

Molecular characterization of influenza virus in intestines and its effect on intestinal microbiota

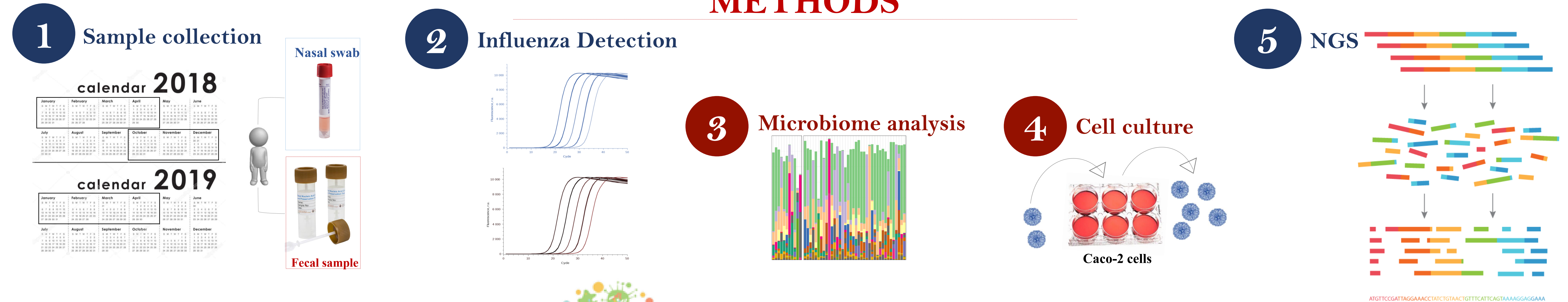
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BACKGROUND

Influenza predominantly causes respiratory illness; with gastrointestinal symptoms commonly reported in about 30% of patients. Influenza virus RNA has been also detected in stools of patients infected with pandemic and seasonal influenza, however, the role and the clinical significance of intestinal infection has not been clearly demonstrated.

Here we aim to (i) study the impact of influenza infection on intestinal microbiota; and (ii) characterize influenza viruses isolated from fecal samples of infected patients and their potential role in virus transmission.

