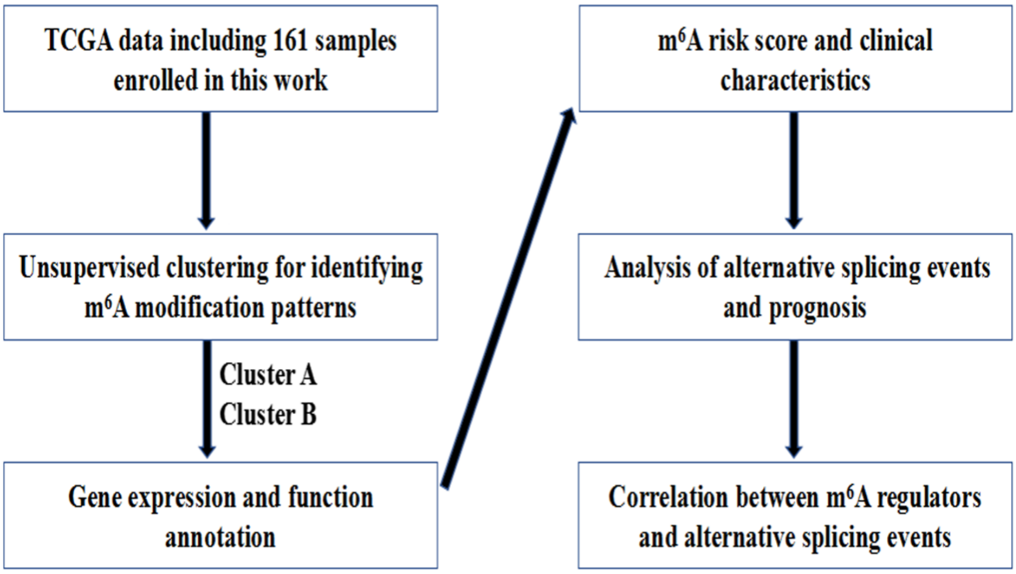
Supplementary Information for

Profiling the m^{6}A regulated RNA expression patterns and alternative splicing features in esophageal carcinoma

Supplementary Information

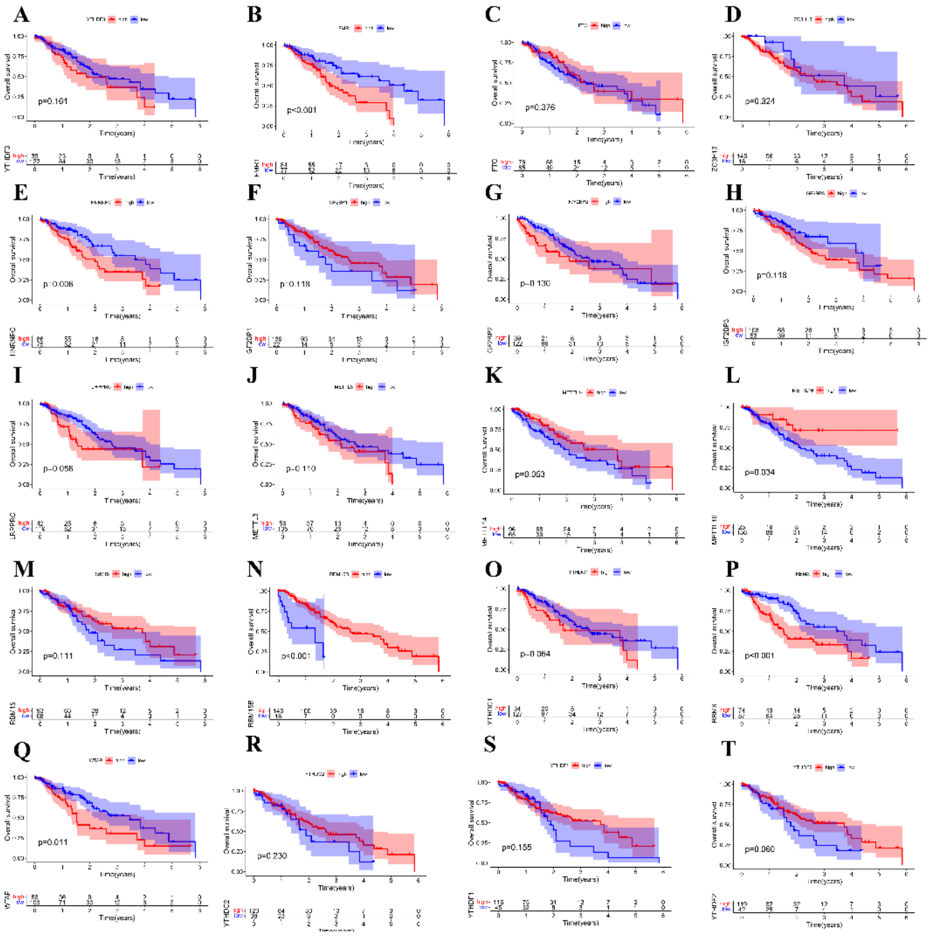
Supplementary Figures:

Figure. S1.



