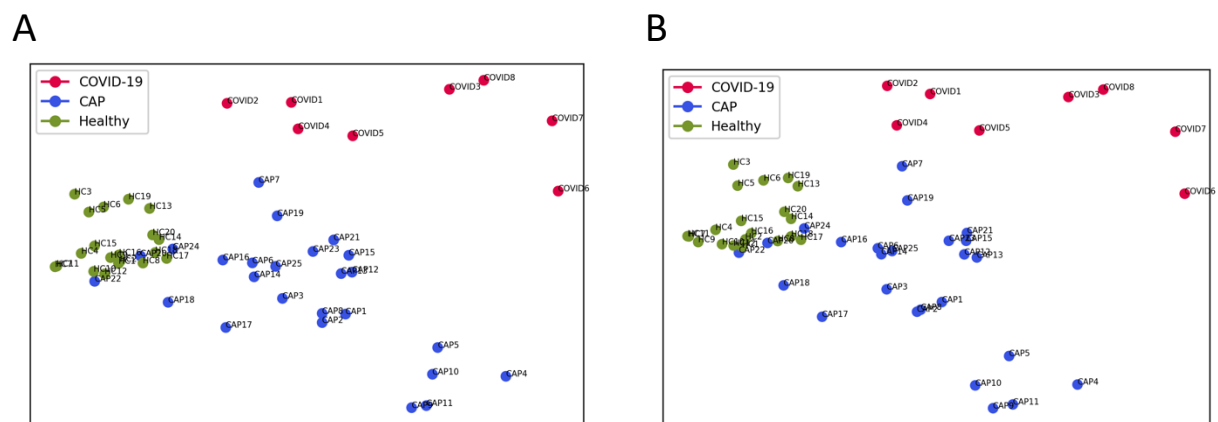


Functional pathways in respiratory tract microbiome separate COVID-19 from community-acquired pneumonia patients

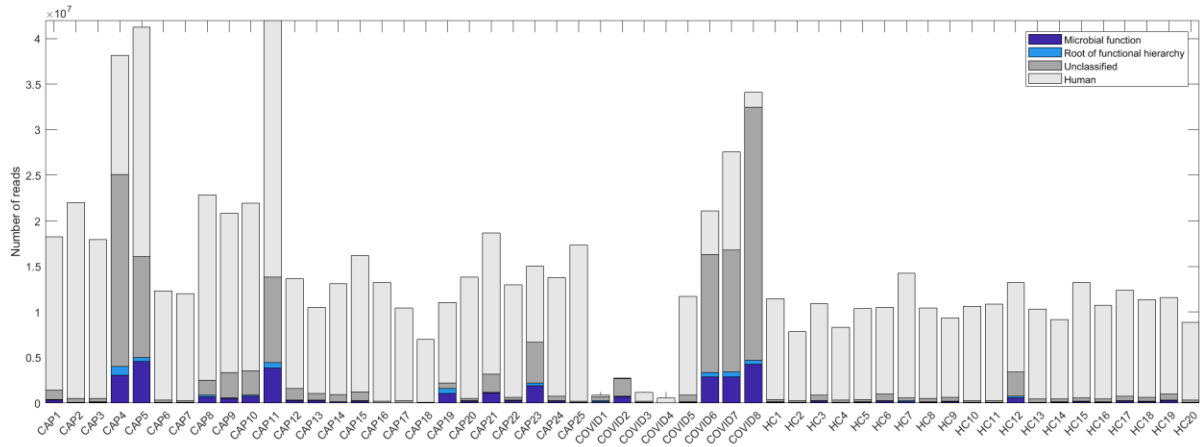
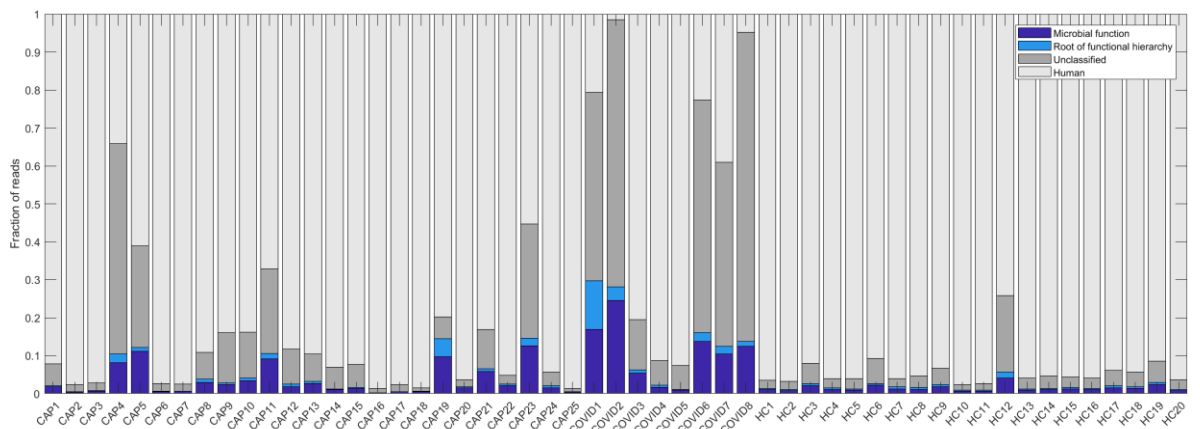
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Under review (2020)

