

Figure S1. Validation of RRP9 in hepatocellular carcinoma tissue microarray. (A) Tissue microarray analysis of cohort 1 (n=54). (B) Tissue microarray analysis of cohort 1 (n=19). (C) Tissue microarray analysis of cohort 2 (n=31). (D) Tissue microarray analysis of cohort 2 (n=22) Scale bar, 1.5 mm.

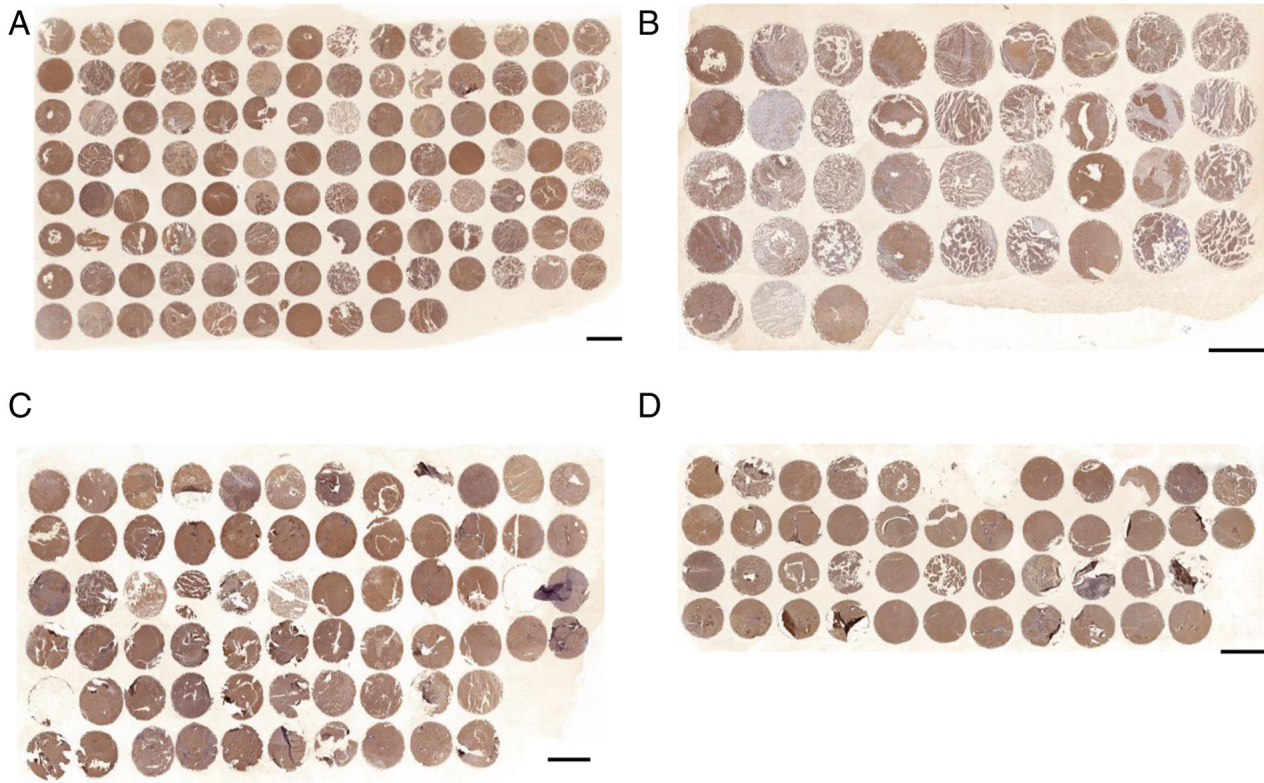


Figure S2. Mechanism of CCNA2 in hepatocellular carcinoma. (A) Co-IP assay showing the interaction between RRP9 and CCNA2 in 293T and (B) 97h cells. (C) Western blot analysis of CCNA2 protein expression following CCNA2 overexpression in 97h cells and knockdown in HLF cells. (D) Western blot analysis of PI3K/AKT/mTOR signaling pathway proteins following CCNA2 knockdown in HLF cells. (E) Western blot analysis of PI3K/AKT/mTOR signaling pathway proteins following CCNA2 overexpression in 97h cells. * $P < 0.05$, ** $P < 0.01$. RRP9, ribosomal RNA processing 9; CCNA2, cyclin A2; KD, knockdown; OE, overexpression; WT, wild-type; IP, immunoprecipitation; IB, Immunoblotting; p-, phosphorylated.

