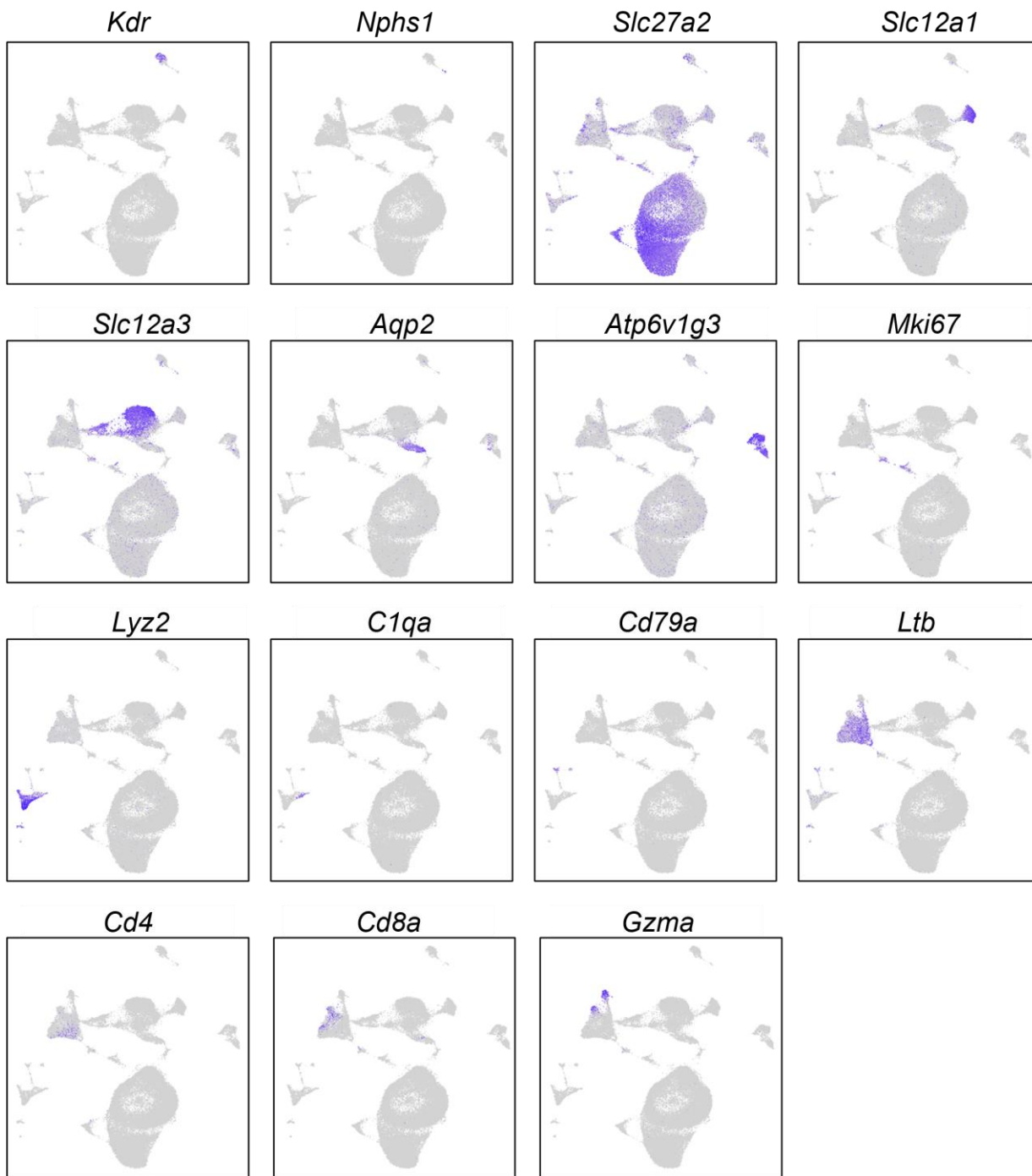

Supplementary information

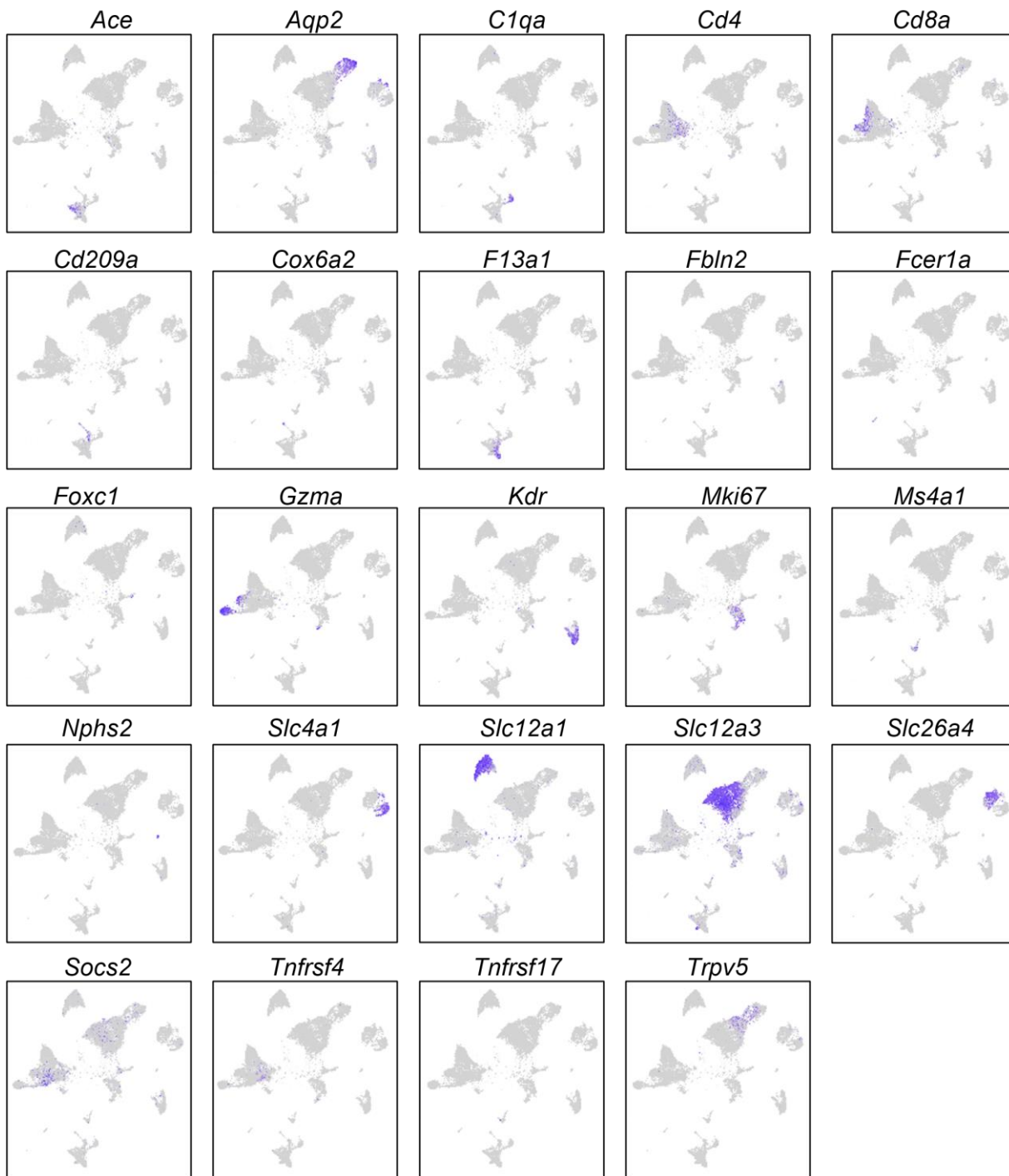
**Single-cell analysis identifies the
interaction of altered renal tubules with
