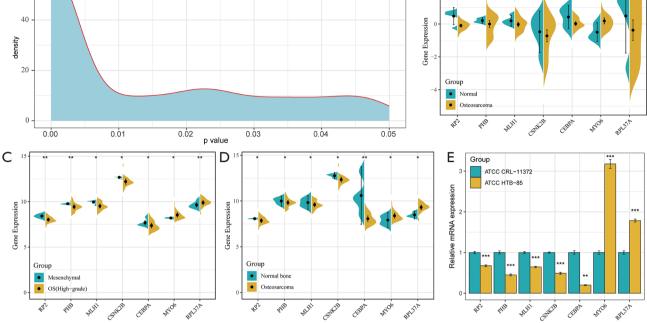
Supplementary

A



В

Figure S1 The expressions of 7 genes in different cohort study. A: The significance distribution of the model's prognostic classification on a thousand random sampling data set. B: Expression difference of 7 genes in GSE19276 data set; C: Expression difference of 7 genes in GSE42352 data set; D: Expression difference of 7 genes in GSE36001 data set; E: The expression differences of 7 genes between CRL-11372 and HTB-85 cell lines. \*P<0.05, \*P<0.01, \*P<0.001.

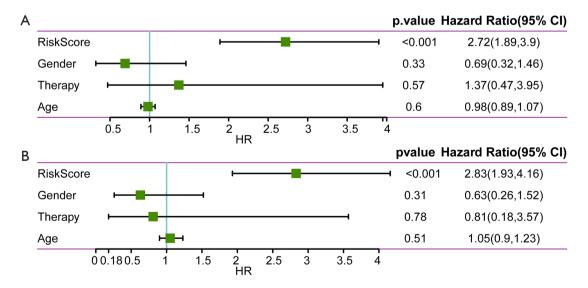


Figure S2 Univariate analysis and multivariate analysis of Riskscore. A: Univariate analysis of the relationship between Riskscore and other clinical characteristics in the TARGET dataset. B: The relationship between Riskscore and other clinical features was analyzed by multivariate analysis in the Target dataset.

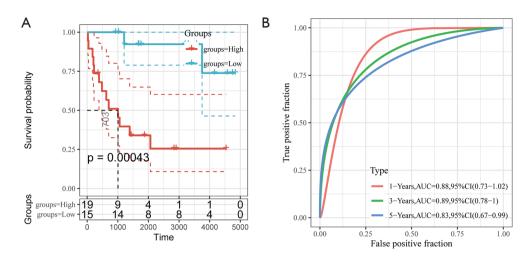


Figure S3 Prognostic ability of Riskscore in GSE16091 dataset. A: Prognostic differences between high and low risk groups in the GSE16091 validation set. B: ROC analysis in the GSE16091 validation set.