

Supplementary data

Table S1, nutritional composition of piglet diets. Table S2, histopathological scoring criteria for the colon. Table S3, primer sequences used in the present study. Figure S1, differences in relative abundance of colonic microorganisms. Figure S2, differential analysis of KEGG pathways at the third hierarchical level.

Table S1. Nutritional composition of piglet diets

Category	Value
Apparent digestible energy (MJ/kg)	3.16
Crude protein (%)	16.69
Crude fibre (%)	4.21
Crude Ash (%)	5.43
NaCl (%)	0.55
Total Phosphorus (%)	0.67
Calcium (%)	0.80
Moisture (%)	12.93

Note: The diet used in this study was piglet compound feed (Hainan Liyuan Feed Co., Ltd.). Apparent digestible energy was determined in accordance with GB/T 26438-2010. Crude protein, crude fibre and crude ash were determined in accordance with GB/T 18868-2002. NaCl, total phosphorus and calcium were determined in accordance with DB21/T 2048-2012. Moisture was determined in accordance with GB/T 6435-2014.

Table S2. Histopathological scoring criteria for the colon

Score	Histological features
0	Normal colonic mucosa with intact epithelium
1	Mucosa with scattered inflammatory cell infiltration
2	Dense mucosal infiltration without submucosal spread and intact epithelium
3	Moderate inflammatory cell infiltration of mucosa and submucosa, epithelial hyperplasia, goblet cell exfoliation
4	Marked inflammatory cell infiltration of mucosa and submucosa with crypt abscesses, thrush cells and crypt shedding
5	Marked inflammatory cell infiltrate in the mucosa extending into the submucosa with crypt shedding and haemorrhage

Table S3. Primer sequences used in the present study

Genes	Primer sequence (5'-3')
<i>β-actin</i>	TGGCACCACACCTTCTACAACG TCTTCTCACGGTTGGCTTTGGG
<i>IL-1β</i>	GTGTCTGTGATTGTGGCAAAGGAG AGGACGATGGGCTCTTCTTCAAAG
<i>TNF-α</i>	CAACGGCGTGAAGCTGAAAGAC ATGCGGCTGATGGTGTGAGTG
<i>IL-8</i>	CTGCCTGGACCCCAAGGAAAAG ACTGCTGTTGTTGTTGCTTCTCAG
<i>TGF-β1</i>	GCTGTGGCTGCTAGTGCTGAC GAATGGCCTCGATGCGCTTCC
<i>IL-22</i>	AGCCCTTTTCCTTCTGGAGAC GGTCAAGCTTGCA GTGATGA
<i>ZO-1</i>	TGATGATCGTCTGTCCTACCTGTC CCGCCTTCTGTATCTGTGTCTTC
<i>MUC1</i>	AGCGGAAGCAGGCACCTATAAC AGAATACAGACCAGCACCAGCAG
<i>CLDN1</i>	TGTGGATGTCCTGCGTGTCG AAGTGGTGTTTCAGATTCAGCAAGG

