

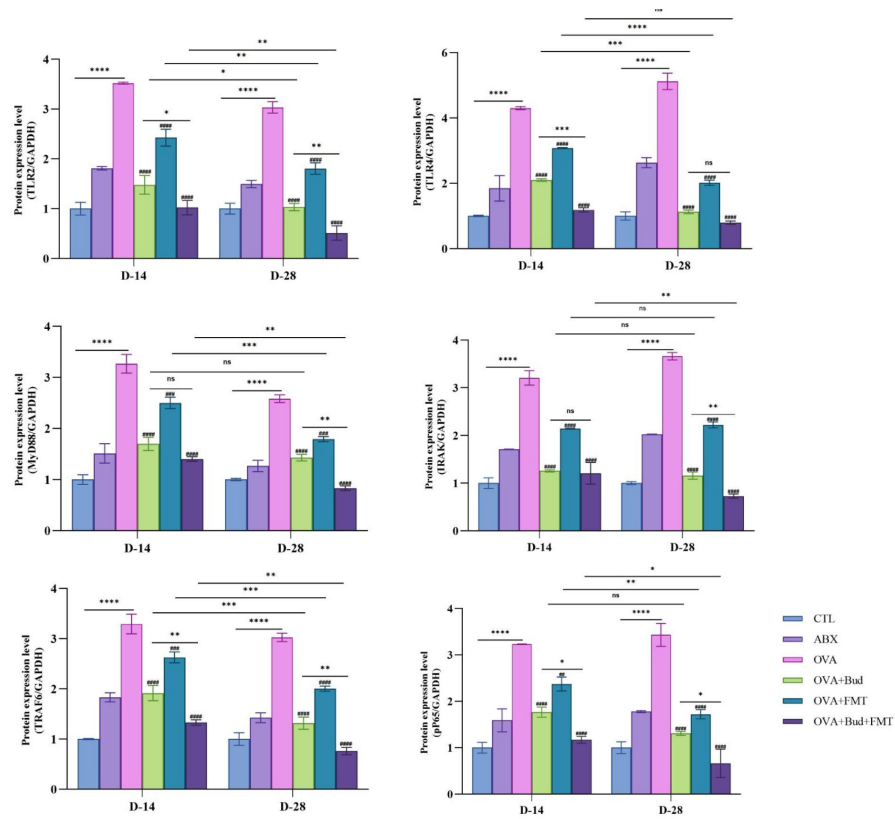


Figure S1. Relative protein expression levels of TLR4, TLR2, IRAK, MyD88, TRAF6 and p-P65 in lung tissues at D-14 and D-28.

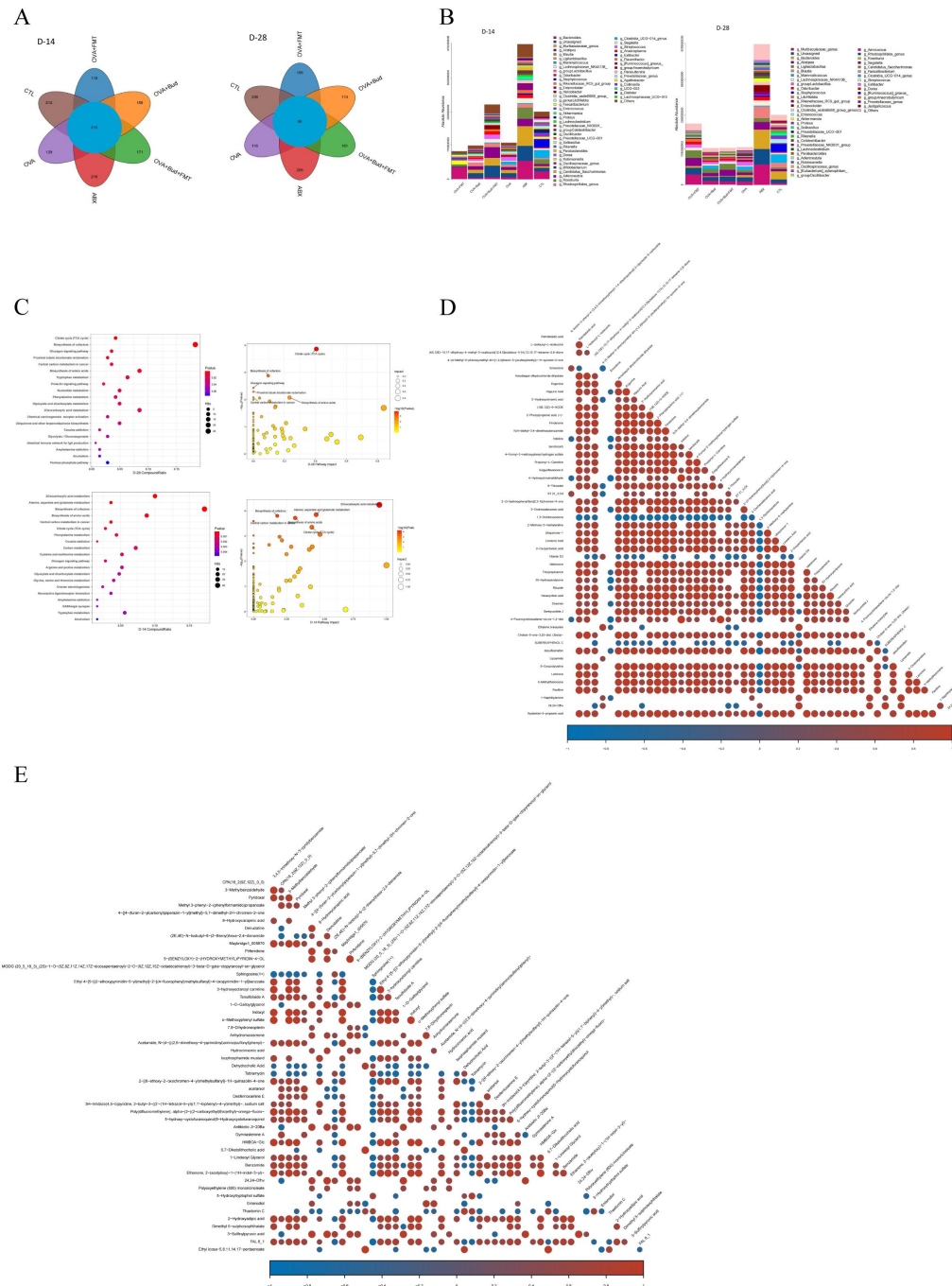


Figure S2. (A) Venn diagrams showing shared and unique OTUs among different groups at D-14 and D-28. (B) Relative abundance of GM at the genus level at D-14 and D-28. (C) Metabolic pathway enrichment analysis was performed based on differential metabolites at D-14 and D-28. The left panels display enriched pathways ranked by compound ratio and statistical significance, where dot size represents the number of matched metabolites (hits) and color indicates adjusted P values. The right panels show pathway topology analysis, with the x-axis representing pathway impact and the y-axis indicating $-\log_{10}(P \text{ value})$. (D) Correlation heatmap of significantly altered metabolites. Red and blue colors indicate positive and negative correlations, respectively, with color intensity reflecting the strength of the correlation.