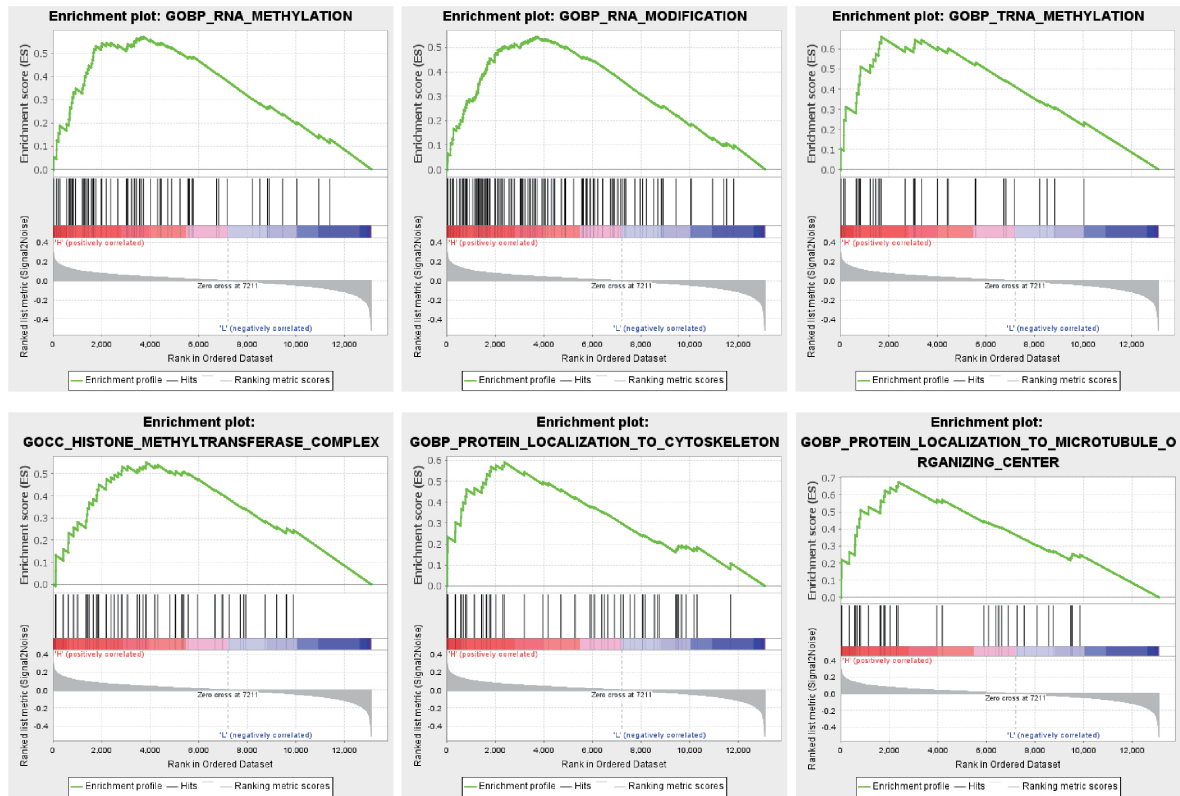


**Figure S1** Identification of m6A-related differential gene expression and differential gene identification for high and low RBM15 expression in esophageal squamous carcinoma. (A) Heatmap of the expression of 16 m6A methylation-related genes of GSE67269-GPL571 in esophageal squamous carcinoma and normal tissues from GEO database. (B) Significant difference ranking of m6A-related genes in esophageal squamous carcinoma and surrounding normal tissues. (C) Wayne plots of the results of GEO database analyses with differences in results and TCGA database of m6A-related genes affecting the prognosis of esophageal squamous carcinoma taken as intersections. (D) Bubble plots of functional enrichment of genes differing between high and low RBM15 expression groups. The value of the horizontal coordinate is calculated by counting the ratio of the number of differentially expressed genes annotated to a specific GO term to the number of all genes annotated to that GO term. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ . Q value represents adjusted P value.



