

SUPPLEMENTARY MATERIALS

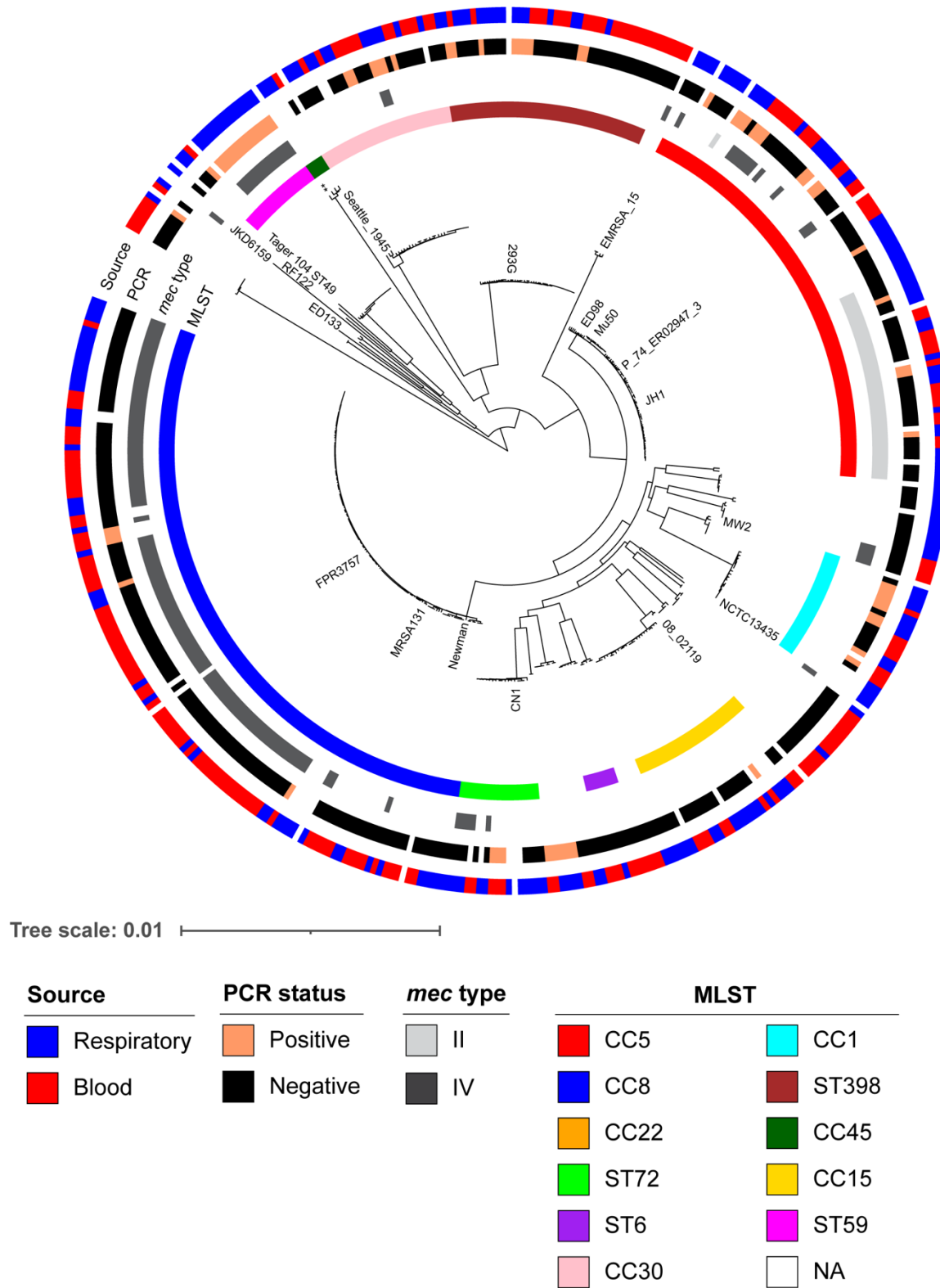
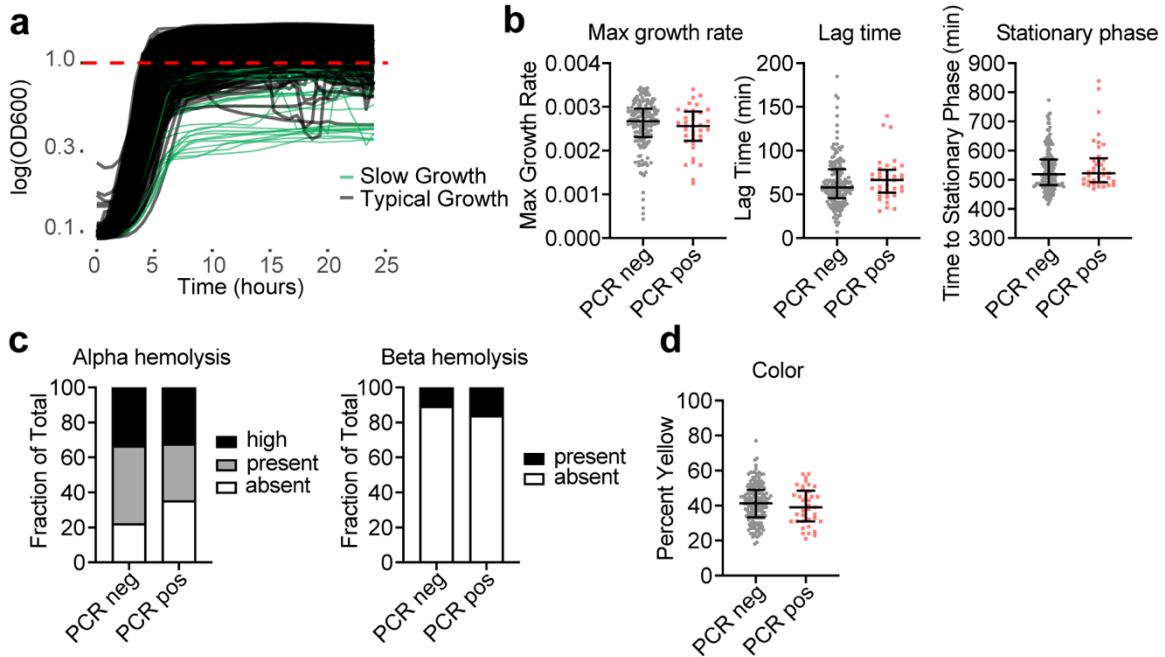


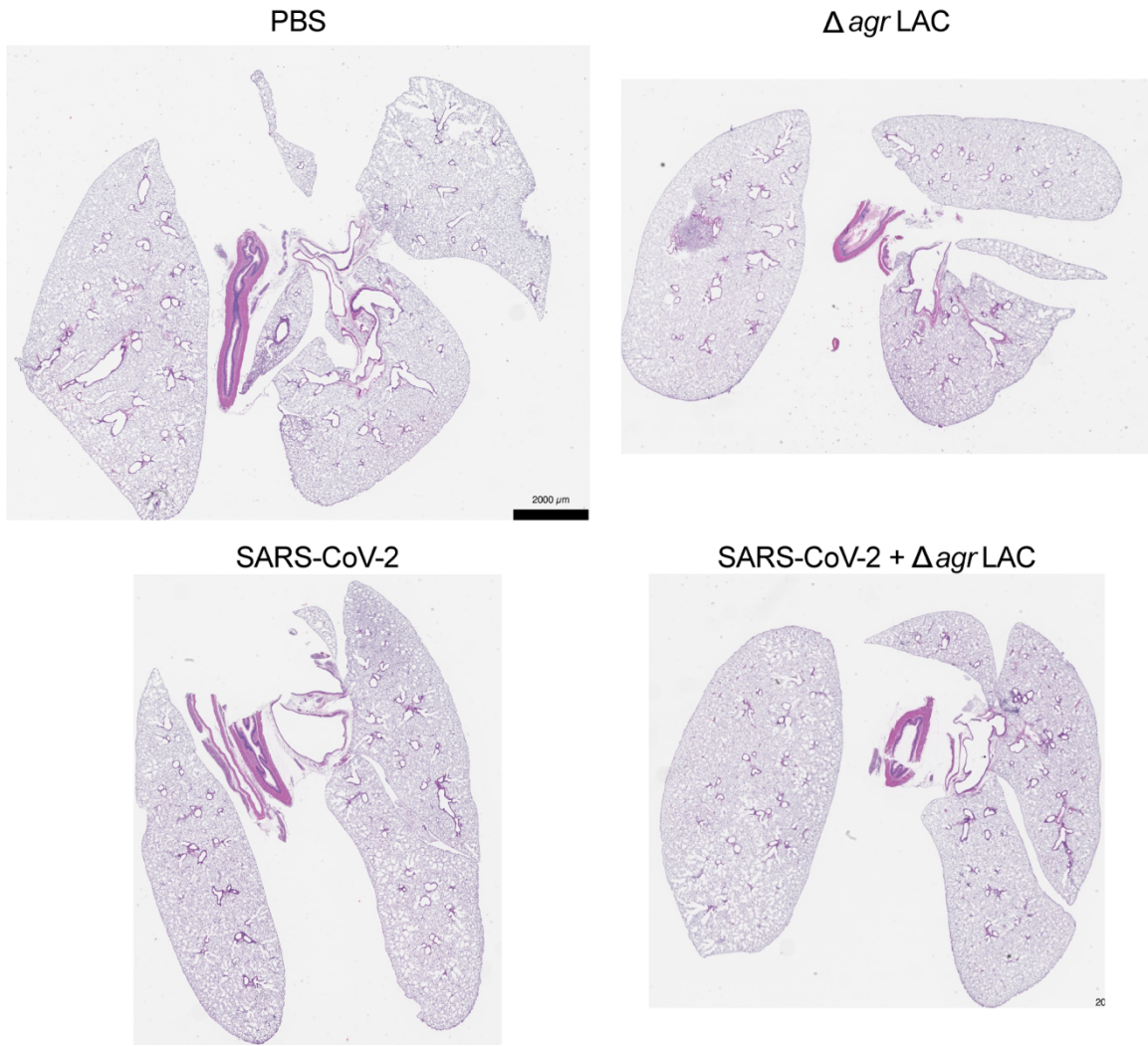
Figure S1. Phylogenetic analysis of *S. aureus* isolates.

