

Figure S1 Structural analysis of rumen microbial communities **(A)** Core-pan gene dilution curves; **(B)** Venn diagram of genes among the three groups; **(C)** PCA analysis; **(D)** Anosim analysis graphs.

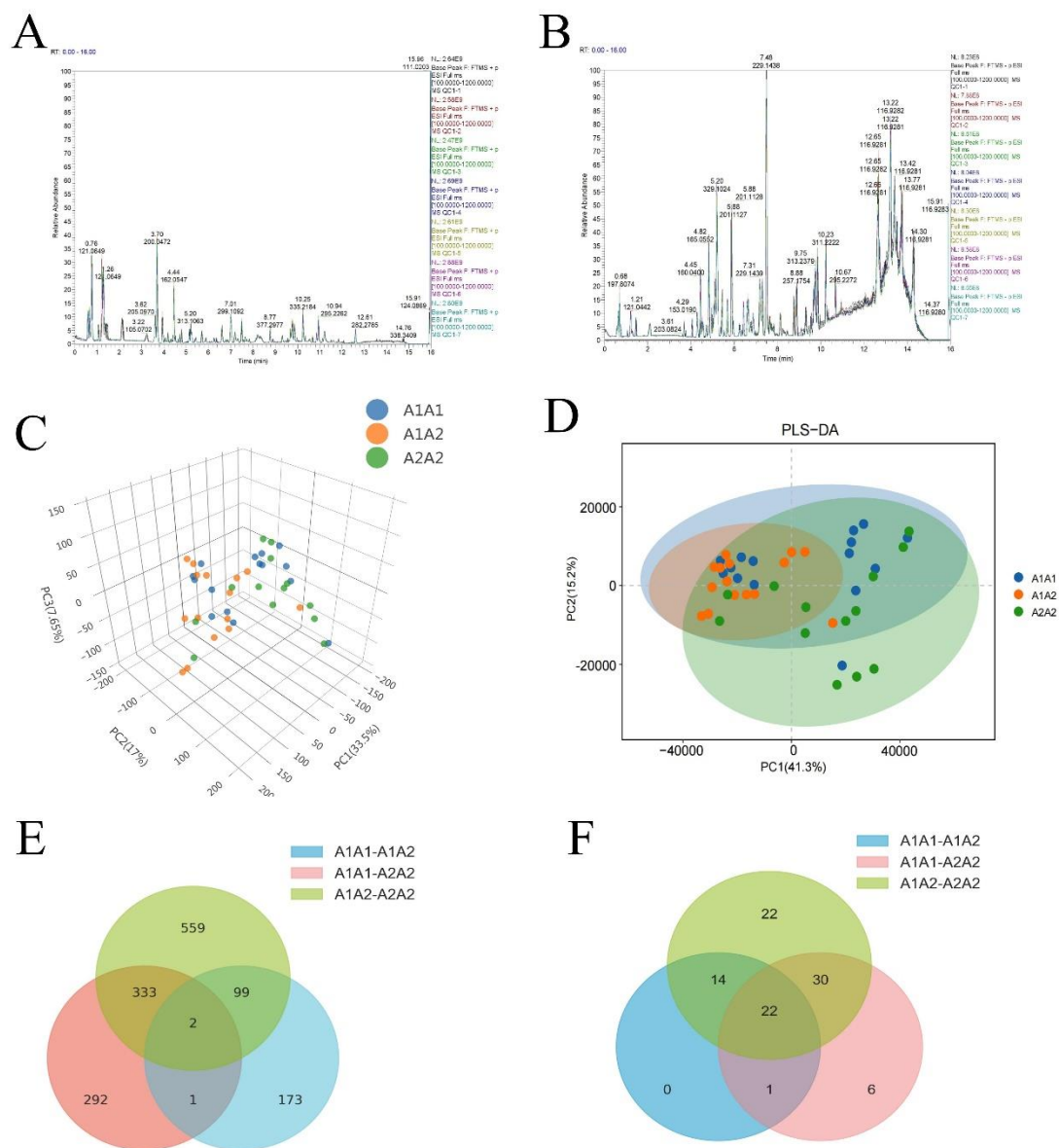


Figure S2 The TIC plot in **(A)** Positive and **(B)** Negative ion mode **(C)** PCA of the three metabolomes; **(D)** PLS-DA of the three metabolomes; **(E)** Wayne plots of the three differential metabolites; **(F)** Wayne plots of the three differential metabolic pathways.

