## Methods

### Ethics declarations

We conducted a retrospective study of electronic medical and laboratory records. This study was approved by Life Medical Ethics Committee at Wuhan University (WHU-LFMD-IRB2023001).

### Overview of the study design

This project was performed at a single hospital in Wuhan, China. We included COVID-19 outpatients and inpatients admitted to the Renmin Hospital of Wuhan University between 7 December 2022 and 5 January 2023. COVID-19 was diagnosed according to the presence of SARS-CoV-2 in respiratory swabs or COVID-19 Coronavirus Rapid Antigen tests. Cases were included based on criteria from the World Health Organization and China's Coronavirus Pneumonia Diagnosis and Treatment Plan (provisional $10^{th}$ edition). Data were manually extracted from the electronic medical records that were included in a quality improvement database. We examined the time and date of admission of the hospital visit, analyses and diagnoses of COVID-19, and the microbiological test results. Each positive microbiological nucleic acid test result was reviewed by at least one infectious disease physician and was included if that result represented a clinically significant coinfection.

### Characterization of the microbiome of the respiratory tract

Coinfection was defined by clinical signs and/or symptoms of infection and further detection of a pathogen by microbiological nucleic acid tests. Sputum samples were subjected to nucleic acid tests to detect respiratory bacteria (*Acinetobacter baum*annii, *Escherichia coli*, St*reptococcus pneumonia*, *Klebsiella pneumonia*, *Mycoplasma pneumoniae*, *Staphylococcus aureus*, *Haemophilus influenzae*, methicillin-resistant *Staphylococcus aureus*, *Legionella pneumophila*, *Stenotrophomonas maltophilia*, *Legionella pneumophila, Pseudomonas aeruginosa, Mycoplasma pneumonia,* and *Chlamydophila pneumoniae*) and other respiratory viruses (rhinovirus, bocavirus, parainfluenza virus, coronaviruses, respiratory syncytial virus, Influenza A virus, Influenza A/H1N1, Influenza A/H3N2, Influenza B virus, human metapneumovirus, and human adenovirus).

**Statistical Analysis**

SPSS 24.0 statistical software was used for statistical analysis of the data. The count data were described statistically by frequency and component ratio, and compared between groups. $\chi 2$ test was used for those meeting the test conditions, or Fisher exact probability method or Cochran-Mantel-Haenszel test was used. The test level was $\alpha = 0.05$. $P < 0.05$ indicated statistically significant difference.