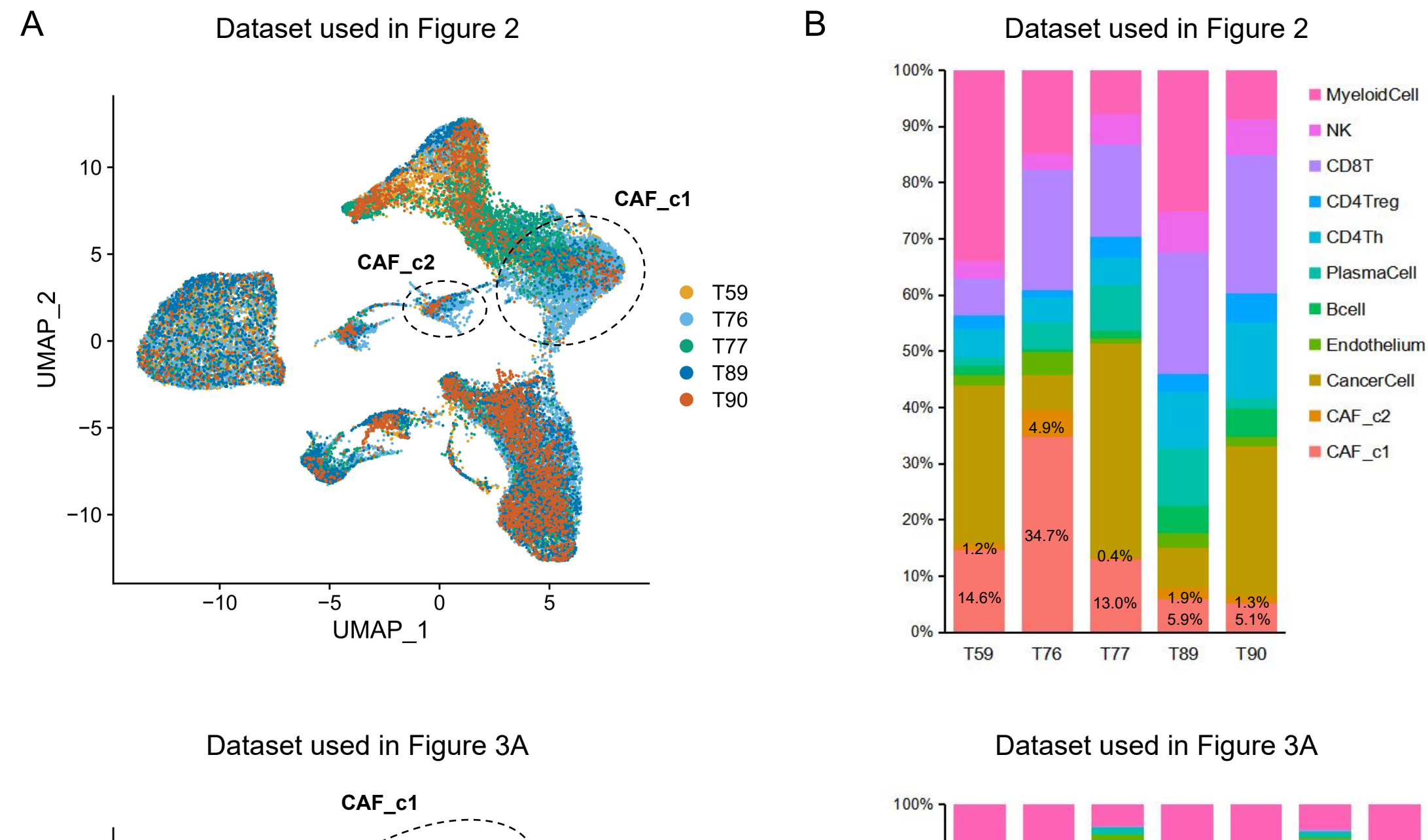
