## **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.

Figure S1

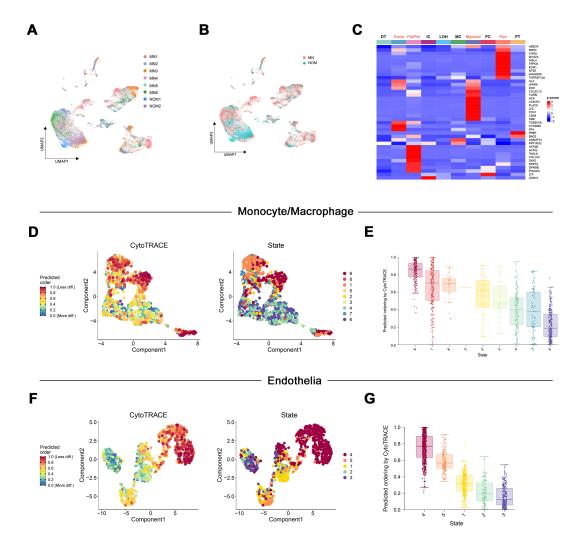


Figure S2 Relative expression of differentially expressed genes identified in Olink proteomics across each single-cell clusters.

Figure S2

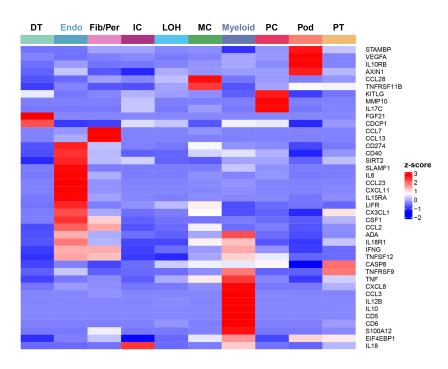


Figure S3 Results of reverse mendelian randomization in the discovery and validation cohort.

Figure S3

## **Reverse MR Discovery Cohort** Exposure Method nSNP p.val Outcome OR (95% CI) Membranous nephropathy Inverse variance weighted 2 0.1512981 SLC1A5 1.0180 (0.9935 - 1.0432) Membranous nephropathy Inverse variance weighted 2 0.7097524 TRIM4 0.9959 (0.9745 - 1.0178) 0.8 0.9 1 1.1 1.2 **Validation Cohort** OR (95% CI) Method nSNP p.val Exposure Outcome MR Egger 0.5713079 SLC1A5 0.9720 (0.9065 - 1.0422) Membranous nephropathy 0.1890696 1.0153 (0.9925 - 1.0386) Weighted median SLC1A5 Inverse variance weighted 3 0.2657683 SLC1A5 1.0194 (0.9855 - 1.0545) Simple mode 0.4390346 SLC1A5 1.0125 (0.9871 - 1.0387) 1.0150 (0.9933 - 1.0372) 0.3091441 SLC1A5 Weighted mode MR Egger 0.5039997 TRIM4 0.9734 (0.9228 - 1.0269) Membranous nephropathy Weighted median 0.5007744 TRIM4 0.9929 (0.9723 - 1.0138) Inverse variance weighted 3 0.6066593 TRIM4 0.9946 (0.9741 - 1.0155) 0.9915 (0.9649 - 1.0188) Simple mode 0.6009102 TRIM4 0.9927 (0.9702 - 1.0158) 0.5962285 TRIM4 Weighted mode 0.8 0.9 1 1.1 1.2

Figure S4 UMAP visualization of TRIM4 expression in endothelial cells.

Figure S4