basophils orchestrating kidney fibrosis**

In the format provided by the
authors and unedited



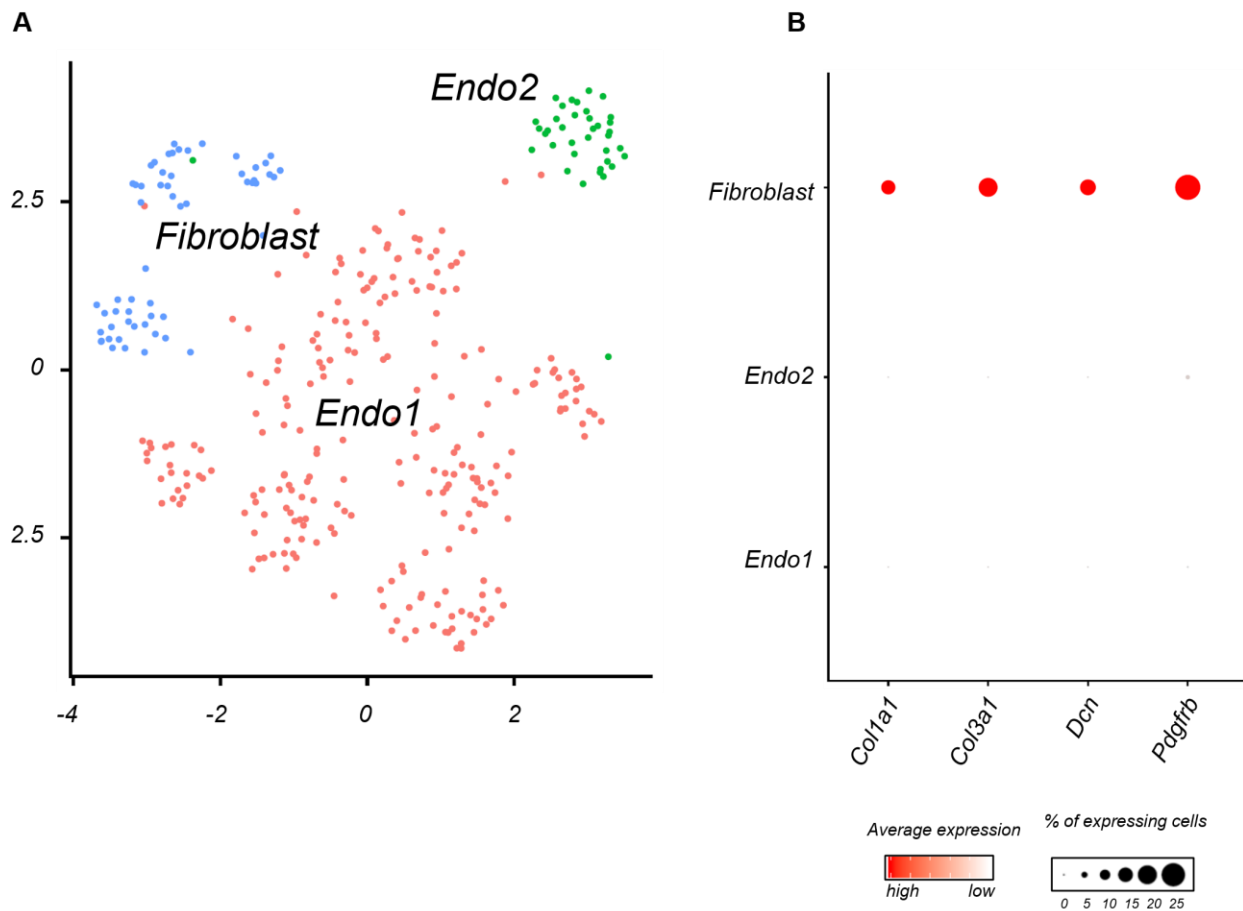
Supplementary Fig 1: Marker gene expression in sham and UUO kidneys in the entire dataset

