

Table S1. Complete list of differential metabolites identified by untargeted metabolomics in rumen fluid of Texel-Kazakh crossbred rams (VIP > 1.0, P < 0.05). Detailed data are provided in the supplementary file Table_S1_Differential_Metabolites.xlsx.

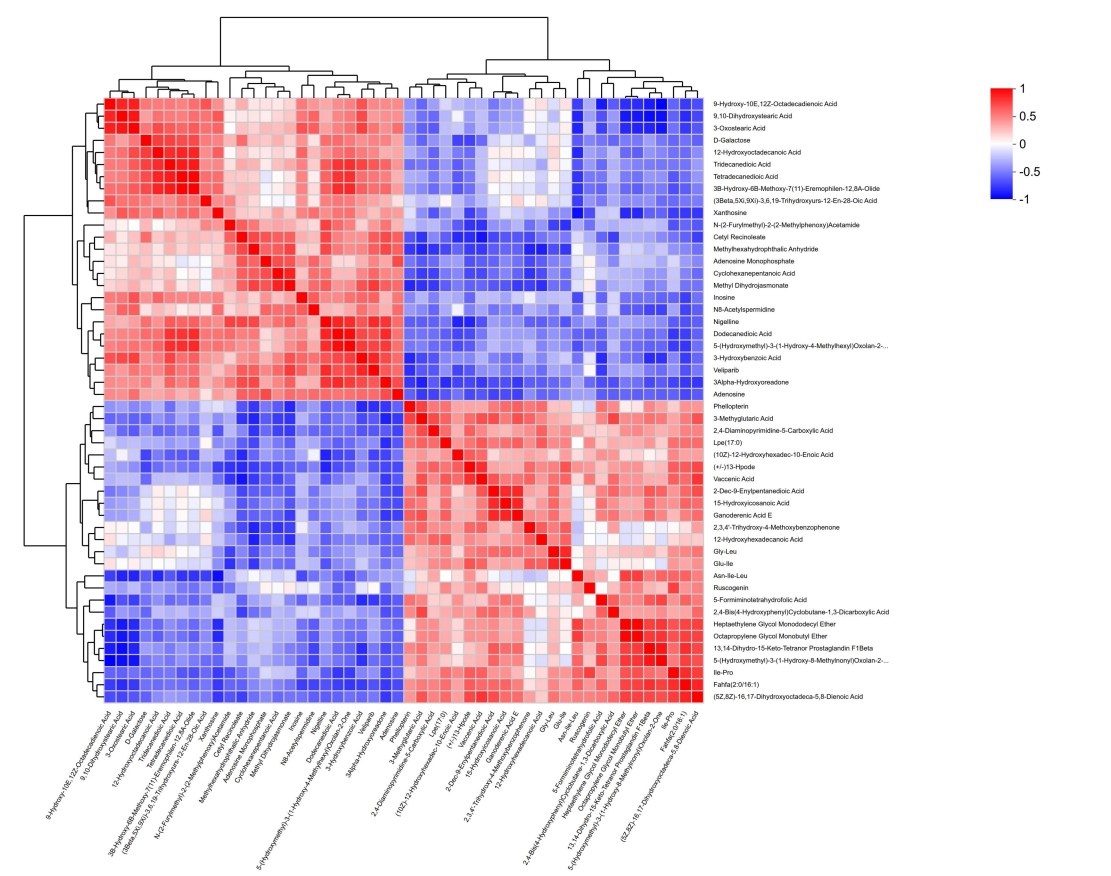


Fig. S1. Hierarchical clustering heatmap of the top 50 differential metabolites ranked by VIP value in rumen fluid of Texel-Kazakh crossbred rams. Rows represent metabolites and columns represent individual samples (n = 10 per group). Color scale indicates Z-score normalized metabolite abundance (red, high abundance; blue, low abundance). Dendrograms on the left and top display hierarchical clustering results of metabolites and samples, respectively. CON = control group; THY = thymol group.

