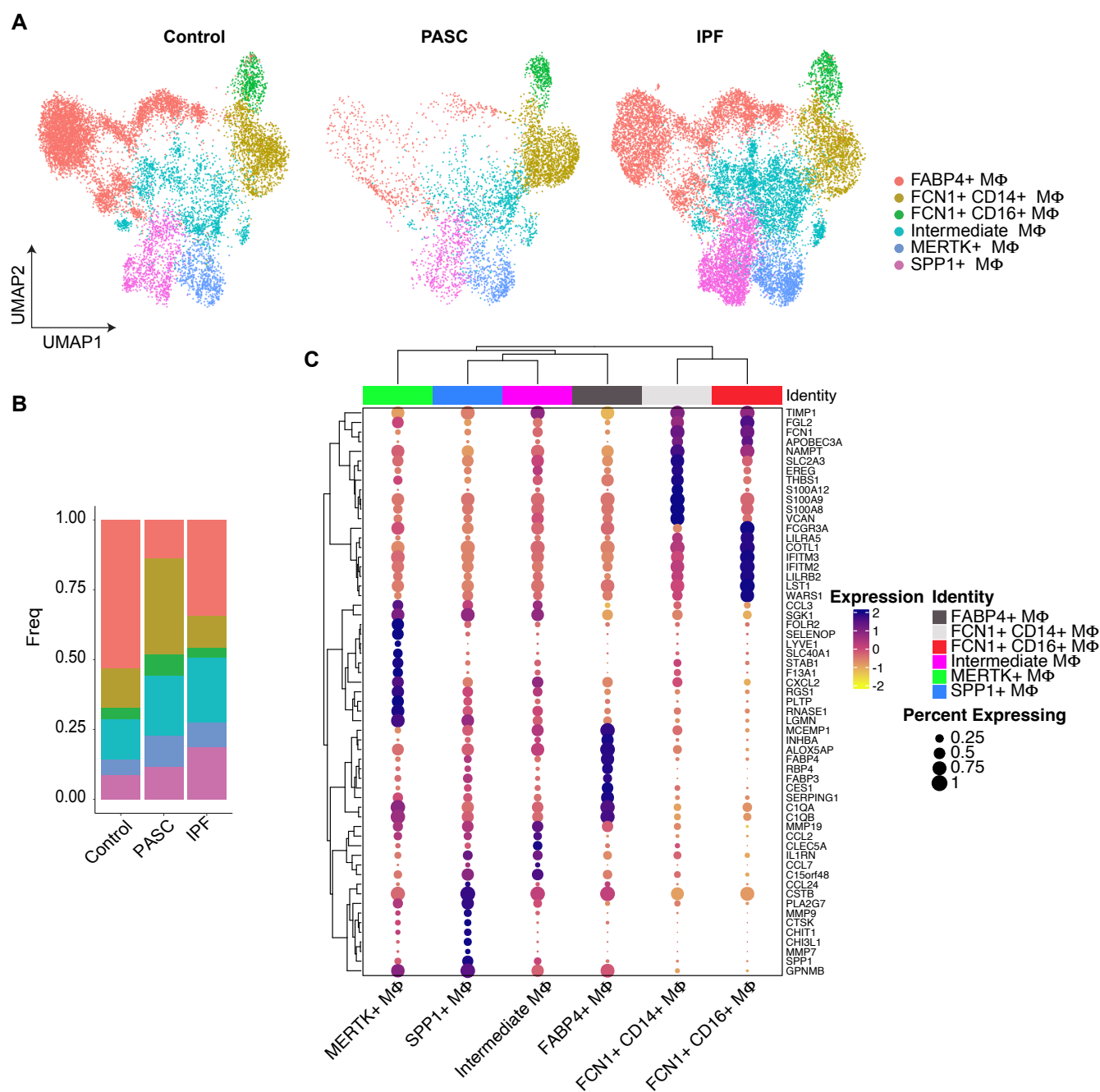


Supplemental Figure 1. Analysis of epithelial and immune sub-population.