Feature plots of marker gene expression (blue) in the single cell atlas



Supplementary Fig 2: Marker gene expression in sham and UUO kidneys in non-PT cells

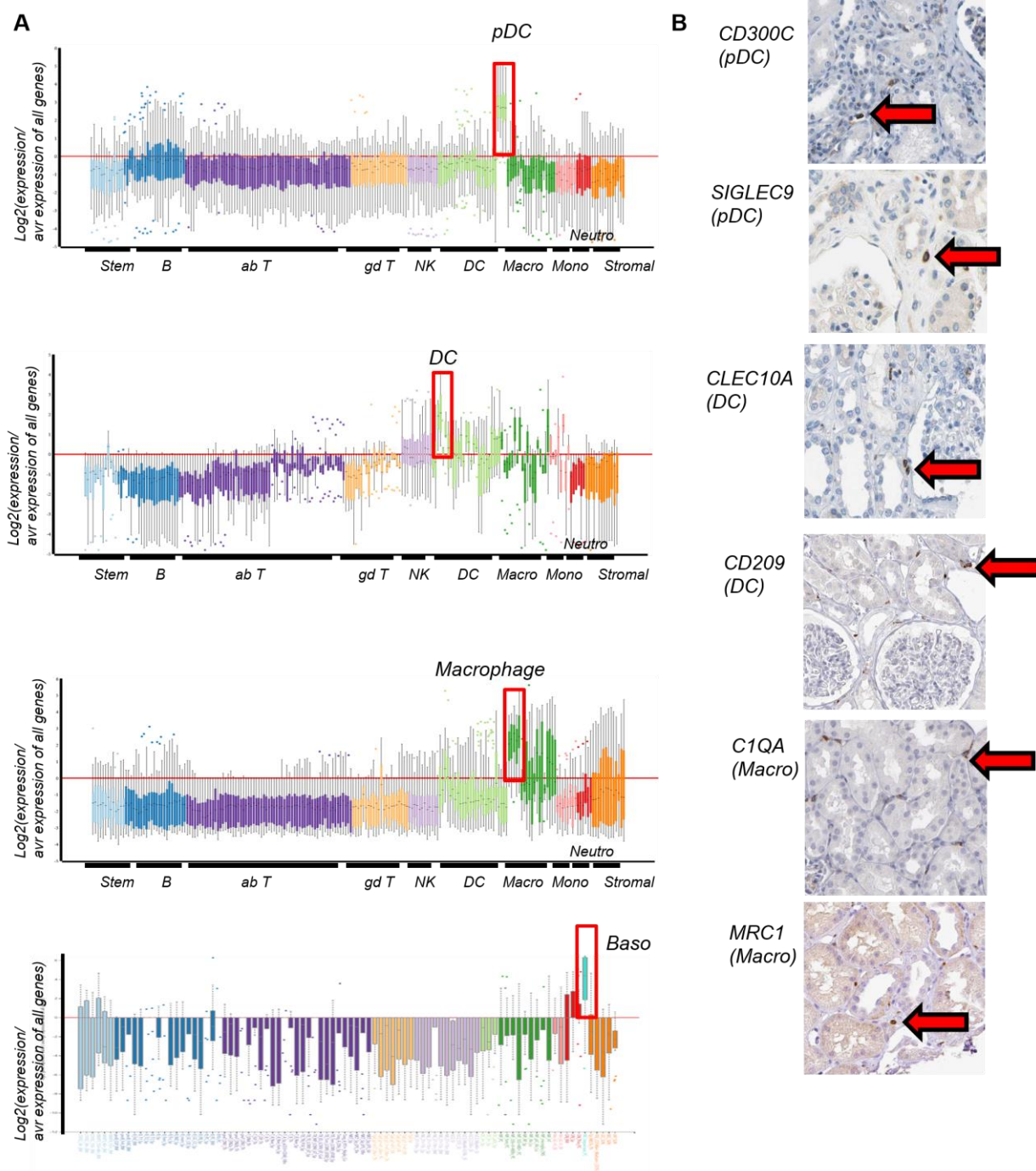
Feature plots of marker gene expression (blue) in the single cell atlas



