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Characterizing smoking-induced transcriptional heterogeneity in the human bronchial epithelium at single-cell resolution

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The human bronchial epithelium is composed of multiple distinct cell types that cooperate to defend against environmental insults. While studies have shown that smoking alters bronchial epithelial function and morphology, its precise effects on specific cell types and overall tissue composition are unclear. We used single-cell RNA sequencing to profile bronchial epithelial cells from six never and six current smokers. Unsupervised analyses led to the characterization of a set of toxin metabolism genes that localized to smoker ciliated cells, tissue remodeling associated with a loss of club cells and extensive goblet cell hyperplasia, and a previously unidentified peri-goblet epithelial subpopulation in smokers who expressed a marker of bronchial premalignant lesions. Our data demonstrate that smoke exposure drives a complex landscape of cellular alterations that may prime the human bronchial epithelium for disease.

INTRODUCTION

The human bronchus is lined with a pseudostratified epithelium that acts as a physical barrier against exposure to harmful environmental insults such as inhaled toxins, allergens, and pathogens (1, 2). The bronchial epithelium is a complex tissue, predominantly composed of ciliated, goblet, club, and basal epithelial cells. These cell types cooperate to perform mucociliary clearance, which is the process that mediates the capture and removal of inhaled substances (1, 2). Goblet cells secrete components of a mucosal lining that entraps inhaled particulate matter, which is propelled out of the airways by mechanical beating of ciliated cells (1, 2). Club cells secrete components of a mucosal lining that entraps inhaled particulate matter, which is propelled out of the airways by mechanical beating of ciliated cells (1, 2). Club cells have both secretary (3) and progenitor (4) functions, and basal cells are multipotent progenitors responsible for normal tissue homeostasis (5–7). Interplay among these cells is required for proper function and long-term maintenance of the bronchial epithelium, but exposure to substances, such as tobacco smoke, might alter or injure specific cell types and lead to tissue-wide dysfunction.

Inhalation of tobacco smoke exposes the bronchial epithelium to toxins, carcinogens, and free radicals (8–11), but cellular injuries and abnormalities associated with this exposure are complex and have not been fully characterized. Previous studies have described smoking-induced epithelial changes, such as increased goblet cell numbers (12–14) and reduced ciliary length (15, 16). Robust transcriptomic alterations have also been observed in the bronchial epithelium of smokers, involving the up-regulation of genes linked to xenobiotic metabolism and the oxidative stress response (17, 18). Furthermore, it has been reported that a subset of gene expression alterations detected in smokers persists years after smoking cessation (18). However, the aforementioned transcriptomic studies profiled bronchial tissue in “bulk,” masking cell type–specific contributions to the smoking-associated gene expression signature.

To overcome the limitations of bulk tissue analyses, we used single-cell RNA sequencing (scRNA-Seq) to profile the transcriptomes of individual bronchial cells from healthy never and current smokers. We identified bronchial subpopulations using an unsupervised machine learning algorithm and immunostained bronchial tissue from independent cohorts of never and current smokers to validate robust smoking-associated findings. In the airways of smokers, we described a metabolic response specific to ciliated cells, a shift in the presence of club and goblet cells, and the emergence of a previously uncharacterized epithelial subpopulation.

RESULTS

scRNA-Seq was used to identify bronchial subpopulations in the airways of never and current smokers

Bronchial brushings were procured by bronchoscopy from the right mainstem bronchi of six healthy current smokers and six healthy never smokers (table S1), and single ALCAM+ epithelial cells (19) and CD45+ white blood cells (WBCs) were isolated from each donor (Fig. 1A and fig. S1). The CEL-Seq scRNA-Seq protocol (20) was used to profile the transcriptomes of 84 epithelial cells and 11 WBCs from each of the 12 donors (1140 total cells: 1008 epithelial cells and 132 WBCs). Low-quality cells were excluded from downstream analyses, leaving 796 cells (753 epithelial cells and 43 WBCs) (figs. S2 and S3) expressing an average of 1817 genes per cell. Expression of known marker genes for bronchial cell types was detected in largely nonoverlapping cells, including KRT5 for basal cells, FOXJ1 for ciliated cells, SCGB1A1 for club cells, MUC5AC for goblet cells, and CD45 for WBCs (Fig. 1B). Given the relatively small number of donor bronchial epithelial cells, we were able to use a relatively small number of cells for robust statistical analyses.
of subjects, we sought to determine whether smoking-associated gene expression changes identified in these donors reflected those observed in a larger, independent cohort of never and current smokers. Data from all cells procured from each donor were combined to generate in silico bulk bronchial brushings. Analysis of differential expression between never and current smoker in silico bulk samples revealed associations that were highly correlated (Spearman’s \( r = 0.45 \)) with those observed in a previously published bulk bronchial brushing.

