Map your data to the Human Lung Cell Atlas

The Human Lung Cell Atlas (Sikkema et al., biorXiv 2022) is a consensus reference model of the lung and nose. This reference was built by integrating data from 107 individuals and 14 datasets, and then re-annotating all cells in a consensus manner based on originally published labels and inputs from 6 experts.

Mapping your own lung single-cell or single-nucleus data to the HLCA will greatly speed up the analysis of your dataset. Upon mapping we can project consensus labels from the HLCA to your data and, using mapping uncertainty, highlight which cells seem different from healthy cells in the atlas. Depending on your experimental setup, these cells might represent novel cellular identities or cells particularly affected by disease.

**HLCA**
beta.fastgenomics.org/p/hlca

**Mapping with scArches**
beta.fastgenomics.org/analyses/scarches