

Stanford team creates cellular atlas of the human lung

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A team of researchers from multiple departments at Stanford University has created a cellular atlas of the human lung that highlights the dozens of cell types that comprise parts of the lungs. In their paper published in the journal *Nature*, the researchers describe their work (mostly involving single-cell RNA sequencing) and some of the things they learned about the lungs during their effort.

To create the atlas, the researchers collected [tissue samples](#) from bronchiole, bronchi and alveolar regions of the lungs, along with associated [blood samples](#). Each of the samples was broken down into its cellular components, which were then sorted by type: immune, epithelial, endothelial or stromal.

The researchers generated transcriptomes for approximately 75,000 cells. Using markers, the team then clustered the cells to reveal 58 distinct cell populations. In so doing, they were able to generate expression profiles for 91 percent of lung types—and also found 14 lung cell types not previously known to science. They also found

approximately 200 markers that could be used to identify the unknown types they found.

The team found they were able to use the resulting atlas to trace hormone targets in the lungs. In so doing, they found that some [hormone receptors](#) were expressed widely across different parts of the lungs, while others were not. And as part of this secondary effort, the researchers also identified areas where 233 genes are expressed that could be used by scientists working on understanding and curing a wide variety of lung diseases.

The researchers also used their atlas to compare human and mice lungs. They found that mice lack approximately 30% of human lung cell types, and humans lack approximately 5% of mouse lung cell types. They suggest this finding indicates there may have been more diversification of early mammalian species than previously thought.

The researchers suggest the atlas could be used by a wide variety of medical researchers, noting that it provides new insights into the regulation, interaction and function of [lung cells](#) and types.

More information: Kyle J. Travaglini et al. A molecular cell atlas of the human lung from single-cell RNA sequencing, *Nature* (2020). [DOI: 10.1038/s41586-020-2922-4](https://doi.org/10.1038/s41586-020-2922-4)

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