

Origin and Function of Myofibroblasts in Kidney Fibrosis

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Supplementary Figures and Figure Legends:

Figure S1

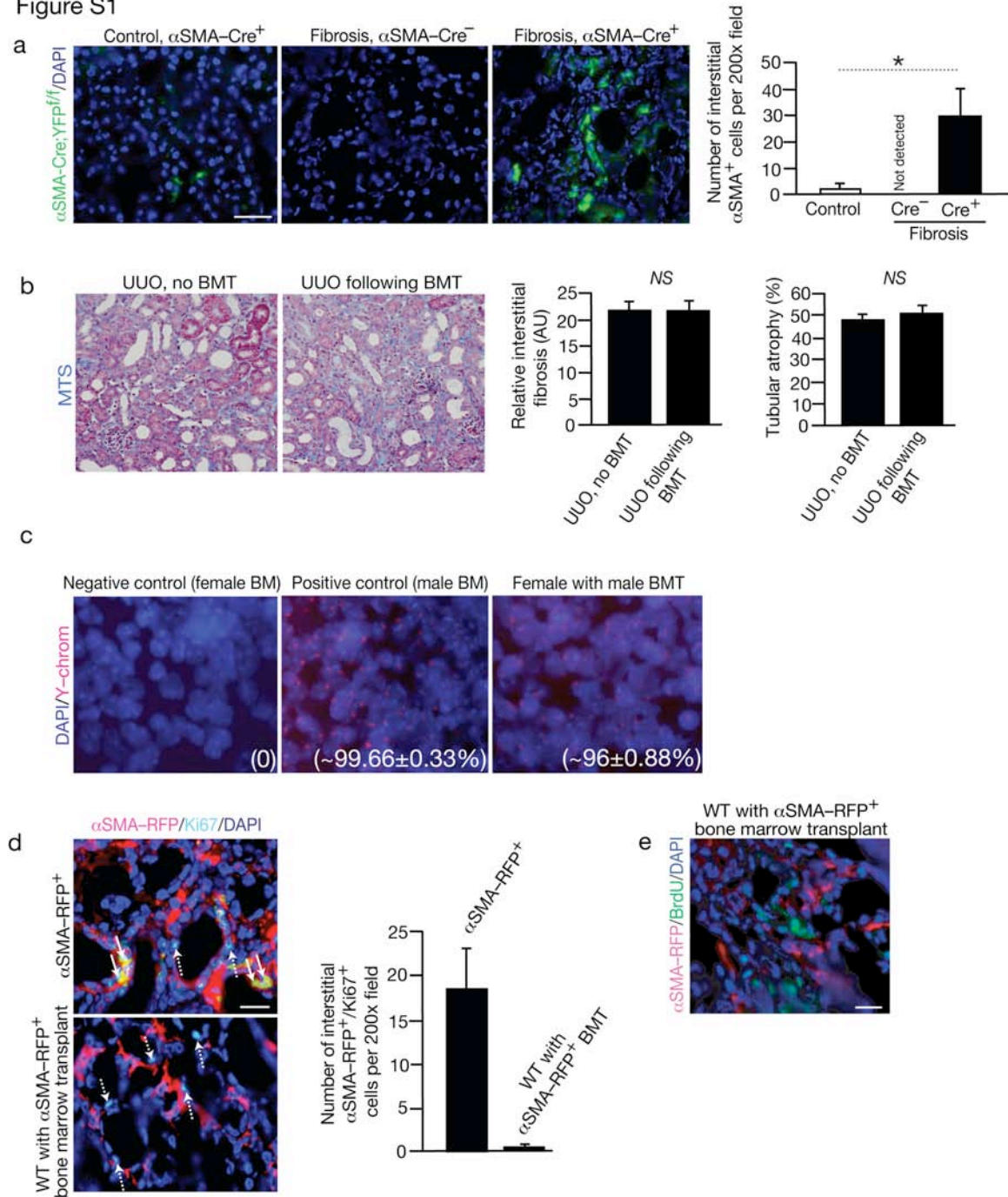


Figure S1. Lineage tracing of α SMA⁺ cells and bone marrow transplant supporting data