**Figure S2** Graph of the results of GSEA analysis for RBM15 positively regulates modifications.

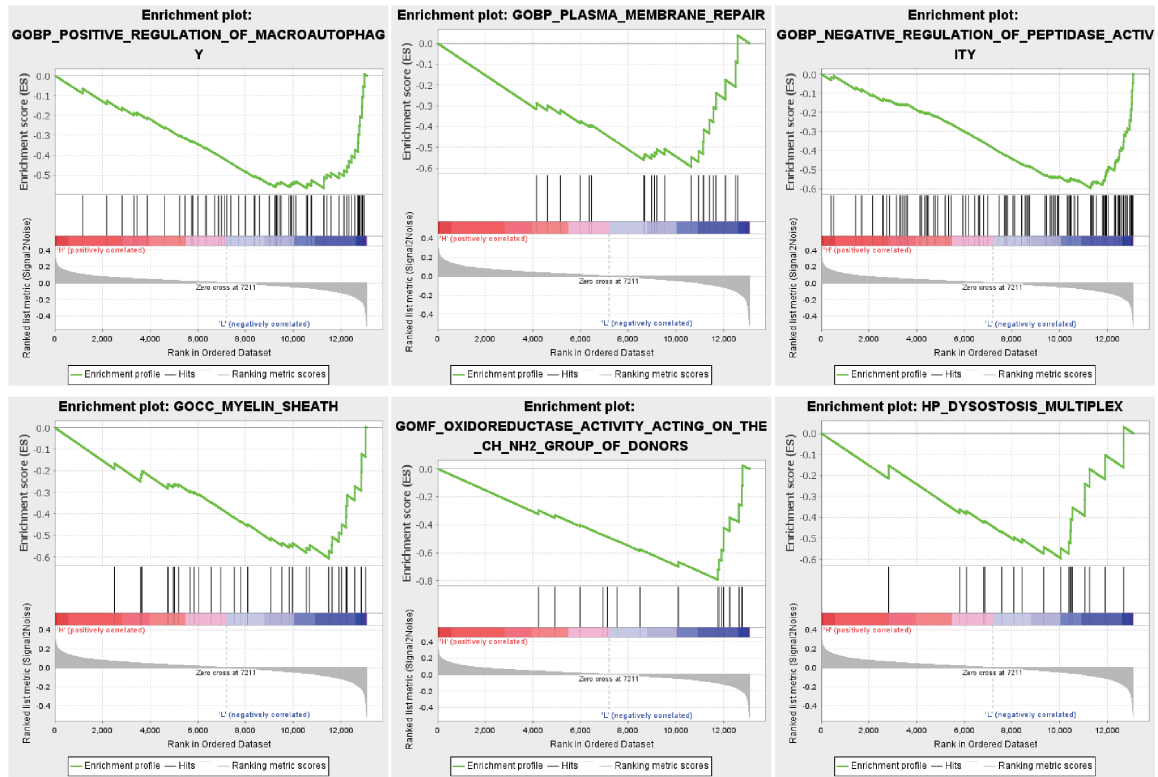
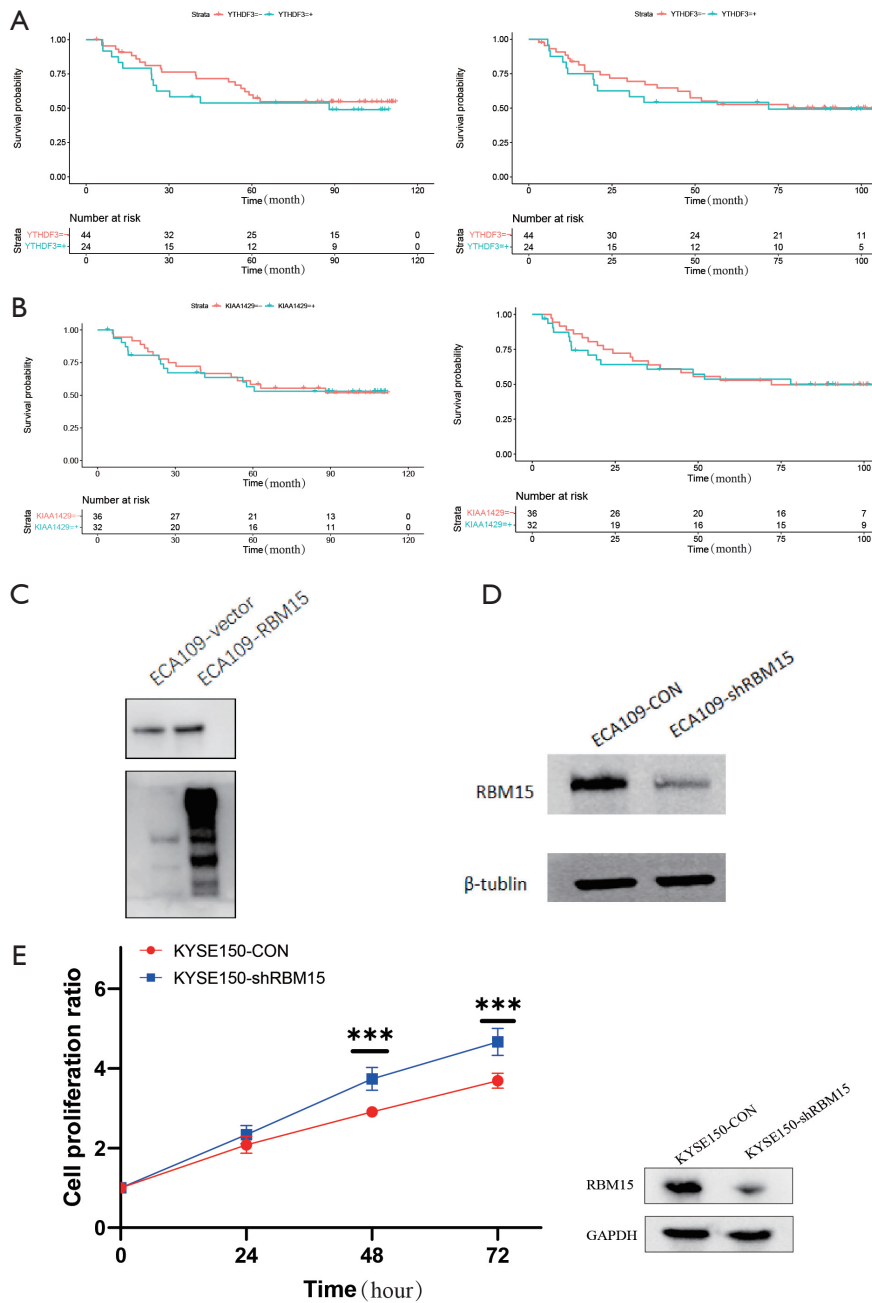


