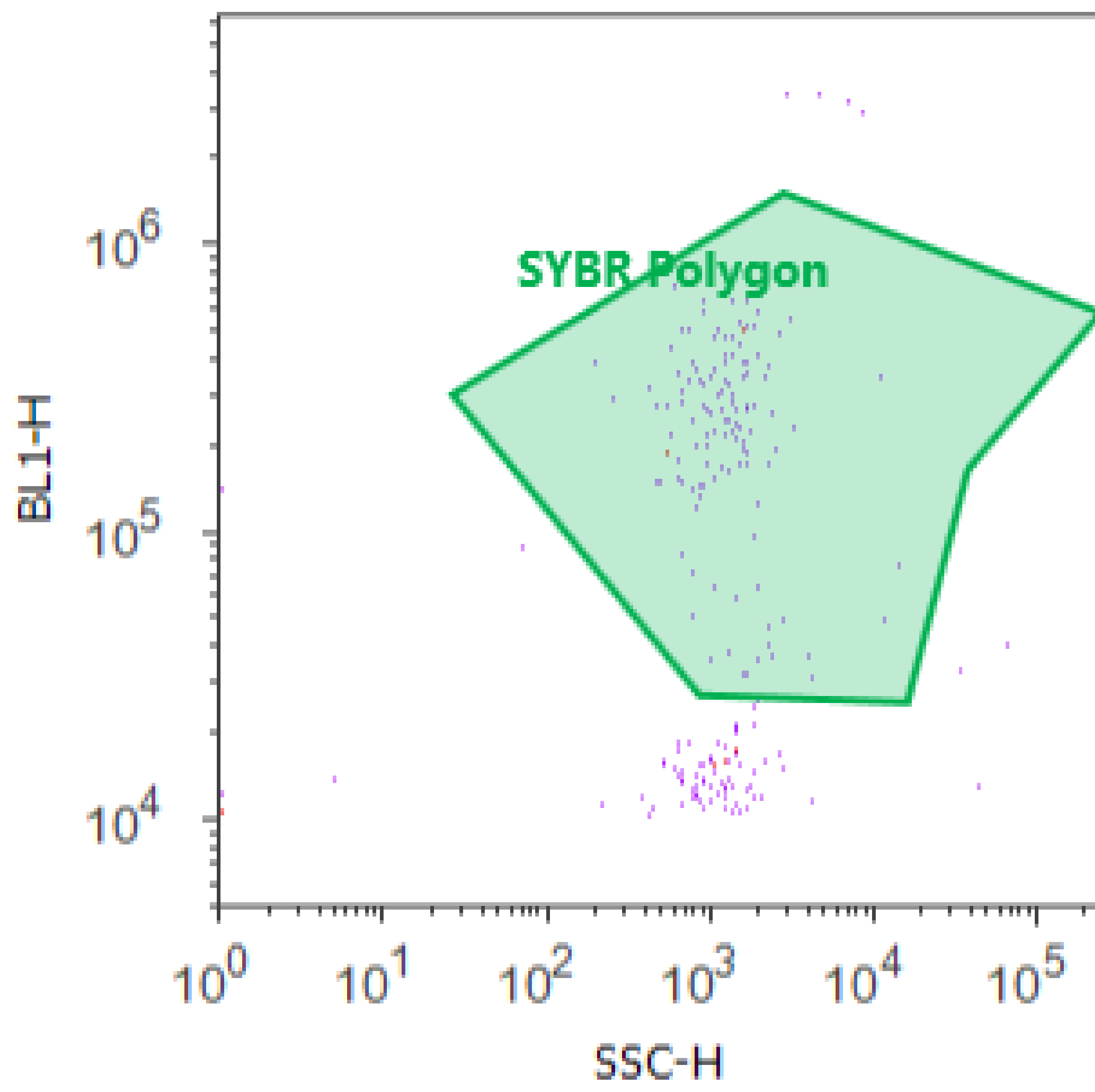


Control



Sample

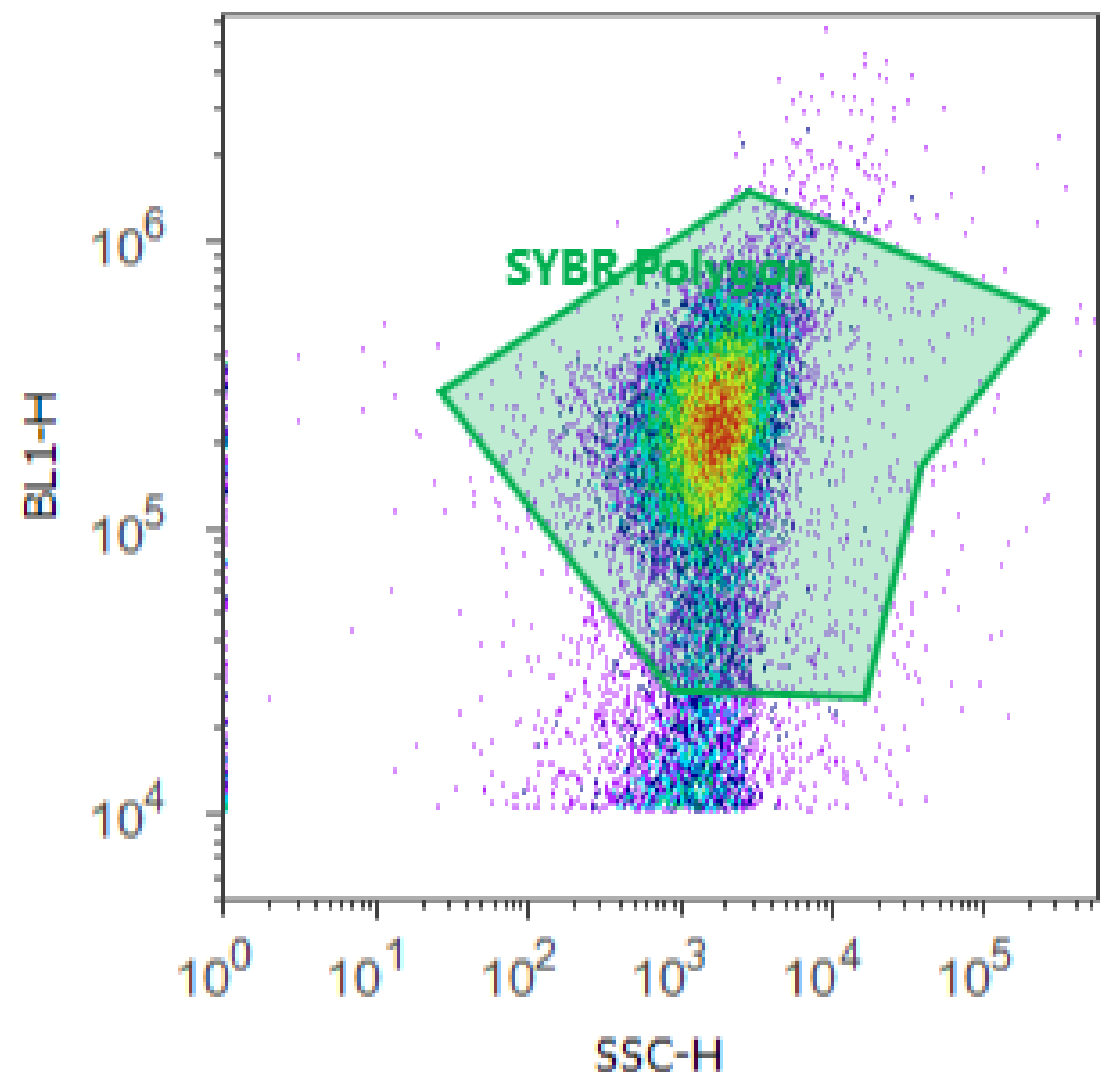


Figure S1: Representative density plots of gated SYBR polygon derived bacterial counts for a SYBR stained .2 μ m filtered milliQ control and a SYBR stained sample.

