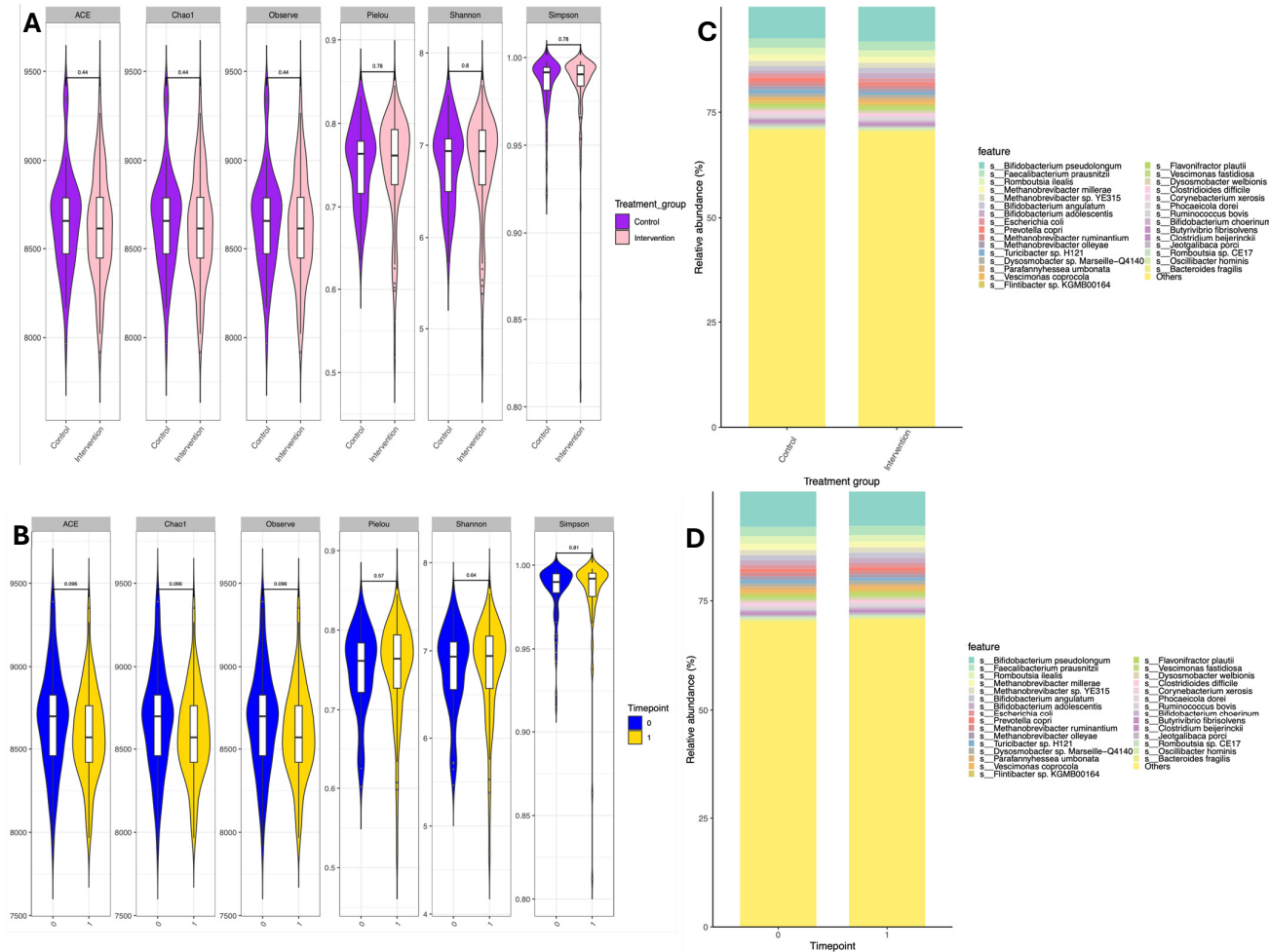
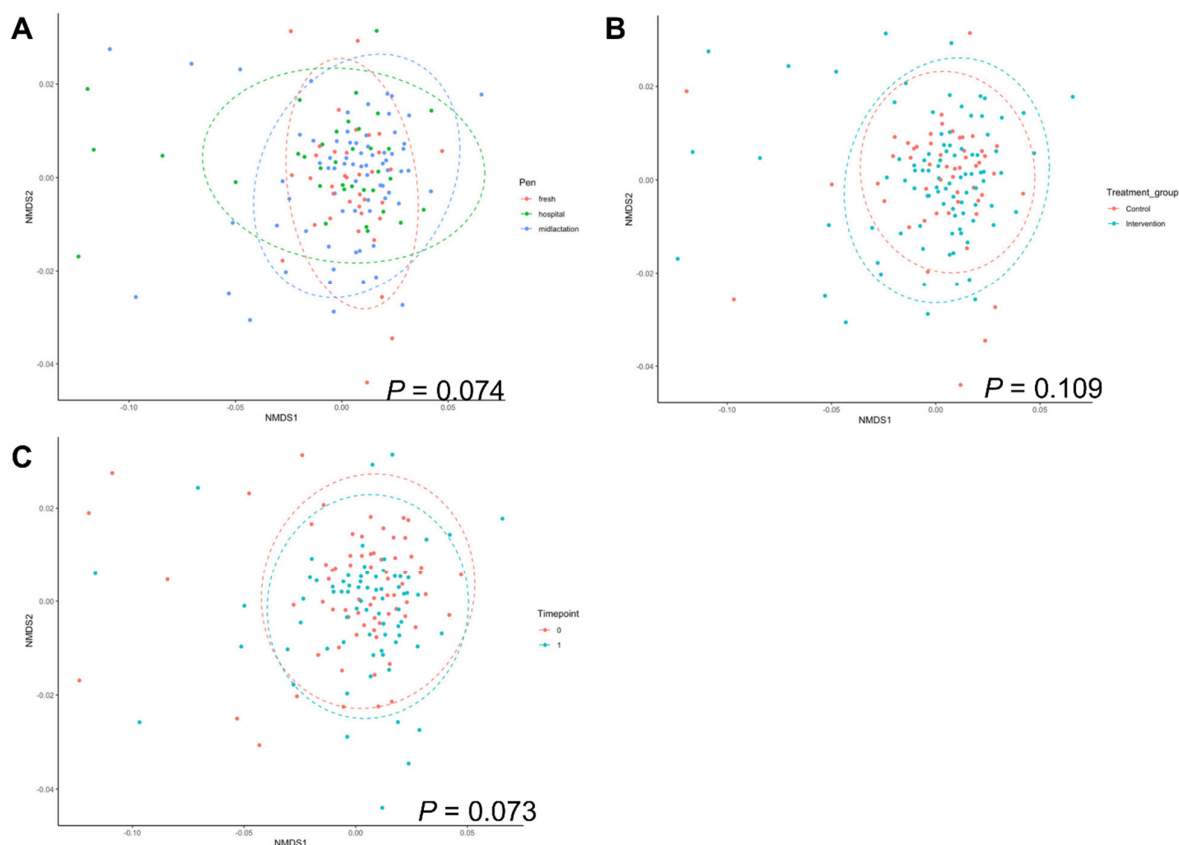


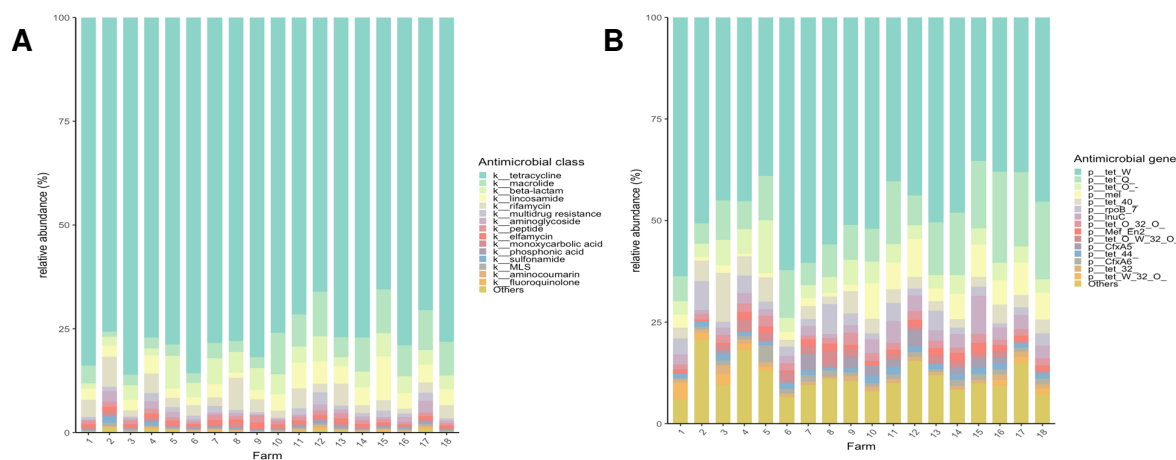
Supplementary Materials



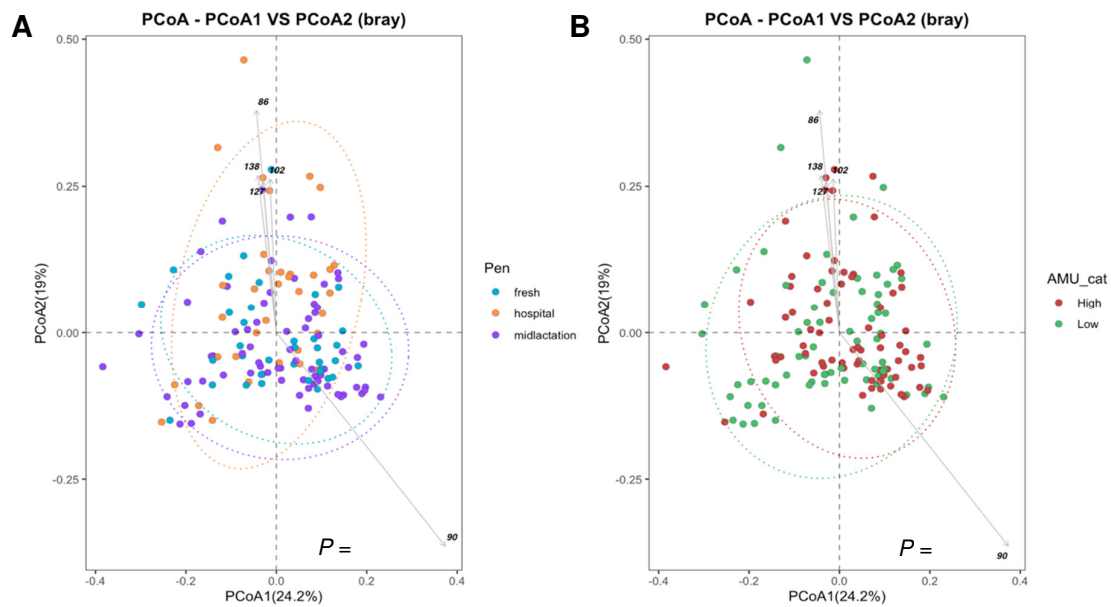
Supplementary Figure S1. Fecal microbiome analysis of pooled samples collected from the fresh cows, hospital, and mid-lactation pens. Alpha diversity at the species level comparing (A). Treatment groups (control, intervention) (B). Sampling time points (Before starting the intervention, T1, 6 months after completing the intervention, T2). P -values represent pairwise comparisons based on the Wilcoxon Sum Rank Test. $P < 0.05$ was considered a significant difference. Relative abundance of the top 30 bacteria species by (C). Treatment groups (control, intervention), (D). Sampling time points (Before starting the intervention, T1, 6 months after completing the intervention, T2).



