LIFETIME OMICS

# SUPPLEMENTARY MATERIALS FOR

## Hospital Antimicrobial Stewardship: Profiling the Oral Microbiome After Exposure to COVID and Antibiotics

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**This PDF file includes:**

**Figure S1.** Study Workflow

**Figure S2.** Collinearity between metadata variables including clinical and patient characteristics.

**Figure S3.** Alpha and Beta diversity associated with Broad-Spectrum Sepsis Antibiotics (BSA) for all patients and 5 healthy subjects

**Figure S4.** Bacterial Microbiome Beta Diversity at the Genus Level

**Figure S5.** Bacterial Microbiome Alpha Diversity at the Genus Level

**Figure S6.** Alpha Diversity at the Family level by Disease Severity groups of DNA Viruses, Fungi and Parasites

**Figure S7.** Species Alpha Diversity by BSA groups of **(a)** Fungi and Parasites **(b)** DNA Viruses

**Figure S8.** Maaslin Boxplots showing antimicrobial resistance differences between BSA groups

Other supplementary materials for this manuscript include the following:

**Table S1.** P-values for Correlations shown in Figure S2

MetadataCorrelation_Pvalue.xlsx

**Table S2.** Outcome for 4 False Positives

Supp-Table-4-false-positives-outcome-antibiotics.xlsx

**Table S3.** Nextflow nf-core/viralrecon variant analysis

Coverage-variants.xlsx

**Table S4.** Microbiome read counts by Biobakery (BB) and Kraken (K) and Respiratory Virome Sequencing (RVOP) read counts and genome coverage

Kraken-Biobakery-Read-Stats-Supp-Material-deid.xlsx

**Table S5.** Severity and Controls at Species Level - Significantly reduced bacteria at the species level in COVID-19 compared to healthy subjects (controls)

AR_Maaslin2_Species_significant_results.xlsx

**Table S6**. Severity and Controls at Genus Level- Significantly reduced bacteria at the genus level in COVID-19 compared to healthy subjects (controls)

Masslin_Severity_Healthy_Armstrong_Genus_Level_Significant_Results.xlsx

**Table S7.** Severity and FPs - Significantly reduced bacterial species in COVID-19 patients as compared to false positives

Maaslin_Severity_4FPs_significant_results.xlsx

**Table S8.** DNA Virus, fungi, and parasites - Species/Genus - Significant associations between severity of disease and DNA Virus, fungi, and parasites

DNA-Virus-Fungi-Parasites-Severity.xlsx

**Table S9.** BSA and Bacteria - Significantly reduced bacterial species in patients receiving broad-spectrum sepsis antibiotics

Maaslin-sepsis_bef_significant_results.xlsx

**Table S10.** Species Abundance Table Kraken/Bracken

bracken_c0.1_combined_subshell2.S-reid.txt

**Table S11.** Genus Abundance Table Kraken/Bracken

bracken_c0.1_combined_subshell2.G-reid.txt

**Table S12.** Abundance Table Metaphlan

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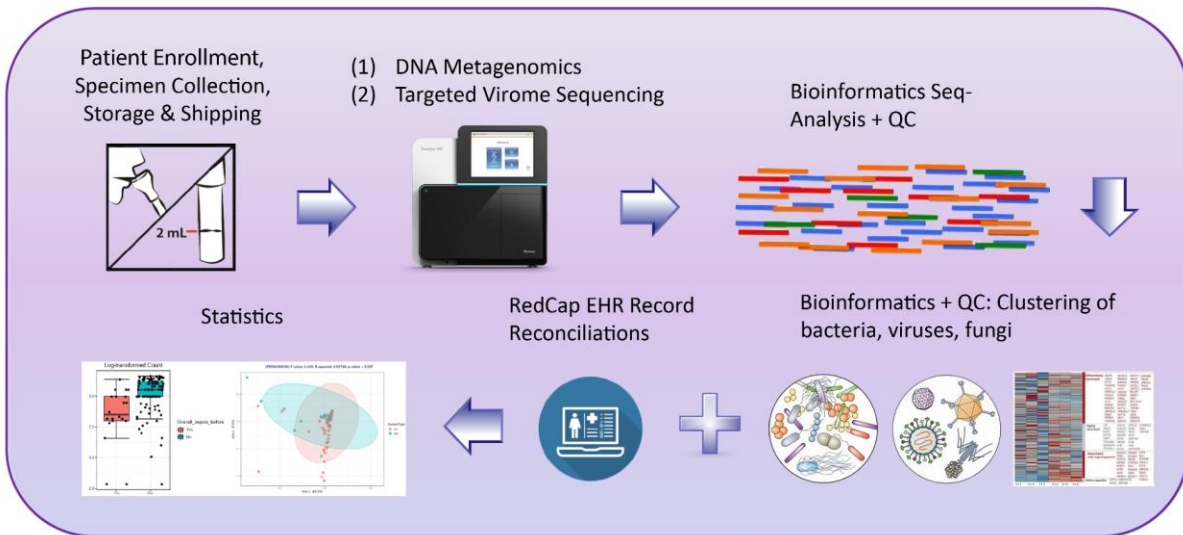claire_metaphlan_concat_01242022_merged_metaphlan_with_Armstrong21_reid.txt

