Supplemental Figures:

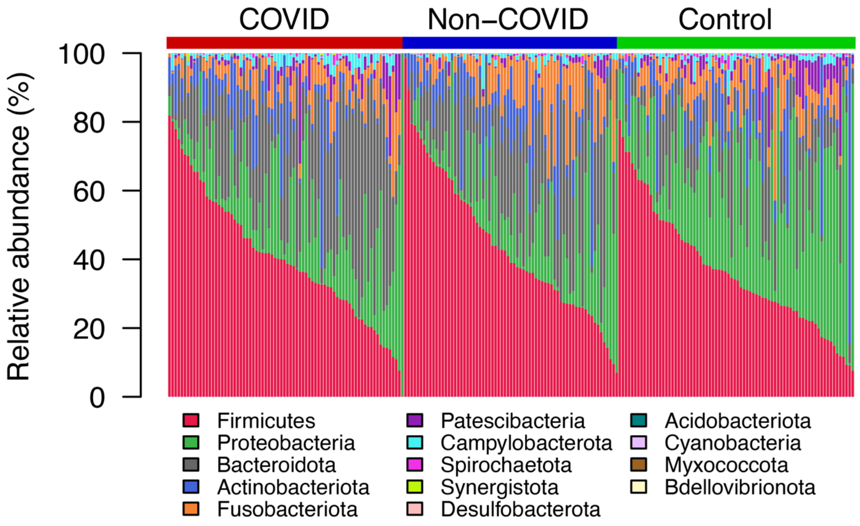

FIG S1 Composition of the naso-oropharyngeal microbiota in each study subject summarized at the phylum level.

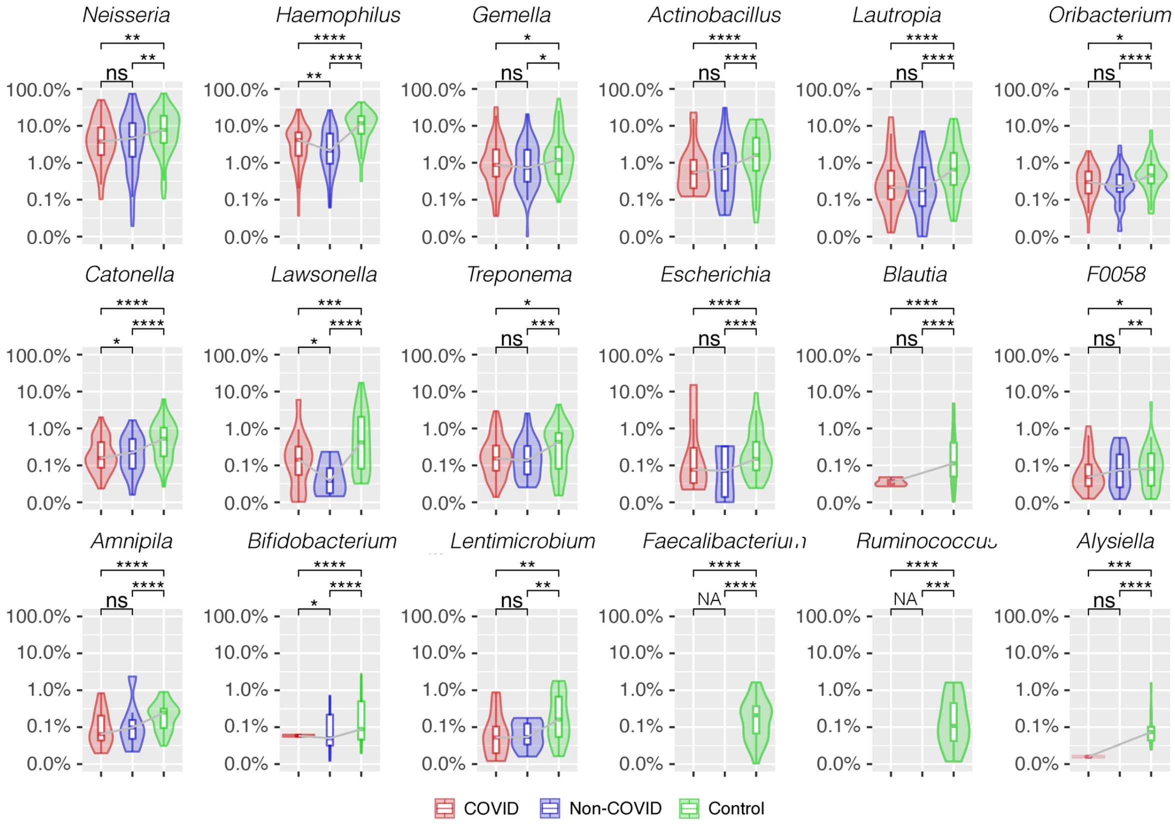

FIG S2 Comparison of the relative abundance of discriminative bacterial genera significantly depressed in both hospitalized COVID and non-COVID patients when compared with local controls. **, $p < 0.01$; ***, $p < 0.001$; ****, $p < 0.0001$; ns, not significant.