To characterize cellular subpopulations beyond known cell type markers, we used latent Dirichlet allocation (LDA) as an unsupervised framework to assign cells to clusters and identify distinct sets of coexpressed genes across all cells (Fig. 1C). LDA divided the dataset into 13 distinct cell clusters and 19 sets of coexpressed genes (Fig. 2, A and B, and figs. S5 to S8). Each cell cluster was defined by the expression of a unique combination of gene sets, and each gene set was defined by a unique expression pattern among clusters (Fig. 2, A and B, and fig. S9). Cell types were defined for 8 of the 13 clusters based on medium to high marker gene expression: Cell clusters C-2 and C-4 expressed \( KRT5 \), C-5 and C-11 expressed \( FOXJ1 \), C-1 and C-8 expressed \( SCGB1A1 \), and C-3 expressed \( MUC5AC \) (Fig. 2C). Cluster C-7 expressed WBC marker \( CD45 \) (Fig. 2C), and Fisher’s exact test was used to show that C-7 was enriched with sorted WBC. C-7 cells also expressed several T cell receptor genes (e.g., \( TRBC2 \) and \( TRGC1 \)), indicating a T cell lineage (fig. S10). Low levels of \( SCGB1A1 \) transcripts were detected in cluster C-10 (\( SCGB1A1^{low} \)), and \( CFTR \) was expressed by cluster C-13, which suggests that these cells may be ionocytes (fig. S11) (21). Marker gene expression was not detected in clusters C-6, C-9, and C-12 (Fig. 2C). Enrichment [false discovery rate (FDR) \( q < 0.05 \)] of current smoker cells was observed in goblet cell cluster C-3, as well as C-9 and C-12, whereas that of never smoker cells was observed in club cell cluster C-1 and basal cluster C-4 (Fig. 2D). Donor-specific contributions of cells to each cluster were variable; however, most of the never and current smokers contributed to each never and current smoker–associated cell cluster, respectively (fig. S12). Furthermore, a subset of gene sets expressed by specific clusters of ciliated, club, goblet, and basal cells, as well as those without a cell type designation, was differentially expressed between never and current smokers in transcriptomic data generated from bulk bronchial tissue (Fig. 2, A and B, and fig. S13) (18). Therefore, smoking-induced gene expression changes reported in bulk tissue are likely driven by alterations to multiple bronchial cell types.

### Ciliated cell subpopulations and smoking-induced detoxification

We characterized transcriptomic similarities and differences among \( FOXJ1^{+} \) clusters C-5 and C-11 to define ciliated cell subpopulations detected in never and current smokers. Our data revealed that both clusters of ciliated cells expressed gene set GS-2 but could be differentiated based on expression of gene set GS-3 by cluster C-5 and gene set GS-7 by cluster C-11 (Fig. 3A). GS-2 contains \( FOXJ1 \), in addition to genes involved with ciliary assembly, maintenance, and function, such as motor protein genes (e.g., \( DYNLL1 \) and \( DNAH9 \)) and intraflagellar transport genes (e.g., \( IFT57 \) and \( IFT172 \)) (Fig. 3A and extended table S3). GS-2 also includes antioxidant genes (e.g., \( PRDX5 \), \( GPX4 \), and \( GSTA2 \)), known transcriptional regulators of ciliogenesis [e.g., \( RFX2 \) (22, 23) and \( RFX3 \) (24, 25)], and surface proteins not
Previously attributed to ciliated cells (e.g., CDHR3 and CD59), GS-3 contains genes with known roles in airway ciliary biology, such as IFT88 (required for ciliary formation) (26–28) and DNAH5 (required for ciliary motility) (29–31). By contrast, gene set GS-7 is enriched with cell cycle–associated genes (extended table S3), such as CDK1 and CCNB1 (G1-S transition) and TOP2A (S-phase DNA replication), as well as the transcription factor HES6. Therefore, clusters C-5 and C-11 likely represent functionally distinct subpopulations of FOXJ1+ ciliated cells.

We found that ciliated cells from current smokers expressed a distinct transcriptional signature. Specifically, the current smoker subset of cluster C-5 FOXJ1+ cells expressed gene set GS-8, which was enriched with genes encoding enzymes implicated in aldehyde and ketone metabolism, such as ALDH3A1, AKR1C1, and AKR1B10 (Fig. 3B). This finding suggested that the gene expression response to toxic aldehydes and ketones present in tobacco smoke (Fig. 3B). This finding suggested that the gene expression response to toxic aldehydes and ketones present in tobacco smoke might be restricted to ciliated epithelial cells. To confirm that this set of enzymes localized to ciliated cells, we immunostained bronchial tissue procured from an independent cohort of never and current smokers [University Medical Center Groningen (UMCG) cohort, table S2] for the aldo-keto reductase AKR1B10, as well as cilia-specific acetylated α-tubulin (Ac-α-Tub) and the luminal cytokeratin KRT8, which is expressed by all nonbasal cells (Fig. 3C). We found that AKR1B10 was robustly expressed in the airways of current smokers, and numbers of AKR1B10+ ciliated cells were significantly higher than those observed in never smokers (P = 7.4 × 10−7; Fig. 3, C and D). AKR1B10 was detected throughout the cytoplasm of smoker ciliated cells, as well as at the base of the cilia (Fig. 3C).

