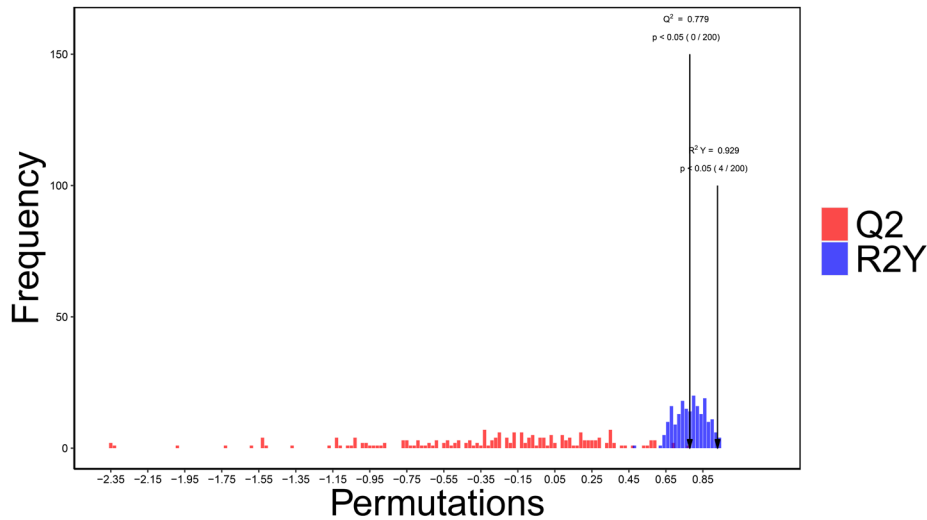


Figure S1. DNA sequence data analysis. (A) Venn diagram. The numbers in the figure show the unique or shared OTUs in each group. (B) Graph showing the difference in Goods_coverage between groups. Dilution curve (C) and abundance rank curve (D) of ASV. “*” indicates a significant difference in statistics (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

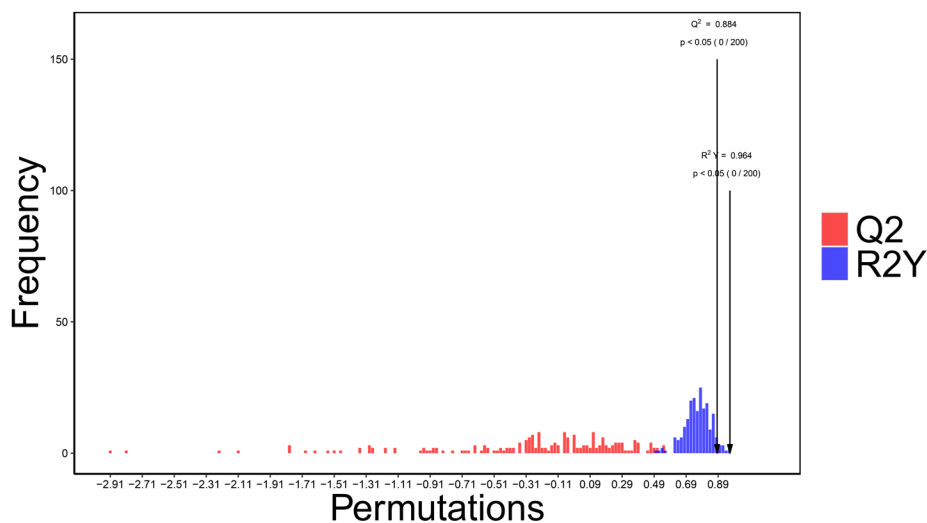


Figure S2. Significant differences in bacterial taxa between groups were determined by linear discriminant analysis and effect size (LEfSe). LDA scores were calculated for bacterial taxa that were differentially enriched among different groups.

