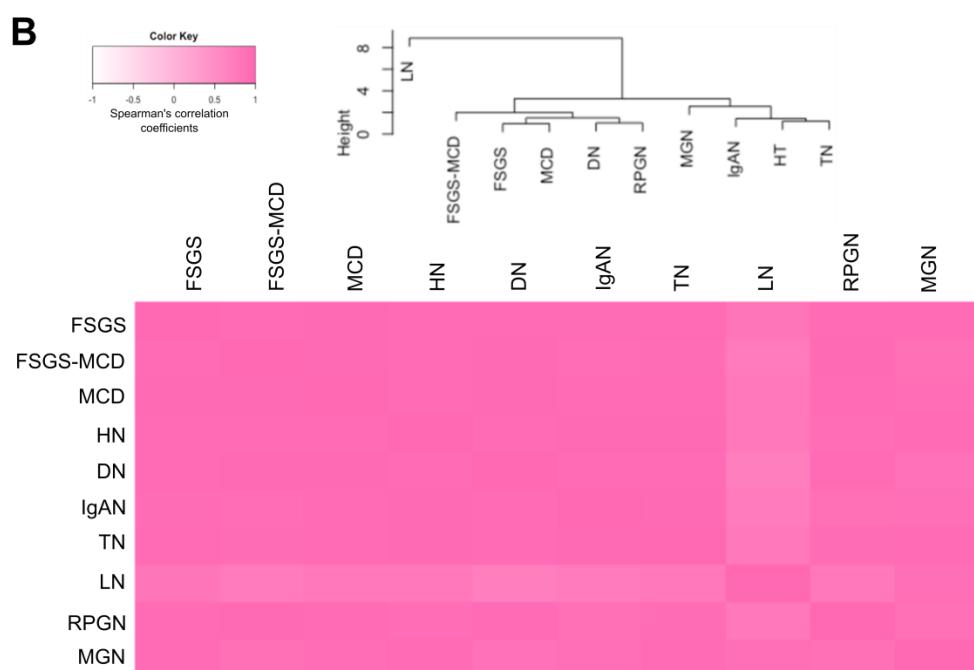
83 **Supplementary Figure 2. Histopathological abnormalities on kidney biopsies from patients**  
84 **with uric acid crystal deposits.** (A) Kidney biopsy shows epithelioid granulomas with colorless  
85 ghost-like UA crystals (black arrows, magnification: x100). The patient was a 75 years-old man  
86 with CKD, creatinine 3.8 mg/dl and proteinuria 1.6 g/24 hours. (B) UA granuloma with spindle  
87 shaped UA crystals including giant cell formation containing more than 30 nuclei (black arrow)  
88 (PAS stain, magnification: x200). (C) Low power of kidney biopsy containing both cortex and  
89 medulla shows diffuse interstitial fibrosis and focal glomerulosclerosis in the cortex, and  
90 undissolved crystal deposits (black arrow) in the medulla. The patient was a 47 years-old man  
91 with a history of biopsy proven IgA nephropathy, now presenting with proteinuria 2 g/24  
92 hours (Trichrome stain, magnification: x40). (D) UA crystal deposits visualized under a  
93 polarizable light microscope (white arrow, same biopsy as in C).

94

95

96

97      **2.3 Supplementary Figure 3**



98

99

100

101

102

103

104 **Supplementary Figure 3.** (A and B) Public available Affymetrix Human Genome arrays  
105 predicting gene expression profiles from different human CKD disease entities <sup>10</sup>: lupus  
106 nephritis (LN), rapidly progressive glomerulonephritis (RPGN), membranous  
107 glomerulonephritis (MGN), IgA nephropathy (IgAN), hypertensive nephropathy (HN), diabetic  
108 nephropathy (DN), focal segmental glomerulosclerosis (FSGS), minimal change disease (MCD),  
109 and one dataset of patients were labeled as overlap of FSGS-MCD, and healthy tissue from  
110 tumor nephrectomy (TN) as control. (A) Normalized gene expression of inflammatory genes  
111 of CKD entities illustrated as heat map. (B) Hierarchical clustering of CKD entities based on the  
112 expression of the gene set of interest using the Spearman's correlation coefficient illustrated  
113 as heat map.