(a) Visualization of YFP⁺ cells in non-fibrotic contralateral (Control) kidney of α SMA-Cre⁺;YFP^{fl/fl} mice, and fibrotic kidneys of α SMA-Cre⁺;YFP^{fl/fl} and α SMA-Cre⁻;YFP^{fl/fl} mice (used as negative control) 10 days post UUO. Graph depicts the quantitative analysis of YFP⁺ cells per visual field in control and fibrotic kidney in α SMA-Cre⁺;YFP^{fl/fl} mice. (b) Representative Masson Trichrome staining (MTS) and morphometric analyses of kidneys of mice 10 days post UUO ('UUO, no BMT', $n = 5$) and of mice day 10 post UUO which received bone marrow transplant 4-5 weeks prior to UUO ('UUO following BMT'; $n = 5$). (c) Representative Y-chromosome FISH labeling of bone marrow cells cyto-spinned from female ($n = 1$), male ($n = 1$), and female mice transplanted with bone marrow from a male donor ($n = 3$). Percentages represent the relative number of Y-chromosome labeled nuclei. (d) Immunolabeling for Ki67 in fibrotic kidney of α SMA-RFP mice and WT mice transplanted with bone marrow from α SMA-RFP donor. Dashed arrows point to RFP⁻/Ki67⁺ cells and filled arrows point to RFP⁺/Ki67⁺ cells. Quantitation of α SMA-RFP⁺/Ki67⁺ myofibroblasts in fibrotic kidney. (e) Immunolabeling for BrdU in fibrotic kidney of α SMA-RFP mice and WT mice transplanted with bone marrow from α SMA-RFP donor (mice were euthanized 1-2 hours post BrdU injection). AU: Arbitrary Units. DAPI(blue): nuclei. Scale bar: 50 μ m. Data is presented as mean \pm s.e.m. *t*-test, **P* < 0.05, NS: not significant.