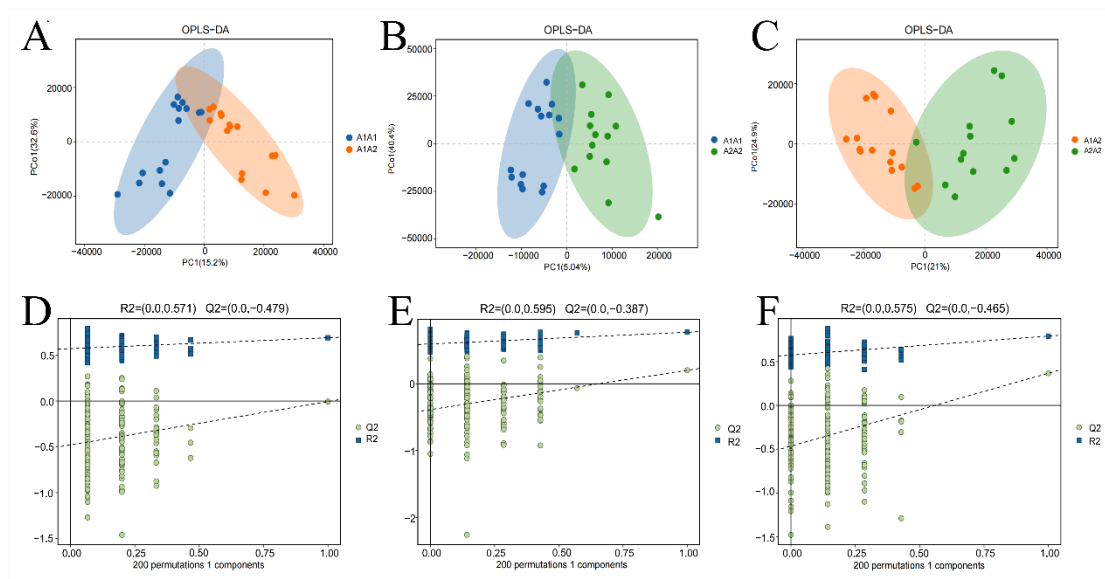


Figure S3 (A-C) OPLS-DA of rumen metabolites for groups A1A1, A1A2, and A2A2; (D-F) OPLS-DA replacement test plots (Further replacement tests of the OPLS-DA model for positive and negative ion pattern data showed that the model was valid for evaluation).

