Electronic Supplementary Material (ESI) for Food & Function.

Supplementary table 1 The configuration of stock solution in simulated gastrointestinal tract

	Stock solution volume (mL)	Storage solution concentration (g/L)
KCl	250	37.3
KH_2PO_4	250	68
$NaHCO_3$	250	84
NaCl	250	117
$MgCl_2(H2O)_6$	100	30.5
$(NH_4)_2CO_3$	100	48
$CaCl_2(H_2O)_2$	100	43.8 (0.3 mol/L)

Supplementary table 2 The components of SGF and SIF[a]

Form	Stock conc. (mol/L)	SGF (pH = 3)		SIF (pH = 7)	
		Vol. of stock (mL)	Conc. in SGF (mmol/L)	Vol. of stock (mL)	Conc. in SIF (mmol/L)
KCl	0.50	17.50	6.90	13.60	6.80
KH_2PO_4	0.50	2.25	0.90	1.60	0.80
$NaHCO_3$	1.00	31.25	25.00	85.00	85.00
NaCl	2.00	29.50	47.20	19.20	38.40
$MgCl_2(H2O)_6$	0.15	1.00	0.10	2.20	0.33
$(NH_4)_2CO_3$	0.50	1.25	0.50	-	-
$CaCl_2(H_2O)_2$[b]	0.30	-	1.50	-	0.60

a) The composition and configuration of the simulated digestion solution were shown in the international convention, and the final constant volume was 1000 mL.

b) In order to prevent calcium precipitation, $CaCl_2(H_2O)_2$ was added before *in vitro* digestion.

Supplementary table 3 The primer's sequences for the genes

Gene	Forward (5'-3')	Reverse (5'-3')
G6Pase	CTCTTTCCCATCTGGTTCCATCTTA	GGAGCTGTTGCTGTAGTAGTCGG
Gck	AGGAGGCCAGTGTAAAGATGT	CTCCCAGGTCTAAGGAGAGAAA
Glut4	CCATTCCCTGGTTCATTGTG	ACGGCAAAT AGAAGGAAGAC
IRS-1	GGTTGCAGGCCCAGTTGTTG	CTGGTGCAGCACTGATCTAC
PPARα	AGAGCCCCATCTGTCCTCTC	ACTGGTAGTCTGCAAAACCAAA
GK	ATGTCGCTTTCCAACAAGCTG	GCTCCATTGTCCAAGCAGAAT
Serbp1c	GCAGCCACCATCTAGCCTG	CAGCAGTGAGTCTGCCTTGAT
Fas	ATGCTGTGGATCTGGGCTGTC	CAGTTTCACGAACCCGCCTC
Acc1	GCACGTTCGATAGCACACCAC	ATGGCATACATACCAATCTCTCTA
Nrf2	TCTTGGAGTAAGTCGAGAAGTGT	GTTGAAACTGAGCGAAAAAGGC
Gpx-1	AGTCCACCGTGTATGCCTTCT	GAGACGCGACATTCTCAATGA
Ho-1	AAGCCGAGAATGCTGAGTTCA	GCCGTGTAGATATGGTACAAGGA
CD14	TAGACCTTAGTCACAATTCAC	TTCCTATCCAGCCTGTTG
ZO-1	ACCCGAAACTGATGCTGTGGATAG	AAATGGCCGGGCAGAACTTGTGTA
occludin	TTGAAAGTCCACCTCCTTACAGA	CCGGATAAAAAGAGTACGCTGG
claudin3	ACCAACTGCGTACAAGACGAG	CAGAGCCGCCAACAGGAAA
β-actin	TGTCACCAACTGGGACGATA	GGGGTGTTGAAGGTCTCAAA

Detailed information of analysis of colonic flora profiles by 16S rDNA gene sequencing

Supplementary table 4 PCR amplification and 16S rDNA sequencing

Region	Primers	Length of PCR product (bp)
V3-V4	341F (5’-CCTACGGGNGGCWGCAG-3’) 805R (5’-GACTACHVGGGTATCTAATCC-3’)	465

The 5' ends of the primers were tagged with specific barcods per sample and sequencing with universal primers. PCR amplification was performed in a total volume of 25 μL reaction mixture containing 25 ng of template DNA, 12.5 μL 2×PCR Premix, 1 μL of each primer, and PCR-grade water to adjust the volume. The PCR conditions to amplify the prokaryotic 16S fragments consisted of an initial denaturation at 98 ℃ for 30 sec; 32 cycles of denaturation at 98 ℃ for 15 sec, annealing at 54℃ for 20 sec, and extension at 72 ℃ for 20 sec; and then final extension at 72 ℃ for 5 min. The PCR products were confirmed with 2% agarose gel electrophoresis. The amplicon pools were prepared for sequencing and the size and quantity of the amplicon library were assessed on Agilent 2100 Bioanalyzer (Agilent, USA) and with the Library Quantification Kit for Illumina (Kapa Biosciences, Woburn, MA, USA), respectively. The libraries were sequenced on NovaSeq PE250 platform.

Data analysis

Samples were sequenced on an Illumina NovaSeq platform according to the manufacturer's recommendations, provided by LC-Bio. After dereplication using DADA2, we obtained feature table and feature sequence. Alpha diversity and beta diversity were calculated by normalized to the same sequences randomly. Then according to SILVA (release 132) classifier, feature abundance was normalized using relative abundance of each sample. Alpha diversity is applied in analyzing

complexity of species diversity for a sample through 5 indices, including Chao1, Observed species, Goods coverage, Shannon, Simpson, and all these indices were calculated with QIIME2. Beta diversity was also calculated by QIIME2. The feature sequences were annotated with SILVA database for each representative sequence. The diagrams were implemented using the R package (v3.5.2).