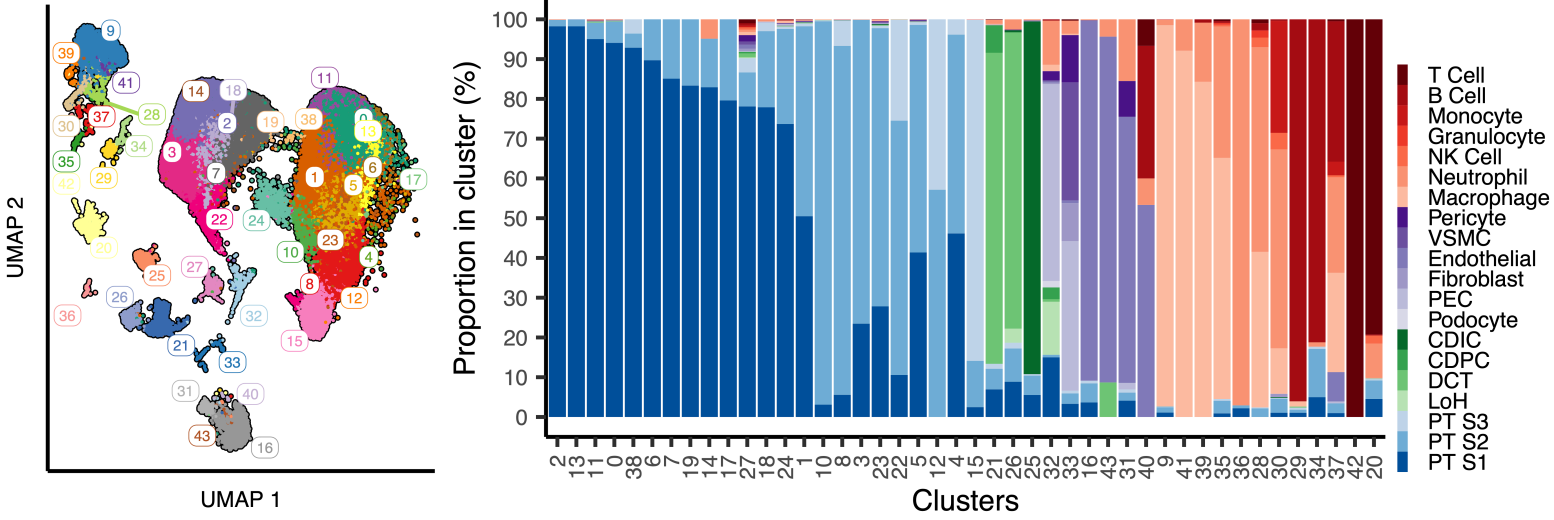
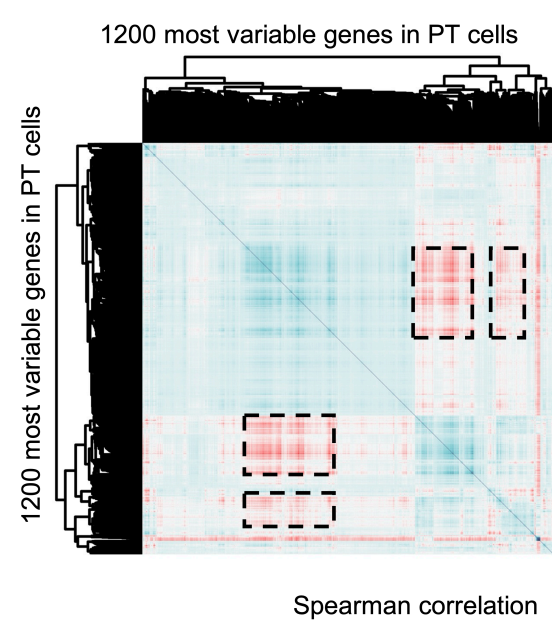


