Building a single-cell atlas of the nasopharyngeal mucosa to investigate SARS-CoV-2 infection

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The nasal cavity serves as a crucial interface where numerous pathogenic and commensal bacteria, viruses first interact with the cells of our body. Understanding the cell types that line this interface in healthy individuals and how these cell types and their gene expression changes during an infection can provide insights into the progression of various diseases. Recently, during the COVID-19 pandemic, several groups have conducted single-cell RNA sequencing on samples collected from the nasopharyngeal cavity to investigate SARS-CoV-2 infections in greater detail. Using the data generated in these studies, we are building an atlas of the nasopharynx at a single cell level. We have identified six studies, of which we selected three studies with a total number of 1732267 cells from 328 individuals. Using Harmony, we have combined all these datasets and are currently re-annotating the cell types, including rarer cell types and sub-types. Next, we aim to investigate changes in the cell populations in terms of age, sex, and disease status. Taken together, this study will build a baseline atlas that can guide or assist future single cell RNA sequencing studies of the nasopharyngeal interface.