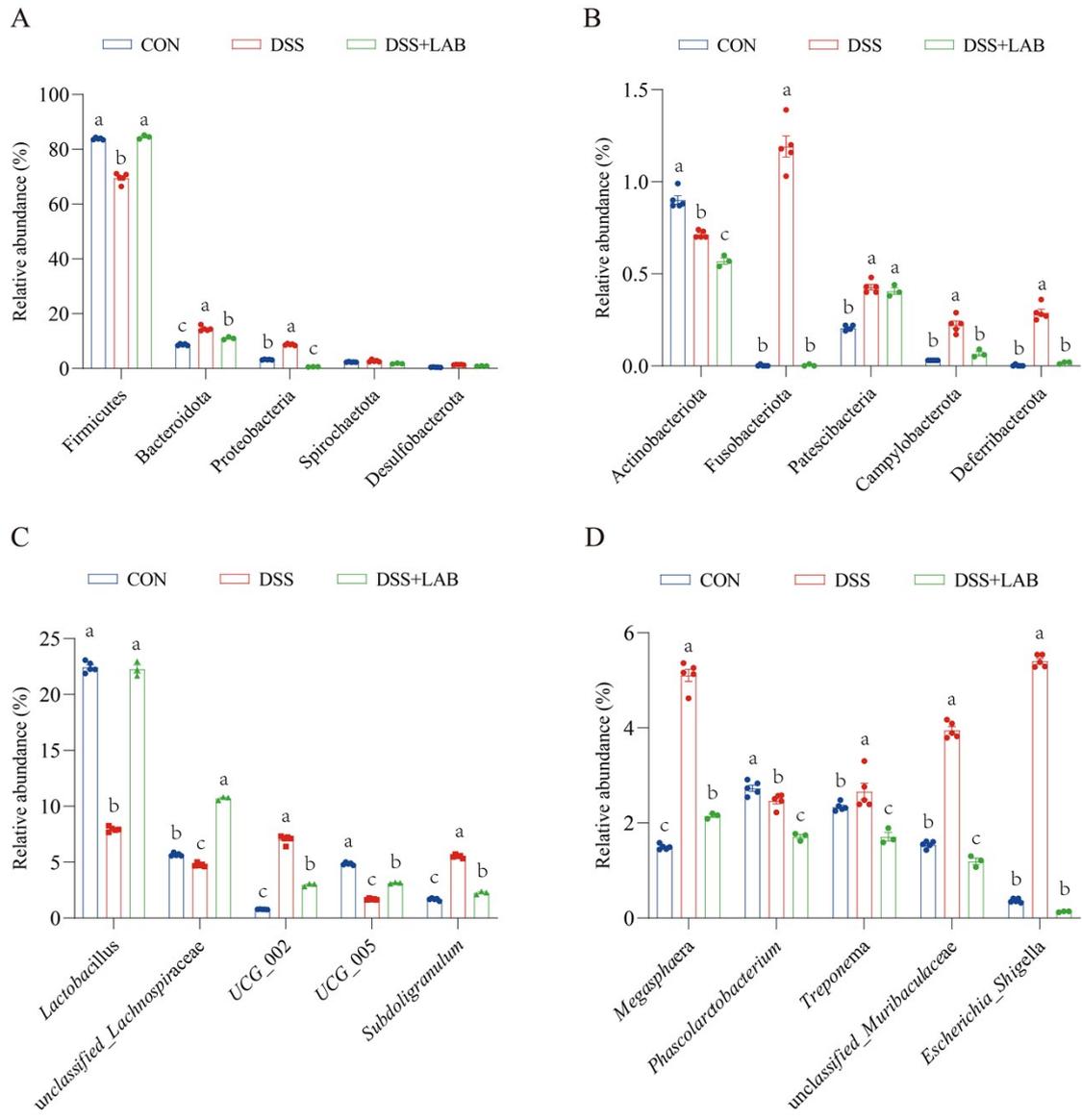
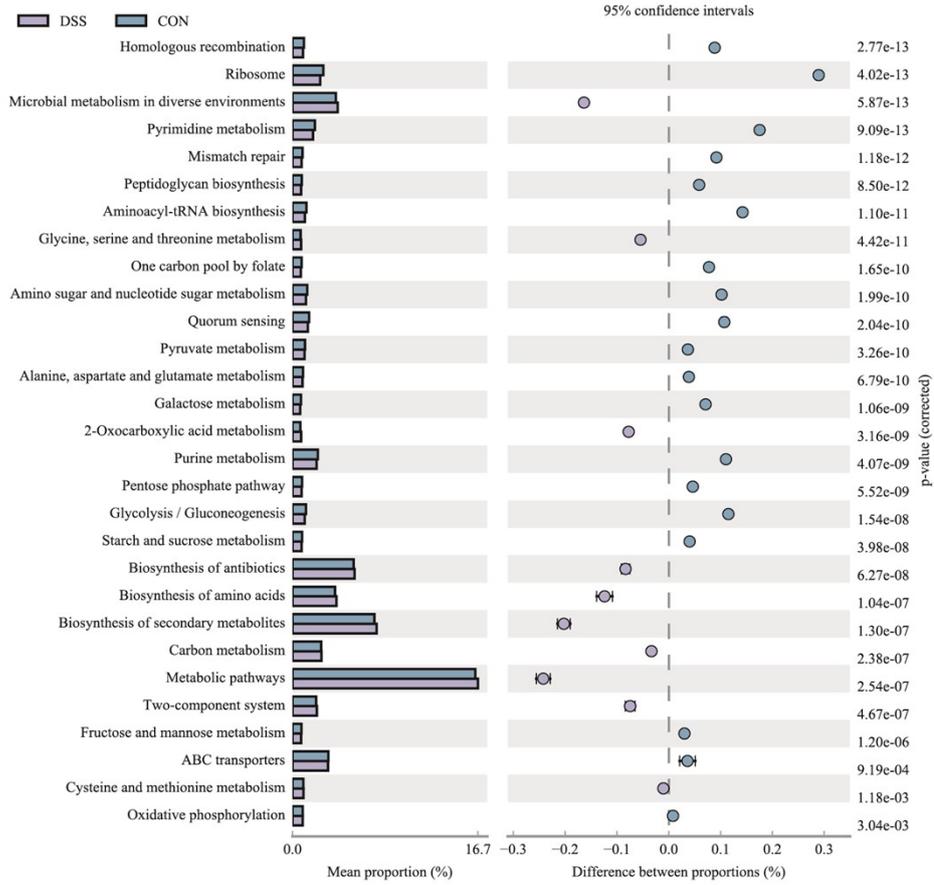


