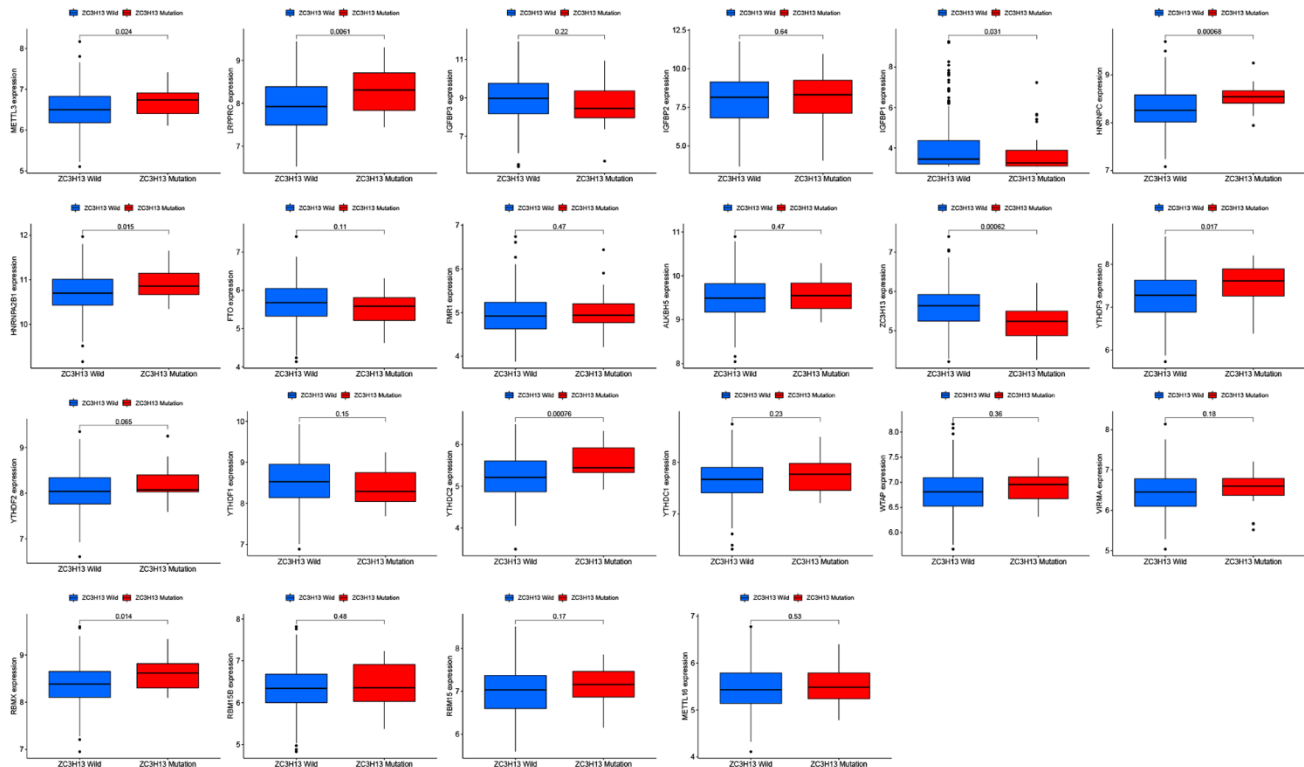
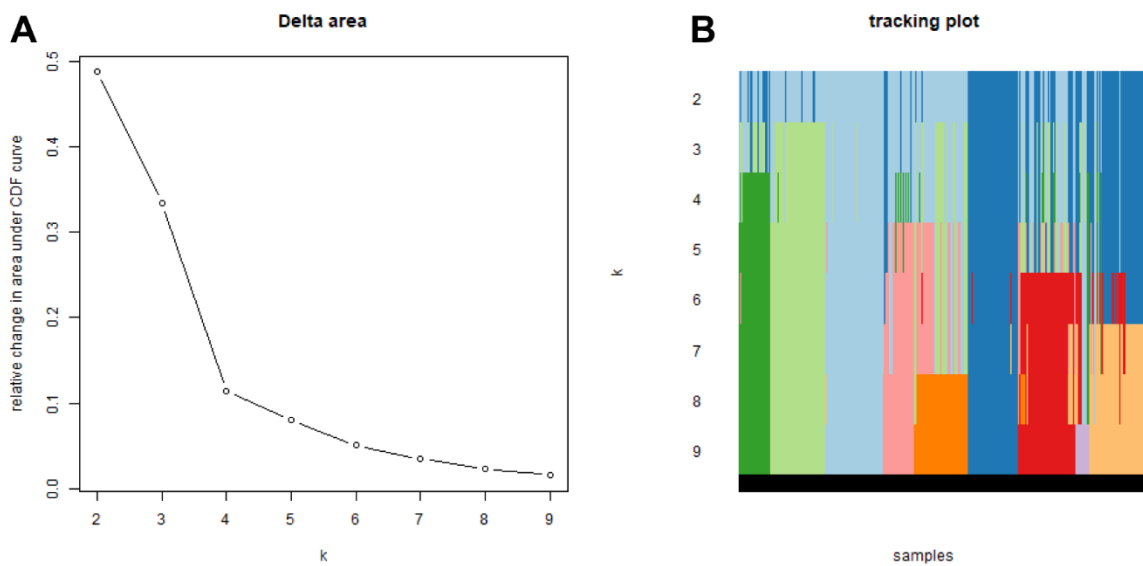