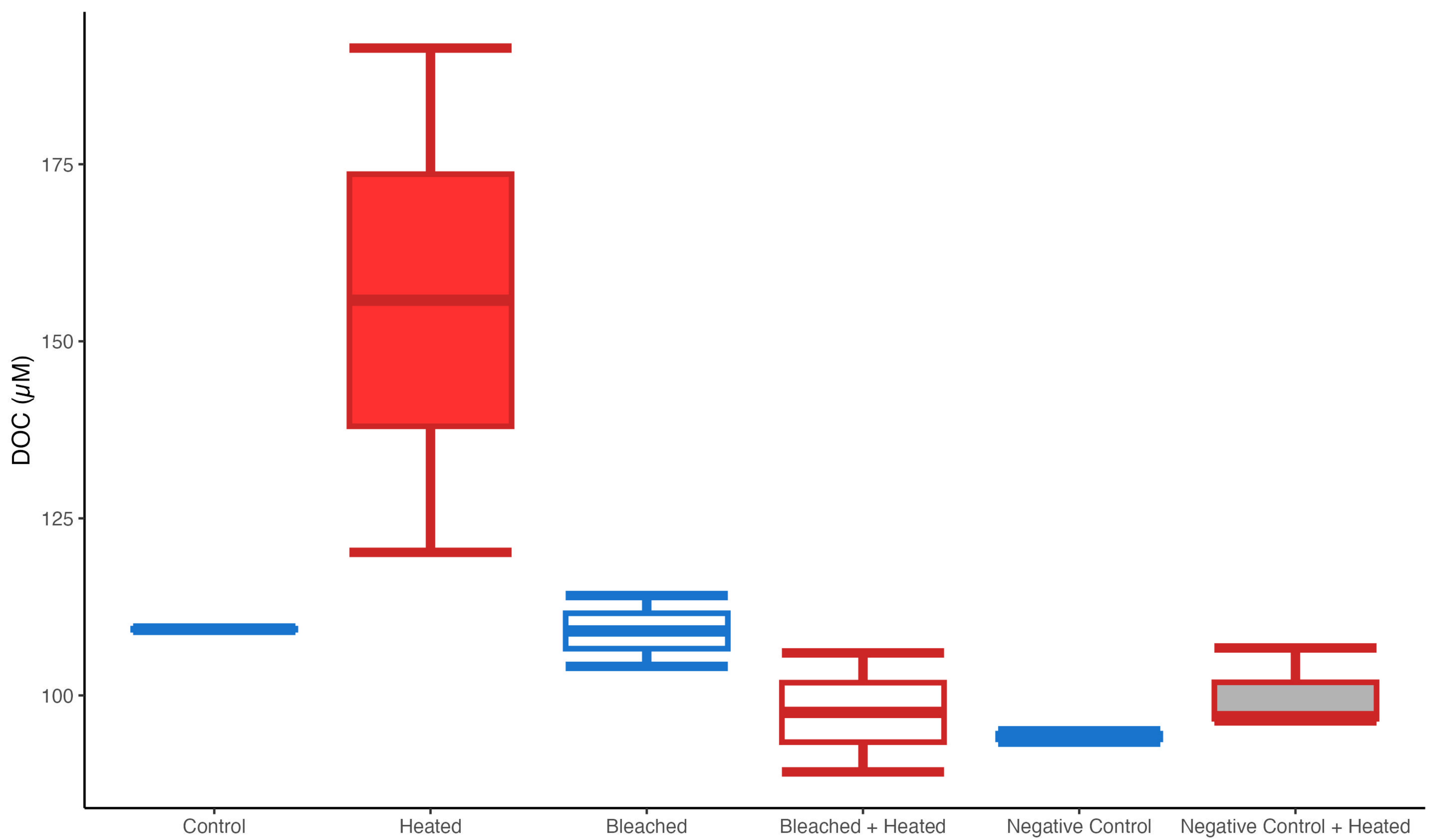


Figure S2: Box and whisker plots of raw DOC exudate concentrations (μM) for the 6 treatments.μ

