

Supplementary Materials

Fecal microbiome does not represent whole gut microbiome

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Figure S1

Pig #1			Pig #2			Pig #3		
		Distance (m)			Distance (m)			Distance (m)
	Stomach	0.13		Stomach	0.12		Stomach	0.15
	Small intestine_1	1.63		Small intestine_1	1.62		Small intestine_1	1.05
	Small intestine_2	5.03		Small intestine_2	5.02		Small intestine_2	5.15
	Small intestine_3	9.13		Small intestine_3	8.62		Small intestine_3	10.05
	Small intestine_4	12.53		Small intestine_4	12.42		Small intestine_4	14.15
	Small intestine_5	15.93		Small intestine_5	17.52		Small intestine_5	18.45
	Small intestine_6	21.13		Small intestine_6	21.72		Small intestine_6	22.55
	Large intestine_1	21.39		Large intestine_1	22		Large intestine_1	22.78
	Large intestine_2	22.27		Large intestine_2	22.84		Large intestine_2	23.76
	Large intestine_3	22.92		Large intestine_3	23.44		Large intestine_3	24.36
	Large intestine_4	23.67		Large intestine_4	24.16		Large intestine_4	24.89
	Large intestine_5	24.39		Large intestine_5	24.76		Large intestine_5	25.49
	Large intestine_6	25.08		Large intestine_6	25.36		Large intestine_6	26.14
	Large intestine_7	25.73		Large intestine_7	25.84		Large intestine_7	27.04

Figure S1. The photographs showing the 14 sampling locations in the GI tracts. The sampling locations within the GI tract were determined based on the anatomical feature: the stomach (Stomach), the duodenum (Small intestine_1), the jejunum (Small intestine_2 ~ Small intestine_5), the ileum (Small intestine_6), the cecum (Large intestine_1), the colon (Large intestine_2 ~ Large intestine_6) and the rectum (Large intestine_7). Stomach represent the sample of the mixed luminal contents within the whole stomach. Distance represents the distance from the endpoint of pharynx to the sampling point.

Figure S2

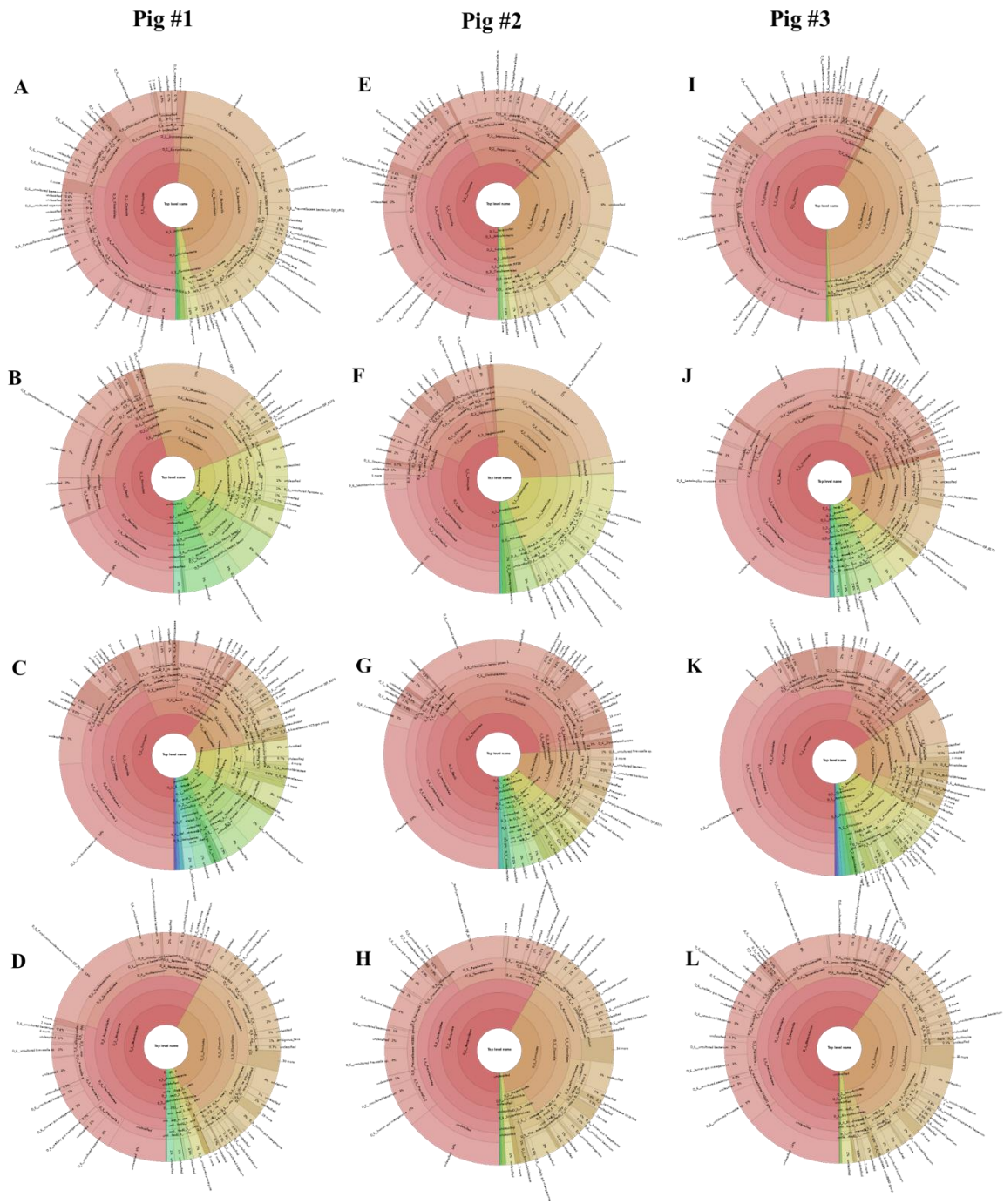


Figure S2. The composition of microbiomes at 4 different locations of the GI tract and feces of Pig #1~3. Clades are labeled according to the species. The corresponding phylum is depicted in the first inner layer and the outer circle represents class, order, family, genus, and species level. Pig #1 (**A**) Feces, (**B**) Stomach, (**C**) Small intestine, (**D**) Large intestine; Pig #2 (**E**) Feces, (**F**) Stomach, (**G**) Small intestine, (**H**) Large intestine; Pig #3 (**I**) Feces, (**J**) Stomach, (**K**) Small intestine, (**L**) Large intestine.