Supplementary Fig 3: Sub-clustering of the endothelial and fibroblast clusters

(A) UMAP showing 3 different sub-groups (Endo1, Endo2, and Fibroblast) within cluster 2.

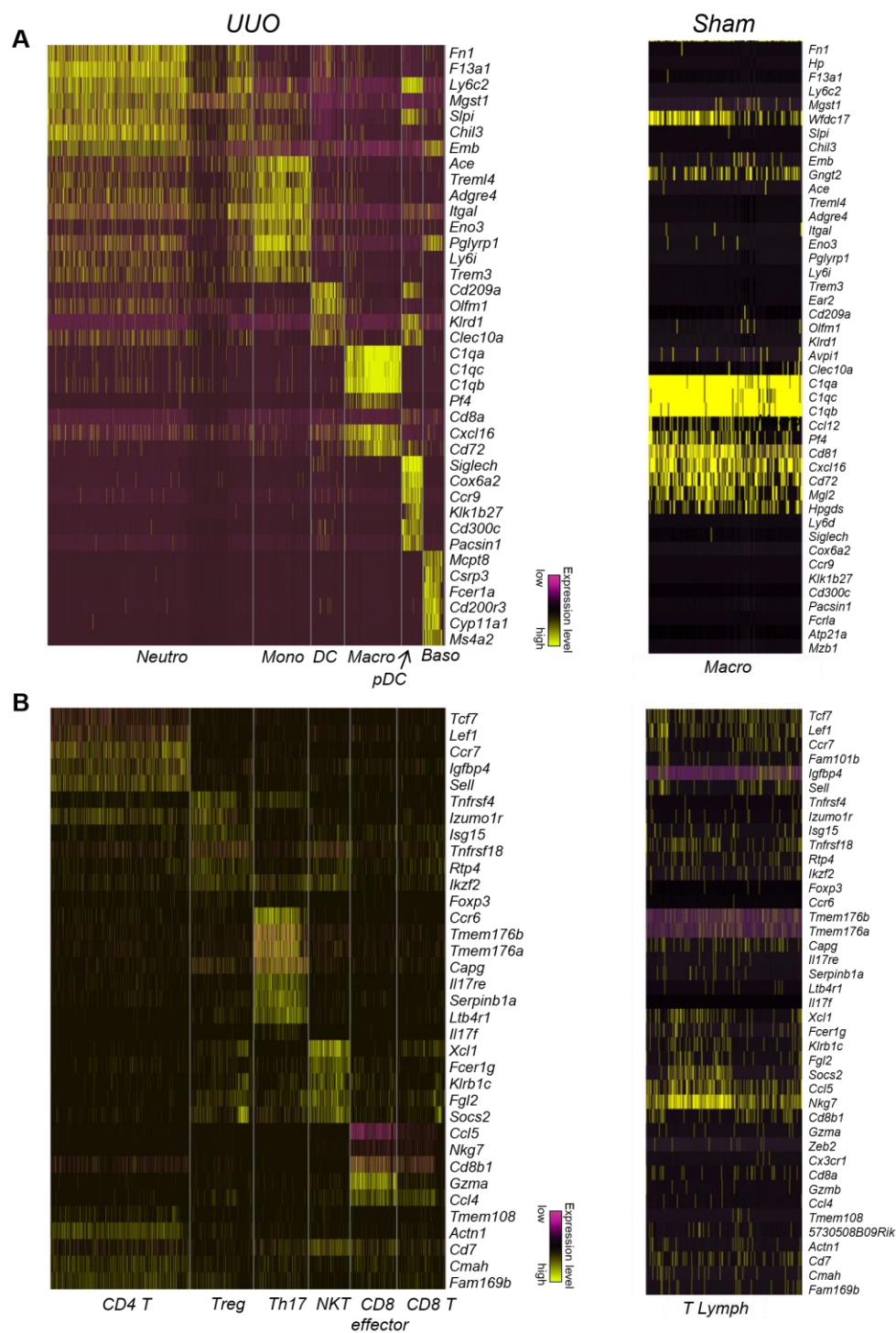
(B) Bubble plot showing the expression pattern of Col1a1, Col3a1, Dcn, and Pdgfrb in each cell cluster.



Supplementary Fig 4: Distribution of immune cell in various tissues.

(A) Gene set enrichment of pDC, DC, macrophage, and basophils markers identified in the current study in the published ImmGen atlas.

(B) The representative image of marker genes from human proteome atlas version 21.0 (<https://www.proteinatlas.org/>).