A



B



C

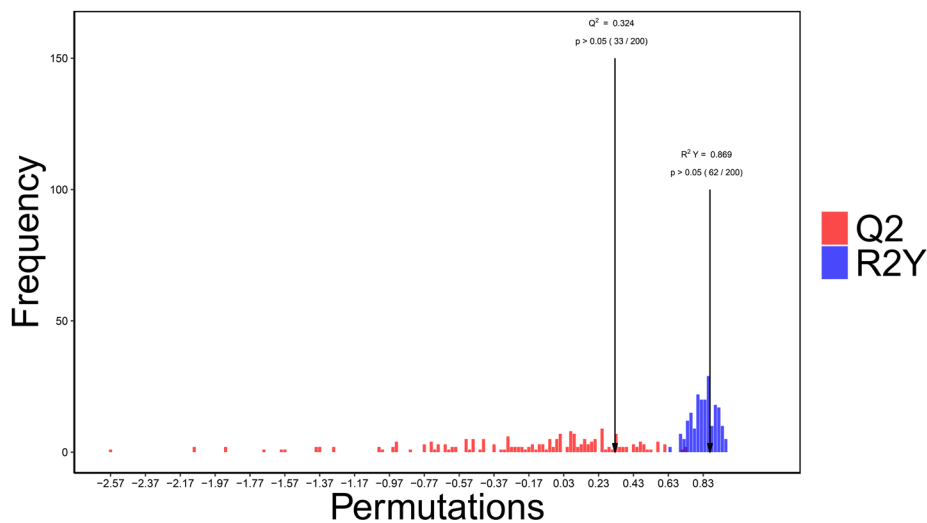
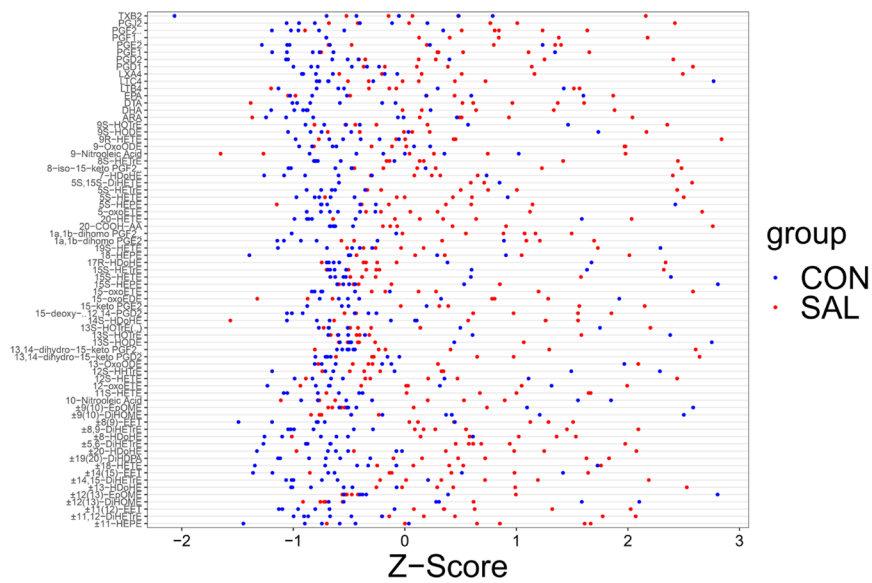
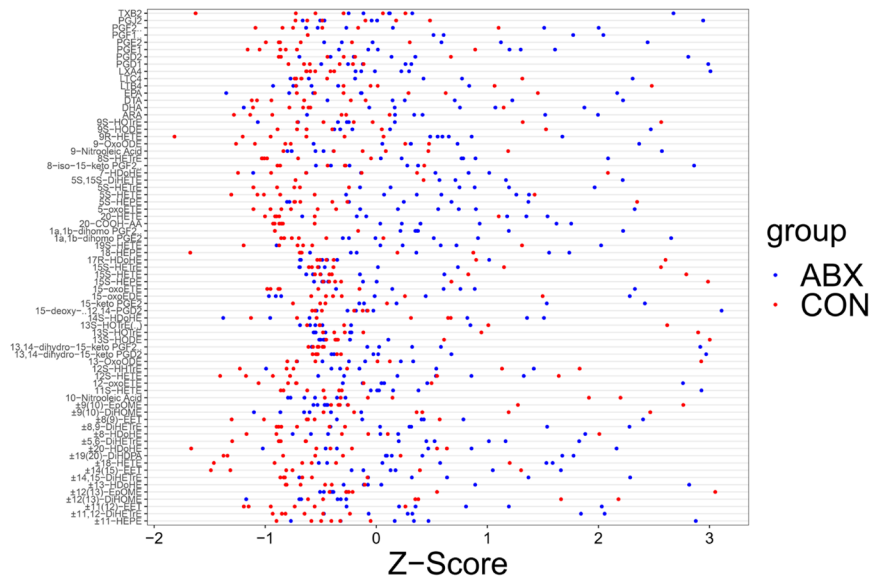


