

Supplementary Figure S1

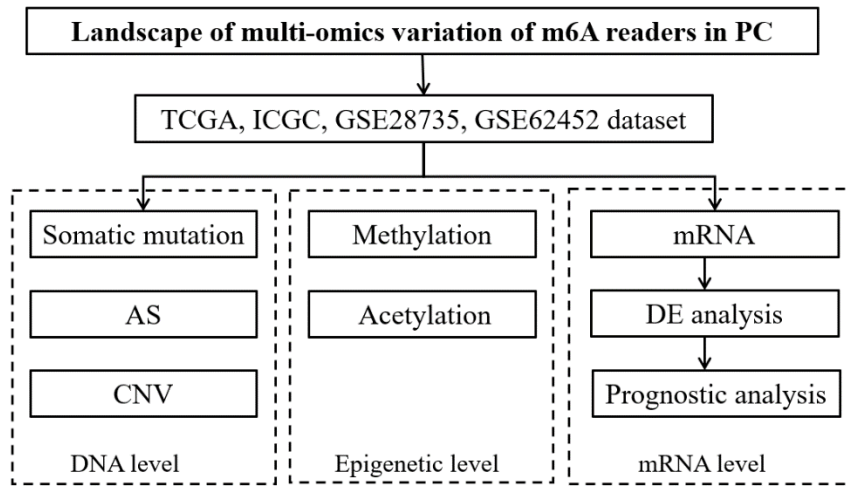


Fig.S1 The workflow of Result 1: Landscape of multi-omics variation of m6A readers in PC.

Supplementary Figure S2

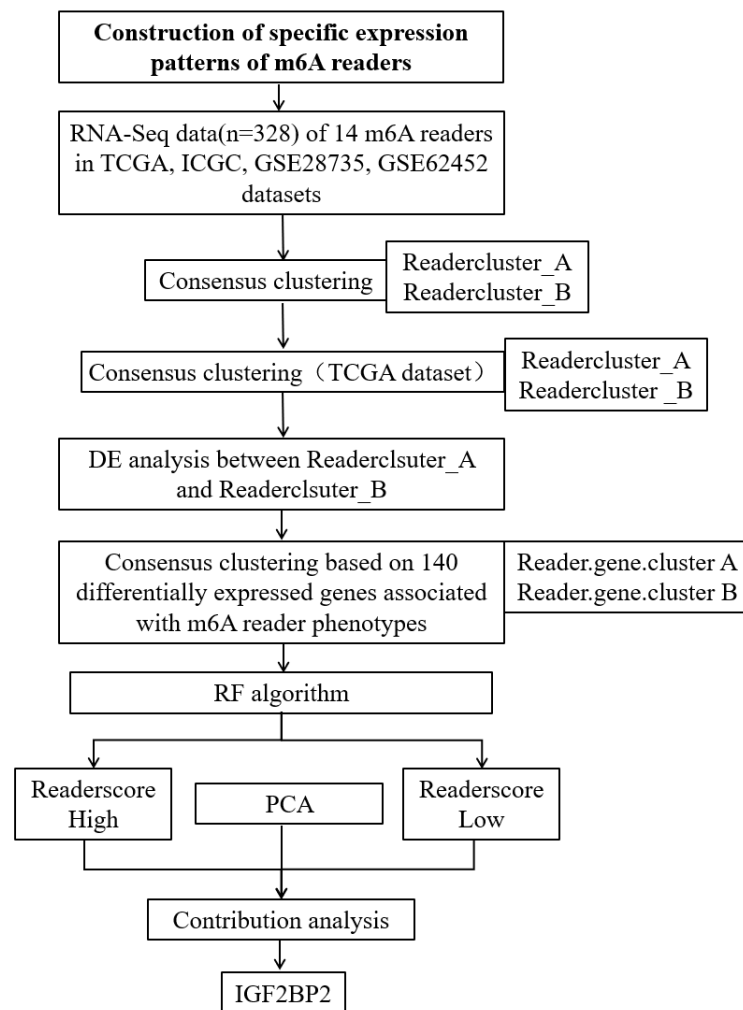


Fig.S2 The workflow of Result 2-3: Ceneration of m6A readers phenotype-related expression patterns and screening of key gene.

