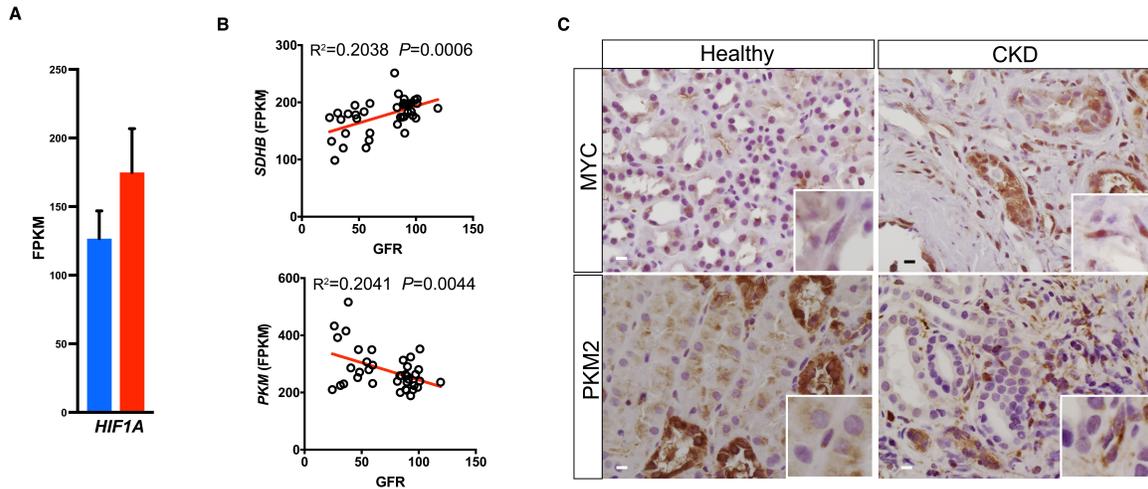


**Supplemental Data**

**Interleukin-1 $\beta$  Activates a MYC-Dependent Metabolic Switch in Kidney  
Stromal Cells Necessary for Progressive Tubulointerstitial Fibrosis**

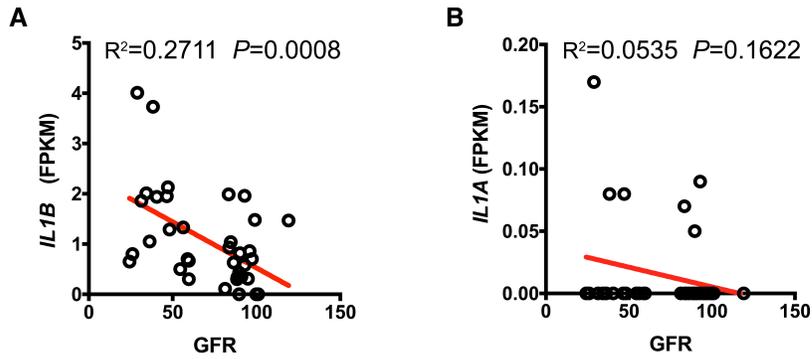
Dario R. Lemos, Michael McMurdo, Gamze Karaca, Julia Wilflingseder, Irina A. Leaf, Navin Gupta, Tomoya, Miyoshi, Koichiro Susa, Bryce G. Johnson, Kirolous Soliman, Guianghai Wang, Ryuji Morizane, Joseph V. Bonventre and Jeremy S. Duffield.

