**Supplementary File 1.**

**Methods:** *Single Cell Sequencing Data Retrieval and Analysis*

Normalised count matrix data from a published single cell mRNA sequencing study [1] of the human lung was retrieved from publicly available resource (<https://www.genomique.info/cellbrowser/HCA/>). Cell annotation was retrieved from the metadata and cell type and airway region were assigned according to previous analysis [1]. Data was further processed using R-tools and Seqgeq software (BD/FloJo, Ashford, USA), where dimensionality reduction using tSNE was applied to principal component analysis of cell type specific marker expression only. Results were visualised as tSNE plots indicating regional and cell type specific cell groupings (Figure 2A-B). Count data was further extracted for select genes involved in chemical biotransformation and transport and average values were calculated for each cell type, also subcategorised based on region. Average gene expression count values were then visualised using a heatmap organised by cell type (Figure 2C). Genes (excluding cell marker genes) were then clustered using hierarchical methods to group for similar expression.

[1] Marie Deprez et al., A Single-Cell Atlas of the Human Healthy Airways. Am J Respir Crit Care Med . 2020 Dec 15;202(12):1636-1645. doi: 10.1164/rccm.201911-2199OC. PMID: 32726565