# A SINGLE CELL ATLAS OF THE HUMAN MIDDLE TURBINATE

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## BACKGROUND

**Single cell RNA-sequencing (scRNA-seq)** analyzes the entire transcriptome of individual cells and is now considered the gold standard for defining cell types and phenotypes. Cells are grouped based on similarity of their expression profiles using cluster analysis, and "marker" genes with statistically significant differences between cells in one cluster and cells in all other clusters are then used to identify cell types.[1,2]

The focus of our lab is the study of the neurodevelopmental etiology of **schizophrenia**. Prior research has shown that neural progenitor cells can be cultured from olfactory neuroepithelium obtained from turbinate biopsies.[3] The **middle turbinate** was selected for this study as it is readily accessible via in-office biopsy and plays a significant role in sinonasal desease.

## OBJECTIVE

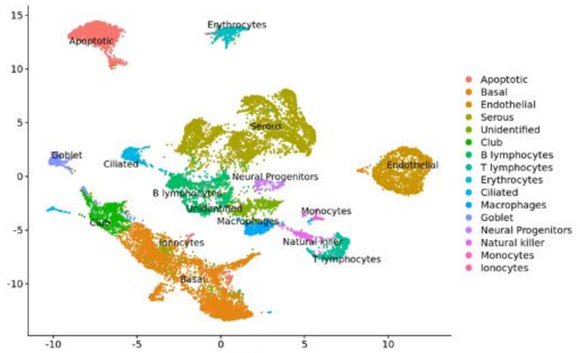
To create the first single cell transcriptome catalog of the human middle turbinate, including identification and characterization of cultured neural progenitors derived from olfactory neuroepithelium (CNON).

## METHODS

- Samples were obtained from the head of the middle turbinate using cupped forceps.
- After the specimen was prepared per lab protocol, cells were dissociated, suspended, and counted.
- Single cell libraries were then prepared according to the 10x Genomics protocol and sequenced using NovaSeq 6000 (Illumina).
- Sequencing data were processed using Cell Ranger, and clustering and gene expression analysis was performed using Seurat.
- Cell types were annotated through expression profiling of single cells using known markers and data from other single cell studies.

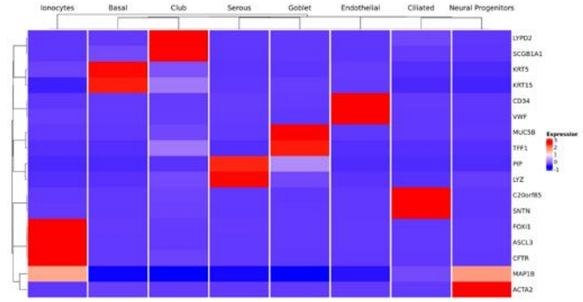
## RESULTS

### AGGREGATE ANALYSIS OF CELLS



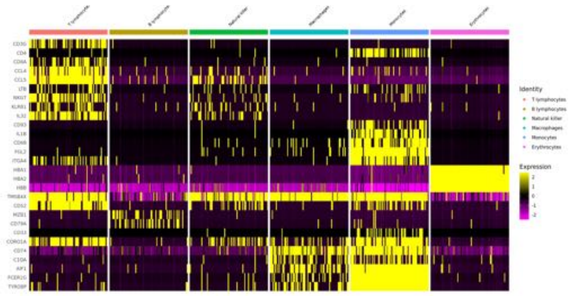

UMAP dimensionality reduction plot of 21,565 human middle turbinate cells from sample SEP310 (healthy donor). Clusters were labeled as 14 unique cell types according to known markers.

### RESPIRATORY EPITHELIAL CELL TYPES




Heatmap using average expression of marker genes for respiratory epithelial cell types.

### BLOOD CELL TYPES

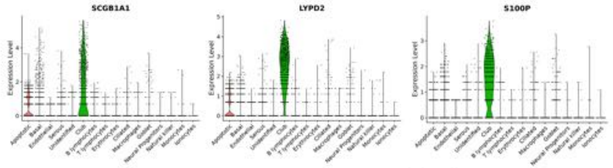



Heatmap using average expression of marker genes for blood cell types.

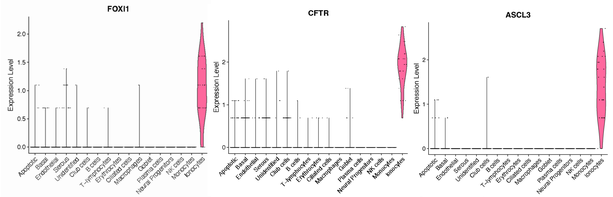
## DISCUSSION

This is the first description of club cells and pulmonary ionocytes in nasal turbinates, establishing potential links in the study of comorbid COPD and cystic fibrosis, respectively, in patients with CRS.

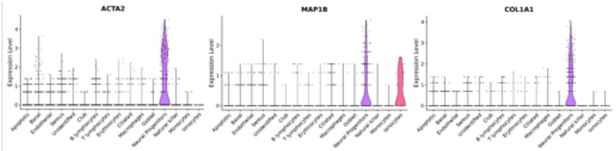
Neural progenitor cells were identified by genetic profiling; their ability to differentiate into neurons in vivo has yet to be demonstrated.




Violin plots show the expression distribution of various markers of **club cells**. Each dot represents a single cell.




Violin plots show the expression distribution of various markers of **pulmonary ionocytes**. Each dot represents a single cell.




Violin plots show the expression distribution of various markers of **cultured neural progenitor cells derived from olfactory neuroepithelium (CNON)**. Each dot represents a single cell.

## CONCLUSIONS

This atlas provides the first comprehensive cellular stratification of gene expression profiles in healthy middle turbinate epithelium.

In conjunction with subsequent research demonstrating cell type homogeneity, stability in cell culture, and similarity to a cell type in embryonic brain,[4] this database provides the genetic framework in using CNON to study neurodevelopmental disorders.

Future studies include spatial transcriptomic analysis of a partial middle turbinectomy specimen to correlate gene expression data to specific locations on the turbinate and comparing gene expression data between schizophrenia and control samples.

## REFERENCES

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