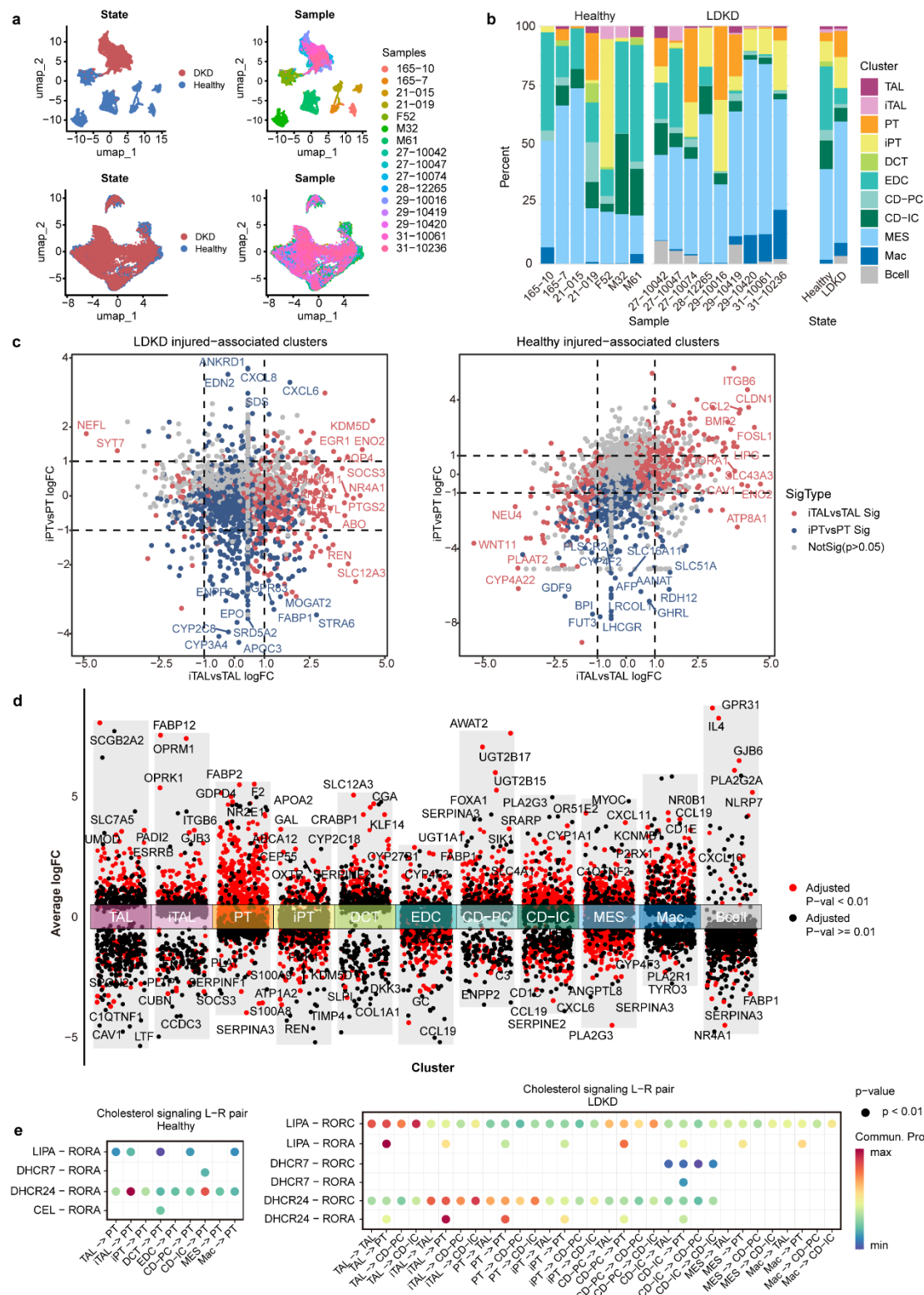
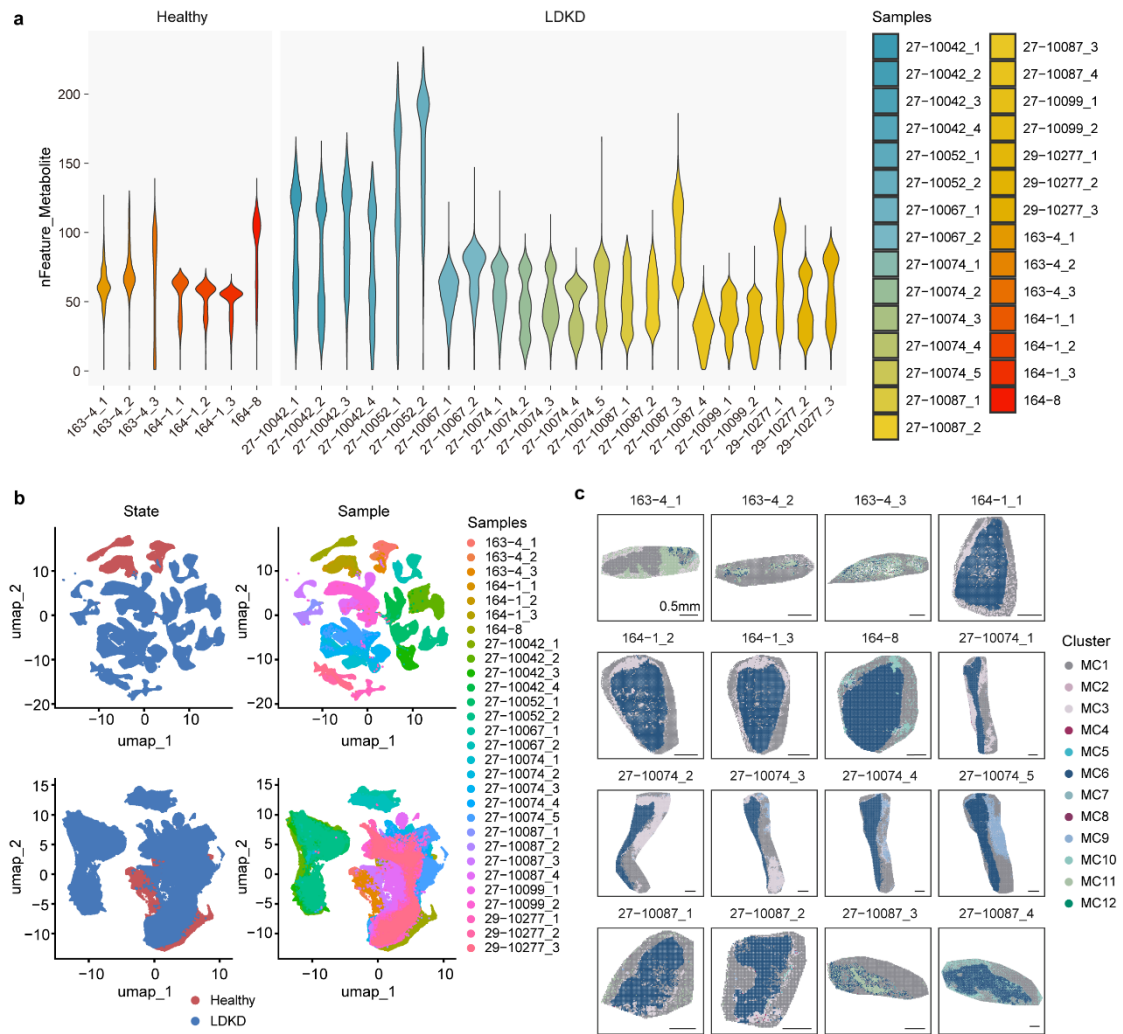


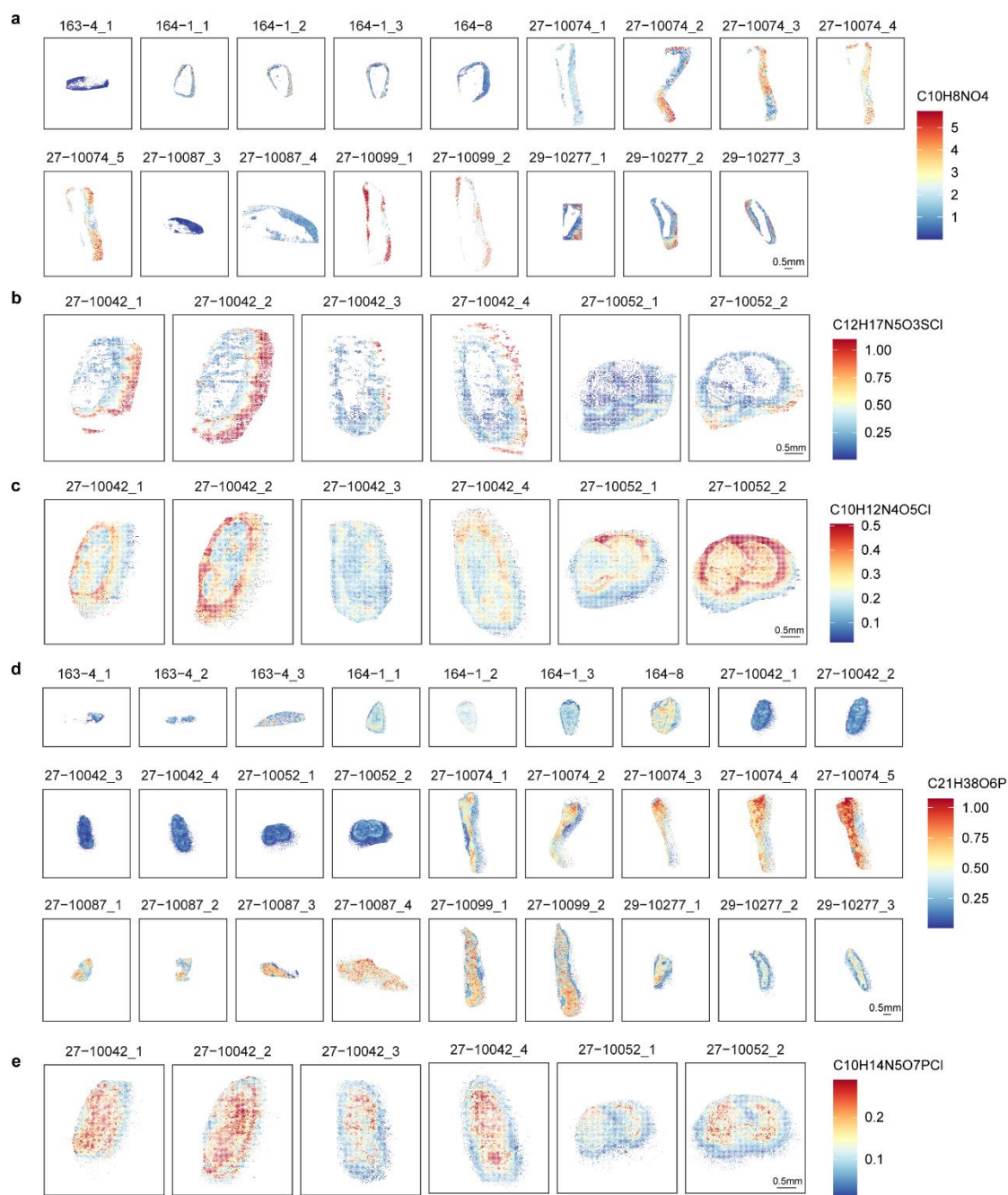
Supplementary Figure 1. Single-cell RNA Sequencing (scRNA-seq) analysis reveals kidney cell types in LDKD and healthy donors. (a) Clinical profiles of participants in the study. (b-c) Violin plot of UMI counts, gene numbers, mitochondrial gene proportions, and ribosomal gene proportions in samples from healthy (b) and LDKD participants. (d) UMAP plot of LDKD and healthy samples before (upper) and after (lower) batch effect correction. (e) UMAP plot of kidney cells in LDKD and healthy samples respectively. Different colors correspond to distinct cell types. (f) The proportions of cell types in LDKD and health samples. Wilcoxon test. Only significant p-values are displayed on the right side of each cluster.