Figure S3. Histogram of replacement test results for OPLS-DA model. The horizontal coordinate represents the accuracy of the replacement test random model, and the vertical coordinate represents the number of random models. The red bar represents the number of occurrences of Q2 value obtained from the replacement test, and the blue bar represents the number of occurrences of R2Y value obtained from the replacement test. The p-value is the ratio of the number of stochastic models in the permutation test that outperforms the original model divided by the number of all stochastic models in the permutation test. The model is considered optimal when the p-value is less than 0.05.

A



B



C

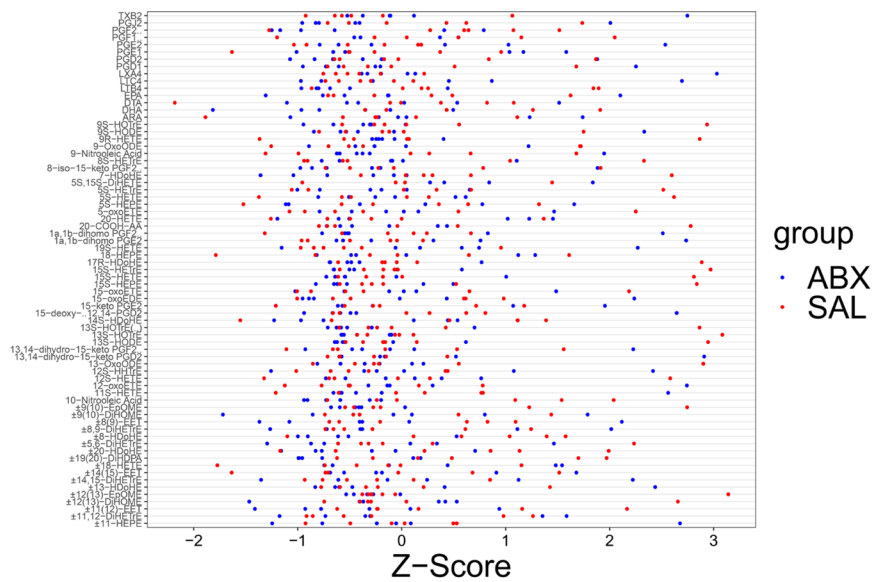


Figure S4. Relative values of the Z-score for the three comparison groups (SAL vs. CON, ABX vs. CON, and ABX vs. SAL). Only the top 20 substances with up- and down-regulated multiples in each comparison group are shown here. The abscissa represents the Z-score, the ordinate represents the metabolites, and the points of different colors represent the samples of various groups.

