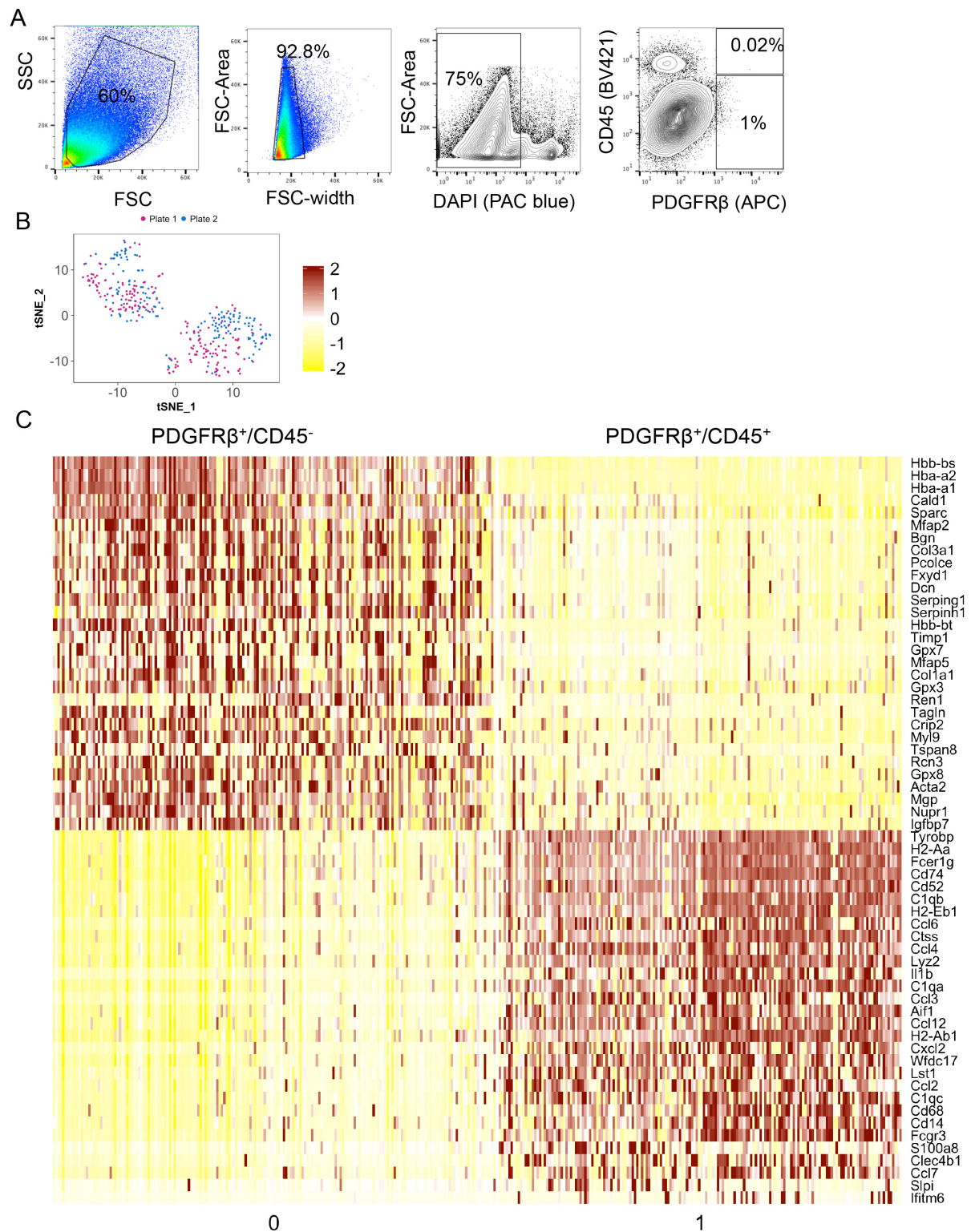


Supplementary Figure S1 Trichrome staining and representative gating for flow cytometry of whole kidneys

(A-B) Non-injured contralateral (CLK) kidneys and injured unilateral ureteral obstructed (UUO) kidney of the CD45.1 parabiont were trichrome stained and the interstitial fibrosis was quantified. Scale bars 50µm. ***p<0.001 by unpaired t-test.