Supplementary Figure S3

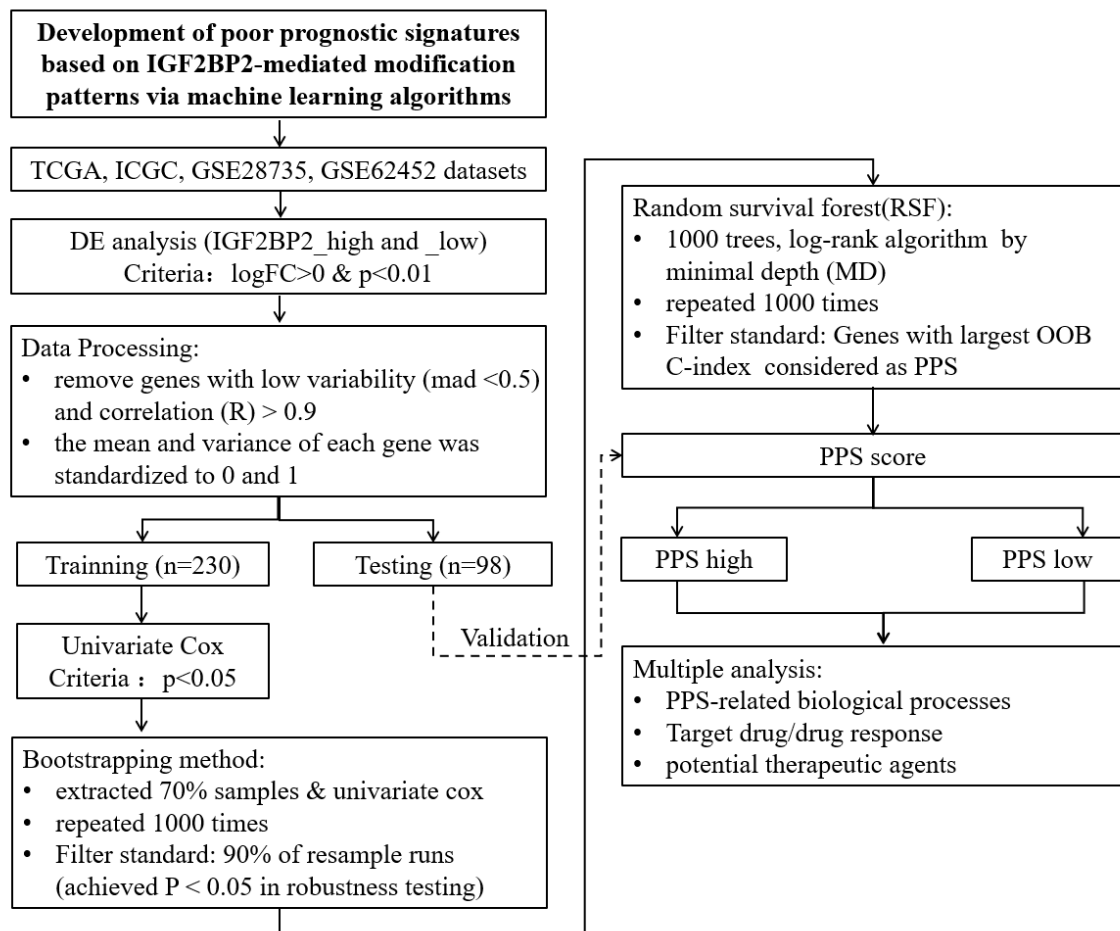


Fig.S3 The workflow of Result 4-5: Development of poor prognostic signatures based on IGF2BP2-mediated modification patterns via machine learning algorithms.

