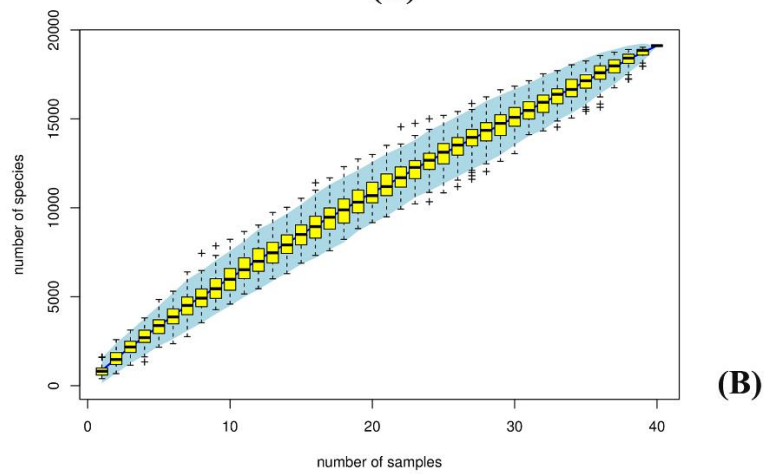
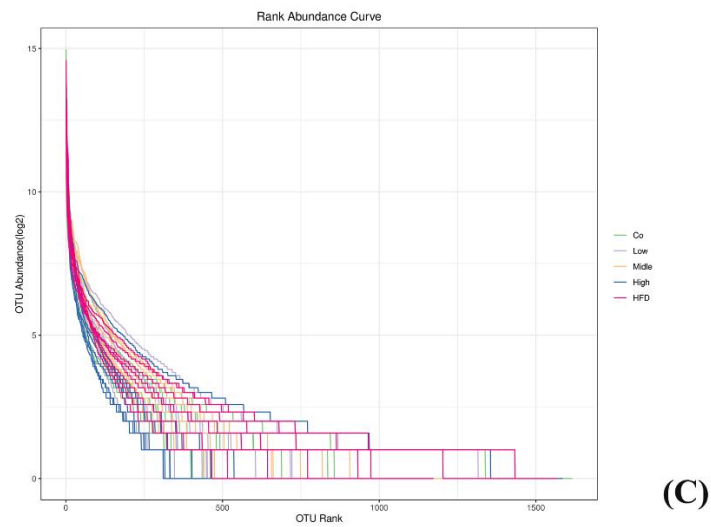


(A)



(B)



(C)

Figure S2 Rarefaction curve (A); Shannon index curve (B) and rank abundance curve (C). Co, control group; HFD, high-fat diet; Low, 10% flaxseed group; Middle, 20% flaxseed group, High, 30% flaxseed group.

