Supplementary Table legends

Supplementary Table 1: Demographic and clinical characteristics of participants included in the spatial transcriptomics study are provided.

Supplementary Table 2: Demographic and clinical characteristics of single-nucleus sequencing samples used for dataset integration are summarized.

Supplementary Table 3: Differentially expressed genes between annotated cell types in the CosMx dataset are listed.

Supplementary Table 4: Differentially expressed genes between annotated cell types in the Xenium dataset are listed.

Supplementary Table 5: Differentially expressed genes between annotated cell types in the imputed dataset are provided.

Supplementary Table 6: Differentially expressed genes between spatial niches in the CosMx dataset are presented.

Supplementary Table 7: Differentially expressed genes between spatial niches in the Xenium dataset are presented.

Supplementary Table 8: Differentially expressed genes between spatial niches in the imputed dataset are presented.

Supplementary Table 9: Differentially expressed genes between DKD and control samples in the imputed dataset are listed.

Supplementary Table 10: Cell–cell interactions identified within PT, iPT, LOH, and iLOH niches are detailed.

Supplementary Table 11: Cell–cell interactions identified within DCT, glomerular, vascular, fibroblast, immune, CD, and CNT niches are detailed.

Supplementary Table 12: Differentially expressed genes between center-cell iPT microenvironments in the CosMx dataset are listed.

Supplementary Table 13: Differentially expressed genes between center-cell iLOH microenvironments in the CosMx dataset are listed.

Supplementary Table 14: Differentially expressed genes between center-cell iPT microenvironments in the Xenium dataset are listed.

Supplementary Table 15: Differentially expressed genes between center-cell iLOH microenvironments in the Xenium dataset are listed.

Supplementary Table 16: Differentially expressed genes between injured tubular microenvironments within a 20 μm surrounding region in the CosMx dataset are presented.

Supplementary Table 17: Differentially expressed genes between injured tubular microenvironments within a 20 μm surrounding region in the Xenium dataset are presented.

Supplementary Table 18: Differentially expressed genes between injured tubular microenvironments within a 20 μm surrounding region in the imputed dataset are presented.

Supplementary Table 19: All identified cell–cell interactions within the injured tubular microenvironment are provided.

Supplementary Table 20: All identified cell–cell interactions within the injured tubular immune microenvironment are provided.

Supplementary Table 21: All identified cell–cell interactions within the glomerular immune microenvironment are provided.

Supplementary Table 22: Spatially variable genes identified across niches are listed.

Supplementary Table 23: Spatially variable genes identified in the B cell–predominant immune microenvironment and the profibrotic injured tubular microenvironment are listed.

Supplementary Table 24: Clinical characteristics of B− and B+ DKD patient groups are summarized.

Supplementary Table 25: Differentially expressed genes between B+ and B− groups in bulk sequencing data from the TRIDENT cohort are listed.

Supplementary Table 26: Elastic net modeling results from the TRIDENT cohort are presented.

Supplementary Table 27: Plasma proteomics validation results in the UK Biobank cohort are provided.

Supplementary Table 28: Genes assayed in the Xenium and CosMx spatial transcriptomics panels are listed.

Additional References:

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