

**Supplementary Figure 1 scRNA-seq analysis of enterocyte subclusters.** A: Selected dysregulated genes in enterocyte subclusters, including Slc22a5, Slc25a37, Slc47a1, Abcg2, Slc26a3, and Slc46a1; B: Representative enriched GO terms for differentially expressed genes in enterocyte subcluster 2 compared with other subclusters on the basis of scRNA-seq data; C: Representative enriched KEGG pathways for differentially expressed genes in enterocyte subcluster 2 compared with other subclusters on the basis of the scRNA-seq data; D: Selected dysregulated genes in enterocyte subclusters, including Cbr1, SUult1b1, Mdh1, Fabp1, and Gsta1; E: Representative enriched KEGG pathways for differentially expressed genes in enterocyte subcluster 1 compared with other subclusters on the basis of the scRNA-seq data; F: Representative enriched KEGG pathways for differentially expressed genes in enterocyte subcluster 3 compared with other subclusters on the basis of the scRNA-seq data; G: Selected dysregulated genes in enterocyte subclusters, including Mki67, Ccnd1, Ube2s, Rack1, Cdk4, and Cbx3. KEGG: Kyoto Encyclopedia of Genes and Genomes.