114

115

116

117

118

119

120

121

122

123

124

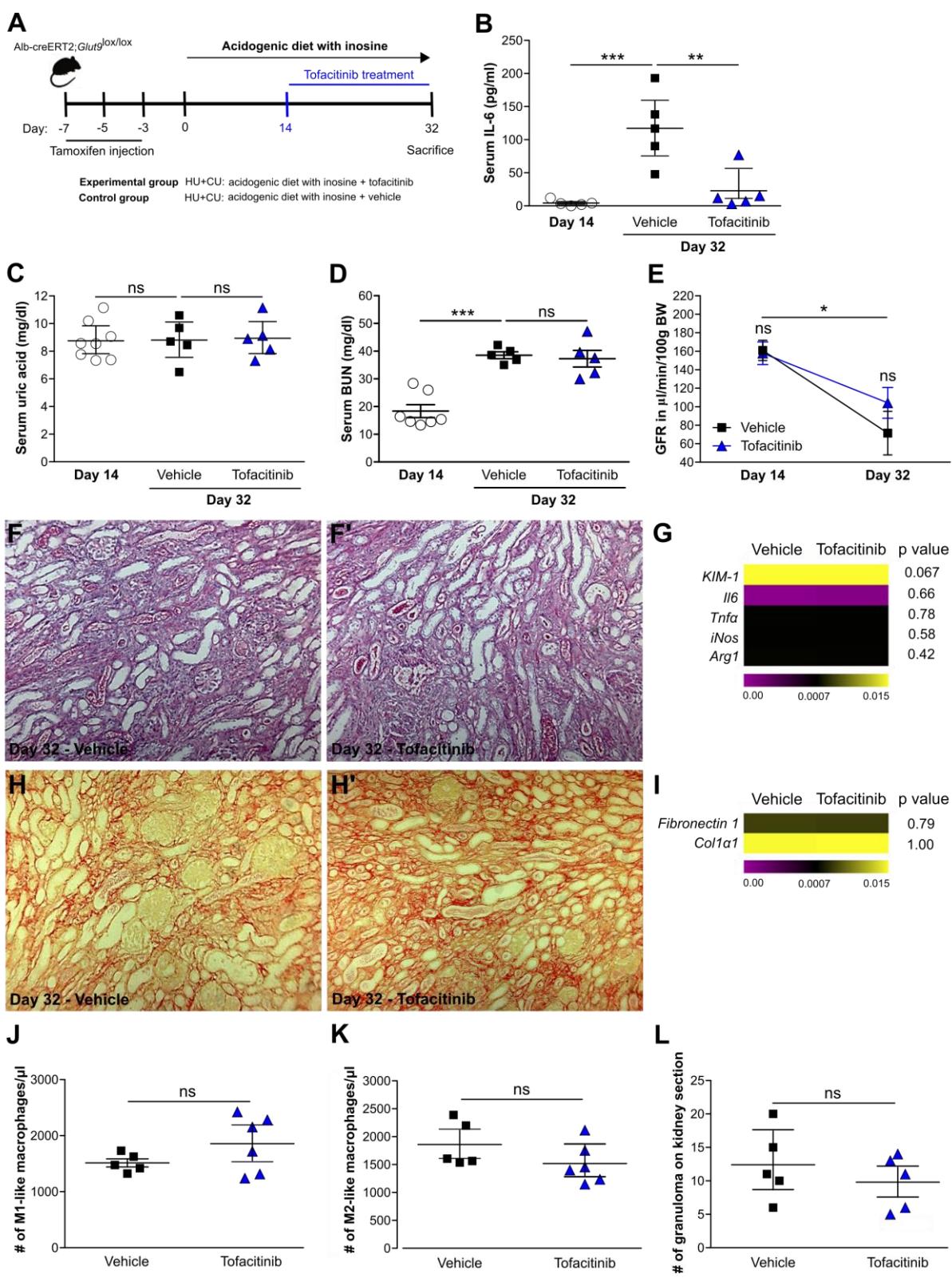
125

126

127

128

## 2.4 Supplementary Figure 4



133 **Supplementary Figure 4. Tofacitinib therapy does not prevent crystalluria, granuloma**  
134 **formation and CKD progression.** (A) Schematic of experimental set up of animal model. Alb-  
135 creERT2;*Gut9*<sup>lox/lox</sup> mice were injected intraperitoneally with tamoxifen and then fed an  
136 acidogenic diet with inosine for 32 days. On day 14, HU+CU mice were injected with tofacitinib  
137 or vehicle (control) every alternate day. (B) Serum IL-6 levels of tofacitinib- and vehicle-treated  
138 HU+CU mice on day 32 (n = 5 mice per group). (C - E) Serum uric acid (C) and blood urea  
139 nitrogen (BUN) levels (D), and glomerular filtration rate (GFR) (E) of tofacitinib- and vehicle-  
140 treated HU+CU mice on day 14 and 32 (n = 5 mice per group, one- or two-way ANOVA). (F)  
141 Representative images of periodic acid-Schiff (PAS, magnification: x200) staining illustrating  
142 tubular injury in tofacitinib- and vehicle-treated HU+CU mice on day 32. (G) Intrarenal mRNA  
143 expression levels of the kidney injury marker (*KIM-1*), interleukin 6 (*Il6*), tumor necrosis factor  
144 (*Tnf*) $\alpha$ , inducible nitric oxide synthase (*iNos*), arginase 1 (*Arg1*) of tofacitinib- and vehicle-  
145 treated HU+CU mice on day 32 (n = 5 mice per group, Student's t-test). (H) Representative  
146 images of Picro sirius red staining illustrating interstitial fibrosis in tofacitinib- and vehicle-  
147 treated HU+CU mice on day 32. Magnification: x200. (I) Intrarenal mRNA expression levels of  
148 the fibrosis marker *Fibronectin 1* and collagen (*Col*) $1\alpha 1$ . (J and K) Absolute number of kidney  
149 M1-like macrophages (J, CD45 $^+$ MHCII $^+$ F4/80 $^{hi}$ CD11b $^+$ CD11c $^{lo}$ CX3CR1 $^+$ CD206 $^-$ ) and of M2-like  
150 macrophages (K, CD45 $^+$ MHCII $^+$ F4/80 $^{hi}$ CD11b $^+$ CD11c $^{lo}$ CX3CR1 $^+$ CD206 $^+$ ) on day 32 determined  
151 by flow cytometry (n = 5 mice per group, Student's t-test). (L) Number of crystal granulomas  
152 on PAS-stained kidney sections (n = 5 mice per group, Student's t-test). Data are mean  $\pm$  SD. \*  
153 p<0.05; \*\* p<0.01; \*\*\* p<0.001; ns, not significant.

