

Supplementary Figures Here

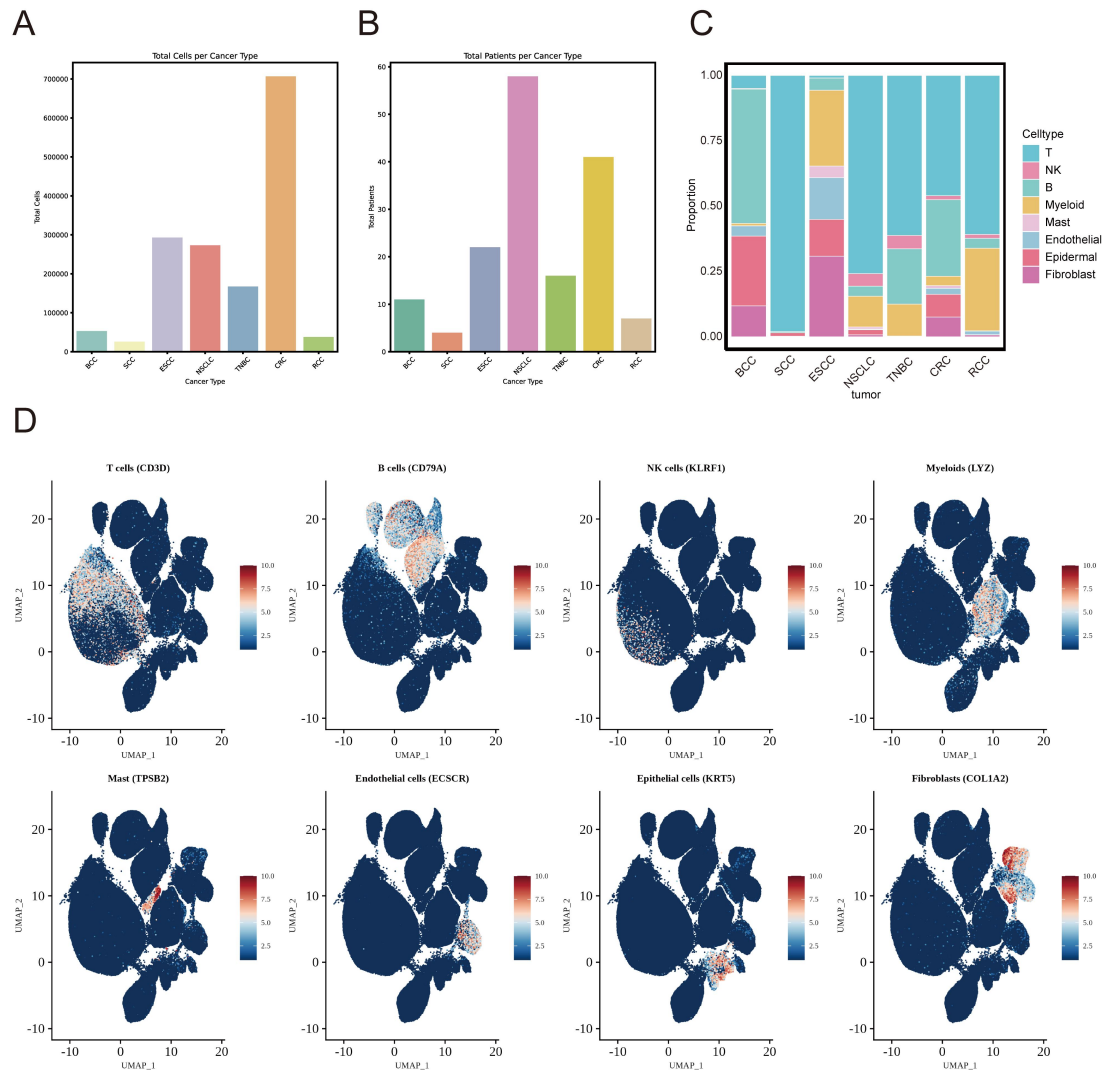


Figure S1 Information on patient cohorts and cell populations.

