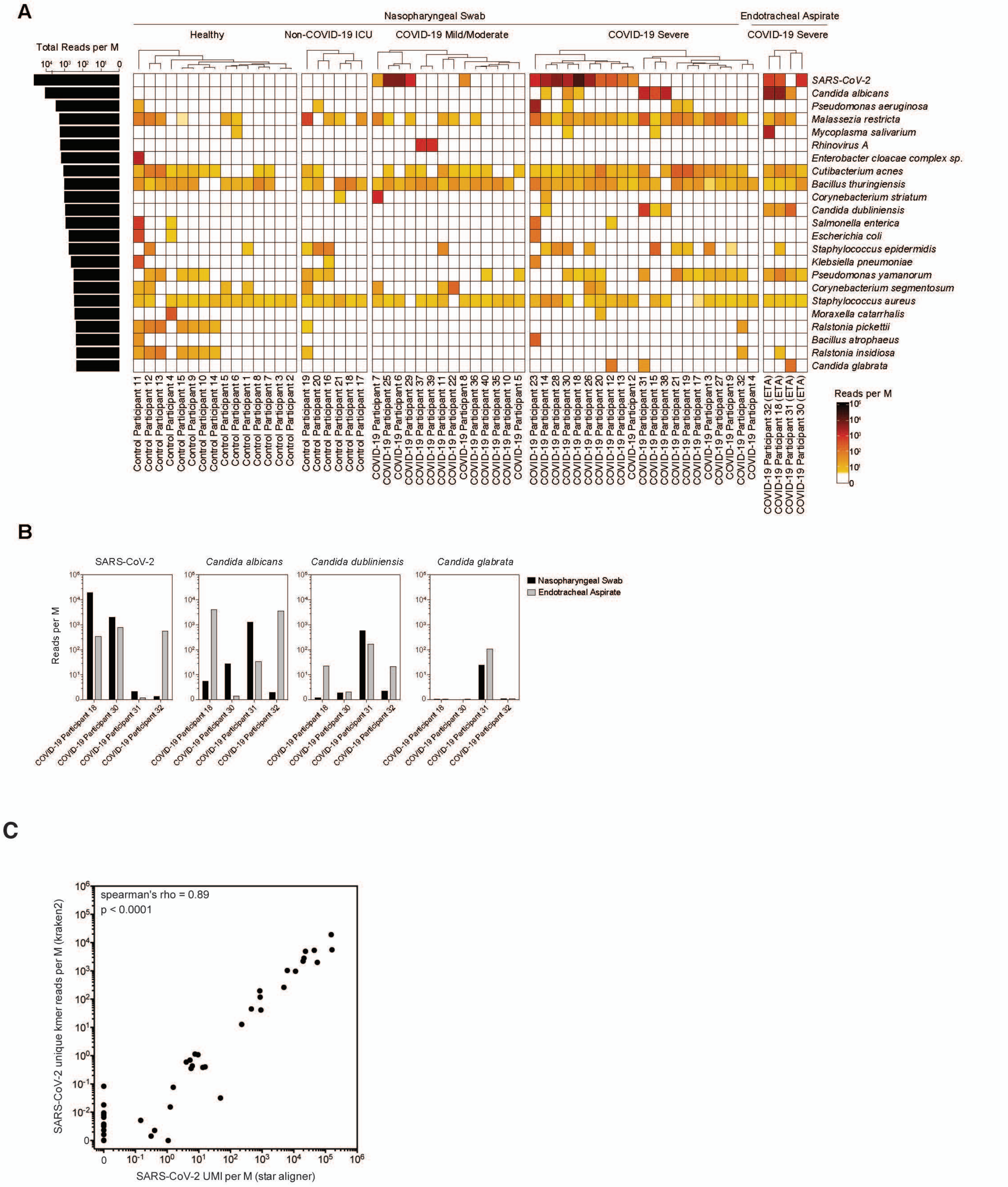