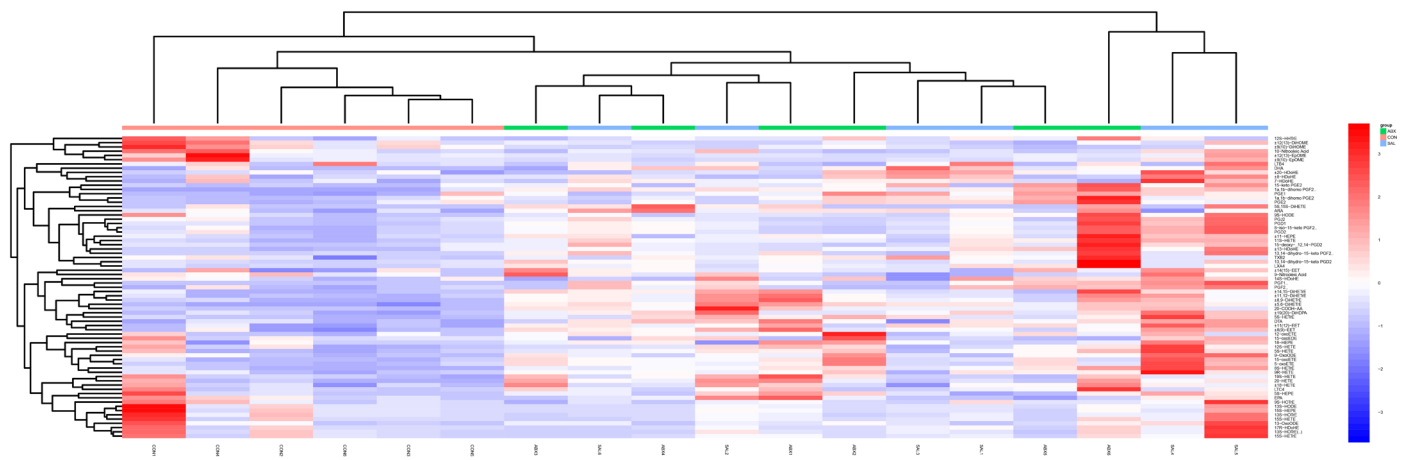
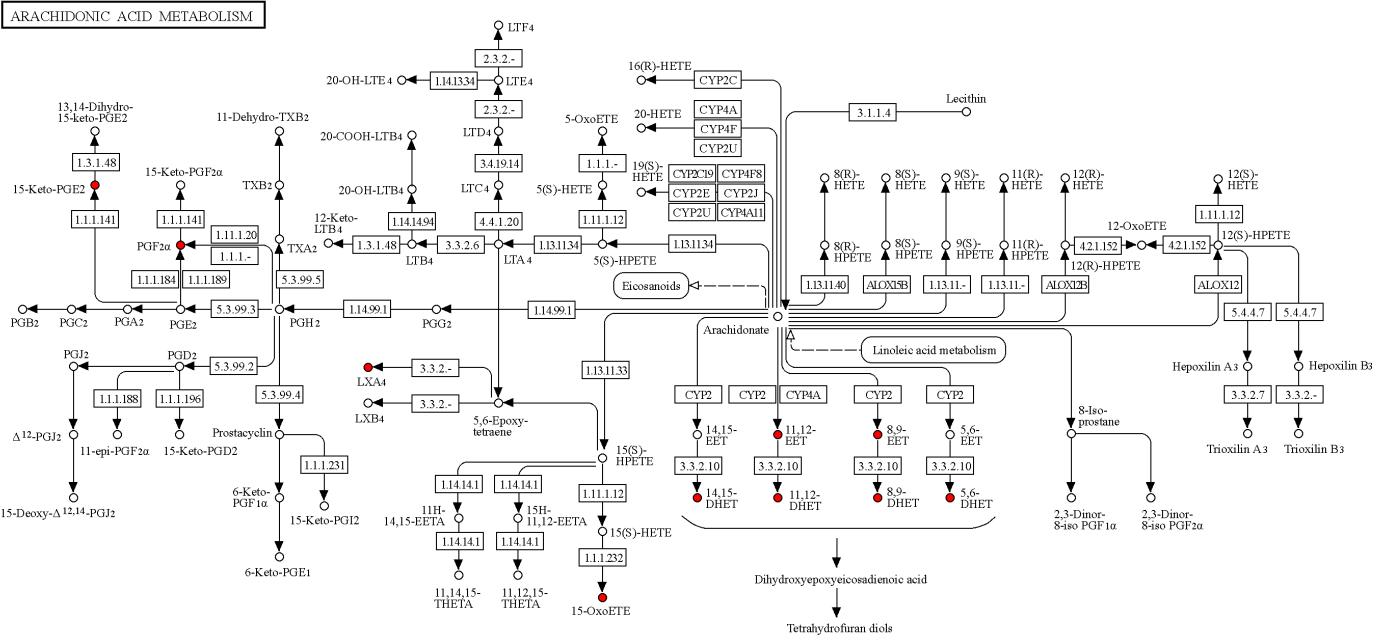


