

RETRACTED ARTICLE: Long noncoding RNA SNHG6 functions as a competing endogenous RNA by sponging miR-181a-5p to regulate E2F5 expression in colorectal cancer

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Background: Long noncoding RNAs (lncRNAs) have been identified as a novel class of regulators implicated in diverse biological processes in human cancers. Currently, evidence have shown that SNHG6, a cancer-associated lncRNA, exerts critical functions in gastric cancer and hepatocellular carcinoma; however, its role in colorectal cancer (CRC) remains unclear.

Methods: The expression of SNHG6 was determined by quantitative real-time PCR in CRC tissues and cells. SNHG6 was downregulated by using RNAi technology. Cell proliferation was examined by MTT and clone formation assays. Cell migration and invasion were determined by wound healing and transwell assays. Fluorescence in situ hybridization assays were performed to examine subcellular localization of SNHG6 in CRC cells. Fluorescence reporter and Western blot assays were used to explore the potential mechanisms of SNHG6 in CRC progression.

Results: In this study, we found that SNHG6 was significantly upregulated in CRC tissues and cell lines, compared with normal tissues and normal colorectal epithelial cell line NCM460, respectively. The expression of SNHG6 was positively correlated with tumor size, advanced TNM stage, and distant metastasis. Survival analyses revealed that SNHG6 was significantly associated with poor clinical outcomes and could serve as an independent prognostic factor. Loss-of-function studies demonstrated that SNHG6 knockdown inhibited CRC cell proliferation, induced G0/G1 arrest, promoted apoptosis, suppressed CRC cell migration and invasion, and restrained tumor growth. Mechanistic investigations showed that SNHG6 acted as a competing endogenous RNA for miR-181a-5p and attenuated the inhibitory effect of miR-181a-5p on E2F5.

Conclusion: Taken together, these results demonstrated that SNHG6 plays a crucial role in CRC progression via miR-181a-5p/E2F5 axis. Therefore, SNHG6 may serve as a prognostic and therapeutic biomarker in CRC.

Keywords: SNHG6, colorectal cancer, miR-181a-5p, E2F5, proliferation

Introduction

Colorectal cancer (CRC) is the third most commonly diagnosed malignancy in males and the second in females worldwide, with an increasing incidence each year in many countries.¹ Despite the advances of surgical methods and chemotherapeutic management of CRC, the clinical outcome of CRC remains unsatisfactory. Like many other cancers, the tumorigenesis of CRC is a complex process involving both genetic and epigenetic changes.² In recent years, intensive investigations have identified a great many biomarkers for CRC characterization and prognosis. Among them, noncoding

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RNAs have been proved to be a critical factor participating in CRC pathogenesis.^{3,4}

Long noncoding RNAs (lncRNAs) are defined as a class of noncoding RNAs that are longer than 200 nucleotides and lack significant protein-coding ability.⁵ Although previous studies have identified thousands of lncRNAs, the majority of them have not been characterized.⁶ Growing evidence have suggested that lncRNAs play crucial roles in a wide range of cellular processes, such as cell proliferation, differentiation, migration, invasion, and apoptosis, and cell cycle progression.⁷ Aberrant lncRNA transcriptions have been shown to contribute to the initiation and progression of different human cancers with lncRNAs functioning as oncogenes or tumor suppressors.^{8,9} For instance, a study showed that lncRNA HOTTIP, which was highly expressed in small-cell lung cancer, acted as an oncogene to enhance chemoresistance by binding miR-216a and regulating the expression of BCL-2.¹⁰ Another study showed that upregulated HNF1A-AS1 promoted colon cancer cell viability, migration, and invasion via miR-34a/SIRT1/p53 feedback loop.¹¹ In multiple myeloma, upregulation of lncRNA MEG3 was found to promote osteogenic differentiation of mesenchymal stem cells by activating BMP4 transcription.¹² Moreover, studies have proved that lncRNAs, such as HOTAIR, CCAT1, and HNF1A-AS1, could also be used as potential diagnostic and prognostic biomarkers on account of their clear correlations with clinical characteristics and outcomes in CRC patients.^{4,11,13}

SNHG6, located in chromosome 8q11.1, is a newly identified lncRNA, which has been reported to be upregulated in gastric cancer (GC),¹⁴ hepatocellular carcinoma (HCC),^{15,16} and CRC.¹⁷ Further investigation revealed that SNHG6 participated in the regulation of epithelial–mesenchymal transition (EMT) and chemoresistance.^{14–16} Additionally, SNHG6 could function as a competing endogenous RNA (ceRNA) by sponging miR-101-5p, thereby modulating the expression of ZEB1.¹⁴ Although a recent study revealed that SNHG6 promotes tumor growth via p21 in CRC,¹⁸ the biological functions and underlying mechanisms of SNHG6 in CRC remain largely unknown, which prompted us to explore the role of SNHG6 in CRC. In this study, we determined the expression and clinical significance of SNHG6 in CRC. The biological functions and potential mechanisms of SNHG6 were also explored by in vitro and in vivo assays. Our study for the first time demonstrated that SNHG6 may act as a ceRNA to regulate the expression E2F5, a critical transcription factor,¹⁹ by sponging miR-181a-5p, thus providing novel insight into the mechanism of CRC progression.