**Figures**



**Figure S1.** Study Workflow

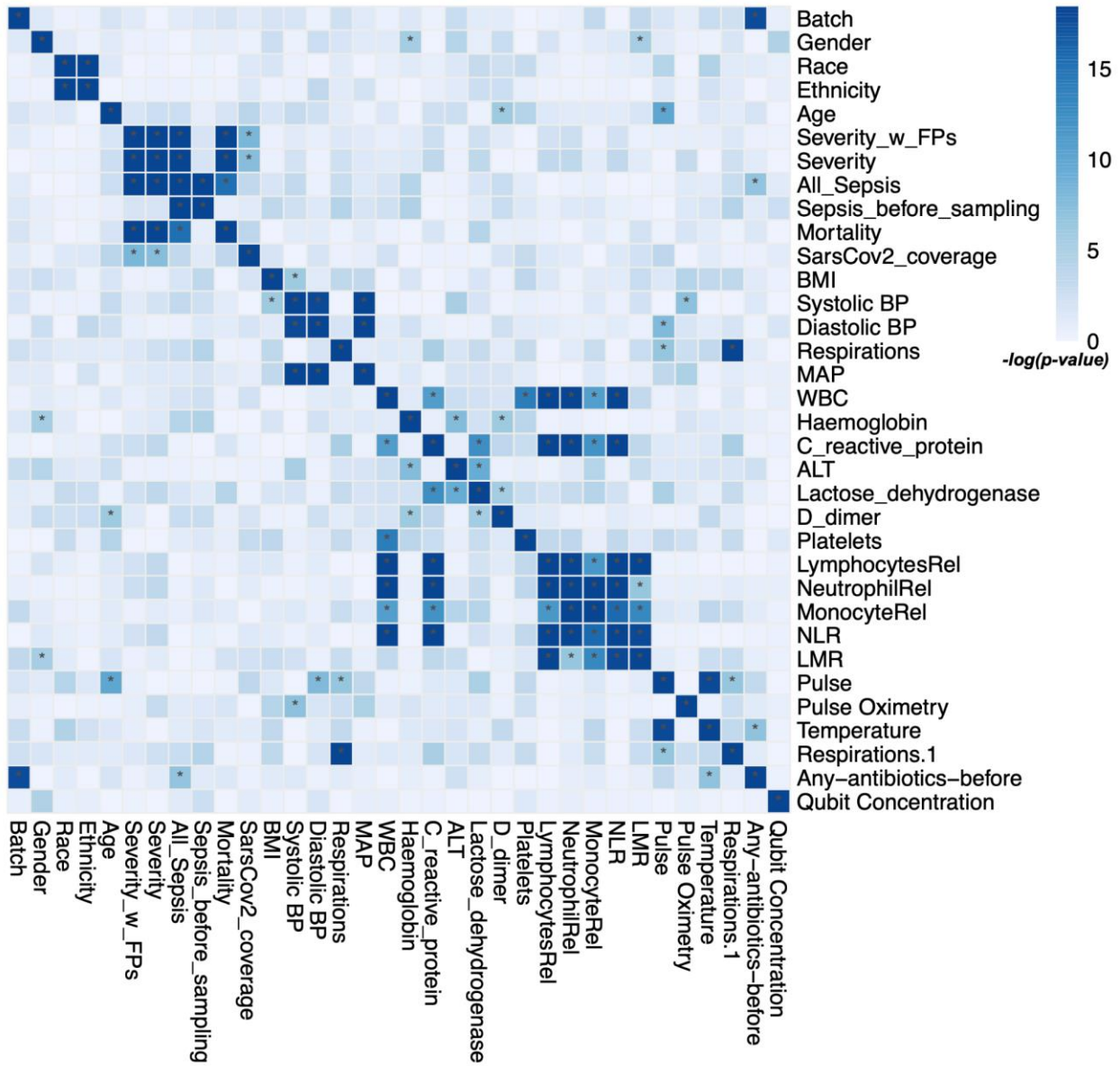**Figure S2.** Collinearity between metadata variables including clinical and patient characteristics. * refers to p-value<0.005. -log(p-value) of feature correlation has been calculated with three different tests based on data types (Kruskal-Wallis, Spearman, Chi-Squared). For model verification, we observe that race and ethnicity, as well as severity and mortality, as expected, are significantly correlated.
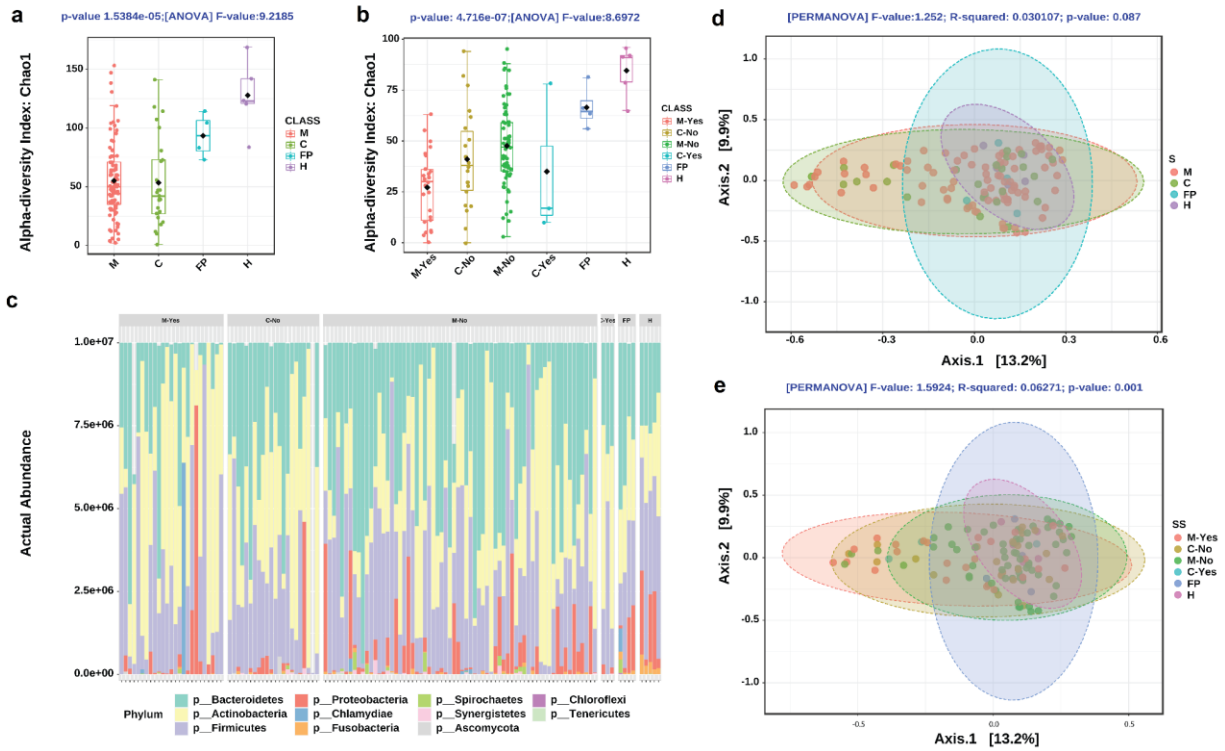
