

Supplementary table 1: The ESCA patient-specific information details used in this research.

Supplementary table 2: The ESCA patient-specific information details of paraffin-embedded tissue microarray.

Supplementary table 3: Summary of detailed antibody information used in this research.

Supplementary table 4: Differential gene expression of CD8⁺T cell subsets from the scRNA-seq data.

Supplementary table 5: Differential gene expression of distinct CD8⁺TRMs cluster from the scRNA-seq data.

Supplementary table 6 : The tissue residence, exhaustion, cytotoxicity, naivety and cell cycle genes signatures of TRMs scores.

Supplementary table 7: The TFs and their driver regulators of each SCENIC analysis module and the Gene Ontology (GO) enrichment analysis result of these TFs and driver regulators

Supplementary table 8: The full-length α and β chains of TCRs from distinct CD8⁺TRMs cluster.

Supplementary table 9: Differential gene expression of myeloid cell cluster from the scRNA-seq data