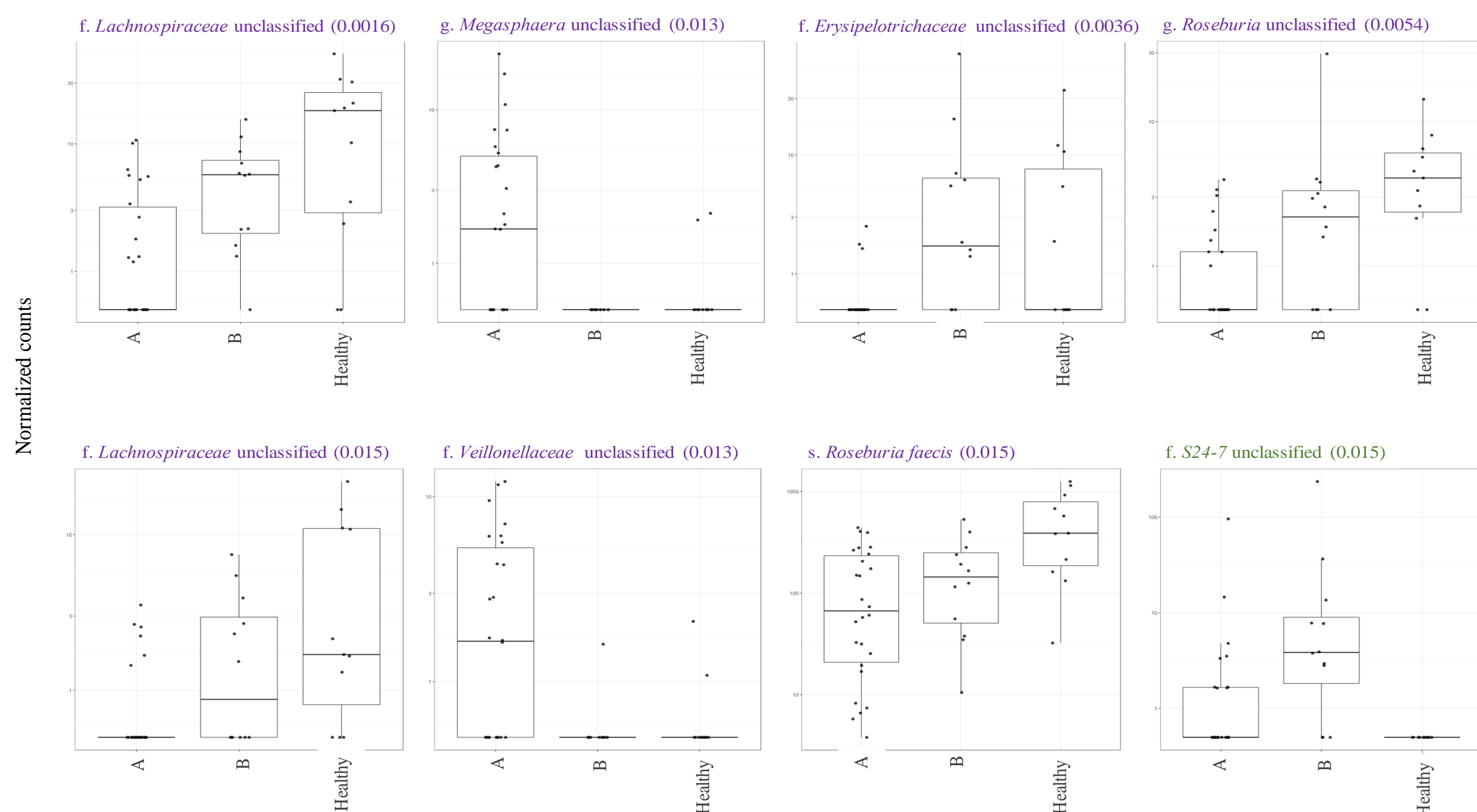
METHODS



RESULTS

MICROBIOME

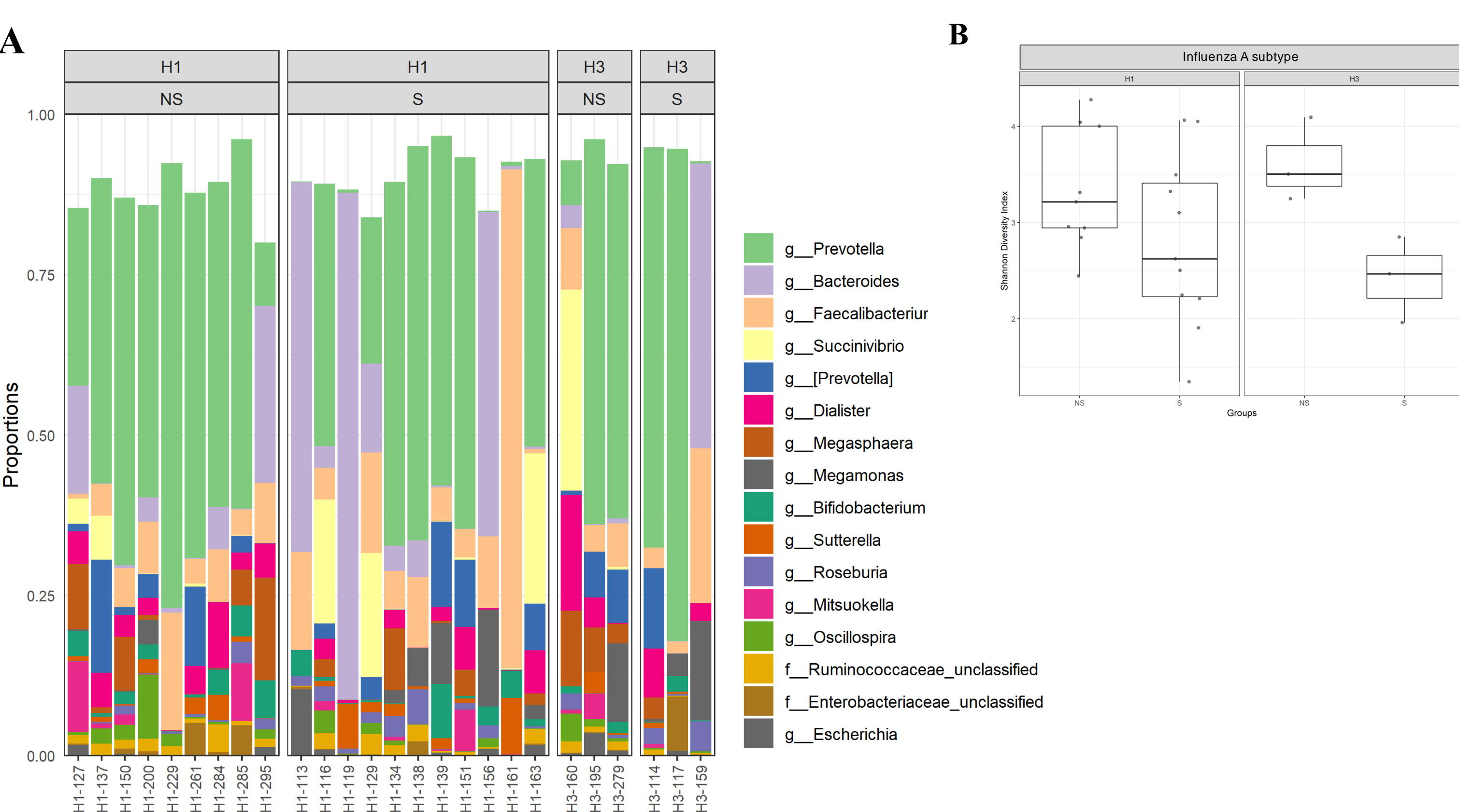
1. Changes in gut microbiota composition is directly related to influenza type. A total of 10 OTUs were found to be differentially abundant among influenza A- and B infected patients. Of these, the relative abundance of 6 OTUs were significantly higher in influenza B patients while 4 OTUs were more abundant in influenza A patients.



