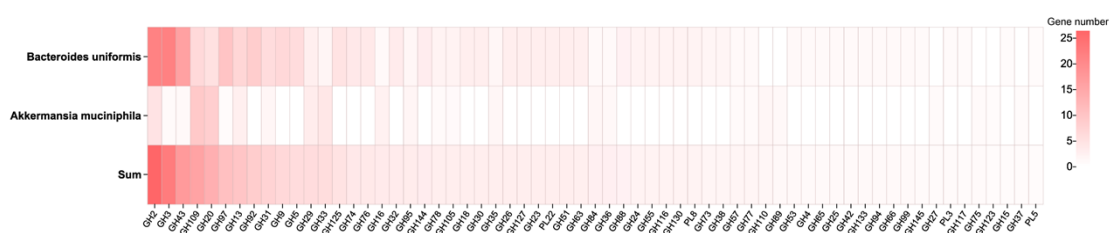
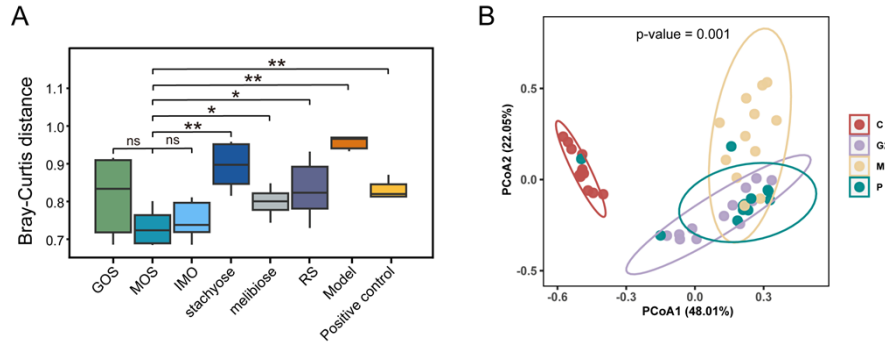


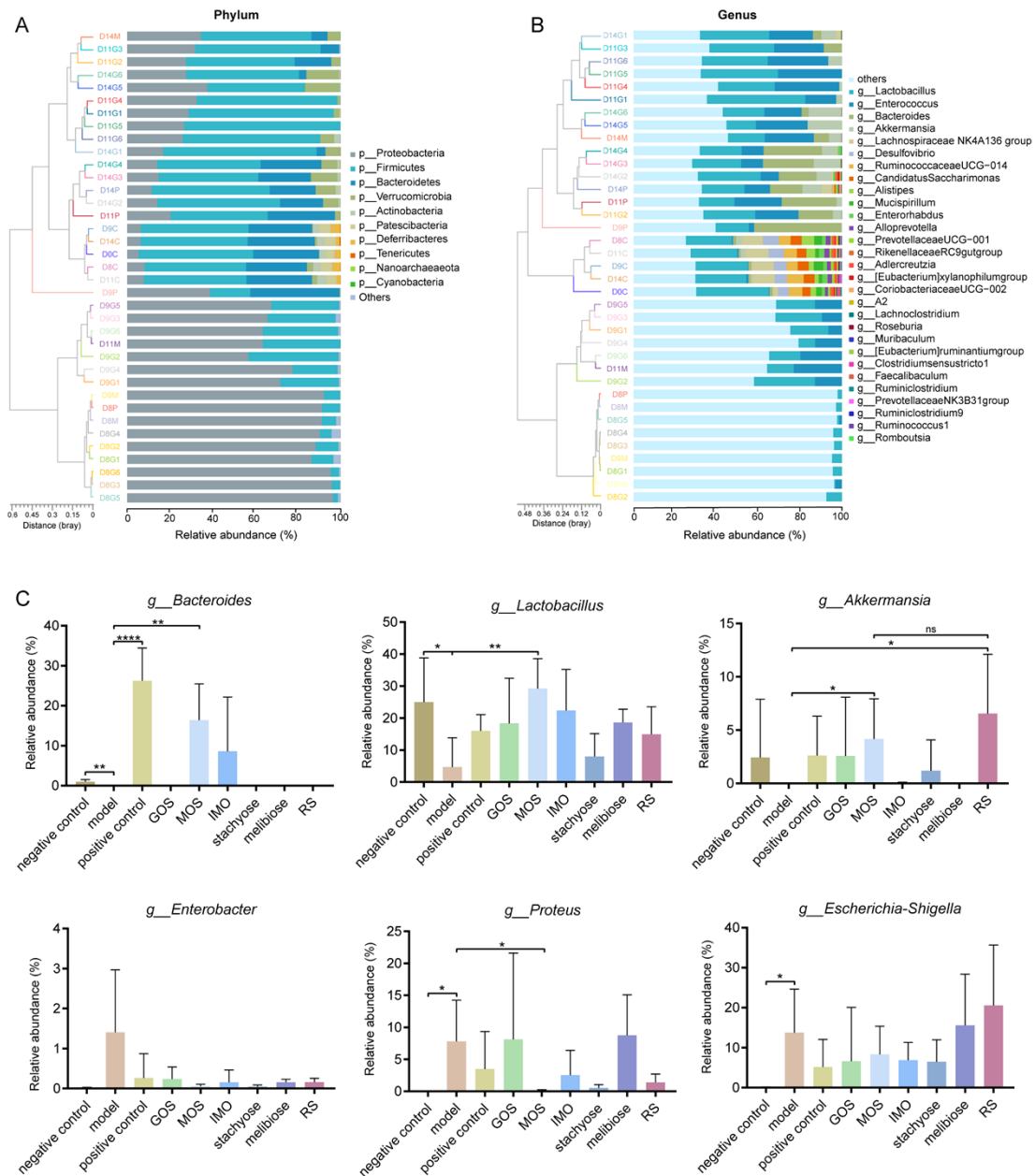
Supplementary Figure 1. Growth curve of bacterial co-culture. Growth curves of the OD_{600} absorbance values of *Akkermansia muciniphila* and *Bacteroides uniformis* under different forms of dietary fiber.