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**Club cell depletion and goblet cell expansion in the airways of smokers**

Our data revealed that the largest cluster of SCGB1A1+ cells, C-1, was enriched with never smoker cells (Fig. 2D), indicating that this subpopulation of club cells was depleted from the airways of smokers. C-1 cells distinctly expressed high levels of gene set GS-19, which contains MUC5B, in addition to SCGB3A1 and transcription factors TCF7, FOS, and JUN (Fig. 4A). However, SCGB1A1 (included in gene set GS-17) was also highly expressed by cluster C-8, which was not affected by smoking status (Fig. 2D). Therefore, these results indicate that smoking is associated with a decrease in MUC5B+ SCGB1A1+ (C-1) club cell content. Furthermore, gene set GS-13, which contains immunologically relevant genes BPIFB1 (32) and PIGR (33) (Fig. 4A), was expressed by SCGB1A1+ cells (C-1 and C-8) as well as MUC5AC+ cluster C-3, indicating that there may be functional overlap among club and goblet cells.

The MUC5AC+ goblet cell cluster C-3 was significantly enriched with current smoker cells (Fig. 2D), which is consistent with previous studies showing that smoking is associated with increased bronchial...
goblet cell abundance (12–14). Cluster C-3 expressed gene set GS-1, which contains the goblet cell marker gene MUC5AC as well as several genes with known roles in goblet cell biology, such as SPDEF (34), AGR2 (35), and TFF3 (36) (Fig. 4A). Genes associated with the unfolded protein response are present in GS-1 (e.g., KDLER3 and DNAJC10) (extended table S3). We also identified several unique goblet cell surface markers (e.g., CLDN10, TSPAN8, and TSPAN13), as well as a transcription factor (NKX3-1) whose role in the goblet cell transcriptional program is unknown (Fig. 4A). Therefore, these data indicate that smoking is associated with increased numbers of MUC5AC+ goblet cells.

To confirm smoking-associated shifts in club and goblet cell numbers, we immunostained bronchial tissue procured from an independent cohort of never and current smokers (UMCG cohort, table S2) for markers of club (MUC5B) and goblet (MUC5AC) cells (Fig. 4B). Imaging data revealed cell subpopulations that exclusively express MUC5B or MUC5AC, as well as those that coexpress both MUC5B and MUC5AC (Fig. 4B). The airways of never smokers contained similar numbers of MUC5B+, MUC5B+, MUC5AC+, and MUC5AC+ cells (Fig. 4, B and F). The bronchial epithelium of current smokers, however, took on two distinct phenotypes: tissue regions described as “morphologically normal” (MN), which were similar to never smokers, and regions characterized by high MUC5AC+ cell density, referred to as goblet cell hyperplasia (GCH) (Fig. 4B and fig. S15). In the MN smoker tissue, we observed a significant decrease in MUC5B+ cells ($P = 0.02$) (Fig. 4C) and a significant increase in MUC5AC+ cells ($P = 1.5 \times 10^{-6}$) (Fig. 4E), relative to never smokers, but no change in MUC5B+ MUC5AC+ content was observed (Fig. 4D). Differences between smoker GCH and never smoker epithelium, however, were more pronounced. Near-complete loss of MUC5B+ cells was observed in smoker GCH ($P = 1.8 \times 10^{-5}$; Fig. 4C), along with a significant loss of MUC5B+ MUC5AC+ cells ($P = 0.02$; Fig. 4D), relative to never smokers. GCH-associated alterations were accompanied by a 13-fold increase in MUC5AC+ cells ($P = 7.4 \times 10^{-7}$; Fig. 4, E and F). Additional immunostaining for KRT5 expression in the same bronchial tissue revealed that basal cell...
content was not affected by smoking status and did not vary between
MN and GCH regions (fig. S16). Overall, these findings indicate
that smoking is associated with a loss of club cells, increased num-
bers of goblet cells, and substantial GCH airway remodeling.

The bronchial airways of smokers contain a previously
unidentified subpopulation of PG epithelial cells

We sought to establish the identity of cluster C-9, which was strongly
enriched with current smoker cells and did not express established
cell type marker genes (e.g., KRT5, FOXJ1, SCGB1A1, and MUC5AC)
(Fig. 2C). C-9 cells expressed high levels of gene set GS-12, which
contains the luminal cytokeratin KRT8 (Fig. 5A). Additional cyto-
keratin genes were also present in GS-12, such as KRT13 and
KRT19, as well as antioxidant genes, such as TXN and GPXI (Fig. 5A).
Cluster C-9 also expressed gene set GS-16, which was detected at
low levels in MUC5AC+ cells (C-3) and contained the xenobiotic
metabolism gene CYP1B1 (Fig. 5A). Furthermore, high expression
of gene set GS-15 was detected in both C-9 and MUC5AC+ cells
(C-3) (Fig. 5, A to C), suggesting that this cluster may have a functional
relationship with goblet cells. GS-15 contains several genes previously
reported to be persistently up-regulated after smoking cessation
(e.g., CEACAM5, CEACAM6, and UPK1B) (18), one of which has
been explicitly linked to lung squamous cell carcinoma (SCC) and premalignancy (CEACAM5) (37).