Supplementary Figure S1

A

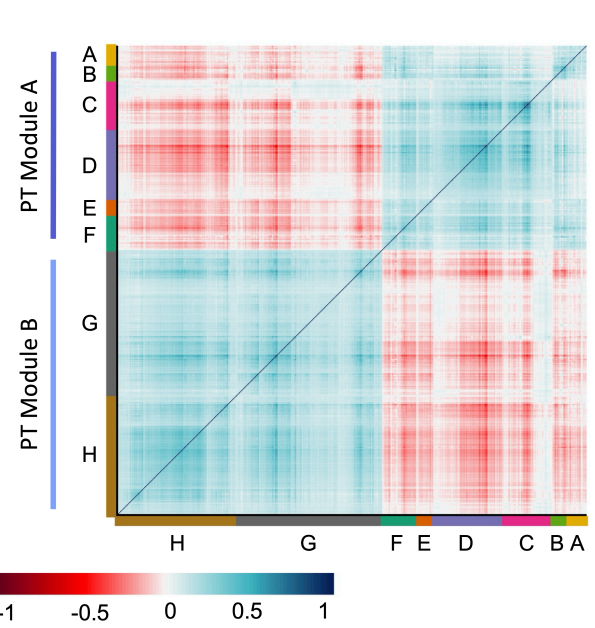


B

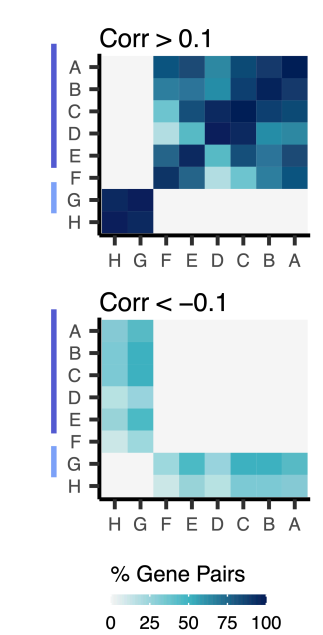


C

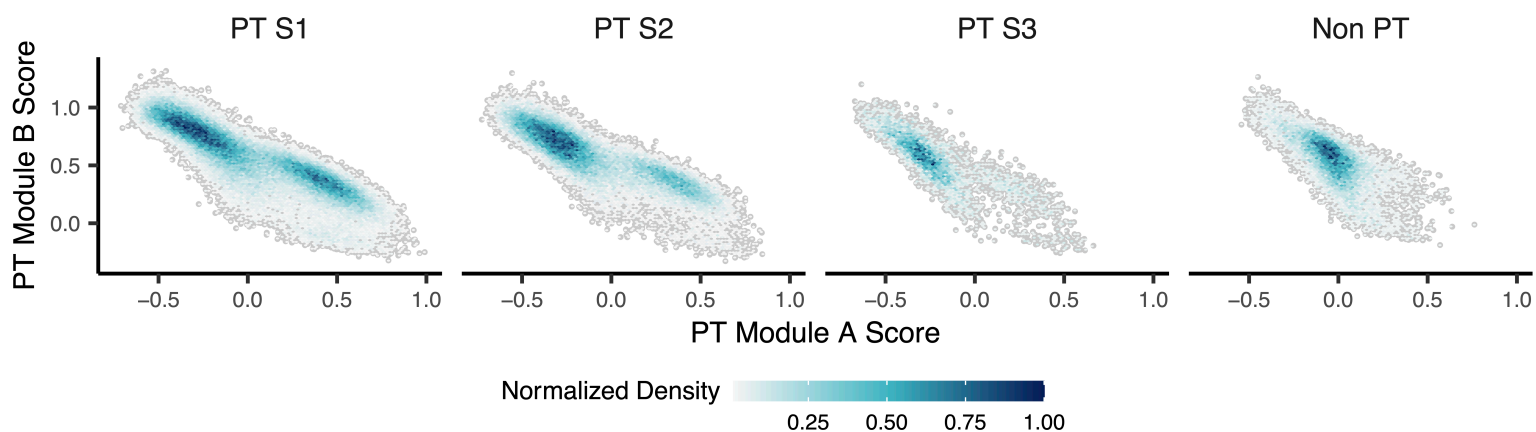
Anti-correlated expression of genes in PT cells



D



E



Supplementary Figure S1: Single-cell RNA sequencing on flow-sorted renal cells. **(A)** UMAP plot depicting cells from kidneys of Control mice colored by UMAP clusters (left). Cell-type composition of each cluster (right). PT – Proximal Tubule; LoH – Loop of Henle; DCT – Distal Convoluted Tubule; CD – Collecting duct, PC – Principal Cell, IC – Intercalated; PEC – Parietal epithelial cell; VSMC – Vascular Smooth Muscle Cell; NK – Natural Killer cell. **(B)** Correlation heatmap for 1,200 most-variable genes expressed in PT cells in kidneys of Control mice after hierarchical clustering. Two areas with high degree of anti-correlation marked by black rectangles. **(C)** Heatmap depicting pairwise Spearman correlations that were highlighted by black rectangles in (B). Hierarchical clusters of genes depicting anti-correlated expression are labelled A-F (PT Module A) and G-H (PT Module B). **(D)** Proportion of gene-pairs between each cluster of genes with Spearman correlations above 0.1 (top) or below -0.1 (bottom). **(E)** Density plot depicting distribution of PT S1, PT S2, PT S3, and non-proximal tubular (Non PT) cells based on the expression scores for PT Module B against PT Module A. **(A-E)** scRNA-seq data shown for n = 3 female (3F) and n = 1 male (1M) Control mice.