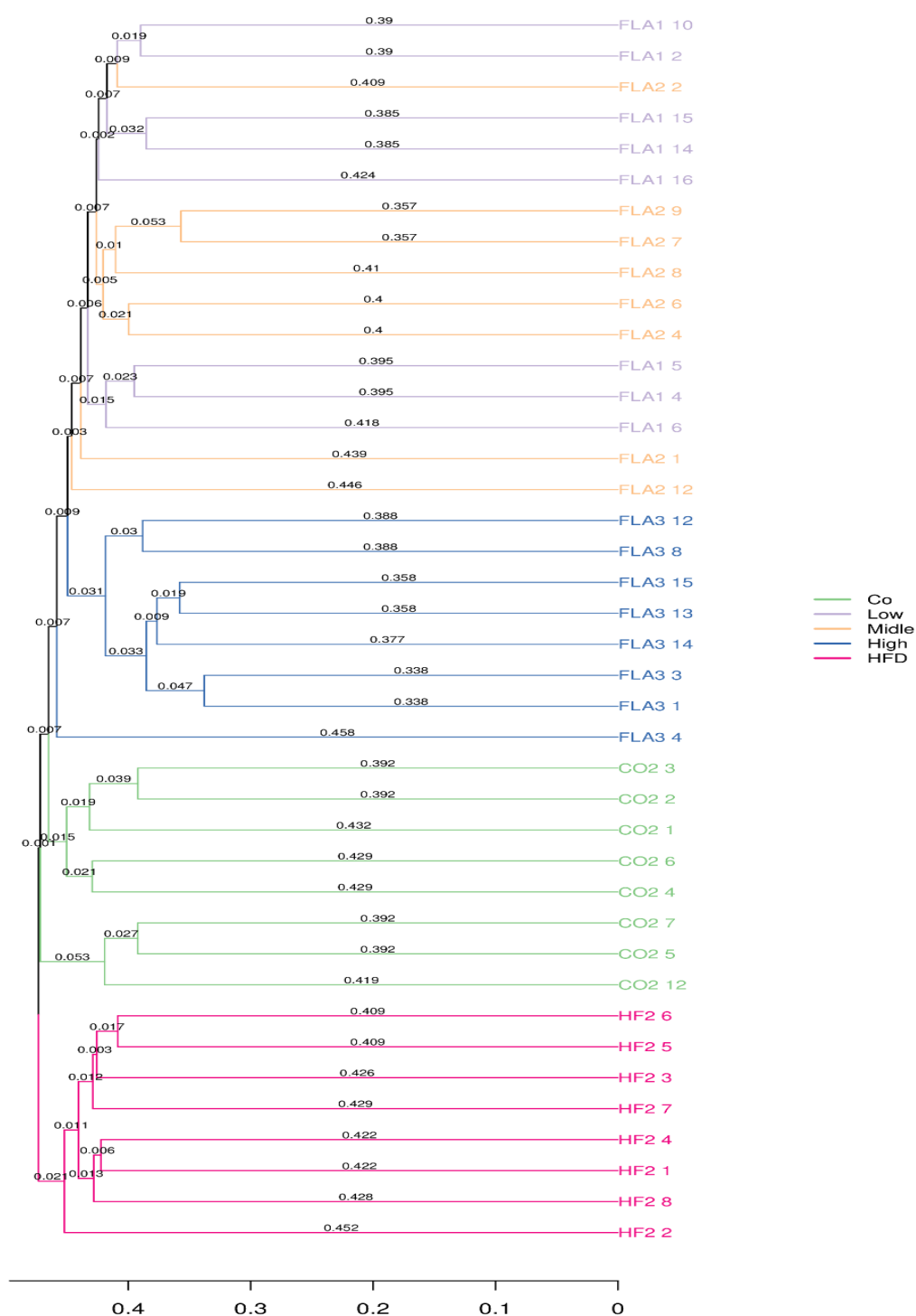


Figure S3. Hierarchical clustering based on the Jaccard similarity of fecal content microbial composition in control (n = 8), three LFA-fed (n = 8 each group) and HFD (n = 8) groups.



Figure S4. Lefse analysis between the CO, HFD and FLA-fed groups.