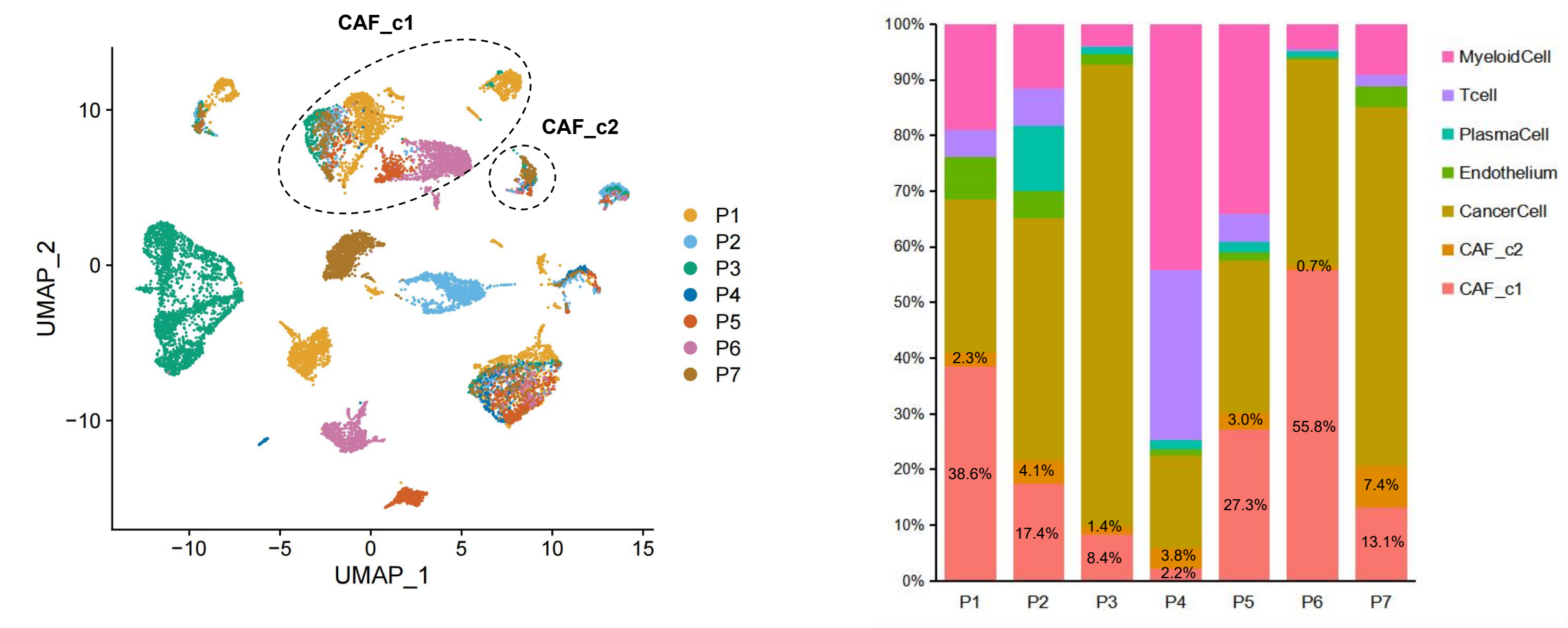
Figure S1





