SUPPLEMENTAL FIGURE LEGENDS

Figure S1: Single-Cell RNA-Seq Analyses of Week 15 and Week 17 Human Fetal Kidneys Showing Transcriptional Changes during Differentiation of human NPCs to Podocytes (Related to Figure 1A-E)

(A) Unsupervised clustering of Week 15 kidney cells from both Zone 1 and Zone 2 displayed in a tSNE plot with annotation of cluster identities. In parentheses are differentially expressed genes used for cluster identification).

(B) tSNE plot of Week 15 kidney cells colored by their original zonal identities.

(C) Violin plots of differentially expressed genes used to classify 21 clusters of Week 15 cells.

(D) and (E) Bar graphs presenting zonal contribution in Week 15 kidney (D) or Week 17 (E) clusters

(F) and (G) Volcano plots with annotations of genes that are differentially expressed between Zone 1 and Zone 2 of Week 15 (F) or Week 17 kidney (G).

Figure S2: Pseudotime Analyses Showing Transcriptional Changes during Human Podocyte Development (Related to Figure 1F-H)

(A) and (B) Pseudotime trajectories from NPCs to Podocytes with cells colored by their cluster identities (A) or zonal identities (B).

(C) Expression of *EYA1, MAFB,* and *TOP2A* along the pseudotime trajectory indicating B3 is mostly comprised of proliferative cells.

(D) Representative EP and LP genes that were used in gene expression correlation analysis to obtain a more complete list of EP and LP genes.

(E) and (F) GO term analyses of human EP gene list (E) or human LP gene list (F) using ToppFun.

(G) and (H) Venn diagrams displaying shared and species-specific EP genes (G) or LP genes (H).

(I) and (J) Fluorescent *in situ* hybridization (I) and quantification (J) showing expression of RPS21 in human developing nephrons. Scale bars denote 50µm.

(K) Dotplot showing expression of OMIM genes associated with glomerulosclerosis and glomerulopathy in the human glomerular cell types and organoid EP and LP. Genes detected in *in vitro* derived podocytes are highlighted red.

B: Branch, hu: human, EP: early podocyte, LP: late podocyte

Figure S3: Examination of *in vitro* Derived Kidney Organoids Containing Podocyte-like Cells (Related to Figure 3)

(A) Schematic diagram of CRISPR-Cas9 targeting of *MAFB* locus in H9 hESC.

(B) IF stains of dd16 and dd28 kidney organoids suggesting formation of nephron-like structures. Scale bars denote 50µm.

(C) Expression levels of NPC markers (*SIX1, SIX2,* and *EYA1*), developing nephron markers (*PAX8, JAG1,* and *HNF1B*), nephron segment markers (*SLC3A1* and *SLC12A1*), early and late podocyte markers (*OLFM3, MAFB,* and *SYNPO, PLA2R1*) along the kidney organoid differentiation protocol.

(D) IF stains showing co-expression of eGFP with MAFB and WT1 in dd28 organoids. Scale bars denote 50µm.

(E) GO term analyses of genes enriched in dd28 MAFB-eGFP+ cells in comparison to MAFB-eGFP- cells using ToppFun.

(F) Hierarchical clustering using the top 2000 most variably expressed genes of transcriptional profiles of eGFP+ hESC-derived podocytes, eGFP- organoid cells, imPods, human fetal RCs and kidneys.

(G) tSNE plot of merged kidney organoid cells colored by their original "differentiation day" identities

(H) Pseudotime trajectories from organoid NPCs to podocytes with cells colored by their cluster identities (left) or "differentiation day" identities (right).

(I) Pseudotime trajectory from organoid NPCs to podocytes with cells colored by their original "differentiation day" identities after removal of proliferative cells.

(J) Expression of *EYA1, MAFB,* and *TOP2A* along the pseudotime trajectory indicating B3 is mostly comprised of proliferative cells.