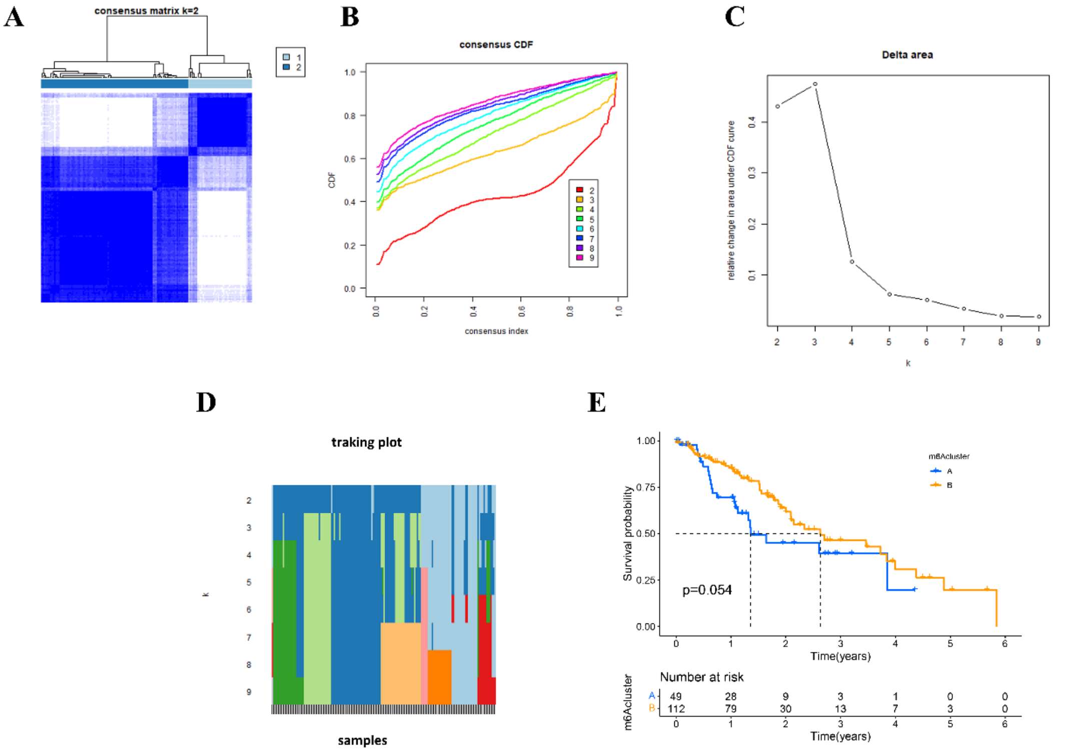
The workflow of this study.

Figure. S2.



(**A-S**). Prognostic signatures based on expression of 20 m^{6}A regulators gene in EC for OS.

Figure. S3.

