

Figure S1. Information on the immunohistochemistry staining of N6-methyladenosine-associated genes in HCC available from the Human Protein Atlas database (version 19.2; <http://www.proteinatlas.org>). Representative staining images of (A) ALKBH5 (<https://www.proteinatlas.org/ENSG00000091542-ALKBH5/pathology/liver+cancer#img>), (B) FTO (<https://www.proteinatlas.org/ENSG00000140718-FTO/pathology/liver+cancer#img>), (C) HNRNPC (<https://www.proteinatlas.org/ENSG00000092199-HNRNPC/pathology/liver+cancer#img>), (D) METTL4 (<https://www.proteinatlas.org/ENSG00000101574-METTL4/pathology/liver+cancer#img>), (E) RBM15 (<https://www.proteinatlas.org/ENSG00000162775-RBM15/pathology/liver+cancer#img>), (F) RBMX (<https://www.proteinatlas.org/ENSG00000147274-RBMX/pathology/liver+cancer#img>), (G) VIRMA (<https://www.proteinatlas.org/ENSG00000164944-VIRMA/pathology/liver+cancer#img>), (H) YTHDC1 (<https://www.proteinatlas.org/ENSG00000083896-YTHDC1/pathology/liver+cancer#img>), (I) YTHDC2 (<https://www.proteinatlas.org/ENSG00000047188-YTHDC2/pathology/liver+cancer#img>) and (J) ZC3H13 (<https://www.proteinatlas.org/ENSG00000123200-ZC3H13/pathology/liver+cancer#img>). HCC, hepatocellular carcinoma.