Figure S3

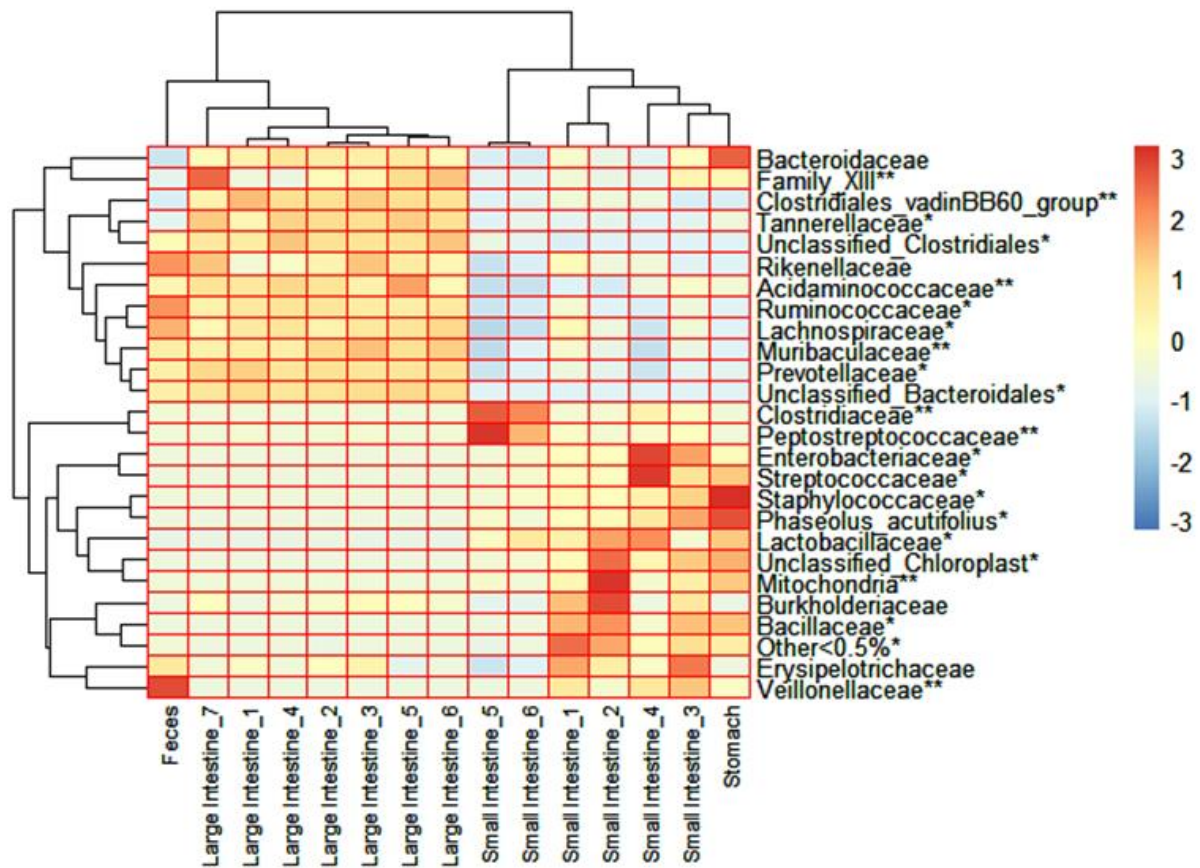


Figure S3. Heatmap of family level taxonomy in each location of the GI tracts based on the correlation distance matrix. p value was corrected by the Benjamini-Hochberg adjustment. $p.adj < 0.01^{**}$, $p.adj < 0.05^{*}$

Figure S4

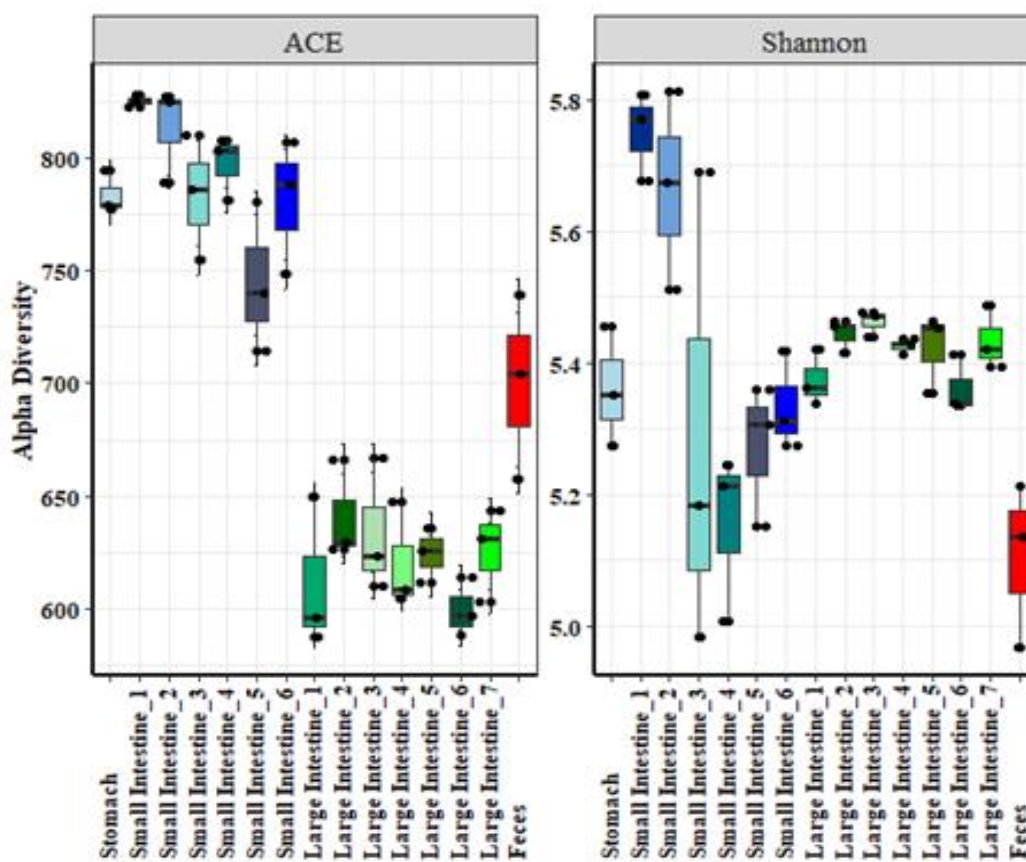


Figure S4. The location-specific chemical diversity in the GI tracts. Boxplot of the alpha - diversity for total chemical compositions of the 3 pigs in each location. Boxplot of the Abundance-based coverage (ACE) estimator ($p < 0.05$) and Shannon diversity ($p < 0.05$) for total chemical compositions of the 3 pigs in each location.