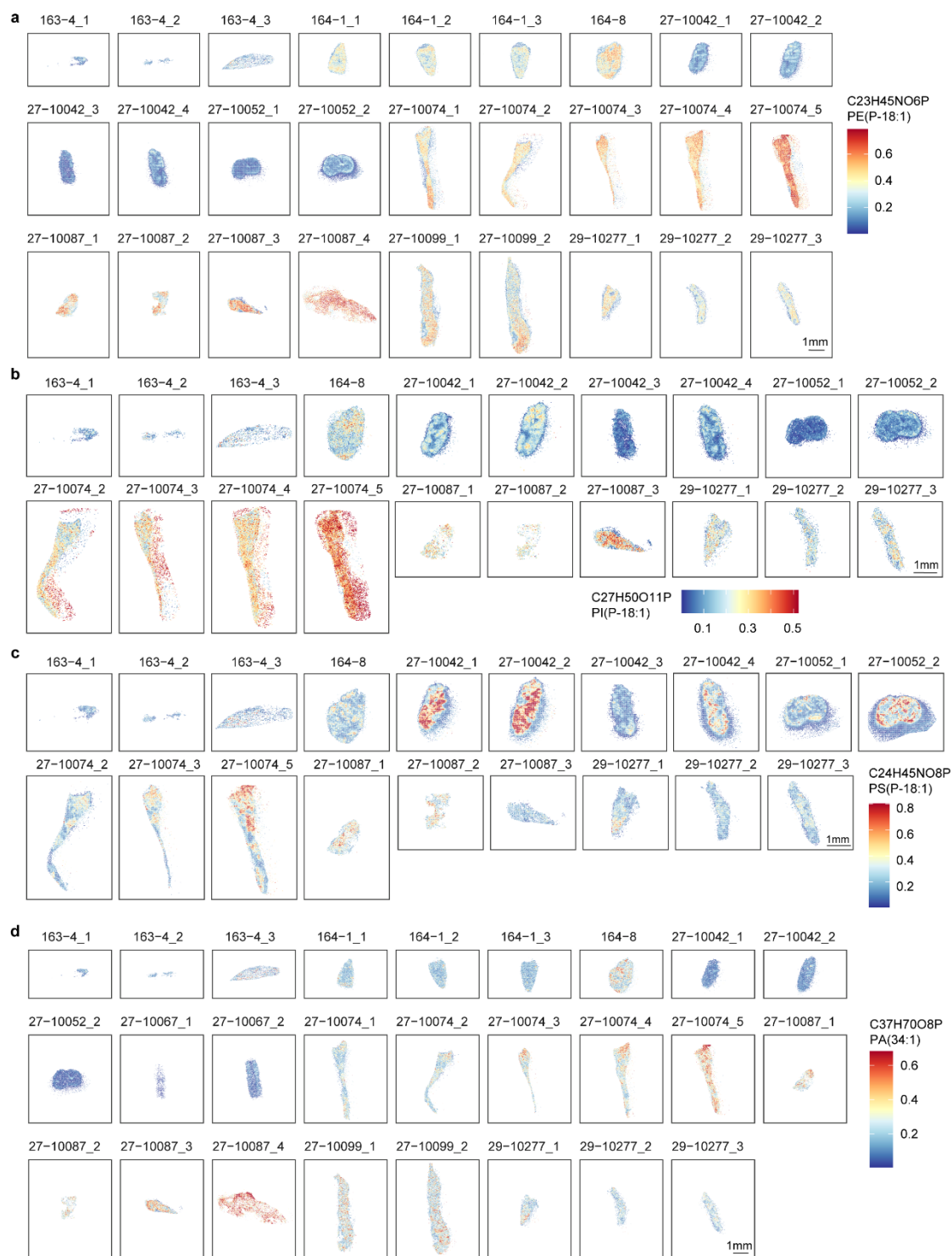
Supplementary Figure 3. Spatial transcriptomics analysis for LDKD and healthy samples. (a) UMAP plot of LDKD and healthy samples before (top) and after (bottom) batch correction. (b) Bar plot of the composition of different cell types in each sample. Only cells with a final proportion exceeding 50% are included. (c) Scatter plot of differentially expressed genes (DEGs) in two comparisons between LDKD and healthy samples. The x-axis represents the avg_logFC for iTAL vs TAL, and the y-axis for iPT vs PT. Point colors indicate significance type, and genes are from lipid-associated pathways. P-values in both comparisons are based on the Wilcoxon test. (d) Highlight