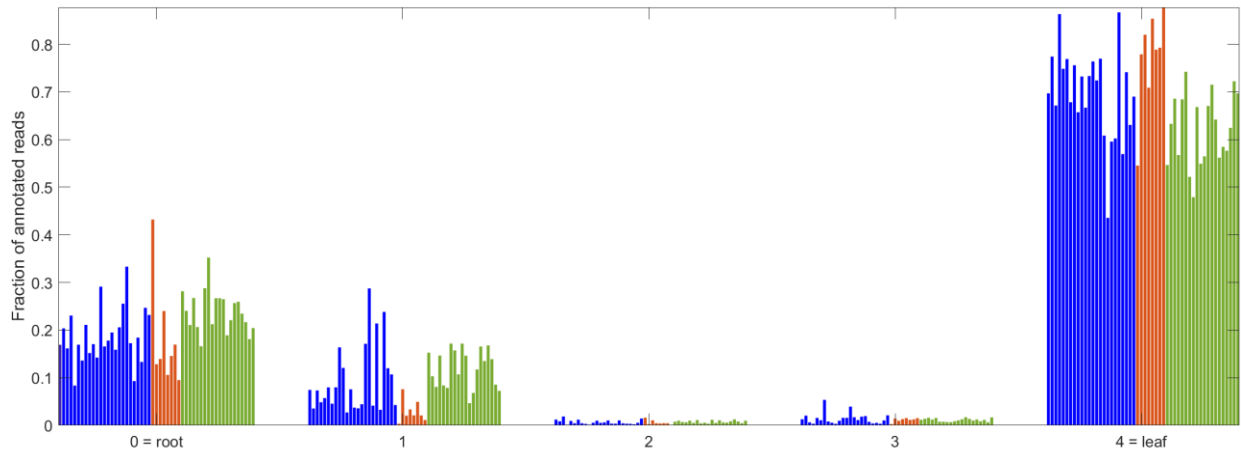
Supplemental Figures S1—S3



Supplemental Figure S1: Multidimensional scaling of pairwise sample distances into a two-dimensional projection. **A.** Using the full database of bacterial and viral sequences. **B.** Using the bacterial subset of the database only.

A**B**

Supplemental Figure S2: Distribution of the annotated reads. The input reads to this analysis were already host filtered by Shen et al., still we filtered additional reads that mapped to human with bowtie2 local alignment mode (light gray in the figure). **A.** Number of reads per sample, including human-mapped and unclassified reads. Light blue reads were classified the root and dark blue to other nodes of the functional hierarchy. The counts per sample are average counts of the two read files for paired end reads, approximating the number of paired reads per sample. **B.** Same data as in (A) scaled to indicate fractions from the total count per sample.



Supplemental Figure S3. Fraction of reads assigned to each functional hierarchy level per sample: CAP (blue), COVID-19 (red), Healthy Control (green).