(A-B) Bar plots summarizing the total number of cells collected by cancer type (A) and the number of patients included (B). (C) Frequency of major cell types across all cancer types. (D) UMAP plot showing the expression of typical marker genes for major cell populations.

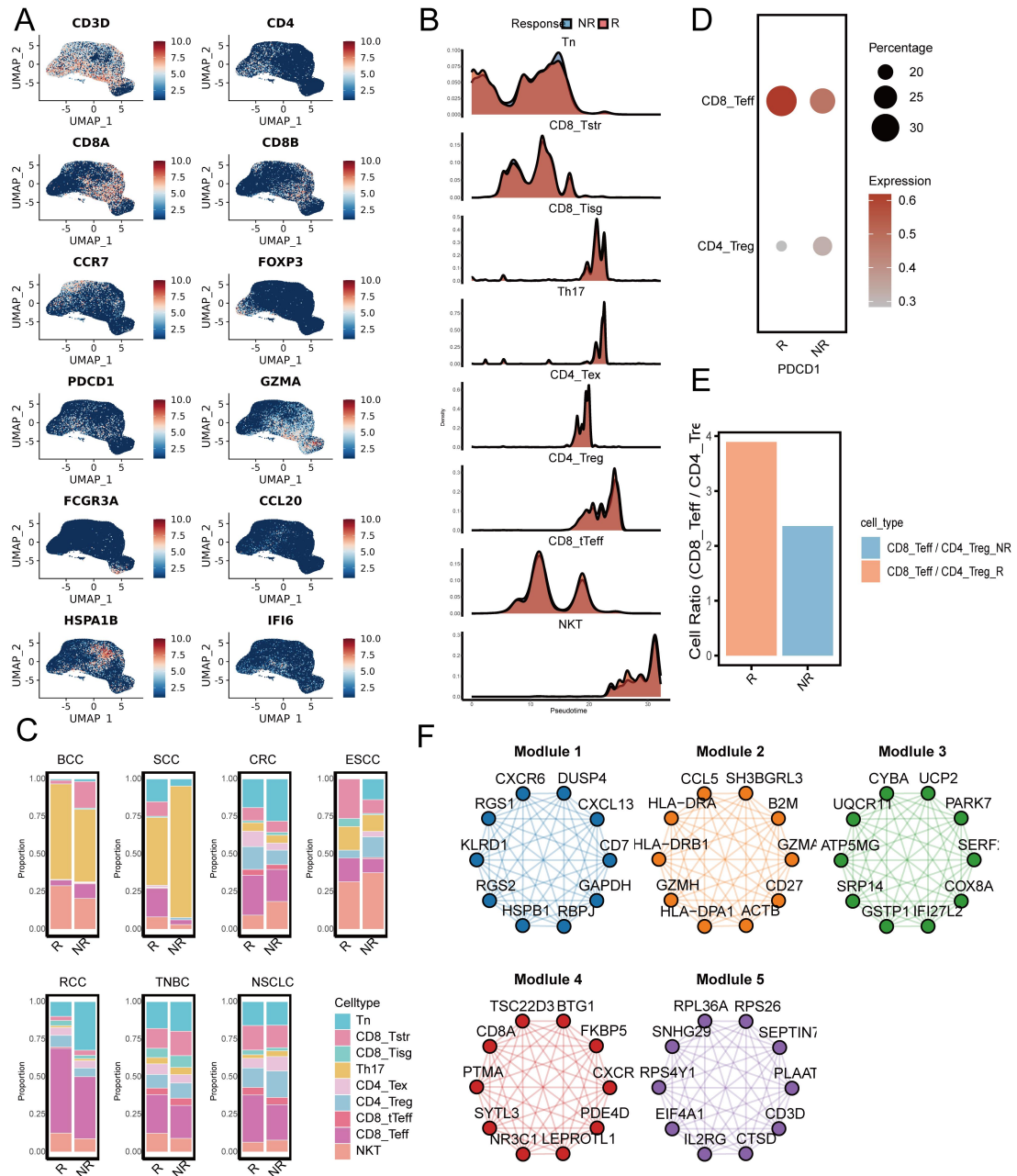


Figure S2 Characteristics of T-cell subpopulations.