Table S1. The row sequencing reads for each sample

Regions	Pig_1	Pig_2	Pig_3	mean $\pm$ SEM
Stomach	137020	134883	120766	130890 $\pm$ 5099
Small intestine_1	125008	109513	133044	122522 $\pm$ 6905
Small intestine_2	142432	113382	161138	138984 $\pm$ 13893
Small intestine_3	175755	113212	132479	140482 $\pm$ 18492
Small intestine_4	147545	116360	131957	131954 $\pm$ 9002
Small intestine_5	147545	141873	140758	143392 $\pm$ 2101
Small intestine_6	136603	119233	138236	131357 $\pm$ 6080
Large intestine_1	127188	138140	126460	130596 $\pm$ 3777
Large intestine_2	139284	154478	154027	149263 $\pm$ 4991
Large intestine_3	136845	145641	143821	142102 $\pm$ 2680
Large intestine_4	136760	149428	123461	136550 $\pm$ 7496
Large intestine_5	138236	150269	126773	138426 $\pm$ 6783
Large intestine_6	110730	138523	146453	131902 $\pm$ 10830
Large intestine_7	126712	159803	125165	137227 $\pm$ 11297
Feces	182421	164087	132822	159777 $\pm$ 14479

Table S2. The relative abundance of intestinal bacteria in the fecal matters at the 14 locations of the GI tract and feces in phylum level

	Phylum	Stomach	Small Intestine_1	Small Intestine_2	Small Intestine_3	Small Intestine_4	Small Intestine_5	Small Intestine_6	Large Intestine_1	Large Intestine_2	Large Intestine_3	Large Intestine_4	Large Intestine_5	Large Intestine_6	Large Intestine_7	Feces
1	D_1__Firmicutes	55.63	47.57	47.90	51.55	68.89	94.02	87.80	38.55	38.90	38.87	40.67	38.82	40.20	35.19	57.59
2	D_1__Bacteroidetes	19.91	21.76	16.55	14.10	5.12	3.98	10.00	59.67	59.74	58.70	57.31	58.95	58.26	63.11	39.96
3	D_1__Cyanobacteria	13.35	2.86	7.47	9.87	5.23	1.34	0.69	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
4	D_1__Proteobacteria	8.03	18.69	22.80	19.39	18.13	0.58	1.50	0.29	0.59	0.85	0.51	0.74	0.52	0.75	0.35
5	D_1__Spirochaetes	0.20	0.69	0.04	0.00	0.20	0.00	0.00	1.07	0.36	1.10	0.95	0.64	0.19	0.25	0.00
6	D_1__Tenericutes	0.08	0.68	0.39	0.87	0.21	0.02	0.00	0.38	0.35	0.46	0.52	0.81	0.81	0.64	0.82
7	D_1__Epsilonbacteraeota	0.00	3.65	1.44	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	D_1__Actinobacteria	2.47	2.69	2.84	3.74	1.81	0.05	0.02	0.04	0.06	0.01	0.03	0.04	0.02	0.06	1.13
9	D_1__Fusobacteria	0.32	0.74	0.57	0.36	0.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10	D_1__Euryarchaeota	0.02	0.49	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	D_1__Chlamydiae	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16
12	D_1__Patescibacteria	0.00	0.18	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table S3. The relative abundance of intestinal bacteria in the fecal matters at the 14 locations of the GI tract and feces in species level