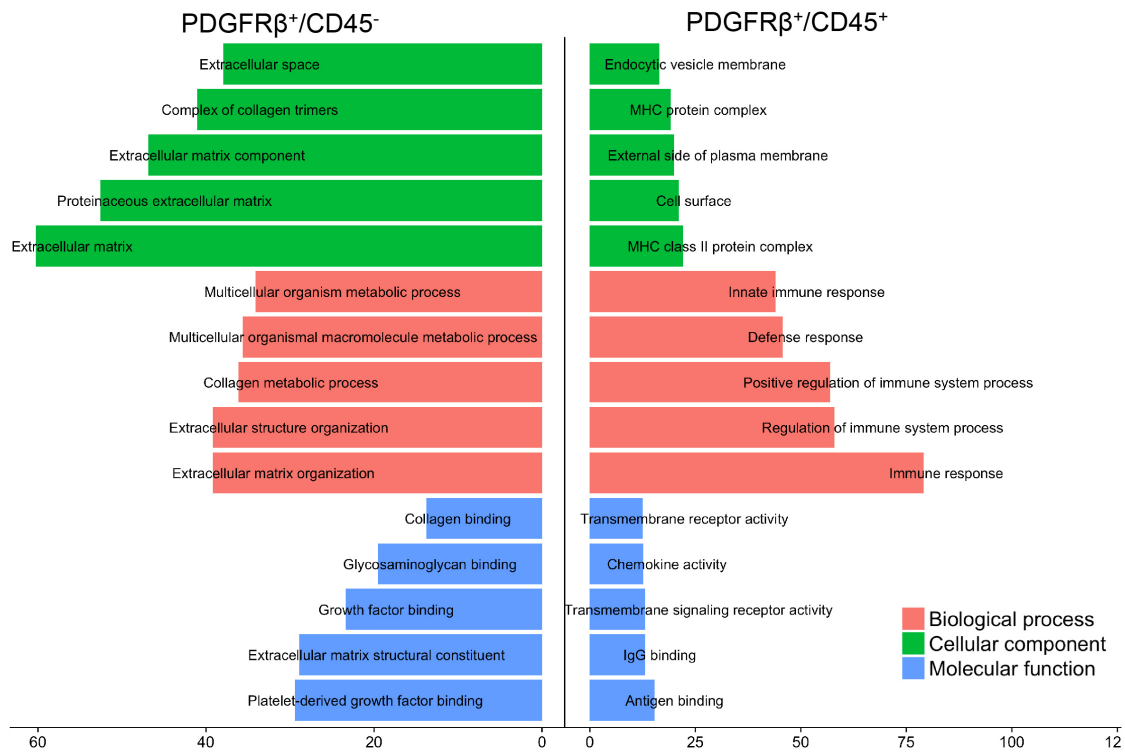
(C) Representative gating for flow-cytometric analysis of the whole kidneys.



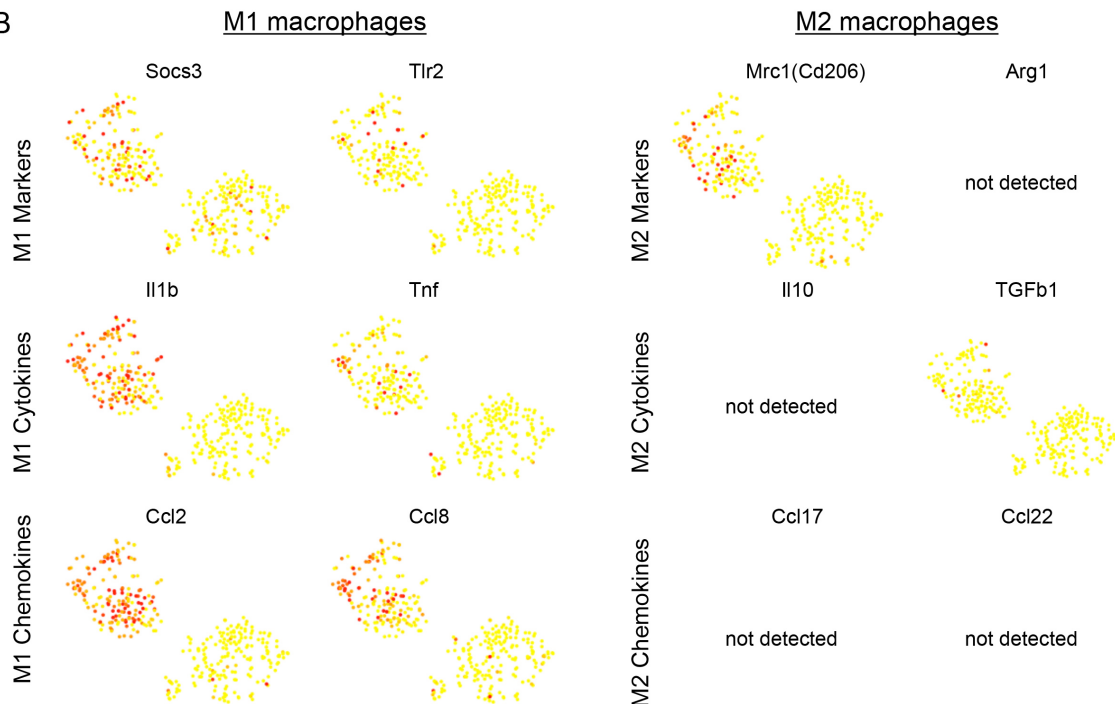
Supplementary Figure S2 Representative gating for FACS and top upregulated genes in single cell RNA-Sequencing clusters of resident and circulating myofibroblasts
 (A) Representative gating for the sorting (FACS) of whole kidneys on single/living (DAPI-) PDGFR β + /CD45+ and PDGFR β - /CD45- cells
 (B) tSNE analysis clusters with respect to the batch.
 (C) Top 30 expressed genes in the two tSNE clusters.

