

Figure S1. Hematoxylin & eosin staining of the duodenum, jejunum, ileum and colon in the DHA and control groups. Scale bar, 20 μ m. Black arrows, enterocytes; black triangles, crypts; red triangles, goblet cells. DHA, dihydroartemisinin.

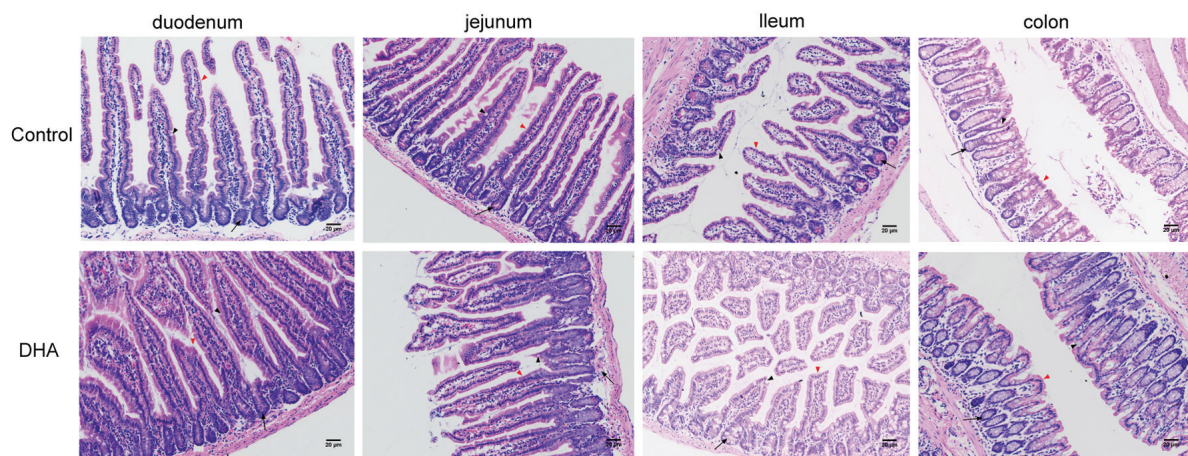


Figure S2. Relative abundance of the gut microbiota in the two groups. (A and B) Relative abundance of the gut microbiota at the bacterial class level in the control and DHA groups. (C and D) Relative abundance of the gut microbiota at the bacterial family level in the control and DHA groups. DHA, dihydroartemisinin.