Figure S2

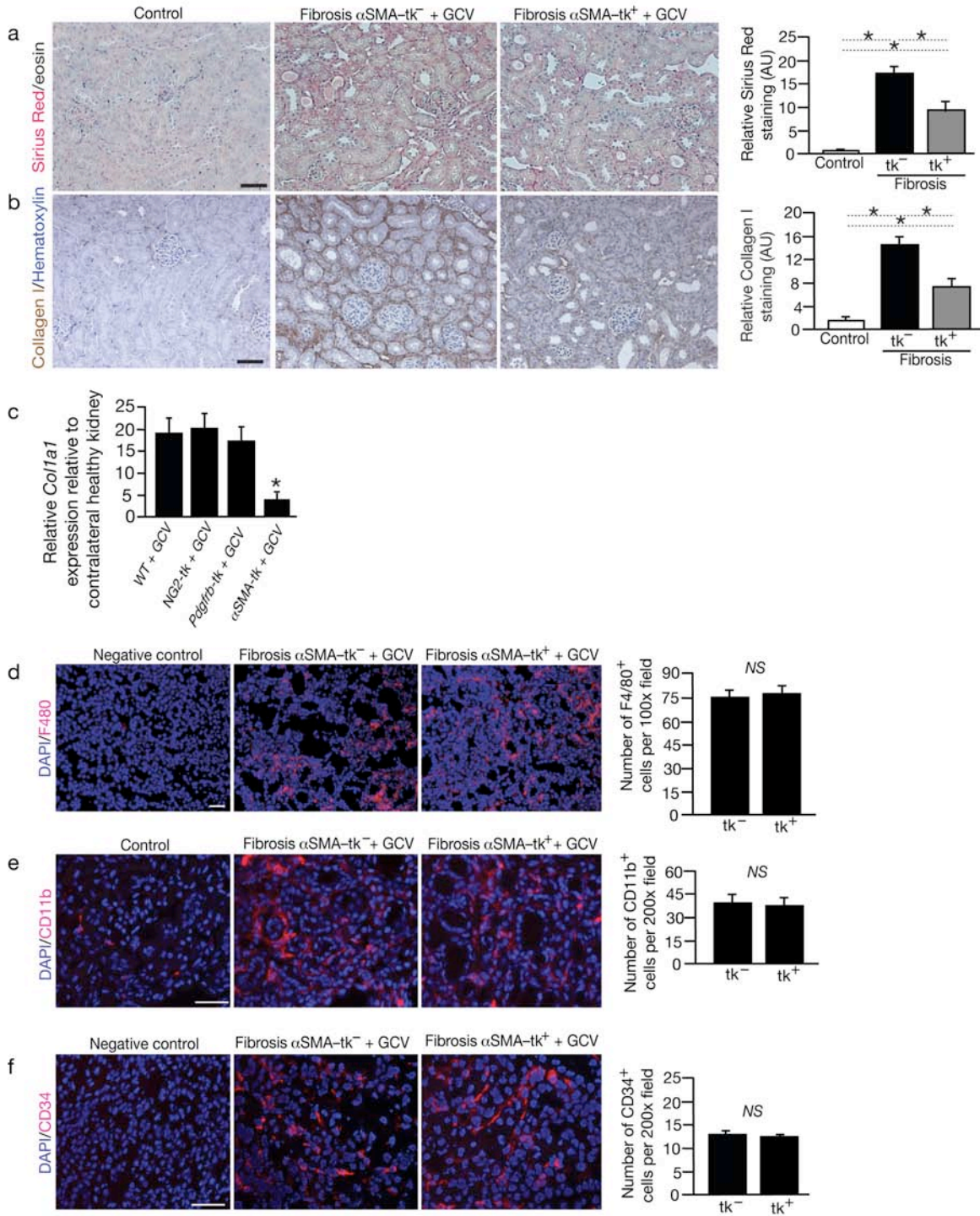


Figure S2. Supporting data for α SMA-tk ablation in UUO-induced renal fibrosis

(a) Representative Sirius Red staining of control (n=5), WT (n=5) and α SMA-tk⁺ (n=5) fibrotic kidneys treated with GCV, and morphometric analysis for relative Sirius red labeling. (b) Representative type I collagen (Collagen I) immunolabeling of control, WT and α SMA-tk⁺ fibrotic kidneys treated with GCV, and morphometric analysis for relative type I collagen staining. (c) Relative *Col1a1* expression by Q-PCR analysis in kidneys of indicated experimental groups, normalized to contralateral healthy kidneys. (d) Representative images and quantification of macrophage infiltration (F4/80⁺) fibrotic kidney from α SMA-tk⁻ and α SMA-tk⁺ mice treated with GCV. (e) Representative images and quantification of macrophage infiltration (CD11b⁺) fibrotic kidney from α SMA-tk⁻ and α SMA-tk⁺ mice treated with GCV. (f) Representative images and quantification of endothelial cells (CD34⁺) fibrotic kidney from α SMA-tk⁻ and α SMA-tk⁺ mice treated with GCV. Negative control: secondary antibody only. Control: contralateral healthy kidney. AU: Arbitrary Units. DAPI(blue): nuclei. Scale bar: 50 μ m. Data is presented as mean \pm s.e.m. *t*-test, **P* < 0.05, *NS*: not significant.