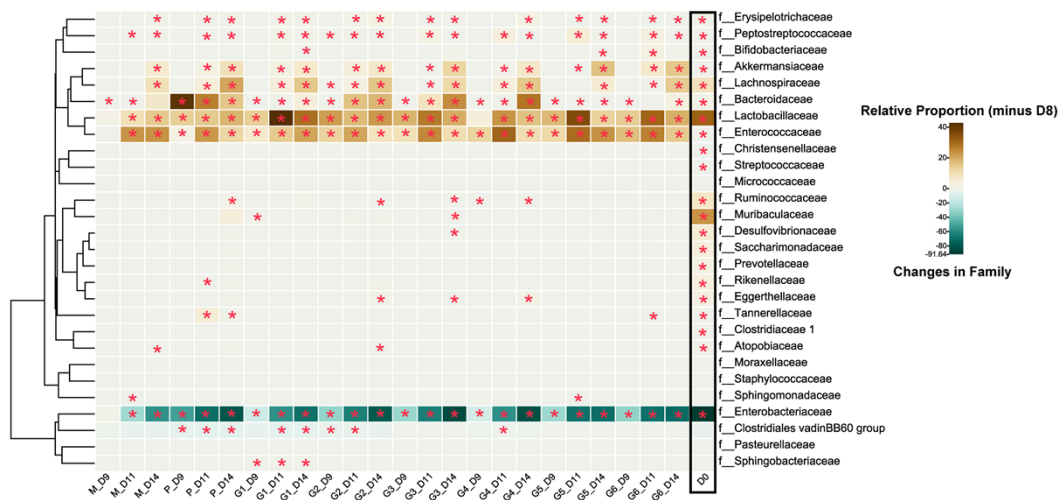
Supplementary Figure 2. CAZyme annotations. CAZyme annotation of *Akkermansia muciniphila* and *Bacteroides uniformis*, considering the average number of genes for glycoside hydrolases (GHs) and polysaccharide-degrading enzymes (PLs) present in more than 70% of strains in each species, was plotted as heat maps, sorted from left to right based on the sum of the average number of genes of the two species.