Figure S5. Results of metabolite cluster analysis. The horizontal coordinates in the graph represent different experimental groups, the vertical coordinates represent the metabolites compared in the group, and the colored blocks in various positions represent the relative expression of the metabolites in the corresponding positions. Red indicates that the substance is highly expressed in the group in which it is contained, and blue means that the substance is lowly expressed in the group in which it is included.

A SAL vs. CON



B ABX vs. CON

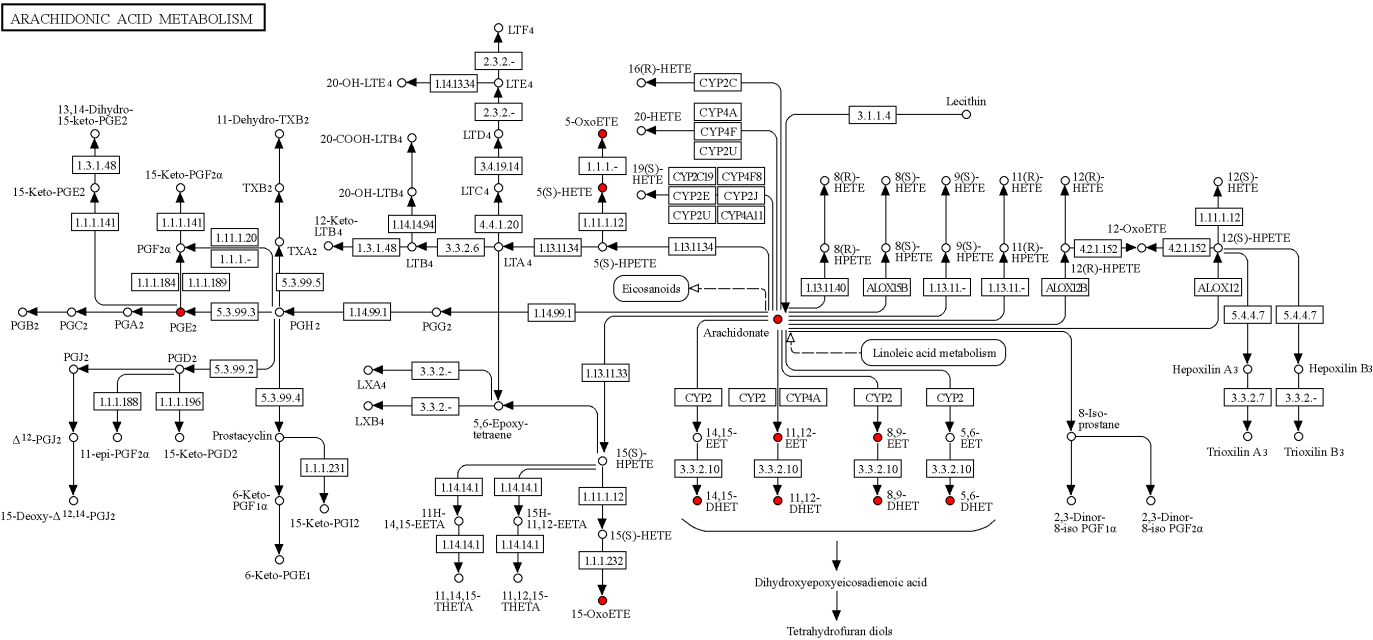


Figure S6. KEGG enrichment pathway map of the differential metabolites in the SAL and ABX groups. (A) KEGG enrichment analysis of the differential metabolites in the SAL group. (B) Results of KEGG enrichment analysis of the differential metabolites in the ABX group. Red represents significant metabolite upregulation.