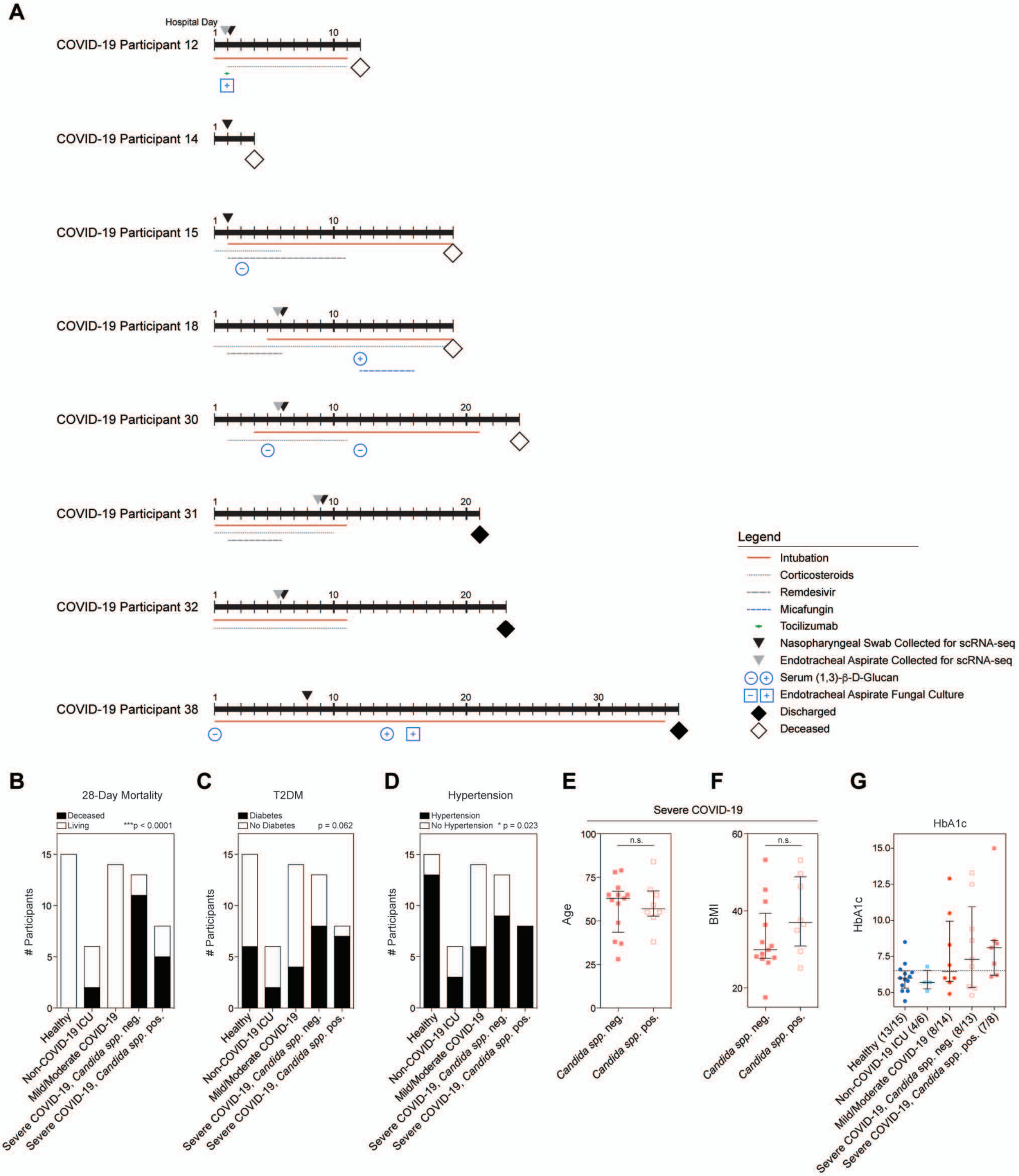