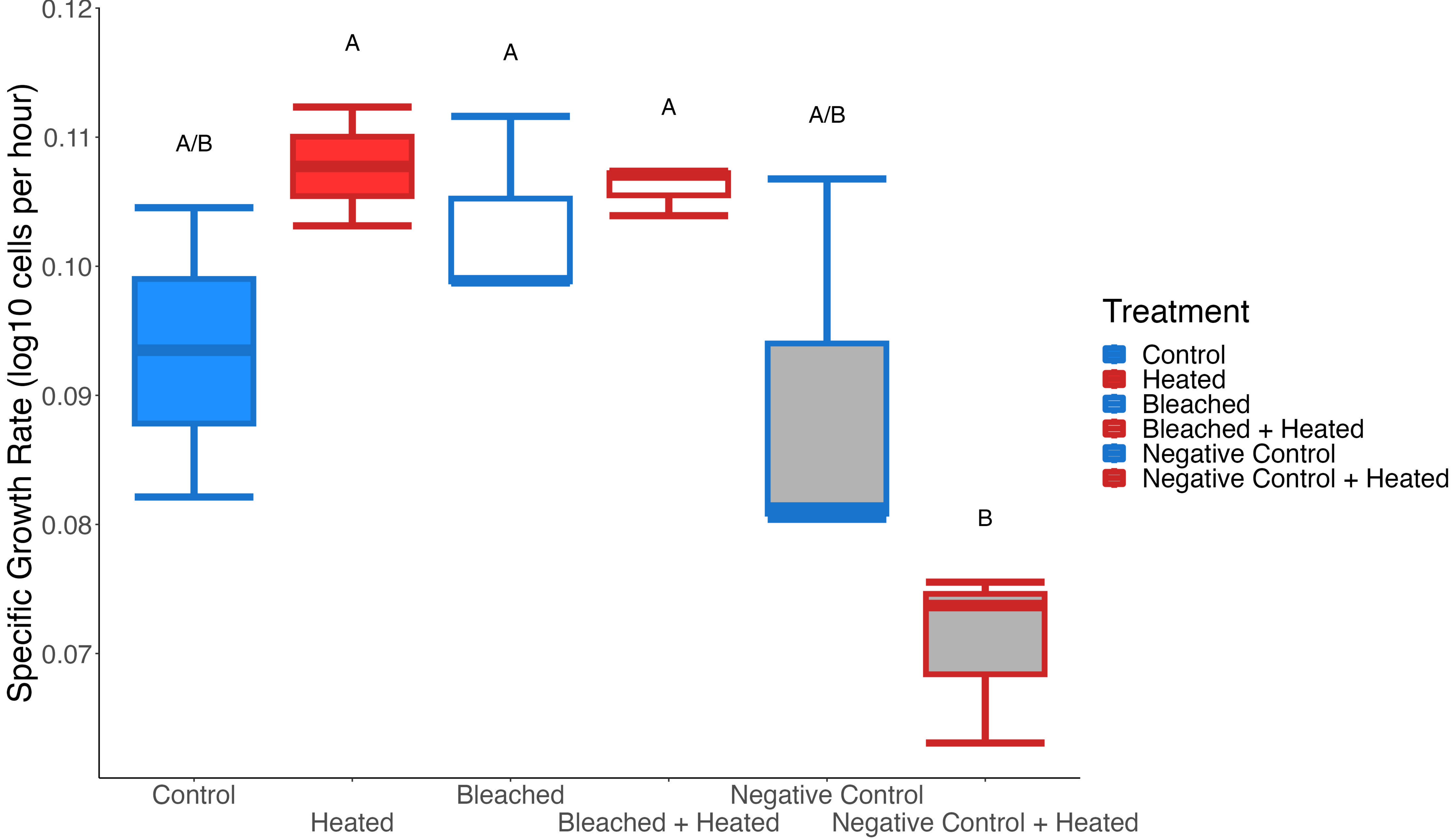


Figure S3: Box and whisker plots of bacterial specific growth rate, in log₁₀ cells per hour, for the 6 treatments. Significant differences between treatments (Tukey post-hoc test, p<0.05) are denoted by letters above each boxplot.