Figure S3

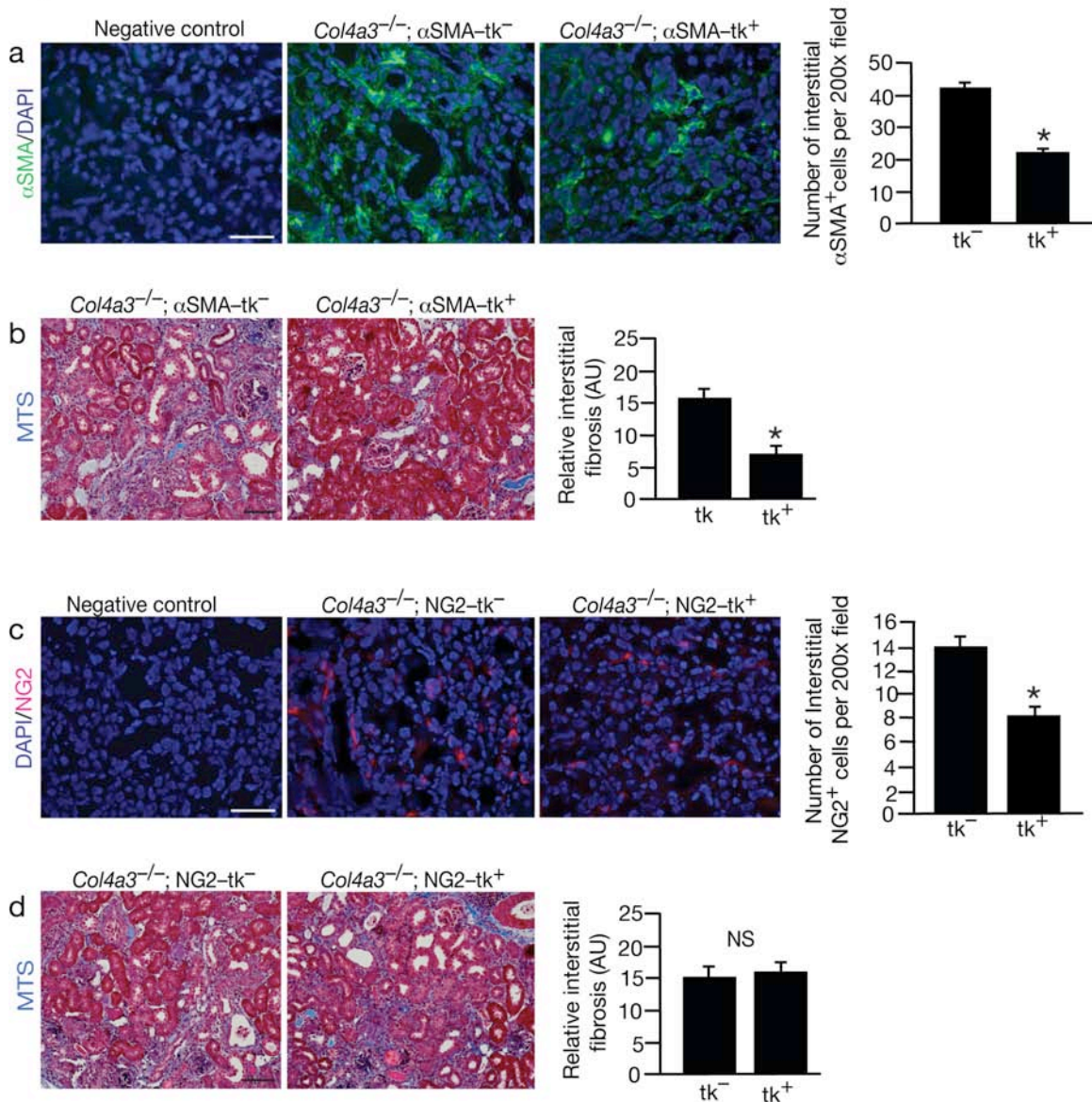


Figure S3. Ablation of α SMA⁺ cells but not NG2⁺ cells improves fibrosis in *Col4a3*^{-/-} mice

(a) Immunolabeling for α SMA in fibrotic kidney of *Col4a3*^{-/-}; α SMA-tk⁻ (n=5) and *Col4a3*^{-/-}; α SMA-tk⁺ (n=5) mice treated with GCV and quantitation of α SMA⁺ cells per field of view. (b) Representative Masson Trichrome staining (MTS) of

Col4a3^{-/-};αSMA-tk⁻ and *Col4a3*^{-/-};αSMA-tk⁺ mice treated with GCV and morphometric analysis for relative interstitial fibrosis. **(c)** Immunolabeling for NG2 in fibrotic kidney of *Col4a3*^{-/-};NG2-tk⁻ (n=5) and *Col4a3*^{-/-};NG2-tk⁺ (n=5) mice treated with GCV and quantitation of NG2⁺ cells per field of view. **D.** Representative Masson Trichrome (MTS) staining of *Col4a3*^{-/-};NG2-tk⁻ and *Col4a3*^{-/-};NG2-tk⁺ mice treated with GCV and morphometric analysis for relative interstitial fibrosis. Negative control, secondary antibody only. Control: contralateral healthy kidney. AU: Arbitrary Units. DAPI(blue): nuclei. Scale bar: 50μm. Data is presented as mean ± s.e.m. *t*-test, **P* < 0.05, *NS*: not significant.