Supplementary Figure S4

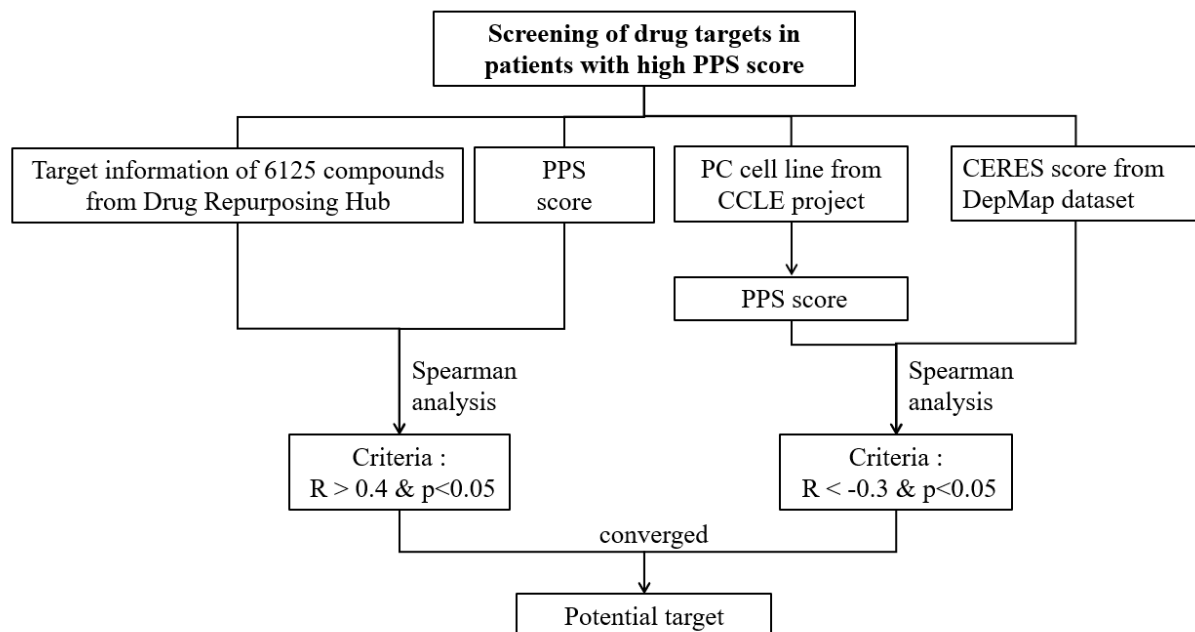


Fig.S4 The workflow of Result 6: Screening of drug targets in patients with high PPS score.

Supplementary Figure S5

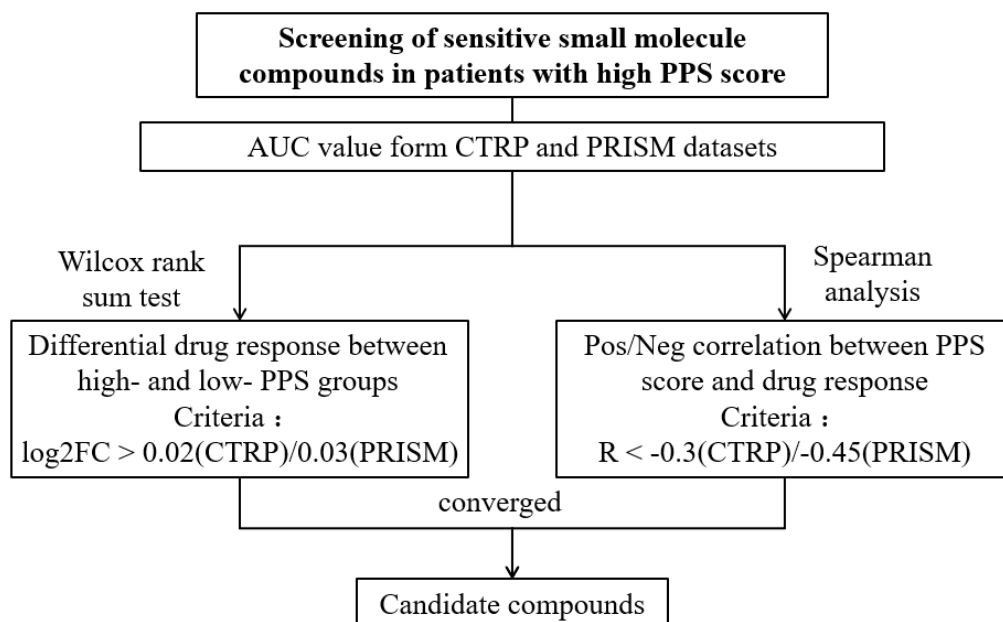


Fig.S5 The workflow of Result 7: Screening of sensitive small molecule compounds in patients with high PPS score.