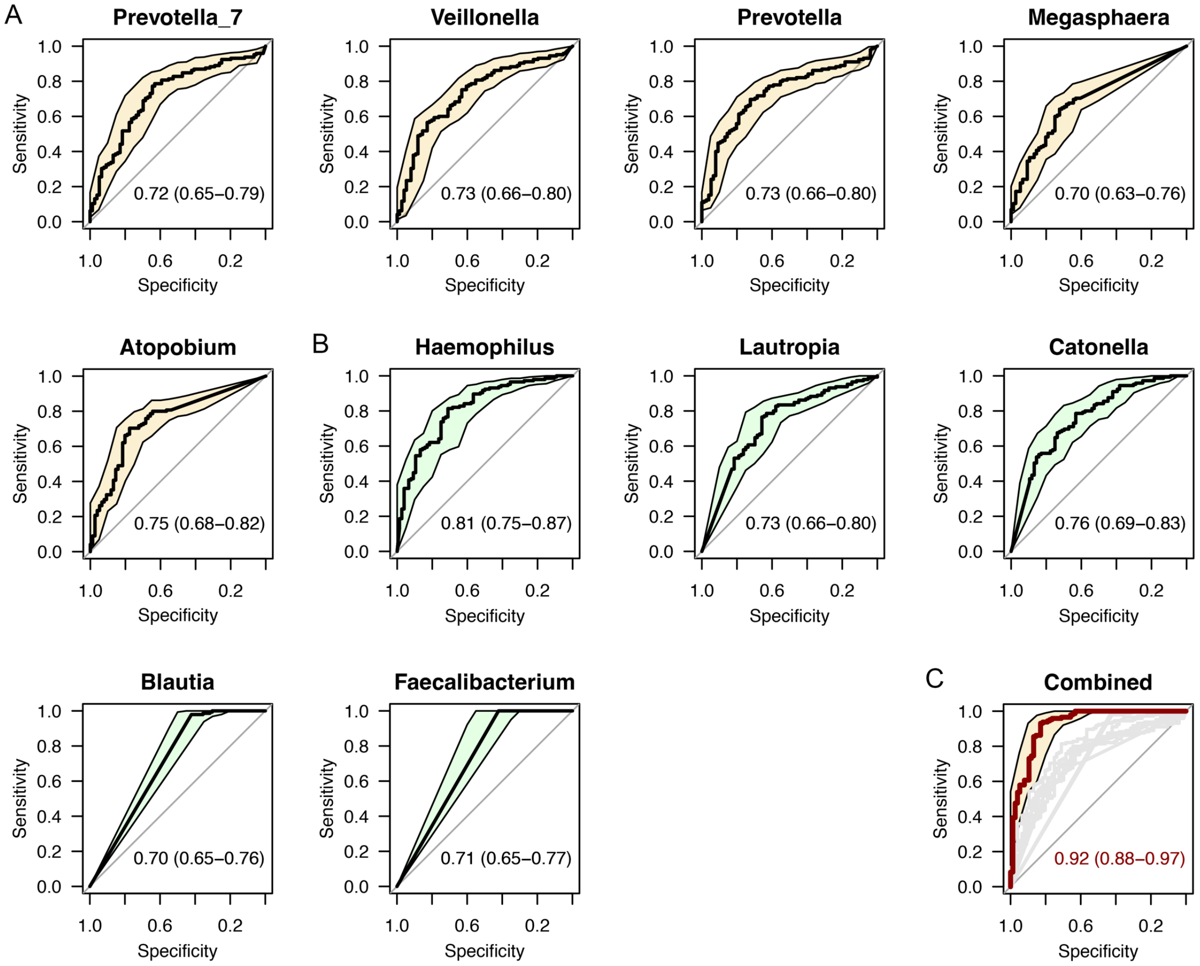

FIG S3 Receiver operating characteristic (ROC) analysis with area under the receiver operating curve (AUC) values distinguishing hospitalized patients (COVID and non-COVID) from local controls. **(A)** Five enriched and **(B)** five depressed bacterial genera with AUC ≥ 0.7 in both COVID and non-COVID patients achieved a combined AUC value of 0.92 **(C)**.

FIG S4 Associations between demographic and clinical parameters and the alpha diversity of the naso-oropharyngeal microbiota in COVID patients. CRP, C-reactive protein; NA, not available. *, $p < 0.05$; ns, not significant.

```
            Df SumOfSqs      R2      F Pr(>F)
Pneumonia    1   0.1444 0.01133 0.8613  0.613
Age          1   0.3315 0.02603 1.9779  0.020 *
Sex          1   0.1847 0.01450 1.1019  0.303
loadSample   2   0.3652 0.02867 1.0893  0.312
loadPeak     2   0.3477 0.02730 1.0372  0.383
crp          2   0.3021 0.02372 0.9012  0.609
Residual    66  11.0631 0.86846
Total       75  12.7387 1.00000
```

FIG S5 PERMANOVA results inferred from weighted UniFrac distance shows no relationship between the beta diversity of the naso-oropharyngeal microbiota in COVID patients and most host variables except age. CRP, C-reactive protein. *, $p <$ 0.05.