A

Top 5 GO terms for each category



B



Supplementary Figure S3 Top gene ontology terms and macrophage polarization markers in the two clusters.

(A) Top 5 gene ontology (GO) terms of the two tSNE cluster for the categories biological process, cellular component and molecular function.

(B) Expression levels of genes that define M1 and M2 macrophages in both tSNE clusters. (Socs3, suppressor of cytokine signaling 3; Tlr2, toll-like receptor 2; Il1b, Interleukin 1b; Tnf, tumor necrosis factor alpha; Ccl2, cc-chemokine ligand 2; Ccl8, cc-chemokine ligand 8; Mrc1, mannose receptor 1; Arg1, arginase 1; Il10, Interleukin 10; TGFb1, transforming

growth factor beta 1; Ccl17, cc-chemokine ligand 17; Ccl22, cc-chemokine ligand 22 Color key denotes the z-score normalized average expression value of selected differentially expressed genes between PDGFR β^+ /CD45 $^-$ and PDGFR β^+ /CD45 $^+$ cells.

Supplementary Table 1: Transcription factors for PDGFRb+/CD45+ cell population in kidney fibrosis

TF	DC	CC	BC	DFC	DCC	DDC	AVG.RANK
Fos	1	2	1	1	1	1	1
Atf3	2	1	2	3	3	2	2
Junb	4	3	3	2	2	3	3
Egr1	6	6	5	4	4	4	4
Maf	3	4	4	6	7	5	4
Batf3	7	5	6	8	9	9	6
Pou2f2	9	7	9	6	7	8	7
Batf	11	12	8	5	5	6	8
Spi1	8	8	7	11	6	7	8
Jun	5	12	11	11	12	12	10
Sub1	11	16	10	8	9	11	11
Irf8	14	14	12	8	9	10	12
Ddit3	11	9	14	11	12	13	13
Stat1	14	10	13	11	12	14	14
Klf6	9	15	15	11	12	15	15
Nfe2l2	17	17	17	11	12	17	16
Mafb	16	11	16	17	17	16	17

TF: transcription factor; **DC**: Degree Centrality; **CC**: Closeness Centrality; **BC**: Betweenness Centrality; **DFC**: Disruptive Fragmentation Centrality; **DCC**: Disruptive Connection Centrality; **DDC**: Disruptive Distance Centrality; **AVG.RANK**: Average Ranking.

Supplementary Table 2: Transcription factors for the PDGFRb+/CD45- cell population in kidney fibrosis

TF	DC	CC	BC	DFC	DCC	DDC	AVG.RANK
Id3	2	1	1	4	4	2	1
Prrx1	4	5	2	1	1	1	1
Nr2f2	3	2	3	4	4	4	3
Tcf21	1	3	5	4	4	6	4
Tsc22d1	10	6	4	2	2	3	5
Heyl	5	4	6	4	4	5	6
Peg3	8	11	7	2	2	7	7
Nfic	7	8	8	4	4	8	8
Zbtb20	8	12	9	4	4	10	9
Hoxd10	6	13	11	4	4	12	10
Hoxa10	14	17	10	4	4	9	11
Snai2	12	15	15	4	4	15	12
Nr1d1	11	19	13	4	4	16	13
Ssrp1	12	14	16	4	4	17	13
Tcf4	19	16	14	4	4	11	15
Nfib	17	18	12	4	4	13	15
Hoxc10	17	7	21	4	4	18	17
Creb3l2	21	9	20	4	4	14	18
Alx1	21	10	22	4	4	19	19
Snai1	15	20	19	4	4	21	20
Zfp948	19	21	18	4	4	22	21
Meis2	24	23	17	4	4	20	22
Klf9	15	22	24	4	4	23	22
Glis2	21	25	23	4	4	24	24
Tead1	24	24	27	4	4	25	25
Thap7	26	27	26	4	4	26	26
Nfix	27	26	25	4	4	27	26
Cers2	27	28	28	4	4	28	28
Ebf1	29	29	29	4	4	29	29
Trp53	30	30	30	4	4	30	30

TF: transcription factor; **DC:** Degree Centrality; **CC:** Closeness Centrality; **BC:** Betweenness Centrality; **DFC:** Disruptive Fragmentation Centrality; **DCC:** Disruptive Connection Centrality; **DDC:** Disruptive Distance Centrality; **AVG.RANK:** Average Ranking.