	Species	Stomach	Small Intestine_1	Small Intestine_2	Small Intestine_3	Small Intestine_4	Small Intestine_5	Small Intestine_6	Large Intestine_1	Large Intestine_2	Large Intestine_3	Large Intestine_4	Large Intestine_5	Large Intestine_6	Large Intestine_7	Feces
1	D_6_uncultured bacterium	0.62 ± 0.52	3.2 ± 1.09	4.42 ± 3.01	4.3 ± 2.1	17.12 ± 8	49.6 ± 13.08	37.43 ± 17.93	0.83 ± 0.43	1.1 ± 0.36	0.89 ± 0.55	0.64 ± 0.34	0.73 ± 0.4	0.4 ± 0.2	0.63 ± 0.21	2.74 ± 1.88
2	D_6_Unclassified_Lactobacillus	15.64 ± 7.79	7.28 ± 4.97	23.41 ± 19.29	1.76 ± 0.23	25.08 ± 17.84	6.37 ± 5.05	13.93 ± 11.32	0.02 ± 0.01	0.34 ± 0.28	0.21 ± 0.17	0.05 ± 0.04	0 ± 0	0 ± 0	0 ± 0	0.2 ± 0.17
3	D_6_Unclassified_Prevotellaceae	2.26 ± 1.45	3 ± 1.51	1.28 ± 0.7	1.39 ± 1.14	0.56 ± 0.43	0.41 ± 0.35	1.25 ± 1.03	9.34 ± 1.55	9.48 ± 2.23	11.09 ± 2.85	9.48 ± 1.55	9.16 ± 2.43	11.16 ± 2.83	10.49 ± 1.57	1.19 ± 0.96
4	D_6_Porphyrimonadaceae bacterium DJF_B175	2.92 ± 1.2	1.16 ± 0.62	1.2 ± 0.23	0.87 ± 0.58	0.58 ± 0.41	0.79 ± 0.5	1.98 ± 1.09	5.7 ± 1.67	8.69 ± 1.82	8.51 ± 1.67	9.58 ± 1.9	9.89 ± 2.47	8.66 ± 1.83	10.65 ± 3.61	0.23 ± 0.19
5	D_6_Unclassified_Clostridium sensu stricto 1	0.7 ± 0.39	0.69 ± 0.32	0.78 ± 0.43	6 ± 4.13	2.53 ± 1.63	12.46 ± 5.78	17.66 ± 7.3	0.28 ± 0.05	0.37 ± 0.08	0.29 ± 0.15	0.31 ± 0.08	0.3 ± 0.1	0.23 ± 0.1	0.16 ± 0.07	0.18 ± 0.15
6	D_6_Unclassified_Staphylococcus	11.47 ± 5.41	1.75 ± 0.61	2.04 ± 1.72	6.04 ± 4.3	3.16 ± 2.06	0.47 ± 0.38	0.77 ± 0.42	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0
7	D_6_Unclassified_Prevotella 9	0.83 ± 0.7	0.5 ± 0.3	0.59 ± 0.5	0.67 ± 0.56	0.23 ± 0.19	0.3 ± 0.23	1.01 ± 0.62	4.37 ± 1.42	2.19 ± 0.27	2.71 ± 0.98	2.5 ± 0.22	3.14 ± 1.19	4.09 ± 1.78	1.55 ± 0.44	7.76 ± 2.98
8	D_6_uncultured Prevotella sp.	1.1 ± 0.26	1.72 ± 0.59	1.6 ± 1	1.22 ± 0.65	0.01 ± 0.01	0.73 ± 0.43	0.62 ± 0.29	3.99 ± 2.13	2.52 ± 0.6	4.01 ± 1.62	3.34 ± 1.44	2.18 ± 0.36	1.97 ± 0.69	4.87 ± 1.75	1.82 ± 0.95
9	D_6_Unclassified_Lachnospiraceae	1.56 ± 1.23	1.3 ± 0.72	0.38 ± 0.2	0.89 ± 0.42	0.21 ± 0.16	0.12 ± 0.09	0.42 ± 0.26	2.58 ± 0.31	2.68 ± 0.65	2.83 ± 0.2	4.73 ± 1.31	2.84 ± 0.67	4.75 ± 1.48	2.69 ± 0.48	1.54 ± 0.72
10	D_6_uncultured bacterium	0.87 ± 0.45	0.67 ± 0.26	0.83 ± 0.43	1.18 ± 1	0.32 ± 0.27	0.4 ± 0.21	1.2 ± 0.22	3.29 ± 1.62	2.95 ± 0.56	2.22 ± 0.6	2.95 ± 1.01	2.32 ± 0.67	4.49 ± 1.06	2.98 ± 0.54	0
11	D_6_Phaseolus acutifolius (tepary bean)	9.82 ± 6.61	1.65 ± 1.06	2.36 ± 1.99	7.27 ± 5.61	3.59 ± 2.25	0.81 ± 0.23	0.28 ± 0.23	0 ± 0	0 ± 0	0.01 ± 0	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0
12	D_6_Escherichia-Shigella	0	0.2 ± 0.1	0.37 ± 0.2	8.94 ± 6.95	11.37 ± 6.89	0.02 ± 0.02	0.76 ± 0.4	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0
13	D_6_human gut metagenome	0.08 ± 0.05	0.24 ± 0.12	0.34 ± 0.17	0.47 ± 0.4	0.52 ± 0.3	0.11 ± 0.06	0.04 ± 0.02	1.92 ± 0.55	1.84 ± 0.5	2.42 ± 0.4	2.87 ± 0.85	3.22 ± 0.41	2.05 ± 0.81	4.53 ± 1.47	0.74 ± 0.48
14	D_6_Unclassified_Ruminococcaceae	0.37 ± 0.16	0.83 ± 0.4	0.66 ± 0.56	0.52 ± 0.28	0.07 ± 0.04	0.08 ± 0.04	0.44 ± 0.36	2.56 ± 0.65	1.93 ± 0.25	2.14 ± 0.18	2.25 ± 0.43	2.46 ± 0.49	2.44 ± 0.84	2.23 ± 0.53	0.79 ± 0.47
15	D_6_Unclassified_Chloroplast	3.51 ± 1.15	1.47 ± 1.19	6.37 ± 5.26	3.19 ± 1.55	1.54 ± 0.7	0.36 ± 0.16	0.48 ± 0.34	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0
16	D_6_Unclassified_Mitochondria	2.59 ± 0.24	1.55 ± 1.15	7.91 ± 6.47	1.95 ± 1.23	0.54 ± 0.46	0.43 ± 0.36	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0

