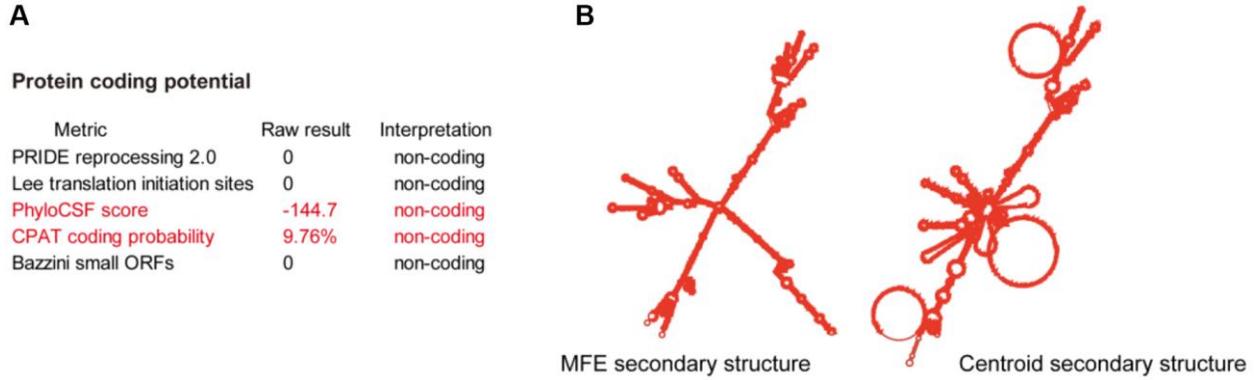
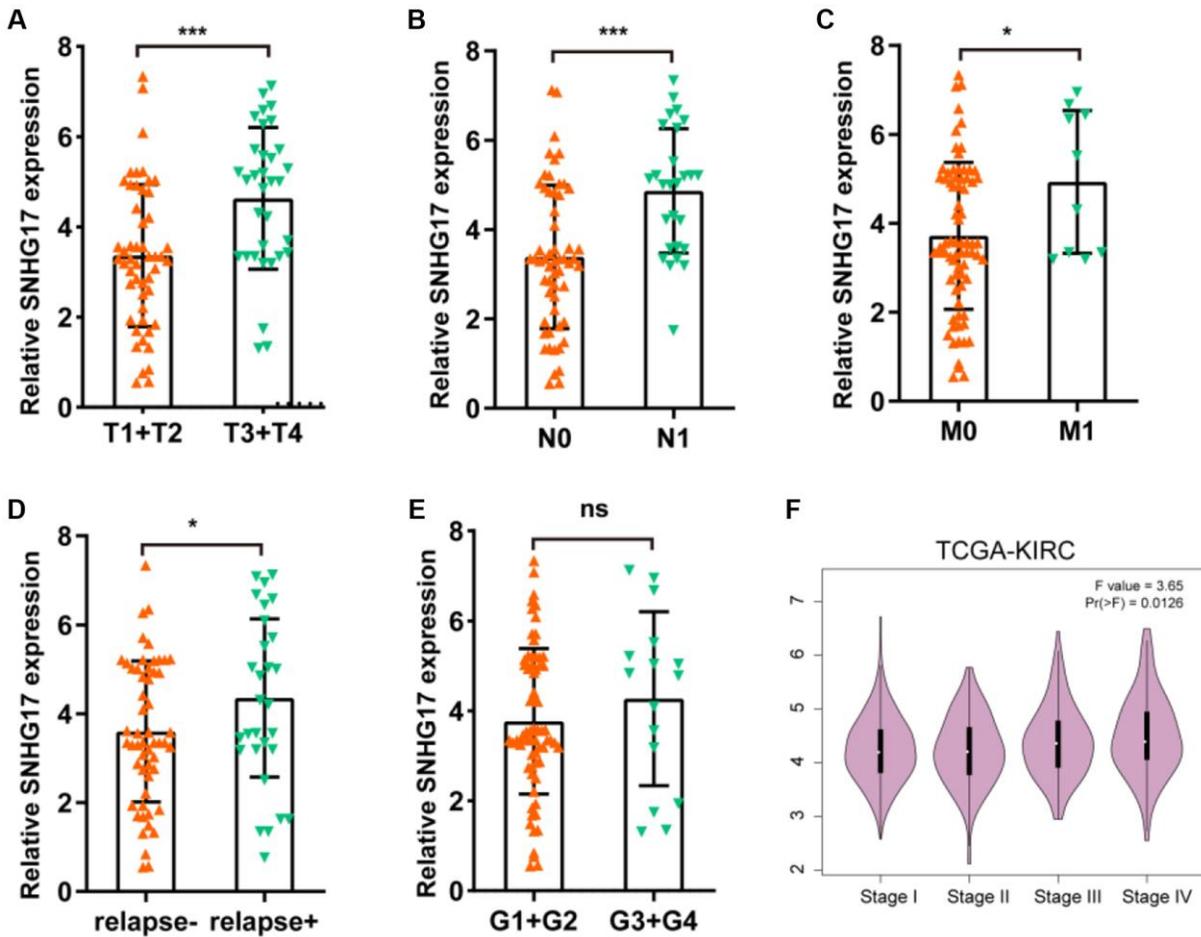