**Figure S3. a.** Alpha diversity boxplots for four groups: moderate (M) and critical (C) COVID-19 groups, false positives (FP), and healthy/control (H) groups. **b.** Alpha diversity boxplots with COVID-19 groups stratified by BSA timing [BSA before or same day as saliva sampling: Yes (Y), No (N)]. **c.** Phyla Abundance Plot. **d.** Beta diversity PCA graphs for the four groups. **e.** Beta diversity PCA graphs with COVID-19 groups stratified by BSA timing.
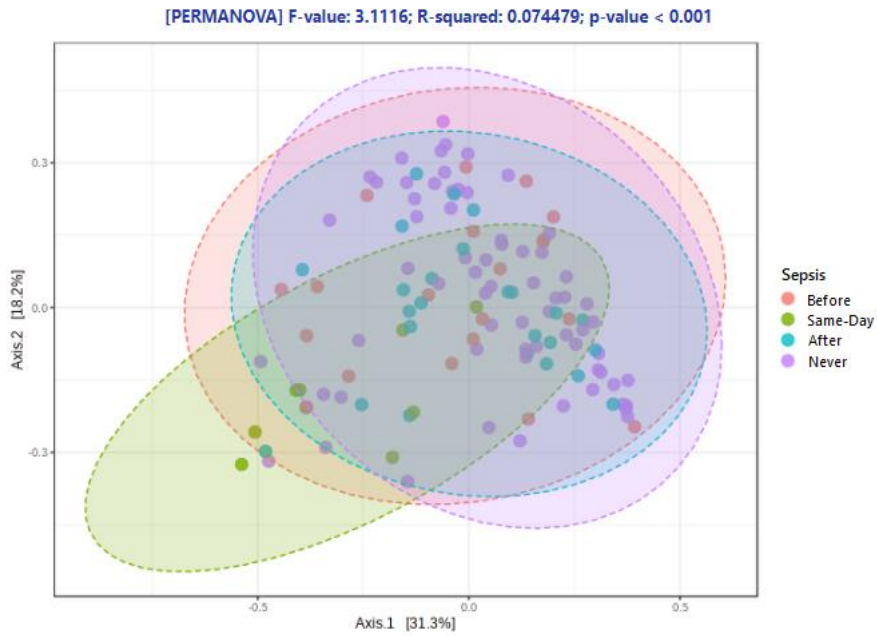
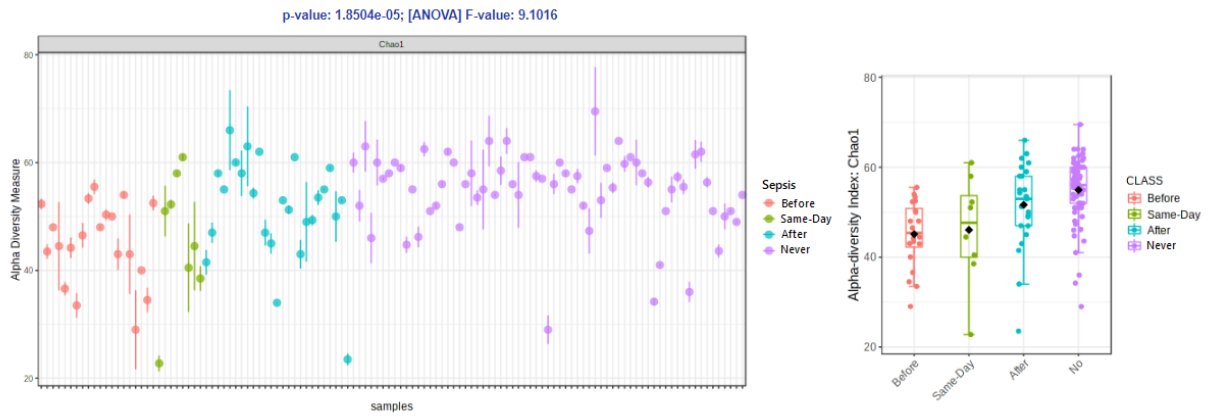**Figure S4.** Bacterial Microbiome Beta Diversity at the Genus Level