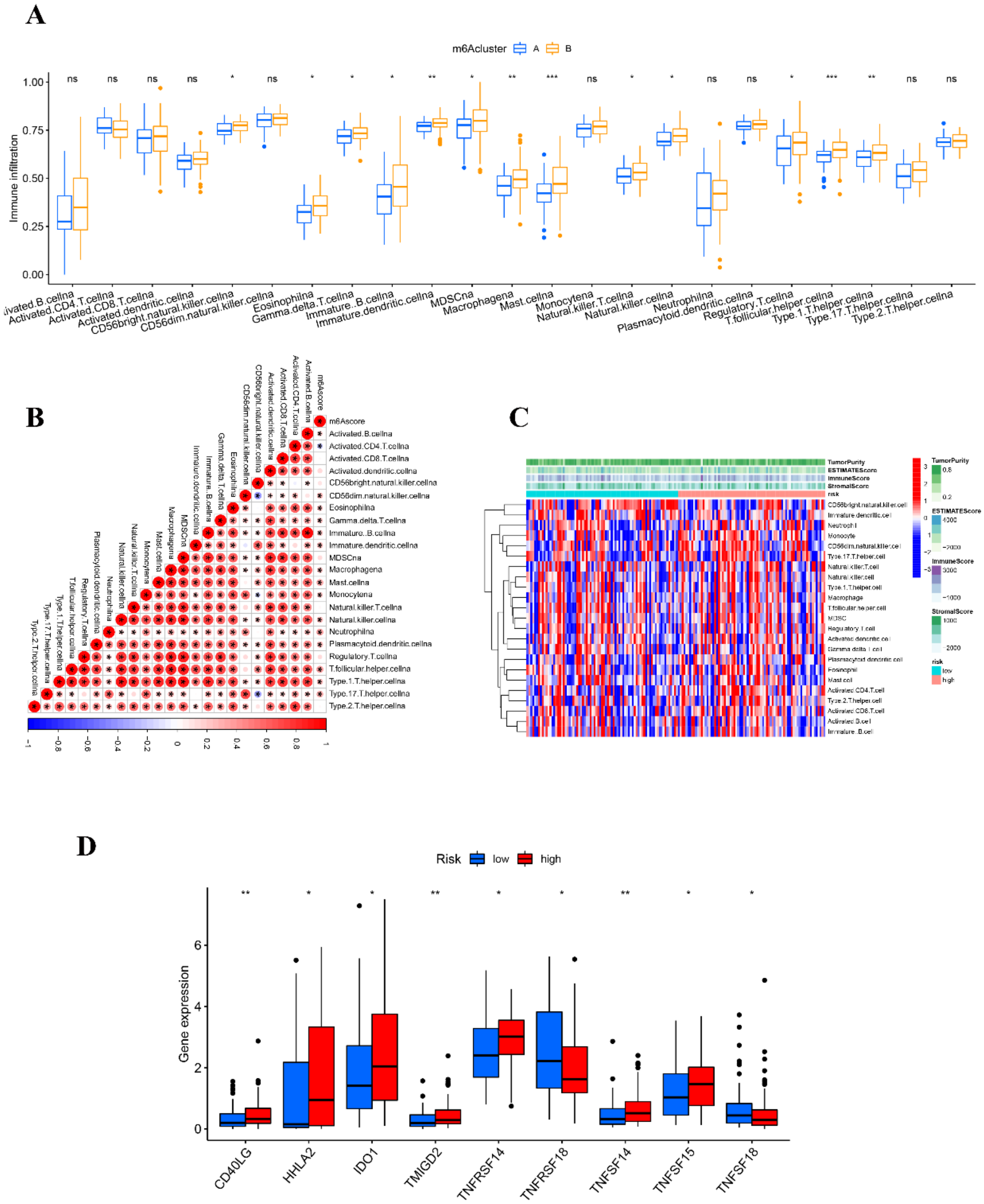


(**A**). Consensus matrices of the m^{6}A risk gene in TCGA cohort for k = 2.

(**B-D**). The corresponding relative change in area under the cumulative distribution function (CDF) curves when cluster number changing from k to k+1. The range of k changed from 2 to 9, and the optimal k = 2.

(**E**). Prognostic signatures based on genecluster in ES for OS. The figure contains three parts: [1]survival differences estimated by Kaplan-Meier survival curve; [2] number of patients in different groups; [3] number censored at different times.