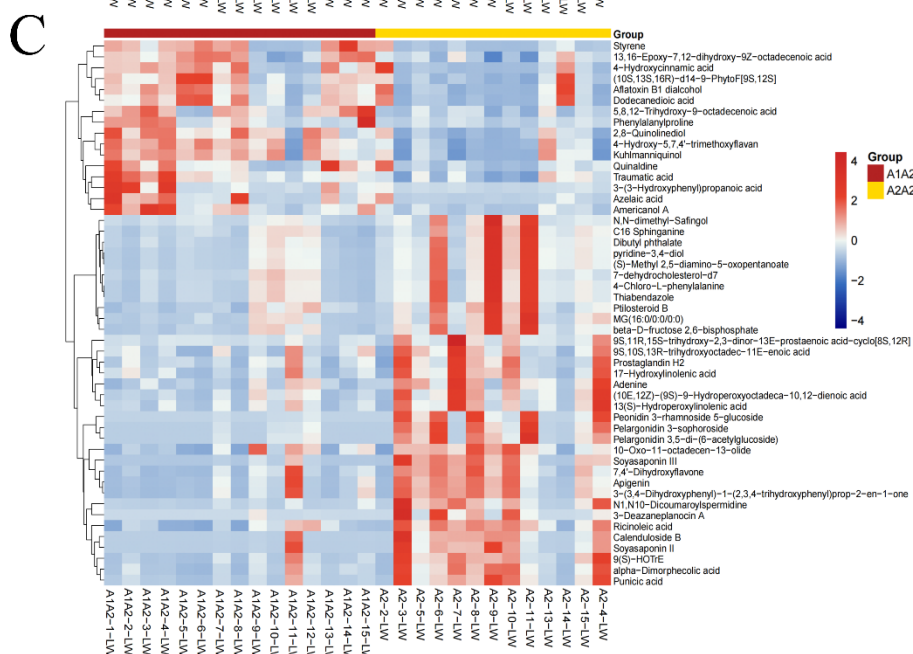
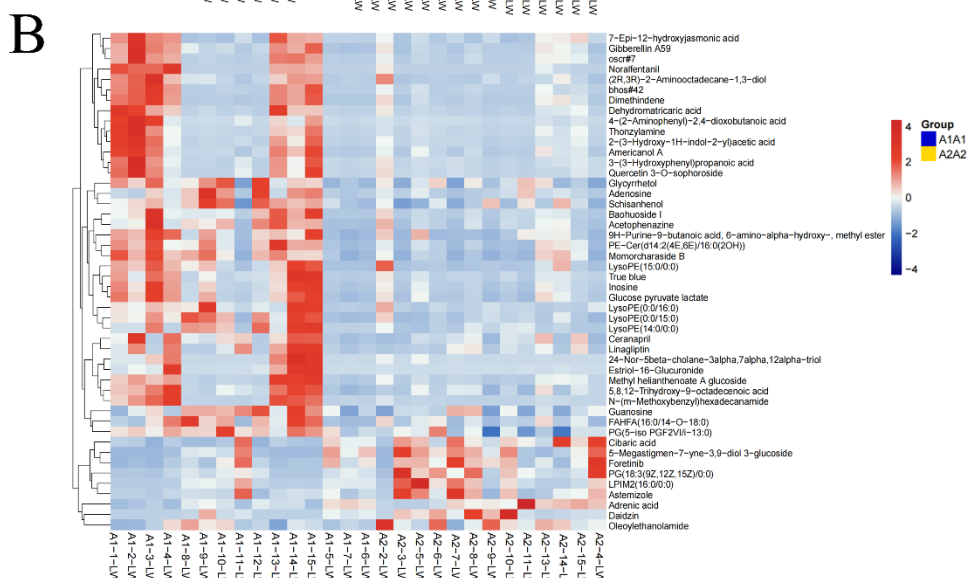
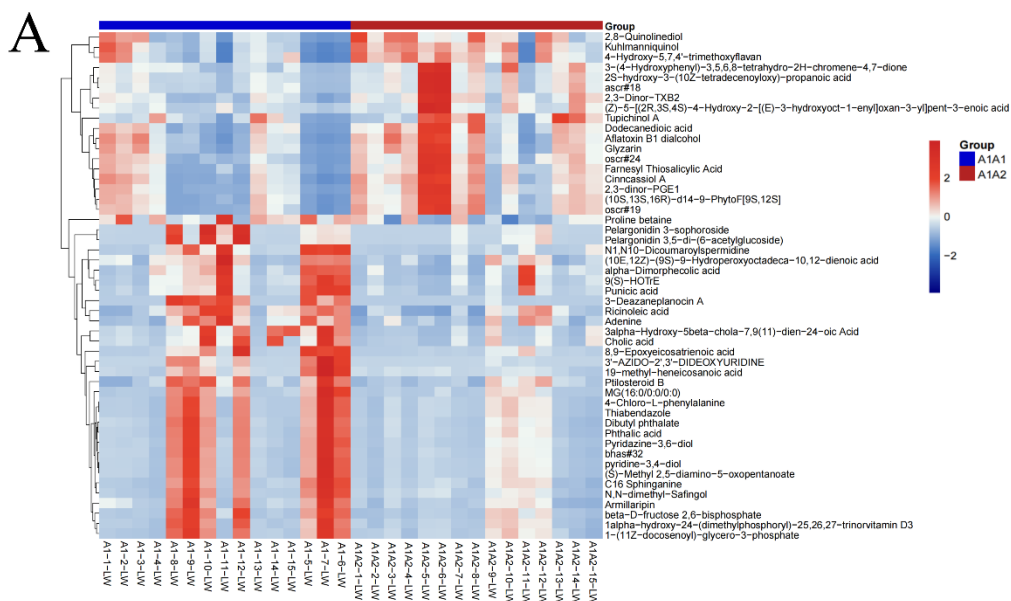