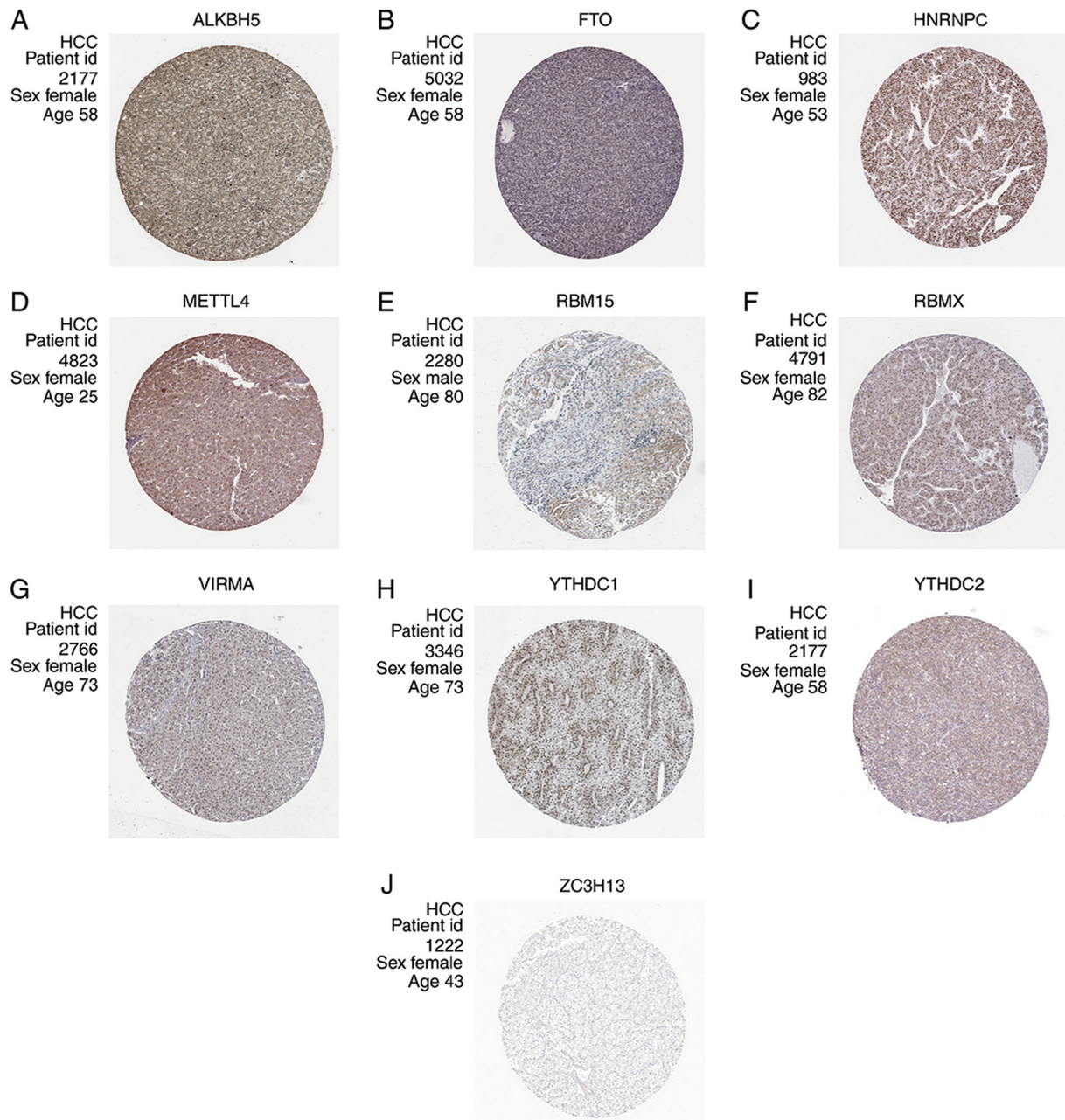


Figure S2. Expression of m6A RNA methylation regulators in HCC with different clinicopathological features. Expression levels of HNRNPA2B1, HNRNPC, IGF2BP1, IGF2BP2, IGF2BP3, METTL4, RBM15, RBM15B, RBMX, VIRMA and YTHDC1 in HCC with different pathological grades and expression levels of HNRNPA2B1, METTL4, RBM15B, RBMX, YTHDF1 and YTHDF3 in HCC with different T stages. Patients with G1/G2 pathological grade were divided into the L group, and patients with G3/G4 grade were divided into the H group. Patients with T1/T2 stage were divided into the L group, and patients with T3/T4 stage were divided into the H group. The y-axis represents log2 expression of the gene. HCC, hepatocellular carcinoma; T stage, tumor stage; H, high; L, low.

