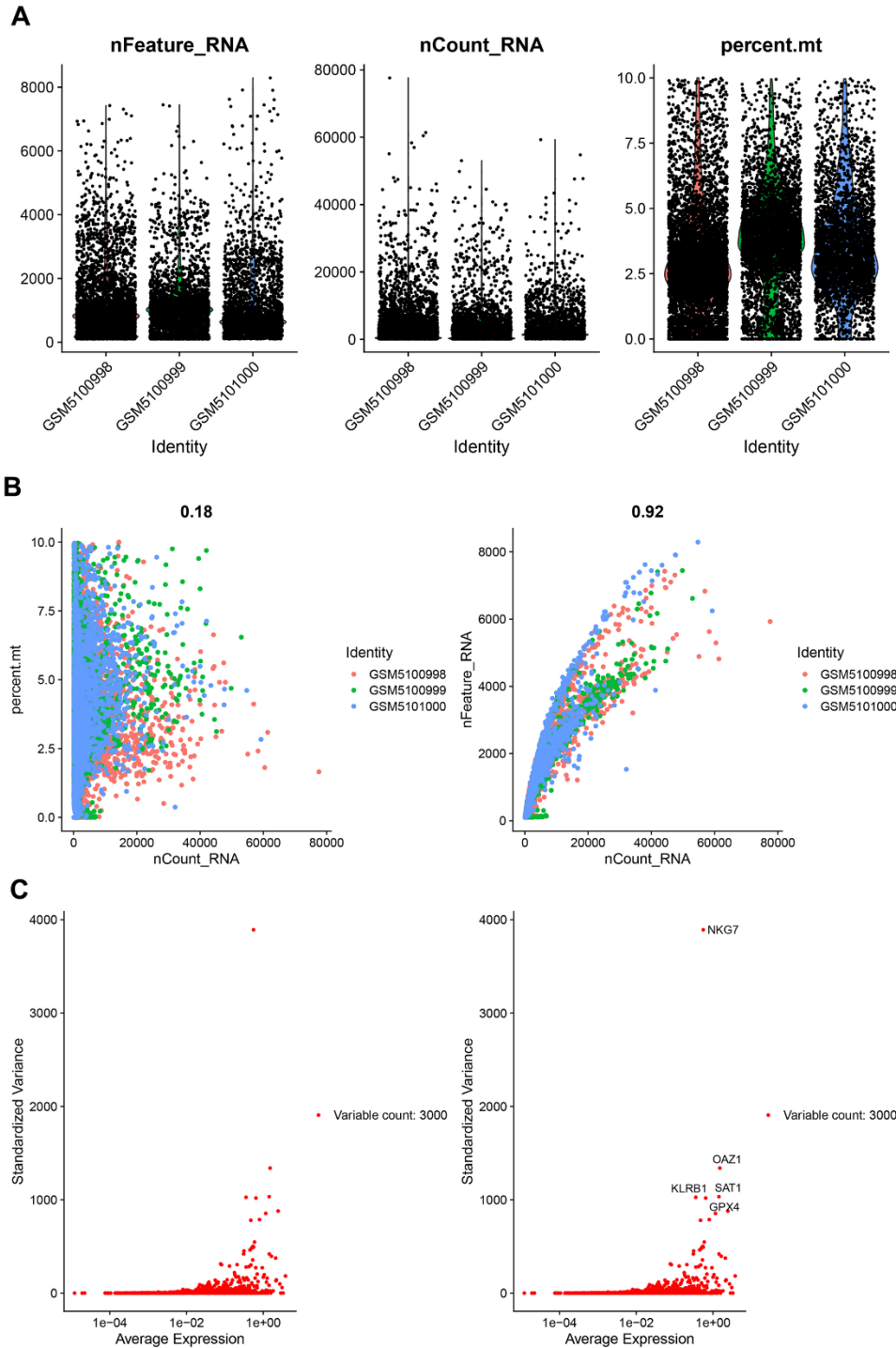
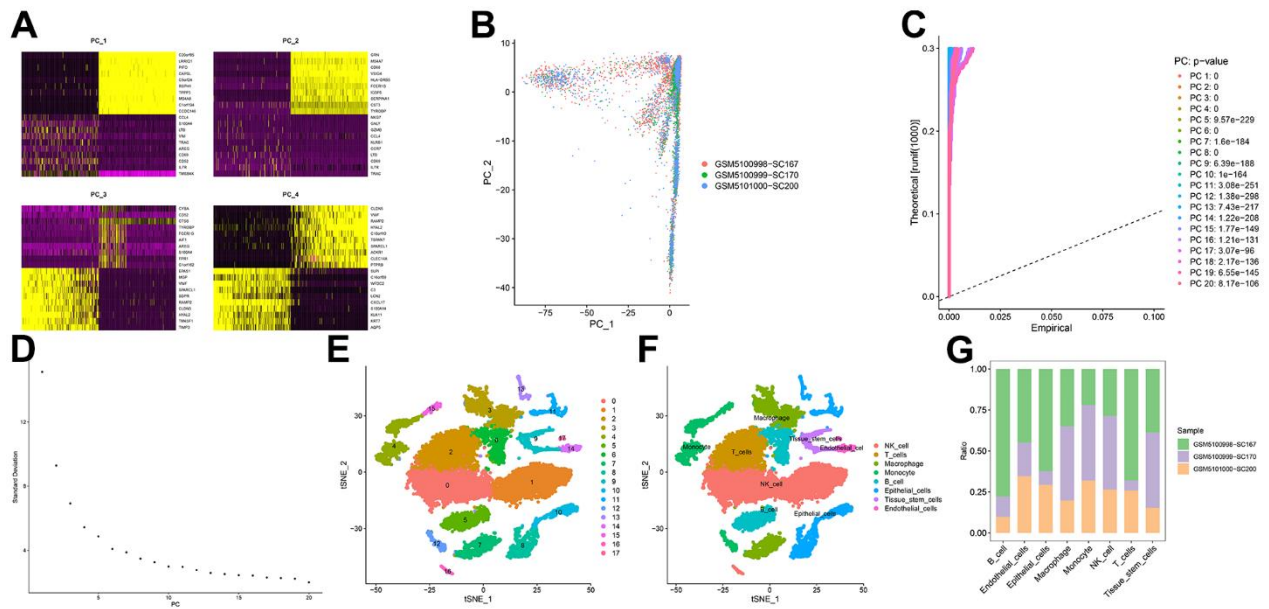


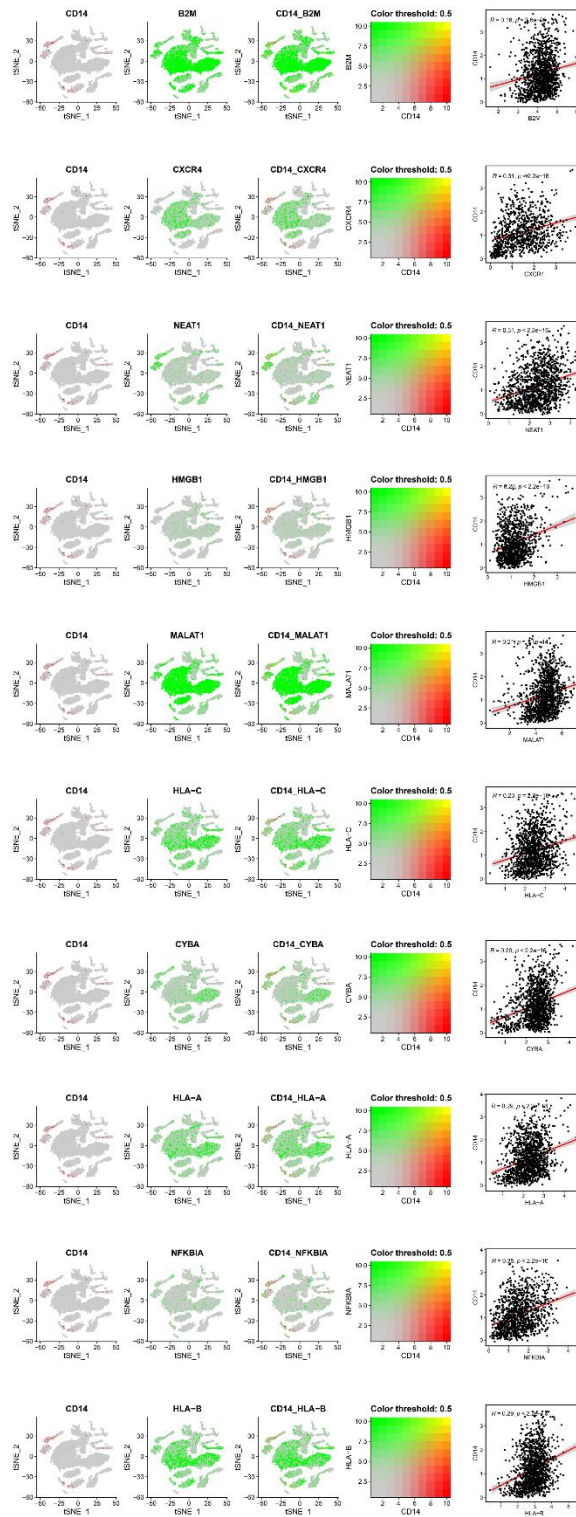
**SUPPLEMENTARY FIGURES**



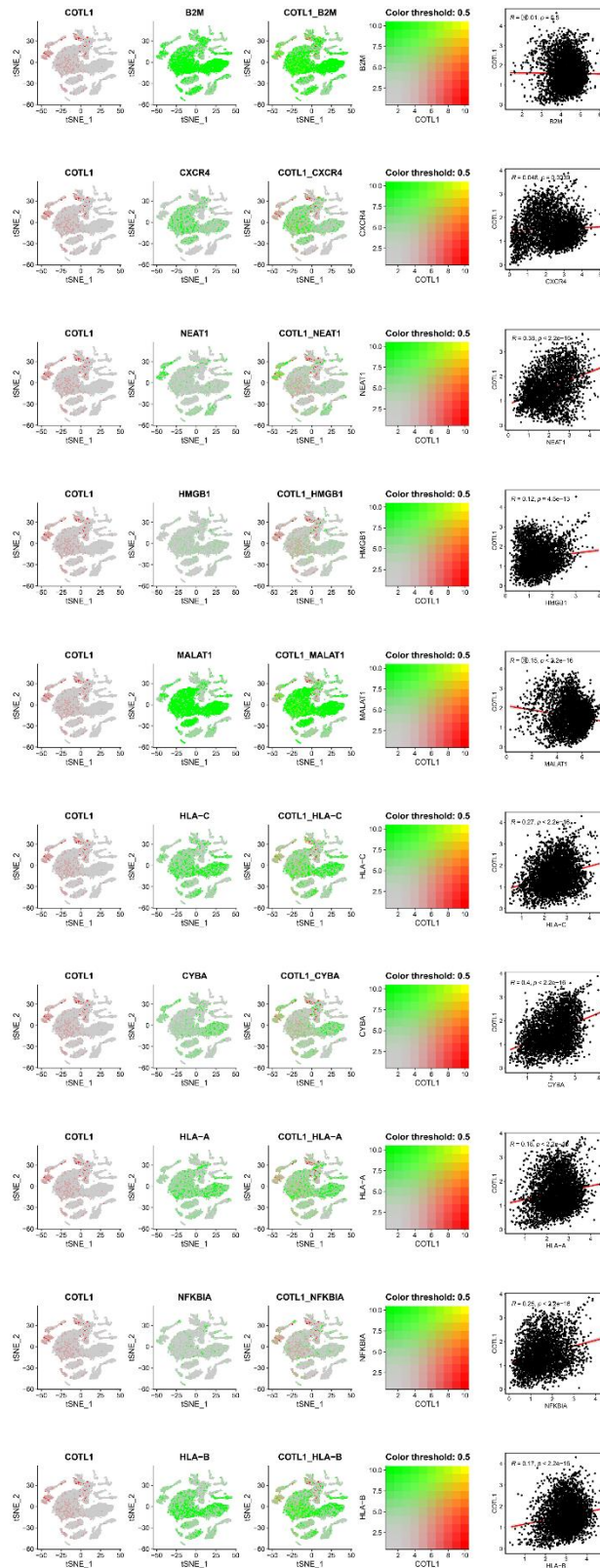
**Supplementary Figure 1. Analysis of single-cell sequencing results from COPD patients. (A)** Quality inspection of single-cell sequencing. Plots from left to right showed the number of cells, the number of genes and the sequencing depth for each sample, respectively. **(B)** Plots from left to right showed the relationship between single-cell sequencing depth and mitochondrial content (correlation coefficient of 0.18) and the number of genes (correlation coefficient of 0.92), respectively. **(C)** Genes that differed between cells, and the 5 genes with the highest standardized variance were flagged.