**Supplemental Figure 1. Meta-transcriptomic classification of reads from nasopharyngeal swabs and endotracheal aspirates**

A. Heatmap of top detected microbes (rows) across all samples (columns). Bar plot on left: total classified reads per million (M) for each microbe listed along heatmap rows. Heatmap colors represent total classified reads per M, dark red: higher abundance, yellow: lower abundance, white: < 10 reads per M.

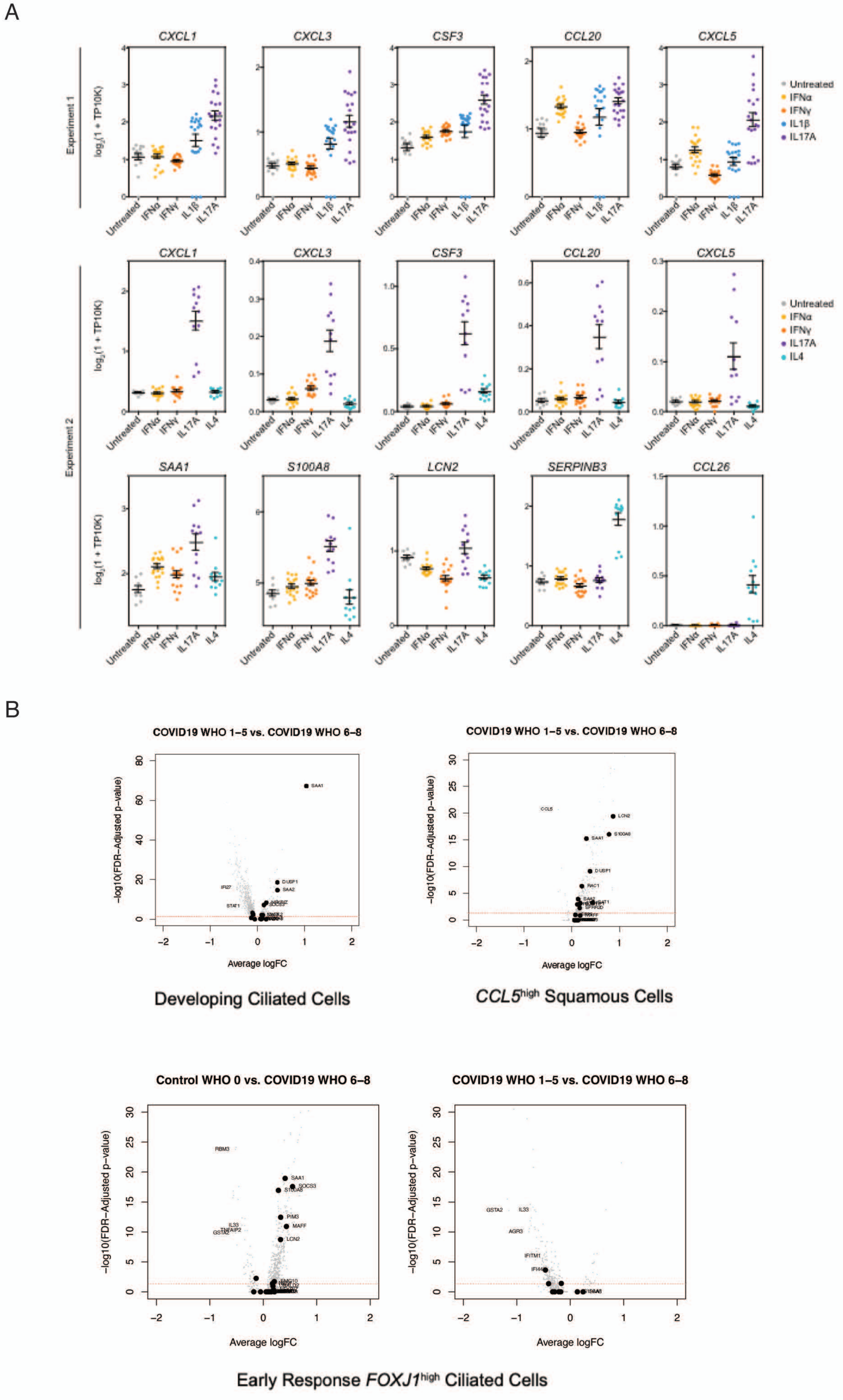
B. SARS-CoV-2 and Candida spp. reads detected from matched nasopharyngeal (NP, black bars) and endotracheal aspirate (ETA, grey bars) samples from the same participants.

C. Abundance of UMI aligning to SARS-CoV-2 RNA for each patient. Y axis: reads detected by metagenomic classification of SARS-CoV-2 RNA. N=56 participants, both Healthy and COVID-19.