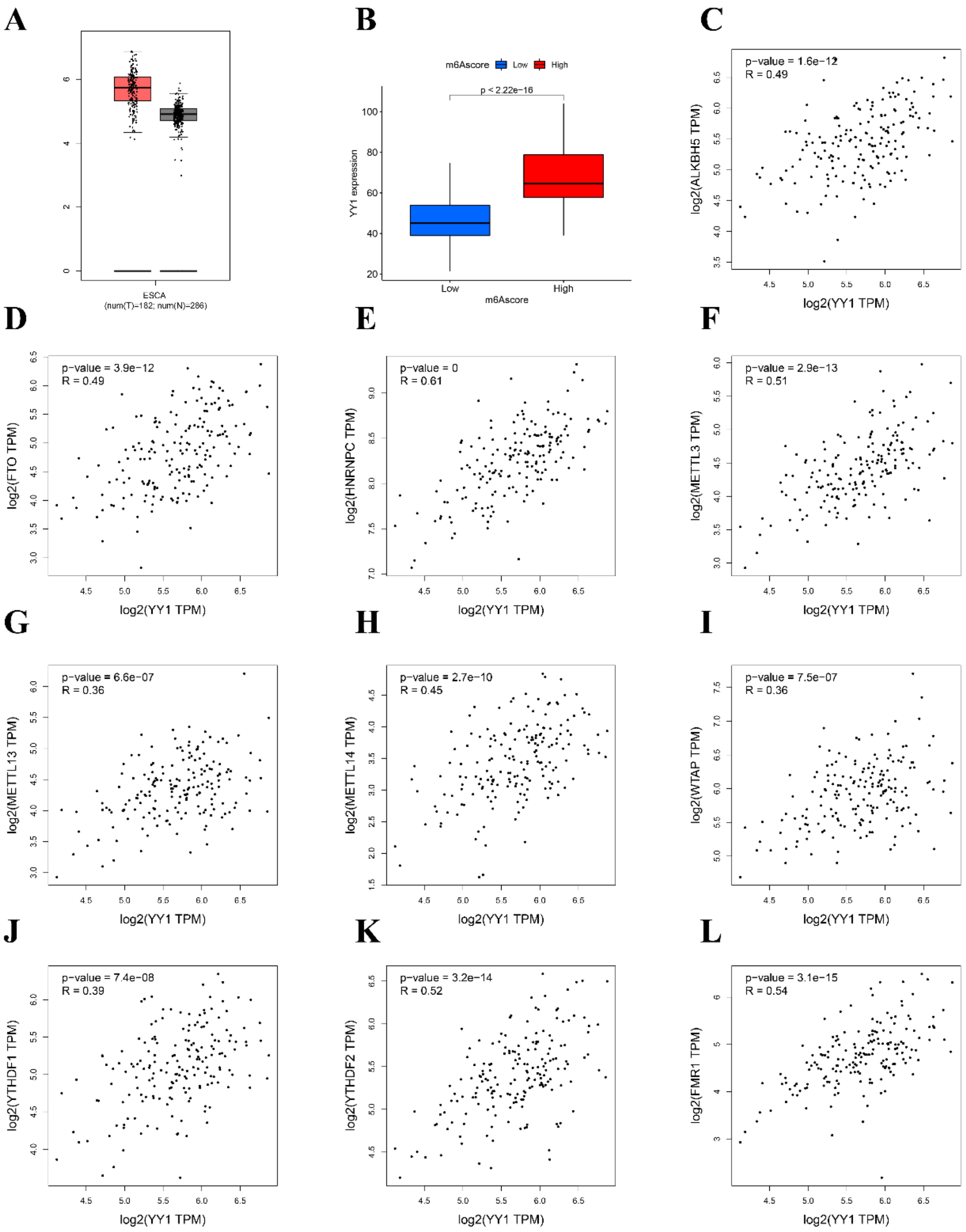
Figure. S4.



(**A**).The abundance of each TME infiltrating cell in two m^{6}A modification patterns. The upper and lower ends of the boxes represented interquartile range of values. The lines in the boxes represented median value, and black dots showed outliers. The asterisks represented the statistical p value (*p< 0.05; **p < 0.01; ***p< 0.001).

(**B**). Correlations between m^{6}Ascore and the known gene signatures in TCGA cohort using Spearman analysis. Negative correlation was marked with blue and positive correlation with orange.

Figure. S5.