154

155

156

157

158

159

160

161    **3. Supplementary Movies**

162    **3.1 Supplementary Movie 1**

163    **3.2 Supplementary Movie 2 – move along z axis**

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180 **4. Supplementary Tables**181 **4.1 Supplementary Table 1.** Murine primer sequences.

182

<b>Mouse genes</b>	<b>Primer sequences</b>	
<i>KIM-1</i>	Forward	5'-TCAGCTCGGAATGCACAA-3'
	Reverse	5'-TGGTTGCCCTCCGTCTCT-3'
<i>Tnfα</i>	Forward	5'-CCACCACGCTCTCTGTCTAC-3'
	Reverse	5'-AGGGTCTGGGCCATAGAACT-3'
<i>Il-6</i>	Forward	5'-TGATGCACTTGCAGAAAACA-3'
	Reverse	5'-ACCAGAGGAAATTTCATAAGGC-3'
<i>iNos</i>	Forward	5'-GAGACAGGGAAGTCTGAAGCAC-3'
	Reverse	5'-CCAGCAGTAGTTGCTCCTCTTC-3'
<i>Arg1</i>	Forward	5'-AGAGATTATGGAGCGCCTT-3'
	Reverse	5'-TTTTTCCAGCAGACCAGCTT-3'
<i>Col1α1</i>	Forward	5'-ACATGTTCAGCTTGTGGACC-3'
	Reverse	5'-TAGGCCATTGTGTATGCAGC-3'
<i>Fibronectin 1</i>	Forward	5'-GGAGTGGCACTGTCAACCTC-3'
	Reverse	5'-ACTGGATGGGGTGGGAAT-3'
<i>FSP-1</i>	Forward	5'-CAGCACTCCTCTCTCTGG-3'
	Reverse	5'-TTTGTGGAAGGTGGACACAA-3'
<i>18s RNA</i>	Forward	5'-GCAATTATTCCCCATGAACG-3'
	Reverse	5'-AGGGCCTCACTAAACCATCC-3'

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197 5. References

- 198 1. Wilson, P.C. *et al.* The single-cell transcriptomic landscape of early human diabetic  
199 nephropathy. *Proc Natl Acad Sci U S A* **116**, 19619-19625 (2019).
- 200 2. Butler, A., Hoffman, P., Smibert, P., Papalexi, E. & Satija, R. Integrating single-cell  
201 transcriptomic data across different conditions, technologies, and species. *Nat Biotechnol* **36**,  
202 411-420 (2018).
- 203 3. Edgar, R., Domrachev, M. & Lash, A.E. Gene Expression Omnibus: NCBI gene expression and  
204 hybridization array data repository. *Nucleic Acids Res* **30**, 207-210 (2002).
- 205 4. Barrett, T. *et al.* NCBI GEO: archive for functional genomics data sets--update. *Nucleic Acids  
206 Res* **41**, D991-995 (2013).
- 207 5. Neusser, M.A. *et al.* Human nephrosclerosis triggers a hypoxia-related glomerulopathy. *Am J  
208 Pathol* **176**, 594-607 (2010).
- 209 6. Berthier, C.C. *et al.* Cross-species transcriptional network analysis defines shared  
210 inflammatory responses in murine and human lupus nephritis. *J Immunol* **189**, 988-1001  
211 (2012).
- 212 7. Ju, W. *et al.* Defining cell-type specificity at the transcriptional level in human disease.  
213 *Genome Res* **23**, 1862-1873 (2013).
- 214 8. Martini, S. *et al.* Integrative biology identifies shared transcriptional networks in CKD. *J Am  
215 Soc Nephrol* **25**, 2559-2572 (2014).
- 216 9. Hodgin, J.B. *et al.* The molecular phenotype of endocapillary proliferation: novel therapeutic  
217 targets for IgA nephropathy. *PLoS One* **9**, e103413 (2014).
- 218 10. Tajti, F., Kuppe, C., Antoranz, A., Ibrahim, M.M., Kim, H., Ceccarelli, F., Holland, C.H., Olauson,  
219 H., Floege, J., Alexopoulos, L.G., Kramann, R., Saez-Rodriguez, J. A functional landscape of  
220 CKD entities from public transcriptome data. *Kidney Int Rep* (2019).

221