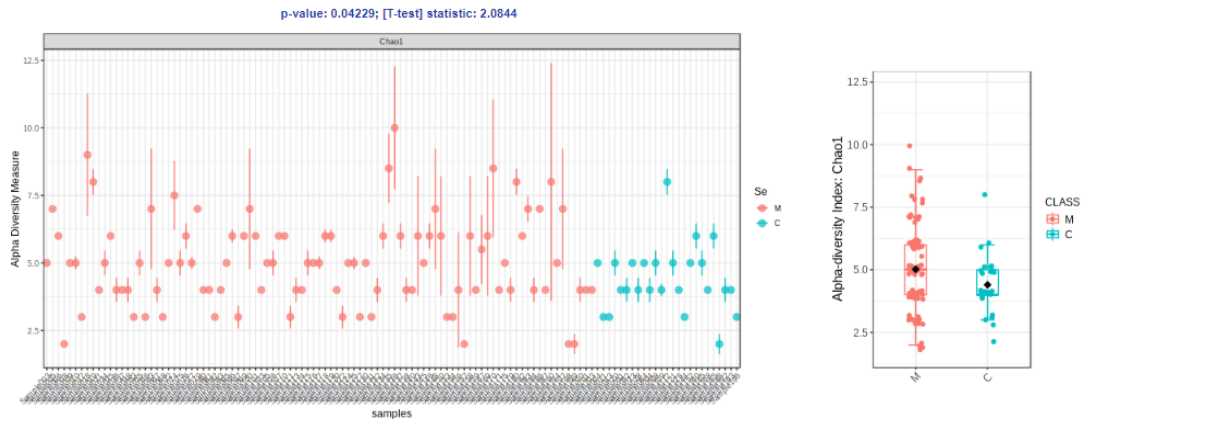**Figure S5.** Bacterial Microbiome Alpha Diversity at the Genus Level

