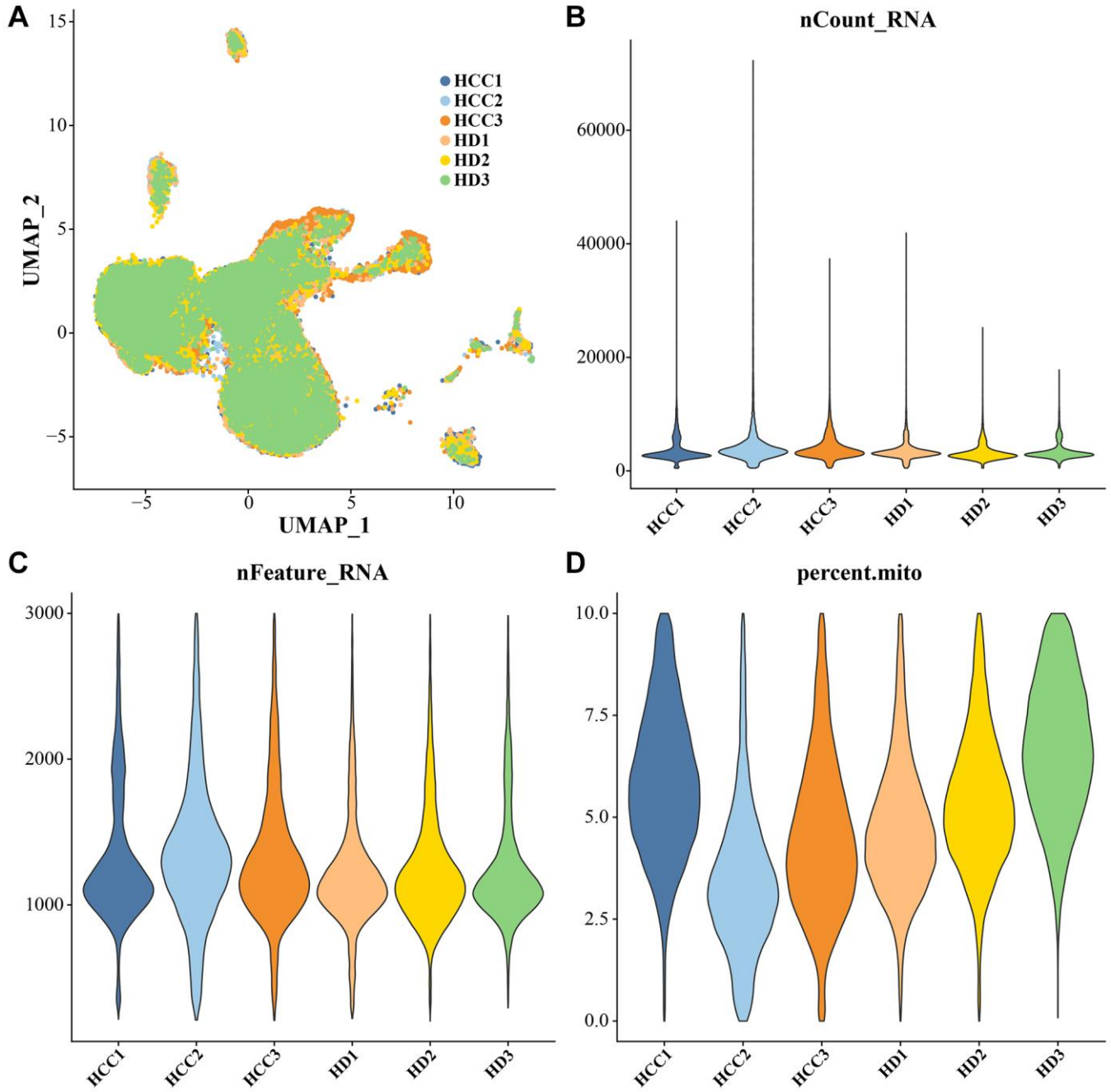
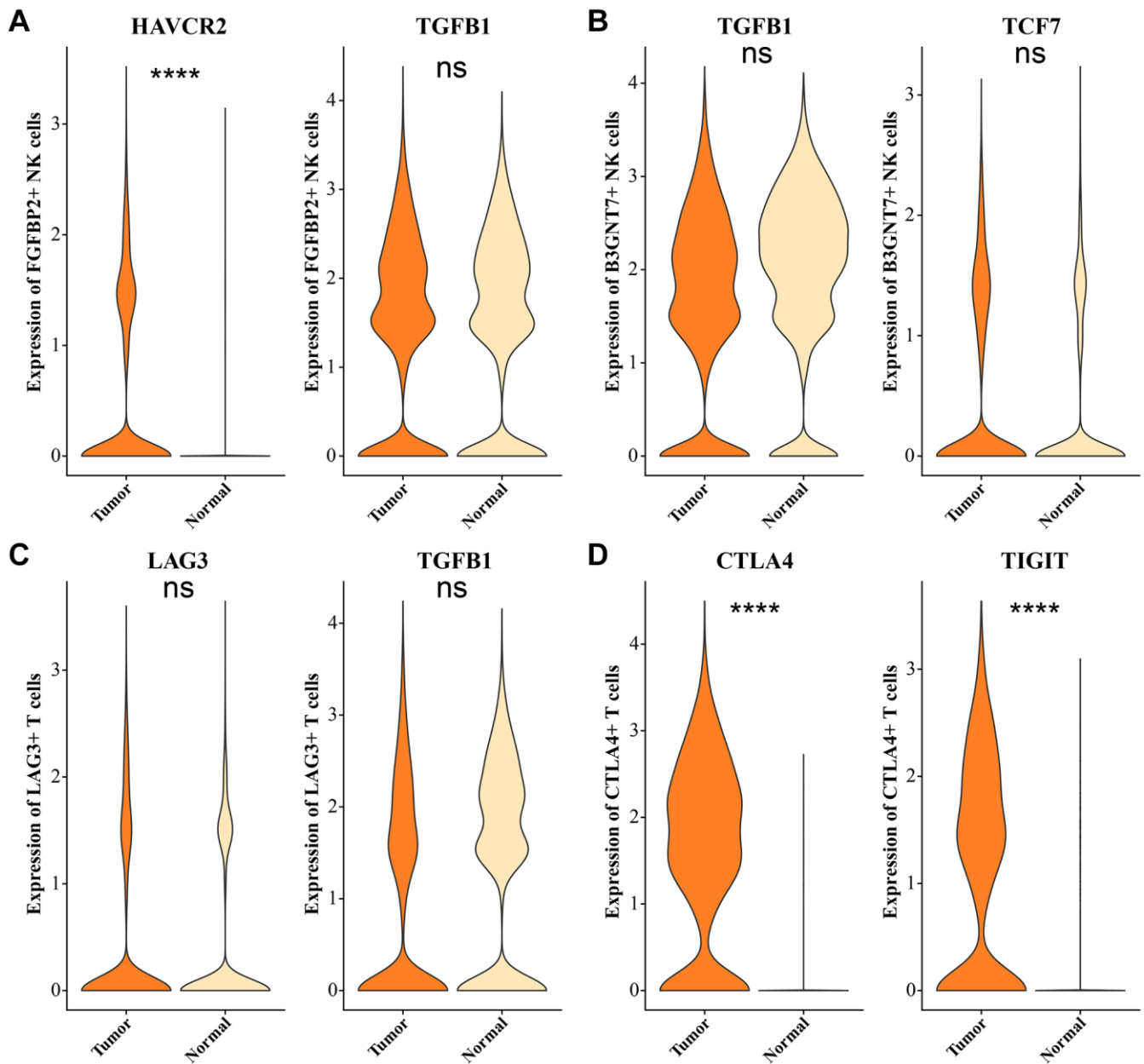


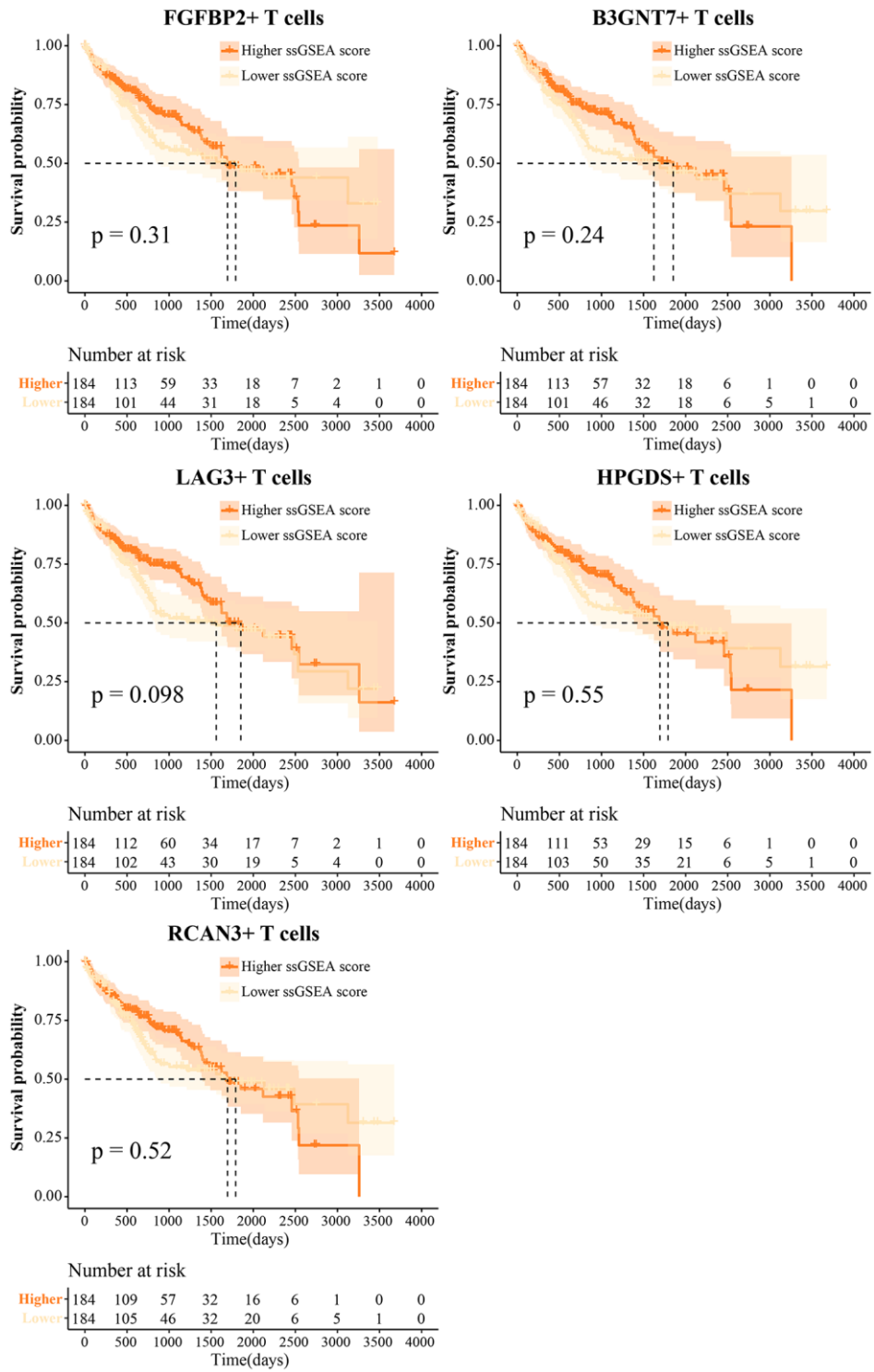
SUPPLEMENTARY FIGURES



Supplementary Figure 1. scRNA-seq data processing. (A) Distribution of cells in six samples after removal of batch effects. (B) Distribution of the number of detected UMIs in the samples after filtering. (C) Number of detected genes in the samples after filtering. (D) Proportion of mitochondrial genes detected in the samples after filtering.



Supplementary Figure 2. Expression levels of marker genes in FGFBP2+ NK cells, B3GNT7+ NK cells, LAG3+ T cells, CTLA4+ T cells. (A) Expression levels of HAVCR2 and TGFB1 in FGFBP2+ NK cells. (B) Expression levels of TGFB1, TCF7 in B3GNT7+ NK cells. (C) Expression levels of LAG3, TGFB1 in LAG3+ T cells. (D) Expression levels of CTLA4, TIGIT in CTLA4+ T cells.



Supplementary Figure 3. K-M curves of HCC patients in the grouping of FGFBP2+ T cells, B3GNT7+ T cells, LAG3+ T cells, HPGDS+ T cells, and RCAN3+ T cells.