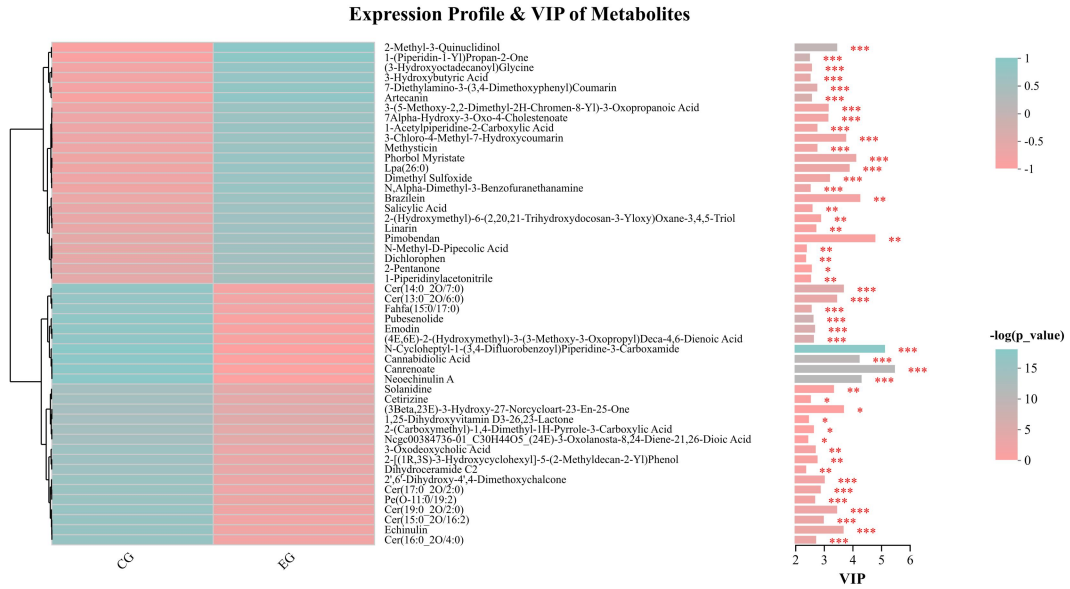


Fig. S2. Expression profile and VIP analysis of the top 50 differential metabolites in rumen fluid of Texel-Kazakh crossbred rams. The heatmap on the left displays relative expression levels of the top 50 differential metabolites across individual samples (red, high expression; blue, low expression). The bar chart on the right shows the VIP value of each metabolite, with bar length representing the contribution of each metabolite to between-group discrimination. Bar color indicates statistical significance (expressed as $-\log_{10} P$ -value). Asterisks denote significance levels ($P < 0.05$, $*P < 0.01$, $**P < 0.001$). CON = control group; THY = thymol group.

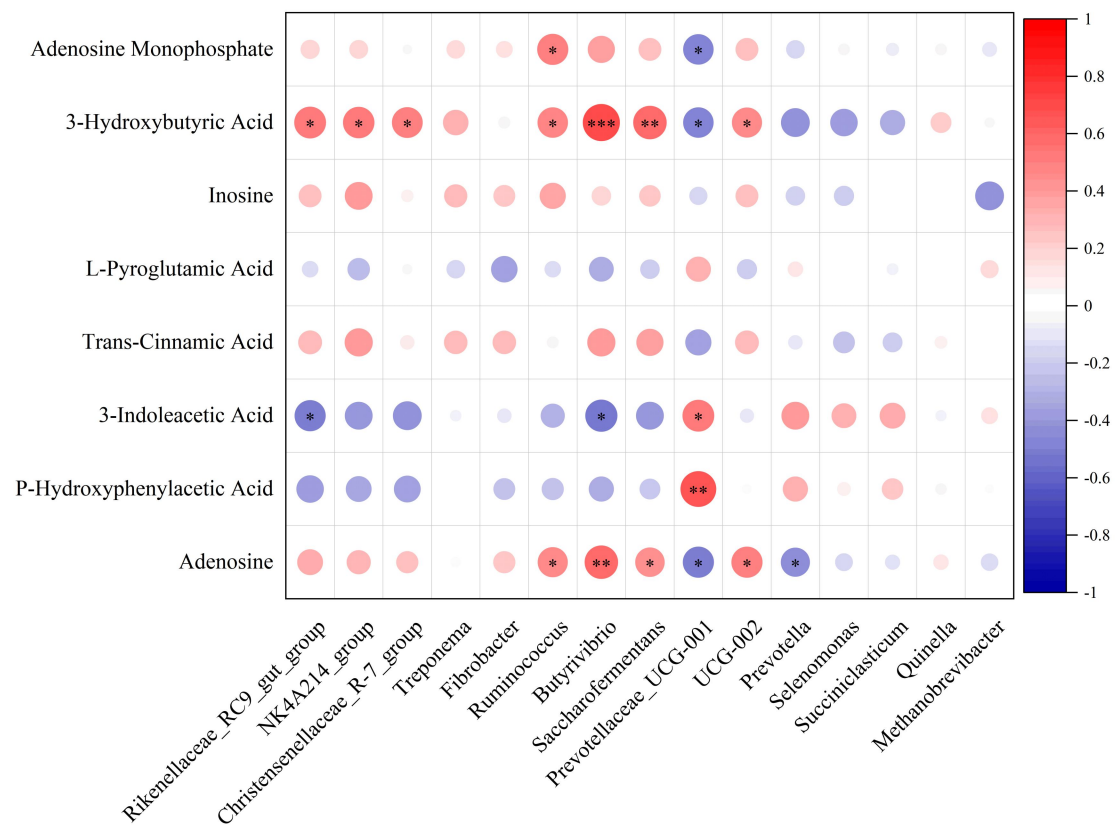


Fig. S3. Spearman correlation heatmap between the 8 key differential metabolites (columns) and 15 core bacterial genera (rows) in rumen fluid of Texel-Kazakh crossbred rams. Metabolites are from significantly enriched KEGG pathways. The color bar on the right indicates the direction of abundance change in the THY group relative to the CON group. $P < 0.05$, $*P < 0.01$, $**P < 0.001$.