

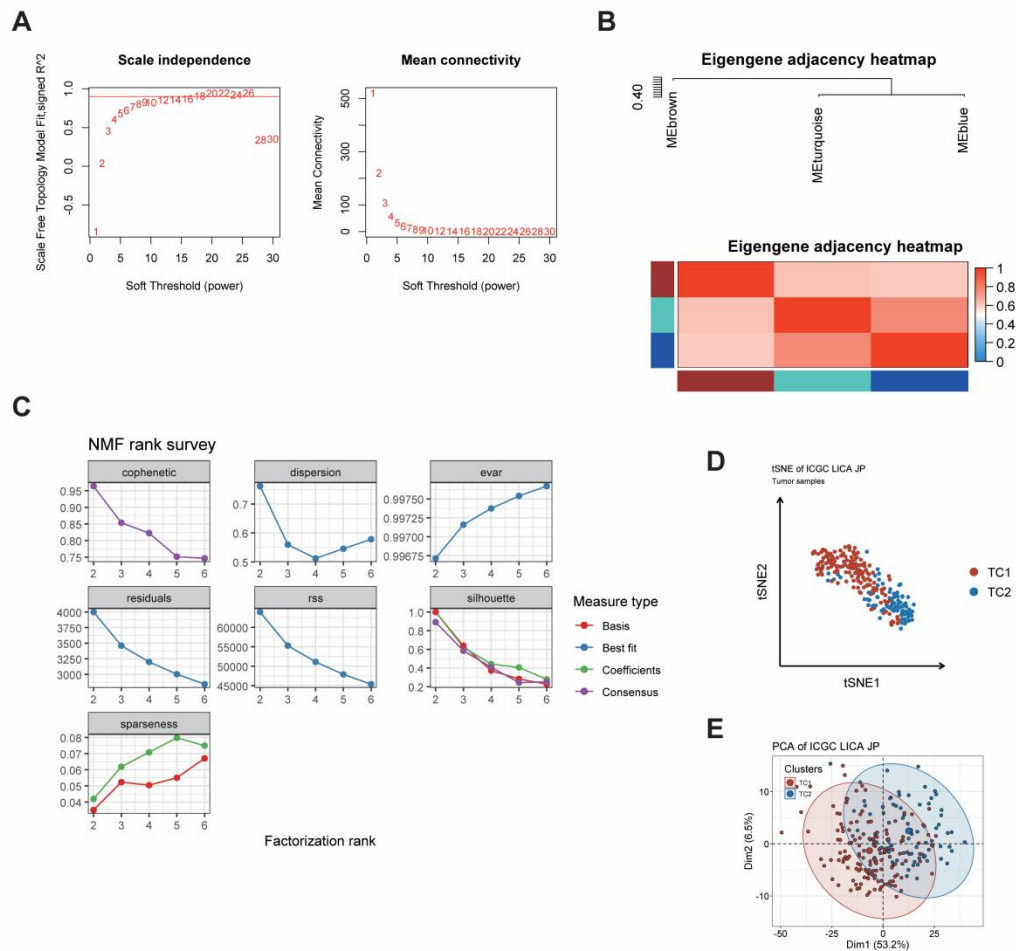


Figure S1

Supplementary Figure S1: WGCNA screening suitable TM-related genes to identify the most pertinent modules associated with TM. (A) Power = 12 was selected as the soft threshold for WGCNA analysis. (B) The interconnection between biological pathways and gene modules. (C) The optimal rank value for NMF-based clustering is 2. (H) The CDF and delta index of consensus clustering. (I) TM clusters were identifiable through PCA and tSNE plots.