(A) UMAP plot showing the expression of typical marker genes in major T-cell subpopulations. (B) Distribution of T cells along pseudotime in R and NR groups. (C) Proportions of T-cell subpopulations in R and NR across different cancer types. (D) Expression of PDCD1 in CD8_Teff and CD4_Treg cells between R and NR groups. (E) Ratio of PDCD1-expressing CD8_Teff to CD4_Treg cells in R and NR. (F) Top ten genes for each gene module.

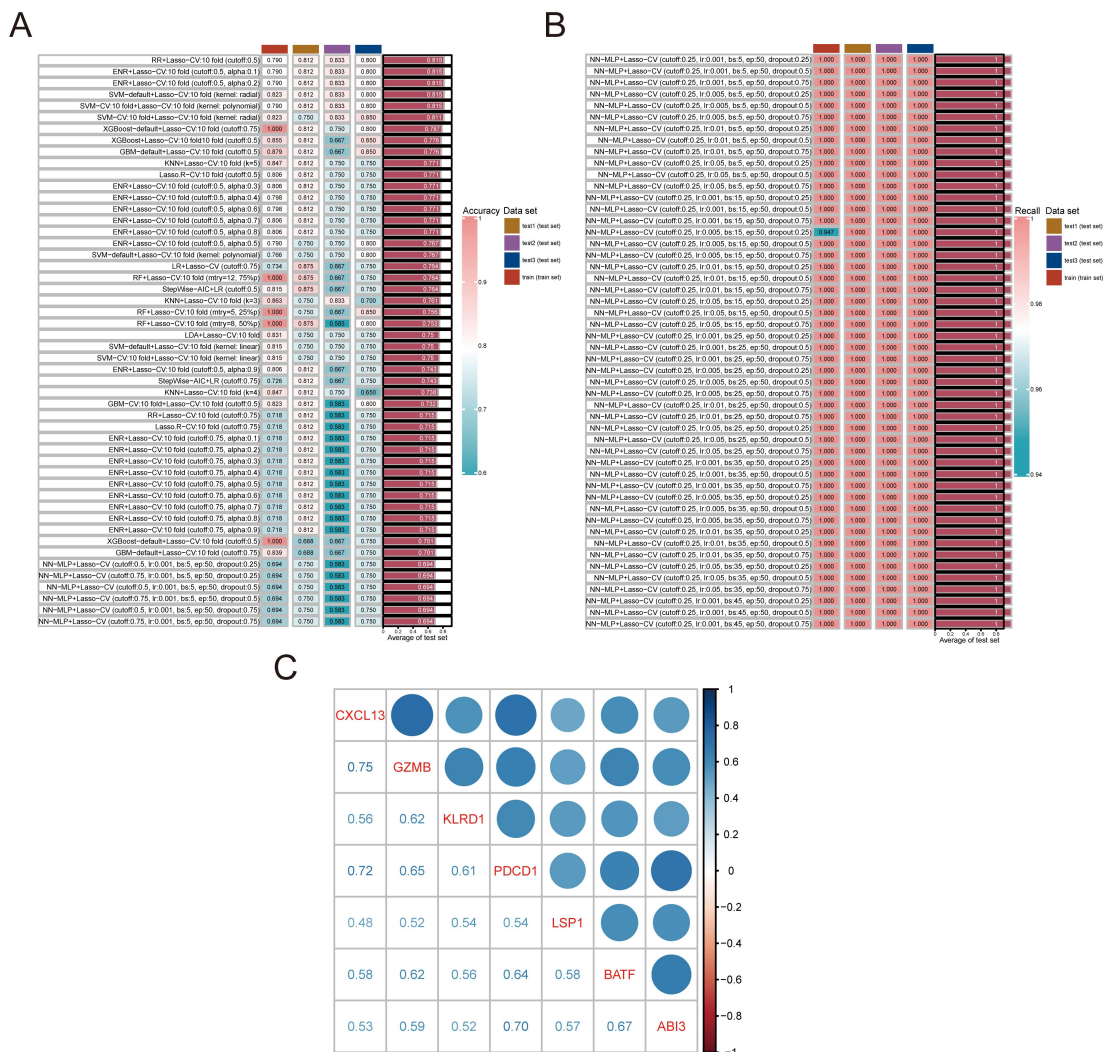


Figure S3 Construction of the ETIRGS model.