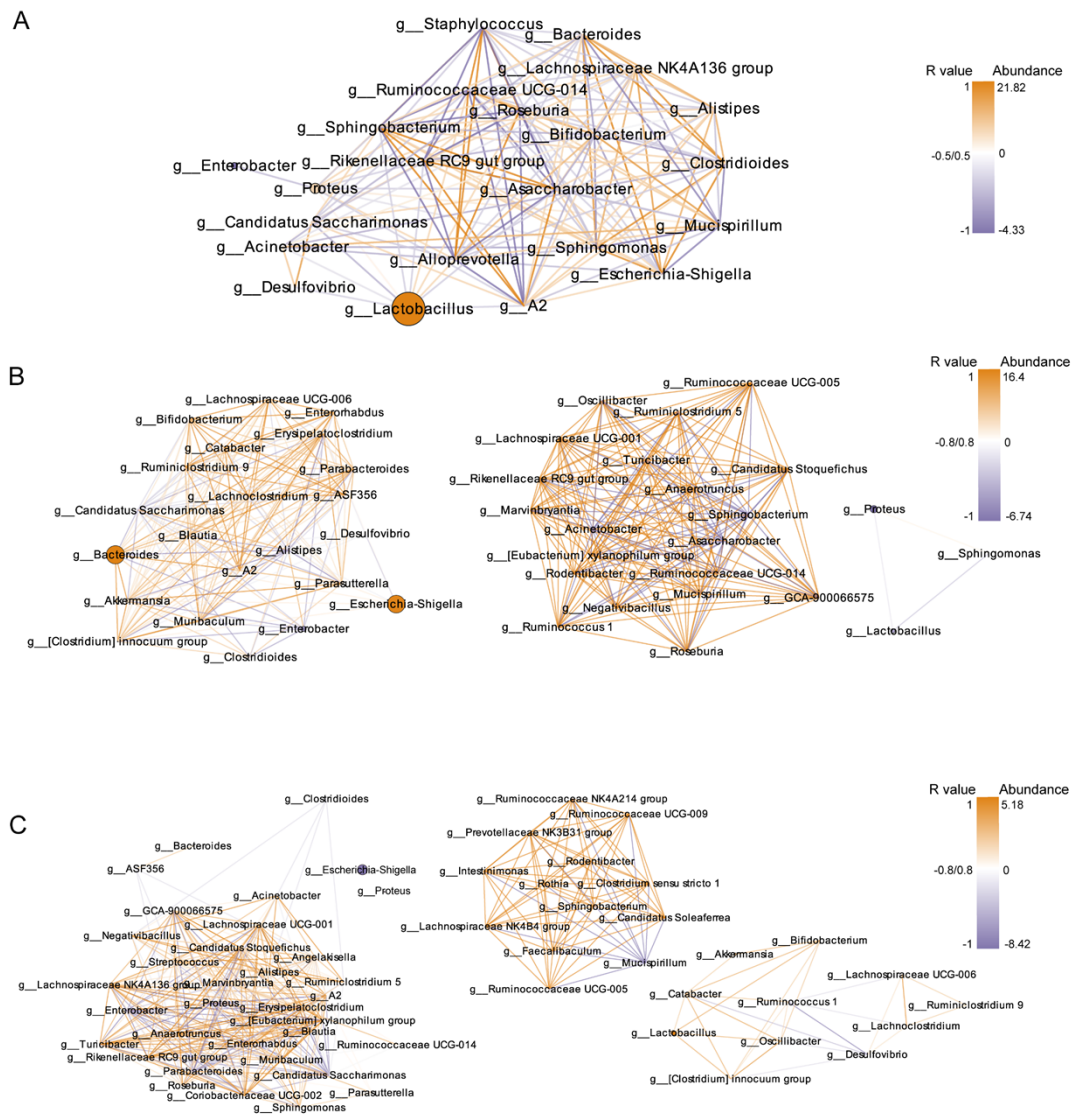
Supplementary Figure 3. Bray–Curtis distance of the intervention groups compared to the negative control group. (A) The Bray–Curtis distance between the intervention and negative control groups on day 9. (B) Microbial communities of the negative control, model, positive, and MOS groups on days 11 and 14. * $p < 0.05$, ** $p < 0.01$. There were six mice in each group.



Supplementary Figure 4. Effects of various dietary fiber types on gut microbiota composition and relative abundance of the main genera. Average relative abundance of each group at the phylum (A) and genus (B) levels. Clustering is based on the Bray–Curtis distance, and different colors represent different phylum/genera. (C) Relative abundance of different genera in different groups. * $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$. There were six mice in each group, totaling 54 mice on days 8, 9, 11, and 14, and one mouse in each group, totaling nine mice on day 0.