Figure S4 **(G-I)** Differential hierarchical cluster analysis of the top 50 metabolites of rumen metabolites in groups A1A1, A1A2 and A2A2 (heat map).

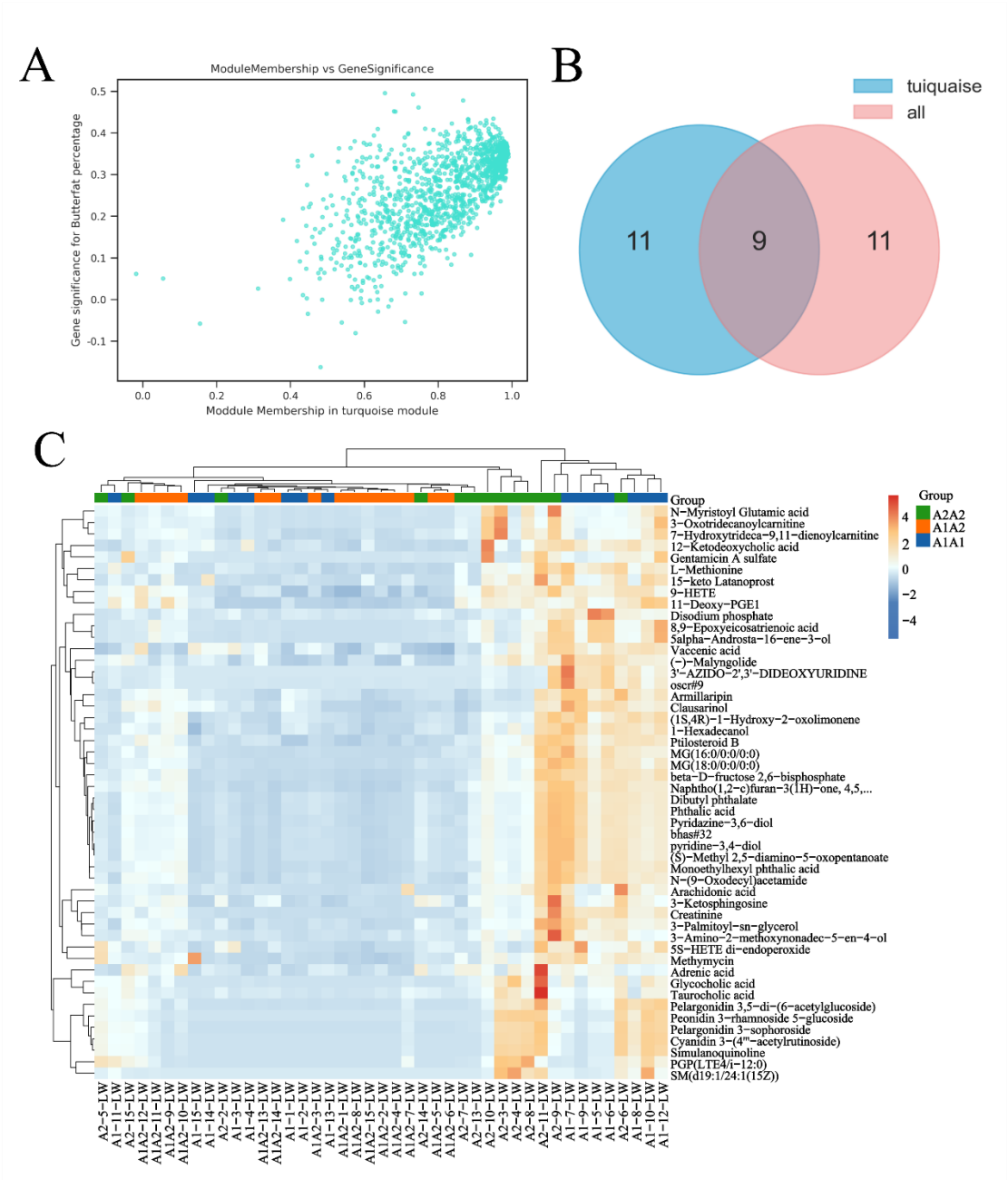


Figure S5 **(A)**Scatter plot of metabolites versus turquoise module members (MM);**(B)** METurquoise metabolite set enrichment analysis (heatmap); **(C)** Wayne plots of METurquoise top 20 differential metabolic pathways and top 20 differential metabolic pathways among the three groups.

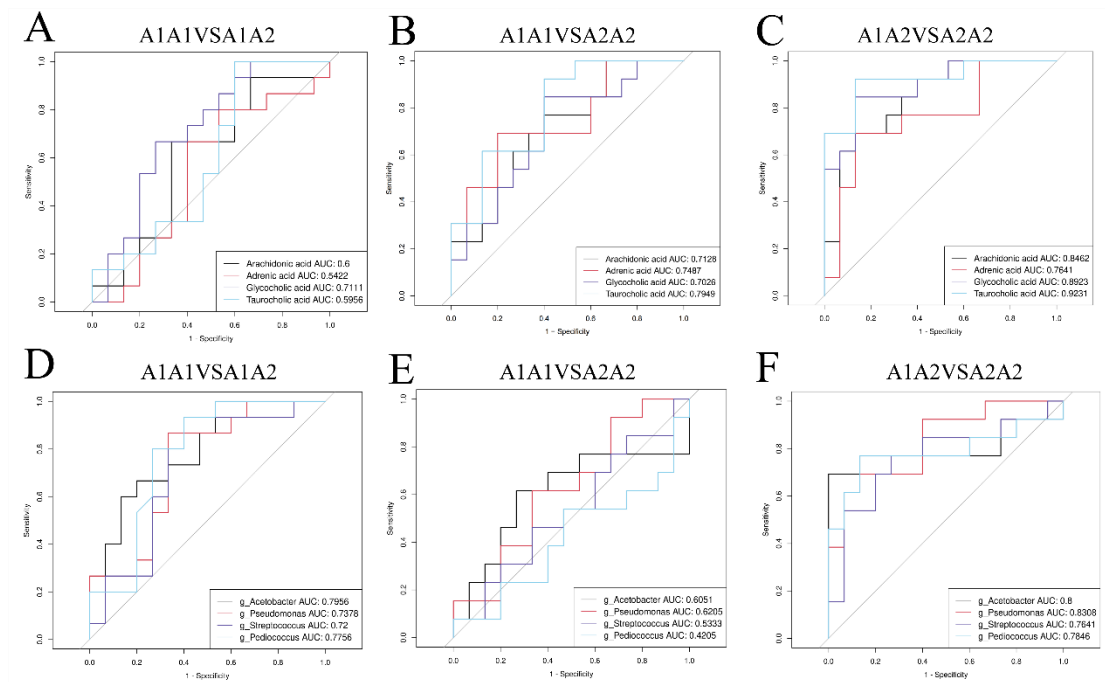


Figure S6 (A-C) ROC curves of AA, AdA, GCA, and TCA; (D-F) ROC curves of *g\_Acetobacter*, *g\_Pseudoxanthomonas*, *g\_Streptococcus* and *g\_Pediococcus*.