



Figure 3-figure supplement 1. Time course proteomic analysis of kidney organoid differentiation.

(A) Gene ontology (GO) term enrichment analysis for cellular component annotations associated with proteins detected in the cellular and ECM fractions of kidney organoids by mass spectrometry (MS). GO terms were considered enriched when False Discovery Rate (FDR) < 0.10. (B) Protein interaction network depicts matrisome proteins identified in kidney organoids by MS over the differentiation time course (nodes represent proteins and connecting lines indicate a reported protein-protein interaction). (C) Principal component analysis (PCA) for the matrix proteins identified by MS in the cellular (left plot) and ECM (right plot) fractions of kidney organoids. (D) Top 15 most abundant BM proteins found in kidney organoids by MS. Proteins were ranked according to their normalized abundance levels (LFQ-intensities). Pooled data are shown as median, error bars indicate the 95% confidence interval for the median. (E) Volcano plots show the log₂-fold change (x-axis) vs. -log₁₀-p-value (y-axis) for proteins differentially expressed in the cellular fraction of kidney organoids from day 14 to 18, and 18 to 25. Key BM proteins significantly up-regulated (FC>1.5, p-value < 0.05, Two-way ANOVA test, *n*=3) are indicated. (F) Pathway enrichment analysis for proteins differentially expressed during kidney organoid differentiation: bar charts depict log-transformed FDR for the top-most enriched pathways (FDR<0.10). Pathway terms shown were simplified.