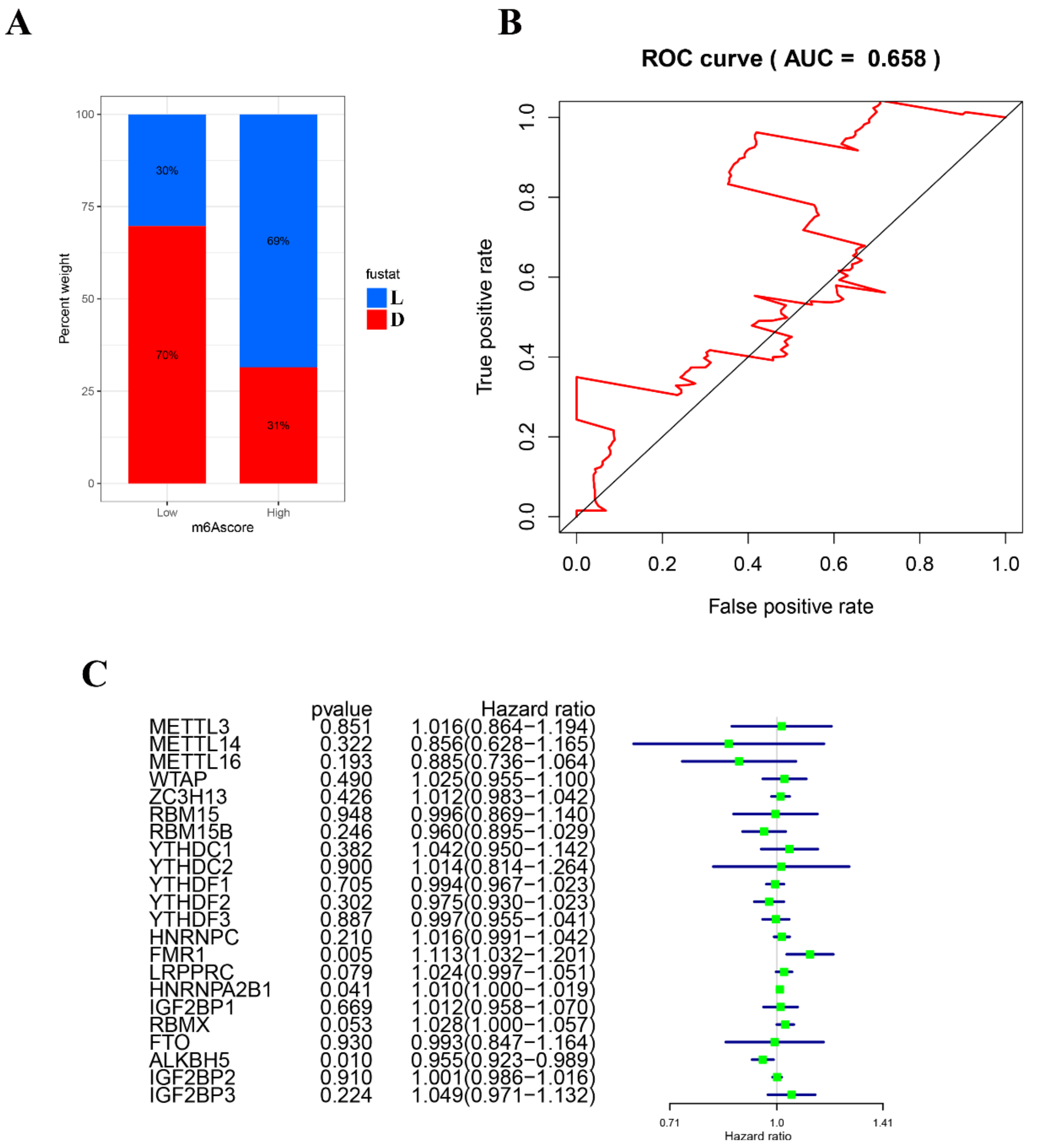


(**A**).The expression of YY1 in cancer and adjacent species.

(**B**). Differences in YY1 expression between low and high m^{6}Ascore groups ($p < 0.0001$, Wilcoxon test).

(**C-L**). The correlation between YY1 and m^{6}A regulators.

Figure. S6.