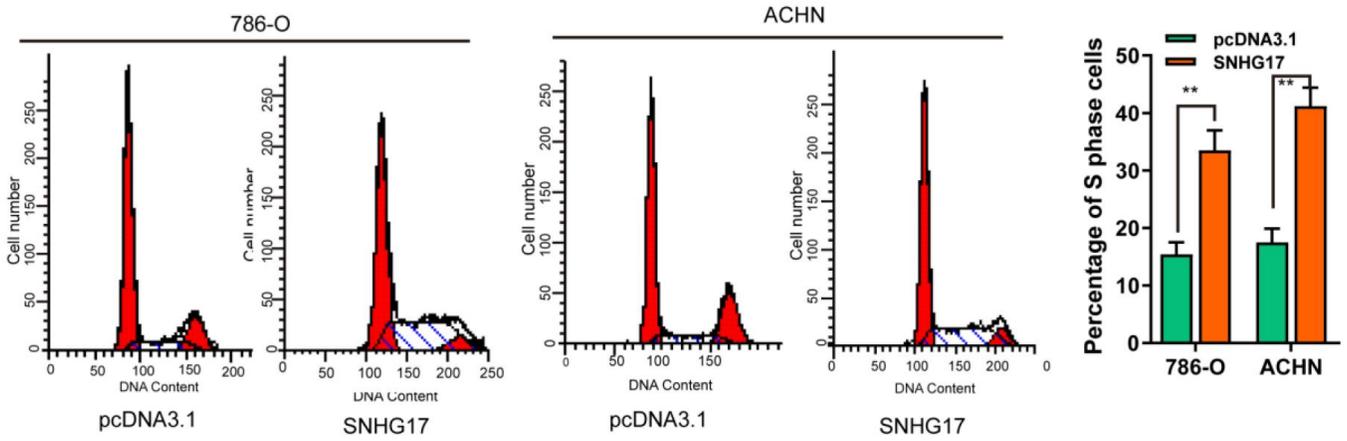
SUPPLEMENTARY FIGURES



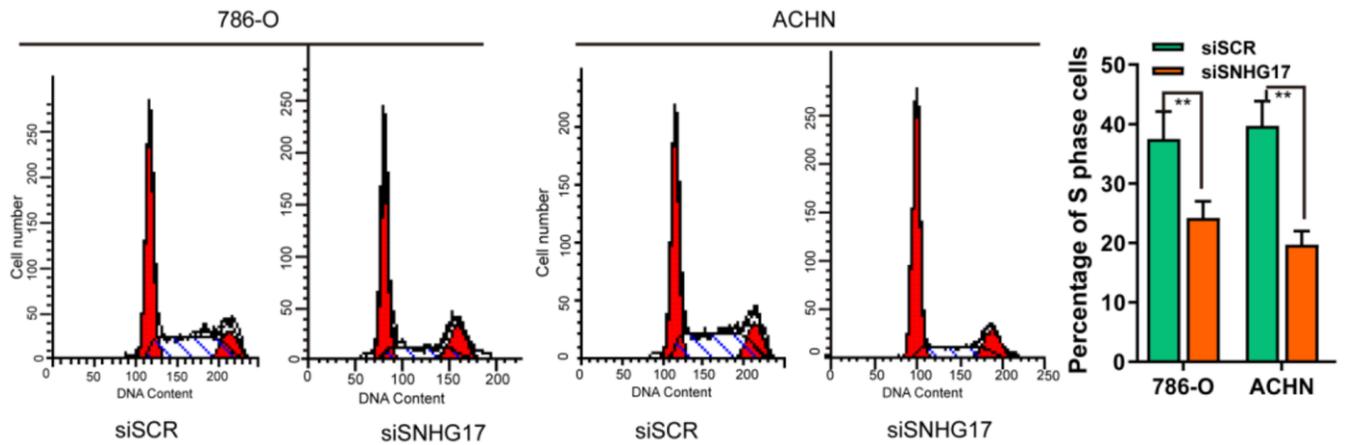
Supplementary Figure 1. (A) Protein coding potential of SNHG17 predicted using LNCipedia (<https://lncipedia.org>). (B) The RNA secondary structure of SNHG17 predicted using RNAfold Webserver (<http://rna.tbi.univie.ac.at/>) based on minimum free energy (MFE) and partition function.



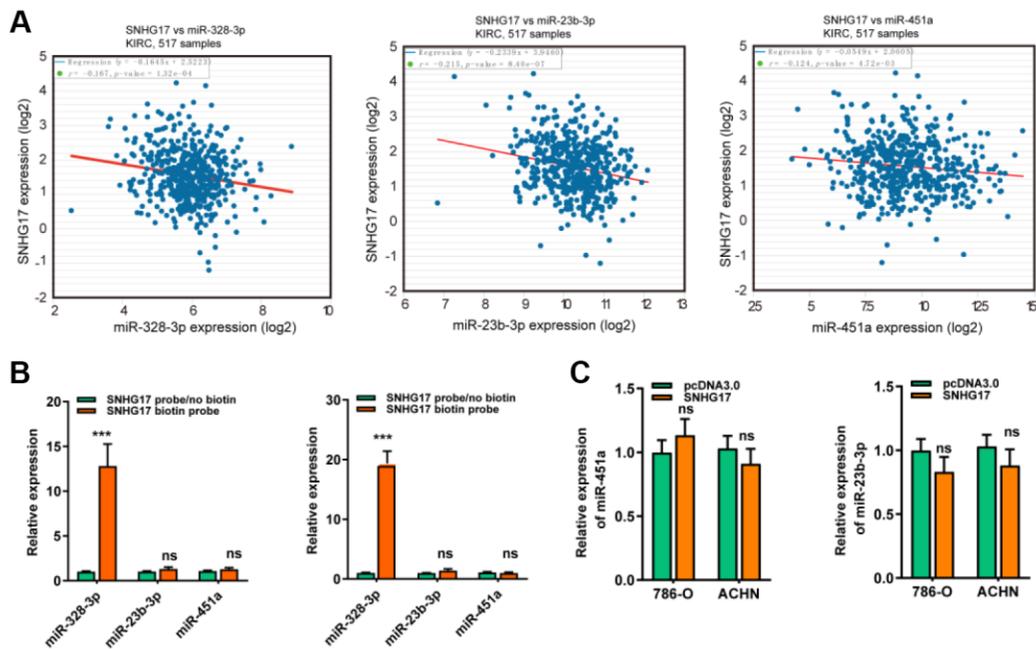
Supplementary Figure 2. Clinical significance of SNHG17 in CRC. RT-PCR assay analysis of the association between expression of SNHG17 and T stage (A) node invasion (B), metastasis status (C), relapse status (D), and tumor grade (E). Data were obtained using the $2^{-\Delta\Delta CT}$ method and were normalized to GAPDH levels. (F) Expression of SNHG17 was significantly associated with aggressive TNM stage according to TCGA-KIRC dataset. ns, not significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.