To validate the presence of cluster C-9 cells in the airways of
current smokers, we immunostained bronchial tissue procured
from a second independent cohort of never and current smokers
[University College London (UCL) cohort, table S3] for KRT8,
MUC5AC (goblet cells), and Ac-α-Tub (ciliated cells). KRT8+
MUC5AC− Ac-α-Tub− cells that were morphologically distinct
from goblet and ciliated cells were detected in significantly higher
numbers in GCH regions of current smokers relative to never
smokers (fig. S17). To confirm that there was functional overlap
between goblet cells and this subpopulation of KRT8+ MUC5AC−

Fig. 4. Smoking is associated with increased numbers of goblet cells and decreased numbers of club cells in the bronchial epithelium. (A) Expression of gene sets GS-19, GS-17, GS-13, and GS-1 in clusters C-1, C-8, and C-3 was visualized by heatmap (z-normalized TPM values). Bronchial tissue procured from an independent cohort of never and current smokers (UMCG cohort, table S2) was immunostained for MUC5B and MUC5AC. (B) Representative images of never smoker tissue, MN current smoker tissue are displayed. Arrows specify examples of MUC5B+, MUC5B+ MUC5AC+, and MUC5AC+ cells. Changes in tissue length (μm)–normalized

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smokers (fig. S17). To confirm that there was functional overlap
between goblet cells and this subpopulation of KRT8+ MUC5AC−
Ac-α-Tub− cells, we immunostained bronchial tissue (UCL cohort, table S3) for CEACAM5, in addition to KRT8 and MUC5AC. Increased numbers of CEACAM5+ KRT8+ MUC5AC− cells were detected in GCH regions of current smokers relative to never smokers (P = 0.004) (Fig. 5, D and E), although variable content among donors was observed. Within current smoker GCH tissue regions, CEACAM5+ KRT8+ MUC5AC− cells were typically found in close proximity to goblet cells (CEACAM5+ KRT8+ MUC5AC+) and were therefore named peri-goblet (PG) cells (UCL cohort, Fig. 5D; UMCG cohort, fig. S18). CEACAM5 expression in goblet cells was phenotypically punctate and colocalized with MUC5AC in both never and current smokers (Fig. 5D and fig. S18). In PG cells, however, CEACAM5 localized to the plasma membrane and cytoplasm (Fig. 5D and fig. S18). Overall, these data indicate that PG cells are a previously unidentified, bronchial epithelial subpopulation associated with smoking-induced GCH.

**DISCUSSION**

Previous transcriptomic studies have shown that smoking is associated with a robust bronchial gene expression signature (17, 18). Interrogation of bronchial tissue at single-cell resolution revealed that elements of this signature were derived from different cell subpopulations. Overall, we found smoking-associated phenotypes that included a metabolic response that localized to ciliated cells, a cell type shift that involved club cell loss and goblet cell expansion, and a previously uncharacterized subpopulation of PG epithelial cells present within regions of GCH (fig. S19).

We identified a gene set (GS-8) specifically expressed by smoker ciliated cells (C-5) that contains genes encoding families of enzymes, such as aldehyde dehydrogenases (e.g., ALDH3A1 and ALDH1A3) and aldo-keto reductases (e.g., AKR1B10 and AKR1C1), capable of breaking down tobacco smoke–derived chemical compounds, such as toxic aldehydes (e.g., formaldehyde and acrolein) and ketones (e.g., acetone and methyl vinyl ketone) (8, 9). This finding suggests that ciliated cells exhibit a cell type–specific coping mechanism that may convey resistance to certain forms of smoking-induced toxicity. Links between this mechanism and previously reported smoking phenotypes, such as reduced ciliary length (15), however, are unclear. This finding might also highlight a protective function with tissue-wide significance, in which the bronchial epithelium’s capacity for detoxification may be compromised if ciliated cells are lost because of injury or disease.
Several studies have reported that smoking is associated with increased mucous production and GCH in the bronchus (12–14, 38–40). Loss of club cells (SCGBlA1) has been reported in smoker bronchioles (11, 12), but this is the first instance in which a similar observation has been made in the mainstem bronchi. We confirmed that GCH is a regional phenomenon interspersed among MN tissue areas. The determinants of GCH prevalence are unclear, but it has been shown that cytokines [e.g., interleukin-13 (IL-13) and (IL-4)] (41–43) and viral infection (e.g., Rhino virus and polyinosinic:polycytidyllic acid) (44, 45) can increase MUC5AC expression and goblet cell abundance. The specific catalyst for GCH in response to smoke exposure is unknown, but reports of its co-occurrence with airway inflammation suggest that immunological interplay may be a factor (14). Furthermore, there is evidence that both basal and club cells are capable of goblet cell differentiation (32, 46). However, the origins of newly formed goblet cells in the airways of smokers have not been explicitly described. Functional implications for goblet cell expansion and club cell loss are unclear, but a similar phenotype has been described in the airways of asthmatics, in which diminished mucosal fluidity, the formation of mucosal plugs, and impaired mucociliary clearance were observed (47, 48). Murine models have also shown that MUC5B loss is associated with impaired mucociliary clearance, airflow obstruction, and respiratory infection (49).

