

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Quality control and metadata information of scRNA-seq data.

File Name: Supplementary Data 2

Description: Cell type marker genes derived from scRNA-seq analysis & marker genes used for annotation.

File Name: Supplementary Data 3

Description: DEG in scRNA-seq data after ambient RNA cleaning.

File Name: Supplementary Data 4

Description: DEG in scRNA-seq data of stroma subclusters.

File Name: Supplementary Data 5

Description: Cell type-specific open chromatin derived from snATAC-seq analysis.

File Name: Supplementary Data 6

Description: Cell type-specific motif enrichment.

File Name: Supplementary Data 7

Description: Regulons and respective target genes inferred by SCENIC.

File Name: Supplementary Data 8

Description: Scaled and binarized regulon activities in each cell type inferred by SCENIC.

File Name: Supplementary Data 9

Description: ChromVAR cell-TF enrichment score matrix.

File Name: Supplementary Data 10

Description: DEG along pseudotime in distinct lineages in scRNA-seq data.

File Name: Supplementary Data 11

Description: Differentially accessible peaks along pseudotime in distinct lineages in snATAC-seq data.

File Name: Supplementary Data 12

Description: Nearest genes of differentially accessible peaks along pseudotime in distinct lineages in snATAC-seq data.

File Name: Supplementary Data 13

Description: GO enrichment of differentially accessible peaks along pseudotime in distinct lineages inferred by GREAT analysis.

File Name: Supplementary Data 14

Description: Nearest genes of differentially accessible peaks at bifurcation events along pseudotime in distinct lineages inferred by GREAT analysis.

File Name: Supplementary Data 15

Description: Proportion of cells in each cell type with accessible chromatin overlapped with kidney disease-associated SNPs.

File Name: Supplementary Data 16

Description: Material Table