of significantly altered genes per cell type. Different colors denote distinct significance types (Wilcoxon test, threshold = 0.5). Top 5 highest/lowest fold change genes are labeled for each cell type. (e) Significant ligand-receptor interactions in the cholesterol metabolism pathway network for LDKD and healthy samples. Significant pairs are identified via permutation testing.



Supplementary Figure 4. Spatial metabolomics analysis for LDKD and healthy samples. (a) Violin plot of metabolite feature numbers in spatial metabolomics samples from LDKD patients and healthy donors. (b) UMAP plot of LDKD and healthy samples before (upper) and after (lower) batch effect correction. (c) Spatial distribution of MCs in samples from remaining LDKD patients and healthy donors. Scale bar, 0.5 mm.



Supplementary Figure 5. Spatial distribution of characteristic metabolites for distinct MCs. Spatial distribution of the metabolites: (a) C10H8NO4, a characteristic metabolite for MC1; (b) C12H17N5O3SCI, a characteristic metabolite for MC2; (c) C10H12N4O5CI, a characteristic metabolite for MC4; (d) C21H38O6P, a characteristic metabolite for MC6; (e) C10H14N5O7PCI, a characteristic metabolite for MC7. Scale bar, 0.5 mm.



Supplementary Figure 6. Spatial distribution of characteristic metabolites for lipid classes. Spatial distribution of the metabolites: (a) C23H45NO6P, annotated as PE(P-18:1); (b) C27H50O11P, annotated as PI(P-18:1); (c) C24H45NO8P, annotated as PS(P-18:1); (d) C37H70O8P, annotated as PA(34:1). Scale bar, 1 mm.

