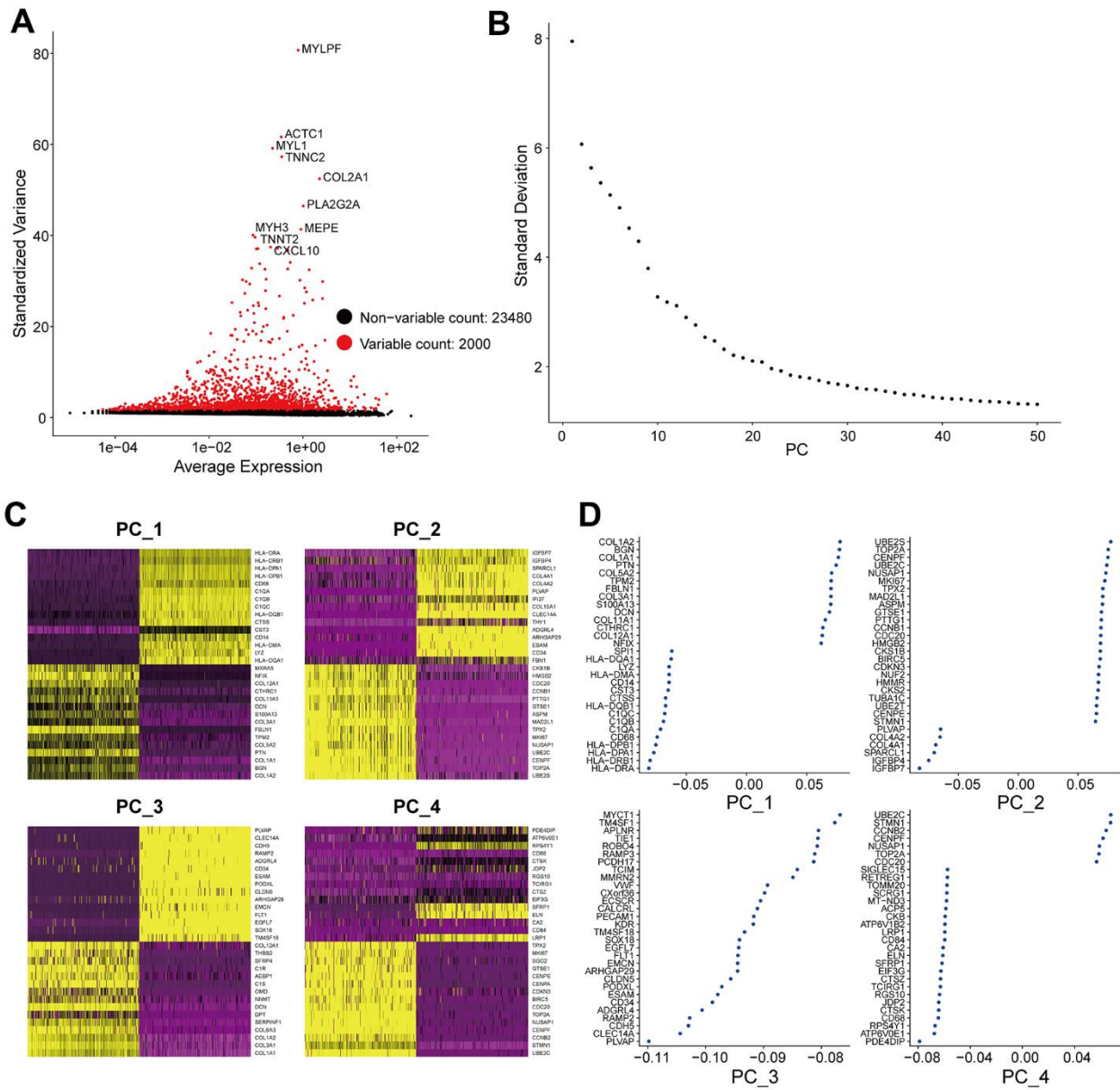Supplementary Figure 1. Processing of single-cell RNA-seq data. (**A**) The characteristic variance diagram of the gene symbols. Each spot represented a gene. Red spots represented highly variable genes with significant differences across cells. (**B**) Principal component sorting elbow graph based on the percentage of variance explained by each one. (**C**) Cluster analysis across each component. The colors ranging from purple to golden yellow represented the expression levels of correlated genes from low to high. (**D**) Correlation analysis of the most altered genes in each component.