



Figure 1 - Supplement 1. **A** Pearson's correlation matrix with hierarchical clustering for whole-transcriptome normalized RNA-seq gene counts from epithelium isolated from the tissues indicated on the axes. **B** Pearson's correlation coefficient for the comparison of whole-transcriptome normalized RNA-seq gene counts between each of the sample types listed on the x-axis and adult small intestinal epithelium. *P*-value indicates the results of an unpaired two-sided Student's *t*-test. **C** Principle component analysis of whole-transcriptome RNA-seq normalized gene counts. Cumulative explained variance for PC1 and PC2 is indicated as a percentage on the x- and y-axes, respectively. **D** Density plot of the Log₂-transformed Fold change in gene expression in epithelium from transplanted HIOs over epithelium from HIOs cultured *in vitro* plotted against the Log₂-transformed Fold change in gene expression in adult small intestinal epithelium over fetal small intestinal epithelium. The intensity of the blue color indicates the density of points in 2-dimensional space. SI, small intestine; tx, transplanted tissue; hPSC, human pluripotent stem cell; HIO, human intestinal organoid