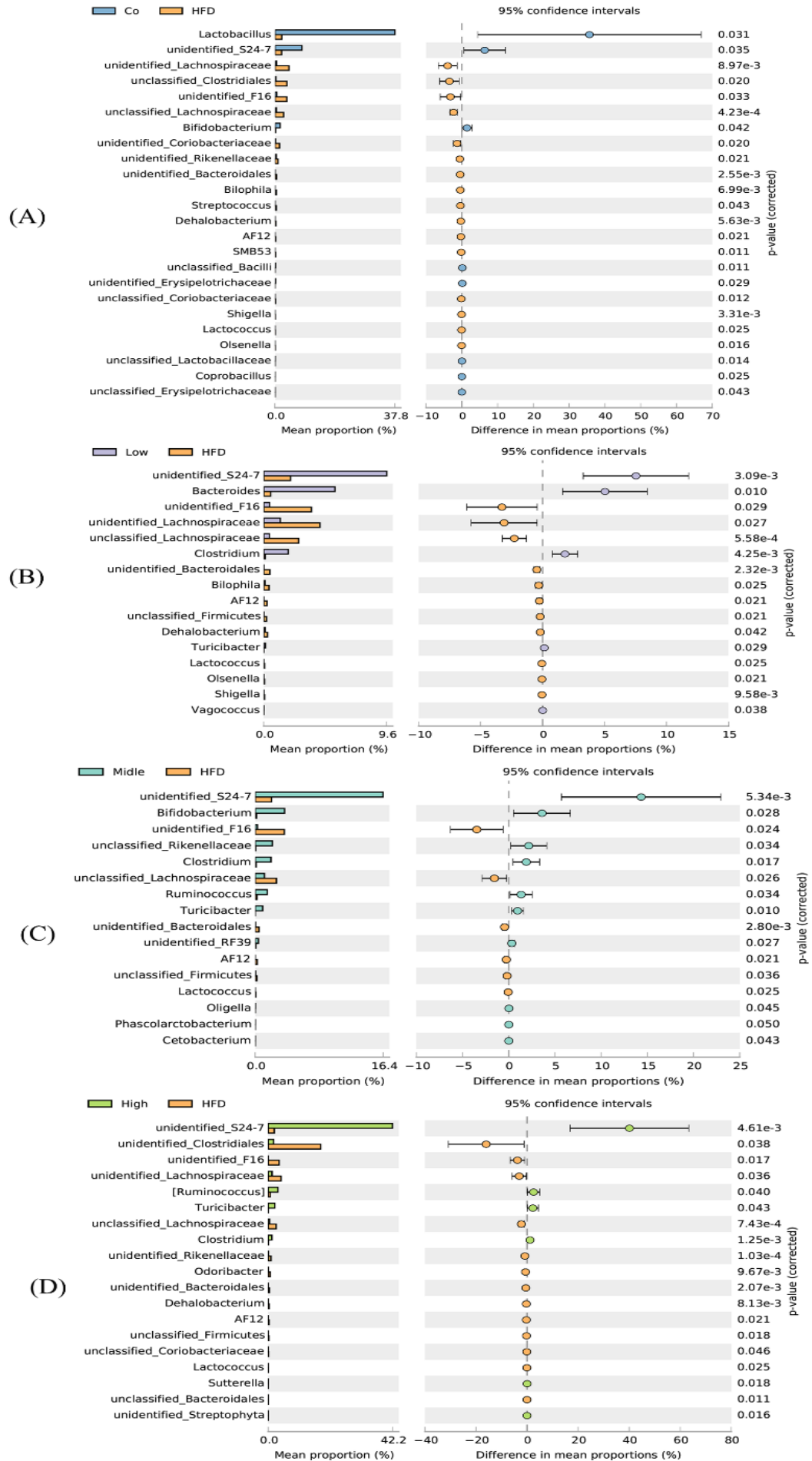


Figure S5. Different bacteria among different dietary groups at five level, (A) CO vs. HFD; (B) Low vs. HFD; (C) Middle vs. HFD; (D) High vs. HFD. Low, 10% flaxseed group; Middle, 20% flaxseed group, High, 30% flaxseed group.