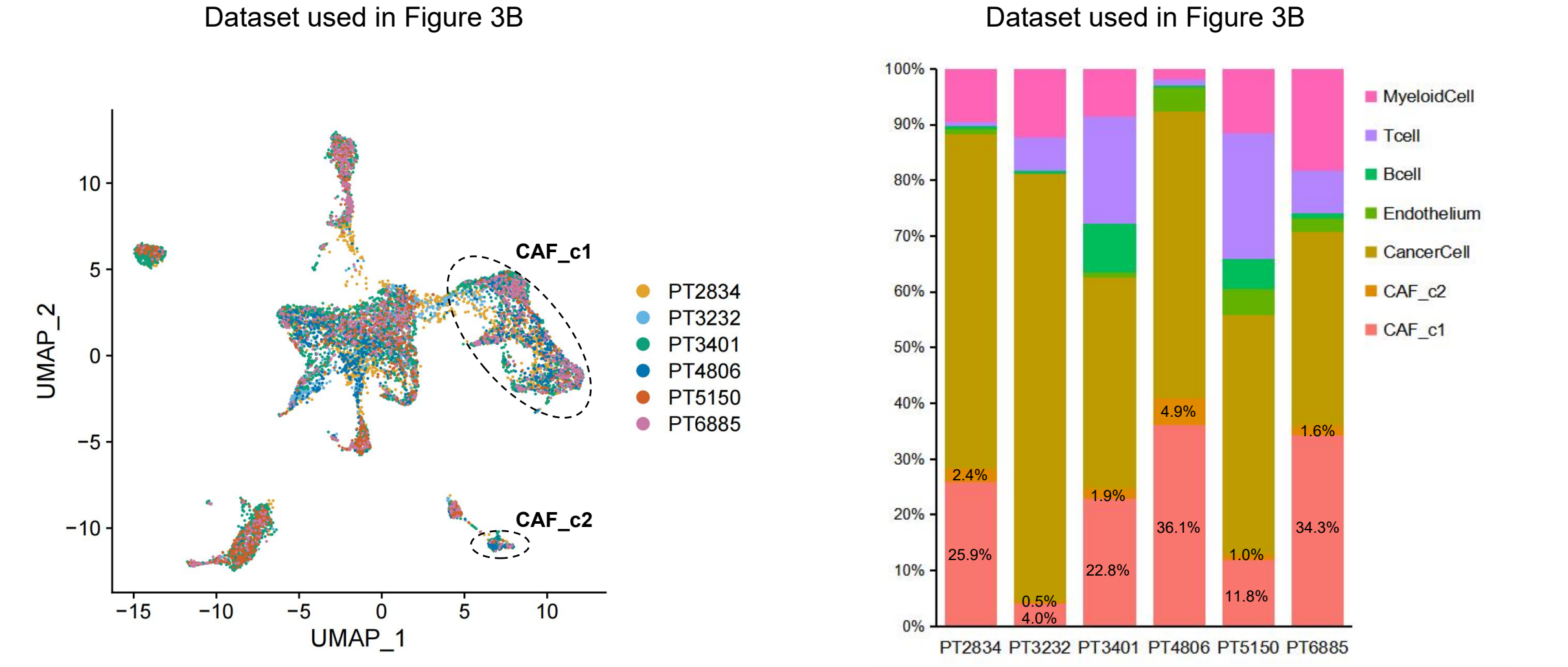


Figure S1. Identification of two CAF subtypes in individual samples. (A) Uniformmanifold approximation and projection (UMAP) analysis showed the distribution of cell phenotypes in individuals samples, the colors indicates different samples. **(B)** The percentage stacking chart of cell proportion in each sample, the colors indicates different cell types.

