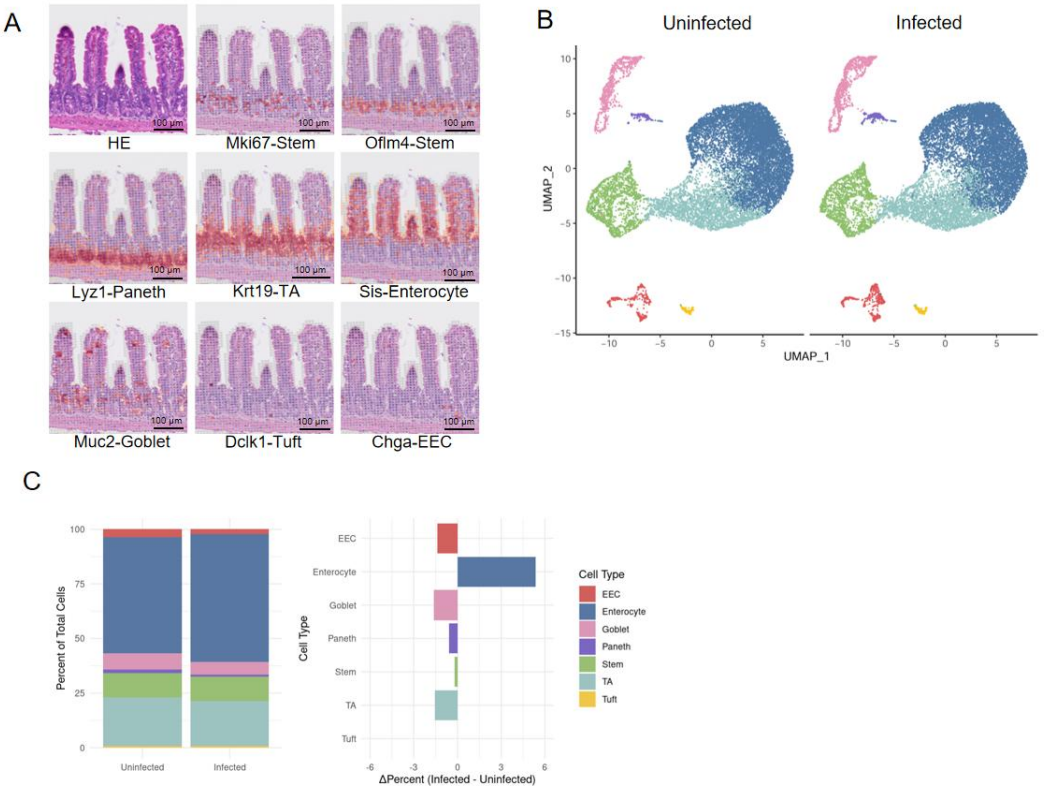
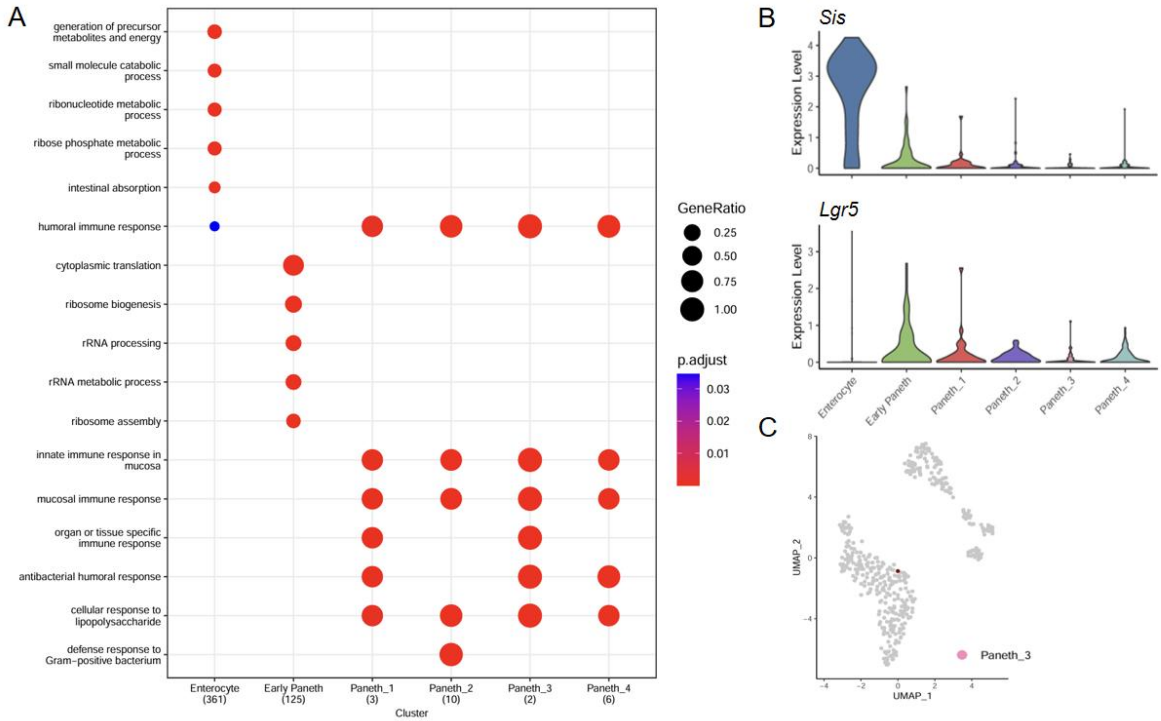
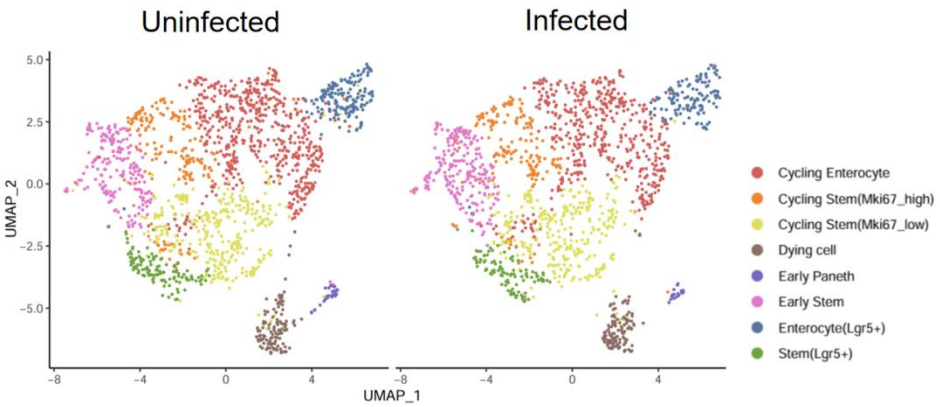


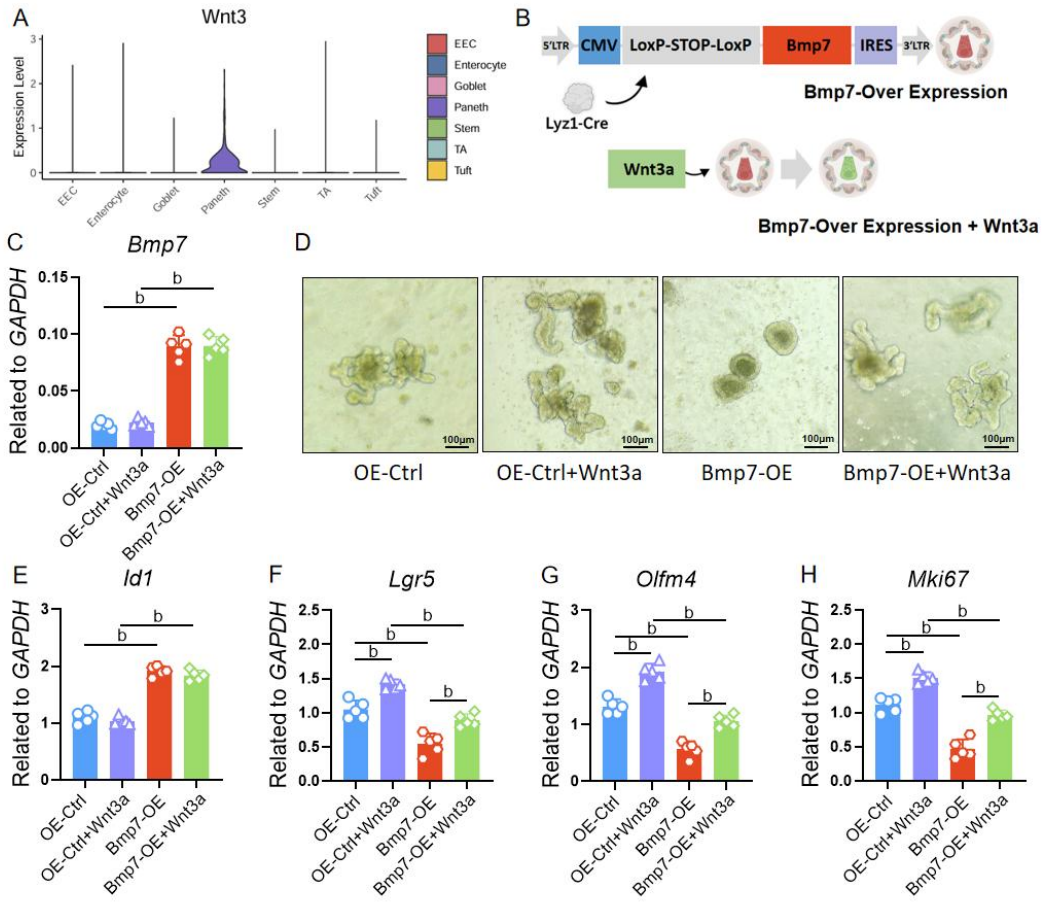
Supplementary Figure 1 Spatial distribution of marker genes across intestinal epithelial cell clusters and statistical comparison between uninfected and infected groups. A: Spatial transcriptomic analysis of marker genes in intestinal epithelial tissue; B: UMAPs of uninfected epithelial cells (Left) versus infected epithelial cells (Right); C: Quantification of percent cells per cluster (Left) and difference in percent of uninfected and infected cells (Right).



Supplementary Figure 2 Enriched GO terms for paneth cells and Infected Paneth cell localization. A: Enriched GO terms for all clusters in paneth cells; B: The expression of marker genes in Enterocyte (Paneth); C: Distribution of paneth cells containing RV genes.



Supplementary Figure 3 UMAPs of uninfected stem cells (Left) versus infected stem cells (Right).



Supplementary Figure 4 Exogenous Wnt3a can rescue the suppressive effect of BMP7. A. Violin plot of *Wnt3* expression across major intestinal epithelial cell types. B. Experimental design for Paneth cell-specific *Bmp7* overexpression (OE) with or without exogenous Wnt3a. Recombinant Wnt3a (200 ng/mL) was added to selected cultures. C. RT-qPCR of *Bmp7* mRNA in four groups (OE-Ctrl, OE-Ctrl+Wnt3a, Bmp7-OE, Bmp7-OE+Wnt3a). Expression is normalized to *GAPDH* (n=5, mean ± SD). E. qPCR of the BMP target *Id1* (n=5, mean ± SD). F-H. qPCR analysis of ISC-associated markers *Lgr5* (F), *Olfm4* (G), and the proliferation marker *Mki67* (H) (n=5, mean ± SD). $^{b}P < 0.01$.