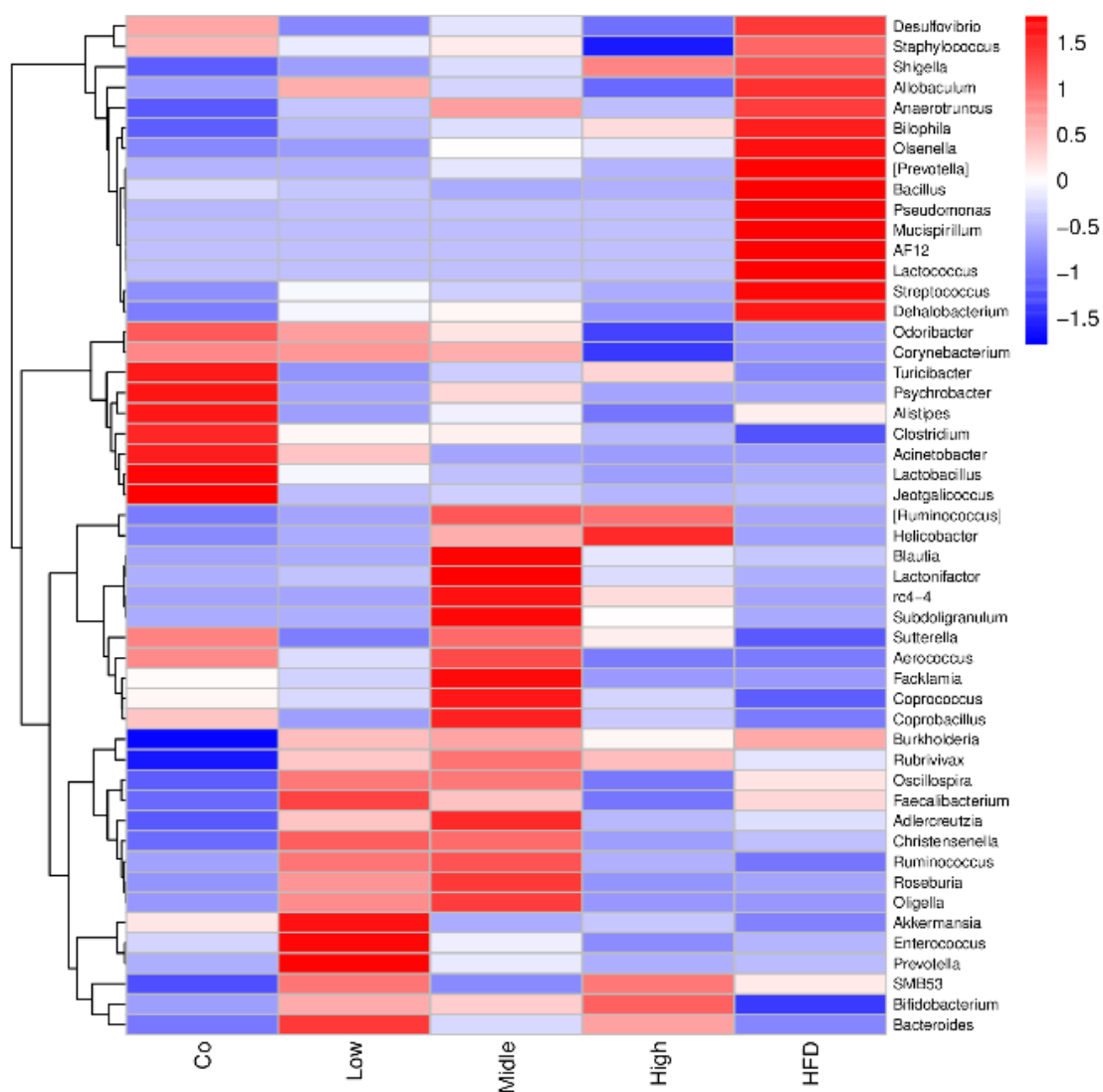


Figure S6. Heatmap analysis of the top abundance of gut microbe at genus level. Co, control group; HFD, high-fat diet; Low, 10% flaxseed group; Middle, 20% flaxseed group, High, 30% flaxseed group.