Supplementary Figure S6

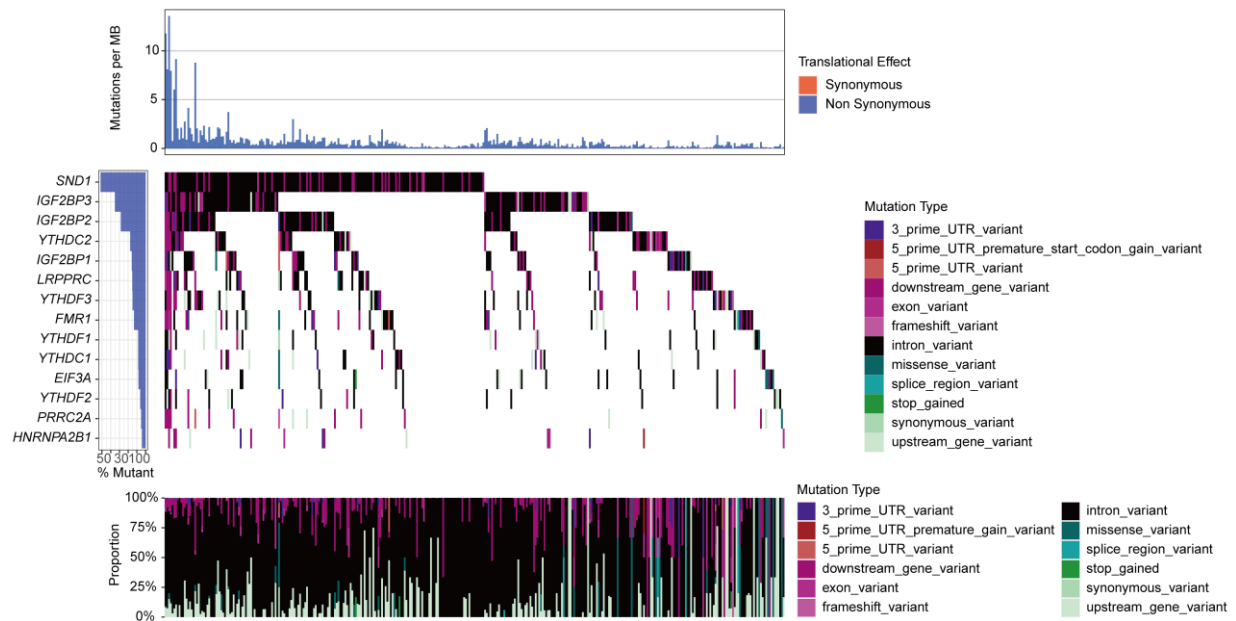


Fig.S6 Mutation waterfall diagram of m6A reader gene in TCGA-PAAD, PACA-AU and PACA-CA: the overall mutation rate of m6A reader gene was low, and the mutation rates of SND1, IGF2BP3 and IGF2BP2 ranked the top three.

