



Figure 5-figure supplement 1. Proteomic analysis of E19 mouse fetal kidney and correlational comparison with kidney organoid proteomics. (A) Gene ontology (GO) term enrichment analysis for cellular component annotations associated with proteins detected by MS in the cellular and ECM. (B) GO biological process annotations enriched for top 100 most abundant proteins detected by MS in the cellular and ECM. (C) Top 20 most abundant BM proteins found in the E19 mouse kidney by MS. Proteins were ranked according to their normalized abundance levels (LFQ-intensities). Pooled data are presented as median, error bars indicate the 95% confidence interval for the median. (D) Comparison of other structural matrix and ECM-associated proteins identified in the E19 mouse kidney and kidney organoids over differentiation. (E) Spearman rank correlation plots depicting the r coefficient values for matrix and BM protein abundance (ECM fraction) comparisons between the E19 mouse kidney and kidney organoids.