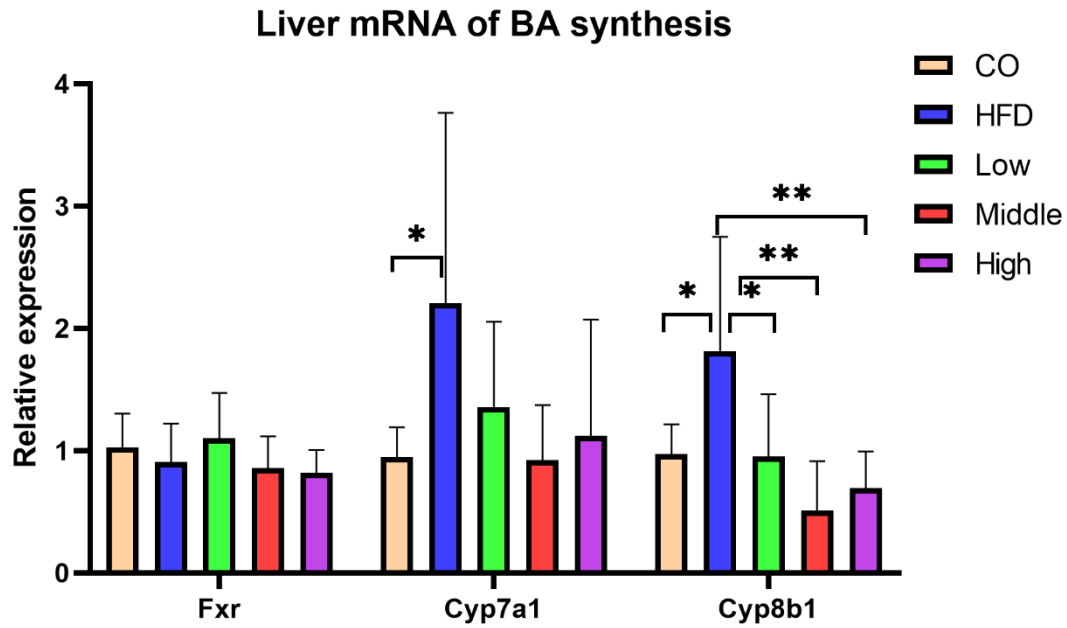


Figure S7. mRNA analysis of liver tissue to evaluate the expression of enzymes responsible for BA synthesis, including Fxr, Cyp7a1 and Cyp8b1. The relative mRNA levels of Fxr, Cyp7a1 and Cyp8b1 for BA synthesis in liver among the five groups. The data are presented as the mean \pm SD. ** $p < 0.01$ (unpaired Student's t-test). $n = 8$ per group.

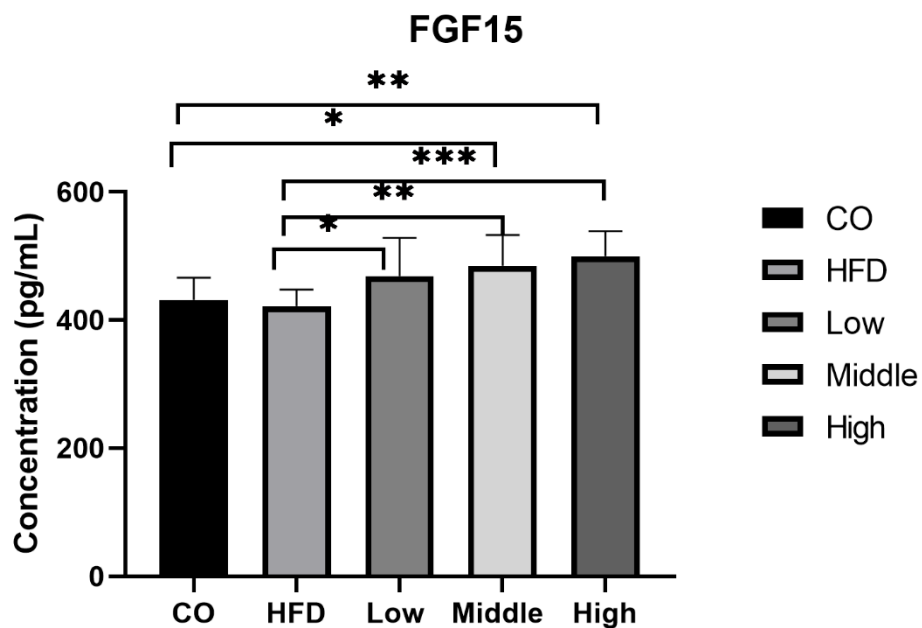


Figure S8. Differences in the plasma FGF15 concentration in five diet group. Serum FGF15 levels were detected by ELISA. Data are presented as the mean \pm SD. ** $p < 0.01$ (unpaired Student's t-test).

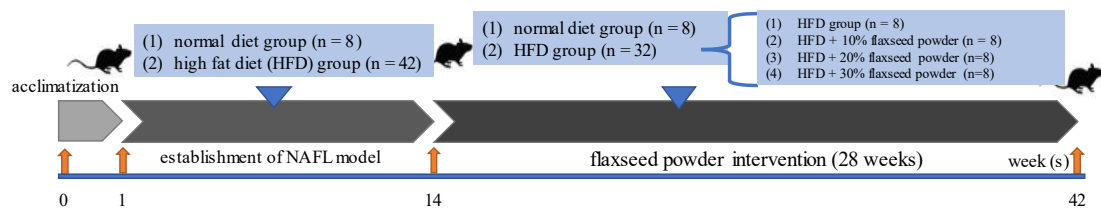


Figure S9. A timeline showing the experimental design.