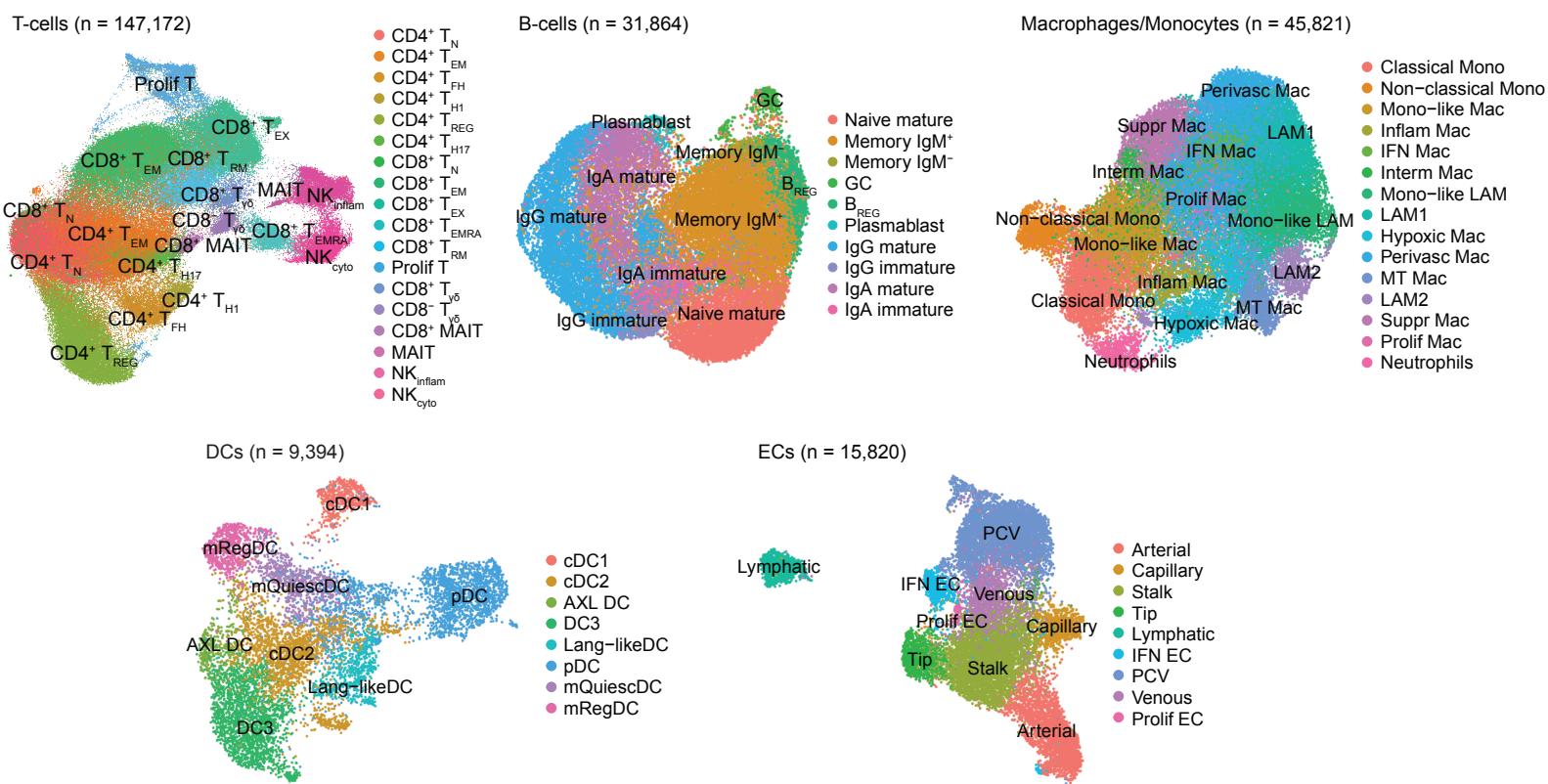
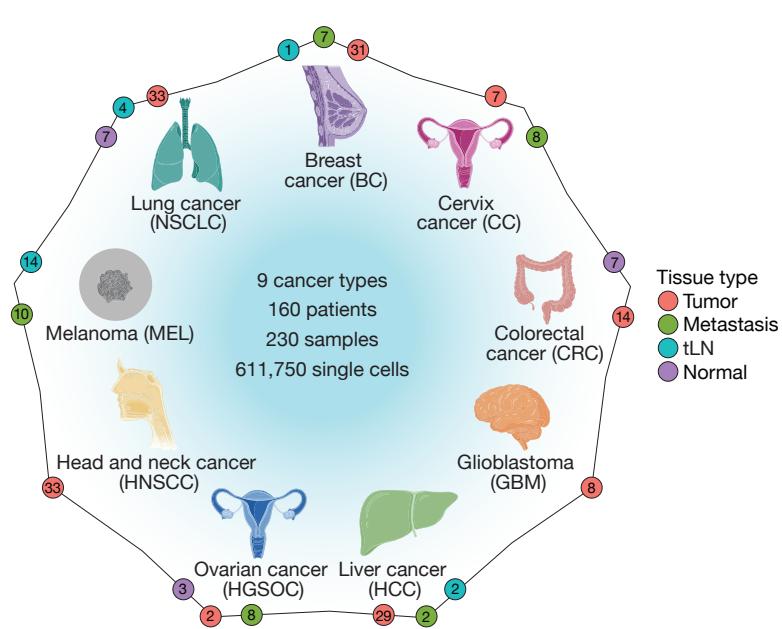


Exploring the tumor microenvironment (TME) with single-cell RNA sequencing (scRNASeq)

The TME plays a crucial role in shaping tumor evolution and determining therapy effectiveness. ScRNASeq has revolutionized our understanding of the TME by enabling detailed insights at the cellular level. While previous studies often focused on a specific cell type and cancer type or combined data from various sources, our approach is distinct. We present a comprehensive, uniform pan-cancer scRNASeq dataset, comprising 611,750 high-quality single-cell transcriptomes from 230 treatment-naïve samples across 9 different cancer types, all generated in-house to minimize technological variability. Within this dataset, we have identified 70 shared subclusters that provide deeper insights into TME heterogeneity.



Welcome to our pan-cancer Shiny apps!

These Shiny apps are designed to facilitate the exploration of gene and gene signature expression across 9 cancer types. It allows users to examine individual gene expression, analyze customizable gene signatures, rank tumors, and explore gene expression changes within specific subclusters. Besides this major app where all 70 shared subclusters can be explored simultaneously, we have individual apps for individual cell types.

Below, you can find links to the Shiny apps for the individual cell types: