

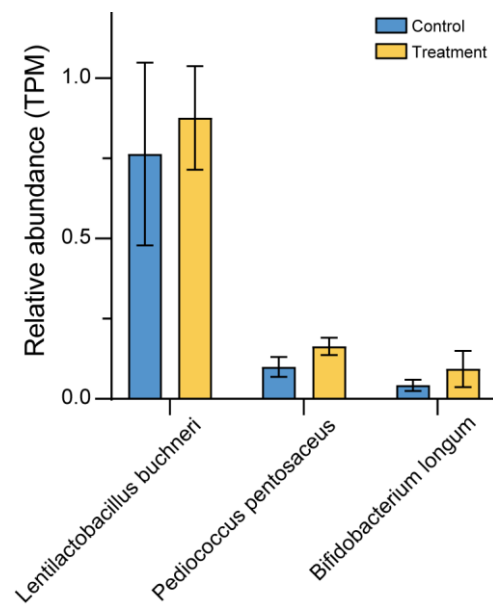


Figure.S1 The relative abundance of DFM in the rumen of Sanhe dairy cow.

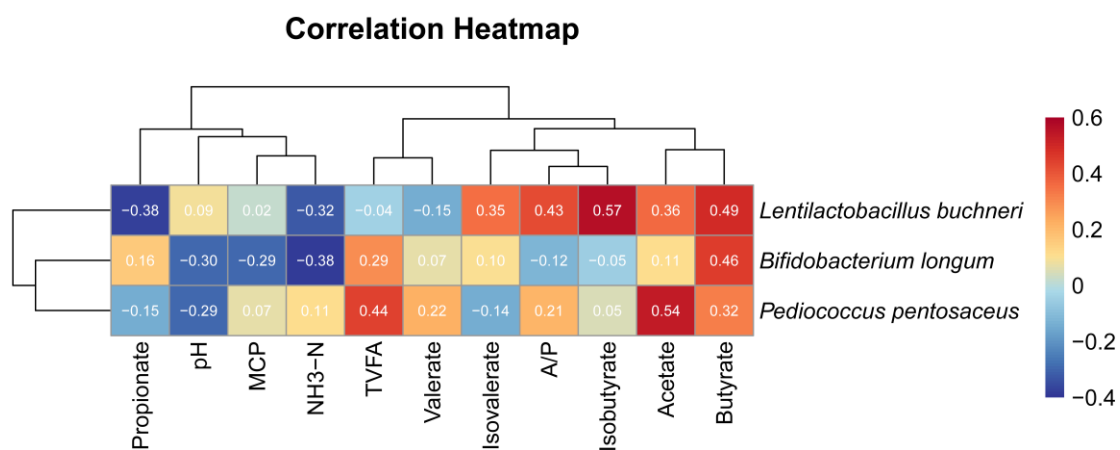


Figure.S2 The spearman correlation analysis between DFM and rumen fermentation parameters. The colors and numbers represent the correlation coefficients between the two.

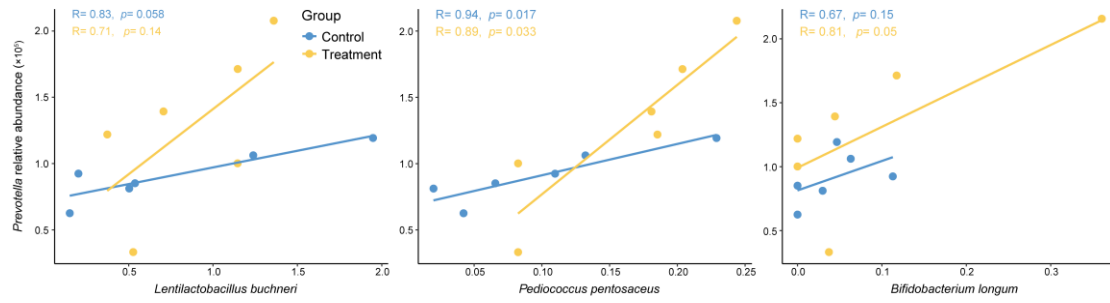


Figure.S3 The spearman correlations between the relative abundance of DFM and *Prevotella*. The blue and yellow line respectively represents the regression line of control and treatment group. Spearman correlation and its statistic significant was calculated using the cor.test function in ggpubr R package.

