

Supplementary Material

Table S1 Affected sub-pathways belonging to the top 10 pathways at KEGG level 2 in the digesta-associated microbiota. Numbers in the same row with different superscripts indicate a significant difference ($P < 0.05$).

KEGG_Pathways	Jejunum	Ileum	Caecum	Colon	SEM	<i>P</i> value
Amino Acid Metabolism						
Amino acid related enzymes	1.43 ^b	1.43 ^b	1.52 ^a	1.53 ^a	0.011	<0.001
Arginine and proline metabolism	1.13 ^b	1.09 ^b	1.26 ^a	1.25 ^a	0.015	<0.001
Alanine, aspartate and glutamate metabolism	1.00 ^b	0.97 ^b	1.09 ^a	1.1 ^a	0.012	<0.001
Cysteine and methionine metabolism	0.91 ^c	0.93 ^{bc}	0.96 ^{ab}	0.97 ^a	0.006	<0.001
Phenylalanine, tyrosine and tryptophan biosynthesis	0.77 ^b	0.72 ^b	0.92 ^a	0.93 ^a	0.018	<0.001
Valine, leucine and isoleucine biosynthesis	0.71 ^b	0.67 ^b	0.79 ^a	0.78 ^a	0.011	<0.001
Histidine metabolism	0.58 ^b	0.56 ^b	0.66 ^a	0.66 ^a	0.010	<0.001
Valine, leucine and isoleucine degradation	0.38 ^a	0.32 ^a	0.24 ^b	0.23 ^b	0.015	<0.001
Tyrosine metabolism	0.37 ^a	0.39 ^a	0.3 ^b	0.30 ^b	0.008	<0.001
Tryptophan metabolism	0.27 ^a	0.22 ^{ab}	0.18 ^b	0.17 ^b	0.010	<0.001
Lysine degradation	0.22 ^a	0.18 ^{ab}	0.13 ^b	0.13 ^b	0.009	<0.001
Lysine biosynthesis	0.77 ^b	0.76 ^b	0.82 ^a	0.82 ^a	0.007	0.002
Glycine, serine and threonine metabolism	0.82 ^{ab}	0.8 ^b	0.85 ^a	0.84 ^{ab}	0.007	0.009
Carbohydrate Metabolism						
Butanoate metabolism	0.74 ^a	0.72 ^a	0.63 ^b	0.63 ^b	0.012	<0.001
Propanoate metabolism	0.65 ^a	0.59 ^a	0.5 ^b	0.51 ^b	0.012	<0.001
C5-Branched dibasic acid metabolism	0.29 ^b	0.27 ^b	0.32 ^a	0.32 ^a	0.005	<0.001
Citrate cycle (TCA cycle)	0.66 ^{ab}	0.64 ^b	0.72 ^a	0.71 ^{ab}	0.010	0.006
Galactose metabolism	0.63 ^b	0.66 ^{ab}	0.73 ^a	0.72 ^{ab}	0.012	0.019
Glycolysis / Gluconeogenesis	1.13 ^{ab}	1.19 ^a	1.09 ^{ab}	1.09 ^b	0.013	0.022
Starch and sucrose metabolism	0.88 ^b	0.95 ^{ab}	0.98 ^{ab}	0.97 ^a	0.014	0.026
Pentose and glucuronate interconversions	0.43 ^b	0.47 ^{ab}	0.47 ^a	0.46 ^{ab}	0.008	0.044
Energy Metabolism						
Methane metabolism	1.2 ^b	1.17 ^b	1.31 ^a	1.33 ^a	0.015	<0.001
Oxidative phosphorylation	1.16 ^{ab}	1.07 ^b	1.26 ^a	1.24 ^a	0.018	<0.001
Carbon fixation pathways in prokaryotes	1.01 ^a	0.98 ^a	1.1 ^b	1.1 ^b	0.011	<0.001
Carbon fixation in photosynthetic organisms	0.59 ^b	0.58 ^b	0.63 ^a	0.63 ^a	0.005	<0.001
Nitrogen metabolism	0.71 ^b	0.71 ^b	0.75 ^{ab}	0.77 ^a	0.007	0.002
Enzyme Families						
Peptidases	1.78 ^b	1.82 ^{ab}	1.92 ^a	1.92 ^a	0.015	0.002
Lipid Metabolism						
Fatty acid metabolism	0.36 ^a	0.31 ^a	0.23 ^b	0.23 ^{ab}	0.013	<0.001
Fatty acid biosynthesis	0.51 ^a	0.51 ^{ab}	0.48 ^b	0.48 ^{ab}	0.004	0.003
Glycerolipid metabolism	0.39 ^a	0.39 ^a	0.37 ^{ab}	0.36 ^b	0.004	0.004
Biosynthesis of unsaturated fatty acids	0.17 ^a	0.16 ^{ab}	0.14 ^{ab}	0.14 ^b	0.005	0.031

