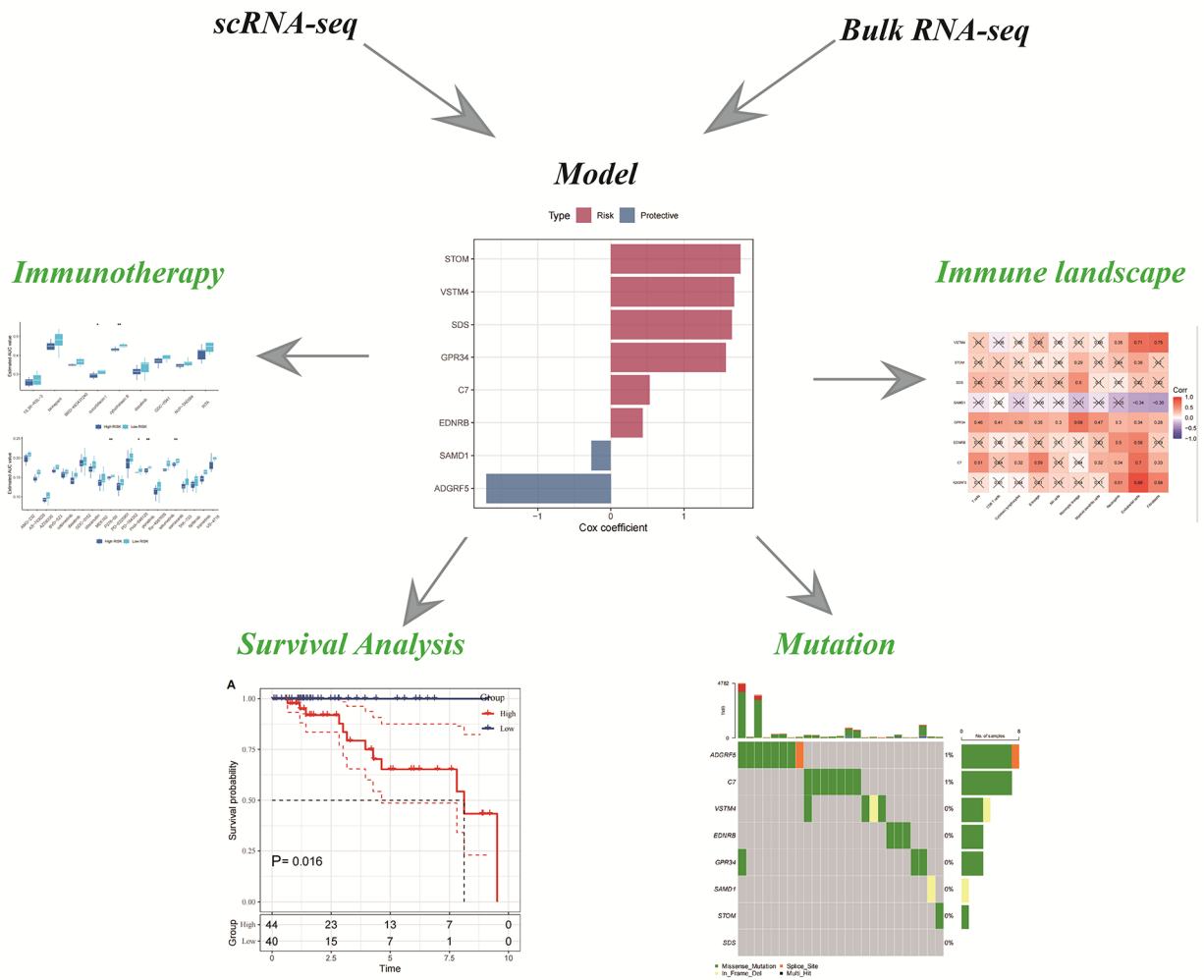