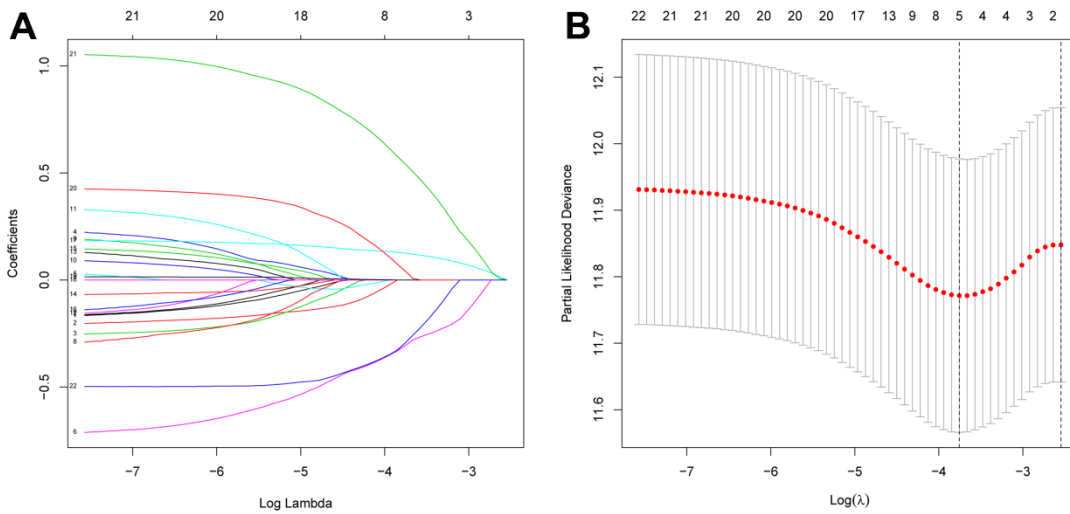
SUPPLEMENTARY FIGURES



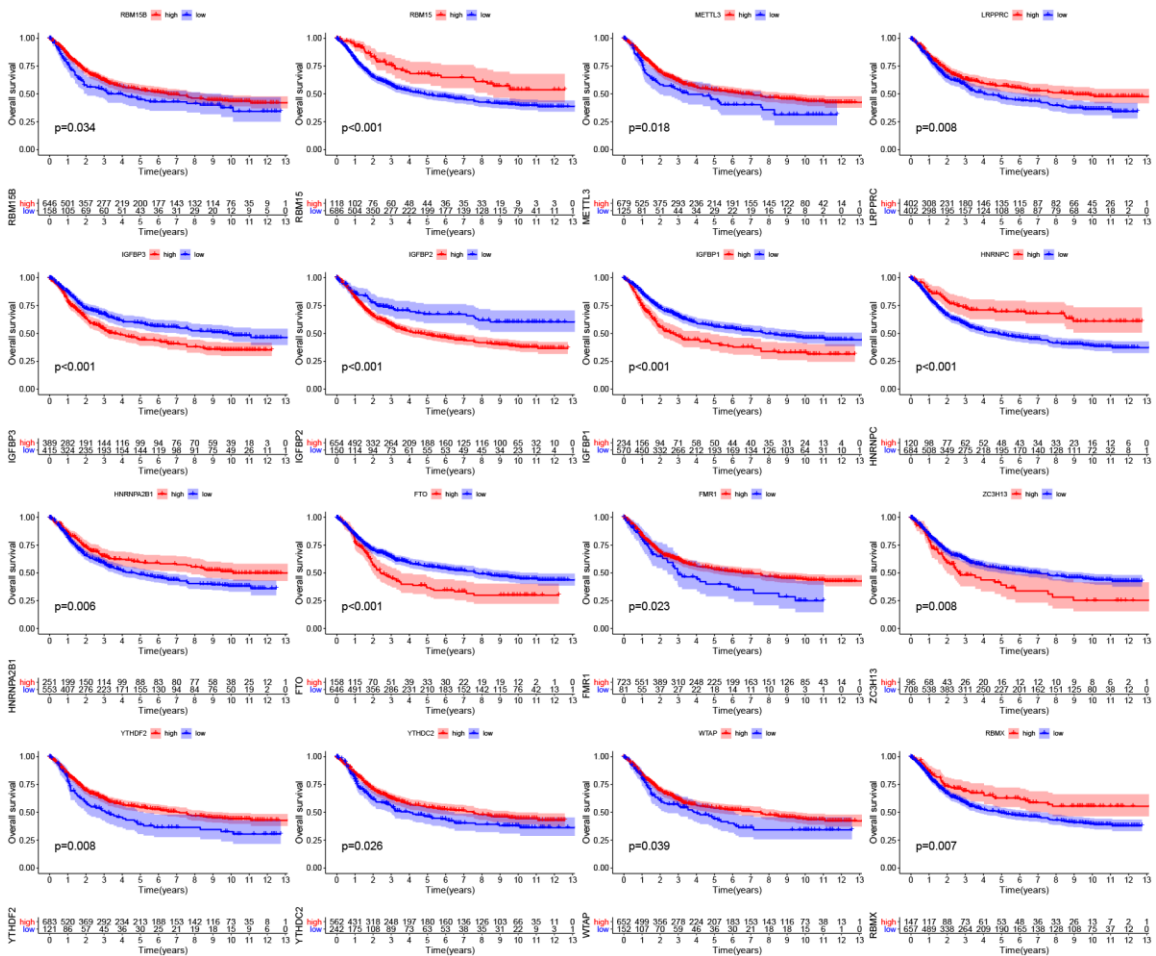
Supplementary Figure 1. Expression levels of 22 m⁶A regulators between ZC3H13 mutant and wild-type in TCGA database.



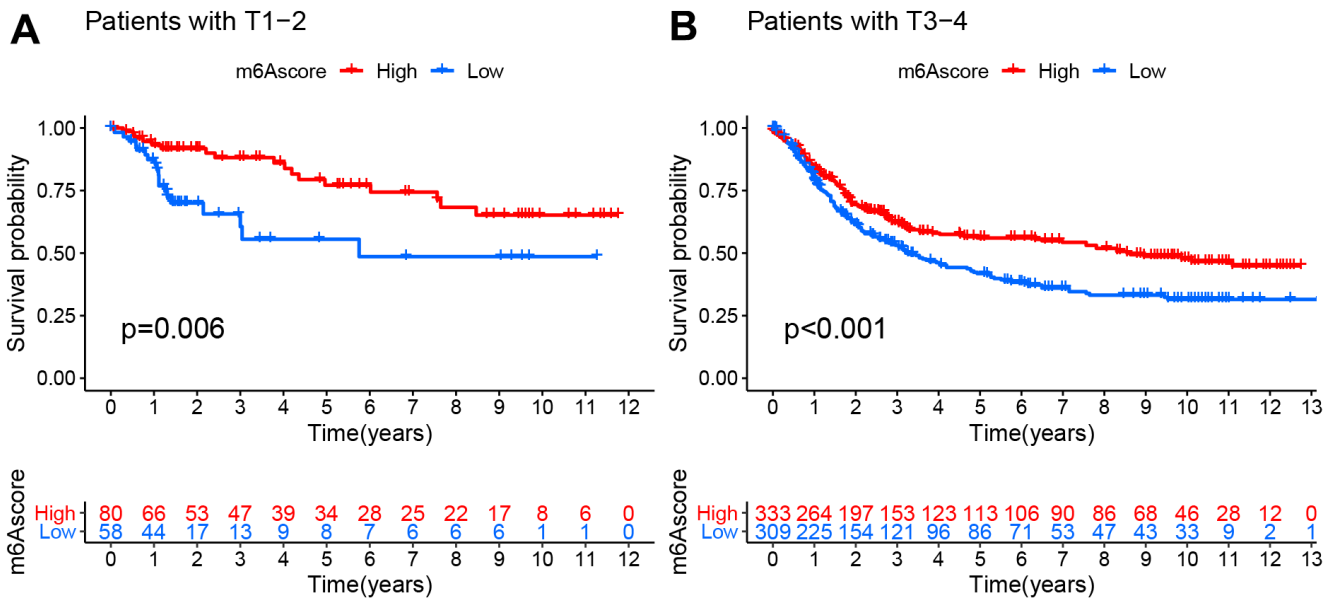
Supplementary Figure 2. Consensus clustering of 22 m⁶A regulators in the TCGA cohort. (A) relative change in area under the CDF in left panel; (B) The cumulative distribution function (CDF) for k=2 to 9 in right panel; relative change in area under the CDF in left panel.



