

Table S1. Relative abundances of significant changed bacteria at different levels (phylum, family and genus) in colon

	Taxonomic group	C_LM (%)	C_MAM (%)	Variation
Phylum	Deferribacteres	0.06±0.04	2.93±1.20	↑*
Family	Lactobacillaceae	9.63±3.14	0.84±0.38	↓*
	Rikenellaceae	1.42±0.23	4.70±0.73	↑**
	Deferribacteraceae	0.06±0.04	2.93±1.20	↑*
	Clostridiales_vadinBB60_group	0.27±0.15	2.13±0.36	↑**
	Erysipelotrichaceae	0.83±0.19	0.21±0.05	↓*
	Unidentified Gastranaerophilales	0.16±0.05	0.80±0.26	↓*
	Coriobacteriaceae	0.34±0.11	0.09±0.02	↓**
	Mollicutes_RF9_group	0.19±0.05	0.08±0.03	↓*
Genus	Lactobacillus	9.63±3.14	0.84±0.38	↓*
	Alistipes	1.34±0.23	3.67±0.34	↑**
	Mucispirillum	0.06±0.04	2.93±1.20	↑*
	Unidentified Clostridiales_vadinBB60	0.27±0.15	2.13±0.36	↑**
	Odoribacter	0.22±0.04	1.24±0.47	↑*
	Marvinbryantia	0.38±0.14	0.99±0.14	↑*
	Lachnoclostridium	0.29±0.08	0.84±0.14	↑*
	Rikenellaceae_RC9_gut_group	0.08±0.03	1.03±0.43	↑**
	Unidentified Gastranaerophilales	0.16±0.05	0.80±0.26	↑*
	Unidentified Erysipelotrichaceae	0.26±0.07	0.03±0.00	↓**
	Unidentified Mollicutes_RF9	0.19±0.05	0.08±0.03	↓*
	Erysipelatoclostridium	0.21±0.06	0.03±0.01	↓**
	Enterorhabdus	0.17±0.04	0.05±0.01	↓*
	Family_XIII_AD3011_group	0.06±0.01	0.02±0.01	↓*
	[Eubacterium]_brachy_group	0.01±0.01	0.04±0.01	↑*
	Massilia	0.02±0.01	0	↓*
	Parvibacter	0.01±0.00	0	↓*

“↑” and “↓” represent the variation when the colonic mucosal microbiota (C_MAM) compared to the colonic luminal microbiota (C_LM).

$n = 6$ for each group. * $P < 0.05$, ** $P < 0.01$.

Table S2. Relative abundance of significant changed bacteria at family and genus levels in duodenum

	Taxonomic group	D_LM	D_MAM	Variation
		(%)	(%)	
Family	Lactobacillaceae	33.65±4.94	8.75±1.52	↓**
	Porphyromonadaceae	0.09±0.06	0.61±0.18	↑*
	Desulfovibrionaceae	0.07±0.03	0.39±0.04	↑**
Genus	Lactobacillus	33.65±4.94	8.75±1.52	↓**
	Marvinbryantia	0.23±0.08	1.17±0.47	↑*
	Ruminiclostridium	0.15±0.11	0.36±0.10	↑*
	Bilophila	0.06±0.02	0.31±0.05	↑**
	Odoribacter	0.06±0.06	0.28±0.09	↑*
	Parabacteroides	0.02±0.01	0.27±0.09	↑*
	Ruminococcaceae_UCG-009	0.02±0.02	0.09±0.02	↑*
	Desulfovibrio	0.01±0.00	0.09±0.02	↑**
	Lachnospiraceae_FCS020_group	0.02±0.01	0.06±0.01	↑*
	Butyricimonas	0	0.06±0.04	↑*
	Ruminococcaceae_UCG-007	0	0.01±0.00	↑*

“↑” and “↓” represent the variation when the duodenal mucosal microbiota (D_MAM) compared to the duodenal luminal microbiota (D_LM).

$n = 6$ for each group. * $P < 0.05$, ** $P < 0.01$.

