

Additional File 1

Unravelling the complexity of bovine milk microbiome: Insights into mastitis through enterotyping using full-length 16S-metabarcoding

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Supplemental Figures S1 – S4

Figure S1. Rarefaction curves plotting the number of species at different sequencing depths for each sample according to their experimental group. The x-axis represents the sequencing depth in number of reads, and the y-axis show the calculated richness at species level.

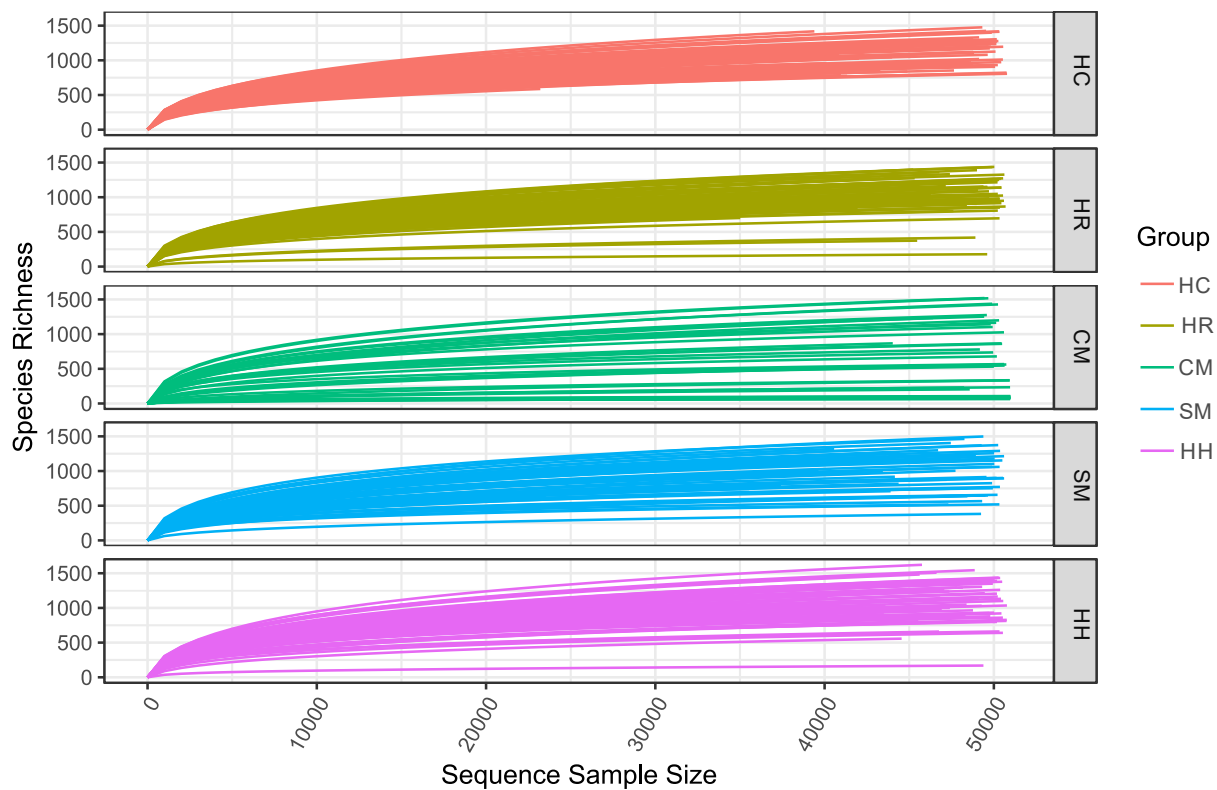


Figure S2. Boxplots showing the alpha diversity indices for species richness (Chao1) and evenness (Shannon) compared between: A) milking phase and B) experimental groups within enterotypes. Each box represent the interquartile range (IQR; Q1 and Q3), with the line inside marking the median. Whiskers extend to the smallest and largest values within 1.5 times the IQR, and points beyond this range considered outliers. Each point represents a sample's diversity score. A non-parametric Kruskal-Wallis test followed by post-hoc Wilcoxon rank sum test was performed for pairwise comparisons. Asterisks denote statistically significant differences (* $p=0.05$; ** $p=0.01$; *** $p=0.001$)