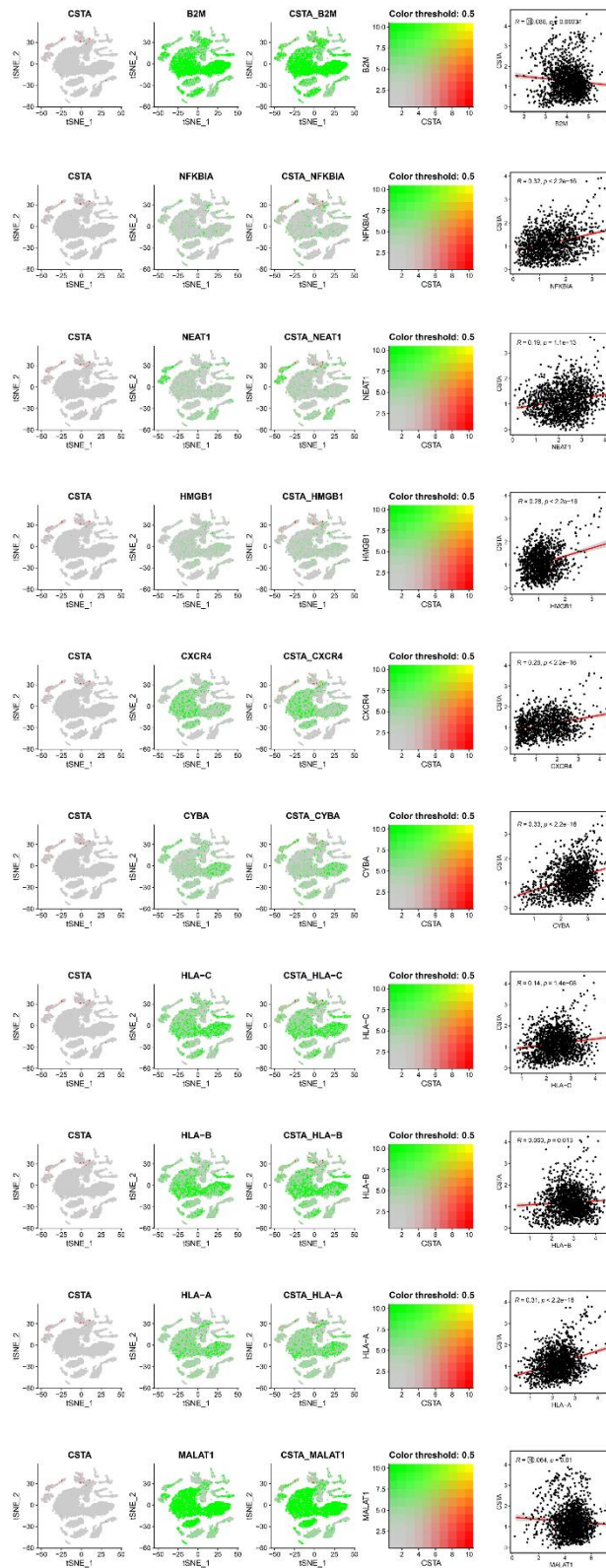
**Supplementary Figure 2. Annotation of cellular subtypes of single-cell samples.** (A) Heatmap of principal component analysis for genes from single-cell sequencing in COPD samples. (B) Distribution of PCs in COPD single-cell sequencing samples, where dots represent cells and different colors represent different samples. (C) Histogram of PCA results of COPD single-cell sequencing samples to show the P-value for each PC. (D) Variogram of each PC in COPD single-cell sequencing samples. (E) Cluster analysis of COPD single-cell sequencing samples. (F) Annotation of cell subtypes in COPD single-cell sequencing samples. (G) Difference in the percentage of cells in COPD samples that were annotated.