Supplementary Figure S7

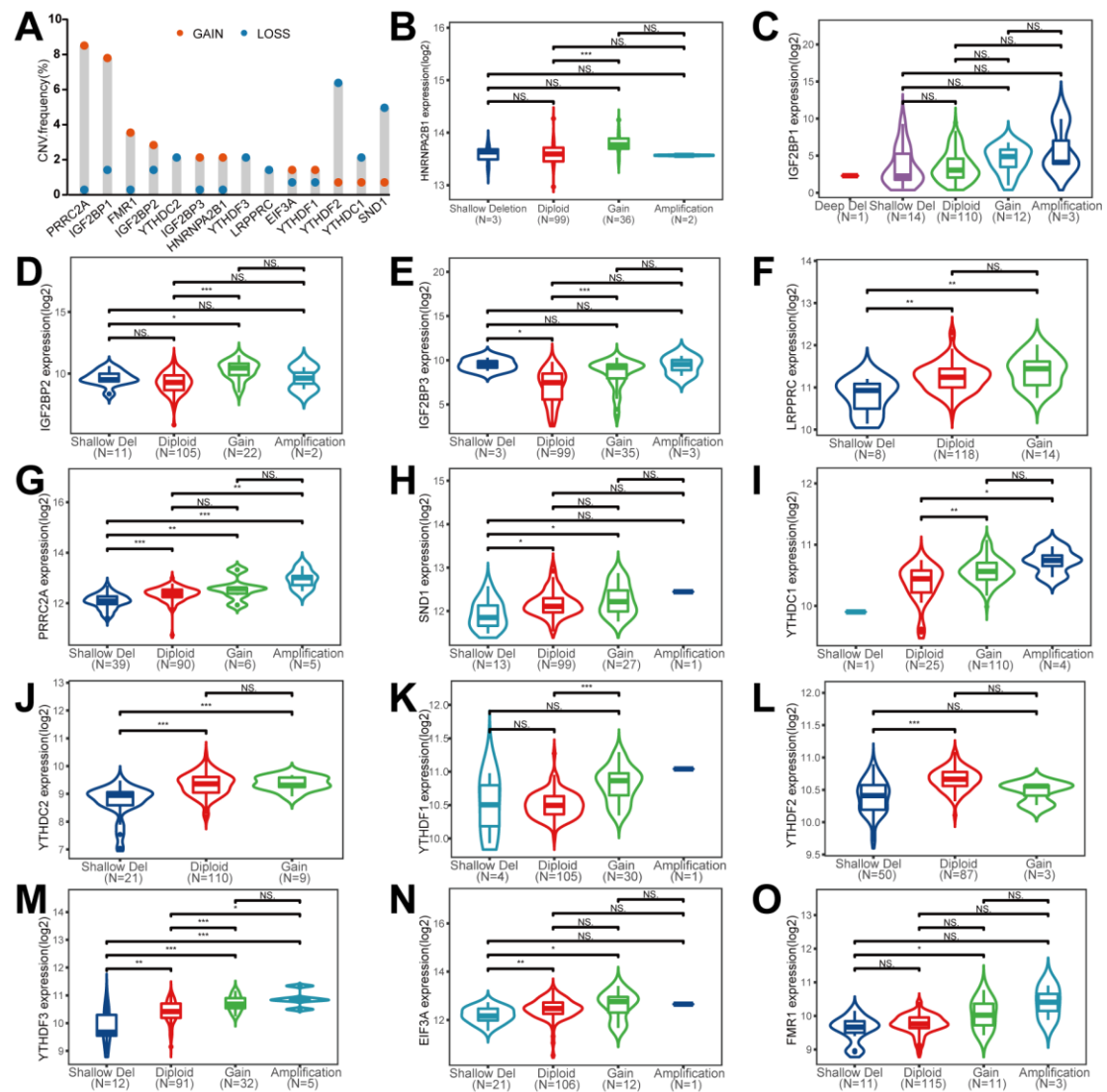


Fig.S7 Map of CNV changes in the m6A reader gene in TCGA-PAAD. (A) bar chart of CNV mutation frequency of 14 m6A readers. (B-O) Violin plot of expression amount of each reader gene versus CNV mutation type.

Supplementary Figure S8

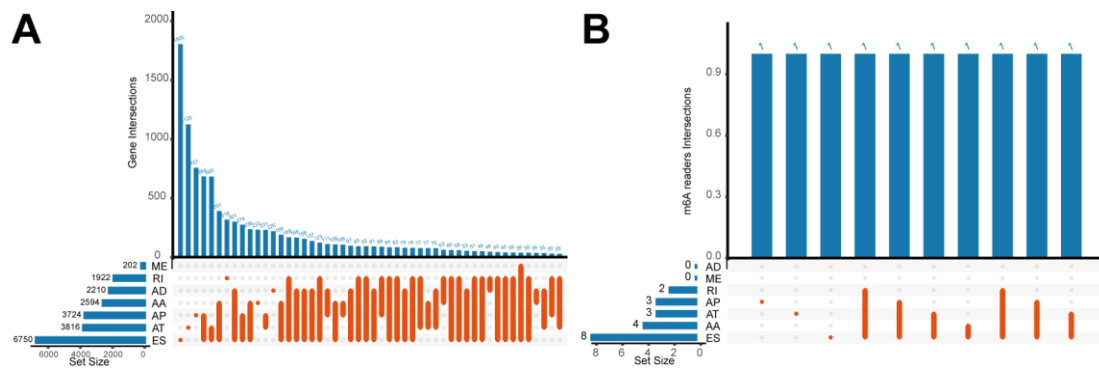


Fig.S8 Map of variable shear events in TCGA-PAAD. (A) UpSet graph for transcriptome-wide analysis of the frequencies of five AS in PC; (B) UpSet diagram of five variable splicing event frequencies in 14 m6A readers.