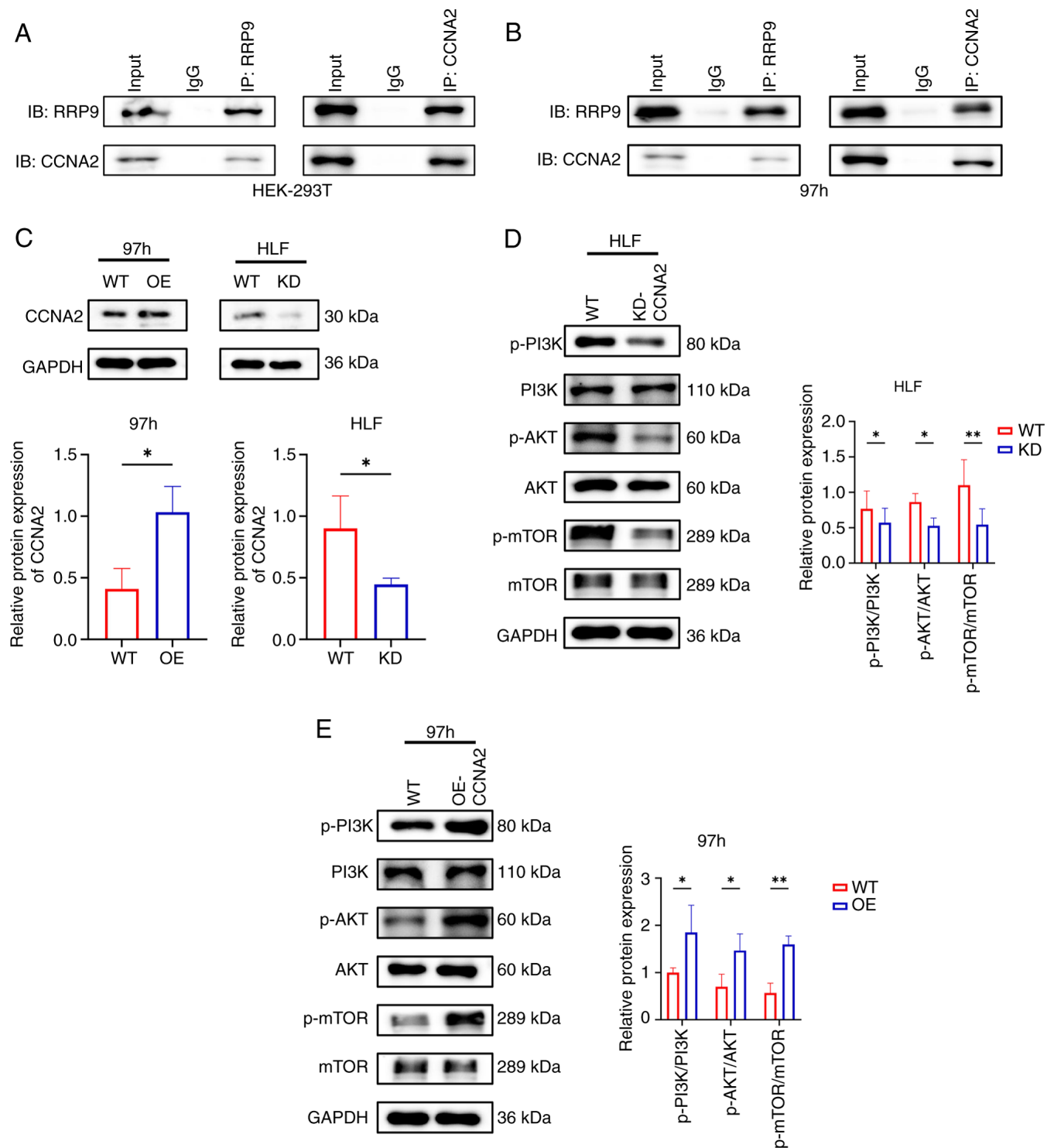


Figure S3. Validation of RRP9 and CCNA2 in hepatocellular carcinoma cell lines. (A) Western blot validation of RRP9 overexpression in Snu449 and (B) Western blot validation of RRP9 overexpression in HLF cells. (C) Western blot validation of RRP9 knockdown in 97h cells. (D) Western blot validation of RRP9 knockdown in Huh7 cells. (E) Western blot validation of CCNA2 knockdown in HLF cells. (F) Western blot validation of CCNA2 overexpression in 97h cells. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, ns $P > 0.05$. RRP9, ribosomal RNA processing 9; CCNA2, cyclin A2; KD, knockdown; OE, overexpression; WT, wild-type.