(A-B) Performance of the top 50 machine learning models based on accuracy (A) and recall (B).

(C) Heatmap showing the correlation among the seven genes included in the ETIRGS model.

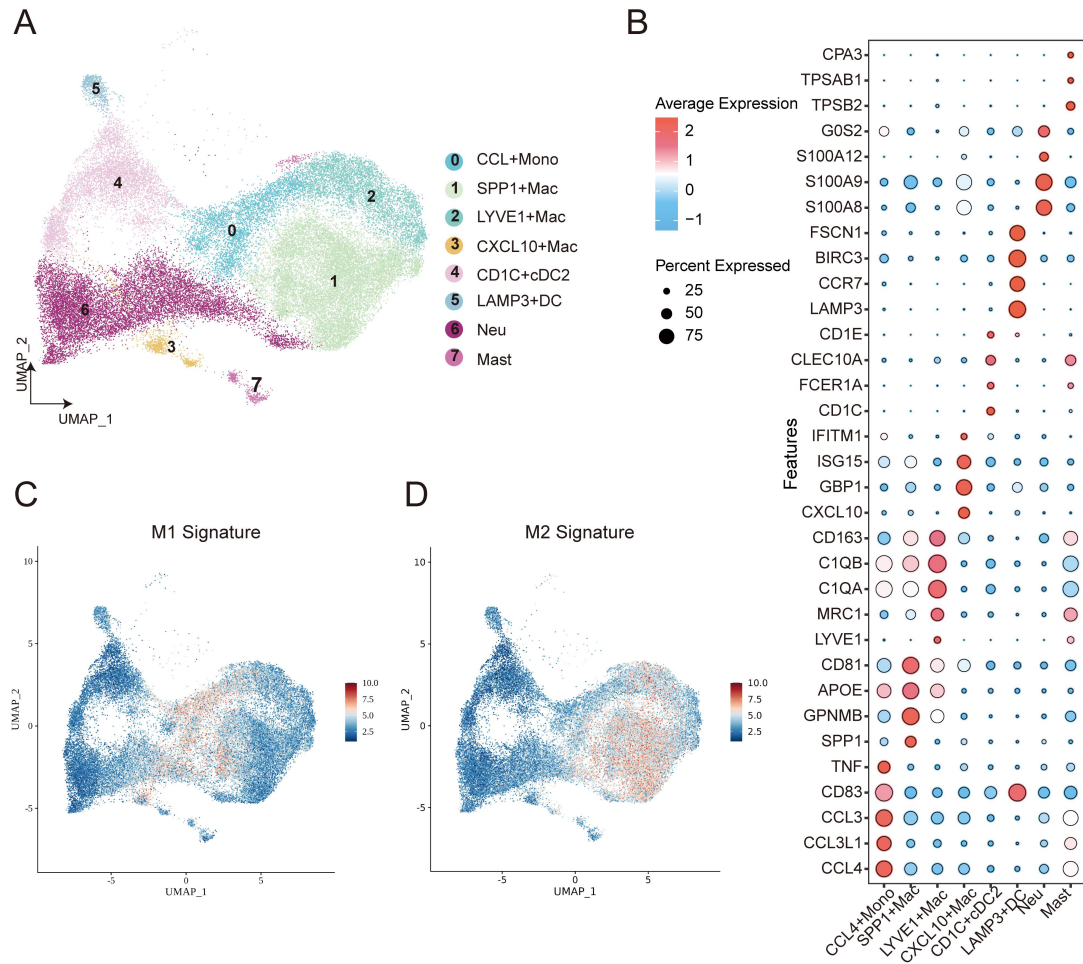


Figure S4 Characteristics of myeloid cells.

(A) UMAP plot displaying the clustering of eight myeloid cell subpopulations. (B) Expression of marker genes in the defined myeloid cell subpopulations. (C-D) UMAP visualization of M1 (C) and M2 (D) macrophage.