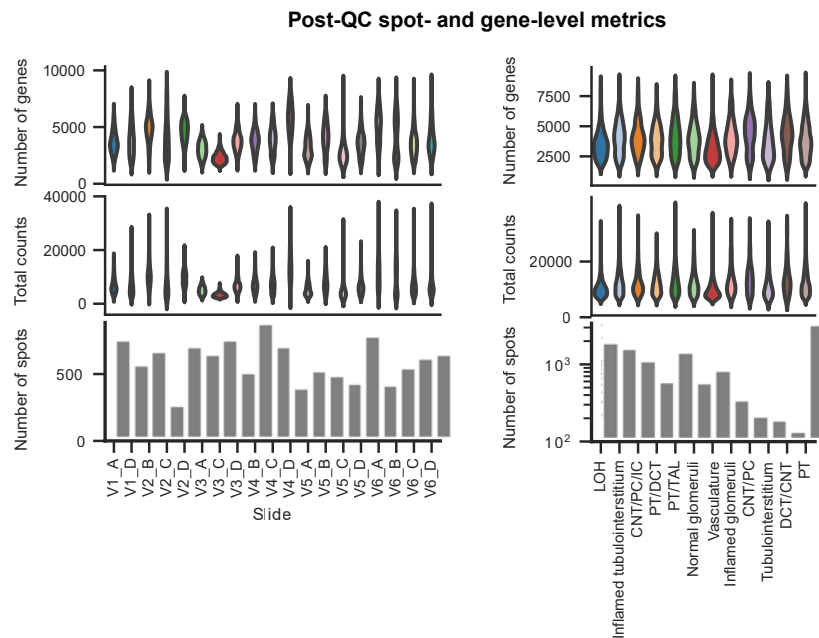
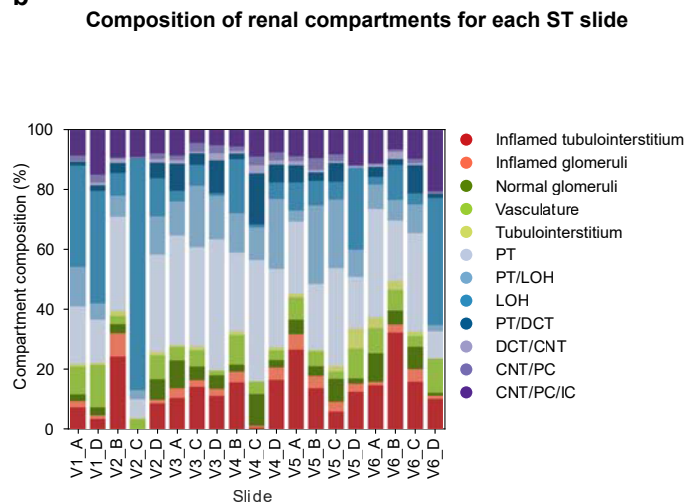


a

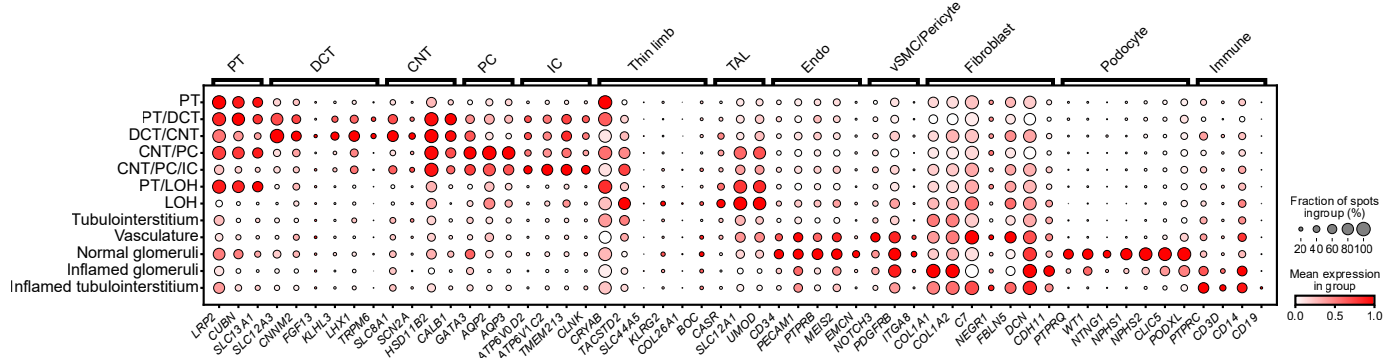


b

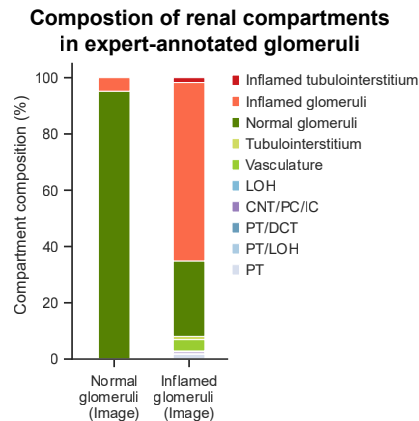


C

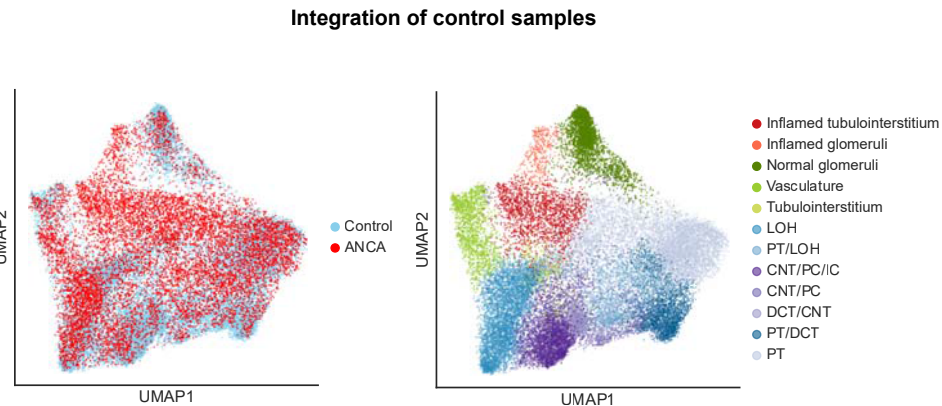
Expression of cell type marker genes in renal compartments



d



e



Supplemental Figure 1: Overview of spatial transcriptomics data from the exploratory group.

a Post-quality control (QC) distributions of number of genes, total UMI counts per spot, and number of spots per Visium ST slide (left) and renal compartment (right). **b** Barplots showing composition of each ST slide. **c** Dot plot showing the expression of marker genes across the renal compartments. **d** Barplots showing the distribution of gene-expression-based annotations compared to expert-based image annotations of normal and inflamed glomerular compartments (x-axis). **e** Joint UMAP-embedding of control and ANCA-GN exploratory group showing condition and renal compartments after the integration of ST slides containing control samples (8 slides and 21,420 spots).

LOH, loop of Henle. CNT, connecting tubules. PC, principal cells. IC, intercalated cells. PT, proximal tubules. DCT, distal convoluted tubules. TAL, thick ascending loop of Henle. vSMC, vascular smooth muscle cells.