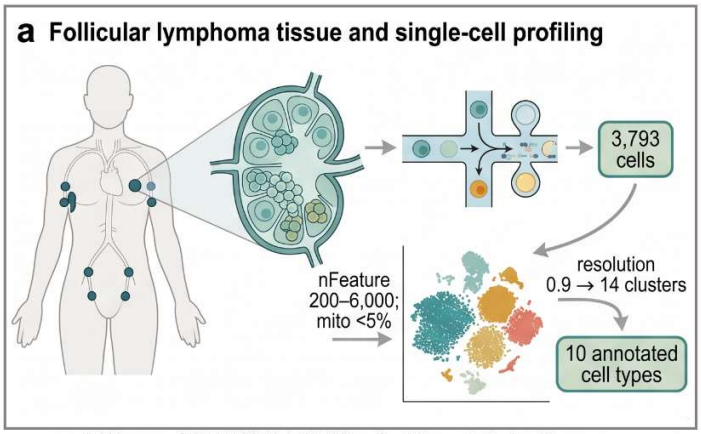
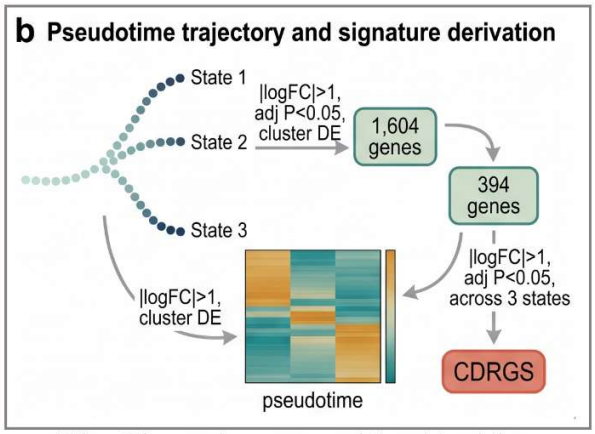
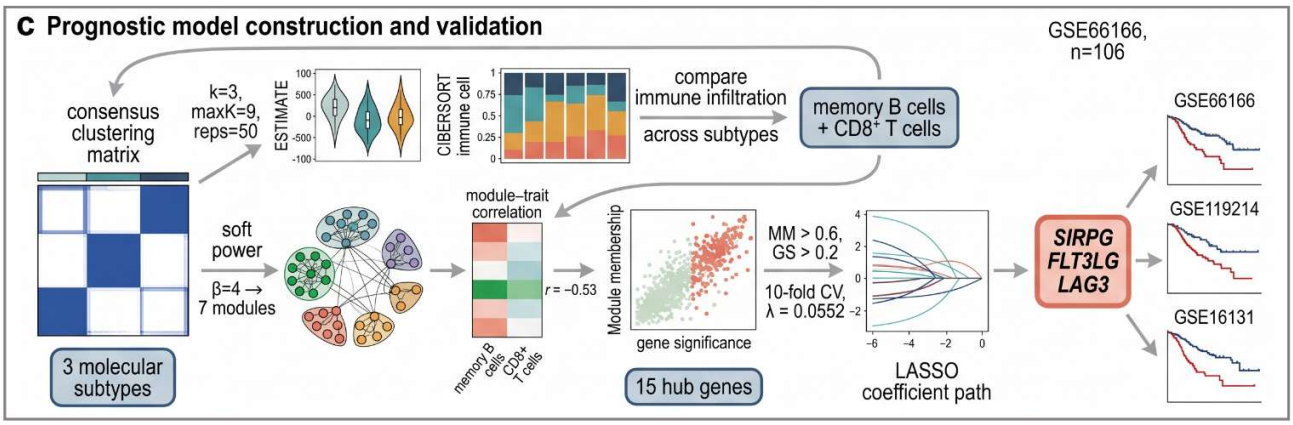


scRNA-seq of GSE182434: 3,793 cells, 10 annotated cell types



Differential expression across pseudotime states defines the cell differentiation-related gene signature



Consensus clustering *resolves three molecular subtypes; comparing immune infiltration between subtypes selects the traits for weighted gene co-expression network analysis, from which the green module, its hub genes, and the three model genes are successively derived, then validated in the training and two independent cohorts.*