**Figure S6.** Alpha Diversity of DNA Virus, Fungi and Parasite at the family level by Disease Severity groups (M: Moderate, C: Critical)
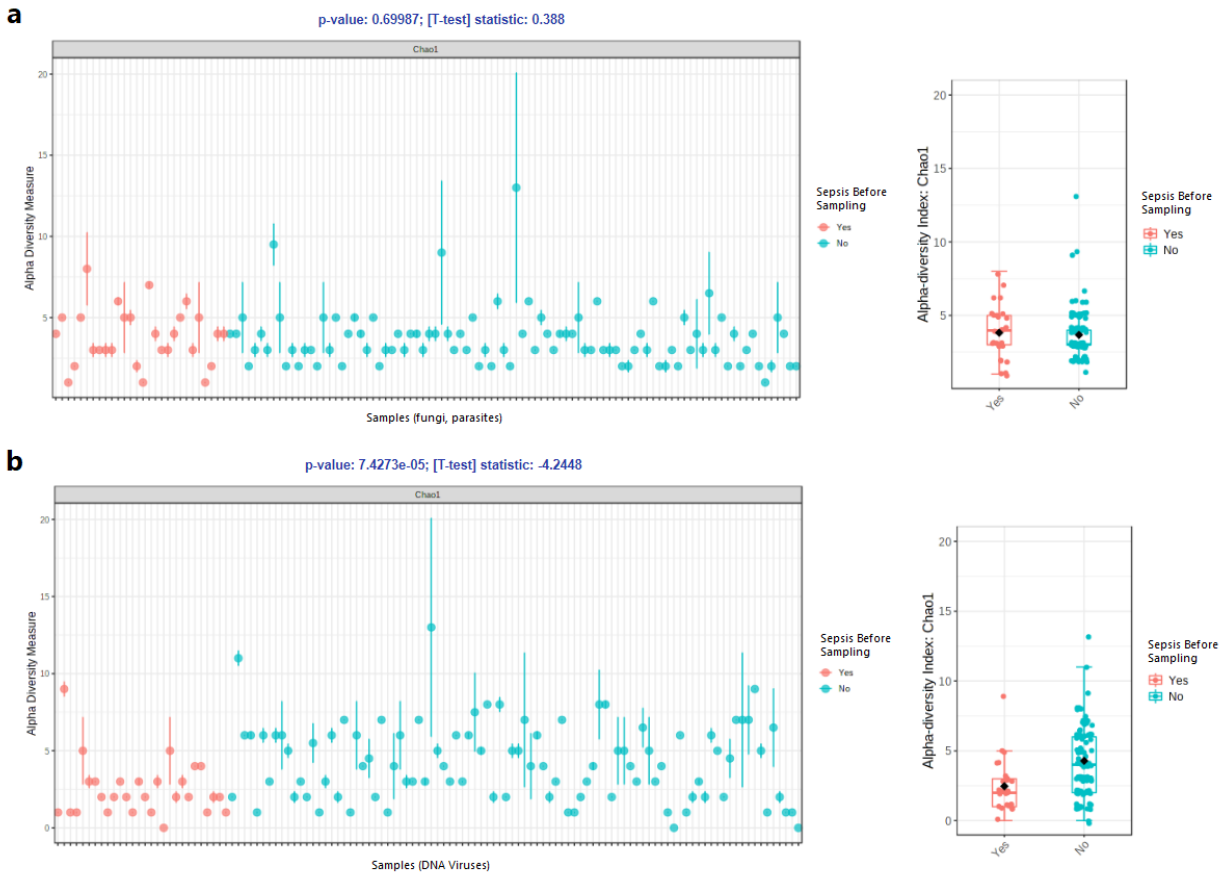