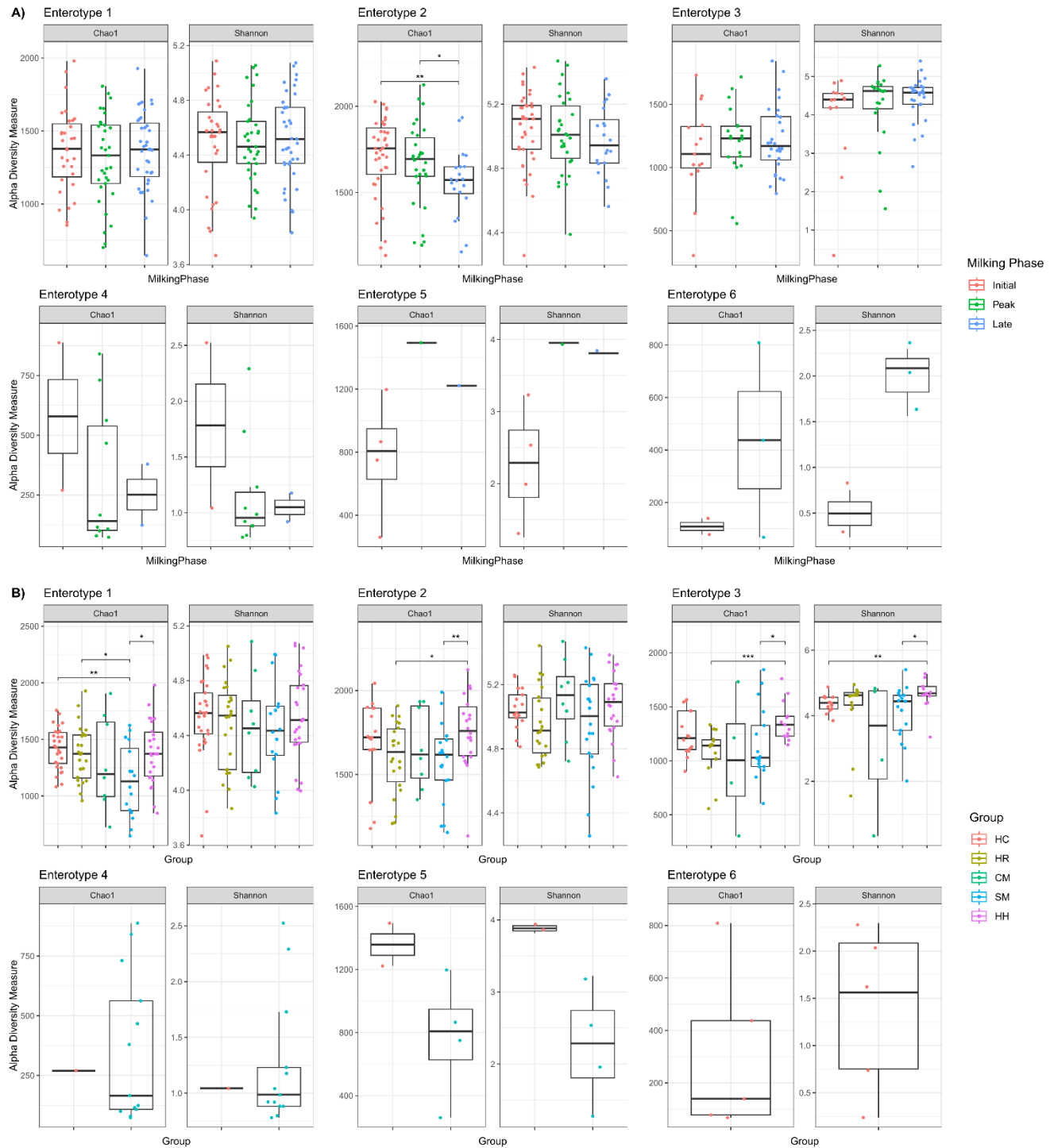


Figure S3. Barplot showing the relative abundance of milk bacterial species in mastitis-associated enterotypes (Enterotypes 4 and 6). The 15 most abundant species within each enterotype are colour-coded according to legend, and the remaining species were grouped into “Other”.