**Supplementary Figure 3. Co-expression analysis of CD14 with immune genes in single-cell sequencing samples.** Scatter plots represent pearson correlation analysis between co-expressed genes.

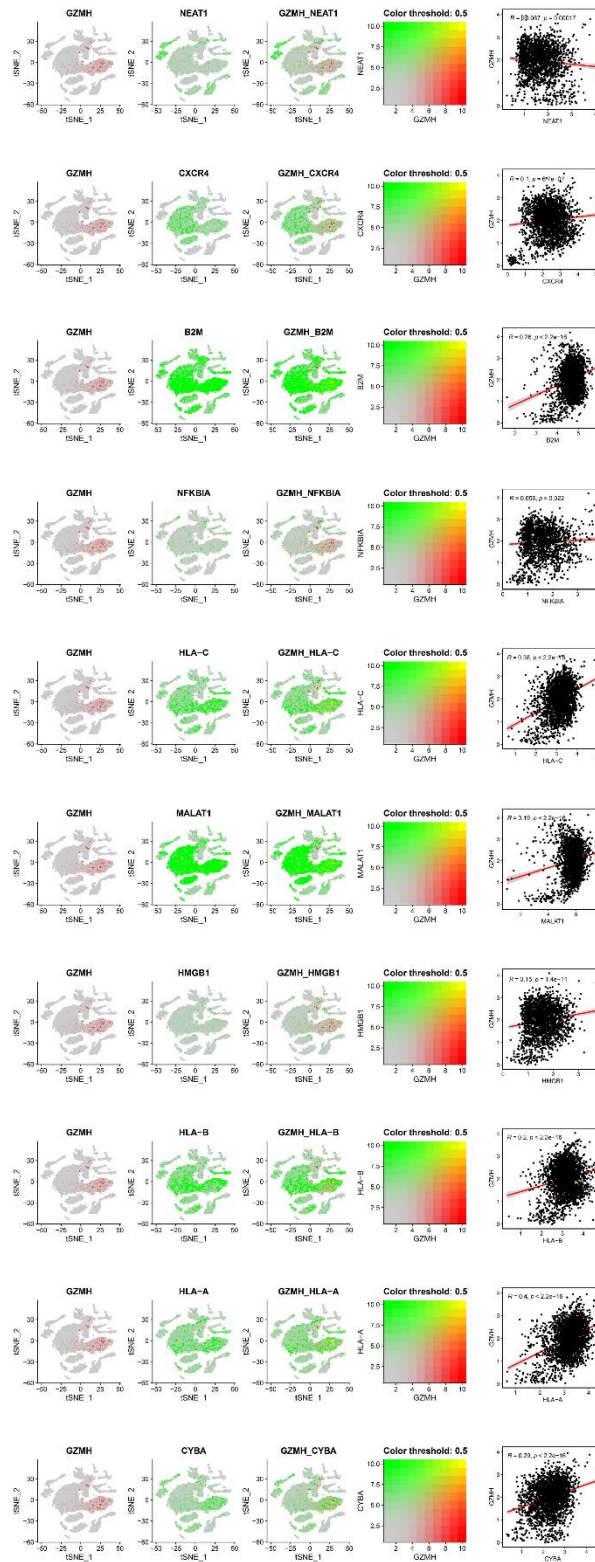


**Supplementary Figure 4. Co-expression analysis of COTL1 with immune genes in single-cell sequencing samples. Scatter plots indicate the Pearson correlation analysis between co-expressed genes.**



**Supplementary Figure 5. Co-expression analysis of CSTA with immune genes in single-cell sequencing samples. Scatter plots indicate the Pearson correlation analysis between co-expressed genes.**





**Supplementary Figure 6.** Co-expression analysis of GZMH with immune genes in single-cell sequencing samples. Scatter plots indicate the pearson correlation analysis between co-expressed genes.