Figure S1. Comparison of the single-cell transcriptome data of HCC tumor cells and liver cancer cell lines. (A) Cell populations using principal component analysis. (B) Definition of cell types according to the marker genes. HuH1 and HuH7 represented the HCC cell lines. P1 represents the tumor cells from an HCC patient T and B represents the T cell and B cell. (C) Heat map of the marker genes. (D) Expression of important genes in all cells. Dots in red illustrate the high expression level of the gene. Dots in grey illustrate the low or no expression of the gene. HCC, hepatocellular carcinoma.

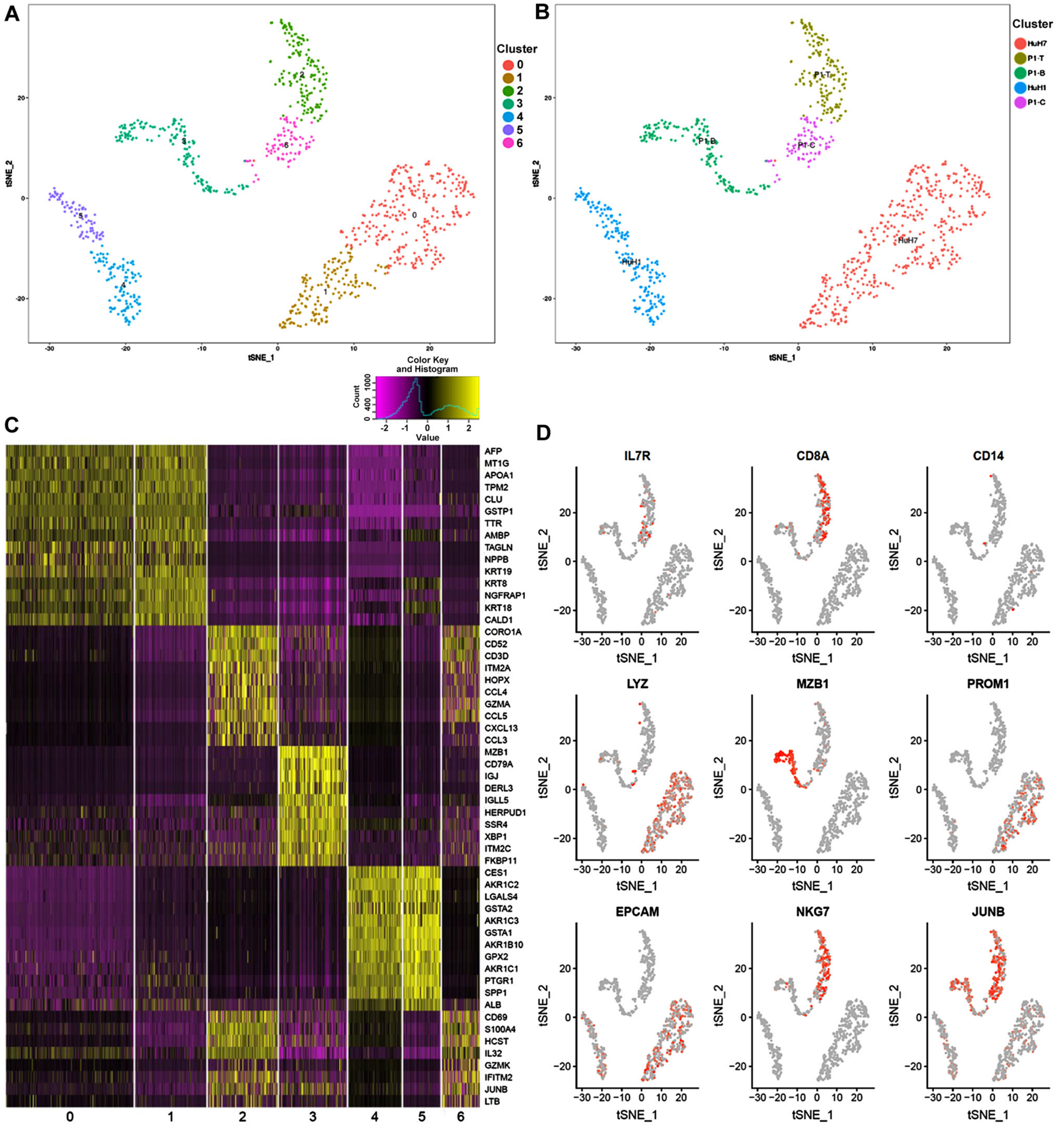

Figure S2. Expression level of cell population- and cell type-specific expressed genes. (A) Scatter plots for gene expression of cell population-specific expressed genes. (B) Box plots for gene expression of cell type-specific expressed genes in (a) HuH7 cells, (b) P1T and P1C cells, (c) P1B cells and (d) HuH1 cells.

