

SUPPLEMENTARY MATERIALS FOR

HOSPITAL ANTIMICROBIAL STEWARDSHIP: NON-BACTERIAL SALIVA MICROBIOME EMERGES AS A BIOMARKER OF COVID-19 SEVERITY

Patricia Buendia^{1*}, Krystal Fernandez¹, Castle Raley², Ali Rahnavard³, Keith A. Crandall³, Jose Guillermo Castro⁴

¹Lifetime Omics, Miami, FL 33133

²The GWU Genomics Core, Milken Institute School of Public Health, The George Washington University, Washington, DC 20052

³Computational Biology Institute, Department of Biostatistics and Bioinformatics, Milken Institute School of Public Health, The George Washington University, Washington, DC 20052

⁴Division of Infectious Diseases, Leonard M. Miller School of Medicine, University of Miami, Miami, FL 33136

This PDF file includes:

Figure S1. Collinearity between metadata variables including clinical and patient characteristics.

Figure S2. Bacterial Microbiome Alpha Diversity

Figure S3. Bacterial Microbiome Beta Diversity

Figure S4. Clinical metadata values significantly associated with the abundance of a particular bacterial species

Figure S5. a Alpha Diversity of Fungi and Parasites **b** Alpha Diversity of DNA Viruses

Figure S6. Maaslin Boxplots showing antimicrobial resistance differences between BSA groups

Figure S7. Study Design

Other supplementary materials for this manuscript include the following:

Table S1. 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 S2. Nextflow nf-core/viralrecon variant analysis

[Coverage-variants.xlsx](#)

Table S3. Significantly reduced bacterial species in COVID-19 patients as compared to false positives

[Maaslin_Severity_4FPs_significant_results.xlsx](#)

Table S4. Significantly reduced bacterial species in patients receiving broad-spectrum sepsis antibiotics

[Maaslin-sepsis_bef_significant_results.xlsx](#)

Table S5. Broad-Spectrum Sepsis Antibiotics

[Broad Spectrum Sepsis Antibiotic.xlsx](#)

