

Figure S1. Prognostic value of m6A RNA methylation regulators in patients with ccRCC with different clinicopathological features in TCGA cohort. (A) Low histological grade; (B) high histological grade; (C) low pathological stage; (D) high pathological stage. *P<0.05, **P<0.01, ***P<0.001. m6A, N⁶-methyladenosine; ccRCC, clear cell renal cell carcinoma; TCGA, The Cancer Genome Atlas; HR, hazard ratio; CI, confidence interval.

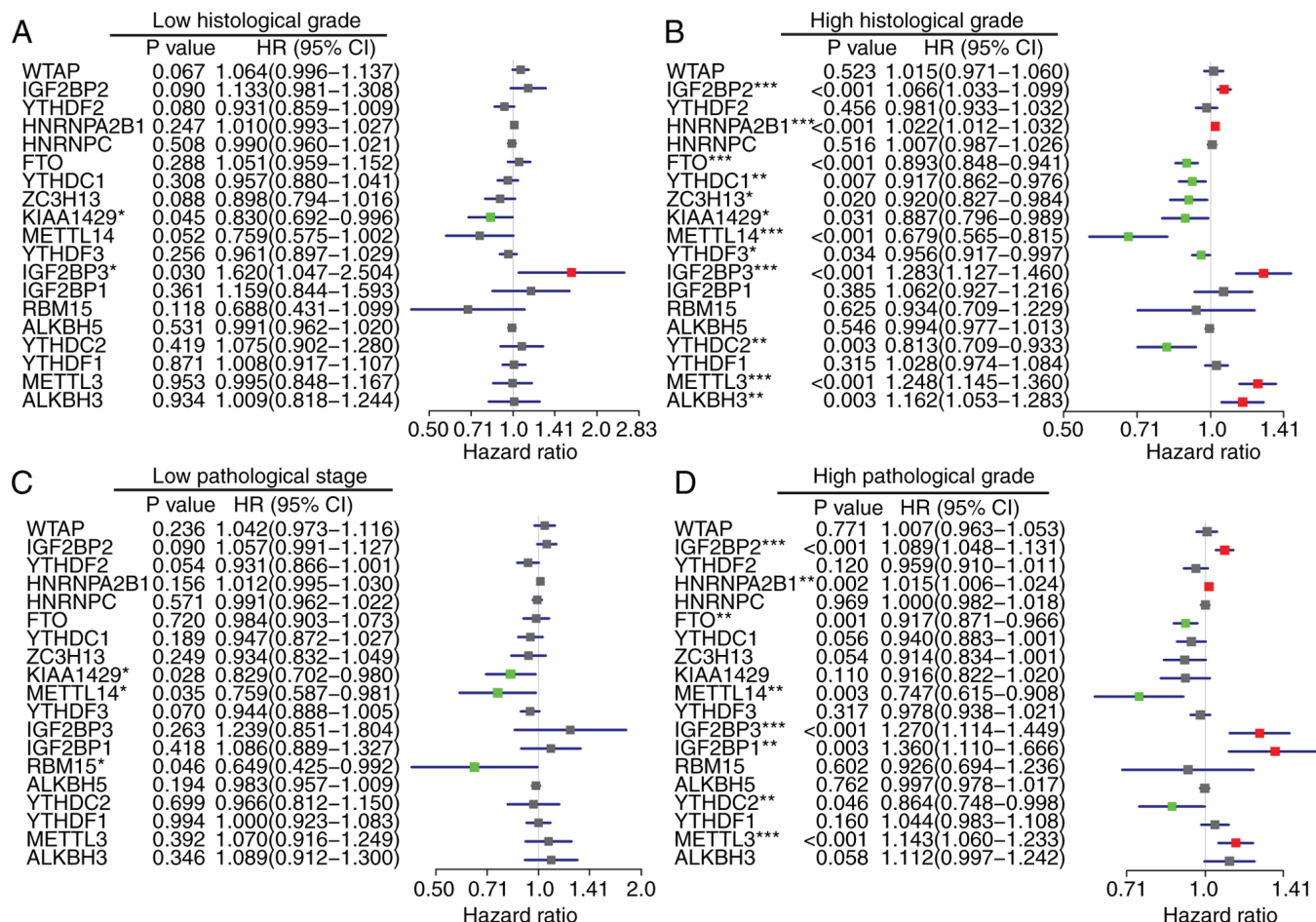


Figure S2. Kaplan-Meier survival curves of patients with ccRCC. (A-H) OS and DFS of patients with different pathological stages or histological grades in TCGA cohort. (I and J) OS of patients with different pathological stages in the ICGC cohort. ccRCC, clear cell renal cell carcinoma; TCGA, The Cancer Genome Atlas; ICGC, International Cancer Genome Consortium; OS, overall survival; DFS, disease-free survival.

