

Figure S1 The clinical data of the 374 HCC samples in TCGA LIHC datasets. HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; LIHC, liver hepatocellular carcinoma.

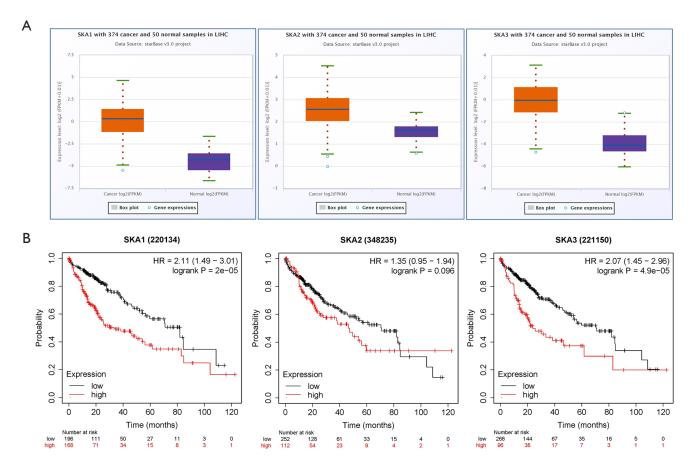


Figure S2 The SKA family was highly expressed in HCC. (A) The expression level of SKA1, SKA2 and SKA3 in the normal liver samples (n=50) and the HCC samples (n=374), as indicated by the TCGA LIHC data set. (B) Kaplan-Meier overall survival curves of patients with HCC in the TCGA cohort (log-rank test). SKA, spindle and kinetochore-associated; SKA1, spindle and kinetochore-associated complex subunit 1; SKA2, spindle and kinetochore-associated complex subunit 2; SKA3, spindle and kinetochore-associated complex subunit 3; HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; LIHC, liver hepatocellular carcinoma.

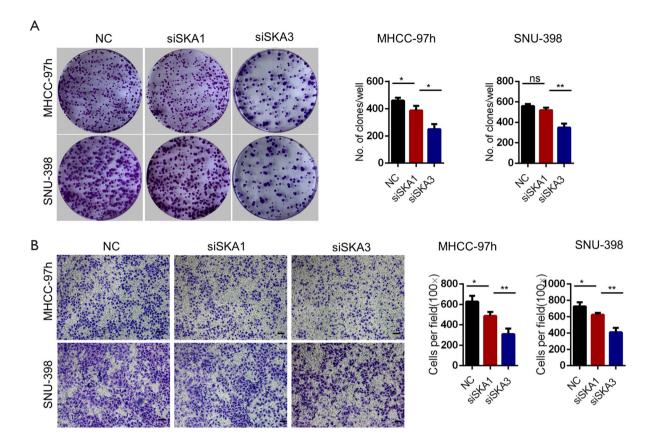


Figure S3 SKA3 had stronger effects on proliferation and migration than SKA1 in HCC. (A) Representative images of colony formation assay in indicated cells staining with crystal violet solution. (B) Representative images of Transwell migration assay in indicated cells staining with crystal violet solution (scale bar: 200 μm). For the statistical analysis (Student's *t*-test), *, P<0.05; **, P<0.01. ns, not significant; SKA1, spindle and kinetochore-associated complex subunit 3; HCC, hepatocellular carcinoma.

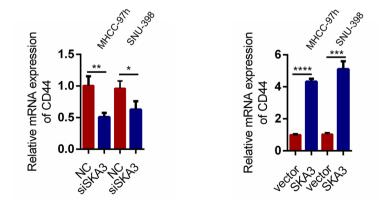


Figure S4 The expression of CD44 were tested by qRT-PCR in indicated cells. For the statistical analysis (Student's *t*-test), *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.001; ****, P<0.0001. SKA3, spindle and kinetochore-associated complex subunit 3; qRT-PCR, quantitative reverse transcription-polymerase chain reaction.

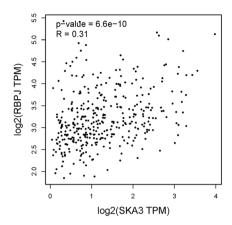


Figure S5 Correlations between RBPJ and SKA3 in TCGA HCC tumor are denoted with Pearson's correlation coefficients. SKA3, spindle and kinetochore-associated complex subunit 3; TCGA, The Cancer Genome Atlas; HCC, hepatocellular carcinoma; TPM, transcript per million.