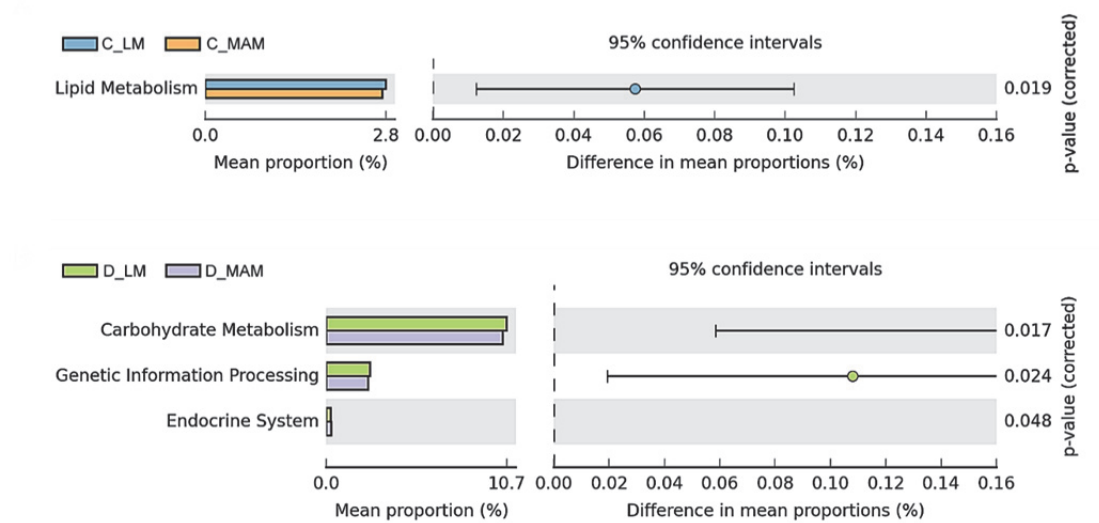


Fig. S1 Predicted microbial function comparison based on KEGG level-2. CC: colonic luminal content; CM: colonic mucosa; DC: duodenal luminal content; DM: duodenal mucosa. Statistics were conducted by two-sided Welch's t-test and Benjamini–Hochberg FDR correction, and the *P* values of different functions lower than 0.05 were shown.

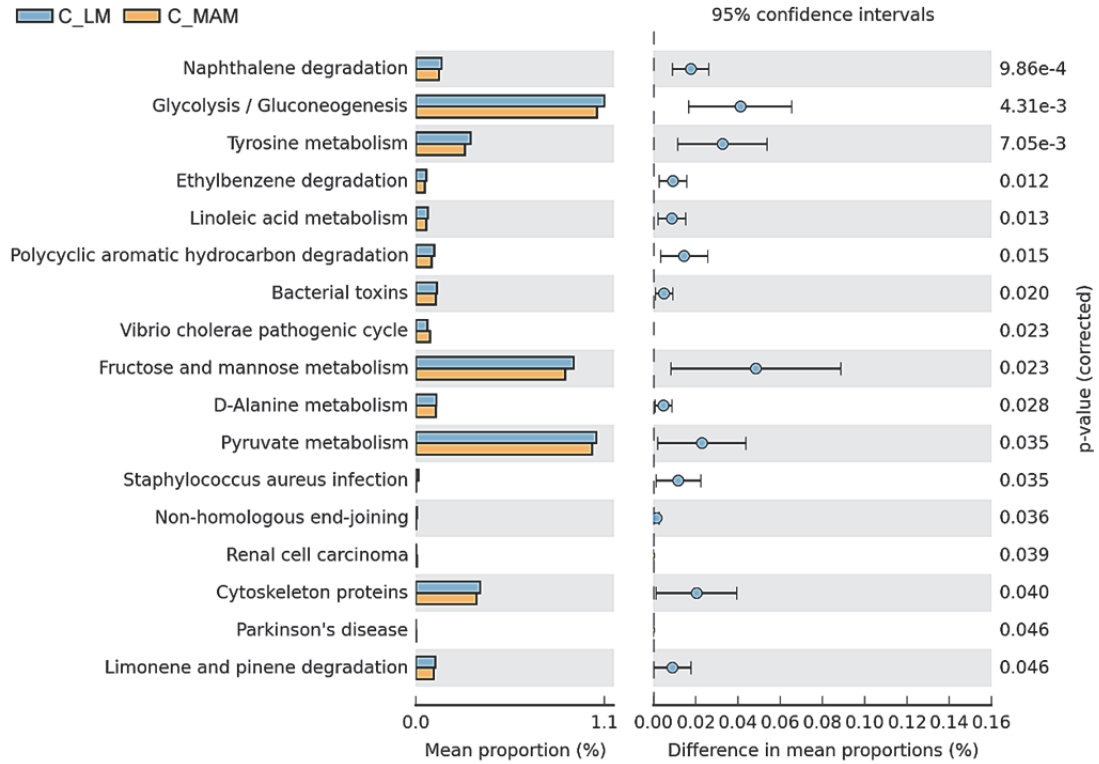


Fig. S2 Colonic predicted microbial function comparison based on KEGG level-3. CC: colonic luminal content; CM: colonic mucosa. Statistics were conducted by two-sided Welch's t-test and Benjamini–Hochberg FDR correction, and the *P* values of different functions lower than 0.05 were shown.



Fig. S3 Duodenal predicted microbial function comparison in based on KEGG level-3.

DC: duodenal luminal content; DM: duodenal mucosa. Statistics were conducted by two-sided Welch's t-test and Benjamini–Hochberg FDR correction, and the *P* values of different functions lower than 0.05 were shown.

Table S1. Relative abundances of significant changed bacteria at different levels (phylum, family and genus) in colon

	Taxonomic group	C_LM (%)	C_MAM (%)	Variation
Phylum	Deferribacteres	0.06±0.04	2.93±1.20	↑*
Family	Lactobacillaceae	9.63±3.14	0.84±0.38	↓*
	Rikenellaceae	1.42±0.23	4.70±0.73	↑**
	Deferribacteraceae	0.06±0.04	2.93±1.20	↑*
	Clostridiales_vadinBB60_group	0.27±0.15	2.13±0.36	↑**
	Erysipelotrichaceae	0.83±0.19	0.21±0.05	↓*
	Unidentified Gastranaerophilales	0.16±0.05	0.80±0.26	↓*
	Coriobacteriaceae	0.34±0.11	0.09±0.02	↓**
	Mollicutes_RF9_group	0.19±0.05	0.08±0.03	↓*
Genus	Lactobacillus	9.63±3.14	0.84±0.38	↓*
	Alistipes	1.34±0.23	3.67±0.34	↑**
	Mucispirillum	0.06±0.04	2.93±1.20	↑*
	Unidentified Clostridiales_vadinBB60	0.27±0.15	2.13±0.36	↑**
	Odoribacter	0.22±0.04	1.24±0.47	↑*
	Marvinbryantia	0.38±0.14	0.99±0.14	↑*
	Lachnoclostridium	0.29±0.08	0.84±0.14	↑*
	Rikenellaceae_RC9_gut_group	0.08±0.03	1.03±0.43	↑**
	Unidentified Gastranaerophilales	0.16±0.05	0.80±0.26	↑*
	Unidentified Erysipelotrichaceae	0.26±0.07	0.03±0.00	↓**
	Unidentified Mollicutes_RF9	0.19±0.05	0.08±0.03	↓*
	Erysipelatoclostridium	0.21±0.06	0.03±0.01	↓**
	Enterorhabdus	0.17±0.04	0.05±0.01	↓*
	Family_XIII_AD3011_group	0.06±0.01	0.02±0.01	↓*
	[Eubacterium]_brachy_group	0.01±0.01	0.04±0.01	↑*
	Massilia	0.02±0.01	0	↓*
	Parvibacter	0.01±0.00	0	↓*

“↑” and “↓” represent the variation when the colonic mucosal microbiota (C_MAM) compared to the colonic luminal microbiota (C_LM).

$n = 6$ for each group. * $P < 0.05$, ** $P < 0.01$.