Supplementary Figure S9

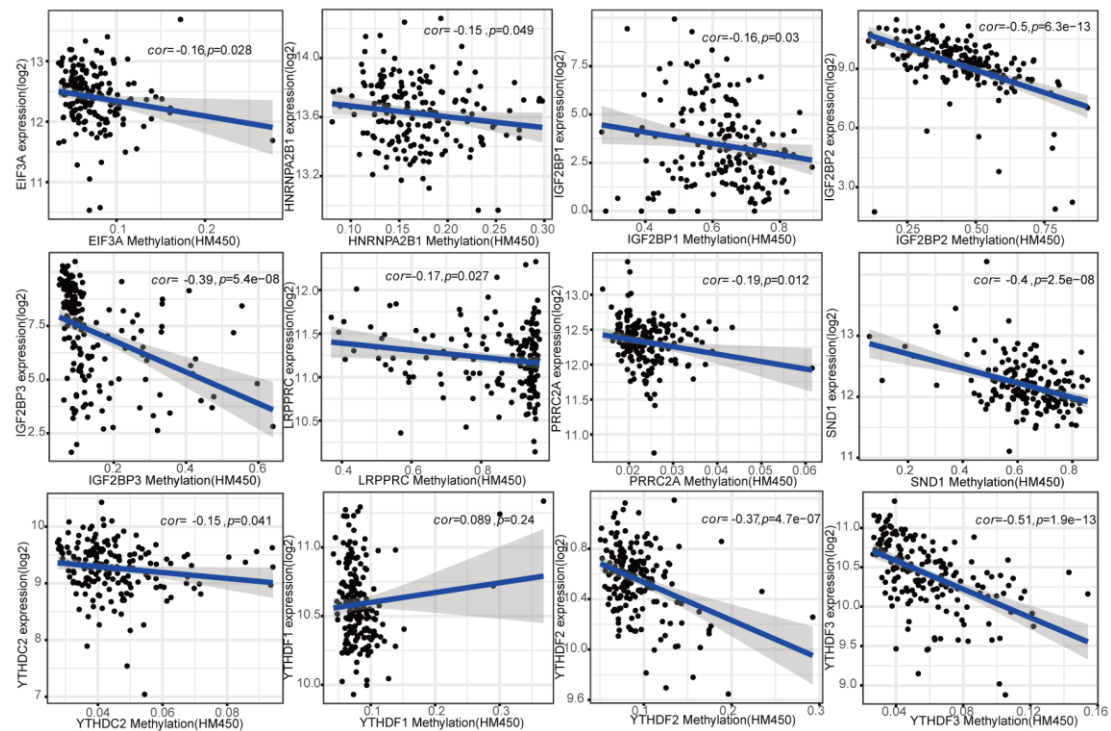


Fig.S9 Correlation plot between the expression of 12 m6A readers and methylation signal values in TCGA-PAAD. (Due to missing data of genes RBMX and HNRNPC, only 12 m6A readers were included in this correlation map).

Supplementary Figure S10

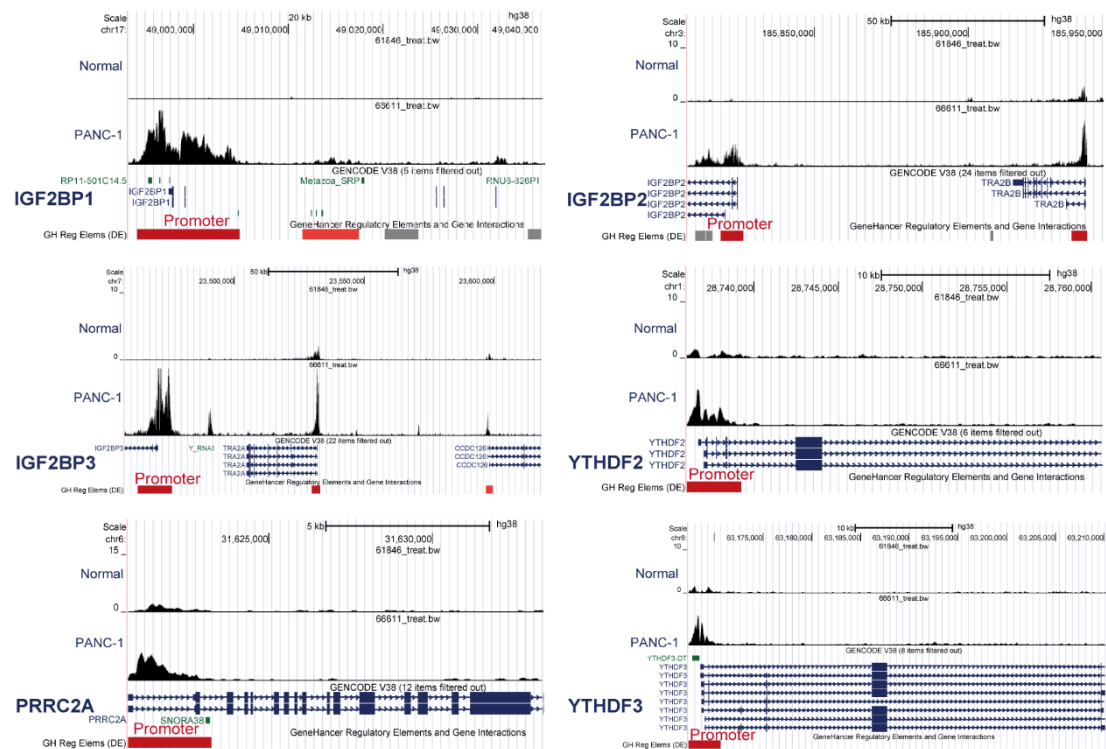


Fig.S10 Comparison of histone H3K27ac acetylation modification peaks in the promoter regions of IGF2BP1, IGF2BP2, IGF2BP3, YTHDF2, YTHDF3, and PRRC2A between PANC-1 cell line and normal human pancreatic cell line.

