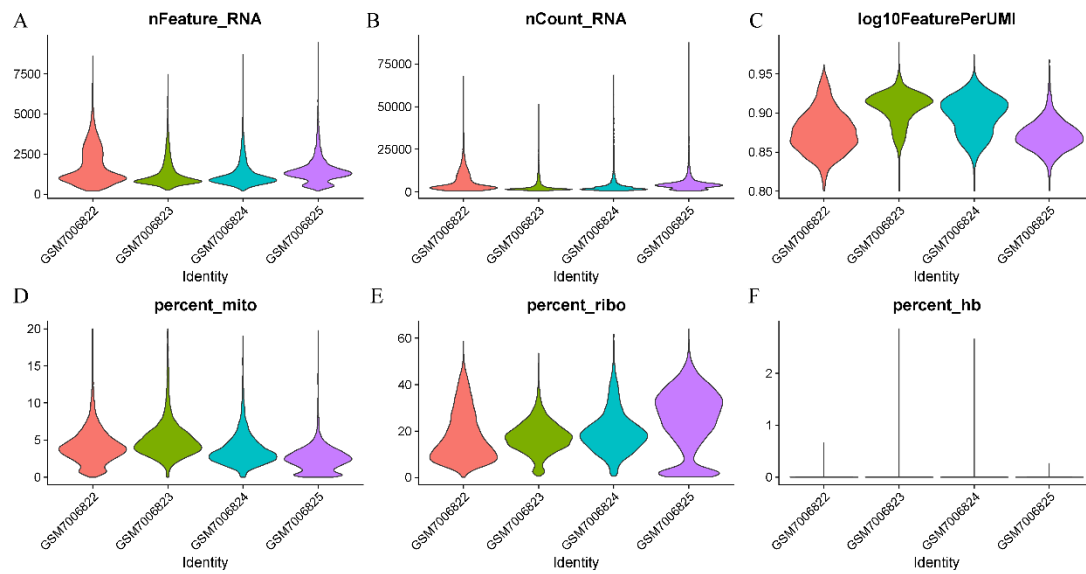
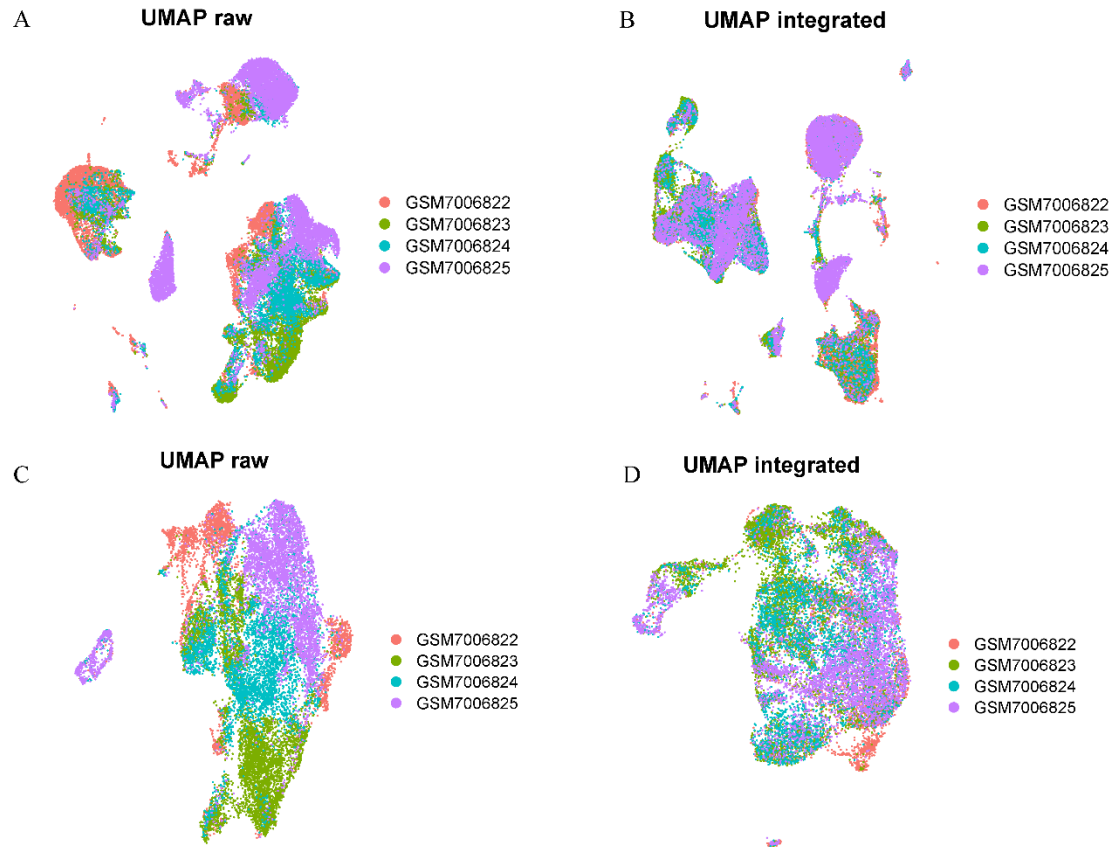


## Supplementary Figures



**Supplementary Figure 1** The schematic of the quality control standards used for the single-cell data in the study. (A) Genes detected per cell was set to  $\geq 200$ . (B) Total number of RNA reads detected per cell was set to  $\geq 500$ . (C) Log10 of the ratio of the number of gene features to the number of UMIs for each cell was set to  $\geq 0.8$ . (D) The proportion of reads to mitochondrial genes was set to  $\leq 20\%$ . (E) No threshold was set for the proportion of reads to ribosomal genes. (F) The proportion of reads to hemoglobin genes was set to  $\leq 3\%$ .



**Supplementary Figure 2** UMAP before and after the removal of batch effect. (A) UMAP of the overall sc-RNA data before the removal of batch effect. (B) UMAP of the overall sc-RNA data after the removal of batch effect. (C) UMAP of the extracted T cells sc-RNA data before the removal of batch effect. (D) UMAP of the extracted T cells sc-RNA data after the removal of batch effect