**Figure S7. a** Alpha Diversity of Fungi and Parasite Species by BSA groups (Yes: Early BSA, No: Early BSA) **b** Alpha Diversity of DNA Virus Species by BSA groups
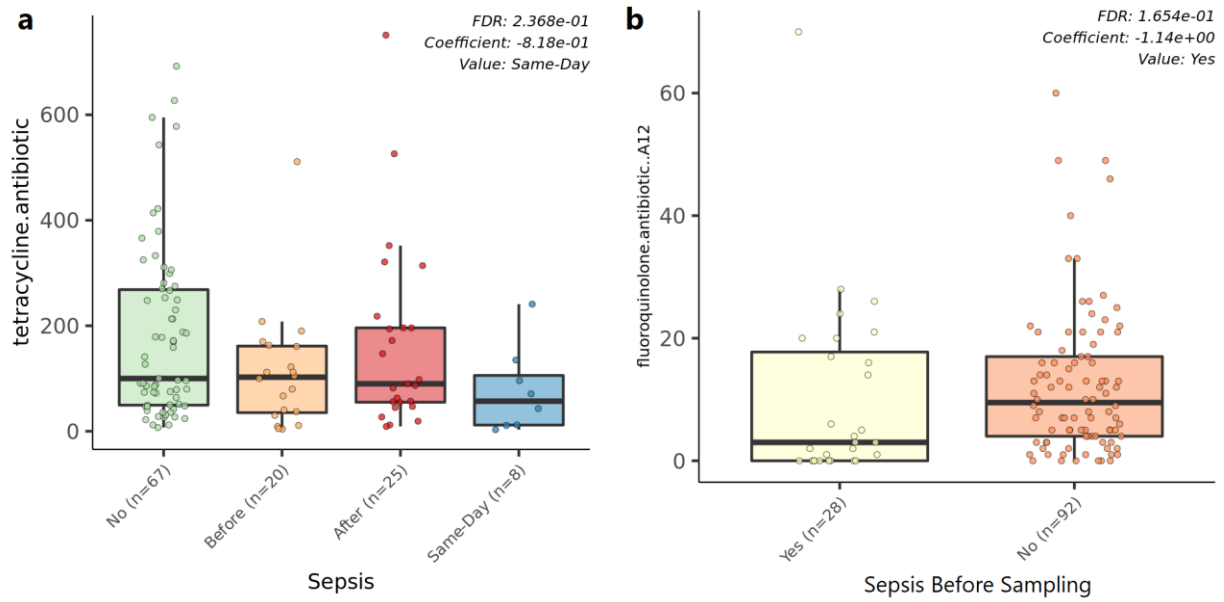
**Figure S8. a** Maaslin Boxplots showing abundance of genes with tetracycline resistance among the 4 sepsis BSA groups (Early BSA: Before and Same-Day), **b** Maaslin Boxplots comparing mixed class fluoroquinolone and tetracycline (A12) resistance to among the 2 sepsis BSA groups (Yes: Early BSA, No: No Early BSA)