Figure S3 Graph of the results of GSEA analysis for RBM15 negatively regulates modifications.



**Figure S4** Survival analyses of KIAA1429, YTHDF3 and results of Western blot. (A) The K-M curve illustrates the prognostic effect of YTHDF3 on esophageal squamous carcinoma. On the left, K-M curves depict survival analysis based on YTHDF3 expression for DSS, while on the right, a separate K-M curve shows the analysis for DFS. YTHDF3 = + for YTHDF3 high expression group; YTHDF3 = - for YTHDF3 low expression group. (B) The K-M curve illustrates the prognostic effect of KIAA1429 on esophageal squamous carcinoma. On the left, K-M curves depict survival analysis based on KIAA1429 expression for DSS, while on the right, a separate K-M curve shows the analysis for DFS. KIAA1429 = + for KIAA1429 high expression group; KIAA1429 = - for KIAA1429 low expression group. (C) RBM15 overexpression ECA109 cell line was constructed using plasmid transfection method, and Western blot verified its overexpression. (D) RBM15 knockdown ECA109 cell line was constructed using lentiviral infection method, and Western blot verified its knockdown. (E) Cell viability of KYSE150 cells after RBM15 knockdown in KYSE150 cells was measured with CCK-8 assay. And RBM15 knockdown KYSE150 cell line was constructed using lentiviral infection method, and Western blot verified its knockdown. \*\*\*,  $P < 0.001$ .