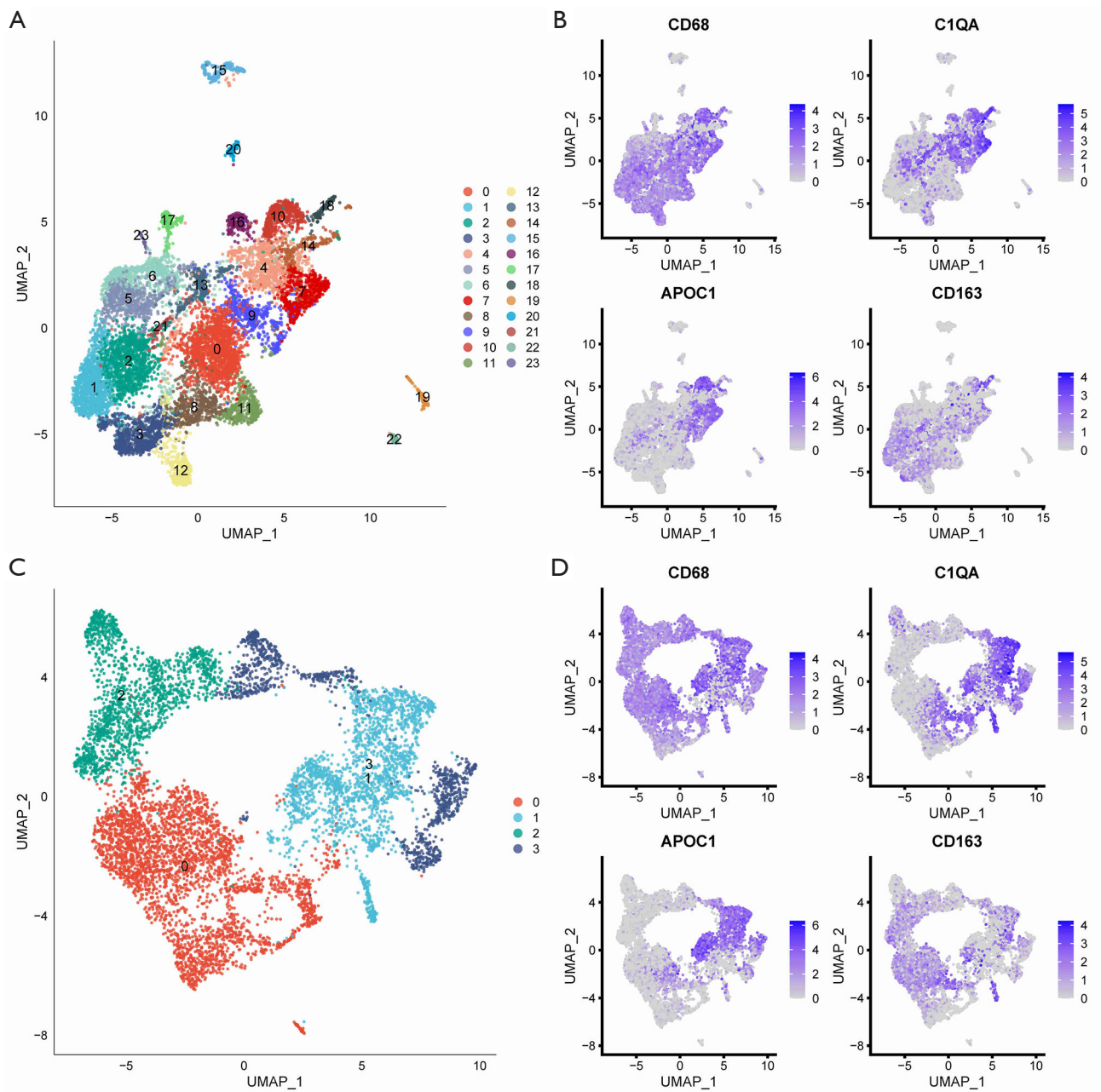