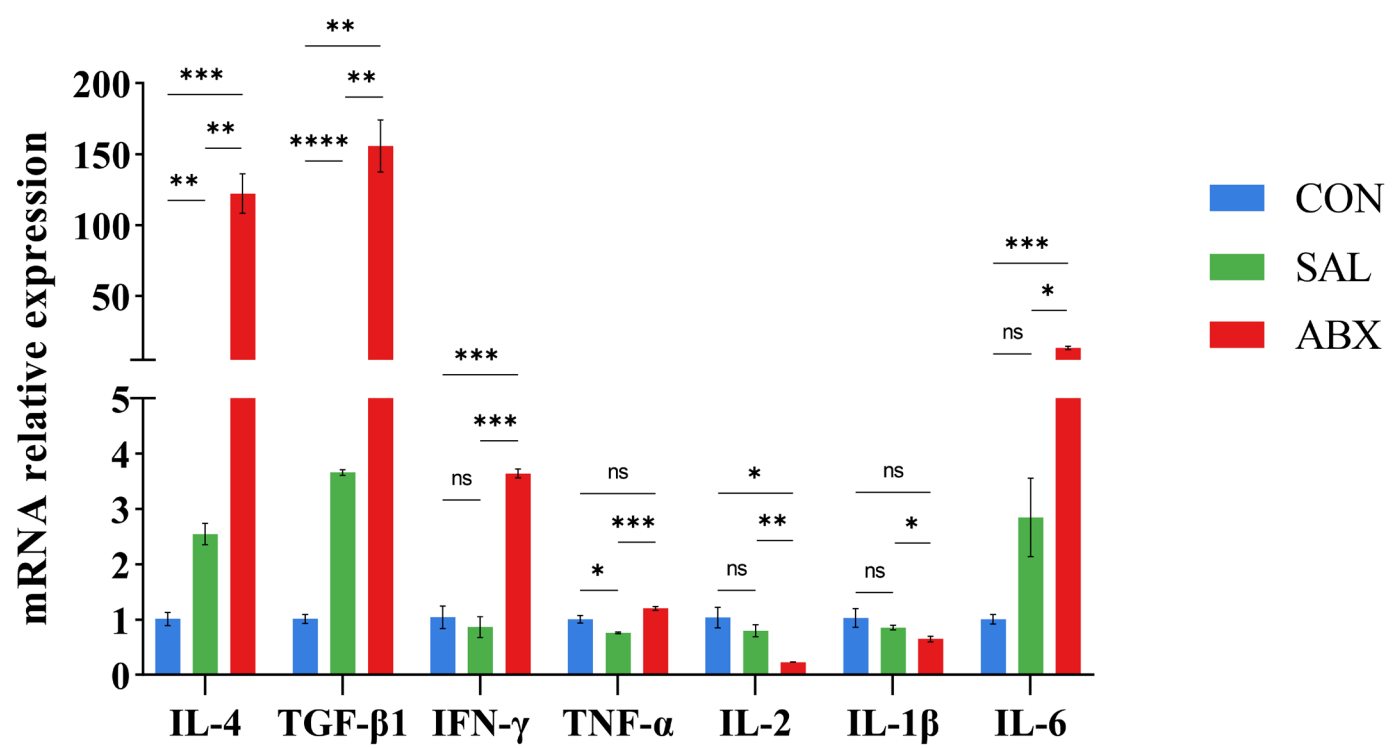


Figure S7. Relative mRNA levels of inflammatory factors in cecum tissue. “*” indicates a significant difference in statistics (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