**Supplemental Figure 2. Participant characteristics and clinical course**

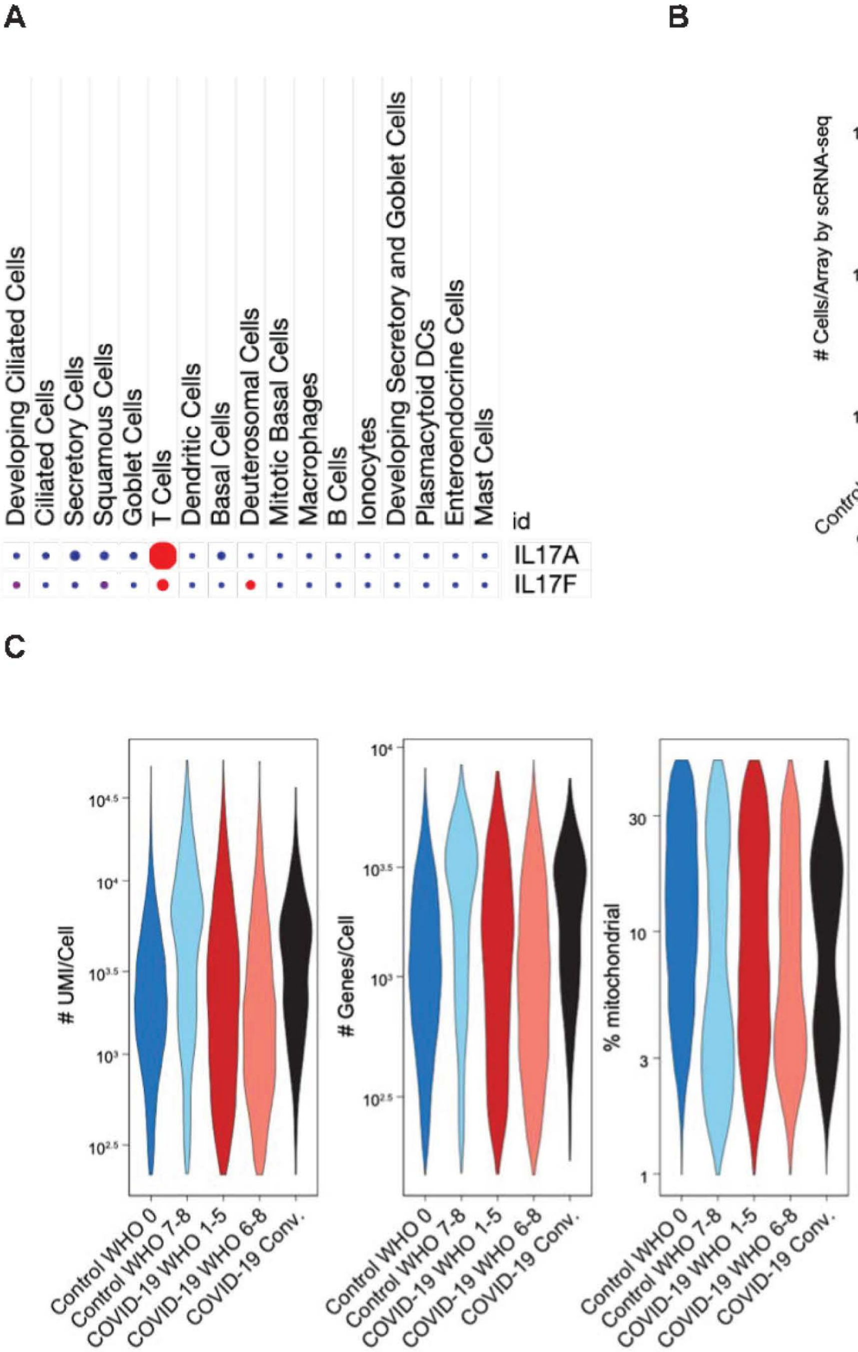
- **A.** Hospital timelines for 8 participants with *Candida spp.* detected from scRNA-seq NP or ETA samples.
- **B.-D.** Select categorical demographic and clinical information from study participants by disease cohort: 28-day mortality (**B**), type 2 diabetes mellitus (T2DM) (**C**), and chronic hypertension (**D**). Statistical testing by multi-group chi-square test, significance result is reported above each plot.
- **E.-F.** Select continuous demographic and clinical information among participants with severe COVID-19, separated by detection of *Candida spp.*: age (**E**) and BMI (**F**). Statistical testing using student's t-test. Lines represent median +/- interquartile range.
- **G.** Hemoglobin A1c (HbA1c) for each study participant by disease cohort. Dashed line at HbA1c 6.5%. Group differences non-significant by Kruskal-Wallis test. Numbers in parenthesis reflect patients per group with available data in medical record.



**Supplemental Figure 3. Expression of select genes among human nasal basal cells by stimulation condition.**

A. Expression of select genes among human nasal basal cells presented on by different cytokine simulation condition across 2 separate experiments.

B. Volcano plots of differential gene expression in selected epithelial cells comparing mild to severe COVID-19.



**Supplemental Figure 4. Quality control analysis**

A. Dot plot representing expression abundance of IL17A and IL17F according to cell type across all patients. Dot size corresponds to % of cell type expressing each gene.

B. Number of high-quality cells/array recovered for single-cell RNA-seq by disease group. Statistical testing by Kruskal-Wallis test ($p = 0.37$) with Dunn's post hoc testing, all $p > 0.05$. Dark blue circles: Healthy ("Control WHO 0"); light blue squares: Non-COVID-19 ICU ("Control WHO 7-8"); red circles: Mild/Moderate COVID-19 ("COVID-19 WHO 1-5); pink squares: Severe COVID-19 ("COVID-9 WHO 6-8").

C. Single-cell quality metrics by group (after filtering for low-quality cells). Left: number of UMI per cell. Center: number of genes per cell. Right: % mitochondrial mapping per cell. Blue: Healthy ("Control WHO 0"); light blue: Non-COVID-19 ICU ("Control WHO 7-8"); red: Mild/Moderate COVID-19 ("COVID-19 WHO 1-5); pink: Severe COVID-19 ("COVID-19 WHO 6-8"); black: COVID-19 convalescent (excluded from this study).