

Supplementary Figure Legends

Figure S1 Batch correction and pseudotime starting point estimation in scRNA seq.

(A, B) UMAP visualization colored by sample source (A) and disease state (B). (C) Relative expression of differentially expressed genes identified in bulk transcriptome across each single-cell clusters. (D, E) Macrophage differentiation order identified by Cytotrace. (F, G) Endothelial cell differentiation order identified by Cytotrace. MN, membranous nephropathy; NOM, normal kidney; PT, proximal tubular cells; MC, mesangial cells; Pod, podocytes; LOH, Loop of Henle cells; DT, distal tubular cells; IC, intercalated cells; PC, principal cells; Endo, endothelial cells; Fib/Per, fibroblasts/pericytes; Less diff., less differentiated; More diff, more differentiated.

A

B

C

D

E

F

G

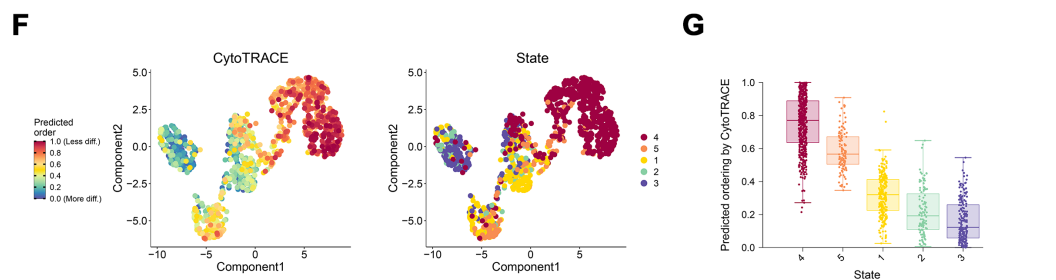


Figure S2 Relative expression of differentially expressed genes identified in Olink proteomics across each single-cell clusters.

Figure S2

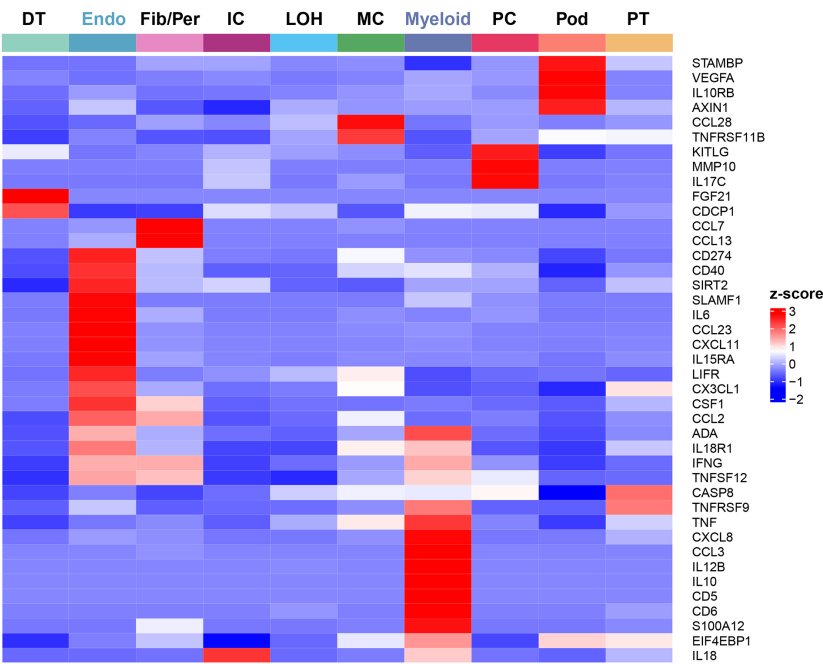


Figure S3 Results of reverse mendelian randomization in the discovery and validation cohort.

Figure S3

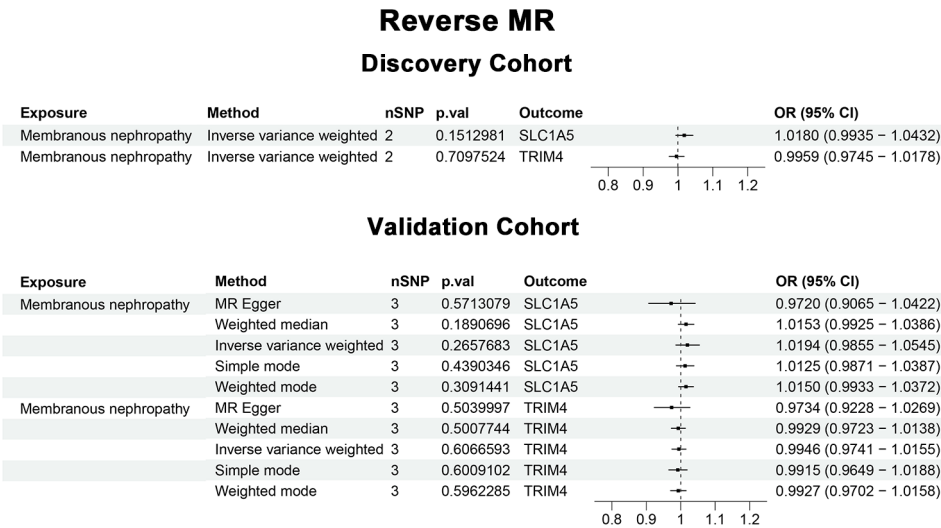


Figure S4 UMAP visualization of *TRIM4* expression in endothelial cells.

Figure S4