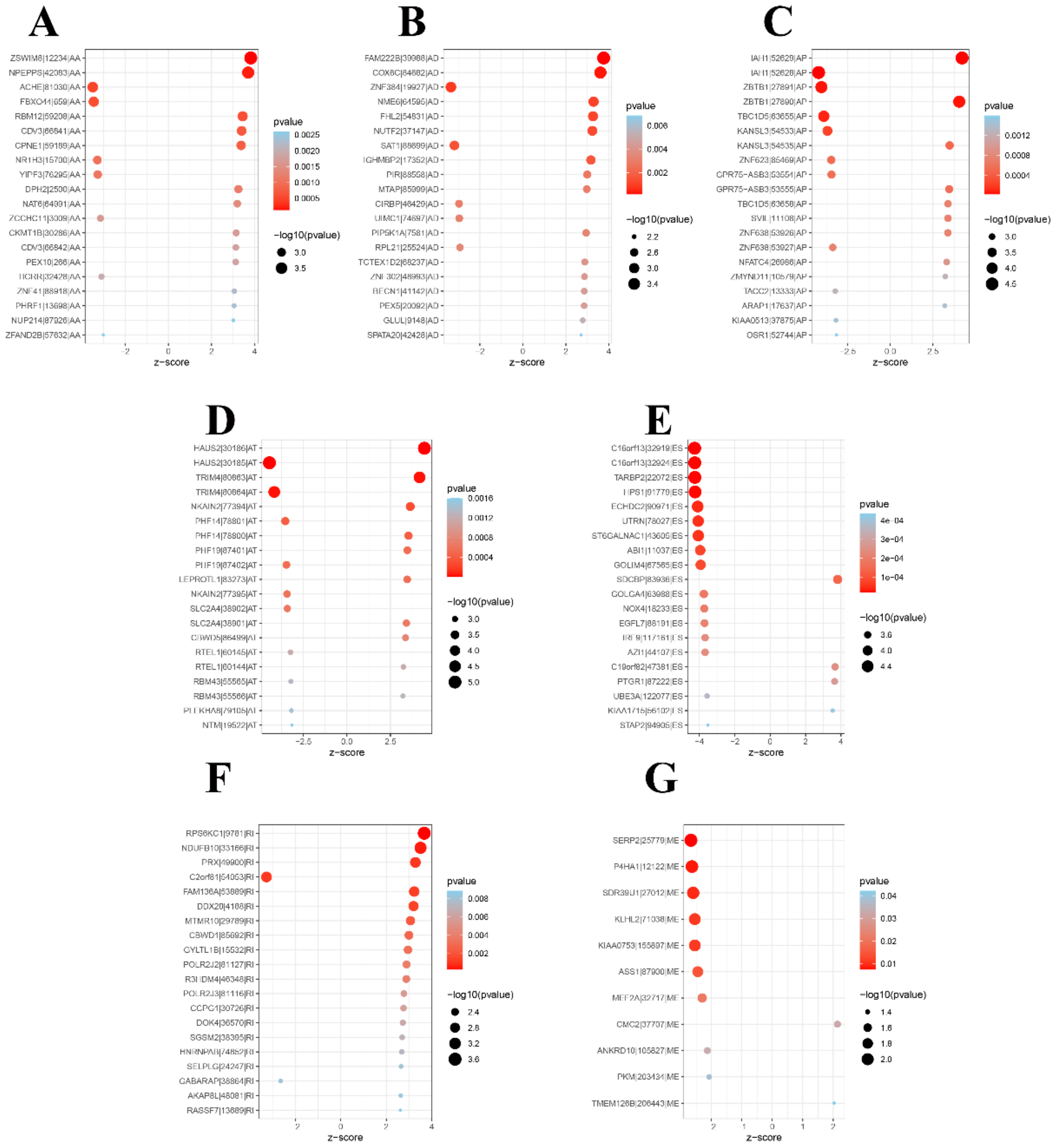


(**A**). The proportion of patients with prognosis in low or high m^{6}Ascore groups.Dead/Survival: 50%/50% in the low m^{6}Ascore groups and 31%/69% in the high m^{6}Ascore groups.

(**B**). Receiver operating characteristic curve for the m^{6}Ascore of esophageal cancer. Note—AUC, areas under the receiver operating characteristics curve.