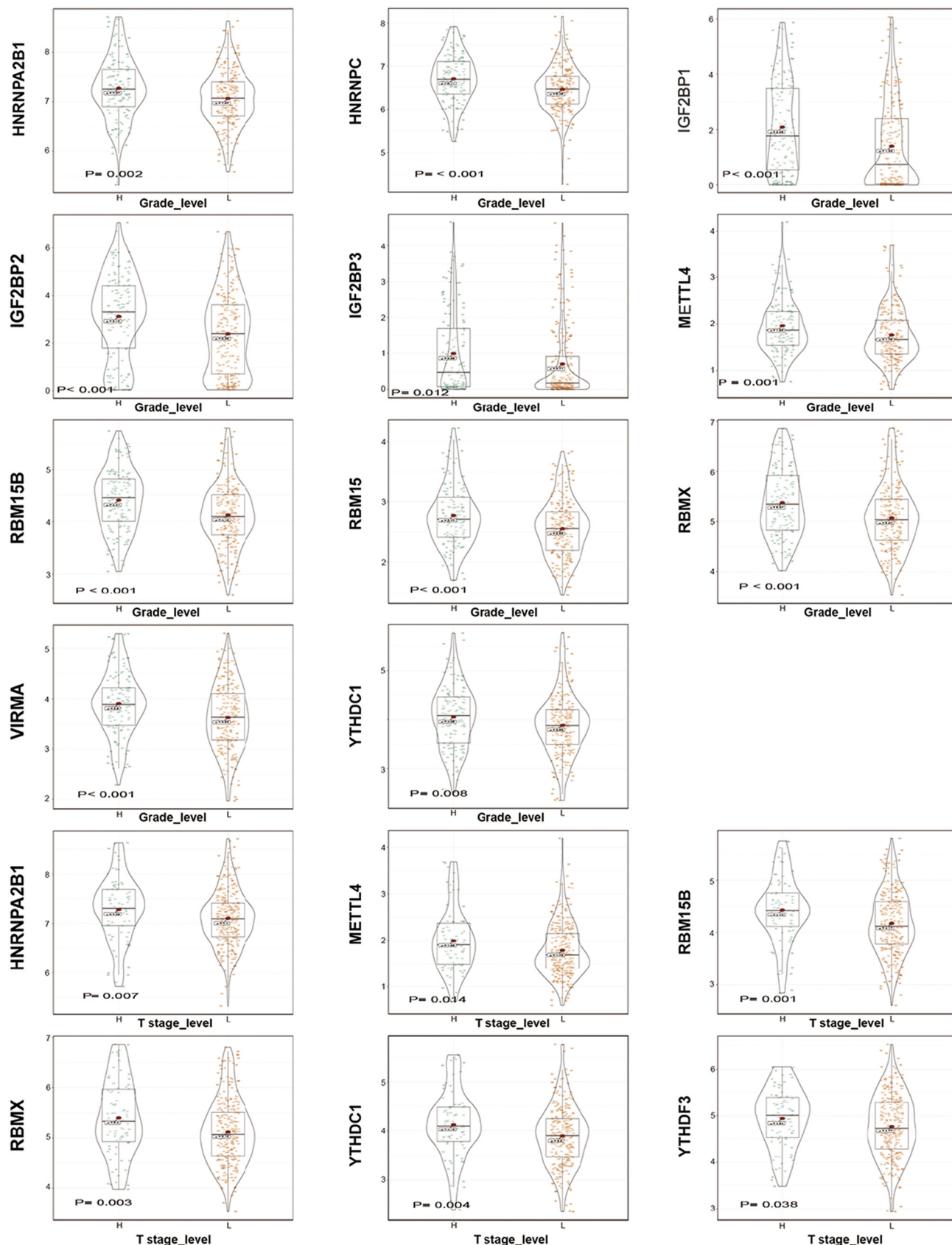


Figure S3. Protein-protein interaction network of the 20 N6-methyladenosine modification regulators.

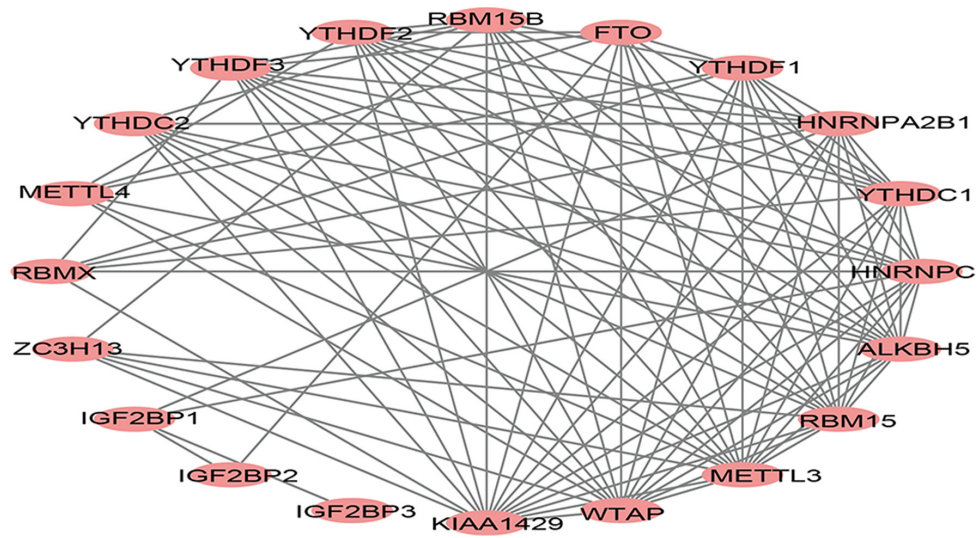


Figure S4. Univariate analysis of the m6A regulators regarding (A) disease-free survival and (B) overall survival.