Fig. S1. Differences in relative abundance of colonic microorganisms. (A) Microorganisms ranked first to fifth at the phylum level. (B) Microorganisms ranked sixth to tenth at the phylum level. (C) Microorganisms ranked first to fifth at the genus level. (D) Microorganisms ranked sixth to tenth at the genus level. Results were expressed as mean \pm SEM (n = 5 in CON and DSS, n = 3 in DSS+LAB), different lowercase letters indicate significant differences.

A



B

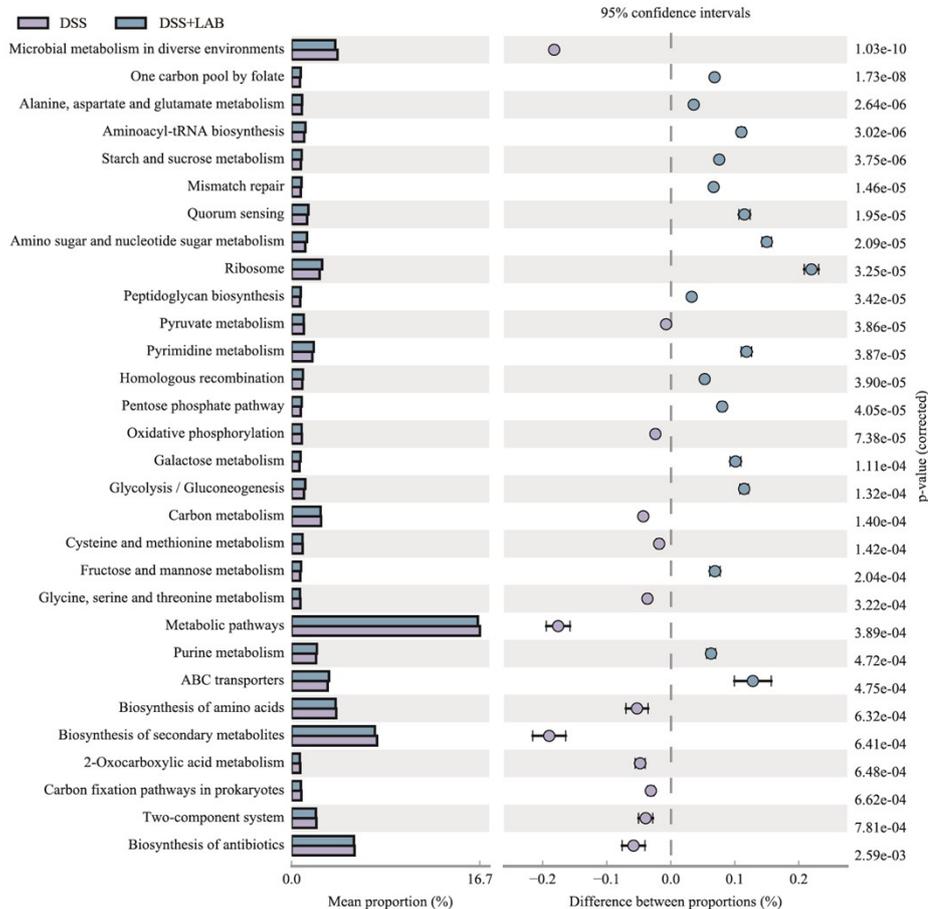


Fig. S2. Differential analysis of KEGG pathways at the third hierarchical level. (A) Between DSS group and CON group. (B) Between DSS group and DSS+LAB group. The left panel of the figure shows the abundance ratio of different functions between the two groups, the middle panel shows the proportion of the difference in functional abundance within the 95% confidence interval, and the right panel shows the *P*-values.

1