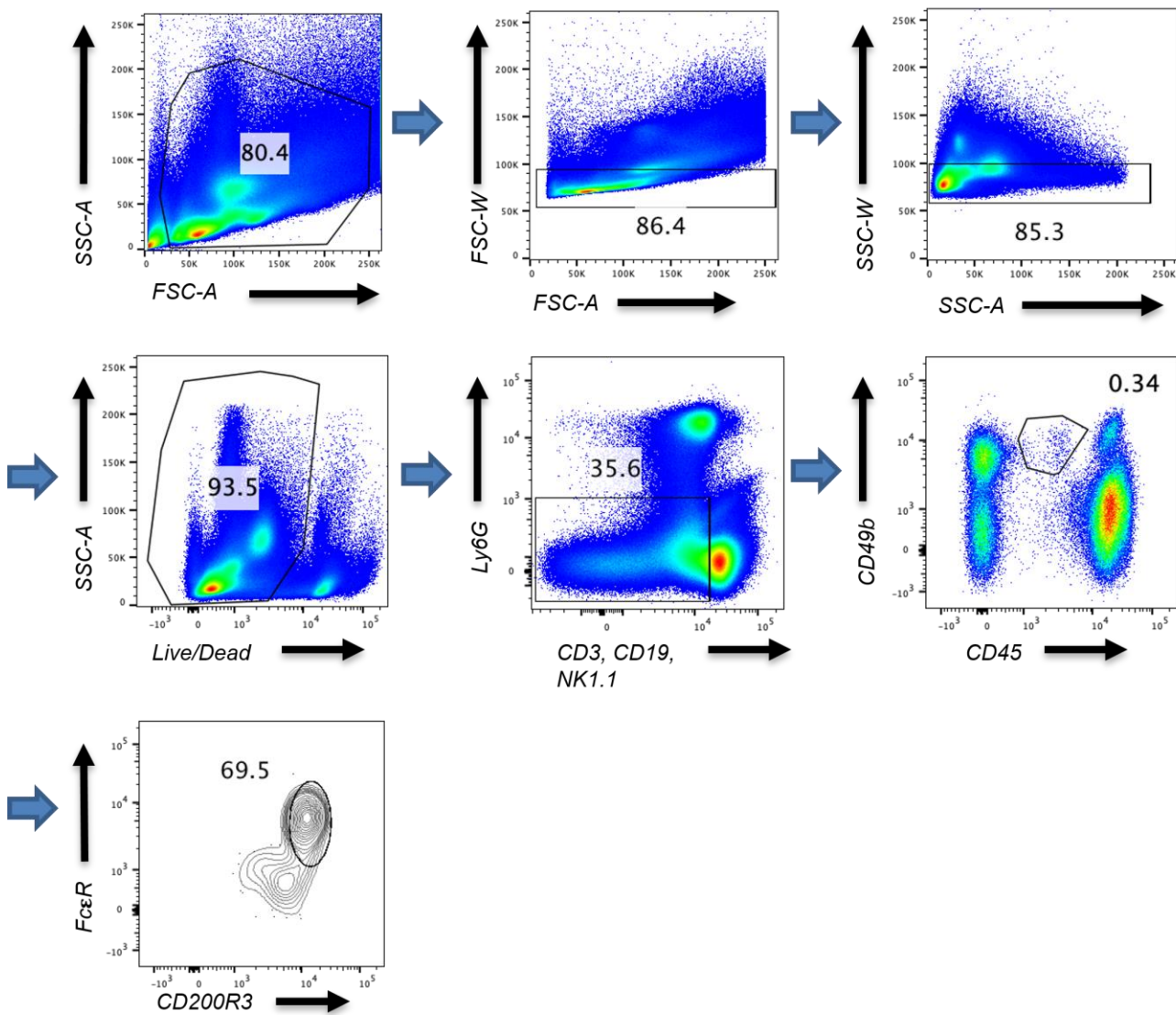


Supplementary Fig 5: Heatmap of immune cell gene expression

(A) Heatmap showing gene expression patterns in myeloid cells in sham and UUO kidneys.