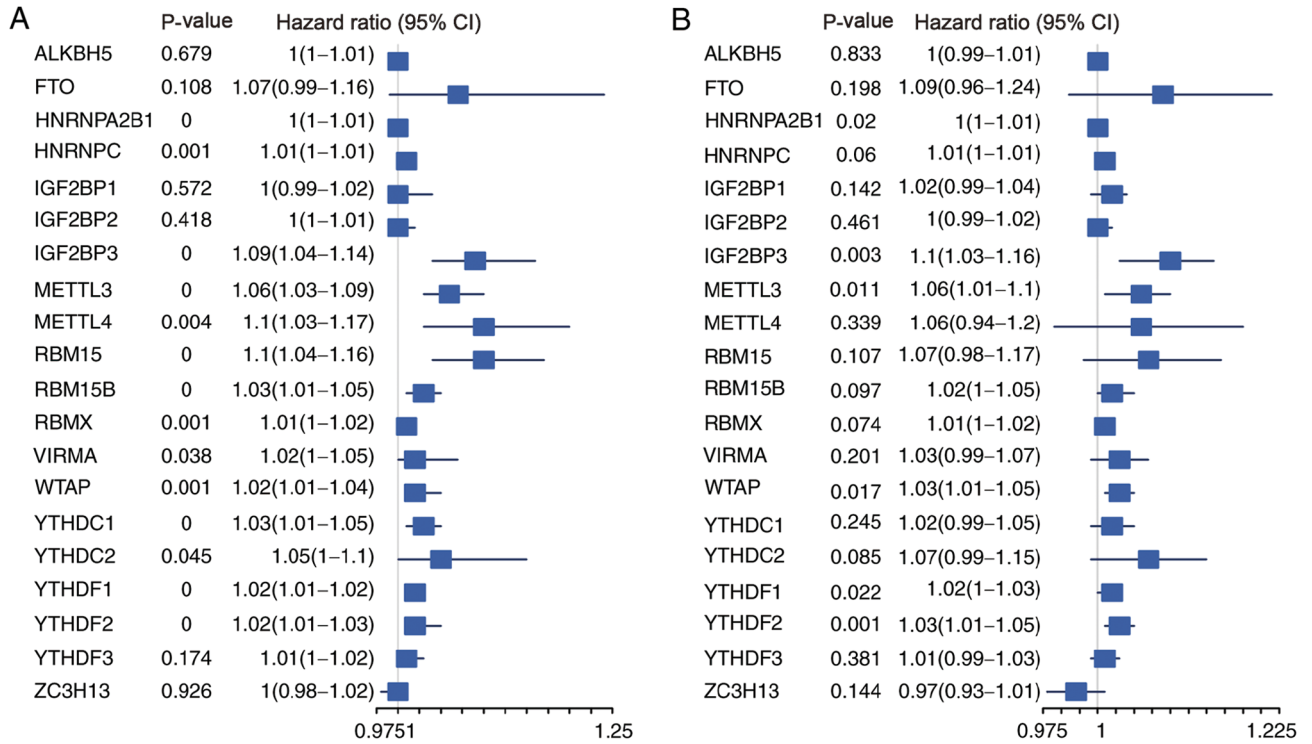




Figure S5. Kaplan-Meier and ROC curves according to the gene signature in the validation cohorts. (A) Survival curves and (B) ROC curves for overall survival in the meta-GEO cohort. (C) Survival curves and (D) ROC curves for disease-free survival in the meta-GEO cohort. (E) Survival curves and (F) ROC curves for overall survival in the International Cancer Genome Consortium cohort. ROC, receiver-operating characteristic; AUC, area under the curve; GEO, Gene Expression Omnibus.