Supplementary Figure S11

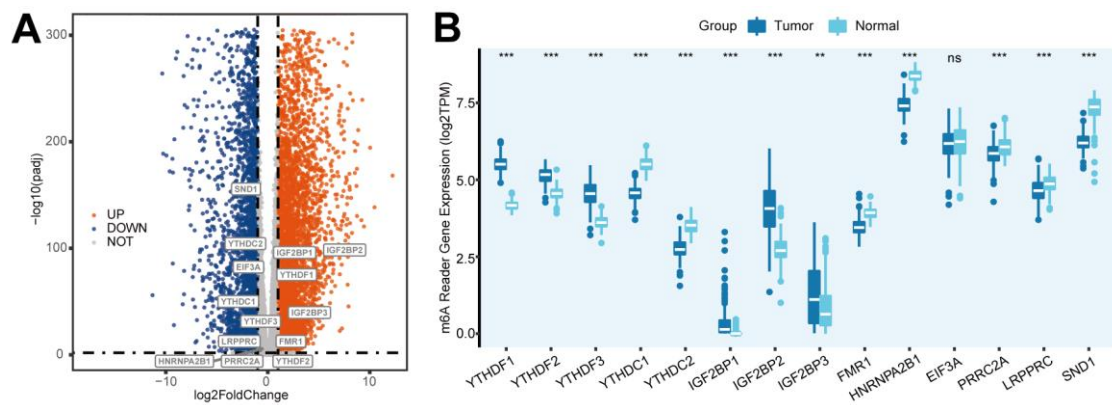


Fig.S11 Analysis of differences between RNA-seq data in TCGA-PAAD and GTEx. (A) volcano plot of differential gene expression analysis between PC tumor samples and normal pancreatic tissue samples; (B) boxplots of expression of 14 m6A readers in PC tumor samples and normal pancreatic tissue samples.

Supplementary Figure S12

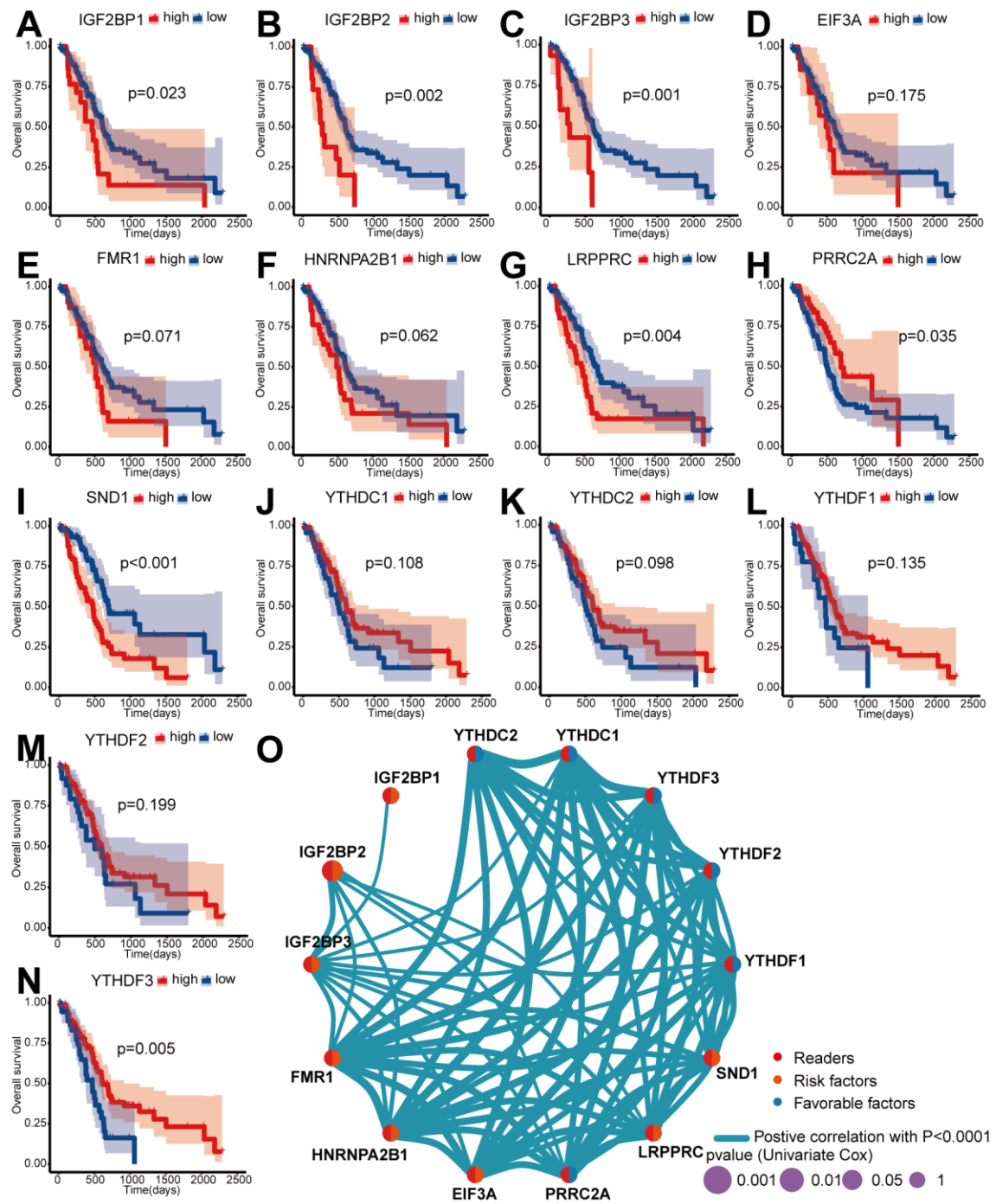


Fig.S12 Relationship between genes of 14 m6A reader genes in TCGA-PAAD and prognosis of PC patients. (A-N) Survival curve drawn by grouping based on the median value of 14 m6A readers' expression; (O) Risk network map among 14 m6A readers.

