**Supplementary Figure 1:** M6A-related genes for prognosis prediction and correlation with TME in GC. (A) Forest plot of 19 m6A-related genes associated with prognosis identified by univariate Cox regression analysis. (B) Clinicopathological features and expression levels of 19 prognostic genes in the two clusters. (C) Kaplan–Meier curves of OS for patients in the two clusters.Expression of PD-L1 (D), immune score (E), and stromal score (F) in the two clusters.Survival analyses of patients by risk score group in the training set (G) and testing set (H). ROC curves of the training set (I) and testing set (J). The risk scores of patients with different ages (K), clusters (L), immune scores (M), and stromal scores in TCGA cohort (N). (O) OS in the high- and low-risk groups in the GSE84437 cohort. (P) ROC curve of GSE84437 dataset. The relationship of risk score with immune score (Q) and stromal score (R) in GSE84437 cohort.; \**P* < 0.05; \*\**P* < 0.01; \*\*\**P* < 0.001. M6A: N6-methyladenosine; TME: Tumor microenvironment; GC: Gastric cancer; CI: Confidence interval; TNM: Tumor-node-metastasis; OS: Overall survival; PD-L1: Programmed cell death-ligand 1; ROC: Receiver operating characteristic; AUC: Area under the curve; TCGA: The Cancer Genome Atlas.

Supplementary Figure 1