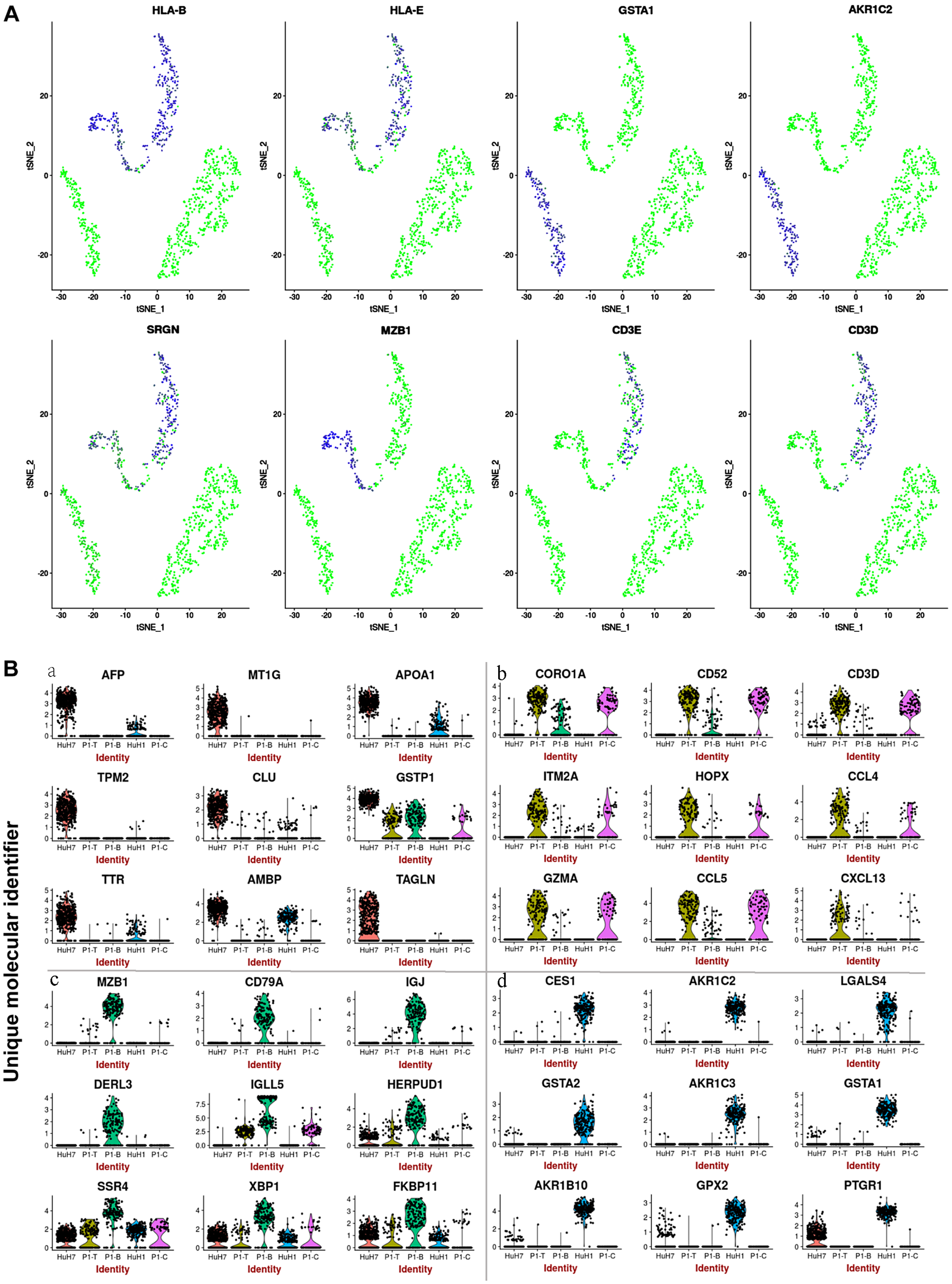

Figure S3. Comparison of the single-cell transcriptome data of PBMCs. (A) Cell populations using PCA. (B) Definition of cell types according to the marker genes. Monocyte indicates the monocyte cells. MS4A1 indicates the MS4A1-positive B cells. (C) Heatmap of the marker genes. (D) Expression of important genes in all cells. Dots in red indicate the high expression level of the gene. Dots in grey indicate the low or no expression of the gene. (E) Protein and protein interactions from the STRING database. (F) Scatter plot of the gene expression correlation of *APOA2*, *JUNB* and *ANXA2*. PCA, principal component analysis; PBMC, peripheral blood mononuclear cells; NK, natural killer cells; MS4A1, Membrane Spanning 4-Domains A1; *APOA2*, apolipoprotein A2; *JUNB*, JunB proto-oncogene; *ANXA2*, annexin A2.