Figure S4

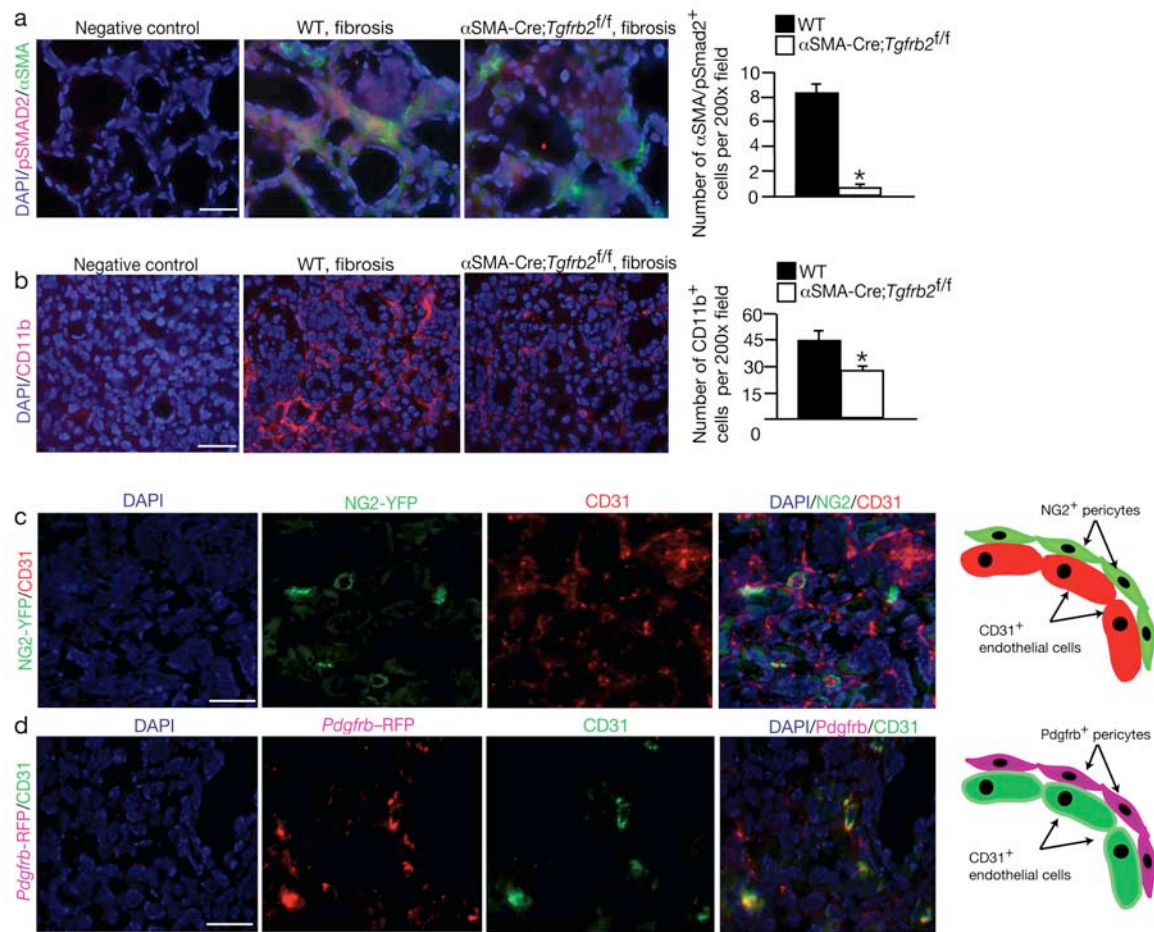


Figure S4. Supporting data for α SMA-Cre;Tgfrb2^{ff} mice and NG2-YFP and *Pdgfrb*-RFP visualization in normal kidney.

(a) Immunolabeling for phosphorylated Smad2 (pSmad2) and α SMA in WT and α SMA-Cre;Tgfrb2^{ff} fibrotic kidneys. Graph depicts quantitation of α SMA/pSmad2 double positive cells per field of view. (b) Immunolabeling for CD11b⁺ macrophages in WT and α SMA-Cre;Tgfrb2^{ff} fibrotic kidneys. Graph depicts quantitation of CD11b⁺ macrophages per field of view. (c) Representative immunofluorescent images showing YFP expression (from NG2-YFP⁺ cells) and

CD31 immunolabeling (endothelial cells) in mouse kidneys and schematic representation of results: NG2⁺ pericytes are noted on the abluminal side of the vessel. (d) Representative immunofluorescent images showing RFP expression (from *Pdgfrb*-RFP⁺ cells) and CD31 immunolabeling (endothelial cells) in mouse kidneys and schematic representation of results: *Pdgfrb*⁺ pericytes are noted on the abluminal side of the vessel. DAPI(blue): nuclei. Scale bar: 50 μ m. Data is presented as mean \pm s.e.m. *t*-test, **P* < 0.05.

