

Correction to: Severe Dysbiosis and Specific *Haemophilus* and *Neisseria* Signatures as Hallmarks of the Oropharyngeal Microbiome in Critically Ill Coronavirus Disease 2019 (COVID-19) Patients

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Several errors appeared in supplementary data for the corrected proof publication of this article (de Castilhos J, Zamir E, Hippchen T, et al. Severe Dysbiosis and Specific *Haemophilus* and *Neisseria* Signatures as Hallmarks of the Oropharyngeal Microbiome in Critically Ill Coronavirus Disease 2019 [COVID-19] Patients. *Clin Infect Dis*; <https://doi.org/10.1093/cid/ciab902>).

- The barplots in Figure S1A were not correctly displayed due to an erroneous jitter function applied.
- The functional profiling of the metagenomes was not described. The data on microbial genes and pathways were

inferred from the HUMAnN3 pipeline (<https://github.com/biobakery/humann>). All statistical analysis were performed by R (version 3.6.1).

- The group assignments in the legends to Figures S3A and S3B contained a minor mistake.
- The legends of Figures S4E and S4D were swapped. The legend of S4D should describe the SARS-CoV-2 load in pharyngeal specimens over time, while the legend of Figure S4E should specify the network visualization of target microbial species.

The publisher regrets these errors.

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