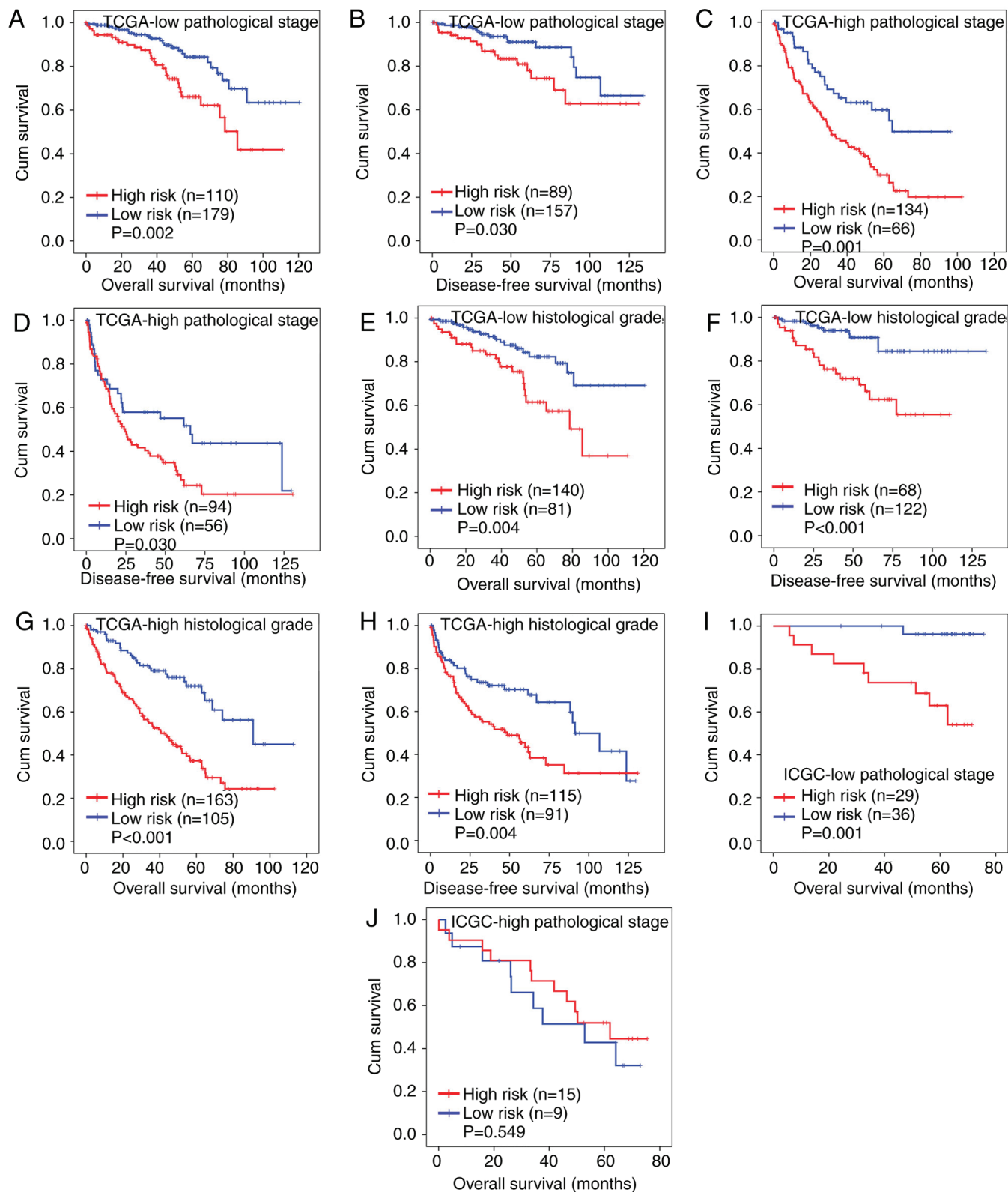


Table SI. Primers used for quantitative PCR.

Primer	Sequence (5'→3')
IGF2BP3	F: AGTTGTTGTCCCTCGTGACC R: GTCCACTTTGCAGAGCCTTC
METTL14	F: CGCCTCCTCCCAAATCTAA R: ACCTCTGTGTGCTCCTCCAC
METTL3	F: ATGGGAAGGAACACTGCTTG R: ATGACTGGTGGAACGAACCT
KIAA1429	F: ATACTGATGGTCTGGTGCTAAGA R: TGGAGGGCTTCCATTAAACTGAT
ALKBH3	F: TACCACTGCTAAGAGCCATCTCC R: ACCTGCTGAGGTTCTTTGAACAC
HNRNPA2B1	F: ACTTTGGCTTTGGGGATTCA R: TCCACGTCCACTGCCATATC
IGF2BP2	F: AGTGGAATTGCATGGGAAAATCA R: CAACGGCGGTTTCTGTGTC
β-actin	F: GTGAAGGTGACAGCAGTCGGTT R: GAAGTGGGGTGGCTTTTAGGAT
F, forward; R, reverse.	