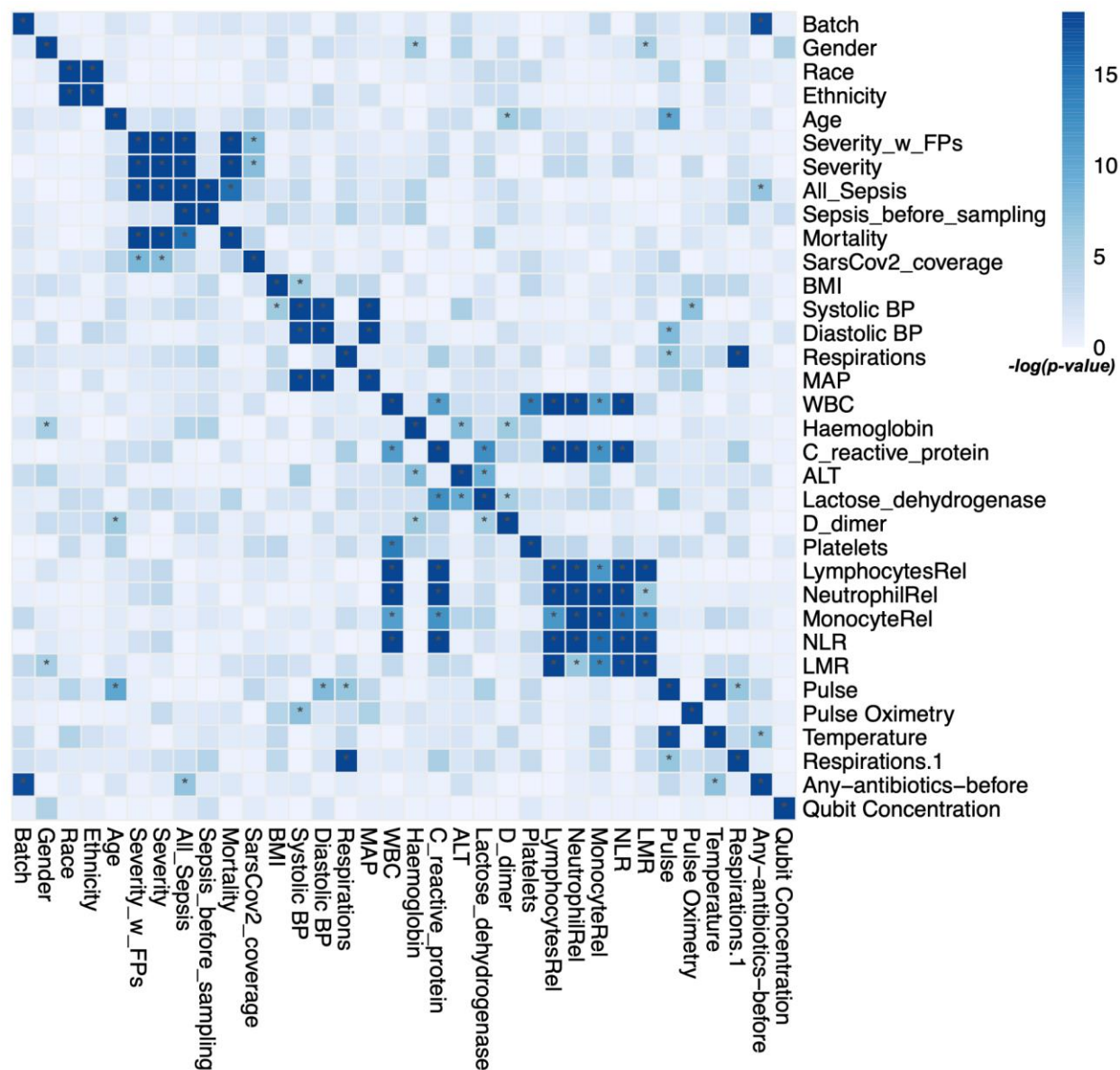


Figure S1. Collinearity between metadata variables including clinical and patient characteristics. * refers to $p\text{-value} < 0.005$. $-\log(p\text{-value})$ of feature correlation has been calculated with three different tests based on data types (Kruskal-Wallis, Spearman, Chi-Squared). As a control, we see significant correlations between Race and Ethnicity, and Severity and Mortality .

