Loupe File Viewing Instructions Kotton Lab, April 2018

This loupe file (named “McCauley and Kotton SCR 2018.cloupe”) contains the scRNA-Seq data (10X Chromium platform) shown in figure 6 of the following publication. The data profiles human iPSC (BU3 NGST)-derived proximal bronchospheres vs distal alveolospheres, when each cell type was sorted from the same day 15 NKX2-1GFP+ progenitor pool (see figure 6) and then further differentiated in parallel in 3D Matrigel cultures as detailed in the publication:

***McCauley, KB et al. “Single cell transcriptomic profiling of pluripotent stem cell-derived SCGB3A2+ airway epithelium.” Stem Cell Reports, April 2018.***

The file may be accessed by downloading the free Loupe browser software available at the 10X Genomics website: https://www.10xgenomics.com/

Once the file is opened with this viewer, the data may be interrogated by typing gene names into the “Gene Exp” window. The cell clusters as portrayed in figure 6 of McCauley et al can be viewed in the “Categories” window by clicking on the down arrow and selecting the term “Clusters”. Alternatively, cells prepared in the distal (alveolosphere) vs proximal (bronchosphere) media may be viewed by selecting the term “library ID”.

Further details and bioinformatics methods are provided in figures S5 and S6 and the supplemental information file available with the publication online.

For questions, please ask Darrell by emailing: dkotton AT bu.edu

Raw datasets used for this analysis can be downloaded from the online Gene Expression Omnibus:

[GSE103920](https://urldefense.proofpoint.com/v2/url?u=https-3A__www.ncbi.nlm.nih.gov_geo_query_acc.cgi-3Facc-3DGSE103920&d=DwMFaQ&c=WO-RGvefibhHBZq3fL85hQ&r=h3GKphfgyQFxyaqpRLTwpPn_XLQyMb0ZiSDbs6DSNwD3k77axWw9Cvy8J8yjknnt&m=c32d5_zD_UqRxr_jlh9FgqZXdkxVqOxZa_1zbTUt3To&s=hbNHERWy4x5PEkL7Zns38WkBgh1UCkBTbzpcYPGwqNg&e=)

Available here: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE103918>

Figure 6, panels a-c:

