Supplementary Figure 2. scRNA-seq derived pseudo-bulk RCA projection on reference sets. In order to emulate a pseudo-bulk dataset from scRNA-seq data, a random sample of 100 single-cells for each of the four patients was selected and the counts from each patient were aggregated by the mean for each gene across the 100 sampled cells. RCA clustering shows high projection scores onto bronchial epithelial tissues for all patients.