Smoking-induced GCH was associated with the presence of a previously uncharacterized subpopulation of CEACAM5+ KRT8+ MUC5AC− PG epithelial cells. The origins of PG cells are unclear, but a KRT8− undifferentiated epithelial subpopulation derived from basal cells, referred to as “suprabasal,” has been described in murine models (46, 50). Suprabasal cells act as intermediate precursors to ciliated and secretory cells during basal cell differentiation under normal conditions (46) and, after injury, as a repair mechanism (50). However, the suprabasal phenotype has not been characterized in the human bronchus, and little is known regarding human intermediate epithelial subpopulations. Furthermore, the involvement of a KRT8+ intermediate state in club cell transdifferentiation (4, 34) has not been explored. Goblet cell differentiation required for the onset and maintenance of smoking-associated GCH might involve a pro-goblet precursor subpopulation, but the explicit role of PG cells in this context requires further investigation.

It has been reported that CEACAM5 expression is persistently up-regulated in the airways of former smokers, whereas genes specifically expressed by goblet cells, such as MUC5AC, SPDEF, and AGR2, return to normal, never smoker levels post-smoking cessation (18). These findings suggest that goblet cell expansion in the airways of smokers is reversible, whereas the emergence of CEACAM5+ PG cells might have long-term implications. The functional consequences of the presence of PG cells are unclear, but irreversible alterations to bronchial epithelial composition might underlie chronic disease states. Although PG cells were identified in this study in the absence of established disease phenotypes, CEACAM5+ KRT5+ cells have been detected in bronchial premalignant lesions and lung SCC (37). CEACAM5 has also been detected in numerous additional cancer types (51, 52), and several genes that are coexpressed with CEACAM5 (i.e., detected in GS-15) have been implicated in carcinogenesis, such as UPK1B (53), MSLN (54, 55), and PSCA (56, 57). Therefore, investigation of mechanisms linking the presence and variable abundance of GCH-associated CEACAM5+ PG cells and premalignant lesion-associated CEACAM5+ KRT5+ cells might provide insight into smoking-induced conditions that promote lung carcinogenesis.

These data demonstrate that human bronchial epithelial exposure to tobacco smoke drives ciliated cell–specific toxin metabolism and leads to both club cell depletion and goblet cell expansion. A novel subpopulation of PG cells was also detected in the bronchial airways of smokers in association with GCH. These results will enable us to more precisely define the landscape of smoking-induced epithelial abnormalities. Future work will use experimental systems to define the consequences of specific, smoke-derived chemical compounds and investigate the recapitulation and reversal of cell and molecular phenotypes observed in this study. Furthermore, these findings may be leveraged to improve diagnostics and develop preventative strategies for smoking-associated lung diseases.

**MATERIALS AND METHODS**

**Bronchial tissue collection for scRNA-Seq**

At Boston University Medical Center, healthy volunteer never smokers (n = 6) and current smokers (n = 6) underwent a bronchoscopy to obtain brushings from the right mainstem bronchus, as described previously (17, 18). Eligible volunteers included subjects who (i) were between the ages of 19 and 55; (ii) did not use inhaled or intranasal medications; (iii) did not have a history of chronic obstructive pulmonary disease, asthma, pulmonary fibrosis, sarcoid, or head and neck/lung cancer; (iv) did not use marijuana; (v) did not have a respiratory infection within the past 6 weeks; and (vi) did not use other tobacco products (i.e., pipe, cigar, and chewing). Spirometry was performed to assess lung function (e.g., FEV1/FVC). Exhaled carbon monoxide (Smokerlyzer Carbon Monoxide Monitor, model EC-50; Bedfont Scientific Ltd.) and urine cotinine (NicAlert; Confirm Biosciences) levels were measured to confirm smoking status. The Institutional Review Board approved the study, and all subjects provided written informed consent.

**Single-cell isolation by FACS**

Bronchial brushings were treated with 0.25% trypsin/EDTA for 20 min and stained for sorting using a BD FACSArIA II. Gating based on forward scatter height (FSC-H) versus forward scatter area (FSC-A) was applied to sort single singlet events (fig. S1A). Dead cells (LIVE/DEAD Fixable Aqua Dead Cell Stain, Thermo Fisher; L34957) and red blood cells expressing GYPB/A (fig. S1B) on their surface [allophycocyanin (APC) anti-CD325a; BioLegend, 306607] were stained and excluded. ALCAM+ epithelial cells [phycoerythrin (PE) anti-CD166; BioLegend, 343903] and CD45+ WBCs (APC-Cy7 anti-CD45; BD, 561863) were stained (fig. S1C) and sorted into 96-well polymerase chain reaction (PCR) plates containing lysis buffer [0.2% Triton X-100, 2.5% RNaseOUT (Thermo Fisher; 10777019)] compatible with downstream RNA library preparation. In each 96-well PCR plate for each subject, we sorted 84 ALCAM+ cells and 11 CD45+ cells and maintained one empty well as a negative control. The plates were frozen on dry ice and stored at −80°C until preparation for sequencing.