**Supplemental Figure 1**



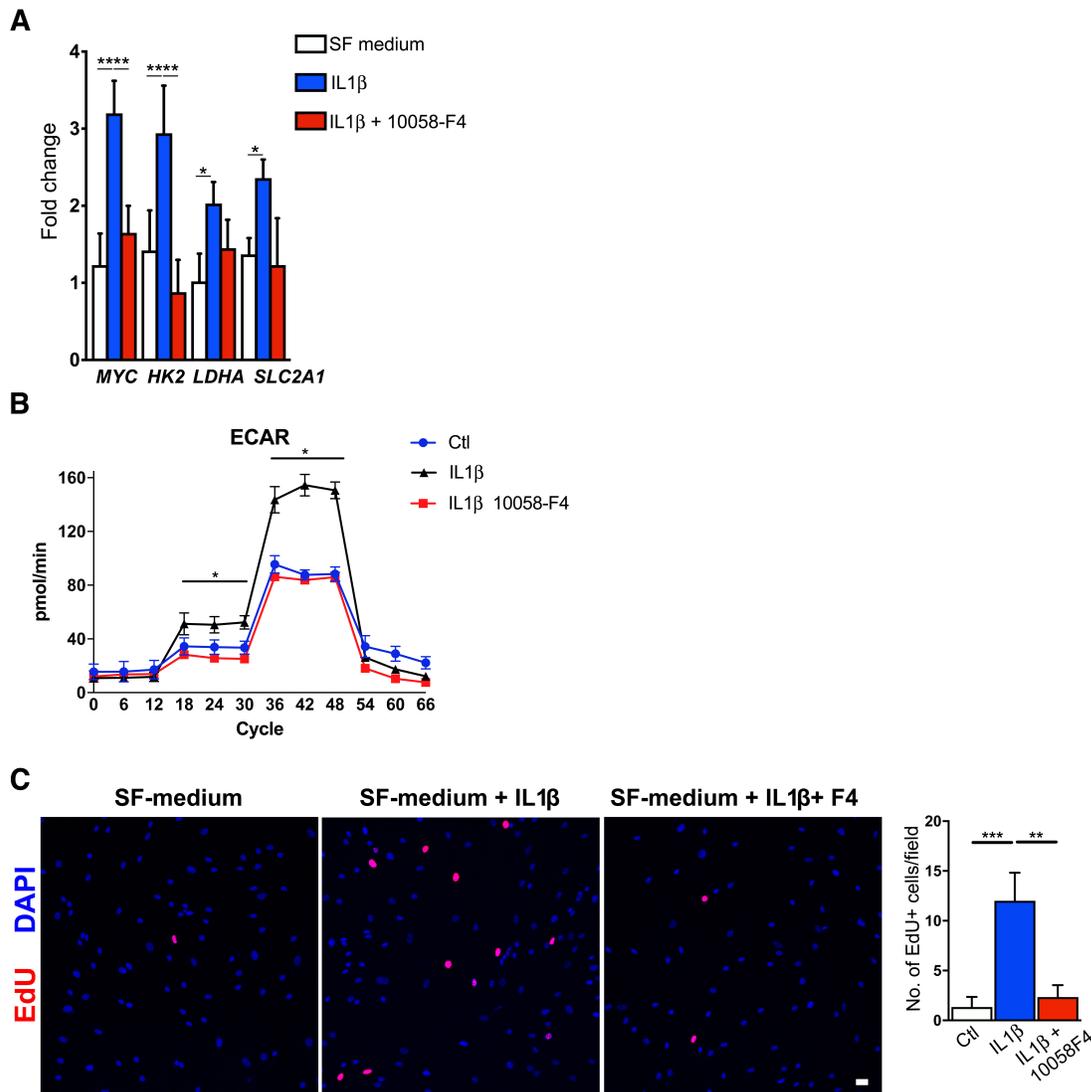
**Supplemental Figure 1.** Relationship of selected genes and proteins involved in metabolism to severity of CKD and cellular localization. (A) *HIF1A* expression in normal *versus* fibrotic human kidneys. Values are mean +/- SD. \**P* < 0.05 vs. 10% fibrosis. Student's *t*-test. (B) Linear regression analysis of eGFR *versus* *SDHB* and *PKM* expression from a cohort of 38 healthy and CKD patients. (C) Representative immunostained images detecting *MYC* and *PKM* isoform 2 (brown stain, counterstained with hematoxylin to show nuclei [blue] in healthy and CKD kidney tissue sections. Insets show higher magnification of a single stromal cell (normal kidney) or SC-derived myofibroblast (CKD kidney). bar = 25 $\mu$ m.

