



Figure S1. Heatmap and clinicopathological features of TMERS-low and TMERS-high group in GSE16011 dataset. *P < 0.001.**

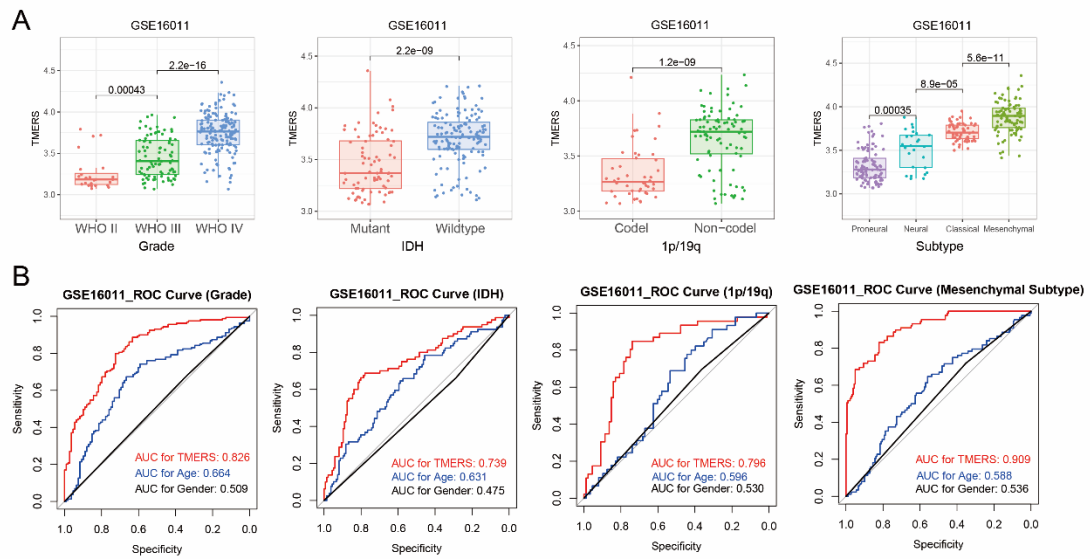


Figure S2. Associations between TMERS and pathological features in GSE16011 dataset. (A) Patients were grouped by WHO grade, IDH mutation status, 1p/19q codeletion status, TCGA molecular subtype. **(B)** The ROC curve evaluated the predictive value of TMERS in pathological features.