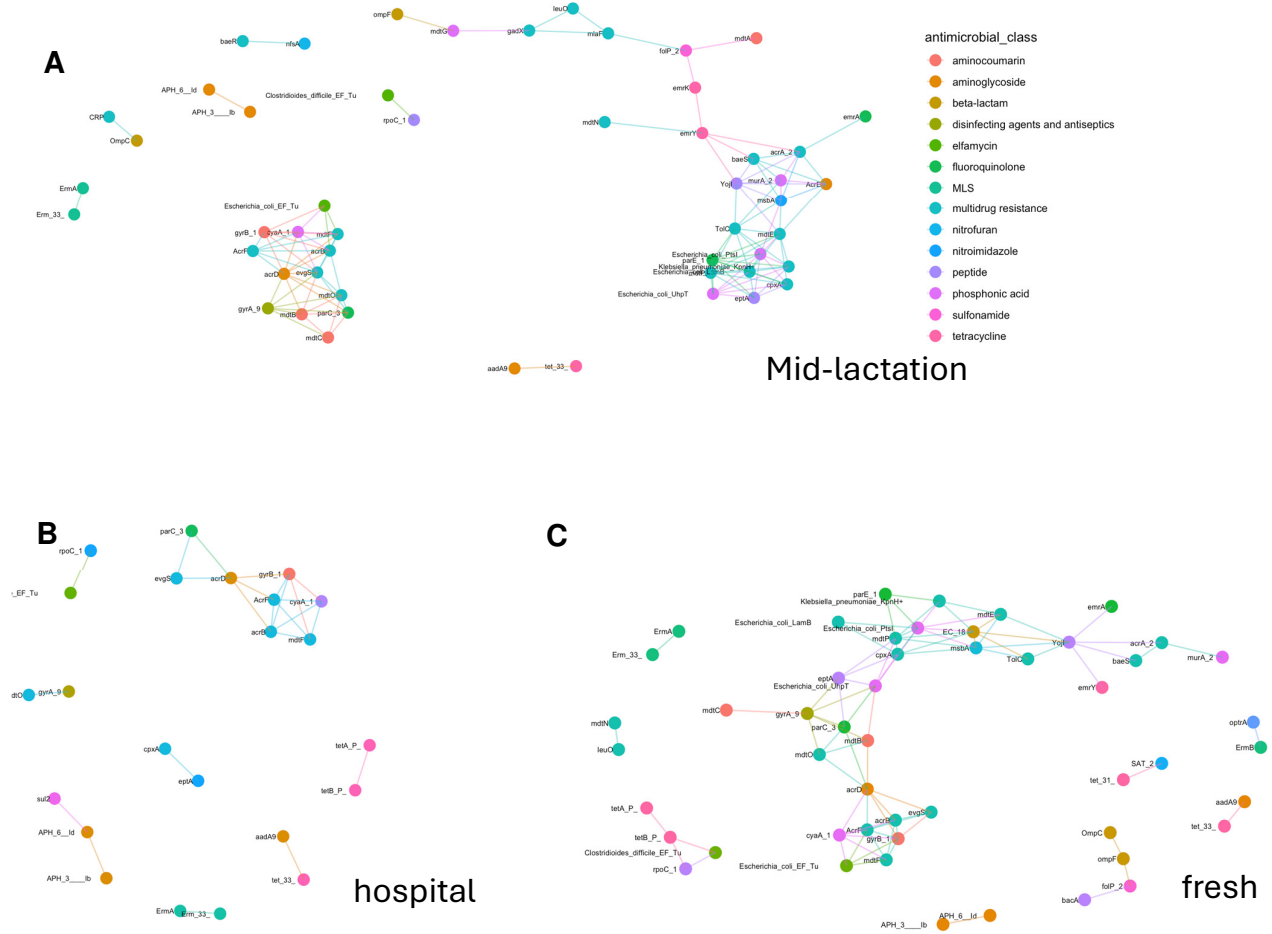
Supplementary Figure S2. Nonmetric multidimensional scaling (NMDS) based on Bray-Curtis dissimilarity of the center log ratio normalized species-level read counts of pooled fecal samples microbiome for (A). Pen (fresh, hospital and mid-lactation), (B). Treatment group (Intervention and control), and (C). Sampling time points (Before starting the intervention, T1, 6 months after completing the intervention, T2). Ellipses correspond to 95% confidence interval. P-values represent PERMANOVA analysis. $P < 0.05$ was considered a significant difference.