Figure S5

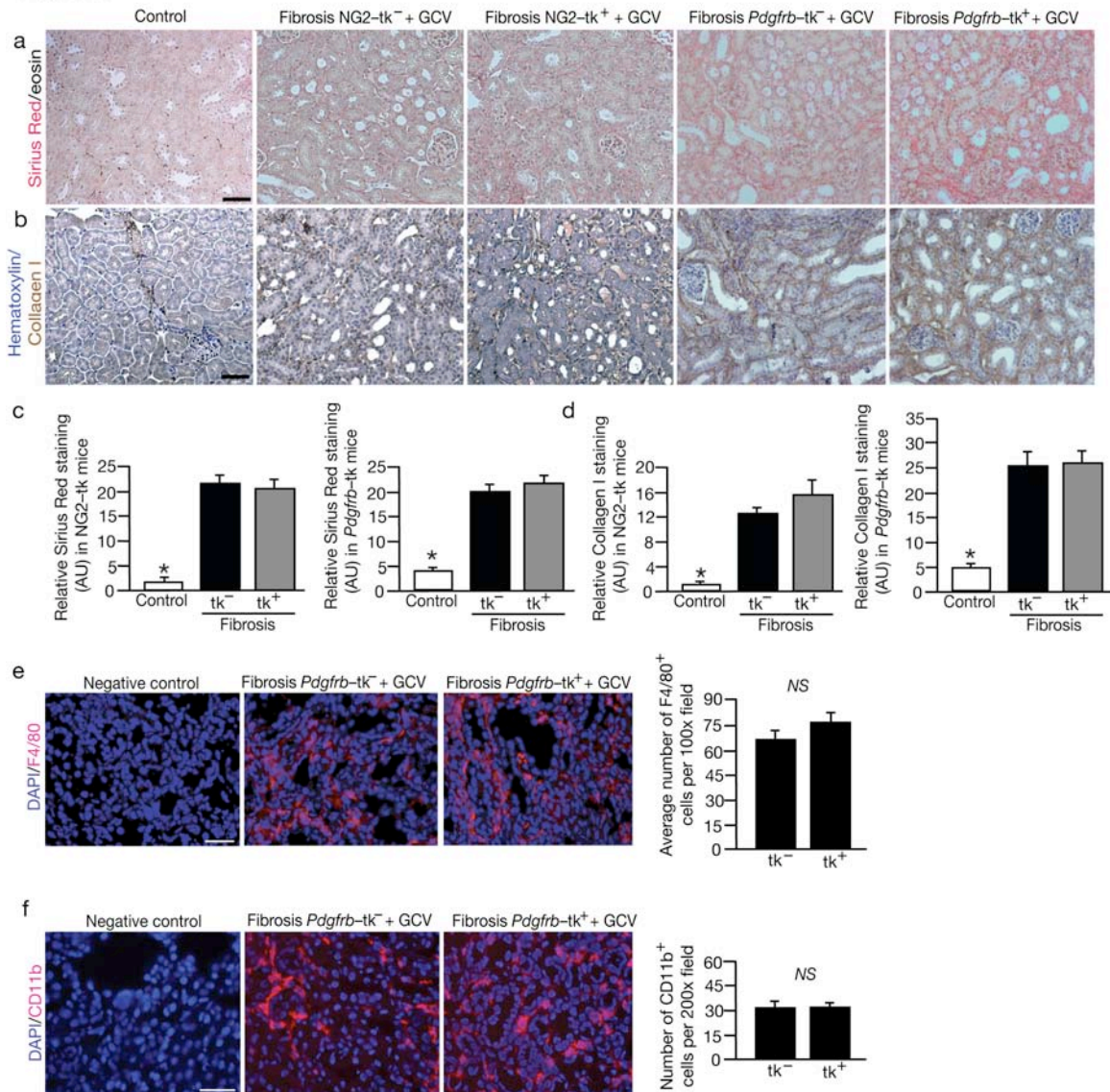


Figure S5. Pericytes do not functionally contribute to fibrosis

(a-b) Representative Sirius red (a), and type I collagen staining (b) of non-fibrotic contralateral (Control) kidney, and fibrotic kidneys from NG2-*tk*⁻, NG2-*tk*⁺, *Pdgfrb*-*tk*⁻ and *Pdgfrb*-*tk*⁺ mice treated with GCV. (c-d) Morphometric analysis for relative Sirius red staining (c), and type I collagen staining (d) of indicated

experimental groups. (e) Representative images and quantification of macrophage infiltration (F4/80⁺) in fibrotic kidney from *Pdgfrb*-tk⁻ and *Pdgfrb*-tk⁺ mice treated with GCV. (f) Representative images and quantification of macrophage infiltration (CD11b⁺) fibrotic kidney from *Pdgfrb*-tk⁻ and *Pdgfrb*-tk⁺ mice treated with GCV. Negative control: secondary antibody only. DAPI(blue): nuclei. AU: Arbitrary Units. Scale bar: 50 μ m. Data is presented as mean \pm s.e.m. *t*-test, **P* < 0.05, NS: not significant.