**Single-cell RNA sequencing**

Massively parallel scRNA-Seq of human bronchial airway cells was performed using a modified version of the CEL-Seq RNA library preparation protocol (20). For each of the 12 recruited donors, one frozen 96-well PCR plate containing sorted cells was thawed on ice, and RNA was directly reverse-transcribed (Thermo Fisher, AM1751) from whole-cell lysate using primers composed of an anchored
poly(dT), the 5’ Illumina adaptor sequence, a six-nucleotide well-specific barcode, a five-nucleotide unique molecular identifier (UMI), and a T7 RNA polymerase promoter. All primer sequences were listed in extended table S1. Samples were additionally supplemented with ERCC RNA Spike-In Mix (1:1,000,000 dilution; Thermo Fisher, 4456740) for quality control. Complementary DNA generated from each of the 96 wells per plate was pooled, subjected to second-strand synthesis (Thermo Fisher, AM1751, and amplified by in vitro transcription (Thermo Fisher, AM1751). Amplified RNA was chemically fragmented (New England BioLabs, E6150) and ligated to an Illumina RNA 3’ adapter (Illumina, RS-200-0012). Samples were again reverse-transcribed using a 3’ adaptor-specific primer and amplified using indexed Illumina RNA PCR primers (Illumina, RS-200-0012). In total, 1152 samples (1008 epithelial cells, 132 WBCs, and 12 negative controls) were sequenced on an Illumina HiSeq 2500 in rapid mode, generating paired-end reads (15 nucleotides for read 1, 7 nucleotides for index, and 52 nucleotides for read 2).

Data preprocessing
Illumina’s bcl2fastq2 software (v2.19.1) was used to demultiplex the sequencing output to 12 plate-level FASTQ files (1 per 96-well plate). A python-based pipeline (https://github.com/yanaoilab/Cel-Seq-pipeline) was used to (i) demultiplex each plate-level FASTQ file to 96 cell-level FASTQ files, trim 52 nucleotide reads to 35 nucleotides, and append UMI information from read 1 (R1) to the header of read 2 (R2); (ii) perform genomic alignment of R2 with Bowtie2 (v2.2.2) using a concatenated hg19/External RNA Controls Consortium (ERCC) reference assembly; and (iii) convert aligned reads to gene-level counts by using a modified version of the HTSeq (v0.5.4p1) python library that identifies reads aligning to the same location with identical UMIs and reduces them to a single count. One UMI-corrected count was then referred to as a “transcript.” The pipeline was configured with the following settings: alignment quality (min_bc_quality) = 10, barcode length (bc_length) = 6, UMI length (umi_length) = 5, cut_length = 35.

Data quality control
The quality of each cell was assessed by examining the total number of reads, total reads aligned to hg19, total reads aligning to genes (pre-UMI correction), total transcript counts, and total genes with at least one detected transcript. Cells were excluded from downstream analyses if the total number of transcripts was not twofold greater than the total background-level transcripts detected in the empty well negative control on each plate (fig. S3). Cells were also excluded from downstream analyses if there was a weak Pearson correlation (r < 0.7) between detected ERCC RNA Spike-In transcript counts (log10) and ERCC input concentration (log10) (amol/ml) (fig. S3). All non–protein-coding genes and genes with less than two transcript counts in five cells were removed from the dataset. The remaining 7680 genes measured across 796 cells were used for subsequent analyses.

LDA implementation and model optimization
LDA from the topicmodels R package (v0.2-6) was used to generate probabilistic representations of cell clusters and gene sets present in the dataset, referred to as Cell-States and Gene-States. The input for the Cell-State model required a counts data matrix where cells were columns and genes were rows, whereas for the Gene-State model, the same matrix was transposed (i.e., genes were columns and cells were rows). Models were fit using the variational expectation-maximization (VEM) algorithm with the following parameters: nstart = 5, seed = 12345, estimate.alpha = TRUE, estimate.beta = TRUE. The given parameter k determined the number of Cell-States and Gene-States to be estimated by the model. The optimal value of k was determined by fivefold cross-validation and evaluation of model perplexity. For the Gene-State model, cells were randomly partitioned into “training” (80%) and “test” (20%) sets, whereas for the Cell-State model, genes were randomly partitioned into training (80%) and test (20%) sets. Models were then fit to the training set, and perplexity was estimated to evaluate model fit for the held-out test set. Fifty iterations of this process were performed for k = 2 to 50, mean perplexity was calculated at each k, and the minimum mean perplexity was selected as the optimal value of k (i.e., k.opt), which was k = 13 for the Cell-State model and k = 19 for the Gene-State model (fig. S6).