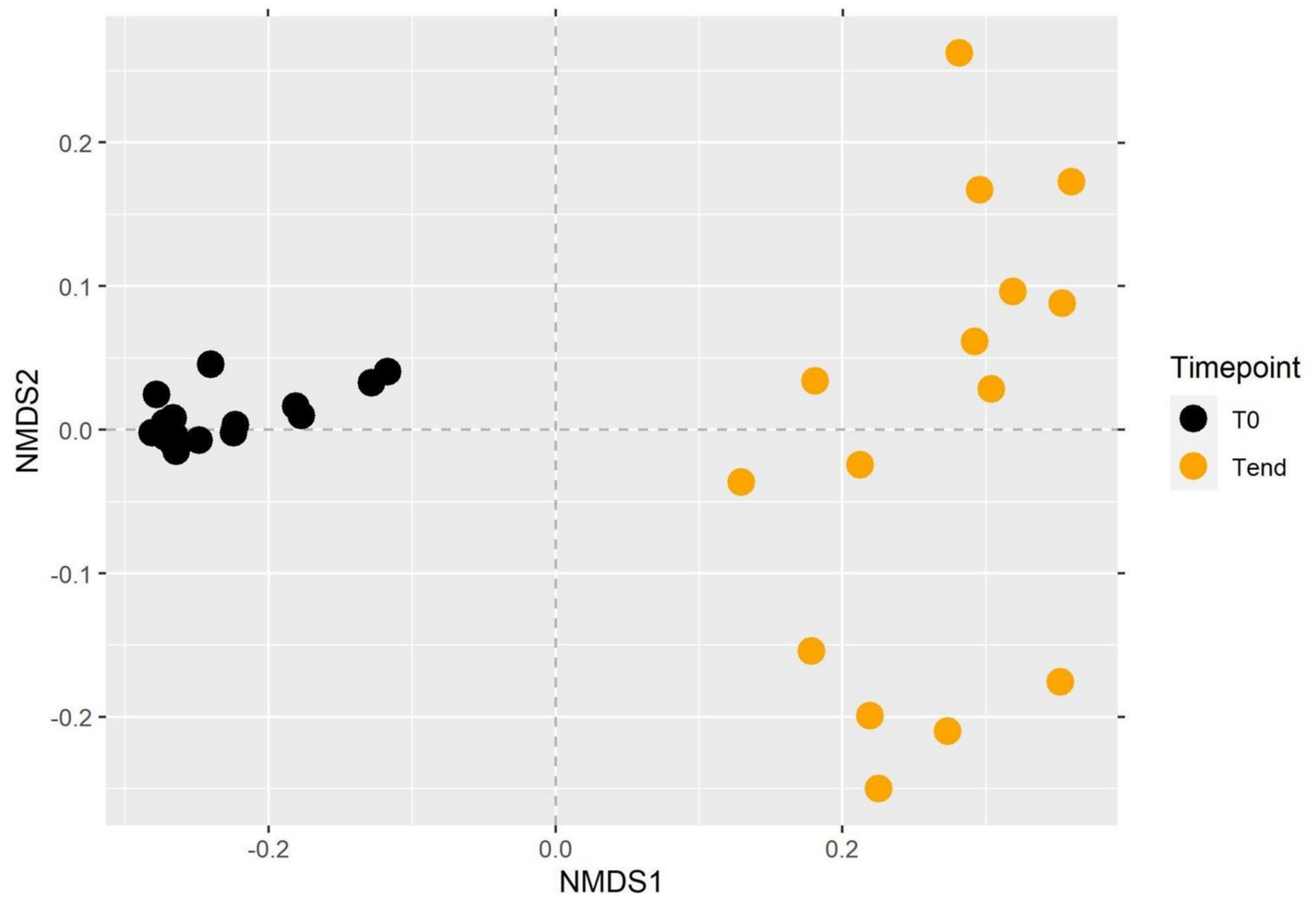


Figure S4: Non-metric multidimensional scaling plot of bacterial communities from start and end of bottle incubation using unifrac dissimilarity.

