Fig. S4 Analysis of scRNA-seq data. (related to Fig. 3)

a Unsupervised clustering of scRNA-seq data of the enriched crypts isolated from WT and *β7⁻/⁻* mice. Left: UMAP plot of cells from WT mice (red) and *β7⁻/⁻* mice (green). Right: unsupervised clusters are overlaid on the UMAP plot and are labeled according to their identity (color coded) based on the expression of cell-type-specific marker genes. **b** UMAP plots of mean expression of known marker genes for the indicated cell type or state. **c** Heatmap shows the relative expression level (row-wise scaled gene expression, color scale) of cell-type specific genes in the indicated clusters. Color code marks the cell type.