## Supplemental Figure 2



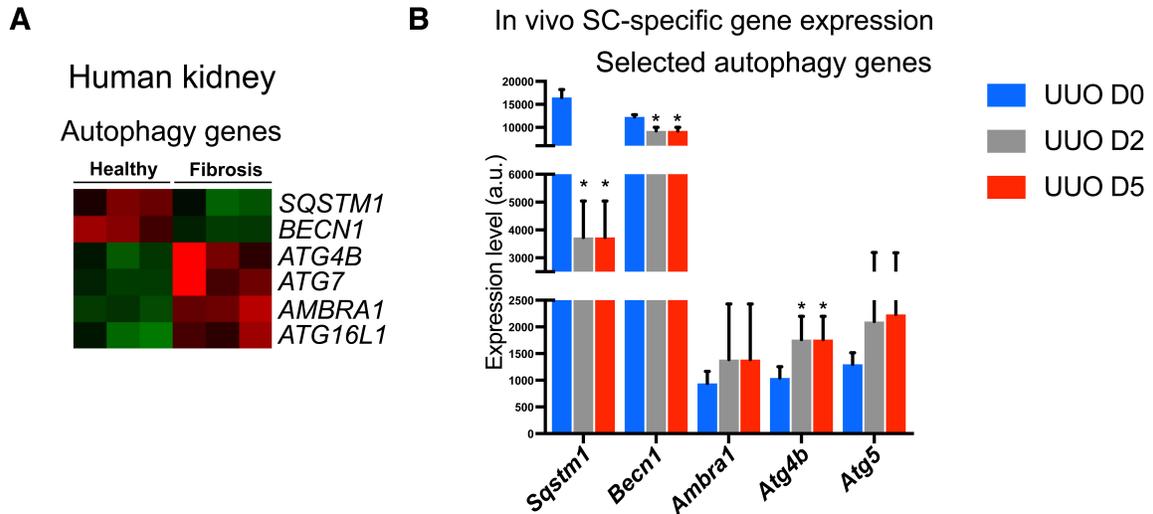
**Supplemental Figure 2.** Relationship of *IL1B* and *IL1A* levels to severity of CKD. (A-B) Linear regression analysis of eGFR versus *IL1B* (A) and *IL1A* (B) expression from a cohort of 38 healthy and CKD patients.

**Supplemental Figure 3**



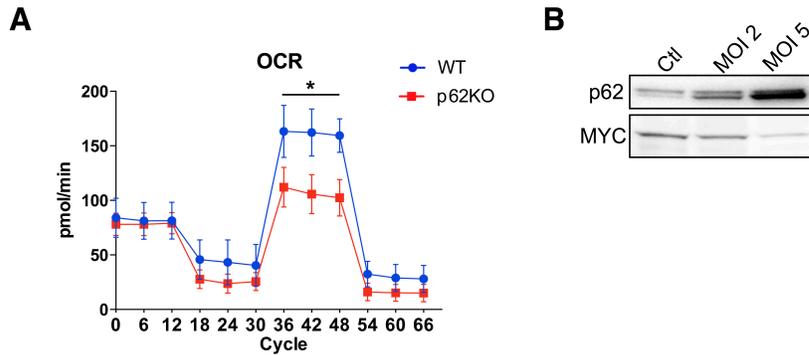
**Supplemental Figure 3.** Effect of the MYC inhibitor 10058-F4 on SC functions in response to IL1 $\beta$ . (A) Graph showing fold change in transcript levels of selected glycolytic pathway genes and MYC, following by IL1 $\beta$  +/- 10058-F4 (10 $\mu$ M) treatment of human kidney SCs. Values are mean +/- SD. \*  $P < 0.05$ , \*\*  $P < 0.01$ . One-way ANOVA. (B) Extracellular acidification rate (ECAR) of human kidney PDGFR $\beta$ + SCs incubated with IL1 $\beta$  for 48 hours in the presence or absence of 10 mM 10058-F4. Points on the curves represent mean +/- SD. \*  $P < 0.05$ . Student's  $t$ -test.  $n = 3$ / point. (C) Images and graph demonstrating EdU incorporation into nuclei of human kidney PDGFR $\beta$ + SCs stimulated with IL1 $\beta$  for 48 hours in the presence or absence of 10058-F4, as a marker of proliferation. A four-hour EdU pulse was applied (bar = 25 $\mu$ m). Values are mean +/- SD. \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ . One-way ANOVA.