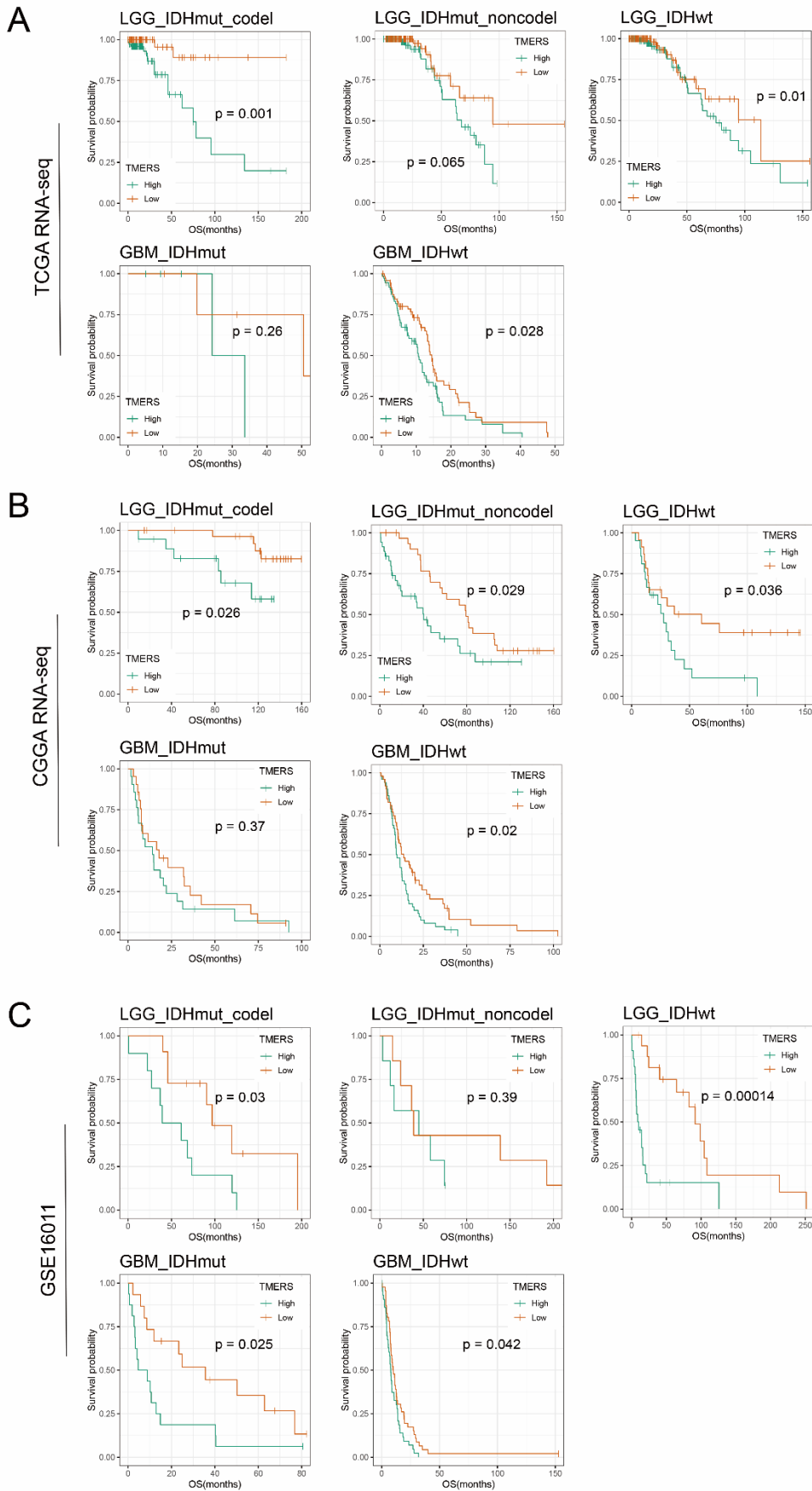


Figure S3. Clinical prognostic value of TMERS. Overall survival prediction of the TMERS in

LGG with IDH-mutant and 1p/19q-codeleted, LGG with IDH-mutant and 1p/19q-intact, LGG with IDH-wildtype, GBM with IDH-mutant, GBM with IDH-wildtype in TCGA dataset (**A**), CGGA dataset (**B**) and GSE16011 dataset (**C**). Survival difference was determined by a log-rank test.

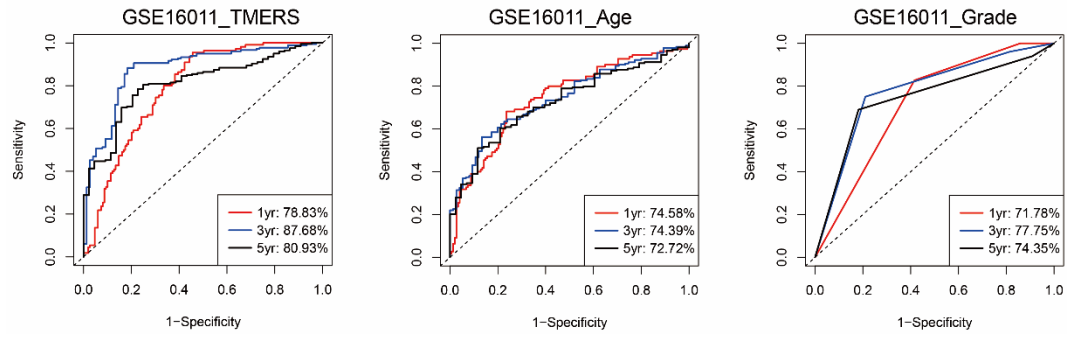


Figure S4. Predictive value of TMERS, age and grade for overall survival in GSE16011 dataset.

(A) 1-year, 3-year and 5-year ROC curves indicated the sensitivity and specificity of TMERS, age and grade in GSE16011 dataset.

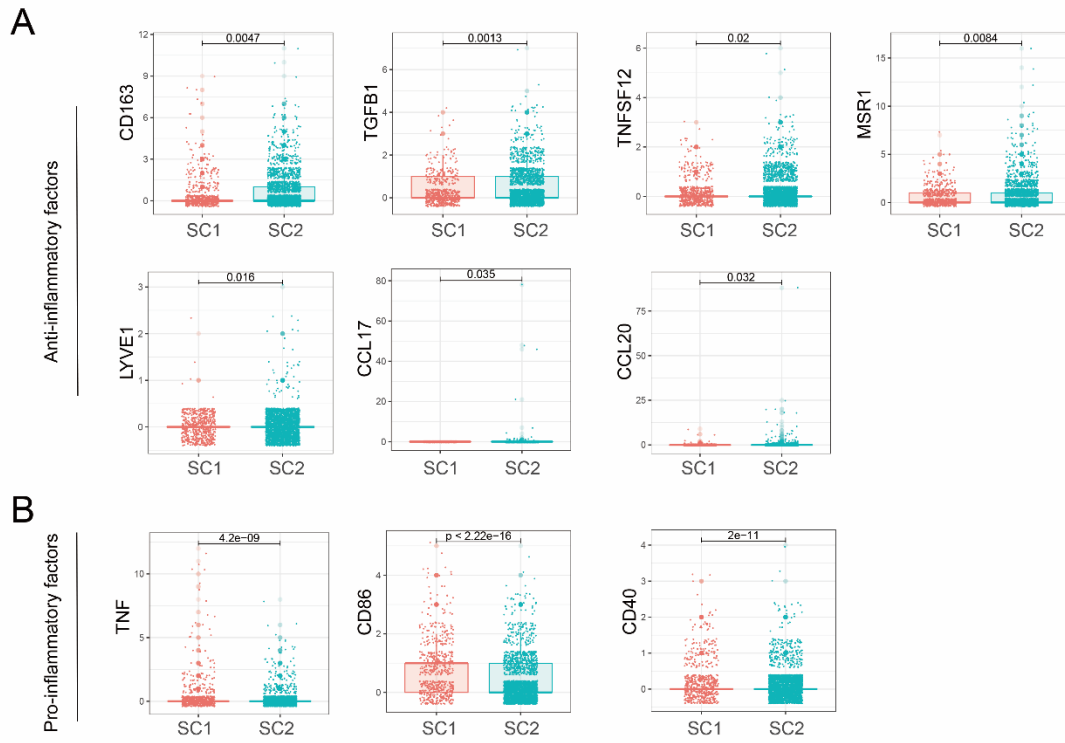


Figure S5. Phenotypic analysis of macrophages in two single-cell sequencing samples. (A) Expression levels of anti-inflammatory factors in macrophages. **(B)** Expression levels of pro-inflammatory factors in macrophages.