Figure S2

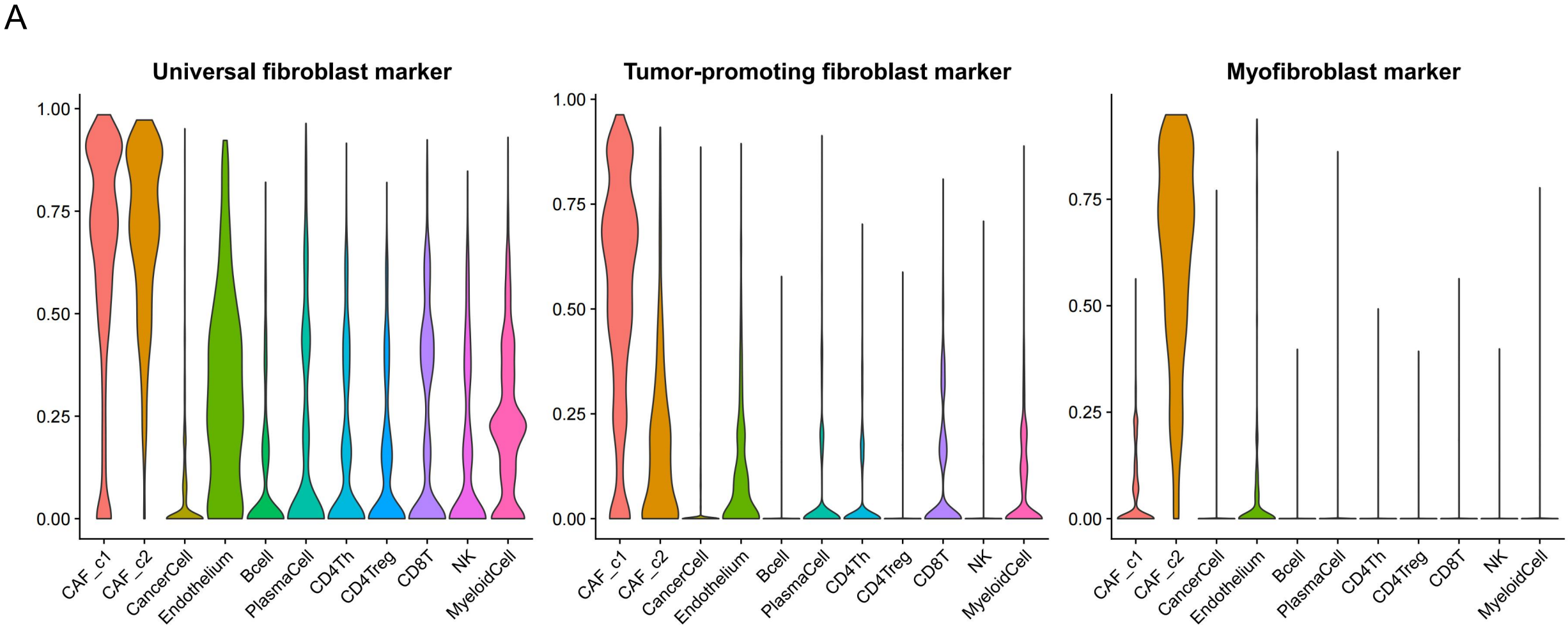


Figure S2. The annotation and function of two CAF subtypes. (A) The cell identity score calculated by UCell based on previously reported fibroblast markers. **(B)** Top 10 enriched Gene Ontology (GO) biological processes in CAF_c1 and CAF_c2, which was calculated by ssGSEA method in R package “GSVA”. The adjusted p-value was calculated by FindMarkers function in R package “Seurat”.

Figure S3

Figure S3. The annotation and function analysis of cancer cells. (A) UMAP analysis of CAF_c1 and cancer cells, in which cancer cells are re-clustered into two subtypes. **(B)** The violin plot of marker genes of CAF_c1, CancerCell_c1 and CancerCell_c2. **(C)** Top 10 enriched Gene Ontology (GO) biological processes in CancerCell_c1 and CancerCell_c2, which was calculated by ssGSEA method in R package “GSVA”. The adjusted p-value was calculated by FindMarkers function in R package “Seurat”. **(D)** Heat map depicting the significant interactions among CAF_c1 and two cancer cell subtypes, the color indicates the number of interactions between two specified TFs. **(E)** Overview of the selected ligand-receptor interactions. P-values (two-tailed permutation test) are indicated by circle size. The means of the average expression level of interacting molecule 1 in cluster 1 and interacting molecule 2 in cluster 2 are indicated by color.

Figure S4

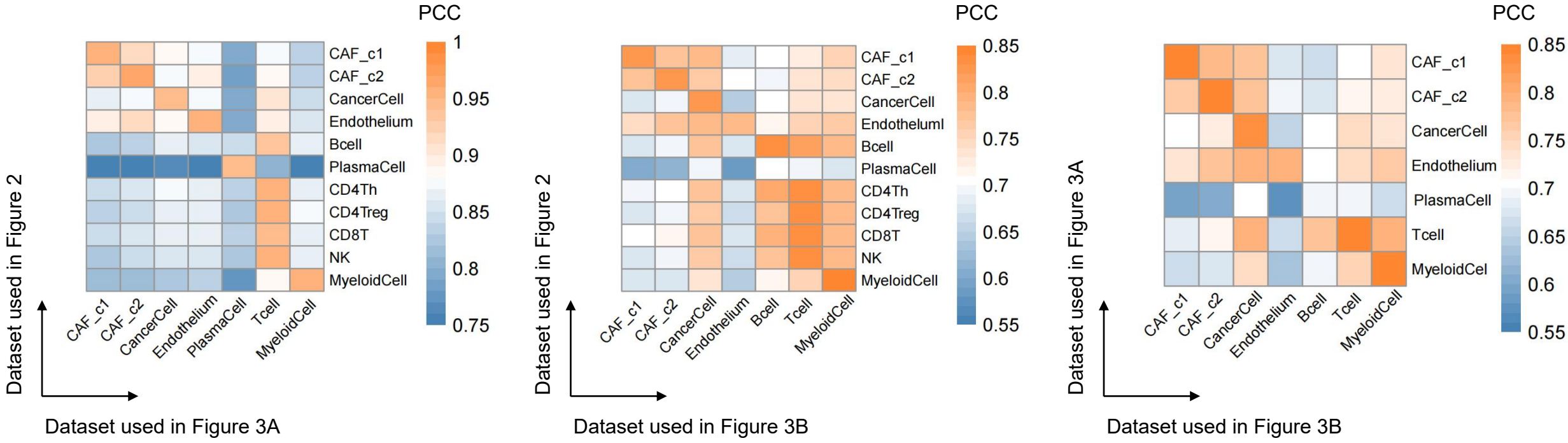


Figure S4. Heatmaps of the correlation matrixes of gene expression profiles between each two datasets. The color indicates the Pearson correlation coefficient (PCC) of a specified cell type in two independent datasets.