17	D_6__uncultured bacterium	0	0.72 ± 0.41	0.34 ± 0.29	0	0.03 ± 0.03	0	0.03 ± 0.03	8.53 ± 6.07	1.13 ± 0.59	0.34 ± 0.14	0.28 ± 0.08	0.2 ± 0.03	0.31 ± 0.15	0.02 ± 0.02	2.71 ± 0.06
18	D_6__uncultured	0.39 ± 0.21	0.93 ± 0.48	0.25 ± 0.21	0.44 ± 0.23	0.18 ± 0.1	0.1 ± 0.08	0.18 ± 0.08	1.31 ± 0.57	2.17 ± 0.92	1.15 ± 0.34	1.15 ± 0.4	0.85 ± 0.2	0.75 ± 0.1	1.29 ± 0.55	0.65 ± 0.29
19	D_6__Unclassified_Faecalibacterium	0.12 ± 0.1	0.33 ± 0.28	0	0.15 ± 0.09	0	0	0.01 ± 0	0.72 ± 0.4	1.27 ± 0.27	0.84 ± 0.65	0.85 ± 0.36	0.22 ± 0.08	0.25 ± 0.14	0.06 ± 0.03	6.21 ± 1.77
20	D_6__Unclassified_Terrisporobacter	0.05 ± 0.04	0.26 ± 0.02	0.19 ± 0.1	0.35 ± 0.18	0.3 ± 0.26	6.47 ± 3.83	2.01 ± 1.12	0.37 ± 0.29	0.26 ± 0.19	0.32 ± 0.2	0.02 ± 0.01	0.02 ± 0.01	0.18 ± 0.13	0.04 ± 0.03	0
21	D_6__uncultured Porphyromonadaceae bacterium	0.59 ± 0.5	0.13 ± 0.11	0.33 ± 0.28	0.28 ± 0.18	0.19 ± 0.16	0	0.53 ± 0.45	0.72 ± 0.48	0.94 ± 0.35	1.23 ± 0.72	1 ± 0.38	1.41 ± 0.86	1.21 ± 0.01	0.77 ± 0.6	1.36 ± 0.89
22	D_6__uncultured bacterium	0	0.63 ± 0.36	0.4 ± 0.34	0	0.06 ± 0.05	0.02 ± 0.01	0.33 ± 0.24	1.07 ± 0.62	1.67 ± 0.57	1.36 ± 1.01	0.53 ± 0.2	1.41 ± 0.97	0.78 ± 0.65	1.48 ± 0.94	0.77 ± 0.31
23	D_6__Lactobacillus mucosae	0.75 ± 0.45	3.31 ± 2.39	1.51 ± 1.27	0.37 ± 0.31	0.96 ± 0.61	0.06 ± 0.05	0.38 ± 0.32	0	0	0	0	0	0	0	0
24	D_6__Helicobacter rappini	0	4.16 ± 3.52	0	0	0	0	0	0	0	0	0	0	0	0	0
25	D_6__Unclassified_Phascolartobacterium	1.07 ± 0.57	0.47 ± 0.34	0.35 ± 0.25	1.24 ± 0.48	0.83 ± 0.46	0	0.05 ± 0.05	1.65 ± 0.73	1.5 ± 0.61	1.25 ± 0.67	2.01 ± 1.14	2.6 ± 1.22	0.69 ± 0.15	1.72 ± 0.87	1.37 ± 1.16
26	D_6__uncultured bacterium	0.78 ± 0.45	0.75 ± 0.22	0.19 ± 0.16	0.84 ± 0.71	0.11 ± 0.09	0.53 ± 0.45	0.04 ± 0.03	0.72 ± 0.55	1.77 ± 0.28	0.92 ± 0.63	2.05 ± 0.47	1.23 ± 0.64	1.33 ± 0.69	3.28 ± 0.93	1.86 ± 1.36
27	D_6__Unclassified_Subdoligranulum	0.79 ± 0.66	0.81 ± 0.19	0.41 ± 0.07	1.92 ± 0.71	0.57 ± 0.34	0.21 ± 0.17	0.39 ± 0.32	1.52 ± 1.01	1.36 ± 0.62	1 ± 0.44	1.64 ± 0.87	1.08 ± 0.53	1.15 ± 0.49	1.11 ± 0.53	2.25 ± 0.53
28	D_6__Unclassified_Streptococcus	3.65 ± 2.11	0.48 ± 0.28	1.26 ± 1.03	2.5 ± 1.14	6.54 ± 2.43	0.24 ± 0.13	0.62 ± 0.33	0	0.06 ± 0.05	0	0	0.01 ± 0	0	0	0.07 ± 0.06
29	D_6__Unclassified_Prevotella 1	0.55 ± 0.29	0	0.07 ± 0.06	0.22 ± 0.19	0.34 ± 0.29	0	0.5 ± 0.42	0.93 ± 0.61	0.71 ± 0.15	1.61 ± 0.81	1.02 ± 0.58	1.65 ± 0.83	1.67 ± 0.8	0.77 ± 0.41	0.13 ± 0.11
30	D_6__Unclassified_Prevotellaceae NK3B31 group	0.69 ± 0.39	0.41 ± 0.34	0.48 ± 0.4	0.15 ± 0.12	0	0	0.07 ± 0.06	1.06 ± 0.57	1.91 ± 0.76	1.13 ± 0.7	1.19 ± 0.66	1.11 ± 0.79	0.99 ± 0.47	0.47 ± 0.17	0

Table S4. α -diversity values for microbiome profiles at the 14 locations of the GI tract and feces

Regions	Observed	ACE	Shannon
Stomach	343.66±97.38	343.6±31.8	4.3±46.8
Small Intestine_1	206.66±17.89	206.6±32.8	4.8±47.8
Small Intestine_2	193.33±147.03	193.3±33.8	4±48.8
Small Intestine_3	289±77.62	289±34.8	4.5±49.8
Small Intestine_4	179.33±46.05	179.3±35.8	3.7±50.8
Small Intestine_5	119.33±51.63	119.3±36.8	2.9±51.8
Small Intestine_6	149.33±64.06	149.3±37.8	3.3±52.8
Large intestine_1	1025±80.5	1025±38.8	5.5±53.8
Large intestine_2	1081.33±175.5	1081.3±39.8	5.7±54.8
Large intestine_3	1054.33±186.78	1054.3±40.8	5.7±55.8
Large intestine_4	988.66±65.0	988.6±41.8	5.6±56.8
Large intestine_5	994±76.09	994±42.8	5.7±57.8
Large intestine_6	1043.66±231.8	1043.6±43.8	5.6±58.8
Large intestine_7	1014±41.61	1014±44.8	5.6±59.8
Feces	168.66±30.82	168.6±45.8	4.7±60.8

Table S5. The relative abundance of intestinal bacteria in the fecal matters at the 14 locations of the GI tract and feces in family level