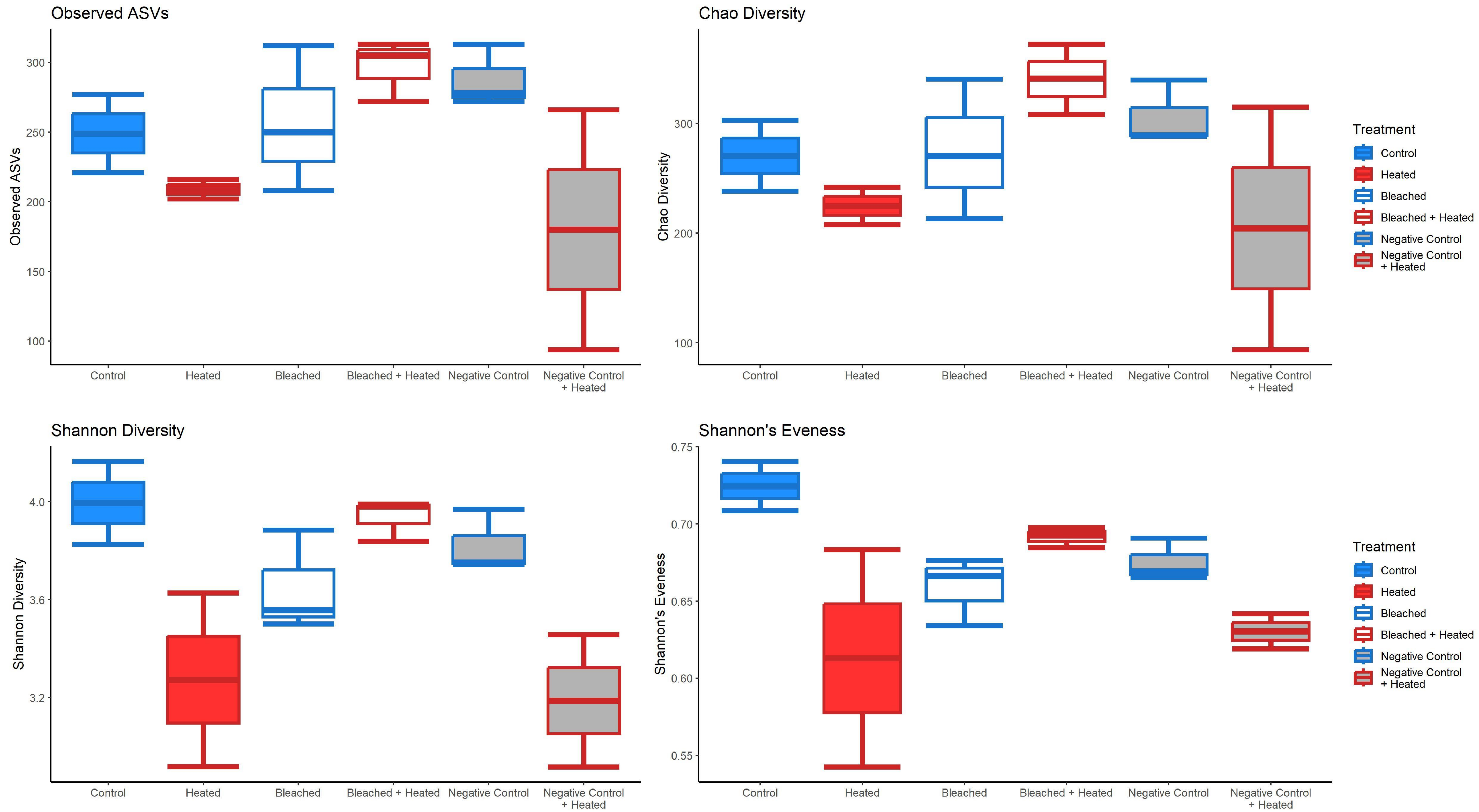


Figure S5: Box and whisker plots of the alpha diversity of the bacterial communities at the end of the incubation

