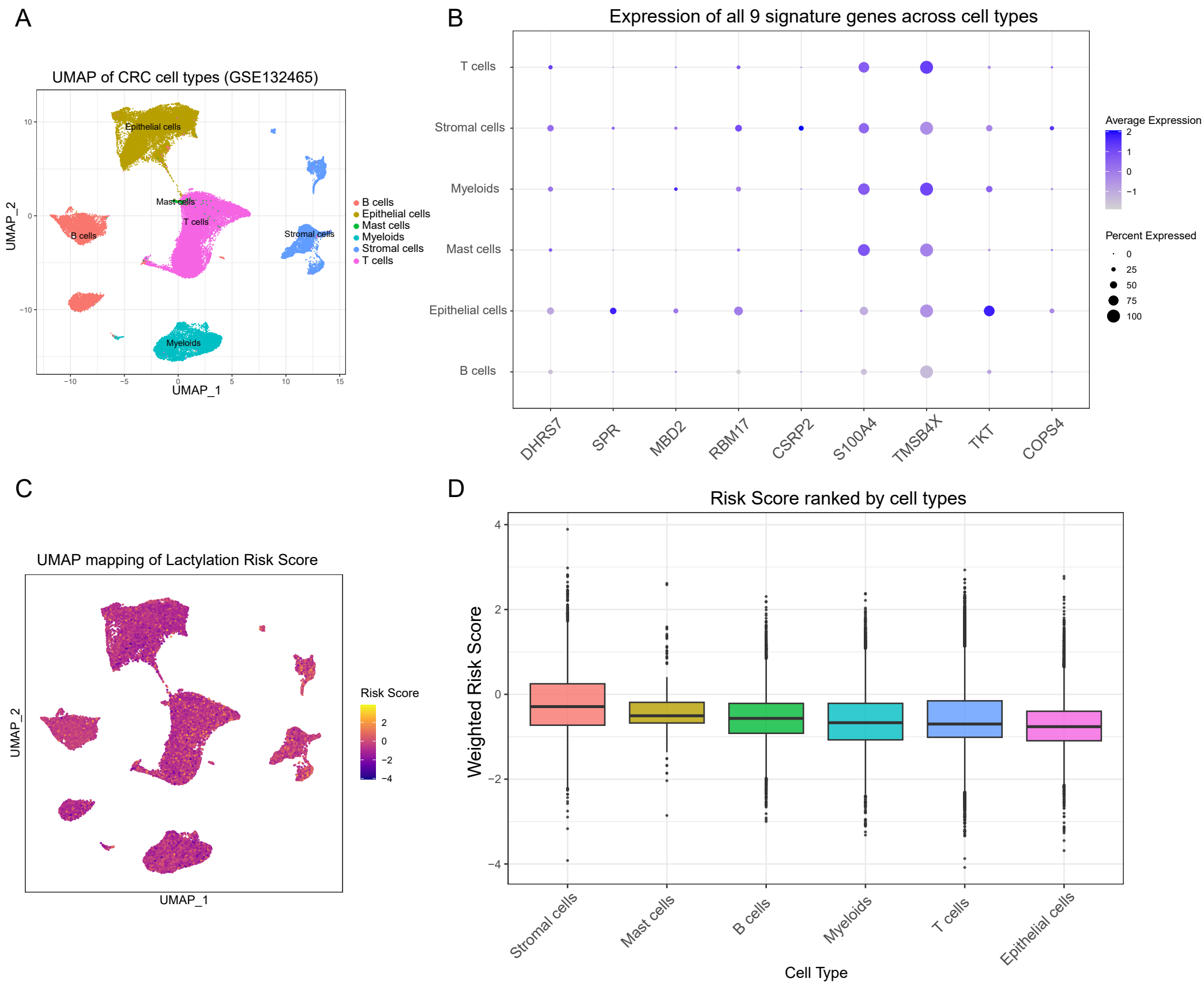




Supplementary Figure S4. Single-cell transcriptomic profiling reveals the expression landscape and risk score distribution of the lactylation-related signature in the colorectal cancer microenvironment. (A) UMAP (Uniform Manifold Approximation and Projection) embedding of single cells from the CRC cohort (GSE132465), colored and annotated by six major cell types: B cells, Epithelial cells, Mast cells, Myeloids, Stromal cells, and T cells. (B) Dot plot illustrating the expression patterns of the nine signature genes across the annotated cell types. The size of the dot represents the percentage of cells expressing the specific gene, and the color gradient indicates the average expression level. (C) UMAP feature plot visualizing the spatial distribution of the calculated 9-gene weighted lactylation risk score at single-cell resolution. (D) Box plots comparing the weighted risk scores across the six cell types. Cell populations are ranked in descending order by their median risk scores, demonstrating that Stromal cells exhibit the highest overall risk score among all subsets.