Figure S6

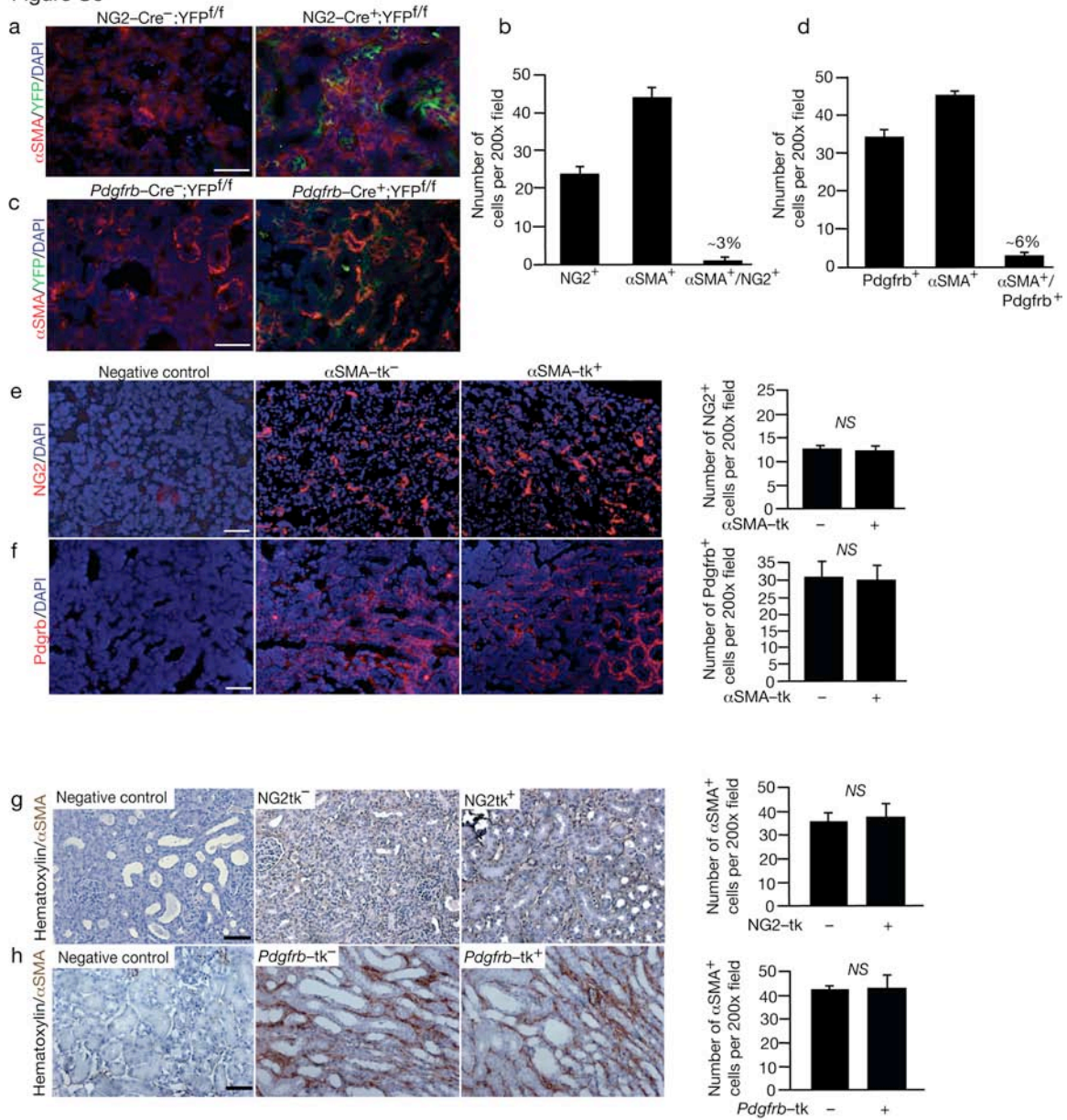


Figure S6. α SMA⁺ myofibroblasts in the fibrotic kidney emerge independently of the vascular pericyte lineage

(a) α SMA immunolabeling of kidneys in lineage tagged NG2-Cre;YFP^{ff} mice, UUO fibrotic kidney ($n = 5$). (b) Relative number of α SMA⁺, NG2⁺, and α SMA⁺/NG2⁺ (double positive) cells per field of view in NG2-Cre+;YFP^{ff} fibrotic kidney. On average 3% of α SMA/NG2 double positive cells were detected. (c)

α SMA immunolabeling of kidneys in lineage tagged *Pdgfrb*-Cre;YFP^{ff} mice. **(d)** Relative number of α SMA⁺, *Pdgfrb*⁺, and α SMA⁺/*Pdgfrb*⁺ (double positive) cells per field of view in *Pdgfrb*-Cre⁺;YFP^{ff} fibrotic kidney. On average 6% of α SMA/*Pdgfrb* double positive cells were detected. **(e)** NG2 immunolabeling of fibrotic kidney from α SMA-tk⁻ and α SMA-tk⁺ mice treated with GCV and number of NG2⁺ cells per visual field in α SMA-tk⁻ and α SMA-tk⁺ fibrotic kidneys. **(f)** *Pdgfrb* immunolabeling of fibrotic kidney from α SMA-tk⁻ and α SMA-tk⁺ mice treated with GCV and number of *Pdgfrb*⁺ cells per visual field in α SMA-tk⁻ and α SMA-tk⁺ fibrotic kidneys. **(g)** α SMA immunolabeling of fibrotic kidney from NG2-tk⁻ and NG2-tk⁺ mice treated with GCV and number of α SMA⁺ cells per visual field in NG2-tk⁻ and NG2-tk⁺ fibrotic kidneys. **(h)** α SMA immunolabeling of fibrotic kidney from *Pdgfrb*-tk⁻ and *Pdgfrb*-tk⁺ mice treated with GCV and number of α SMA⁺ cells per visual field in *Pdgfrb*-tk⁻ and *Pdgfrb*-tk⁺ fibrotic kidneys. Negative control: secondary antibody only. DAPI(blue): nuclei. Scale bar: 50 μ m. Data is presented as mean \pm s.e.m. *t*-test, *NS*: not significant.