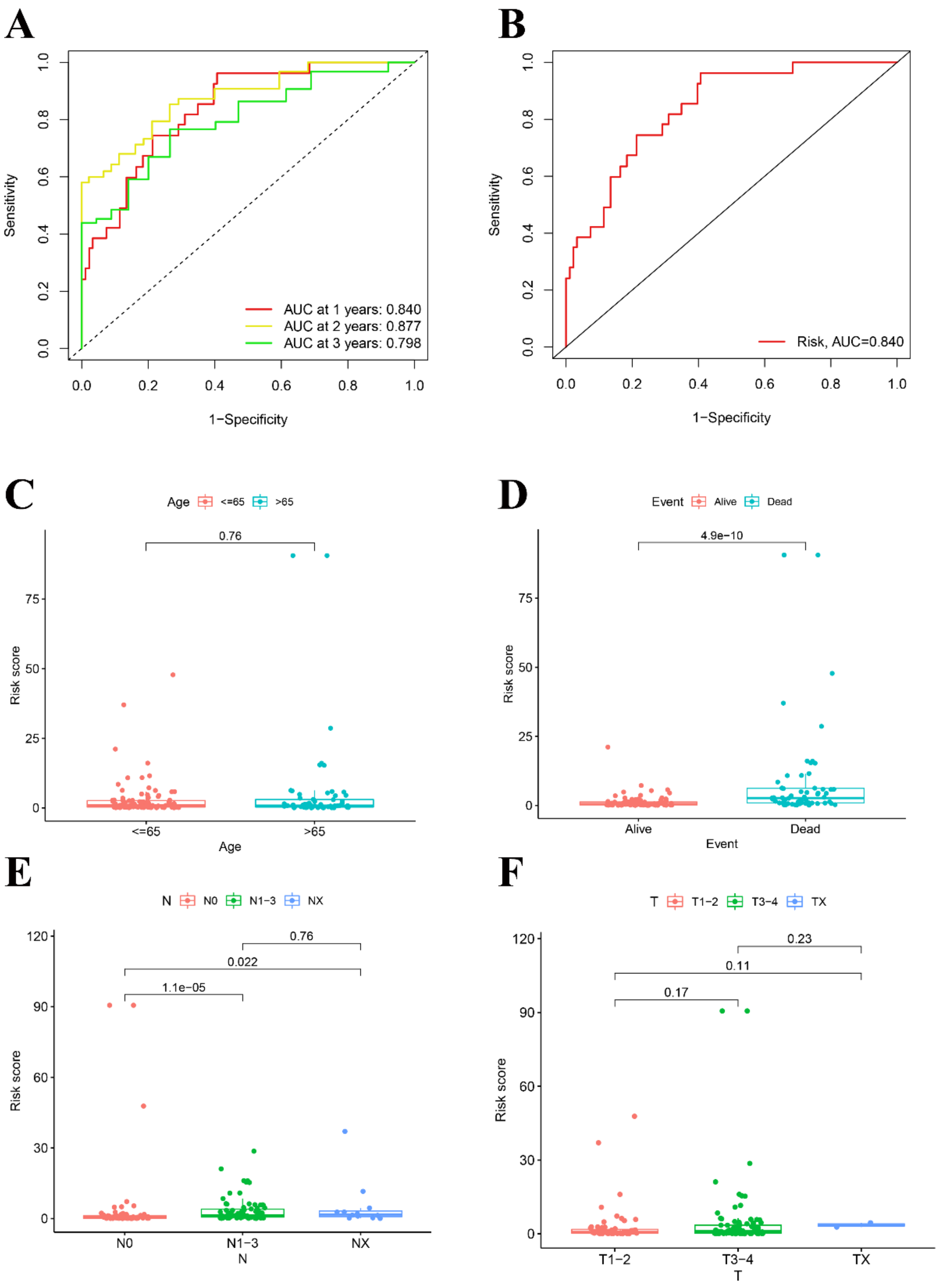
(**C**). DEAS that were simultaneously associated with OS.Univariate and multivariate analysis of DEAS on OS. Unadjusted HRs (boxes) and 95% confidence intervals (horizontal lines) limited to DEAS with $p < 0.05$. Box size is inversely proportional to the width of the confidence interval.