Gene set and cell cluster assignments
Negative binomial generalized linear models were built using the MASS R package (v7.3-45) for each Gene-State (n = 19) and each Cell-State (n = 13), in which States were treated as inferred, independent variables and genes or cells, respectively, were treated as dependent variables. A cell was assigned to a Cell-State if a significant association (FDR q < 0.05) was observed with positive directionality (regression coefficient > 1). Similarly, a gene was assigned to a Gene-State if a significant, positive association was observed (FDR q < 1 × 10^-5, regression coefficient > 1). If multiple State associations were observed for a given gene or cell, assignment was determined on the basis of the strongest State association (i.e., minimum FDR q). Additional metrics for gene set and cluster assignment include State Specificity and State Similarity. LDA (see the previous section) also assigned a probability to each gene (or cell) for each Gene-State (or Cell-State), and State Specificity was calculated by dividing that probability by the sum of probabilities across all Gene-States (or Cell-States). A minimum State Specificity of 0.1 was required for gene or cell assignment. State Similarity was calculated by assessing the cosine (q) similarity between each Gene-State and relative expression of each gene (gene counts divided by total counts for each cell). A minimum State Similarity of 0.4 was required for gene assignment. All downstream analyses used the 785 cells that fit the criteria for Cell-State assignment and 676 genes that fit the criteria for Gene-State assignment. Statistical modeling results, State Specificity, and State Similarity values for all genes, regardless of assignment status, were included in extended table S2.

Data visualization by heatmap and t-SNE
Before heatmap visualization, transcript counts were transformed to z-normalized transcripts per million (TPM). Genes (top to bottom) and cells (left to right) were ordered according to the strength of statistical association (FDR q) with respective assigned Gene-States and Cell-States. The tsne R package v0.1-3 was used for dimensionality reduction by t-distributed stochastic neighbor embedding (t-SNE). Modified parameters include k = 2 and seed = 1234. Input for t-SNE was z-normalized TPM values across genes with at least three transcript counts in three cells (n = 4914 genes). Gene expression overlay onto t-SNE visualization was also performed using z-normalized TPM values.

Functional annotation
The enrichR R package (v0.0.0.9000) was used as an interface for the web-based functional annotation tool, Enrichr, to identify Gene Ontology (GO) terms from the GO Biological Process 2015 library.
significantly associated with each gene set (58, 59). Functional annotation results were listed in extended table S3.

Microarray data processing
Raw CEL files obtained from the Gene Expression Omnibus (GEO) for series GSE7895 were normalized to produce gene-level expression values using the implementation of the Robust Multiarray Average (RMA) in the affy R package (v1.36.1) and an Entrez Gene-specific probeset mapping (17.0.0) from the Molecular and Behavioral Neuroscience Institute (Brainarray) at the University of Michigan (http://brainarray.mbbi.med.umich.edu/).

Comparative analysis of scRNA-Seq and microarray data
Bronchial brushings were reconstructed in silico from the single-cell data by taking the sum of all transcript counts for each gene across all cells procured from each donor. Negative binomial generalized linear models were built using the MASS R package (v7.3-45), modeling transcript counts as a function of smoking status (FDR \( q < 0.05 \); \( n = 593 \) genes). In parallel, using never and current smoker bulk bronchial brushing microarray data (GEO series GSE7895), linear models were built using the stats R package (R v3.2.0), modeling gene-level expression values as a function of smoking status (FDR \( q < 0.05 \); \( n = 689 \) genes). The correlation between test statistics generated from both models was then measured to compare differential expression results (fig. S4A). Using the overlap among smoking-associated genes identified in both models (\( n = 155 \) genes), correlations (Spearman) among in silico bronchial brushings and bulk bronchial brushings were examined (fig. S4B).

Gene set expression analysis in microarray data
Using published microarray data generated from bulk bronchial brushings procured from never and current smokers (GEO series GSE7895), RMA-transformed values for each gene were z-normalized. MetaGene values were then generated by computing the mean z score across all genes in each gene set (GS-1 to GS-19) for each sample. Linear models were built using the stats R package (R v3.2.0), modeling MetaGene expression as a function of donor smoking status and age. For metagenes that were associated with smoking status (FDR \( q < 0.05 \)), but not age, if the mean current smoker value was greater than or less than the mean never smoker value, the gene set was considered to be up- or down-regulated in current smokers, respectively.

Cell type assessment for cell clusters
TPM values for cell type marker genes (KRT5, FOXJ1, SCGB1A1, MUC5AC, and CD45) were z-normalized across all cells. Cluster-specific mean expression was designated high (pink) if expression exceeded 1 SD above the mean value across all cells, medium (white) if expression exceeded one-half of an SD above the mean value across all cells, and low (light gray) if expression exceeded the mean value across all cells. If cluster-specific mean expression was designated high, medium, or low for KRT5, FOXJ1, SCGB1A1, MUC5AC, or CD45 (PTPRC), that cluster was assigned the cell type of basal, ciliated, club, goblet, or WBC, respectively. Cluster-specific mean expression below the mean value across all cells indicated that a given cluster did not express a given marker gene (dark gray).