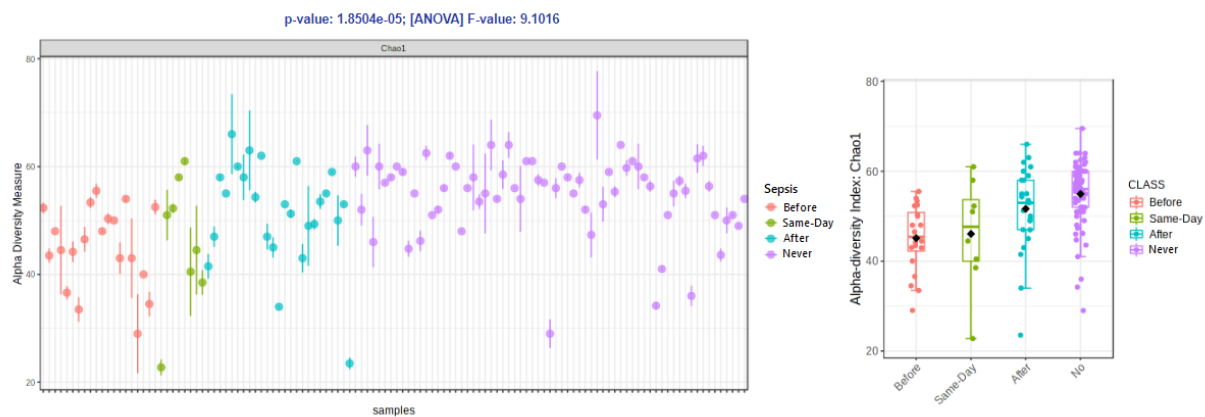


Figure S2. Bacterial Microbiome Alpha Diversity at the Genus Level

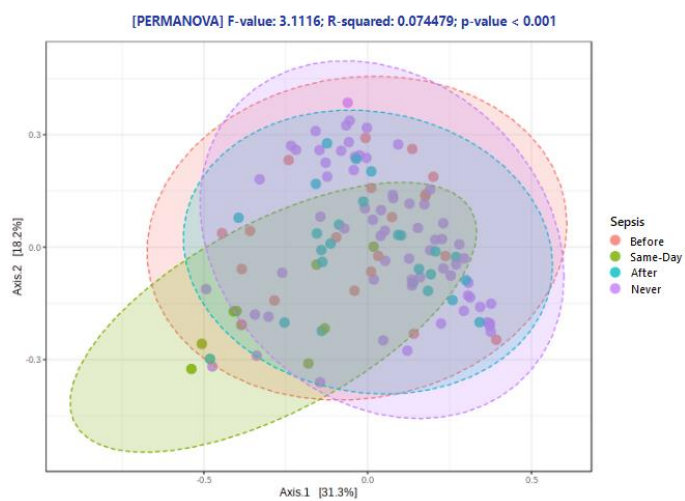


Figure S3. Bacterial Microbiome Beta Diversity at the Genus Level

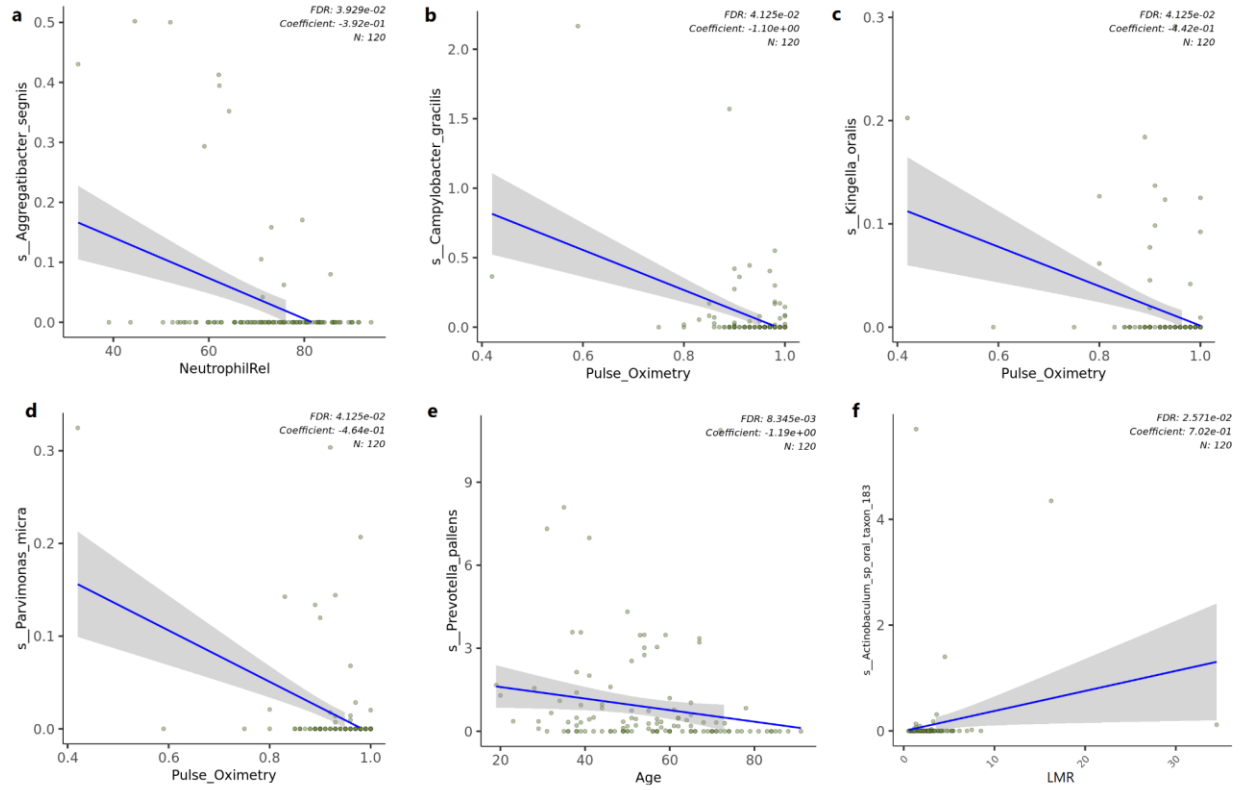


Figure S4. Clinical metadata values significantly associated with the abundance of a particular bacterial species