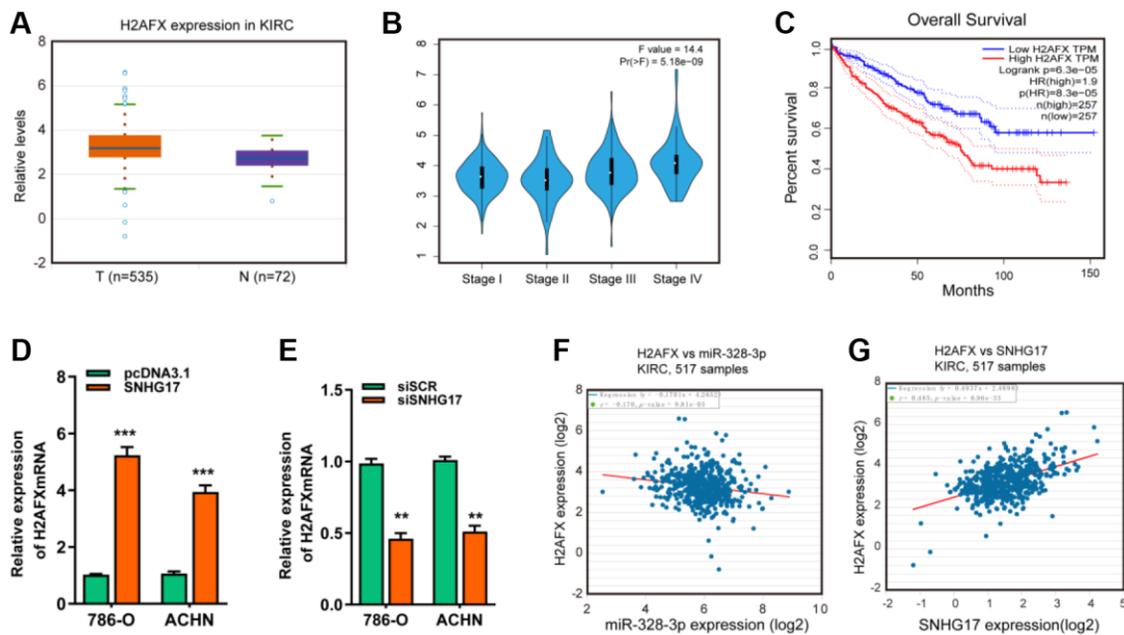
Supplementary Figure 3: Flow cytometry assays were used to detect cell cycle distribution following RCC cells with SNHG17 overexpression



Supplementary Figure 4: Flow cytometry assays were used to detect cell cycle distribution following RCC cells with SNHG17 silencing



Supplementary Figure 5. (A) miR-328-3p, miR-23b-3p, miR-451a were suggested to possess a negative correlation with SNHG17 in human RCC tissue samples according to TCGA-KIRC dataset. (B) RNA pull down assay showed that only miR-328-3p was significantly pulled down by biotinylated SNHG17 in RCC cell lines. (C) qRT-PCR assay analysis of the expression levels of miR-23b-3p or miR-451a in 786-O and ACHN cell lines after transfection with SNHG17 overexpression vectors. ns, not significant; ** $P < 0.01$; *** $P < 0.001$.



Supplementary Figure 6. (A–C) According to TCGA-KIRC dataset, H2AX expression was upregulated, associated with advanced TNM stage and poor survival. (D–E) qRT-PCR assay analysis of the expression levels of H2AX in RCC cells after transfection with the indicated vectors. (F–G) Spearman's correlation analysis of the association between H2AX expression and miR-328-3p (F) or SNHG17 (G) expression in RCC tissues from TCGA-KIRC dataset. ns, not significant; ** $P < 0.01$; *** $P < 0.001$.