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 turbinates.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 disease.

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

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.

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.

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 CGR.

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

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, similarity in cell type in embryonic brain, this database provides the genetic framework in using CNON to study neurodevelopmental disorders. Future studies include spatial transcriptomic analysis of a partial middle turbinate specimen to correlate gene expression data to specific locations on the turbinate and comparing gene expression data between schizophrenia and control samples.

REFERENCES