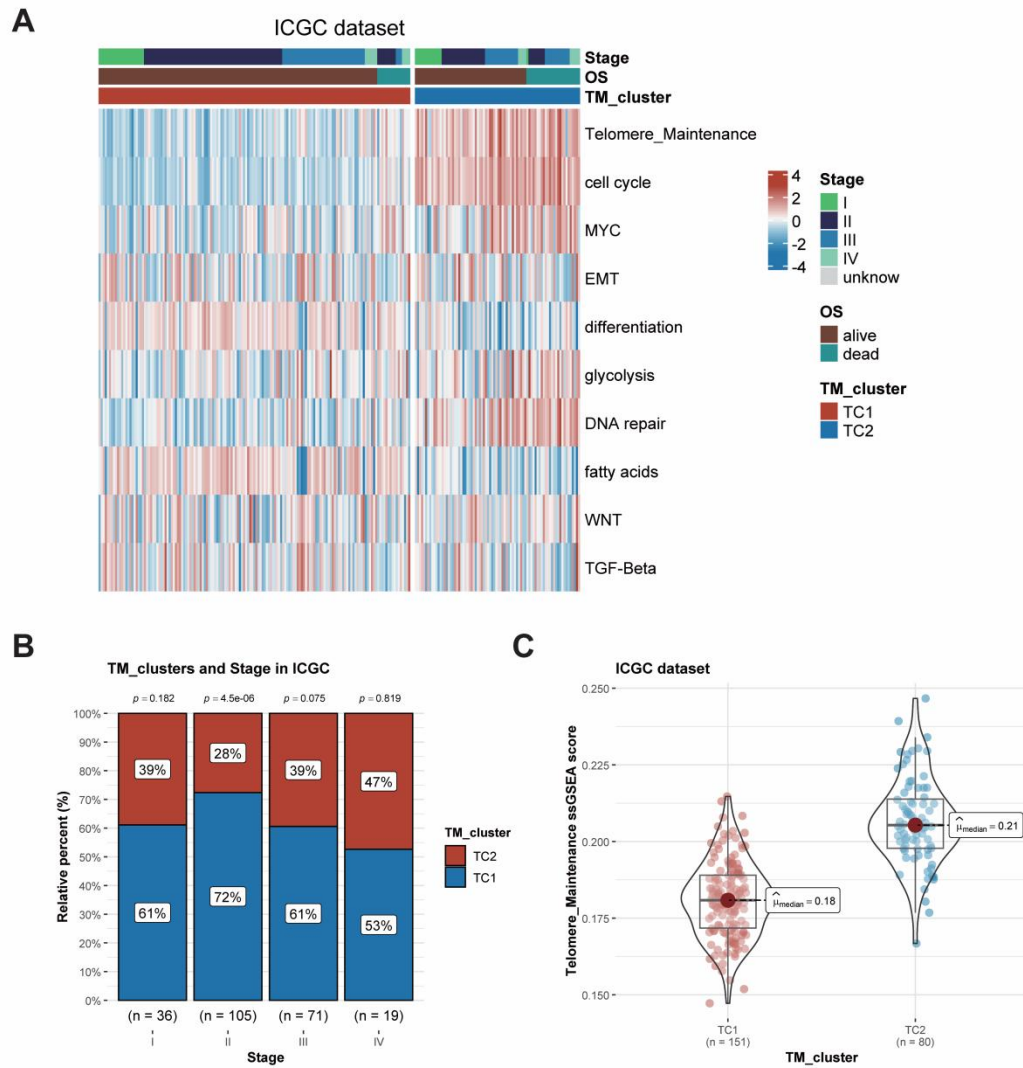
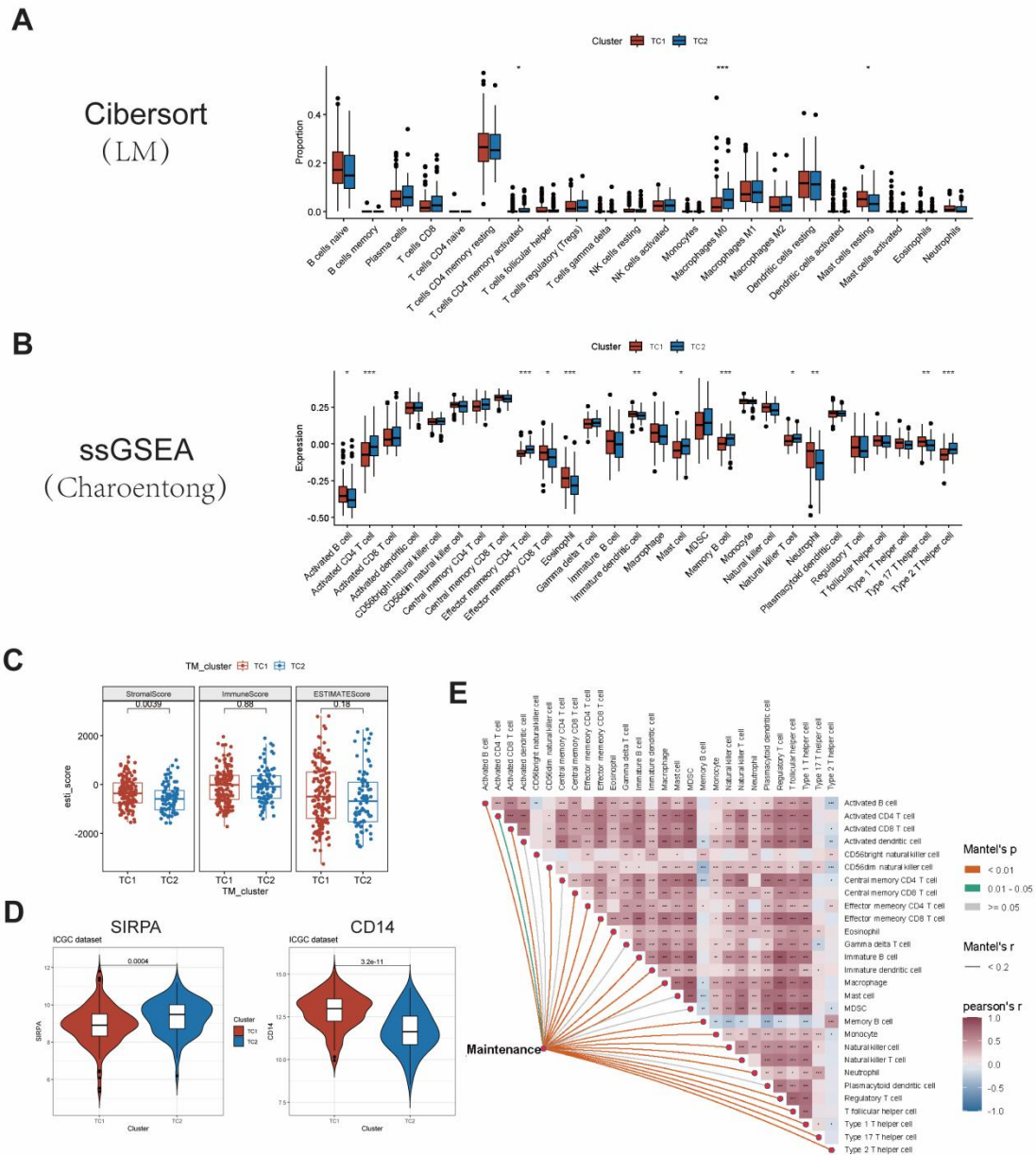