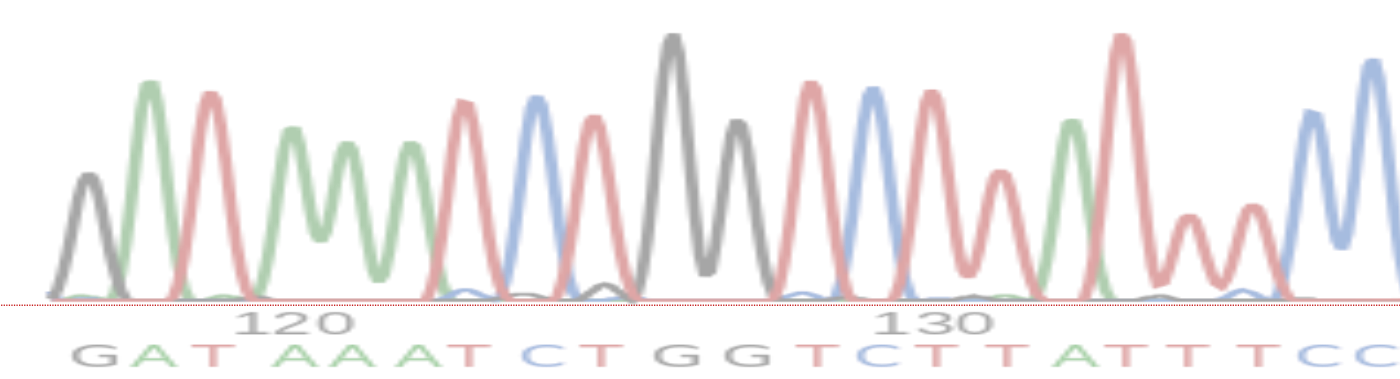
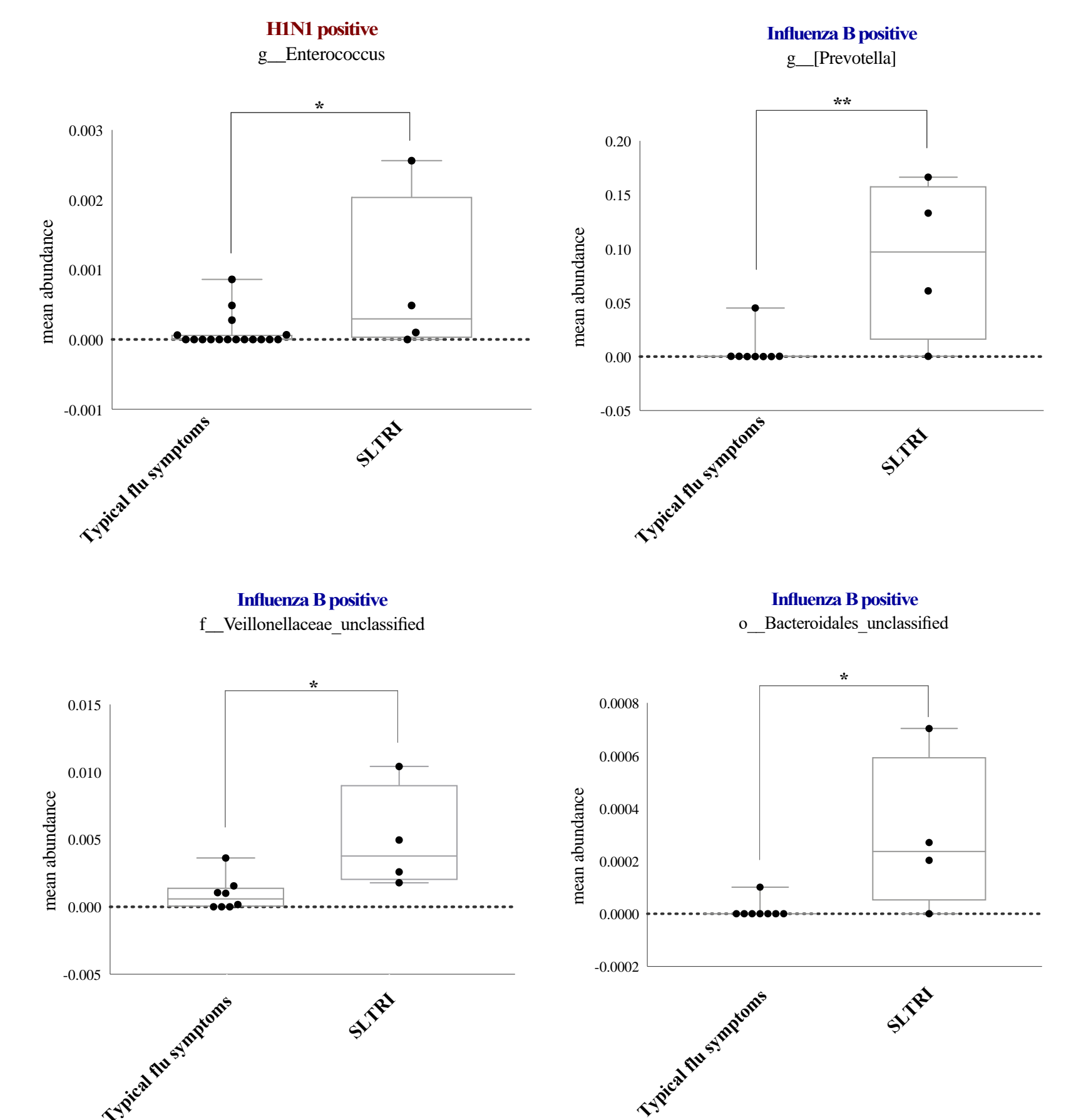
OTUs are colored based on phyla: purple for Firmicutes and green for Bacteroidetes. The Padj value for each OUT is indicated between brackets.