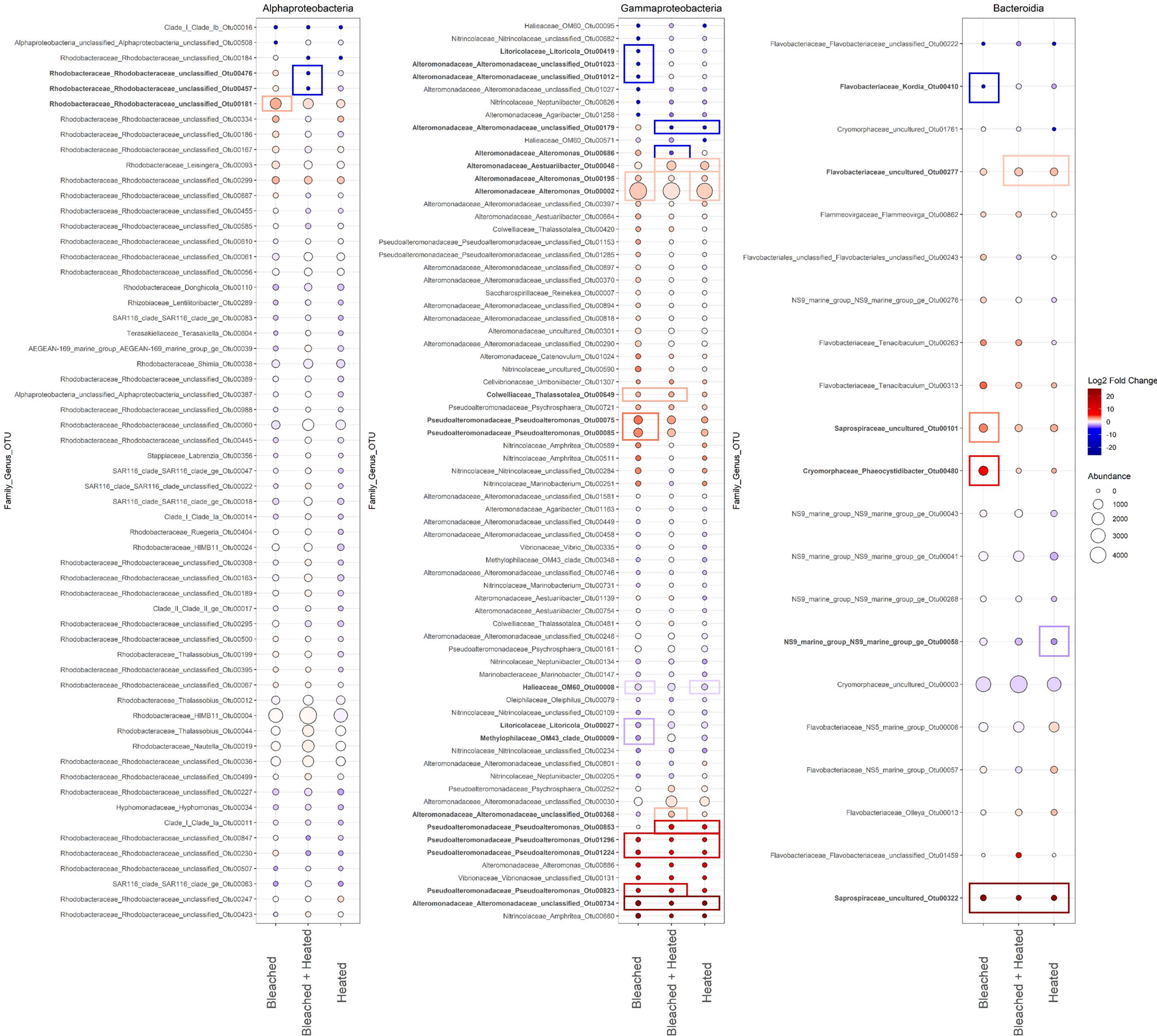


Figure S6: Direct comparison of bacterial OTUs enriched and/or depleted in the three stressed coral treatments relative to the Control corals. The log₂ fold change of the 159 most abundant/prevalent OTUs in the three coral stress treatments compared to the Control treatment. Points are colored by log₂ fold change, with warmer colors indicating more enrichment and cooler colors indicating more depletion relative to the Controls. Point size indicates the mean abundance of a given OTU in a given treatment. OTUs are labeled according to their family, genus, and OTU Number on the y axis. OTUs labeled in bold were determined by DESeq2 to be significantly differentially abundant in at least one of the three treatments compared to Controls (p ≤ 0.05 after FDR). Boxes denote in which treatment there is a significant change and the color of the box indicates whether this was a significant enrichment (red) or depletion (blue).