Supplementary Methods:**Primer sequence:**

Mouse <i>Col1a1</i>	5'-GCTCCTCTTAGGGGCCACT-3' 5'-CCACGTCTCACCATTGGGG-3'
Mouse <i>Acta2</i> (α SMA)	5'-CCAGTTGTACGTCCAGAGGC-3' 5'-GGTGATGATGTCCCAGGGC-3'
Mouse <i>β-actin</i>	5'-GGCTGTATTCCCCTCCATCG-3' 5'-CCAGTTGGTAACAATGCCATGT-3'

Generation of α SMA-Cre mice

A fragment of the cre recombinase gene with 3' UTR was amplified from plasmid p705-Cre (Gene Bridge GmbH, Germany) using the following primers: 5' ATGTCCAATTTACTGACCGTACACC 3' (Forward); 5' CTAATCGCCATCTTCCAGCAGGC 3' (Reverse). The extended α SMA (*Acta2*) promoter (described above) was cloned into the pCR2.1-TOPO vector (Invitrogen) using EcoRI and NotI restriction sites, then this α SMA promoter-TOPO construct and the cre fragment were digested and ligated together. The whole α SMA-Cre construct was released from the vector using SpeI and XbaI before purification and injection into fertilized eggs. The transgenic mice were generated in the Brigham and Women's Hospital Transgenic Core Facility (Boston, MA) on a FVB background and backcrossed at least 10 generations to a BALB/c background. To characterize the specificity of the α SMA-Cre mice, we crossed these mice with R26R-LoxP-Stop-LoxP-YFP mice. In normal kidney, such fate mapping analysis revealed that α SMA-Cre activity is largely undetected. However, some rare positive areas associated with large blood vessel walls and occasional renal epithelial tubules are observed in all mice. In

the fibrosis setting, the α SMA-Cre activity was predominantly seen in renal interstitial cells, some renal tubular epithelial cells and occasional blood vessels.

Generation of α SMA-tk mice

A truncated version of the herpes simplex 1 virus thymidine kinase (HSV1-tk) gene with 3' UTR was amplified from plasmid fsp1-TK¹ using the following primers: 5' ATGCCACGCTACTGCGGG 3' (Forward); 5' GTGGATAACCGTATTACCGCC 3' (Reverse). The extended α SMA promoter was cloned into the pCR2.1-TOPO vector (Invitrogen) using EcoRI and NotI restriction sites, then this α SMA promoter-TOPO construct and the tk fragment were digested and ligated together. The whole α SMA-tk construct was released from the vector using EcoRI and XbaI before purification and injection into fertilized eggs. The transgenic mice were generated in the Brigham and Women's Hospital Transgenic Core Facility (Boston, MA) on a FVB background and backcrossed at least 10 generations to a BALB/c genetic background.

Generation of NG2-Cre mice

Genomic DNA (~5 kb) containing the NG2 (*Cspg4*) promoter and part of NG2 exon 1 was amplified by PCR and a SfiI restriction site was introduced into the reverse primer. The start codon ATG was mutated in the reverse primer (C to A). The PCR product was TA-cloned into the pCR2.1-TOPO vector (Invitrogen). The NG2 promoter was then excised using EcoRI and inserted into p705-Cre vector (Gene Bridge GmbH, Germany). The resulting NG2-Cre construct was released

from the TOPO vector using SfiI and NheI, purified and injected into fertilized eggs (FVB) to generate NG2-Cre transgenic mice. NG2-Cre mice were backcrossed for at least 10 generations to a BALB/c genetic background. To characterize the specificity of the NG2-Cre mice, we crossed these mice with R26R-LoxP-Stop-LoxP-YFP mice. In normal kidney, such fate mapping analysis revealed that NG2-Cre activity is largely restricted to large and small vascular structures including the glomeruli. In the fibrosis setting, the NG2-Cre activity was seen in renal interstitial cells and vascular structures of the kidney.

Supplemental Reference:

1. Iwano, M., *et al.* Conditional abatement of tissue fibrosis using nucleoside analogs to selectively corrupt DNA replication in transgenic fibroblasts. *Mol Ther* **3**, 149-159 (2001).