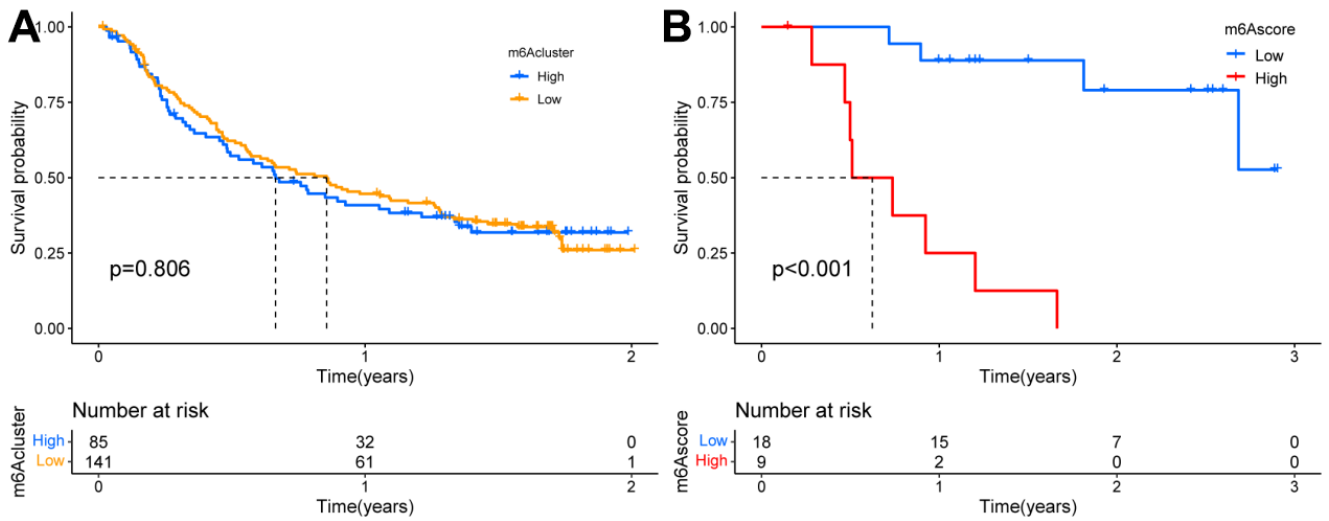
Supplementary Figure 3. Five selection of genes by LASSO Cox regression. (A) Selection of the optimal parameter (lambda) in the LASSO model for STAD. (B) LASSO coefficient profiles of the five genes in STAD. A coefficient profile plot was generated against the log (lambda) sequence.



Supplementary Figure 4. The prognostic subgroup analysis of m⁶A score based on the TCGA cohort.



Supplementary Figure 5. The prognostic clinical status analysis of m⁶A score based on the TCGA cohort. (A) K-M survival analysis in T1-2. (B) K-M survival analysis in T3-4.



Supplementary Figure 6. The prognostic clinical status analysis of m⁶A score between IMvigor210 and GSE78220 cohorts. (A) K-M survival analysis in high and low m6A cluster of IMvigor210. (B) K-M survival analysis in high and low m6A cluster of GSE78220.