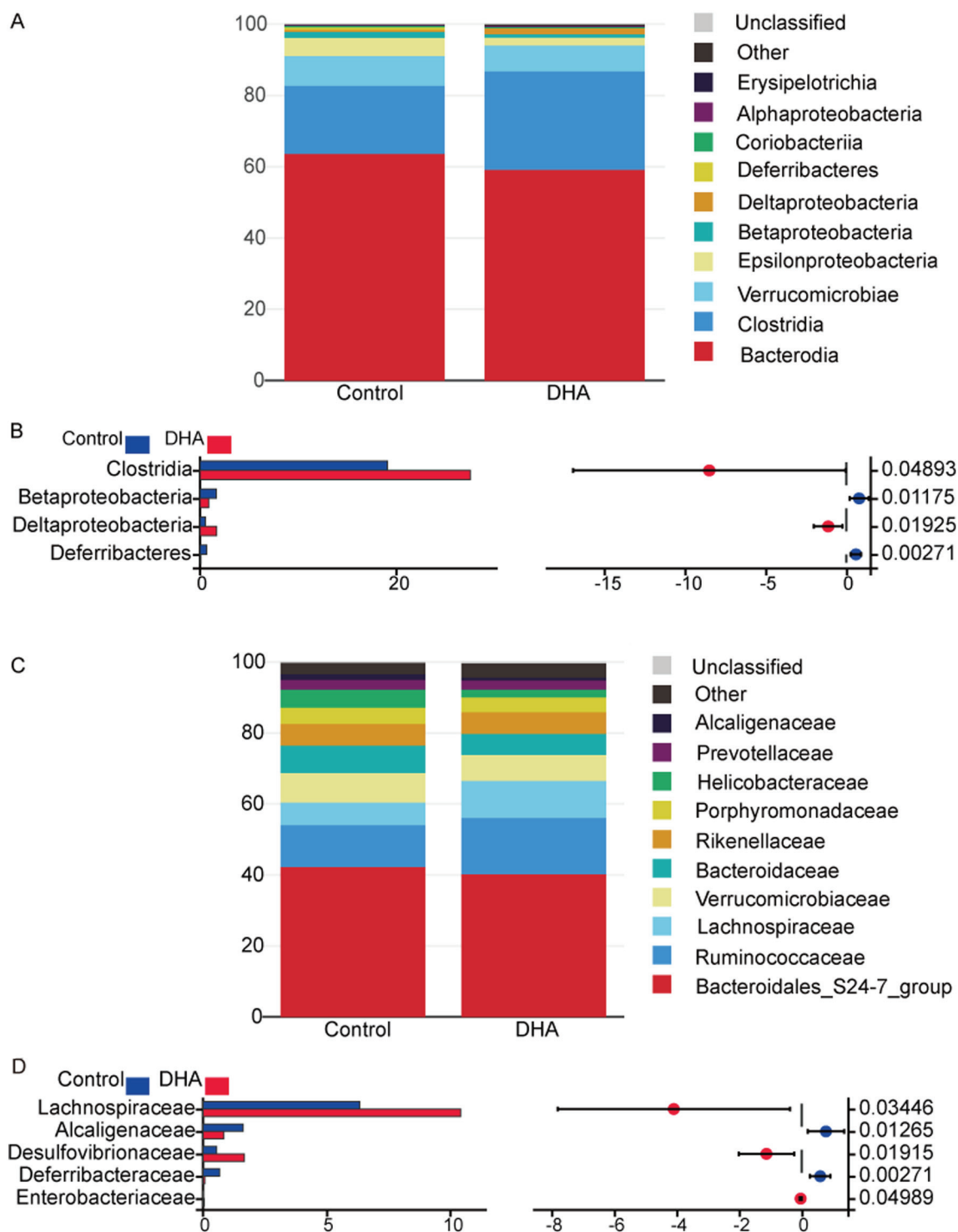


Figure S3. Association between environmental factors and the bacterial taxa. (A) Canonical correspondence analysis presented the correlation of the bacteria with different environmental factors, and LPL-C LPS and TC influenced the structure and composition of gut microbiota most. The longer the arrow, the more effect on the bacteria. (B) Correlation network analysis results demonstrated that LDL-C had positive correlation with Verrucomicrobia, but had negative correlation with Bacteroidetes. HDL-C had positive correlation with Saccharibacteria. TC had positive correlation with Fimicutes, while had negative correlation with Proteobacteria. TG had positive correlation with Defferibacteres, while had negative correlation with Saccharibacteria. Positive correlation, _____; Negative correlation, - - - - -. TG, triglyceride; TC, total cholesterol; LPS, lipopolysaccharide; HDL-C, high density lipoprotein-cholesterol; LDL-C, low density lipoprotein-cholesterol; ALT, alanine aminotransferase; AST, aspartate aminotransferase; DHA, dihydroartemisinin.

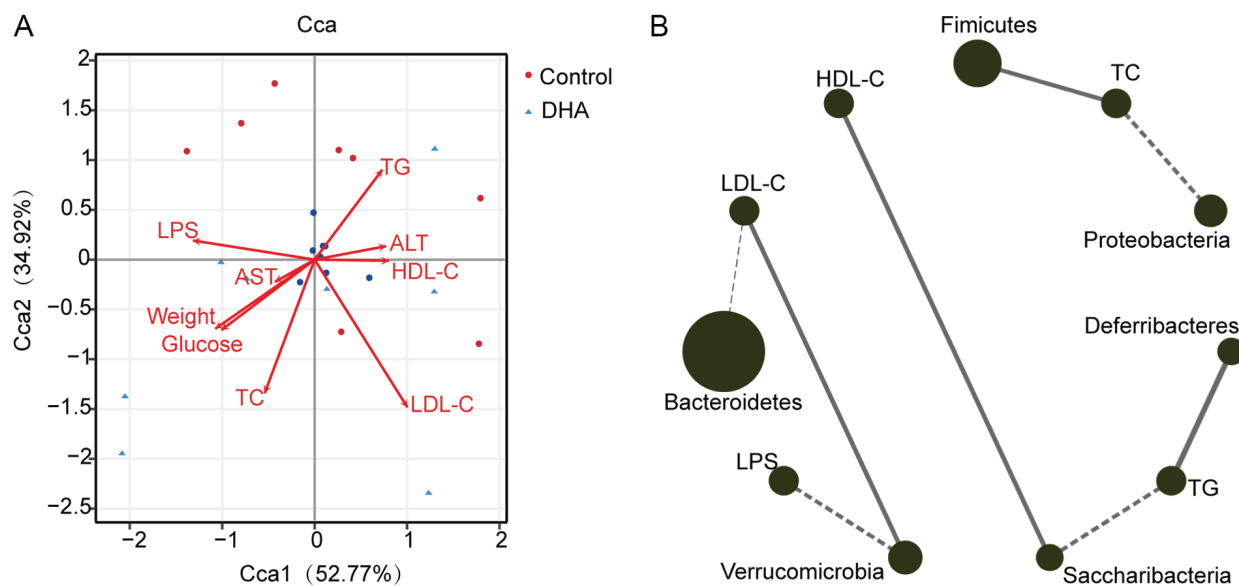


Table SI. Taxonomic composition of the gut bacteria on the class level in the DHA and control groups.

Class	Control (%)	DHA (%)	DHA/Control	P-value
<i>Bacteroidia</i>	63.60755556	59.1167125	0.92939765	0.262323375
<i>Clostridia</i>	19.12884444	27.6200375	1.44389472	0.048932397
<i>Verrucomicrobiae</i>	8.32190000	7.2687500	0.87344837	0.723143799
<i>Epsilonproteobacteria</i>	5.11385556	2.2400000	0.43802567	0.060236738
<i>Betaproteobacteria</i>	1.67271111	0.8847625	0.52893921	0.011751139

Table SII. Taxonomic composition of the gut bacteria on the family level in the DHA and control groups.

Family	Control (%)	DHA (%)	DHA/Control	P-value
<i>Bacteroidales_S24-7_group</i>	42.20567778	40.2162500	0.95286350	0.575344367
<i>Ruminococcaceae</i>	11.84307778	15.8967125	1.34227882	0.113450984
<i>Lachnospiraceae</i>	6.34613333	10.4406000	1.64519077	0.034464044
<i>Verrucomicrobiaceae</i>	8.31984444	7.2687500	0.87366417	0.723672249
<i>Bacteroidaceae</i>	7.75088889	5.9012375	0.76136268	0.101573806