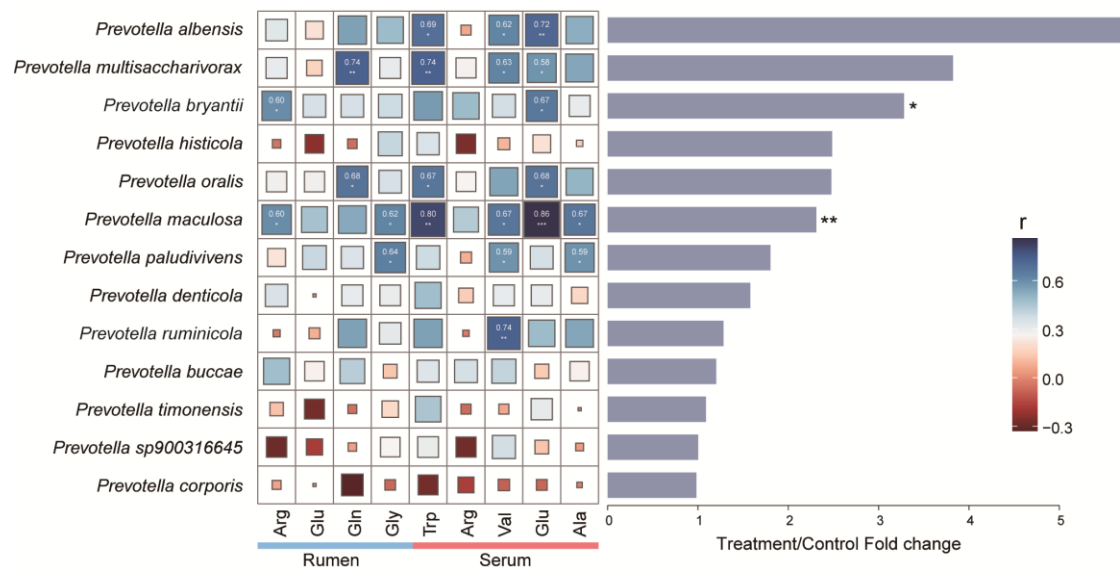


Figure.S4 The associations between significantly enriched amino acids and bacteria associated with milk protein synthesis, with the fold change in the relative abundance of bacteria between the two groups. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

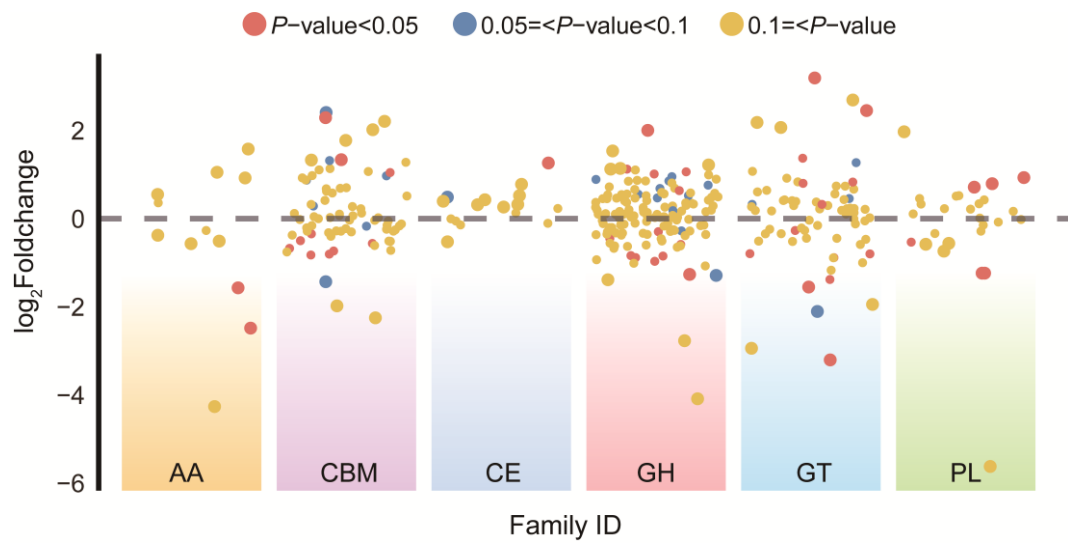


Figure.S5 The differences in relative expression of each enzyme in the six CAZY families, with points enriched above the dotted line in the treatment group and below the dotted line in the control group.