	Family	Stomach	Small Intestine_1	Small Intestine_2	Small Intestine_3	Small Intestine_4	Small Intestine_5	Small Intestine_6	Large Intestine_1	Large Intestine_2	Large Intestine_3	Large Intestine_4	Large Intestine_5	Large Intestine_6	Large Intestine_7	Feces
1	D_4__Prevotellaceae	8.51	14.00	9.47	8.11	2.30	2.44	6.07	43.08	37.55	35.30	35.67	35.69	37.08	41.07	30.44
2	D_4__Ruminococcaceae	4.06	10.39	3.90	8.16	2.95	1.25	2.27	20.03	20.77	18.80	21.40	18.15	19.32	17.09	32.15
3	D_4__Lachnospiraceae	2.43	7.19	4.10	4.76	1.48	0.43	1.11	9.06	7.90	9.37	9.61	9.68	10.80	7.03	12.84
4	D_4__Tannerellaceae	3.27	1.38	1.79	1.45	0.65	0.79	2.06	7.38	11.33	11.03	11.92	12.16	10.69	12.38	1.51
5	D_4__Clostridiaceae	2.68	4.86	5.24	11.79	20.99	74.61	62.57	2.43	2.38	2.55	2.52	2.30	2.59	2.42	3.40
6	D_4__Enterobacteriaceae	2.83	2.53	2.38	10.38	15.14	0.05	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	D_4__Lactobacillaceae	18.01	10.01	22.40	3.37	24.95	5.68	12.64	0.03	0.29	0.18	0.05	0.00	0.00	0.00	0.17
8	D_4__Staphylococcaceae	12.37	1.99	1.76	5.66	3.03	0.41	0.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
9	D_4__Bacteroidaceae	6.32	2.02	1.19	2.32	0.87	0.62	0.53	2.91	3.13	3.10	3.58	3.26	2.45	2.45	0.27
10	D_4__Muribaculaceae	0.93	2.31	1.52	1.60	0.17	0.09	0.94	3.83	4.75	5.43	3.70	4.53	5.06	3.54	3.81
11	D_4__Acidaminococcaceae	1.15	0.44	0.34	1.41	0.92	0.00	0.08	2.47	2.61	2.11	2.86	3.70	1.78	2.63	1.98
12	D_4__Phaseolus acutifolius	9.28	1.59	2.00	6.46	3.49	0.95	0.24	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
13	D_4__Peptostreptococcaceae	0.05	0.96	0.46	1.46	0.78	10.46	6.01	0.45	0.34	0.43	0.07	0.10	0.22	0.11	0.05
14	D_4__Streptococcaceae	4.48	1.29	1.30	3.38	8.60	0.32	0.67	0.00	0.05	0.01	0.00	0.01	0.00	0.00	0.06
15	D_4__Erysipelotrichaceae	0.72	2.39	1.53	2.82	1.01	0.21	0.36	1.05	1.11	1.40	0.81	0.51	0.71	0.80	1.66
16	D_4__Rikenellaceae	0.29	1.22	0.71	0.34	0.73	0.02	0.24	0.79	1.41	2.19	1.01	1.58	1.36	2.21	2.70
17	D_4__Unclassified_Chloroplast	4.02	1.28	5.47	3.37	1.65	0.39	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	D_4__Mitochondria	3.44	1.41	6.82	1.91	0.46	0.37	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
19	D_4__Bacillaceae	2.70	2.91	3.53	2.76	0.40	0.01	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
20	D_4__Unclassified_Bacteroidales	0.07	0.00	0.00	0.00	0.00	0.02	0.08	1.65	1.52	1.66	1.43	1.71	1.61	1.43	1.20
21	D_4__Burkholderiaceae	0.20	1.98	3.19	1.42	0.27	0.04	0.11	0.29	0.59	0.85	0.51	0.74	0.52	0.75	0.27
22	D_4__Family XIII	0.96	0.42	0.18	1.03	0.13	0.02	0.01	0.35	0.86	0.97	0.25	1.64	1.87	2.79	0.05
23	D_4__Unclassified_Clostridiales	0.04	0.00	0.02	0.04	0.02	0.25	0.10	1.07	1.24	1.23	1.53	1.20	1.55	1.14	0.76
24	D_4__Veillonellaceae	0.51	1.42	0.37	2.20	1.51	0.00	0.02	0.00	0.01	0.00	0.01	0.01	0.00	0.00	3.84
25	D_4__Clostridiales vadinBB60 group	0.02	0.35	0.30	0.00	0.28	0.06	0.13	1.35	1.06	1.23	1.08	1.09	1.04	0.76	0.00
26	Other<0.5%	10.67	25.65	20.03	13.81	7.21	0.52	1.35	1.76	1.08	2.16	1.97	1.93	1.34	1.41	2.82

Table S6. The average distance to centroid

Average distance to median		
	Microbiota	LCMS
Feces	0.5275	0.04943
Large Intestine	0.6803	0.0402
Small Intestine	0.6226	0.02662
Stomach	0.5541	0.01587

Table S7. The average distance to NMDS_microbiota

Pig	Sample_type	NMDS1	NMDS2
Pig #1	Stomach	-0.23046582	0.328641759
Pig #1	Small Intestine_1	-0.05588915	-0.00140778
Pig #1	Small Intestine_2	-0.40890828	0.116781626
Pig #1	Small Intestine_3	-0.22723669	0.153418565
Pig #1	Small Intestine_4	-0.06297537	-0.01076643
Pig #1	Small Intestine_5	-0.28810729	0.050342703
Pig #1	Small Intestine_6	-0.14849024	0.002306755
Pig #1	Large Intestine_1	0.184162076	-0.35310399
Pig #1	Large Intestine_2	0.187711426	0.042431759
Pig #1	Large Intestine_3	0.242914337	-0.14497277
Pig #1	Large Intestine_4	0.204314898	-0.18778407
Pig #1	Large Intestine_5	0.320560316	-0.15192814
Pig #1	Large Intestine_6	0.187607462	-0.27534909
Pig #1	Large Intestine_7	0.305109702	0.044777526
Pig #1	Feces	-0.39029501	-0.20168723
Pig #2	Stomach	-0.05256604	-0.06921648
Pig #2	Small Intestine_1	-0.12161189	-0.06211981
Pig #2	Small Intestine_2	-0.25210139	-0.03618984
Pig #2	Small Intestine_3	-0.0290495	-0.01269877
Pig #2	Small Intestine_4	-0.39272402	-0.05175981
Pig #2	Small Intestine_5	-0.29415593	0.019992453
Pig #2	Small Intestine_6	-0.40304868	0.011113888
Pig #2	Large Intestine_1	0.298464487	-0.26853894
Pig #2	Large Intestine_2	0.331584871	-0.09429705
Pig #2	Large Intestine_3	0.26935279	-0.19945359
Pig #2	Large Intestine_4	0.197000842	-0.04451991
Pig #2	Large Intestine_5	0.411501439	-0.04921818
Pig #2	Large Intestine_6	0.358441155	-0.01519688
Pig #2	Large Intestine_7	0.282738094	-0.0216836
Pig #2	Feces	-0.27113653	-0.477476
Pig #3	Stomach	-0.11516625	0.218145938
Pig #3	Small Intestine_1	-0.07988181	0.038901147
Pig #3	Small Intestine_2	0.024721526	0.047881969
Pig #3	Small Intestine_3	-0.31229807	0.188836064
Pig #3	Small Intestine_4	-0.41398329	0.093743401
Pig #3	Small Intestine_5	-0.45470595	0.062978713
Pig #3	Small Intestine_6	-0.34445439	0.040928325
Pig #3	Large Intestine_1	0.336094659	0.098787304
Pig #3	Large Intestine_2	0.290282513	0.193548334
Pig #3	Large Intestine_3	0.252481052	0.298481486
Pig #3	Large Intestine_4	0.249030765	0.162610366
Pig #3	Large Intestine_5	0.337883636	0.167632183
Pig #3	Large Intestine_6	0.245381984	0.378800018
Pig #3	Large Intestine_7	0.229092372	0.250426431
Pig #3	Feces	-0.39718082	-0.28214034