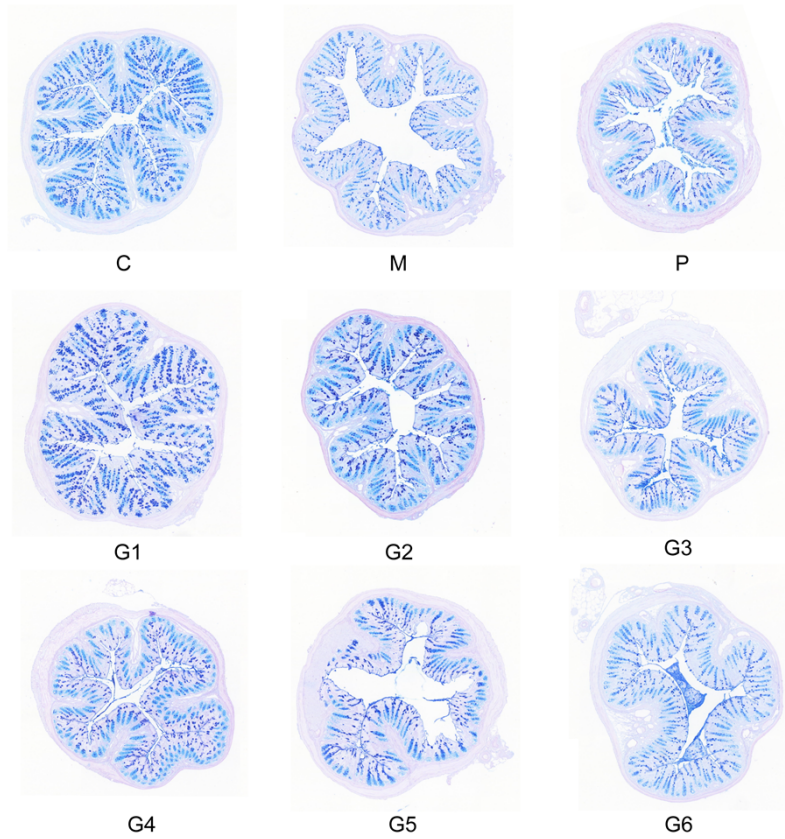
Supplementary Figure 5. Changes in the relative abundance of bacterial taxa at the family level. Clustering analysis based on Bray–Curtis distance ($*p < 0.05$). There were six mice in each group, totaling 54 mice on days 8, 9, 11, and 14, and one mouse in each group, totaling nine mice on day 0.



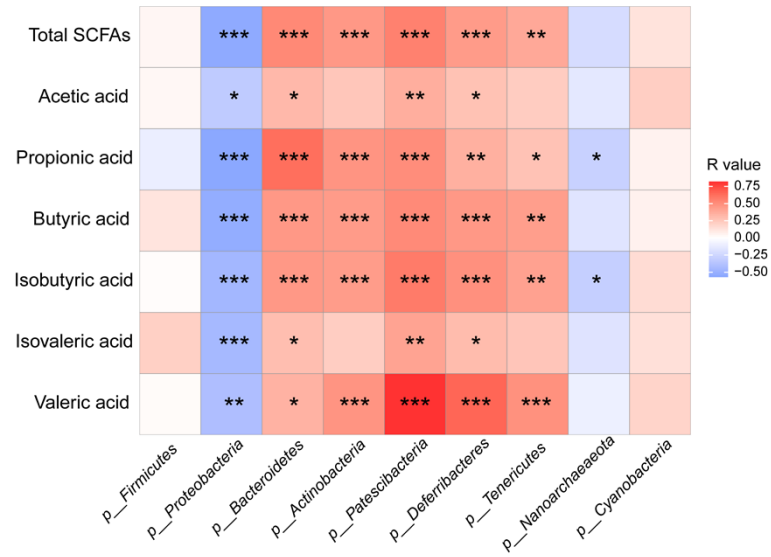
Supplementary Figure 6. Co-occurrence network of gut microbiota in the MOS group.

(A) Dynamic network of microbiota from day 8 to day 9; (B) dynamic network of microbiota from day 9 to day 11; and (C) dynamic network of microbiota from day 11 to day 14. In these networks, the size of the node indicates the variable quantity of genus abundance. Orange nodes indicate increased abundance, and purple nodes indicate decreased abundance of this genus. Similarly, the orange line indicates a positive correlation between the two genera, and the purple line indicates a negative correlation.

There were six mice in each group.



Supplementary Figure 7. AB-PAS staining of the colon tissues. C, negative control group; M, model; P, positive control group; G1, GOS; G2, MOS; G3, IMO; G4, stachyose; G5, melibiose; G6, RS.



Supplementary Figure 8. Spearman's correlation between SCFAs and bacterial phyla in fecal samples. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Clustering analysis based on Euclidean distance. There were six mice in each group.