## Supplemental Figure 4



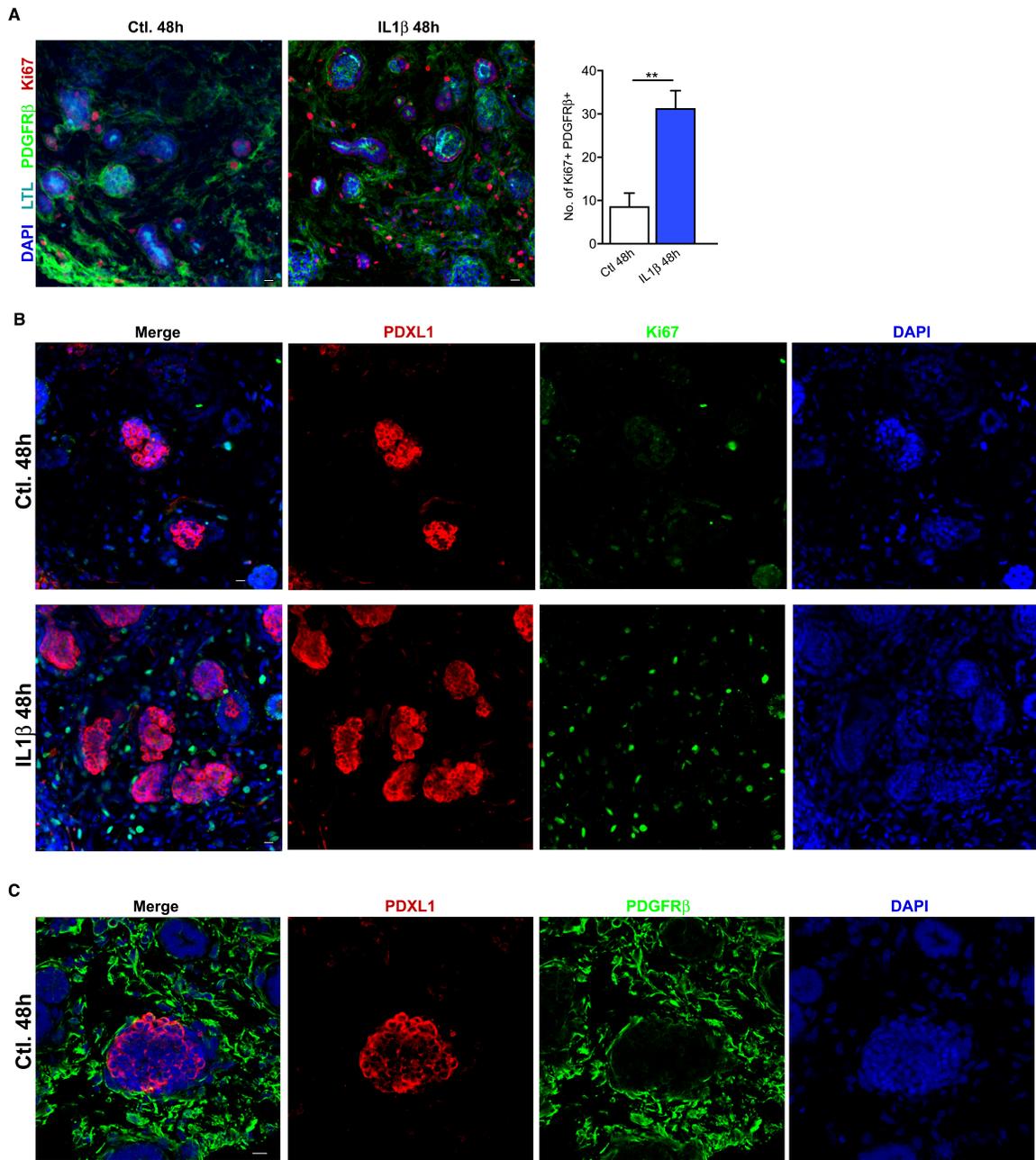
**Supplemental Figure 4.** Effect of kidney disease on transcripts for factors involved in autophagy in human kidney cortex and mouse kidney stromal cells in vivo. (A) Heatmap representing expression of selected transcripts of genes involved in autophagy in normal *versus* fibrotic human kidneys (red = high; green = low). (B) Graph showing in vivo SC-specific expression (absolute units [a.u.]) of translated mRNAs for factors involved in autophagy from UUO day 0 (D0), day 2 (D2) and day 5 (D5) purified from kidneys of *Col1a1-L10a-GFP* mice. Values are mean  $\pm$  SD. \* $P < 0.05$  vs. UUO D0. One-way ANOVA.