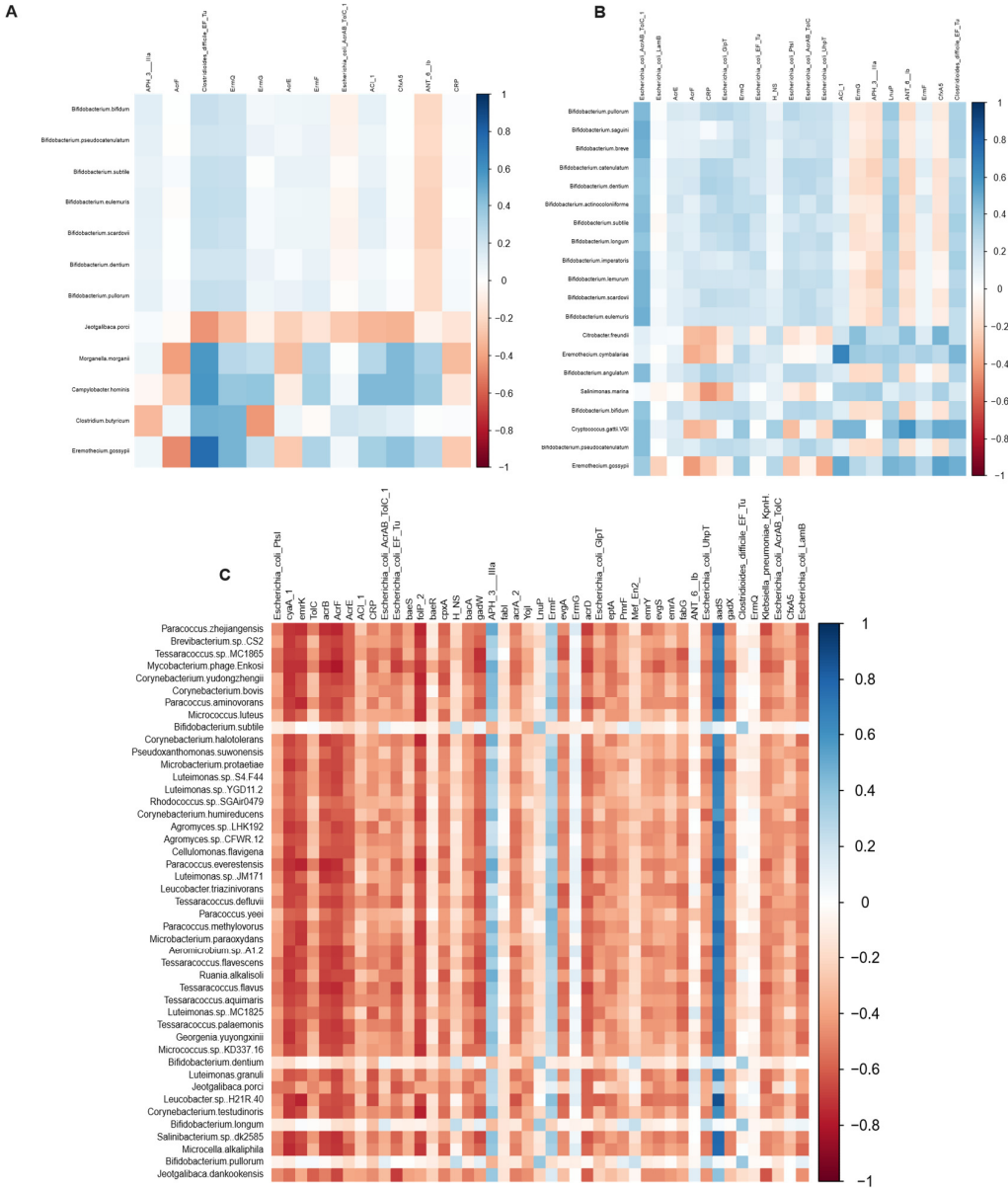
Supplementary Figure S3. Relative abundance of the top 15 (A). Antimicrobial drug classes and (B). Antimicrobial genes presented on pooled fecal samples from dairy cattle stratified by farm of origin. Eighteen farms were included in the study. Farms 1-9 belong to the state of California and 10-18 to the state of Ohio.



Supplementary Figure S4. Principal coordinate analysis (PCoA) based on Bray-Curtis dissimilarity matrix of the center log ratio normalized genes read counts of pooled fecal samples for (A). Pen (fresh, hospital and mid-lactation), (B). Antimicrobial usage level (high and low antimicrobial use at the farm). Ellipses correspond to 95% confidence interval. P-values represent PERMANOVA analysis. $P < 0.05$ was considered a significant difference.



Supplementary Figure S5. Co-occurrence network of antimicrobial resistance genes from pooled fecal samples. Nodes representing AMR genes are color coded by antimicrobial drug class, for (A). mid-lactation, (B). hospital, and (C). fresh cow pens.



Supplementary Figure S6. Correlation plot of antimicrobial resistance genes and bacteria species by (A). Mid-lactation, (B). Fresh, and (C). Hospital pens.