Figure S4: Identification of Mesangial Cells, Glomerular Endothelial Cells and Early/Late Podocytes in Human Week 17, Merged Kidney Organoid and Czerniecki Organoid scRNA-Seq Datasets (Related to Figure 4 and 5)

(A) and (B) Feature plots showing the presence of pericytes (PDGFRB+ GATA3+), mesangial cells (GATA3+ TMEFF2+) and glomerular endothelial cells (PECAM1+ EHD3+) in Week 17 (A), and absence of these cell types in (B) Merged Kidney Organoids.

(C) and (D) Feature plots showing the presence of early podocytes (MAFB+ OLFM3+), late podocytes (MAFB+ TGFBR3+), and late podocytes expressing EP gene (ANXA1+ GFRA3+) in (C) Czerniecki Organoids (Czerniecki et al., 2018), and (D) Wu Organoids (Wu et al., 2018) using the Morizane protocol (M).

(E) and (F) Fluorescent *in situ* hybridization of *OLFM3, PLA2R1, COL4A3, TNNT2* and *MAFB* in human developing nephron. Scale bars denote 50µm.

Figure S5: Heatmaps Presenting Expression of Human Early and Late Podocyte Genes along the *in vivo* Differentiation Trajectory from NPCs to Podocytes (Related to Figure 1H)

NPC: nephron progenitor cell, EP: early podocyte, LP: late podocyte, hu: human.

Figure S6: Heatmaps Presenting Expression of Human Early and Late Podocyte Genes along the *in vitro* Differentiation Trajectory from NPCs to Podocytes (Related to Figure 3H)

NPC: nephron progenitor cell, EP: early podocyte, LP: late podocyte, hu: human, RC: renal corpuscle.



0 Average log fold difference

Zone2-enriched

Zone1-enriched

-1

0

0 Average log fold difference

Zone2-enriched

Zone1-enriched

-1

0



SIX1, SIX2, CBS, CLEC18A, GFRA3, GUCY1B3, HEY1, OLFM3, PAX8, PLVAP, PRSS23, UCP2

AIF1, ANXA1, ARMH4, COL4A3, COL4A4, CPXM1, DDN, F3, GADD45A, NPHS2, PLA2R1, PODXL, PTPRO, SOST, SPOCK2, TCF21, ST6GALNAC3, TGFBR3, TPPP3

F

Gene Ontology of huLP genes

GO: Biological Process	p values
Extracellular matrix organization	9.8E-12
Extracellular structure organization	1.0E-11
Glomerulus development	7.3E-11
Actin filament-based process	9.2E-10
Nephron development	7.1E-09

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Gene Ontology of huEP genes

GO: Biological Process	p values
SRP-dependent cotranslational protein targeting to membrane	2.7E-73
Cotranslational protein targeting to membrane	2.2E-71
Protein targeting to ER	4.0E-71
Establishment of protein localization to endoplasmic reticulum	4.0E-70
Nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	8.7E-67

G









Human LP Signature Genes on in vitro Podocyte Human EP Signature Genes on in vitro Podocyte **Developmental Trajectory** orgNPC orgEP orgLP naNPC orgEP SIX2 FGF10 UCP2 UCP2 CASC1! CASC1! CASC1! CADM1 TPM1 TPM1 TPM1 TMEM1 CRABP3 SIX1 CRABP3 SIX1 CRABP3 SIX1 CRABP3 SIX1 CRABP4 SIX1 CRABP5 SI Relative Expression Le -4 -2 0 2 4 and the second second second second ID1 ID3 HIMGA1 CBS NUSAP1 BIRC5 SLC30A3 SLC32A1 CDKL2 WDR86 RP11-33 CLEC4M GRB14 MGST1 MYC PLOD2 PPAP28 TSPAN8 COL9A1 CCND1 SORL1 ALDH1A1 CLDN7 RBM47 EMX2 CLDN1 MAOB IL1R1 CRTAC1 FBLN2 RP11-444 LHX1 OLFM3 NRP2 KRT19 PMP22 SFXN2 PCDH9 MGAT4C HIST1H2 GFRA3 S10047

