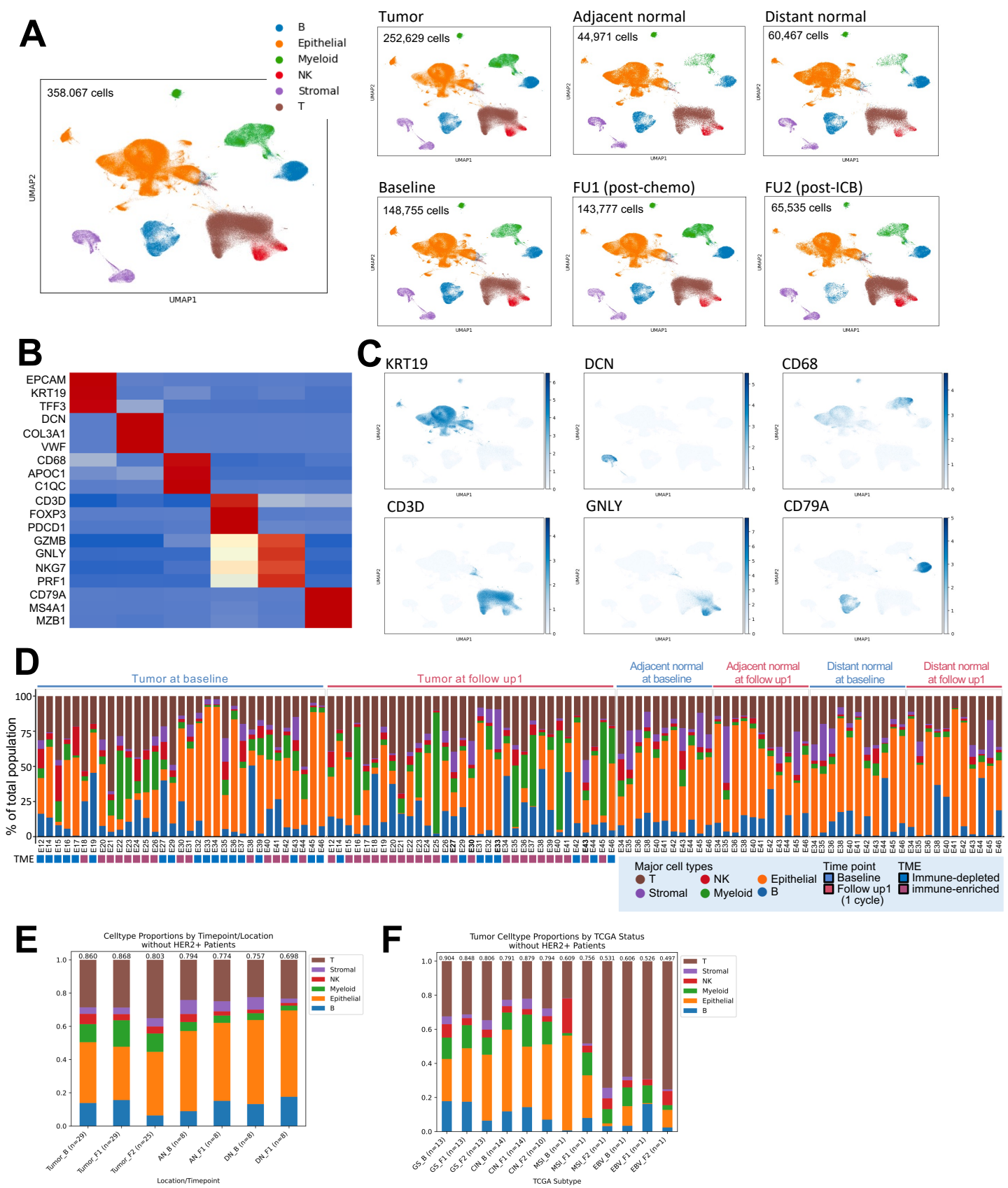

Figure S6. (A) UMAP embedding of single cell transcriptomes obtained from all samples in this trial. Labeled are canonical cell types separated by tumor v.s. normal tissue, and by timepoint. (B) Heatmap and (C) UMAP embeddings showing marker gene expression for broad cell types in (A). (D) Broad cell type composition per sample across tumor and normal tissue. (E) Cell type proportions from scSeq data by timepoint in tumor and normal tissue excluding HER2+ patients. (F) Cell type proportions from scSeq data by timepoint and TCGA classification excluding HER2+ patients.