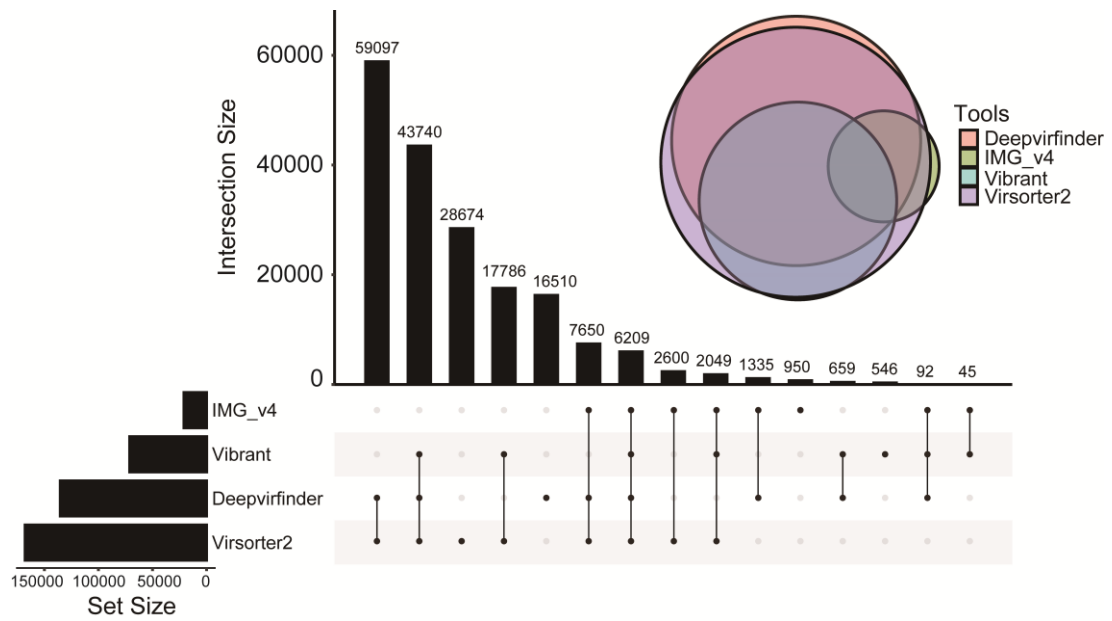


Figure.S6 The overlaps of the viral prediction results using four different methods. The size is the number of predicted virus.

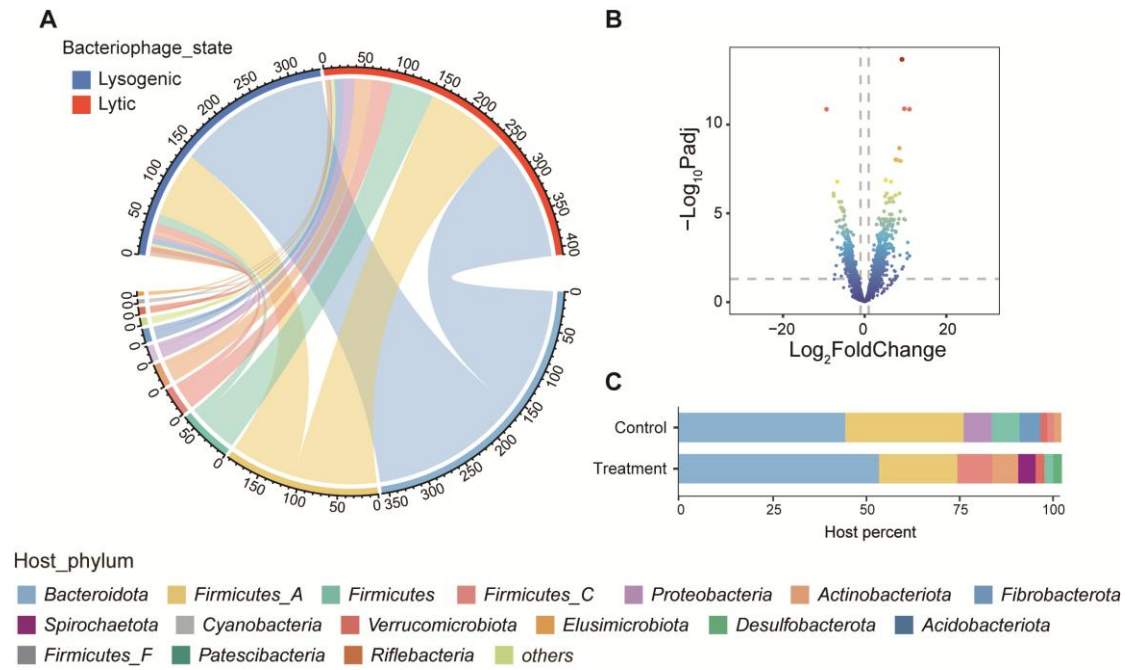


Figure.S7 Viral life state prediction and differential bacteriophage composition between two groups. **A** Lifestyle of bacteriophages infecting different bacteria on phylum level. **B** Differences between the two groups based on bacteriophage rpkms, enriched bacteriophages were distributed on the left in the treatment group and on the right in the control group. **C** Phylogenetic distribution of bacteriophage OTUs significantly different between two groups.