Table S8. The average distance to PcoA_microbiota

	Eigenvalue	Proportion Explained	Cumulative Proportion
PCoA1	1.242593427	0.0597316	0.0597316
PCoA2	0.779425144	0.037467051	0.097198651
PCoA3	0.641864611	0.030854501	0.128053152
PCoA4	0.588918396	0.028309371	0.156362523
PCoA5	0.544051167	0.026152598	0.182515121
PCoA6	0.517244305	0.02486399	0.207379111
PCoA7	0.512450577	0.024633555	0.232012666
PCoA8	0.495189967	0.023803835	0.255816501
PCoA9	0.492878027	0.0236927	0.279509201
PCoA10	0.490559889	0.023581267	0.303090468
PCoA11	0.490163888	0.023562231	0.326652699
PCoA12	0.487974779	0.023457	0.350109699
PCoA13	0.486183516	0.023370894	0.373480593
PCoA14	0.48484432	0.023306519	0.396787112
PCoA15	0.484459969	0.023288043	0.420075155
PCoA16	0.483901595	0.023261202	0.443336357
PCoA17	0.482106647	0.023174919	0.466511275
PCoA18	0.481143242	0.023128608	0.489639883
PCoA19	0.480757554	0.023110068	0.51274995
PCoA20	0.479660647	0.023057339	0.53580729
PCoA21	0.478181145	0.022986219	0.558793509
PCoA22	0.477457424	0.02295143	0.581744939
PCoA23	0.476490558	0.022904953	0.604649891
PCoA24	0.476004775	0.022881601	0.627531492
PCoA25	0.473659322	0.022768855	0.650300347
PCoA26	0.469081328	0.02254879	0.672849137
PCoA27	0.462299437	0.022222784	0.695071921
PCoA28	0.449470686	0.021606104	0.716678025
PCoA29	0.444860167	0.021384476	0.738062502
PCoA30	0.434380488	0.020880717	0.758943219
PCoA31	0.417206255	0.02005515	0.778998368
PCoA32	0.405408308	0.019488021	0.79848639
PCoA33	0.399774983	0.019217227	0.817703616
PCoA34	0.396015862	0.019036525	0.836740141
PCoA35	0.3852891	0.018520889	0.85526103
PCoA36	0.383930088	0.018455561	0.873716591
PCoA37	0.378535532	0.018196244	0.891912835
PCoA38	0.359447248	0.017278668	0.909191503
PCoA39	0.35610653	0.017118079	0.926309582
PCoA40	0.33867184	0.016279992	0.942589574
PCoA41	0.3273338	0.015734971	0.958324545
PCoA42	0.308827087	0.014845351	0.973169896
PCoA43	0.285478304	0.013722973	0.986892869
PCoA44	0.272666968	0.013107131	1

Table S9. The Shannon α -diversity values for chemical profiles at the 14 locations of GI tract and feces

Regions	Observed	ACE	Shannon
Stomach	775 $\pm$ 1.7	777.7 $\pm$ 1	5.3 $\pm$ 0.06
Small Intestine_1	824.3 $\pm$ 2.3	824.7 $\pm$ 2.9	5.7 $\pm$ 0.07
Small Intestine_2	814.3 $\pm$ 21.9	814.4 $\pm$ 21.6	5.5 $\pm$ 0.09
Small Intestine_3	762.3 $\pm$ 19.6	765.1 $\pm$ 18.1	5.1 $\pm$ 0.11
Small Intestine_4	787 $\pm$ 17.3	789.9 $\pm$ 15.1	5 $\pm$ 0.13
Small Intestine_5	721.6 $\pm$ 15	723 $\pm$ 14.5	5.3 $\pm$ 0.03
Small Intestine_6	794.3 $\pm$ 10.9	794.6 $\pm$ 10.6	5.3 $\pm$ 0.06
Large intestine_1	612.3 $\pm$ 28.2	614 $\pm$ 30.7	5.3 $\pm$ 0.04
Large intestine_2	638.3 $\pm$ 19.6	641.8 $\pm$ 21.2	5.4 $\pm$ 0.02
Large intestine_3	633.6 $\pm$ 23.6	637.7 $\pm$ 25.2	5.4 $\pm$ 0.002
Large intestine_4	615.3 $\pm$ 24.8	621.3 $\pm$ 22.6	5.4 $\pm$ 0.01
Large intestine_5	625 $\pm$ 13.8	627.9 $\pm$ 13.8	5.4 $\pm$ 0.05
Large intestine_6	598.6 $\pm$ 9.8	602.3 $\pm$ 10.1	5.3 $\pm$ 0.001
Large intestine_7	630 $\pm$ 5.1	634.9 $\pm$ 7.2	5.4 $\pm$ 0.05
Feces	724.3 $\pm$ 18.4	727.3 $\pm$ 20.1	5.1 $\pm$ 0.04
Total	827	--	--