Supplementary Figure S13

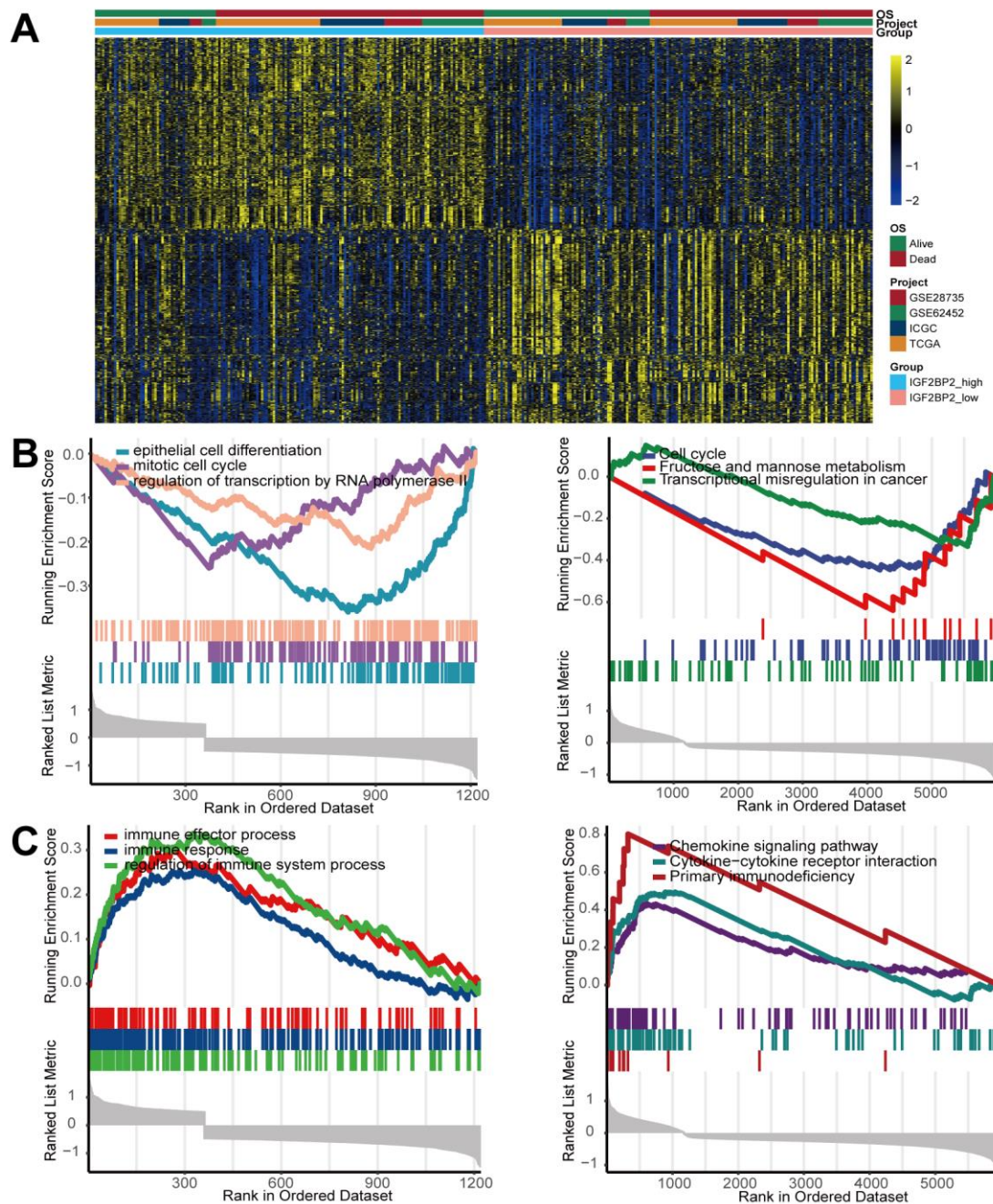


Fig.S13 Screening of differentially expressed genes and pathway enrichment analysis of IGF2BP2 in PC with different expression states. (A) differential gene heat map between high and low IGF2BP2 expression; (B) Enrichment map of differentially expressed genes when IGF2BP2 was highly expressed (left: GO enrichment pathway; Right: KEGG enriched pathway); (C) Enrichment map of differentially expressed genes in IGF2BP2 low expression (left: GO enrichment pathway; Right: KEGG-enriched pathway).