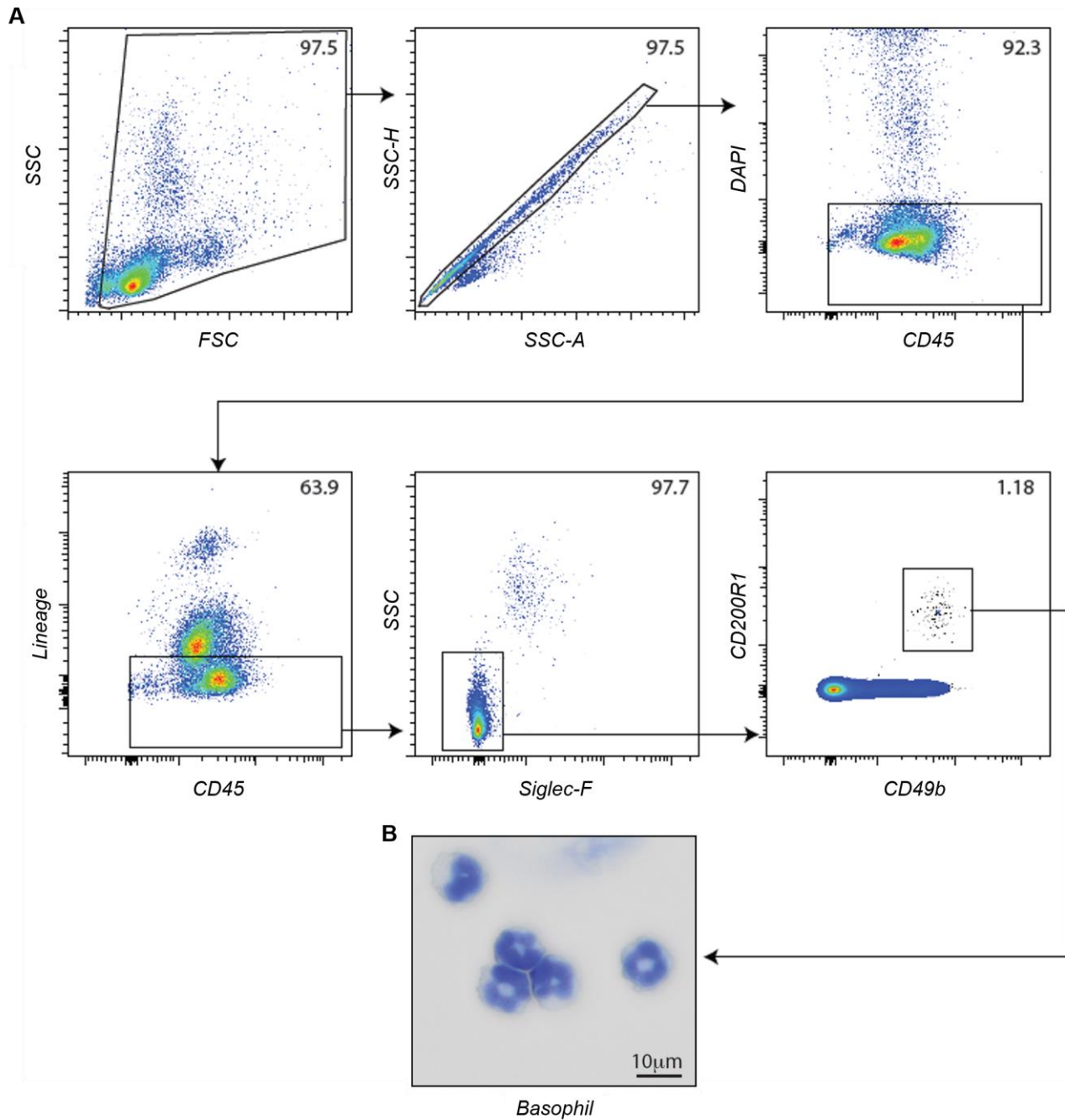
(B) Heatmap showing gene expression patterns in lymphoid cells in sham and UUO kidneys.

Gating strategy for basophils in vivo



Supplementary Fig 6 Gating strategy to identify basophils in the kidney tissue

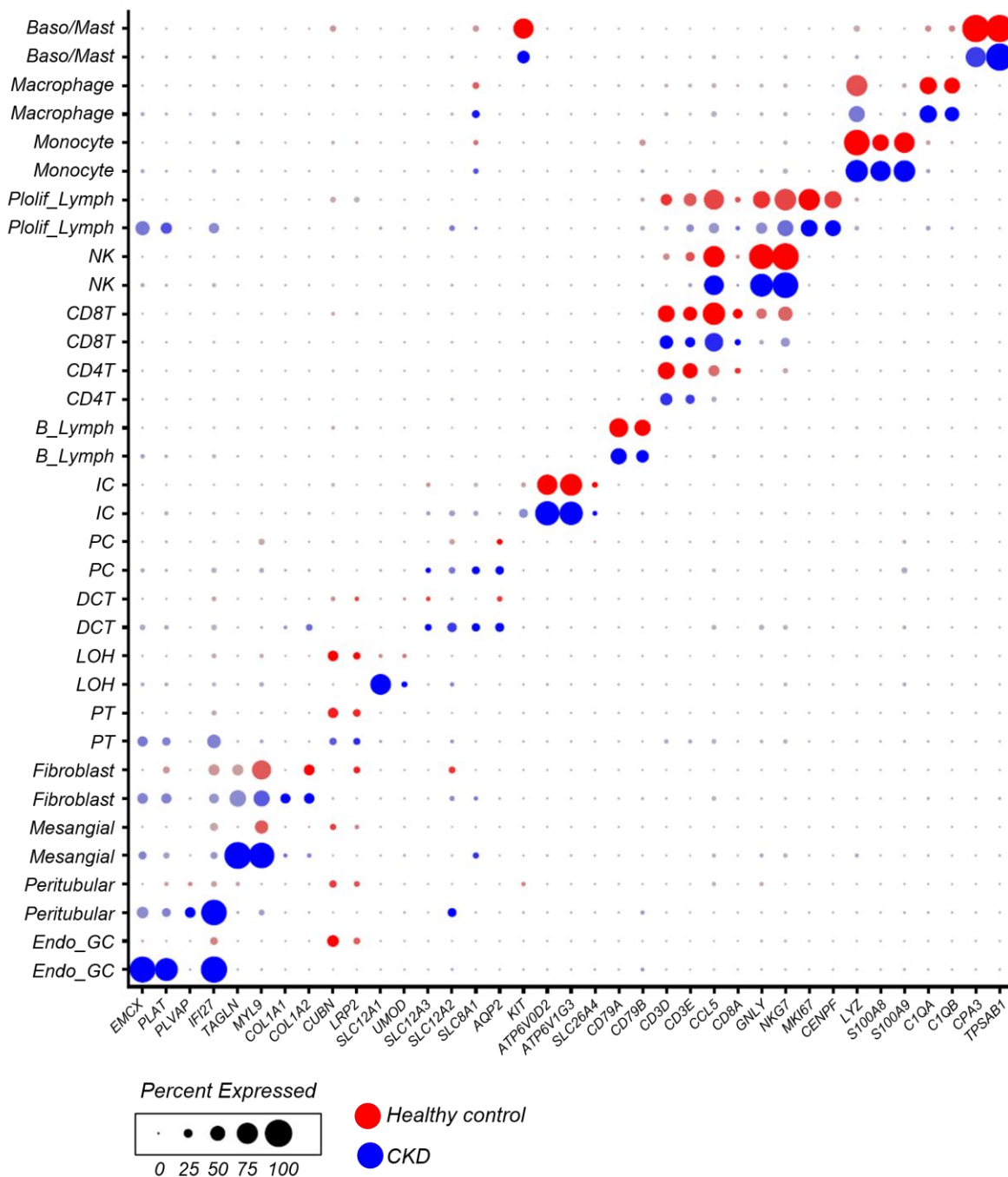
The FACS gating strategy and experimental results.