Figure S2

Supplementary Figure S2: Clinical characteristics of TM clusters in the ICGC database. (A) The distinctions between TCs were unveiled through a meticulous examination of clinical characteristics, alongside an analysis of 10 pathways evaluated via ssGSEA within the ICGC database. (B) Distribution of TCs across varied clinical stages within the ICGC database. (C) The respective ssGSEA scores of TCs revealed that TC2 outperformed TC1 within the ICGC database.



FigureS3

Supplementary Figure S3: Exploration of TME in TCs in the ICGC database. (A) Cibersort analysis revealed the proportion of immune cells present in TCs. **(B)** The ssGSEA analysis demonstrated the varying infiltration levels of immune cells in TCs. **(C)** The ESTIMATE algorithm was utilized to evaluate immune and stromal scores in TCs. **(D)** Differential expression of SIRPA and CD14 in TCs. **(E)** TM was determined through association analysis conducted on various immune cell types (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

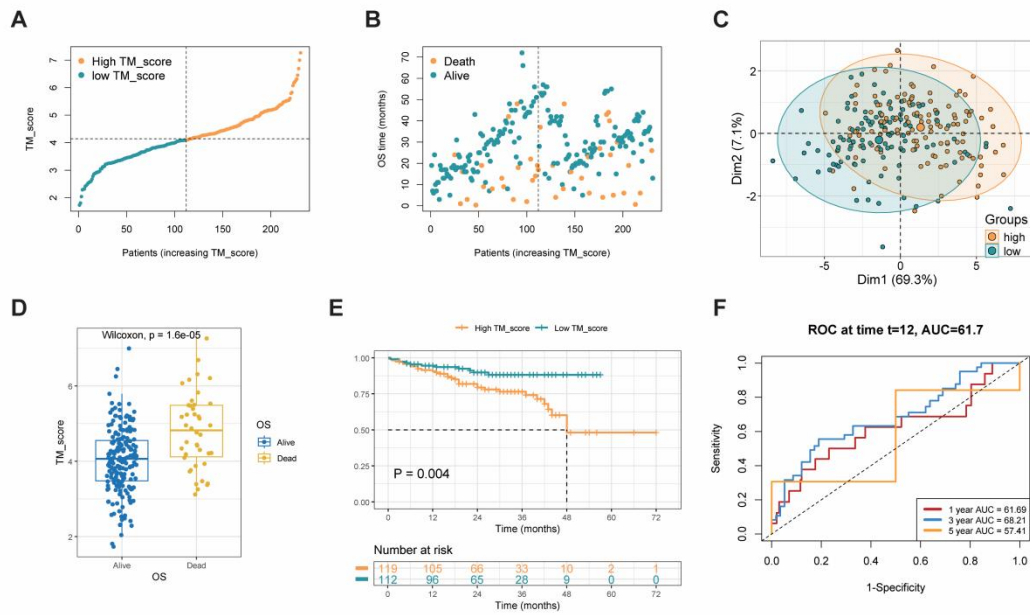


Figure S4

Supplementary Figure S4: Assessment of TM score in the test set. (A-B) Distribution of TM scores among patients with varying overall survival status in the test set. **(C)** PCA analysis revealed the distribution of high and low TM score groups within the test set. **(D)** Patients in the test cohort with dead status attained significantly elevated TM scores. **(E-F)** Survival analysis employing the effective AUC demonstrated that the cohort with elevated TM scores exhibited a significantly poorer prognosis within the test set.