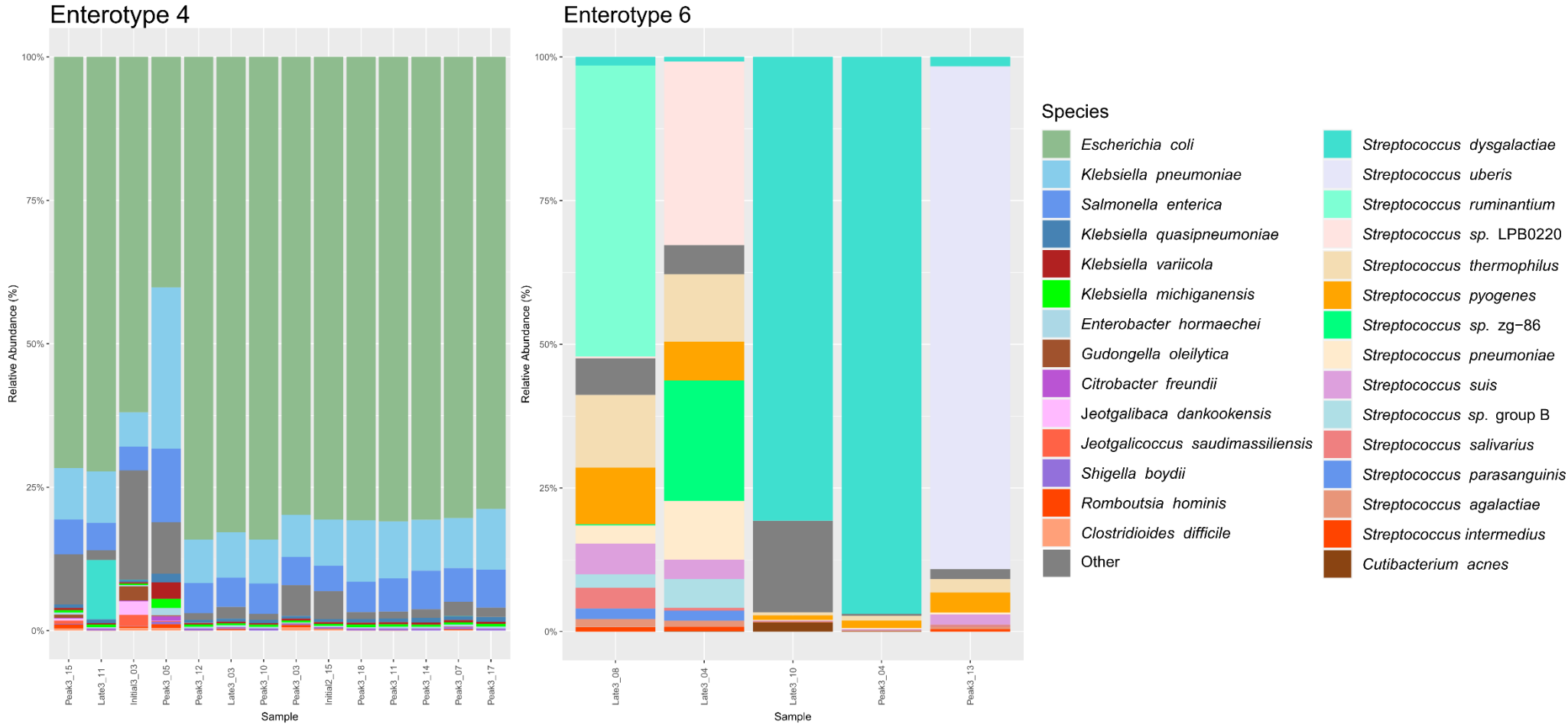


Figure S4. Correlogram displaying significant Pearson correlation coefficients among the top 50 genera, characterised by strong correlations ($p > 0.9$) with at least one other genus. Blank cells indicate non-significant correlations ($p\text{-value} \geq 0.05$). Colours represent correlation coefficient values according to the scale bar provided on the right, while circle sizes are proportional to the magnitude of the correlation coefficients.