Smoking status assessment for cell clusters
To assess smoking status–specific cell enrichment for each cluster, logistic regression was performed using the stats R package (R v3.2.0), modeling each cluster assignment as a function of donor smoking status and the number of cells contributed by each donor. For clusters that were associated with smoking status (FDR \( q < 0.05 \)), but not the number of cells contributed by each donor, the directionality of the regression coefficient was leveraged to assign never or current smoker status.

Gene set expression analysis in cell clusters
Transcript counts were transformed to z-normalized TPM. MetaGene values were then generated by computing the mean z score across all genes in each gene set (GS-1 to GS-19) for each cell. Cluster-specific MetaGene expression was designated high (pink) if mean expression exceeded 1 SD above the mean value across all cells, medium (white) if mean expression exceeded one-half of an SD above the mean value across all cells, and low (light gray) if mean expression exceeded the mean value across all cells. Cluster-specific mean expression below the mean value across all cells indicated that a given cluster did not express a given gene set (dark gray).

Bronchial tissue collection for immunostaining
Bronchial tissue was collected from patients undergoing lung resection. All specimens were procured at least 5 cm from bronchial sites affected by disease diagnoses, and analyses indicated that tissue was histologically normal. The UMCG cohort (table S2) included specimens analyzed in collaboration with the UMCG collected from four never smokers and four current smokers. Specimens were obtained from the tissue bank in the UMCG Department of Pathology. The study protocol was consistent with the Research Code of the UMCG and Dutch national ethical and professional guidelines (“Code of conduct; Dutch federation of biomedical scientific societies”; www.federa.org). The UCL cohort (table S3) included specimens analyzed in collaboration with the UCL collected from five never smokers and five current smokers. Ethical approval was sought and obtained from the UCL Hospital Research Ethics Committee (REC reference 06/Q0505/12). This study was carried out in accordance with the Declaration of Helsinki (2000) of the World Medical Association.

Immunofluorescence
Formalin-fixed paraffin-embedded lung sections were cut at 4 mm, tissue was probed with primary antibodies (listed below) and secondary antibodies with fluorescent conjugates (Invitrogen Alexa Fluor 488, 594, 647), and nuclear staining was performed with 4′,6-diamidino-2-phenylindole (DAPI) (Thermo Fisher, R37606). Immunostaining was performed using the following primary antibodies: mouse anti–Ac-α-Tub (Sigma, T6793), rabbit anti–Ac-α-Tub (Enzo Life Sciences, BML SA4592), rabbit anti-AKR1B10 (Sigma, HPA020280), rabbit anti-CEACAM5 (Abcam, ab131070), chicken anti-KRT5 (BioLegend, 905-901), rat anti-KRT8 (Developmental Studies Hybridoma Bank, University of Iowa; TROMA-1), mouse anti-MUC5AC (Abcam, ab3649), and rabbit anti-MUC5B (Sigma, HPA008246). Imaging of staining panels analyzed in collaboration with investigators at the UMC (table S2) (e.g., AKR1B10/Ac-α-Tub/KRT8: Fig. 3C; AKR1B10/MUC5AC/KRT8: fig. S13; MUC5B/MUC5AC: Fig. 4B; MUC5B/MUC5AC/KRT5: fig. S14; CEACAM5/KRT8/MUC5AC: fig. S18) was performed using a Carl Zeiss LSM 710 NLO confocal microscope at x63 objective magnification at the Boston University School of Medicine Multiphoton Microscope Core Facility. Imaging of staining panels analyzed in collaboration with investigators at the UCL (table S3) (e.g., CEACAM5/KRT8/MUC5AC:
Fig. 5D; KRT8/MUC5AC/Ac-α-Tub: fig. S15) was performed using a Leica TCS Tandem confocal microscope at ×63 objective magnification.

Imaging analysis
All imaging data were analyzed using ImageJ Fiji software. For each image, cells were counted relative to the measured length of the epithelium in micrometers (cells per micrometer). Mean cell counts per micrometer (cells per millimeter) were then calculated for never smokers (treated as the control), and individual values for each image from never and current smokers were calculated relative to the never smoker mean (i.e., relative cells per millimeter). We analyzed three images for each donor and assessed smoking-associated changes using the Wilcoxon rank-sum test. For panels in which MUC5AC was stained, current smoker tissue was assigned the phenotypic status of either MN or GCH based on qualitative assessment of goblet cell density and stratification. For each current smoker, three images of each status were analyzed.

Density and stratification. For each current smoker, three images of either MN or GCH based on qualitative assessment of goblet cell density and stratification. For each current smoker, three images of each status were analyzed.

Table S1. Bronchial brushings were procured from six never smokers and six current smokers.

Table S2. Bronchial tissue was obtained by lung resection from four never smokers and four current smokers.

Table S3. Bronchial tissue was obtained by lung resection from five never smokers and five current smokers.

Supplementary materials
Supplementary material for this article is available at http://advances.sciencemag.org/cgi/content/full/5/12/eaaw3413/DC1

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