

Figure S1 Based on the correlation coefficient R2 in the scale-free network fitting process and the mean connectivity in the scale-free network model, we selected 4 as the power value.

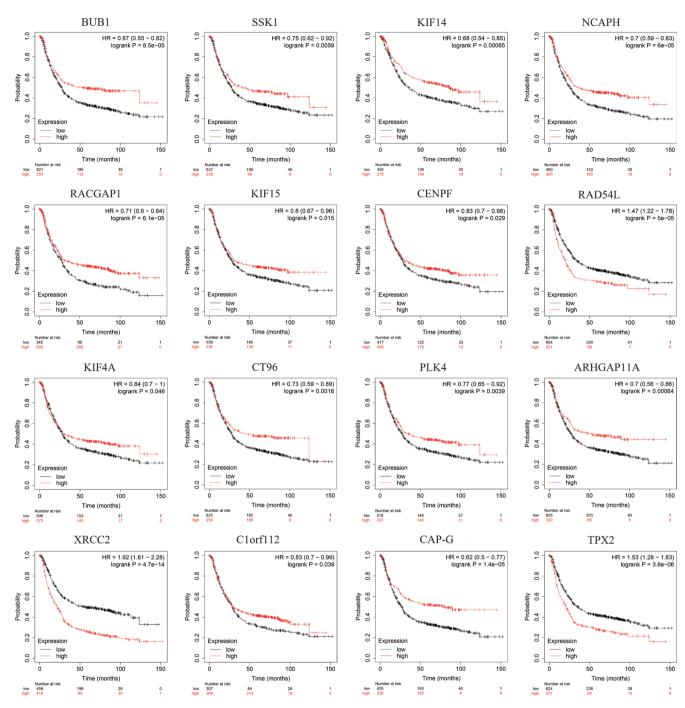


Figure S2 The survival analysis of the key genes using the Kaplan-Meier plotter online tool.

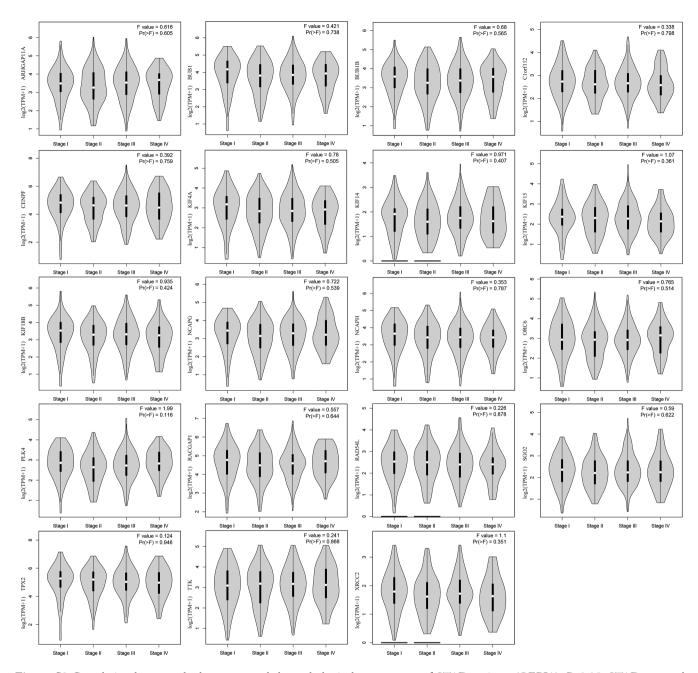


Figure S3 Correlation between the key genes and the pathological tumor stage of STAD patients (GEPIA). P<0.05. STAD, stomach adenocarcinoma; GEPIA, Gene Expression Profiling Interactive Analysis. TPM, Transcripts Per Kilobase of exon model per Million mapped reads.

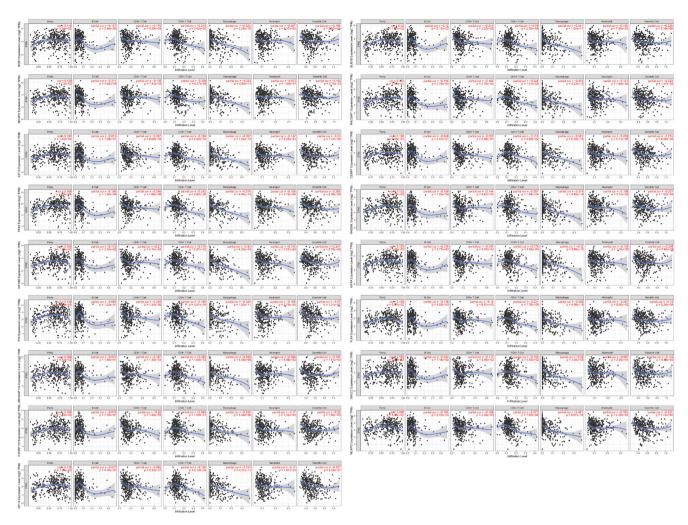


Figure S4 Correlation between the 19 key genes and immune cell infiltration (TIMER).