Figure. S7.



(**A-G**). The bubble plot shows the most significant target genes involved in seven alternative splicing events in patients with esophageal cancer. The red points in the plot represent Events with statistical significance (adj p value < 0.05 and |z-score|>2).

Figure. S8.

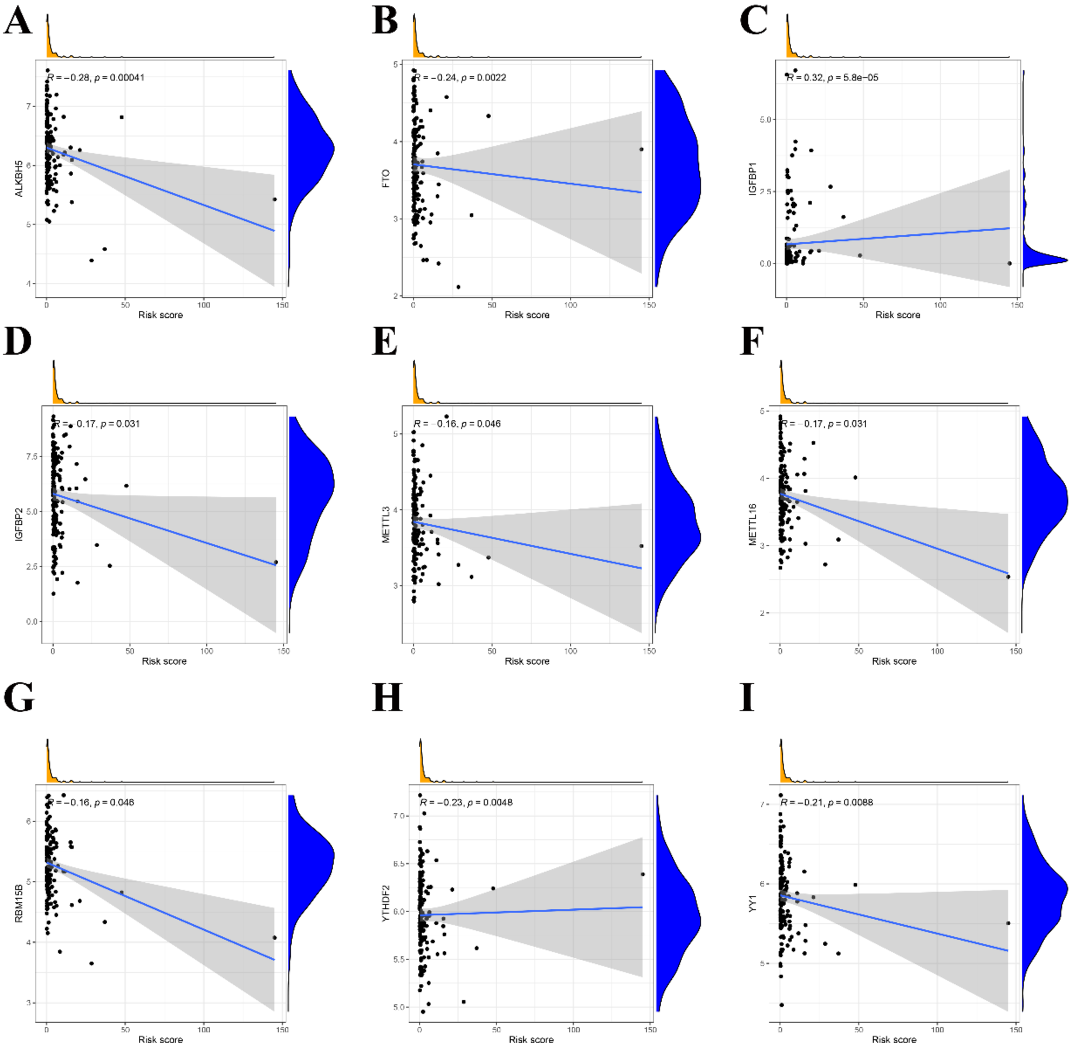


(**A**). The calibration curves of 1-, 2-, and 3-year OS nomogram prediction in the ES cohort. The y-axis showed the observed OS, and the red, yellow and green line indicated the respective performance of the nomogram with 1-, 2-, and 3-year outcomes in the ES cohort.

(**B**). Receiver operating characteristic curve for the alternative splicing risk score of esophageal cancer.

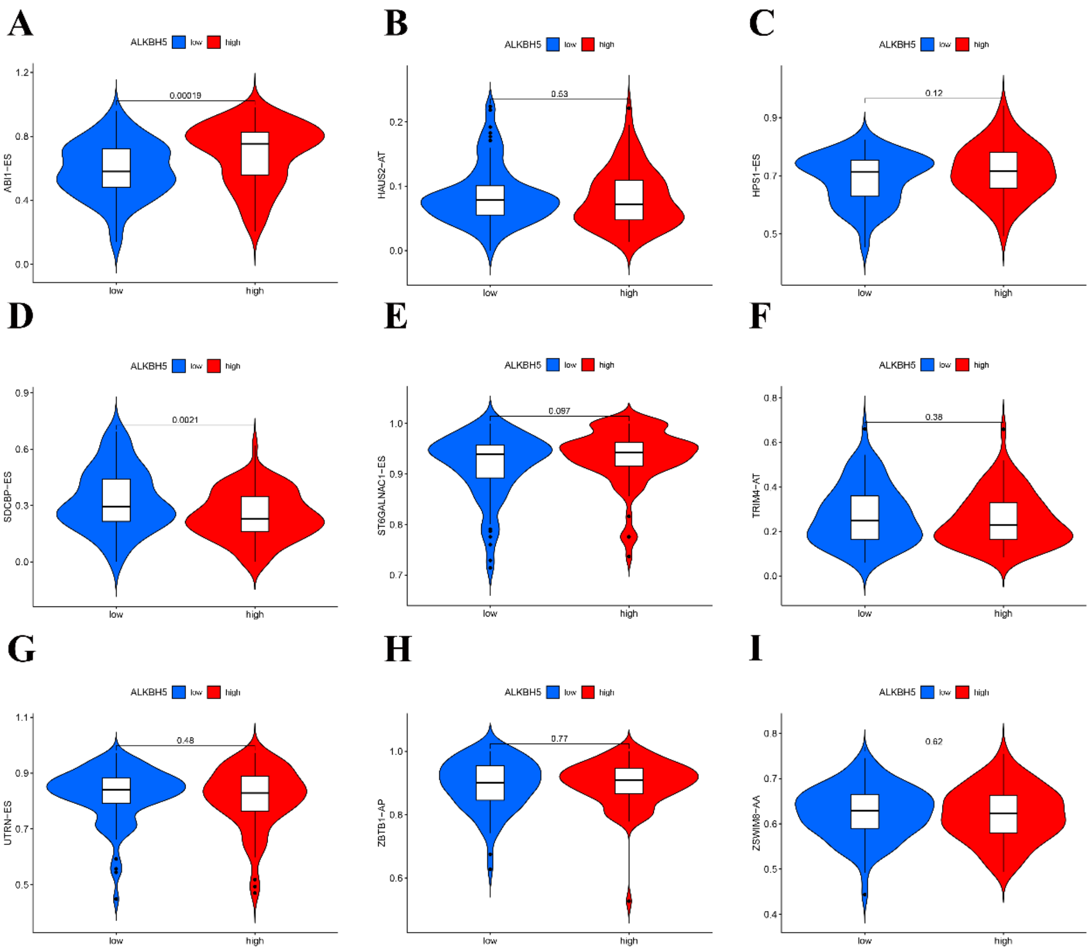
(**C-F**). The correlation between alternative splicing risk score and clinical events in patients with esophageal cancer.

Figure. S9.



(**A-I**). The correlation between expression of ALKBH5and significant alternative splicing events.

Figure. S10.



(**A-I**). The correlation between alternative splicing risk score and the expression of m^6A regulators.