



Supplementary information Fig. S3 Transcriptome analysis of Hyper-organoids

a, GSEA analysis showing enrichment of intestinal epithelial signature genes and colitis-associated regenerative genes in organoids cultured under the indicated conditions.

b, GSEA analysis showing enrichment of an injury-associated regenerative signature across different intestinal epithelium and organoids.

c, d, PCA analysis (c) and correlation matrix (d) of bulk RNA-seq data showing that Hyper-organoids resembled injury-associated epithelial cells more closely than ENR-organoids.