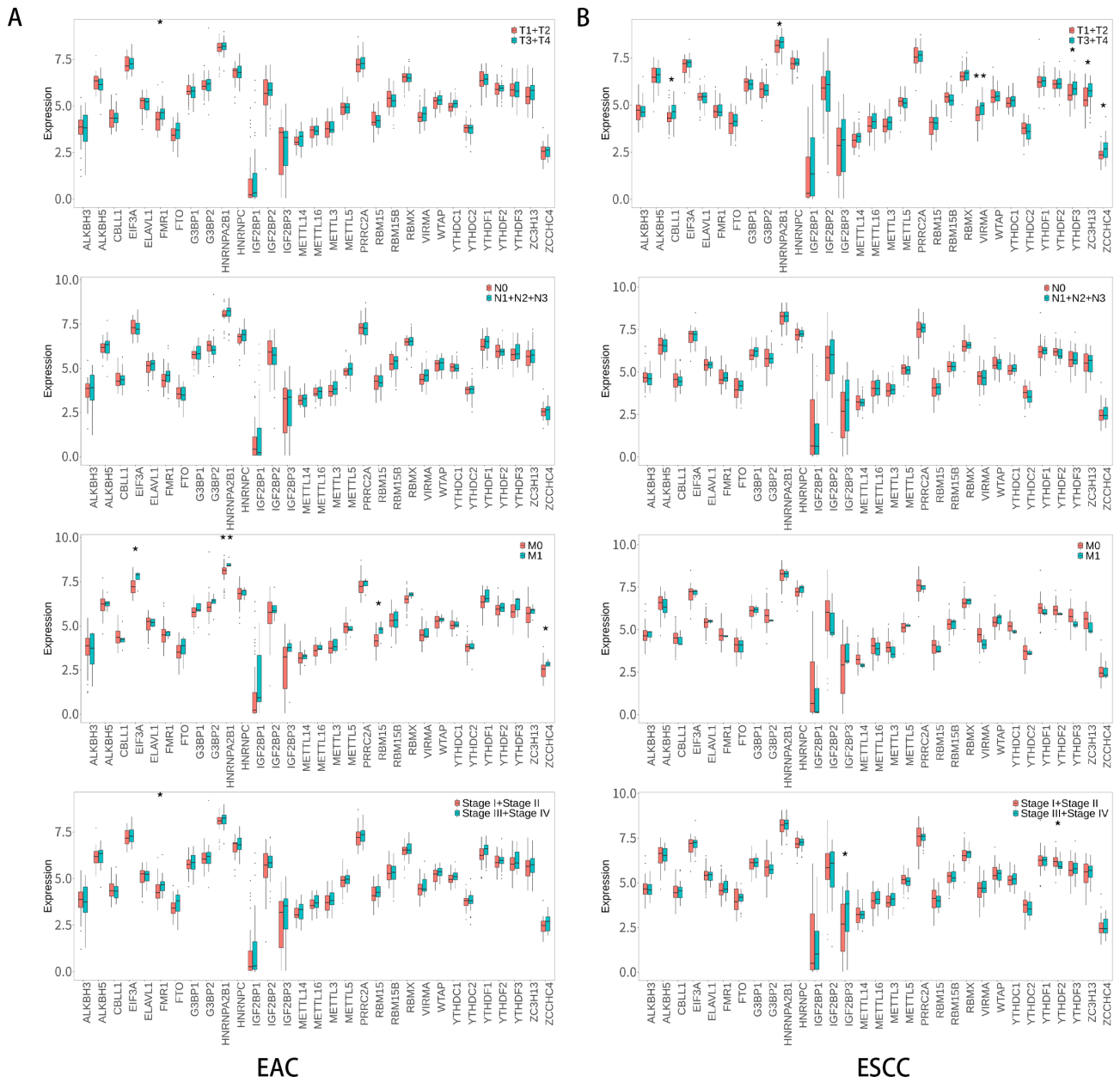


**Figure S1** (A) Classification of the 31 m6A regulators. (B) Genome distribution of the 31 m6A regulators. (C) A comparison of the m6A regulators expression levels in EAC tumors and normal tissues in the TCGA-ESCA dataset. Red represents normal samples and green represents tumor samples. (D) A comparison of the expression levels in ESCC tumors and normal tissues in the TCGA-ESCA and GSE53625 datasets. Red represents normal samples and green represents tumor samples. NS, no significant, \*,  $P < 0.05$ , \*\*,  $P < 0.01$ , \*\*\*,  $P < 0.001$ , \*\*\*\*,  $P < 0.0001$ .



**Figure S2** The association between m6A regulators and tumor stage in (A) EAC and (B) ESCC samples from the TCGA-ESCC cohort. The analysis was performed with four aspects: primary tumor (T stage), regional lymph nodes (N stage), distant metastasis (M stage), and clinical staging. \*,  $P < 0.05$ , \*\*,  $P < 0.01$ .