## Supplemental Figure 5



**Supplemental Figure 5.** Effect on human kidney SCs of deletion of SQSTM1 or lentiviral transduction with a SQSTM1 transgene on oxygen consumption rate (OCR) and MYC protein levels respectively. (A) OCR measurement WT (blue curve) and SQSTM1/p62 KO (red curve) human kidney SCs. Points on the curves represent mean  $\pm$  SD. \* $P$  < 0.05. Student's  $t$ -test.  $n$  = 3 points. Cycle 12-18 = treatment with oligomycin, cycle 30-36 = treatment with FCCP and cycle 48-54 = treatment with rotenone. (B) Representative western blot showing MYC and SQSTM1/p62 levels in human kidney SCs transduced with a lentivirus expressing SQSTM1/p62 under the CMV promoter (Ctl = control virus and MOI = multiplicity of infection of p62 producing virus where MOI = number of viral particles per cell).

Supplemental Figure 6



**Supplemental Figure 6.** Characterization of the effect of IL1 $\beta$  on proliferation in different cellular compartments of human kidney organoids. (A) Low magnification representative immunofluorescence photomicrographs showing Ki67 distribution in human kidney organoids treated with IL1 $\beta$ , where SCs express PDGFR $\beta$ , and proximal tubules express lotus tetragonolobus lectin (LTL). Graph (right panel) quantifying Ki67+ cells in the SC compartment. (Values are mean  $\pm$  SD. \*\* $P$  < 0.01. Student's  $t$ -test.  $n$  = 3 organoids per treatment/time

point. (B) Representative split panel immunofluorescence photomicrographs showing the expression of Ki67 in glomeruli, where anti-podocalyxin antibodies (PDXL1) detect podocytes, in human kidney organoids treated with IL1b. Note podocytes to not express Ki67. (C) Representative immunofluorescence photomicrograph showing distribution of interstitial PDGFRb<sup>+</sup> SCs in relation to organoid glomeruli as detected by anti-podocalyxin antibodies. (bar = 25 $\mu$ m).

**Supplemental Table I**

Gene	Taqman Probe	Species
<i>Acta2</i>	Mm00725412_s1	Mouse
<i>Ccl2 (Mcp1)</i>	Mm00441242_m1	Mouse
<i>Ccl3 (Mip1a)</i>	Mm00441259_g1	Mouse
<i>Col1a1</i>	Mm00801666_g1	Mouse
<i>Ctgf</i>	Mm01192932_g1	Mouse
<i>Cxcl2 (Mip2)</i>	Mm00436450_m1	Mouse
<i>Fn1</i>	Mm01256744_m1	Mouse
<i>Gapdh</i>	Mm99999915_g1	Mouse
<i>Havcr1 (Kim1)</i>	Mm00506686_m1	Mouse
<i>Il1b</i>	Mm00434228_m1	Mouse
<i>Il6</i>	Mm00446190_m1	Mouse
<i>Myc</i>	Mm00487804_m1	Mouse
<i>Sqstm1 (p62)</i>	Mm00448091_m1	Mouse
<i>Tnf</i>	Mm00443258_m1	Mouse
<i>Tgfb</i>	Mm01227699_m1	Mouse
<i>GAPDH</i>	Hs02758991_g1	Human
<i>ACTA2</i>	Hs00426835_g1	Human
<i>COL1A1</i>	Hs00164004_m1	Human
<i>FN1</i>	Hs01549976_m1	Human
<i>HAVCR1 (KIM1)</i>	Hs00930379_g1	Human
<i>HK2</i>	Hs00606086_g1	Human
<i>LDHA</i>	Hs01378790_g1	Human
<i>SQSTM1</i>	Hs01061917_g1	Human
<i>TNF</i>	Hs00174128_m1	Human
<i>MYC</i>	Hs00153408_m1	Human
<i>SLC2A1</i>	Hs00892681_m1	Human
<i>SLC2A3</i>	Hs00359840_m1	Human