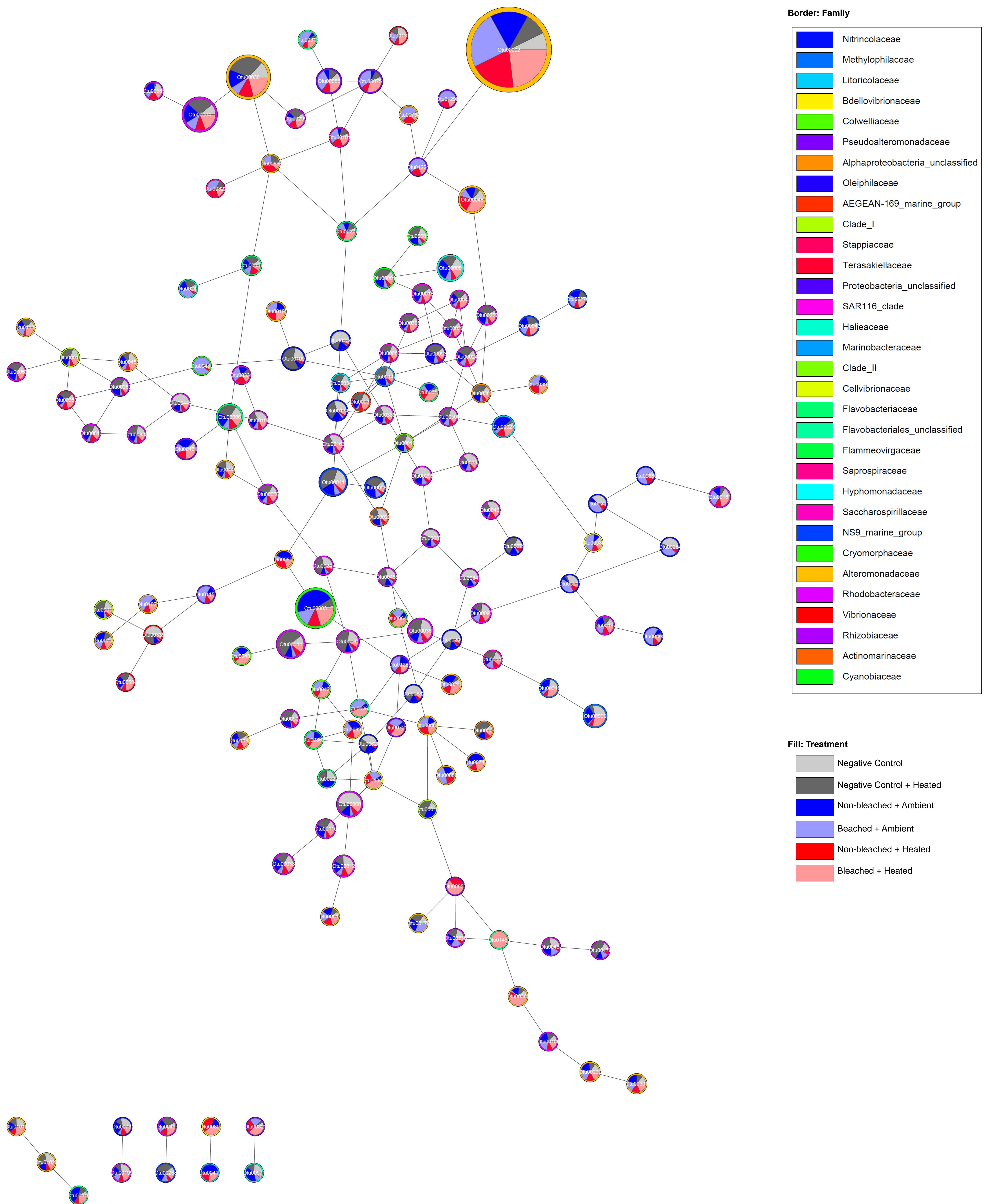


Figure S8: Cooccurrence network of microbial OTUs generated from SpiecEasi and visualized using Cytoscape. Vertices designated significant positive pairwise correlations as defined by SpiecEasi. Nodes represent individual OTUs. Node size indicates mean abundance of a given OTU, node outline is colored according to OTU family, and node fill corresponds to the relative proportion of a given OTU in each of the 6 treatments.