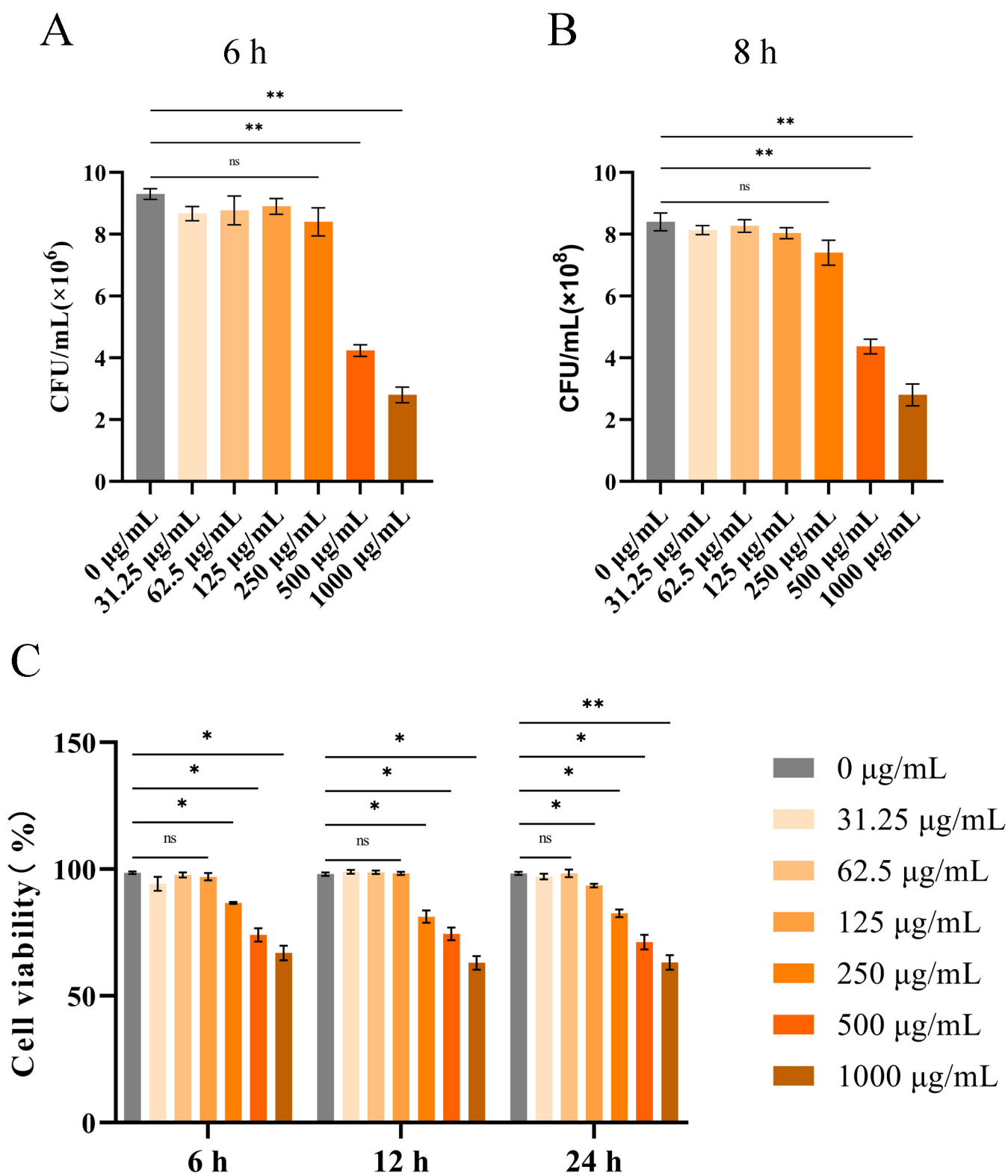


Figure S8. Effect of different concentrations of aspirin at different treatment times on the activity of HD11 cells and *S. Typhimurium*. “*” indicates a significant difference in statistics (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