2. Comparison of intestinal bacteria diversity and composition in influenza-infected patients who were shedding virus in their stools (S) and those who were not (NS).

(A) Microbial profiles (at genus level) of shedders and non-shedders among H1N1 and H3N2 infected patients. (B) Alpha diversity of intestinal microbiota was significantly lower among shedders compared to non-shedders of H1N1 and H3N2 infected patients.

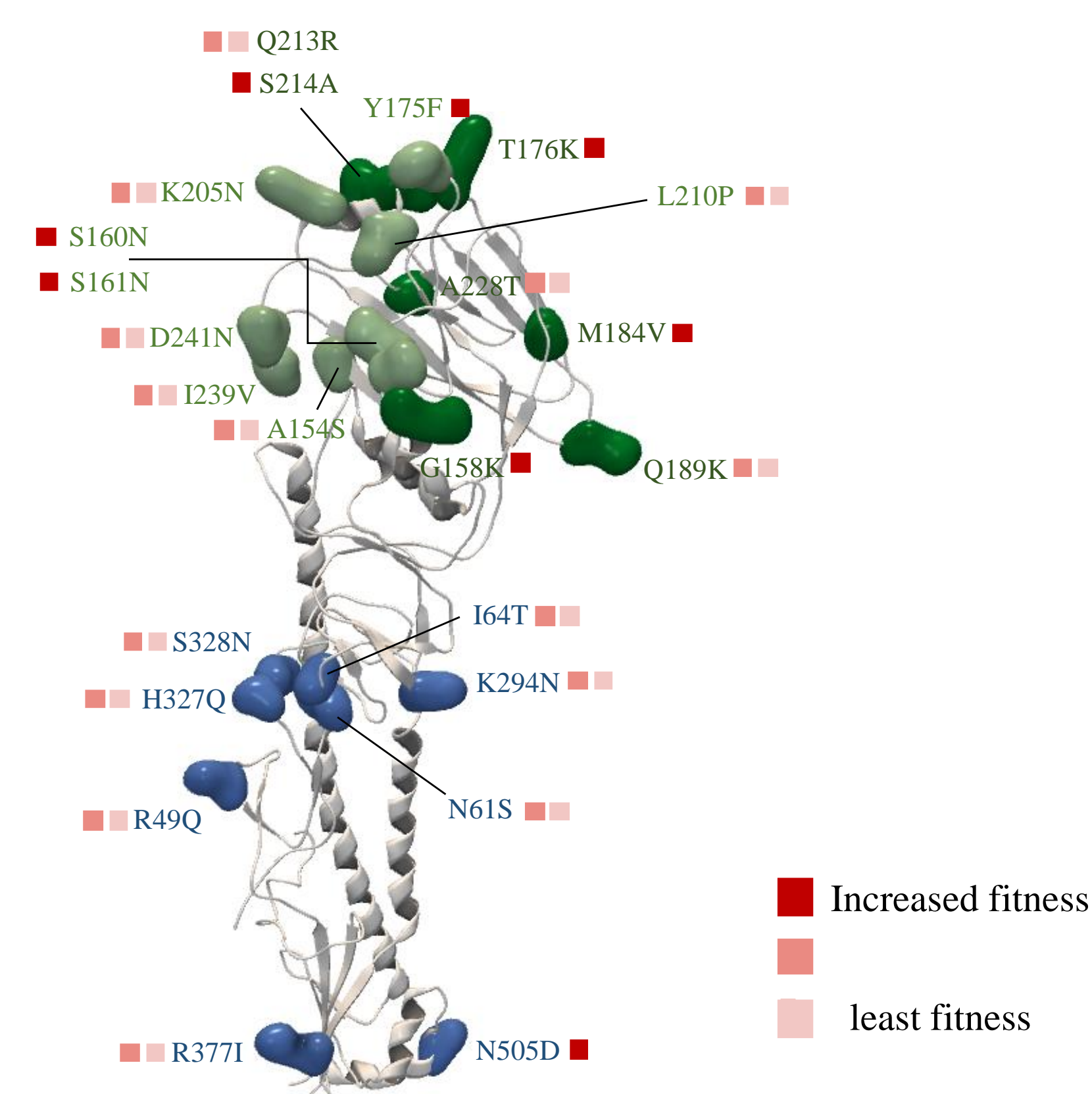


3. Comparison of mean relative abundance revealed higher abundance of 4 genera among patients with severe LRTI (lower respiratory tract infection) compared to patients with typical influenza symptoms.



RESULTS SEQUENCING

1. Mutations detected in HA protein of influenza viruses isolated from intestinal origin



CONCLUSION

Sequencing and microbiome analysis suggest that influenza viruses can affect intestinal environment either by direct intestinal infection or indirectly by modulating intestinal microbiota.

changes in gut microbiota composition in influenza-infected patients are significantly associated with:

- > influenza virus type
- > the presence of viral RNA in intestines of infected patients