Metabolism of Cofactors and Vitamins

Pantothenate and CoA biosynthesis	0.62 ^b	0.59 ^b	0.69 ^a	0.7 ^a	0.009	<0.001
One carbon pool by folate	0.59 ^b	0.59 ^b	0.7 ^a	0.7 ^a	0.010	<0.001
Thiamine metabolism	0.49 ^b	0.48 ^b	0.53 ^a	0.52 ^a	0.005	<0.001
Vitamin B6 metabolism	0.19 ^b	0.17 ^b	0.21 ^a	0.21 ^a	0.004	<0.001
Biotin metabolism	0.15 ^{ab}	0.14 ^b	0.18 ^a	0.18 ^a	0.004	<0.001
Folate biosynthesis	0.4 ^b	0.39 ^b	0.44 ^a	0.44 ^{ab}	0.007	0.003

Replication and Repair

DNA replication proteins	1.18 ^b	1.2 ^{ab}	1.28 ^a	1.29 ^a	0.013	0.002
Mismatch repair	0.81 ^b	0.82 ^{ab}	0.86 ^{ab}	0.86 ^a	0.008	0.015
Nucleotide excision repair	0.39 ^b	0.4 ^{ab}	0.42 ^a	0.42 ^{ab}	0.004	0.027

Membrane Transport

Transporters	6.25 ^{ac}	6.55 ^a	5.57 ^b	5.57 ^{bc}	0.106	<0.001
ABC transporters	3.27 ^a	3.41 ^a	2.83 ^b	2.83 ^b	0.066	<0.001
Phosphotransferase system (PTS)	0.47 ^a	0.6 ^a	0.22 ^b	0.21 ^b	0.034	<0.001
Secretion system	1.49 ^a	1.41 ^{ab}	1.29 ^b	1.29 ^b	0.028	0.003

Table S2 Affected sub-pathways belonging to the top 10 pathways at KEGG level 2 in the mucosa-associated microbiota. Numbers in the same row with different superscripts indicate a significant difference ($P < 0.05$).

KEGG_Pathways	Jejunum	Ileum	Caecum	Colon	SEM	<i>P</i>
Amino Acid Metabolism						
Phenylalanine, tyrosine and tryptophan biosynthesis	0.87 ^{ab}	0.84 ^b	0.89 ^{ab}	0.91 ^a	0.009	0.017
Tyrosine metabolism	0.34 ^{ab}	0.36 ^a	0.32 ^b	0.31 ^b	0.008	0.019
Valine, leucine and isoleucine biosynthesis	0.76 ^{ab}	0.76 ^b	0.79 ^a	0.78 ^{ab}	0.005	0.03
Carbohydrate Metabolism						
C5-Branched dibasic acid metabolism	0.32 ^b	0.32 ^b	0.34 ^a	0.33 ^{ab}	0.003	0.019
Glycolysis / Gluconeogenesis	1.09 ^a	1.09 ^a	1.03 ^b	1.06 ^{ab}	0.006	0.011
Metabolism of Cofactors and Vitamins						
Biotin metabolism	0.16 ^a	0.16 ^a	0.19 ^b	0.18 ^{ab}	0.003	0.017
Pantothenate and CoA biosynthesis	0.65 ^{ab}	0.64 ^b	0.66 ^{ab}	0.68 ^a	0.005	0.027
Membrane Transport						
Phosphotransferase system (PTS)	0.30 ^{ab}	0.34 ^a	0.26 ^b	0.27 ^{ab}	0.01	0.028

Table S3 Correlation between the abundance (relative abundance >1% in at least in one location) and significantly affected microbial genera and KEGG pathways of the mucosa-associated microbiota. Only correlation coefficients with *P* value <0.05 and $|r|>0.5$ are presented.

Genus	KEGG pathway	KO numbers	Correlation coefficient	P Value
Lactobacillus	Glycolysis / Gluconeogenesis	ko00010	0.71	<0.001
Lactobacillus	Valine, leucine and isoleucine biosynthesis	ko00290	-0.65	<0.001
Lactobacillus	C5-Branched dibasic acid metabolism	ko00660	-0.63	<0.001
Lactobacillus	Phosphotransferase system (PTS)	ko02060	0.59	<0.001
Streptococcus	Glycolysis / Gluconeogenesis	ko00010	0.73	<0.001
Streptococcus	Phosphotransferase system (PTS)	ko02060	0.61	<0.001
Streptococcus	Valine, leucine and isoleucine biosynthesis	ko00290	-0.52	0.001
Sphingomonas	Tyrosine metabolism	ko00350	0.78	<0.001
Sphingomonas	Pantothenate and CoA biosynthesis	ko00770	-0.58	<0.001
Sphingomonas	Phenylalanine, tyrosine and tryptophan biosynthesis	ko00400	-0.52	<0.001
Sphingomonas	Valine, leucine and isoleucine biosynthesis	ko00290	0.51	<0.001
Campylobacter	Glycolysis / Gluconeogenesis	ko00010	-0.62	<0.001
Campylobacter	Biotin metabolism	ko00780	0.61	<0.001
Helicobacter	Biotin metabolism	ko00780	0.64	<0.001