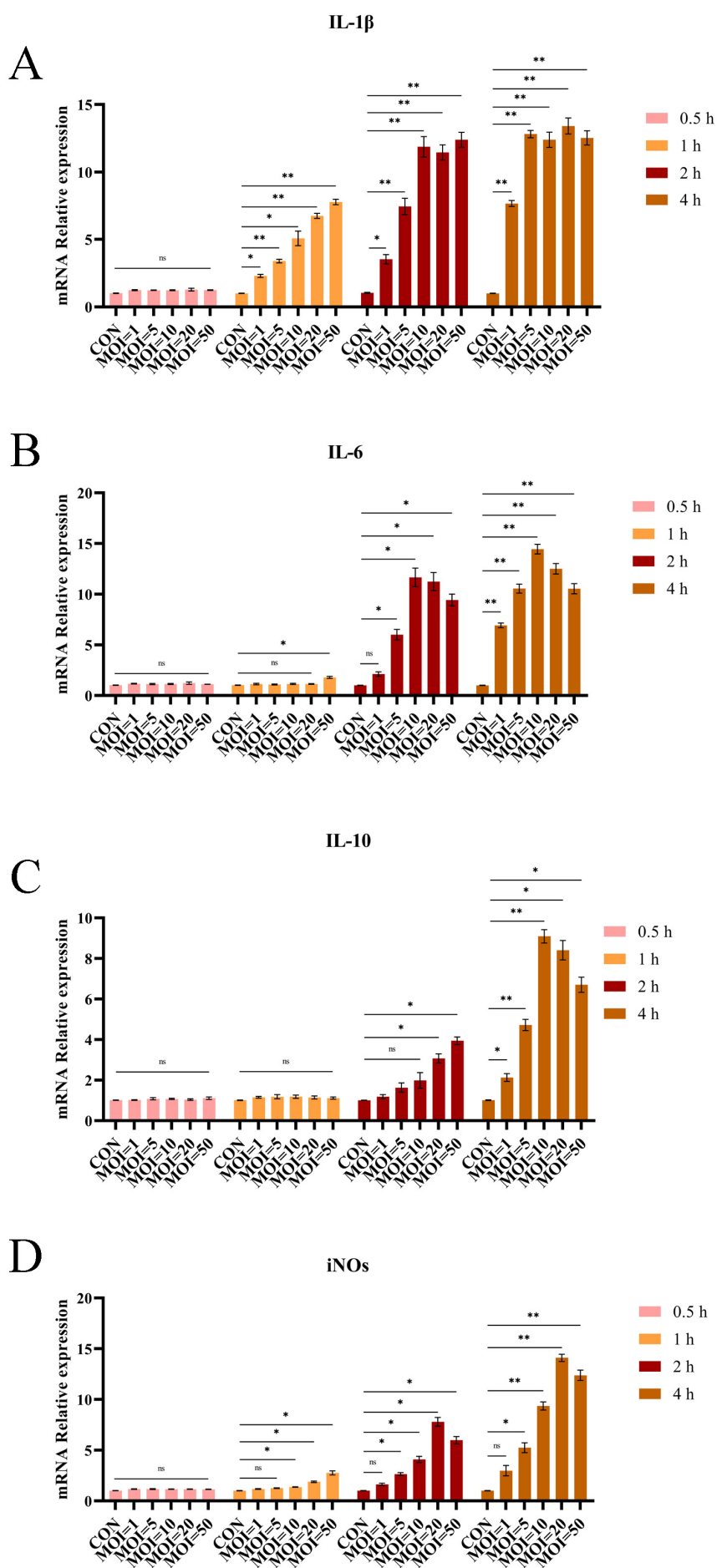


Figure S9. Effect of different infection multiplicities of *S. Typhimurium* on inflammation-related gene expression in HD11 cells within a time gradient. “*” indicates a significant difference in statistics (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).