**Table S1** Primer sequences of reverse-transcriptase polymerase chain reaction

| Gene  | Forward (5'-3')           | Reverse (3'-5')           |
|-------|---------------------------|---------------------------|
| ACTB  | GGCACCCAGCACAAATGAAG      | CCGATCCACACGGAGTACTTG     |
| GPR34 | CGTGGGACTGGTTGGGAACATAATC | GGAGGCAGAAGATGAGTAGGAGGTC |

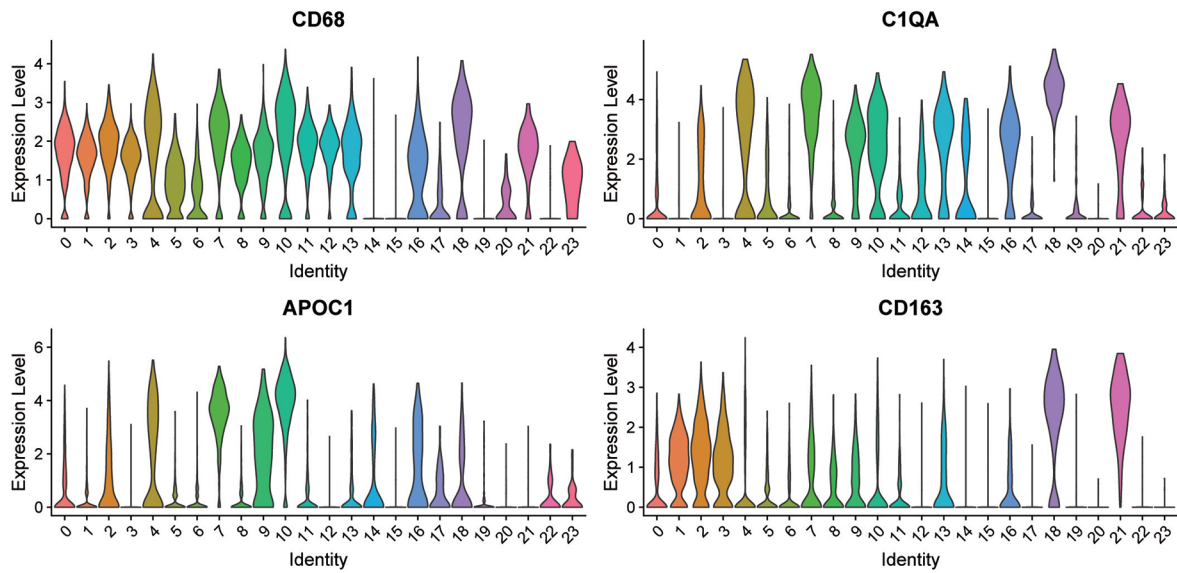


**Figure S1** The flow chart of our study.

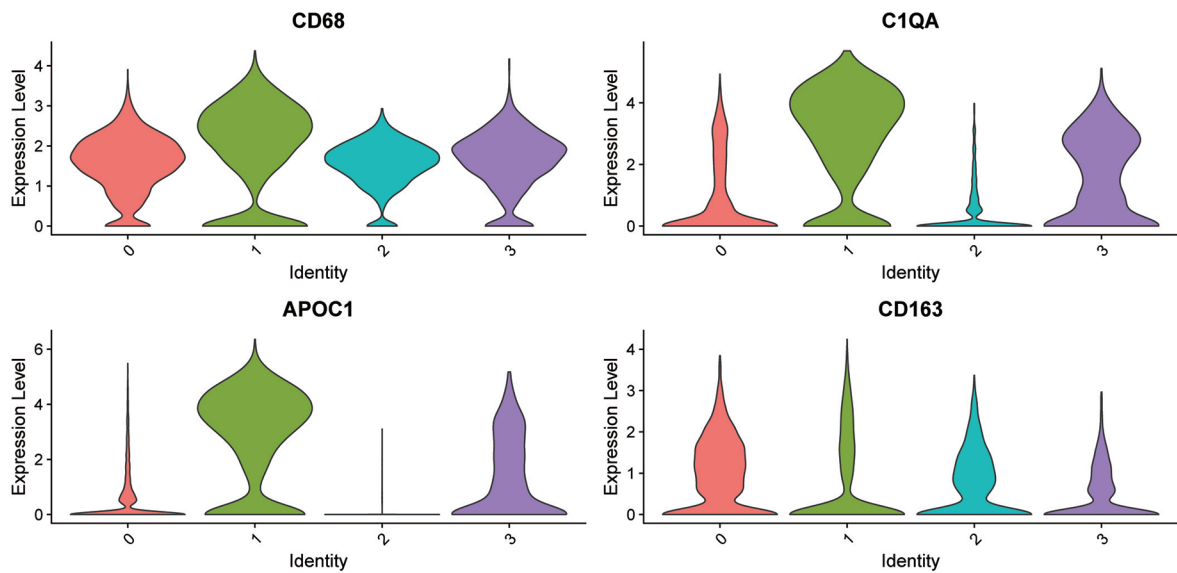


**Figure S2** The clustering of TAM populations and dimensionality reduction. (A) Distribution of subpopulations after clustering of all cells; (B) UMAP diagram of TAM marker gene expression; (C) Distribution of subpopulations after re-clustering of TAMs; (D) UMAP diagram of marker expression in four TAM clusters. TAM, tumor-associated macrophage; UMAP, uniform manifold approximation and projection.

A



B



**Figure S3** Expression patterns of marker genes across clusters and TAM subpopulations. (A) The violin plot showed the different expression of 4 marker genes in 24 clusters. (B) The violin plot showed four marker genes were highly expressed in 4 TAM subpopulations. TAM, tumor-associated macrophage.