Title: *In vivo* gene expression profile of human intestinal epithelial cells: from the viewpoint of drug metabolism and pharmacokinetics

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Figure S1



	ollecting human stinal epithelial cells			
4	RNA isolation cDNA library construct	sequencing using HiSeq 4000	alignment & mapping counting TMM normalization analyses of drug ADM E- related genes	
В	sequencer	HiSeq 4000		
	library	TruSeq Stranded Total RNA Library Prep Kit		
	single or paired	Single-end read		
	number of reads	40-100 million		

reference genome Genome Reference Consortium Human (GRCh) Build 38

R studio/ R-3.5.2 (Counting, TMM normalization)

(A) Working procedure of the sample collection and RNA-seq analysis. (B) Detailed

information of the RNA-seq analysis. This figure was created using Biorender

FeatureCounts / Subread

GeneSpring GX 14.9 (PCA)

Patient information and RNA-seq analysis

TMM / edgeR

TCC-GUI

alignment & mapping STAR RNA-seq aligner

counting

software

(https://biorender.com).

Figure S1

normalization

 $\mathbf{2}$

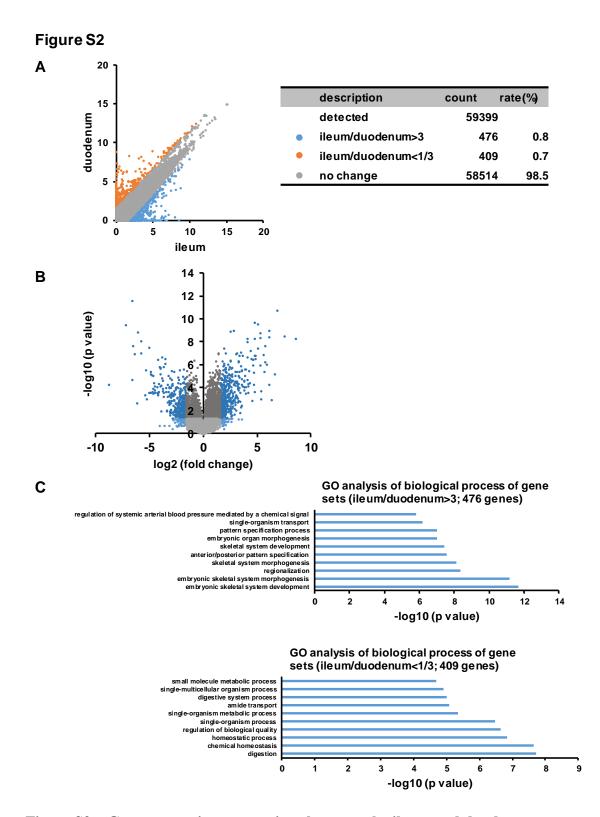


Figure S2 Gene expression comparison between the ileum and duodenum(A) A scatter plot comparing gene expression levels in the ileum with those in the duodenum is shown. (B) A volcano plot comparing gene expression levels in the ileum

with those in the duodenum is shown. (C) GO analysis was performed for gene sets whose gene expression levels were increased more than three-fold or decreased less than three-fold.

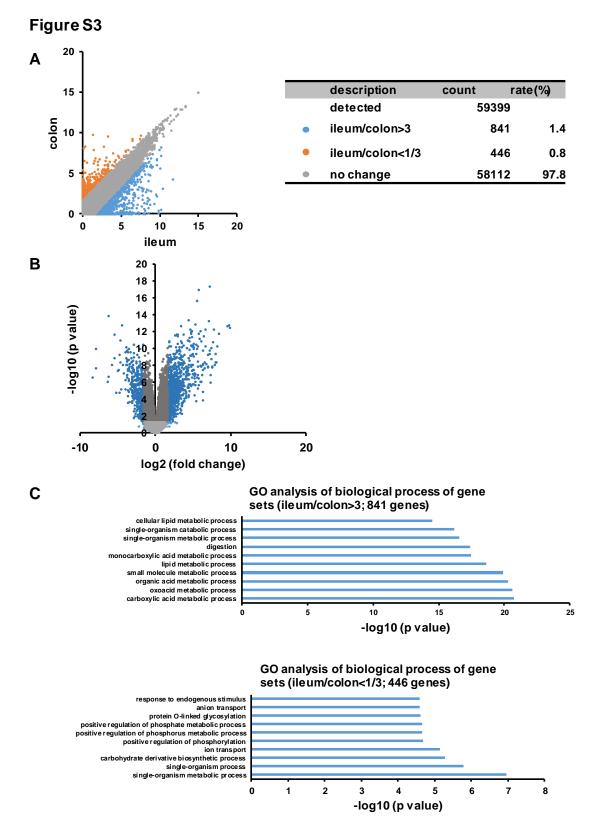


Figure S3Gene expression comparison between the ileum and colon(A) A scatter plot comparing gene expression levels in the ileum with those in the colon

is shown. (**B**) A volcano plot comparing gene expression levels in the ileum with those in the colon is shown. (**C**) GO analysis was performed for gene sets whose gene expression levels were increased more than three-fold or decreased less than three-fold.

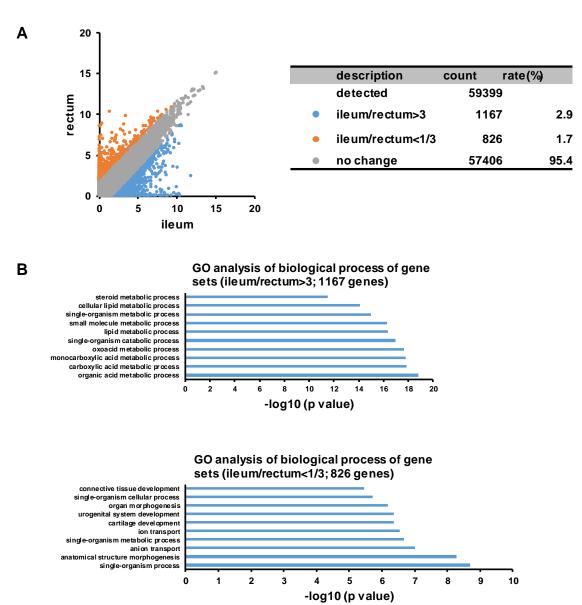


Figure S4



(A) A scatter plot comparing gene expression levels in the ileum with those in the rectum is shown. (B) GO analysis was performed for gene sets whose gene expression levels were increased more than three-fold or decreased less than three-fold.

Figure S5

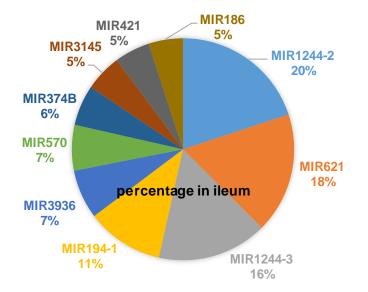


Figure S5 Expression analysis of miRNAs in various regions of the intestinal tract

The expression profile of miRNAs in the ileum is shown.