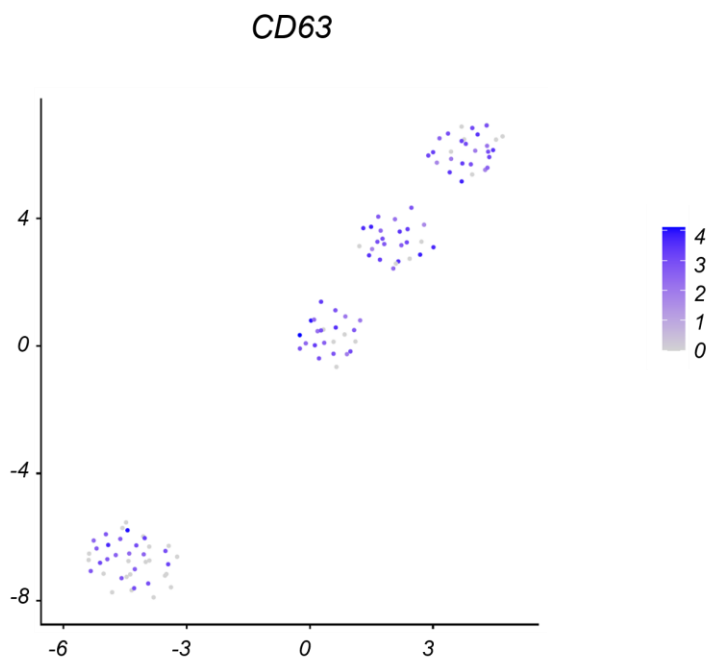
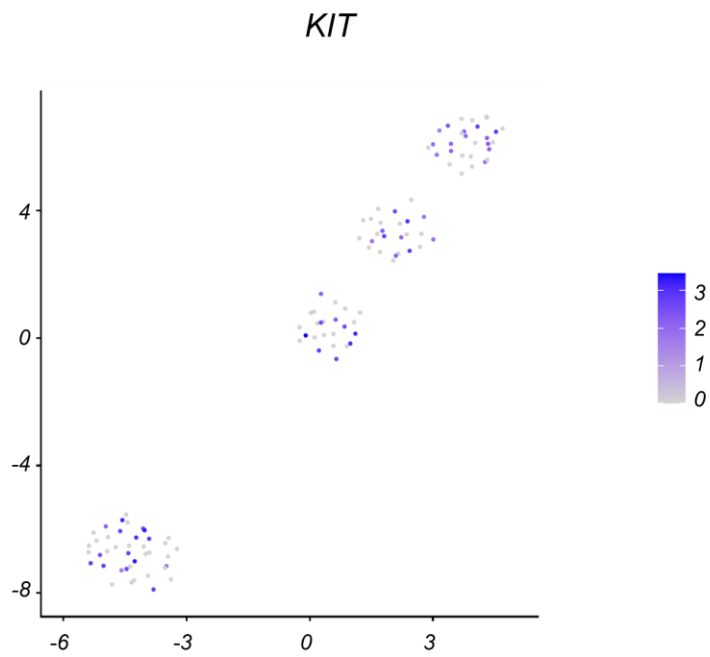
Supplementary Fig 7: Representative gating strategy used for basophils sort purification and basophil cytology

(A) FACS gating strategy. Basophils were identified as CD45 positive live cells that were lineage negative (CD3, CD19, NK1.1, Ly6G, cKit), Siglec-F negative, CD49b positive and CD200R1 positive.