All *S. aureus* isolates collected are indicated (including where multiple isolates were collected from the same patient at different times). Concentric circles represent CC/ST, mec type (Only type II and IV were represented in this collection of isolates. If no mec type is indicated, the strain is mec negative.), SARS-CoV-2 PCR result, and isolate source. \*\* = reference strain CA-347. CC = clonal complex, ST = sequence type, "NA" = other or not categorized.



**Figure S2. Growth, hemolysis, and color of the *S. aureus* isolates.**

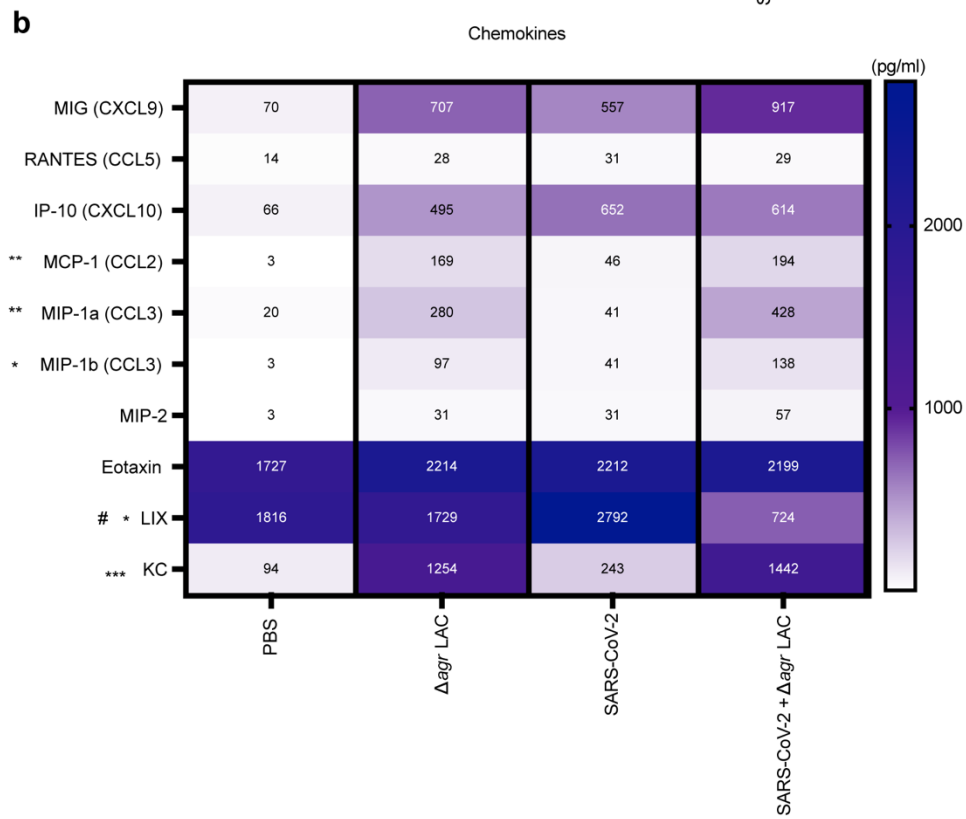
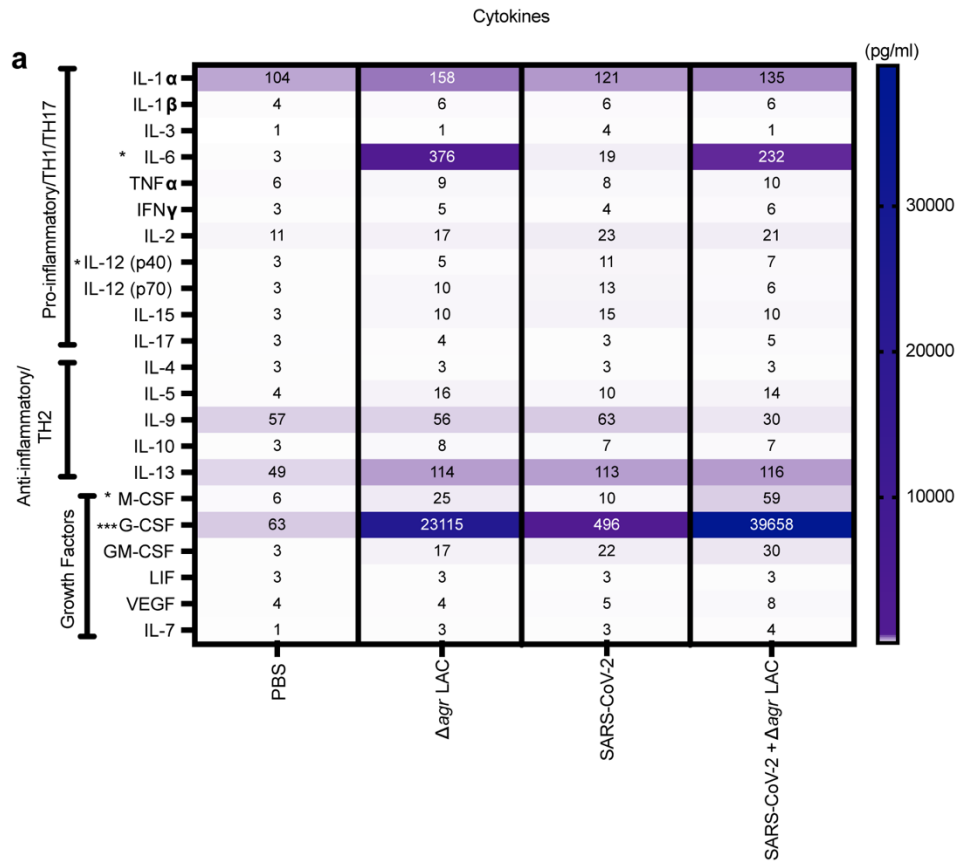
**a.** Growth curves of all isolates analyzed, with those that failed to reach an OD<sub>600</sub> of 1 highlighted in green. **b.** Features of the growth curve of isolates from SARS-CoV-2+ and SARS-CoV-2- patients. **c.** Hemolysis of isolates from SARS-CoV-2+ and SARS-CoV-2- patients. **d.** Color of isolates from SARS-CoV-2+ and SARS-CoV-2- patients when plated on TSA plates ranking from dark yellow (100%) to white (0%). Error bars represent median with interquartile range.  $p > 0.05$  for all plots, Mann-Whitney test (**b,d**), Fisher's exact test (**c**). PCR pos are isolates from SARS-CoV-2+ patients, and PCR neg are isolates from SARS-CoV-2- patients.



**Figure S3. Histology analysis of co-infected lungs.**

H&E staining of sections from lungs of mice infected with the indicated pathogens.

Representative images are shown.



**Figure S4. Cytokine analysis of plasma from co-infected mice.**

**a-b.** Cytokine **(a)** and chemokine **(b)** levels in serum at 4 days post infection. The mean of each group is shown. \* indicates a difference between the SARS-CoV-2 infected group and the coinfecting group, # indicates a difference between the *S. aureus* infected group and the coinfecting group (Student's t-test). \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ .