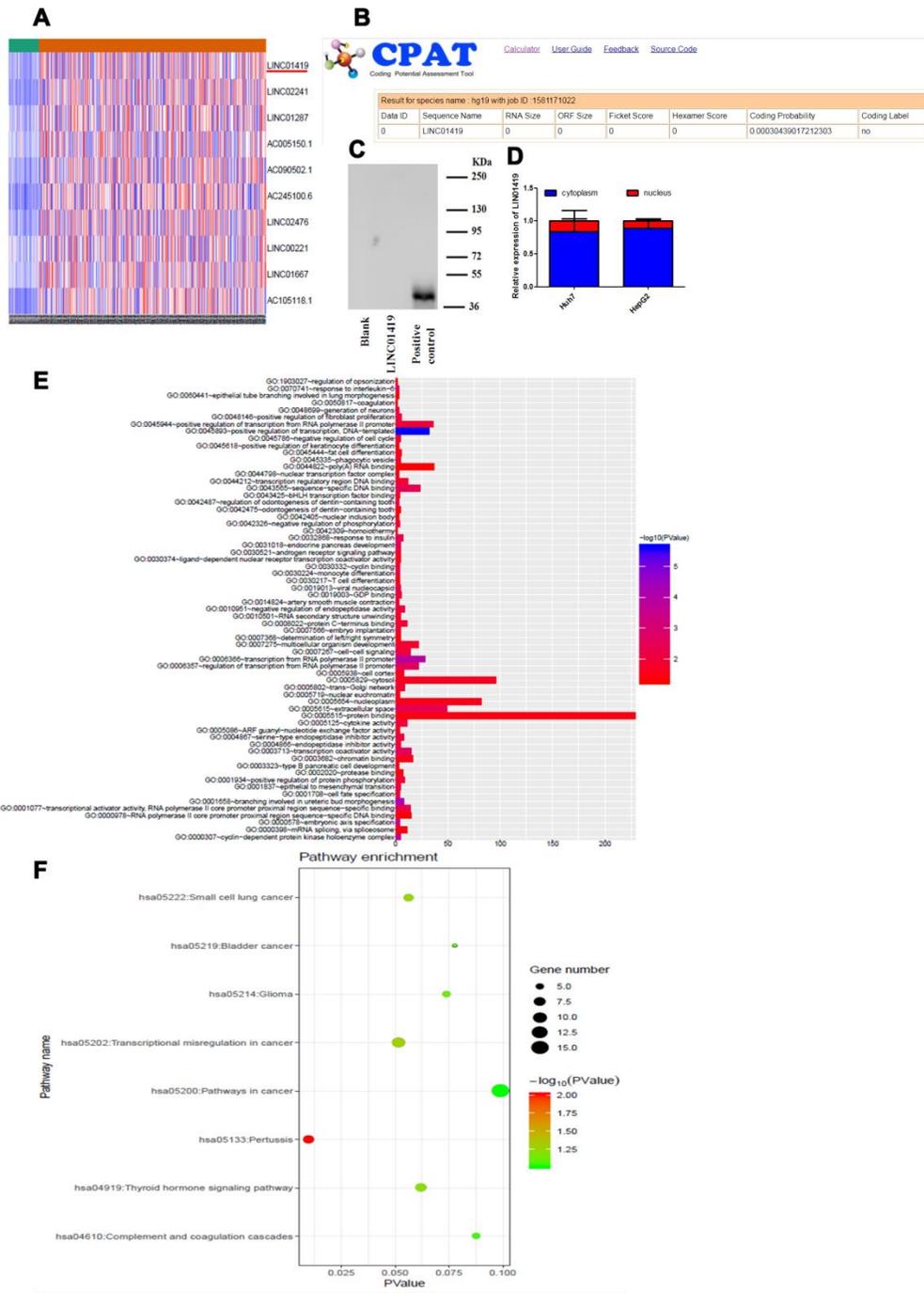
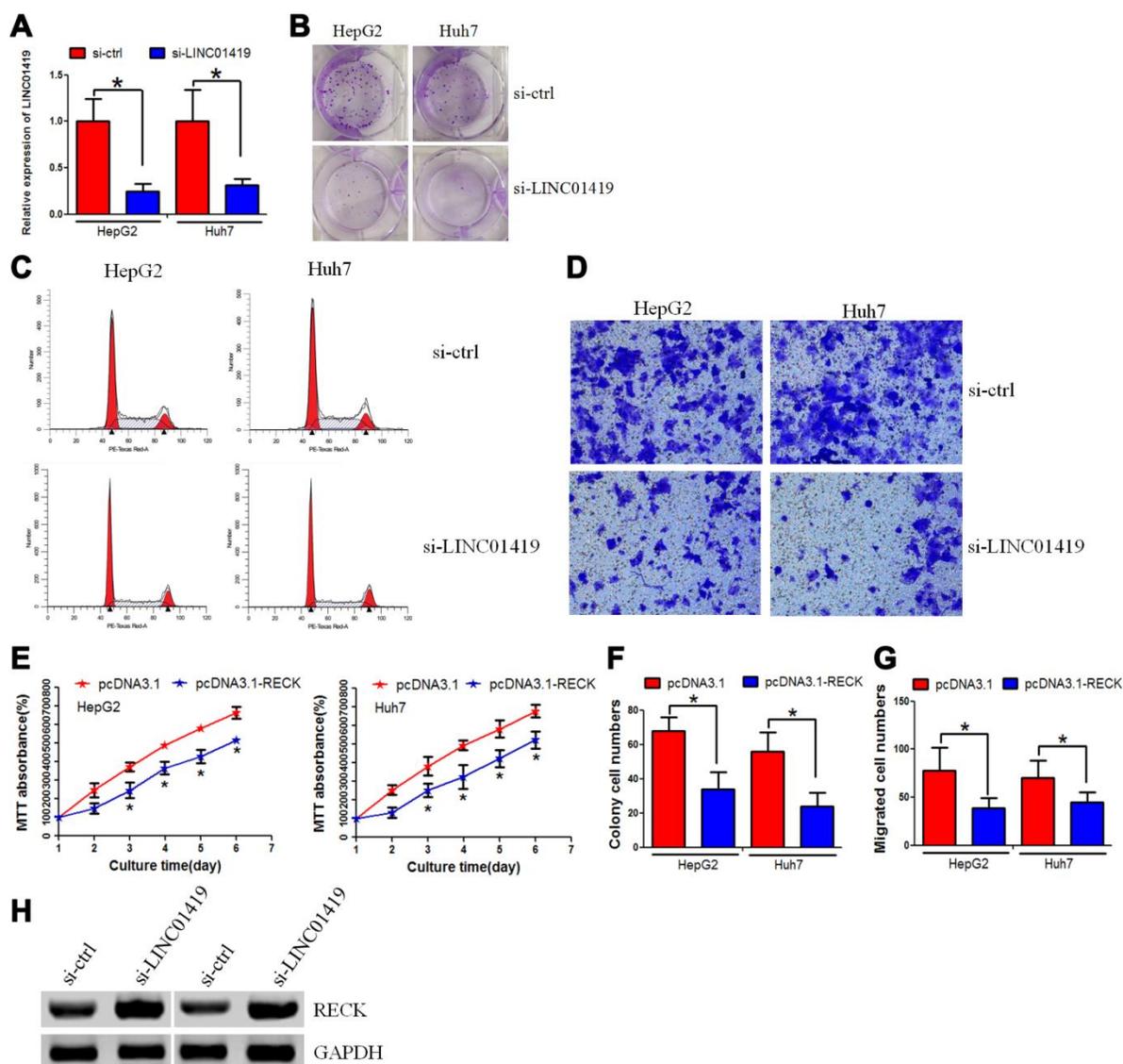


SUPPLEMENTARY FIGURES



**Supplementary Figure 1.** (A) Hierarchical clustering analysis of LincRNAs differentially expressed (fold change > 2; p < 0.05) in HCC and normal tissues in the TCGA cohort. (B) Online bioinformatics analysis indicating protein LINC01419 coding ability. (C) LINC01419 expression levels in cytoplasm and nucleus as examined by RT-PCR assay. (D) Subcellular fractionation and real-time PCR analysis showing that LINC01419 was mainly localized in the cytoplasm. (E) Gene ontology analysis for all genes with altered expression levels after LINC01419 down-regulation. (F) KEGG pathway enrichment for all genes with altered expression levels after LINC01419 down-regulation.



**Supplementary Figure 2.** (A) RT-PCR assay used to examine LINC01419 knockdown efficiency in HCC cells. (B) The colony-forming ability impaired in LINC01419-silenced cells. (C) The cell cycle distribution measured using flow cytometry. (D) The HCC migration ability examined using transwell assays. (E) MTT assay revealed that overexpression of RECK decreased cell growth rate. (F) Colony formation assay revealed that overexpression of RECK impaired cell colony formation ability. (G) Transwell assay revealed that overexpression of RECK decreased cell migration ability. (H) Western blot assay revealed that inhibition of LINC01419 elevated RECK expression level.