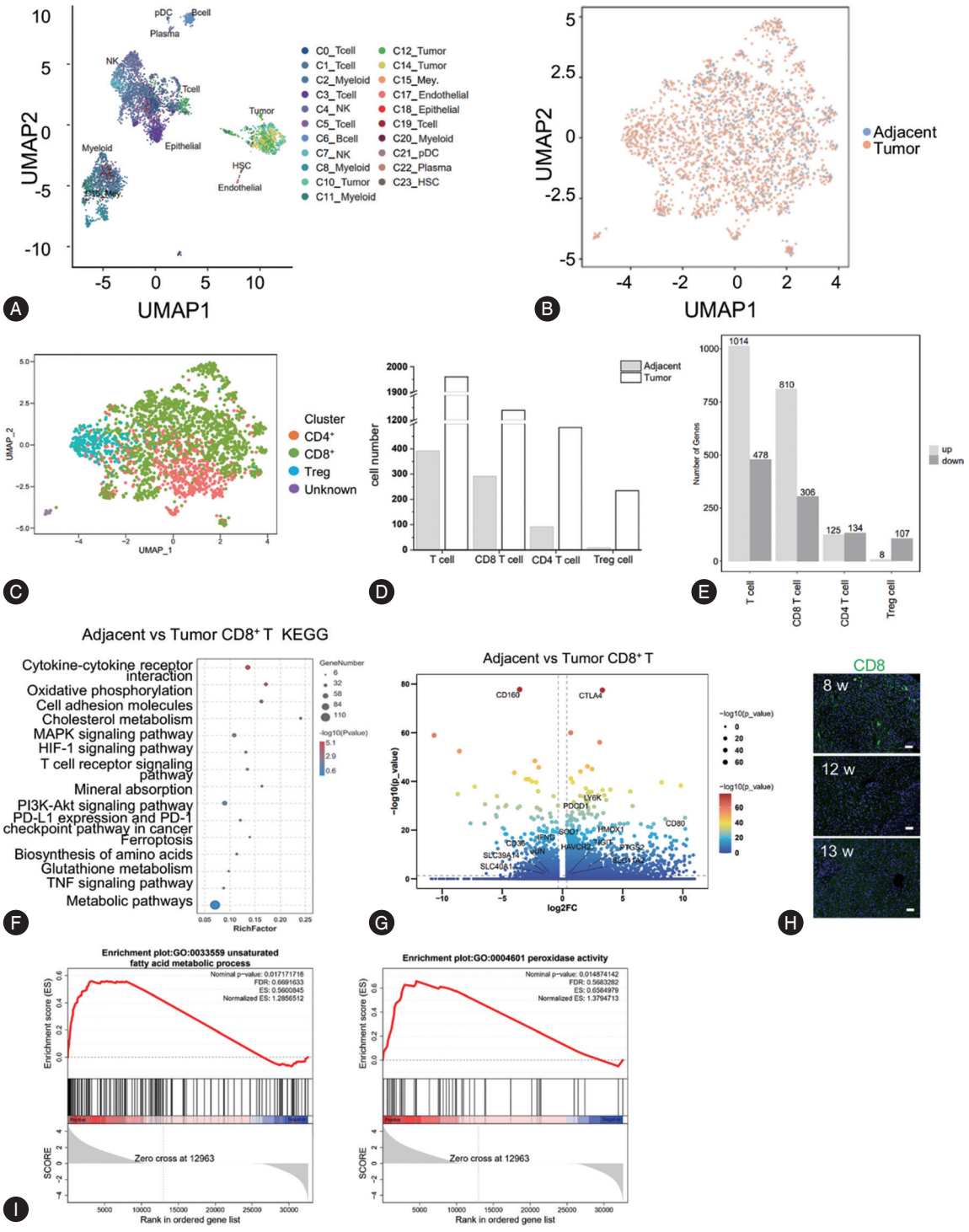

Supplementary Figure 6. Single-cell RNA sequencing of human HCC samples at BCLC A stage. (A) UMAP plots displaying the 24 clusters of cells in scRNA-seq of human HCC samples at early stages and the adjacent liver tissues. (B) UMAP plots showing the proportion of tumor and adjacent. (C) Cell-type annotation of each subpopulation from human HCC samples at early stages and the adjacent liver tissues. (D) Ratio of 4 major cell types showing in bar plots of human HCC tumor and adjacent. (E) Ratio of up and down genes from 4 major cell types showing in bar plots of human HCC tumor and adjacent. (F) Enriched KEGG pathway based on $CD8^+$ T cells from HCC tumors and adjacent tissues. (G) Volcano plot of differentially expressed genes between $CD8^+$ T cells from HCC tumors and adjacent tissues. (H) mIHC staining of CD8 (green) in HTVi HCC tumors at different time points. Scale bar: 50 μm. (I) Gene Set Enrichment Analysis of late-stage $CD8^+$ Tex cells compared with early-stage $CD8^+$ Tex cells in HTVi HCC tumors.