(B) Representative cytology of sort-purified basophils stained with DiffQuik. Scale bar: 10 μ m. Data are representative of two independent experiments.

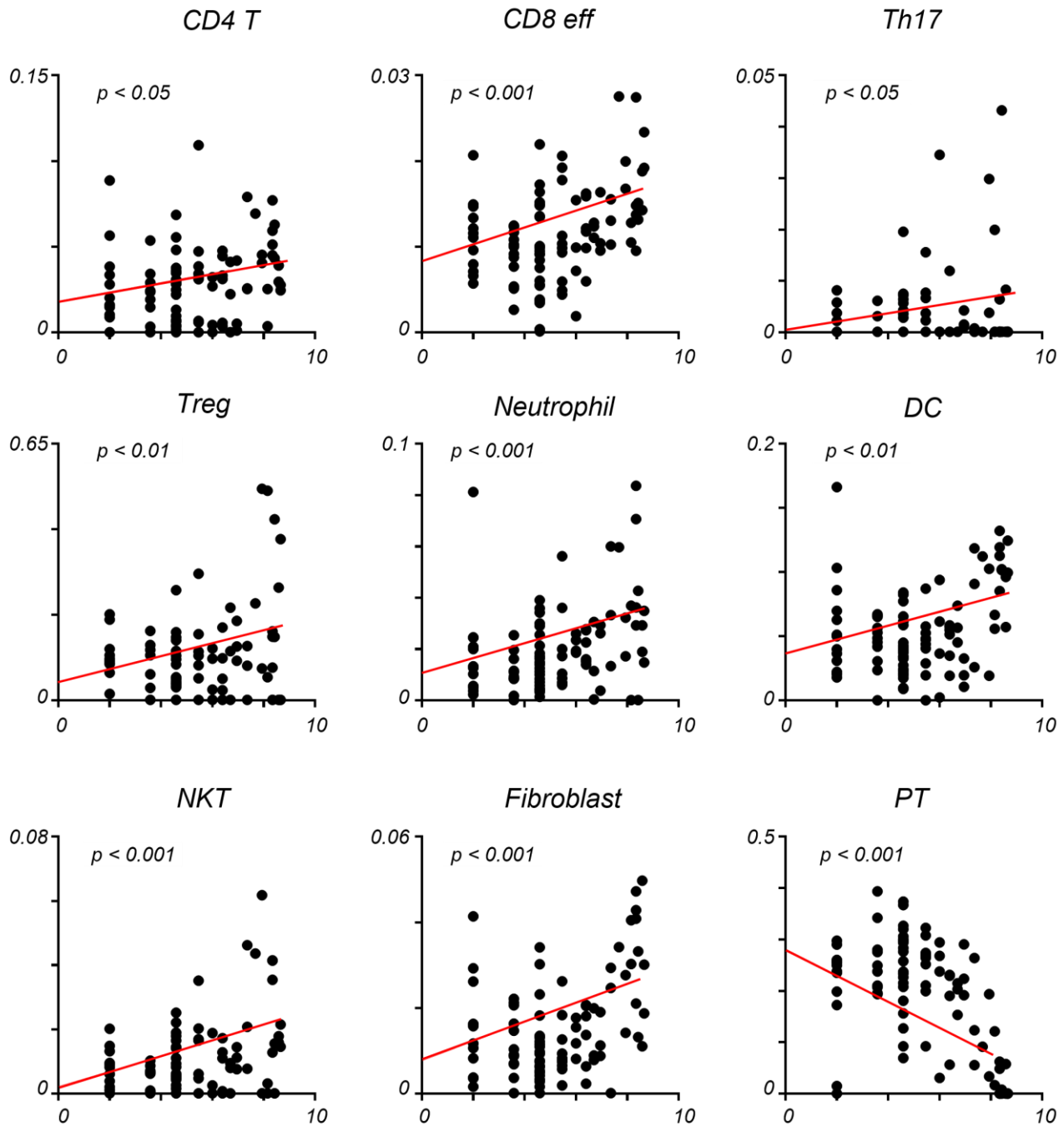


Supplementary Fig 8: Clustering of single cell data from human healthy control and CKD subject. Bubble plots showing expression of cell cluster marker genes in healthy control (red) and CKD kidneys (blue). The circle size represents the percent expression.



Supplementary Fig 9. Expression of KIT and CD63 in basophil/mast cell cluster in the human kidney single cell data

The scatter plot of KIT and CD63 in basophil/mast cell cluster of human kidney samples. Each dot represents a single cell. Dense color indicates higher expression levels.



Supplementary Fig 10. In silico deconvolution analysis of microarray gene expression data of human kidney samples.

Correlation between the percentage (log expression) of kidney fibrosis (x-axis) and each cell fraction (quantified CIBERSORT in silico deconvolution) (y-axis).