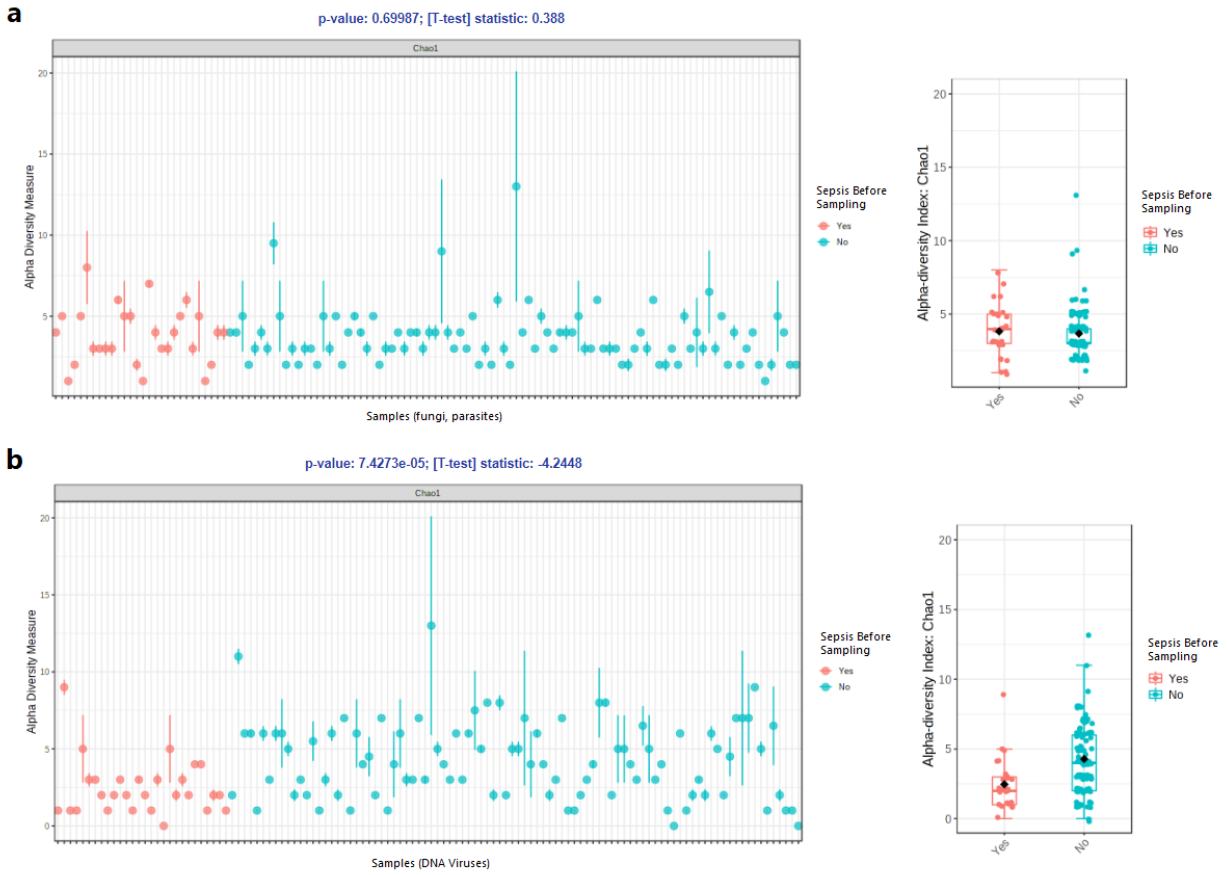


Figure S5. a Alpha Diversity of Fungi and Parasite Species **b** Alpha Diversity of DNA Virus Species