A. UMAP projection and Frequency distribution of each epithelial sub-population in different diagnosis groups.

B. UMAP projection and Frequency distribution of each immune sub-population in different diagnosis groups.

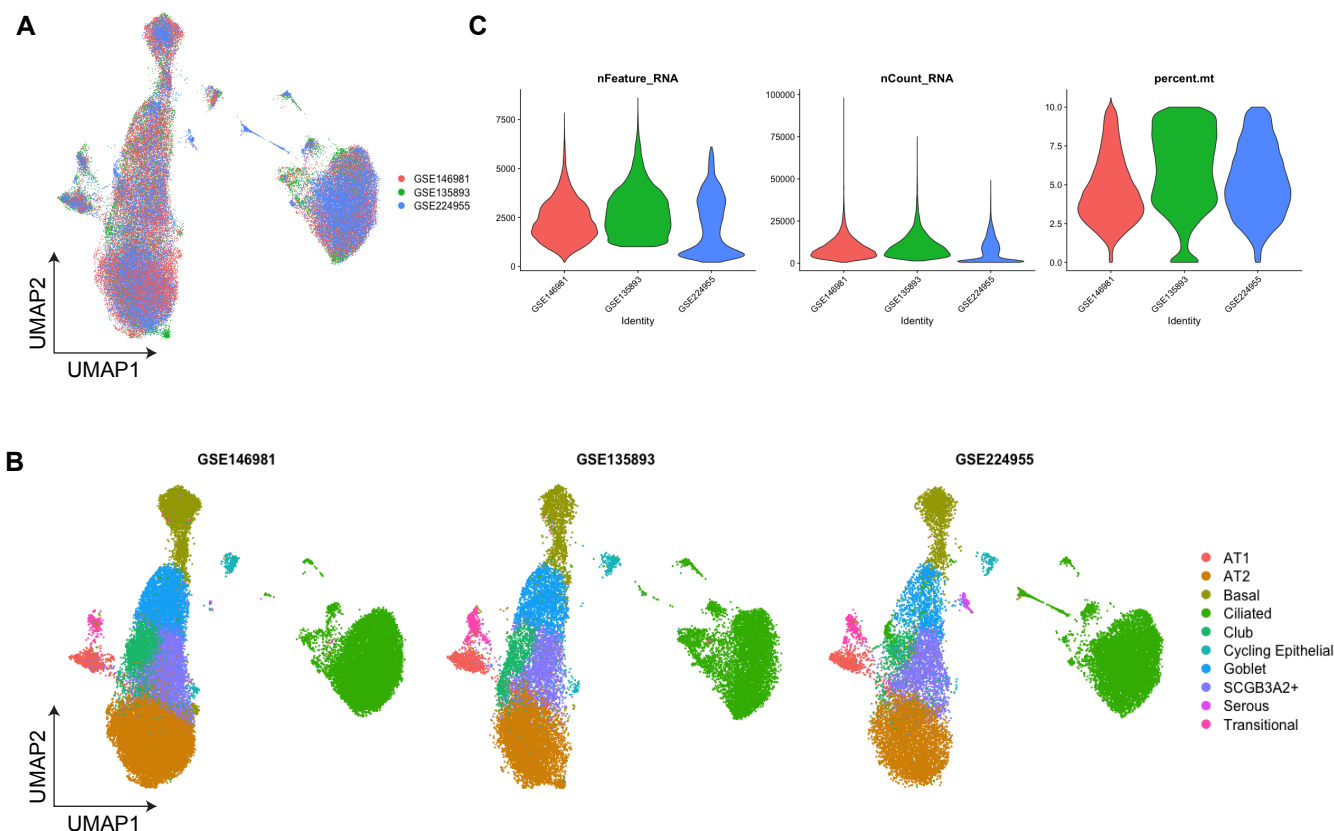


Supplemental Figure 2. Analysis of Macrophage population.

A. UMAP projection of different Macrophage population.

B. Frequency of each Macrophage sub-population in the dataset in different diagnosis groups.

C. Top 10 expression genes of each Macrophage sub-population.



Supplemental Figure 3. Comparison among data sources.

A-B. UMAP projection of epithelial cells from the three different data sources (GSE146981 , GSE135893, GSE224955). GSE146981 and GSE224955 (PASC) were generated by US using the same isolation and sequencing method.

C. number of genes per cell, number of counts per cells detected and percentage of mitochondrial genes per cell of the three different data sources.