Table S10. The average distance to NMDS_LCMS

Pig	Sample_type	NMDS1	NMDS2
Pig #1	Stomach	-0.115288272	0.151673538
Pig #1	Small Intestine_1	-0.402127352	-0.025302151
Pig #1	Small Intestine_2	-0.375521471	0.00084911
Pig #1	Small Intestine_3	-0.033114381	0.108639803
Pig #1	Small Intestine_4	-0.114787026	0.114242684
Pig #1	Small Intestine_5	0.029228465	0.075472885
Pig #1	Small Intestine_6	-0.120575628	0.007327874
Pig #1	Large Intestine_1	0.232396795	0.039948895
Pig #1	Large Intestine_2	0.214954939	0.008089841
Pig #1	Large Intestine_3	0.208486913	0.000163062
Pig #1	Large Intestine_4	0.242110272	-0.001227419
Pig #1	Large Intestine_5	0.200912979	-0.013490251
Pig #1	Large Intestine_6	0.25227102	-0.00212962
Pig #1	Large Intestine_7	0.217456802	-0.018988761
Pig #1	Feces	0.043957697	-0.154528002
Pig #2	Stomach	-0.208682917	0.081164527
Pig #2	Small Intestine_1	-0.432306901	-0.039435474
Pig #2	Small Intestine_2	-0.433161556	-0.043111356
Pig #2	Small Intestine_3	-0.466680214	-0.096270424
Pig #2	Small Intestine_4	-0.157584058	0.036580077
Pig #2	Small Intestine_5	-0.105005497	0.052310045
Pig #2	Small Intestine_6	-0.022193683	0.030196053
Pig #2	Large Intestine_1	0.241811665	0.025850472
Pig #2	Large Intestine_2	0.208280246	-0.004407409
Pig #2	Large Intestine_3	0.235487536	-0.009629749
Pig #2	Large Intestine_4	0.235054467	-0.009131422
Pig #2	Large Intestine_5	0.21370328	-0.021089064
Pig #2	Large Intestine_6	0.256450644	-0.018841192
Pig #2	Large Intestine_7	0.244541213	-0.024222076
Pig #2	Feces	0.178428162	-0.125034775
Pig #3	Stomach	-0.142673743	0.121670625
Pig #3	Small Intestine_1	-0.426869408	-0.055203836
Pig #3	Small Intestine_2	-0.475194037	-0.138081454
Pig #3	Small Intestine_3	-0.161276389	0.096218251
Pig #3	Small Intestine_4	-0.354750435	0.032190125
Pig #3	Small Intestine_5	-0.043455803	0.063772648
Pig #3	Small Intestine_6	-0.243321931	-0.019762355
Pig #3	Large Intestine_1	0.173262802	0.023797958
Pig #3	Large Intestine_2	0.153131384	-0.001897589
Pig #3	Large Intestine_3	0.145317551	-0.018448039
Pig #3	Large Intestine_4	0.162132777	-0.020491979
Pig #3	Large Intestine_5	0.234059476	-0.034404438
Pig #3	Large Intestine_6	0.231297757	-0.038666945
Pig #3	Large Intestine_7	0.177192344	-0.033010932
Pig #3	Feces	0.102643518	-0.103351763

Table S11. The average distance to PcoA_LCMS

	Eigenvalue	Proportion Explained
PCoA1	0.31706581	0.866809644
PCoA2	0.016815817	0.045971882
PCoA3	0.010883827	0.029754726
PCoA4	0.006164843	0.016853743
PCoA5	0.004087907	0.011175716
PCoA6	0.003844625	0.010510619
PCoA7	0.003196137	0.008737753
PCoA8	0.002953713	0.008075001
PCoA9	0.002730647	0.007465174
PCoA10	0.002236955	0.006115495
PCoA11	0.002034125	0.005560989
PCoA12	0.001875659	0.005127767
PCoA13	0.001661337	0.004541841
PCoA14	0.001512746	0.004135617
PCoA15	0.001342651	0.003670604
PCoA16	0.001288409	0.003522314
PCoA17	0.001072214	0.00293127
PCoA18	0.000949402	0.002595519
PCoA19	0.000797758	0.002180949
PCoA20	0.000665676	0.001819857
PCoA21	0.00050512	0.00138092
PCoA22	0.000440137	0.001203268
PCoA23	0.000377215	0.001031248
PCoA24	0.000113054	0.000309072
PCoA25	-2.69E-06	7.35E-06
PCoA26	-4.19E-06	1.15E-05
PCoA27	-4.28E-05	0.000117106
PCoA28	-0.000127077	0.000347409
PCoA29	-0.000161631	0.000441874
PCoA30	-0.000238579	0.00065224
PCoA31	-0.00040947	0.001119429
PCoA32	-0.000463344	0.001266711
PCoA33	-0.000528424	0.001444632
PCoA34	-0.000584558	0.001598094
PCoA35	-0.000752512	0.002057254
PCoA36	-0.000932964	0.002550583
PCoA37	-0.000944218	0.002581349
PCoA38	-0.001156588	0.003161936
PCoA39	-0.001747834	0.004778313
PCoA40	-0.002163787	0.005915465
PCoA41	-0.003539503	0.009676462
PCoA42	-0.005030756	0.013753321

Table S12. The water contents at the 14 locations of GI tract and feces

Locations	Water contents (%)
Stomach	80.27
Small intestine_1	80.67
Small intestine_2	79.38
Small intestine_3	78.04
Small intestine_4	84.39
Small intestine_5	86.49
Small intestine_6	88.52
Large intestine_1	86.65
Large intestine_2	81.04
Large intestine_3	80.18
Large intestine_4	80.12
Large intestine_5	77.38
Large intestine_6	78.28
Large intestine_7	76.27
Feces	48.15

Table S13. The pH values at the 14 locations of the GI tract and feces

Locations	pH
Stomach	3.73±0.55
Small intestine_1	6.39±0.30
Small intestine_2	6.34±0.13
Small intestine_3	5.88±1.44
Small intestine_4	6.20±0.24
Small intestine_5	6.19±0.03
Small intestine_6	6.48±0.15
Large intestine_1	5.86±0.18
Large intestine_2	5.66±0.40
Large intestine_3	6.16±0.32
Large intestine_4	6.10±0.38
Large intestine_5	6.41±0.36
Large intestine_6	6.25±0.29
Large intestine_7	6.35±0.21
Feces	6.40±0.36