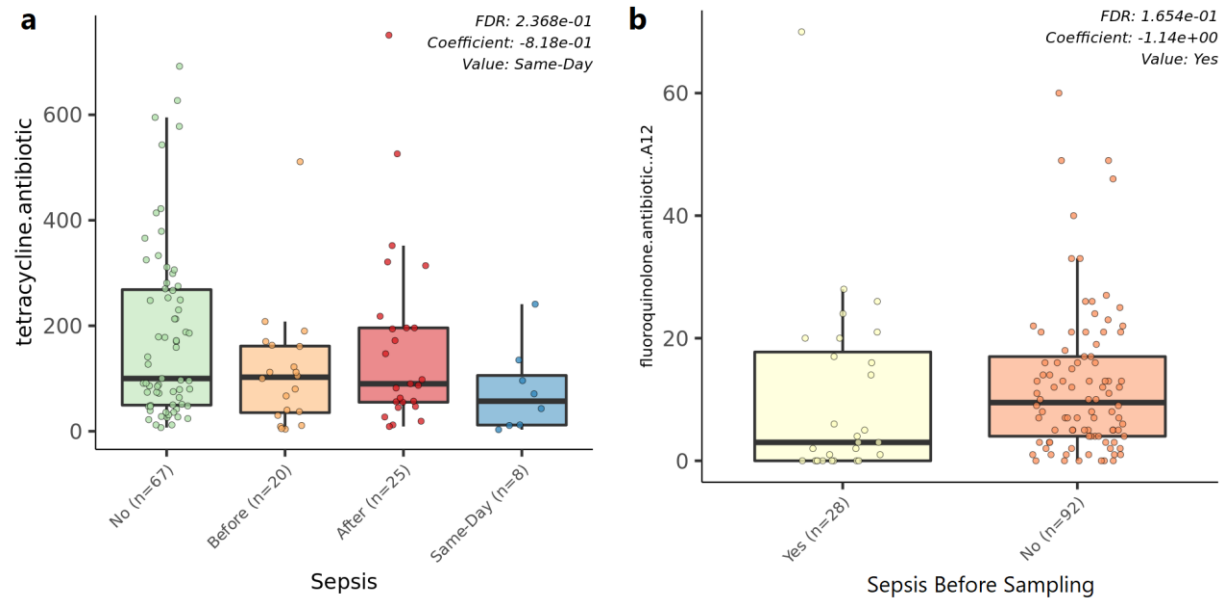


Figure S6. a Maaslin Boxplots showing tetracycline resistance among the 4 sepsis groups, **b** Maaslin Boxplots comparing mixed class fluoroquinolone and tetracycline (A12) resistance to among the 2 sepsis groups

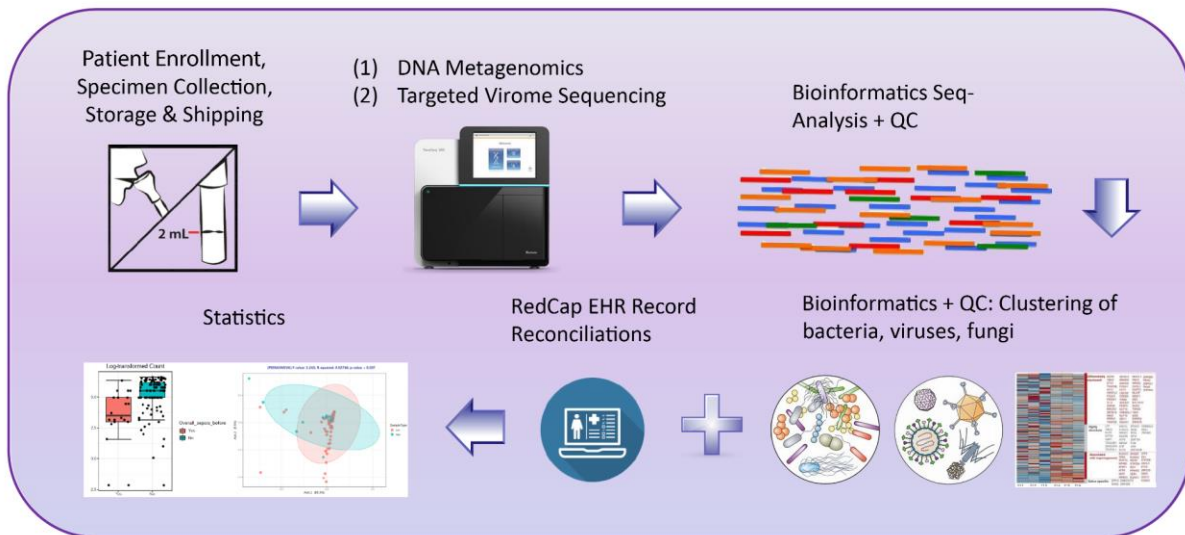


Figure S7. Study Design