Materials and methods

Tissue samples

CRC and adjacent normal tissues were collected from 141 CRC patients during surgery in Weifang People's Hospital, Weifang, Shandong, China. Specimens were transported with liquid nitrogen and stored at -80°C until used. Written informed consent was obtained from all patients. Clinical information including age, gender, tumor size, tumor location, lymphatic invasion, TNM stage, distant metastasis, and venous invasion was collected from medical records. This study was approved by the Institutional Review Committees of Weifang People's Hospital and conducted in accordance with the Declaration of Helsinki.

Cell lines and transfection

All CRC cell lines and HCT116 cell line were purchased from American Type Culture Collection (ATCC, Manassas, VA, USA). All cell lines were cultured in DMEM containing 10% FBS, 100 U/mL penicillin, and 100 mg/mL streptomycin in a humidified incubator at 37°C with 5% CO_2 . The SNHG6 shRNAs, SNHG6 wild-type plasmids, SNHG6 mutant plasmids, pCMV-E2F5 plasmids, and empty vectors were constructed by Jilin Chemical Technology (Shanghai, China). The shRNA sequences used for targeting SNHG6 were as follows: shRNA1, 5'-GCATATAGGTTGCTGTAGA-3'; shRNA2, 5'-GATGTTGATAACATCACAA-3'. The sh-NC sequence used was 5'-CGATAATGCTGTTAGGAGT-3'. The miRNA mimics and inhibitors were synthesized by RiBo Biological Co. LTD (Guangzhou, China). Cell transfection was performed using the Lipofectamine 2000 reagent (Thermo Fisher Scientific, Waltham, MA, USA) following the manufacturer's instructions.

RNA extraction and quantitative real-time PCR (qRT-PCR)

Total RNA was extracted from tissues and cells using TRIzol reagent (Thermo Fisher Scientific). The quality of RNA was evaluated with NanoDrop ND-1000 spectrophotometer. Total RNA was reversely transcribed into cDNA using GoScript RT System (Promega, Madison, WI, USA) following the manufacturer's protocol. qRT-PCR was performed using SYBR Premix EX Taq™ II kit (RR820A; TaKaRa, Kusatsu, China) following the manufacturer's instructions using ABI 7500 (Applied Biosystems, Foster City, CA, USA). All primers were synthesized by Thermo Fisher Scientific. The primer sequences used were as follows: SNHG6, forward 5'-CTCTGCGAGGTGCAAGAAAG-3' and reverse 5'-AATACATGCCGCGTGATCCT-3'; GAPDH,

forward 5'-CGCTCTCTGCTCCTCCTGTTC-3' and reverse 5'-ATCCGTTGACTCCGACCTTAC-3'; miR-181a-5p, forward 5'-ACACTCCAGCTGGGAACATTCAACGCTGTCGG-3' and reverse 5'-TGGTGTCGTGGAGTCG-3'; U6, forward 5'-CTCGCTTCGGCAGCACA-3' and reverse 5'-AACGCTTCACGAATTTGCGT-3'; E2F5, forward 5'-TGCTCACTACCAAGTTCGTGTC-3' and reverse 5'-ACAGCCAAAGTATCAGCAGCC-3'. The relative expression of lncRNA/mRNA and miRNA was calculated using the $2^{-\Delta\Delta C_t}$ method by normalizing to GAPDH and U6, respectively. Each experiment was performed in triplicate.

MTT assay

The MTT assay was performed using Cell Proliferation Reagent Kit I (Roche Applied Science, Penzberg, Germany). CRC cells were seeded in 96-well plates at a density of 2,000 cells per well. At 0, 24, 48, and 72 hours after transfection, MTT reagent (10 μ L) was added to each well and incubated for 4 hours at 37°C. All the experiments were performed in quadruplicate. Then, OD 490 values were detected using a microplate reader (Infinite 200 PRO; Tecan, Männedorf, Switzerland).

Colony formation assay

CRC cells transfected with shRNAs or sh-NC were seeded in 12-well plates at a density of 1,000 cells per well. After incubating for 1 week at 37°C, cells were fixed with formaldehyde for 10 minutes and stained with 0.5% crystal violet for 10 minutes. The number of colonies was counted using ImageJ software (NIH, Bethesda, MD, USA).

Wound healing and transwell assays

For wound healing assay, scrapes were created using a 10 μ L pipette tip. Cells were washed three times with PBS, and serum-free medium was added to wells. The wounds were photographed at 0, 24, and 48 hours. For invasion transwell assay, transwell chambers (8 μ m pore size; Corning Inc., Corning, NY, USA) were prepared with matrigel (Corning Inc.). Cells were collected and washed twice with PBS, and then added to the upper chamber at a density of 2×10^4 cells per chamber in 100 μ L serum-free medium. Then, 700 μ L blood serum medium with 10% FBS was added to lower chamber. After incubation for 24 hours, the lower chamber was fixed with 4% paraformaldehyde for 10 minutes and stained with 0.5% crystal violet for 10 minutes. After washing with PBS, cells were imaged using a Nikon light microscope (Nikon, Tokyo, Japan) and counted by ImageJ software (NIH).

Fluorescence in situ hybridization (FISH) assay

RNA FISH assays were performed to observe the subcellular localization of SNHG6 in NCM460 and HCT116 cells by using FISH kit (Guangzhou Biosense Bioscience Co., Ltd, Guangzhou, China) according to the manufacturer's instructions. The Cy3-labeled SNHG6 probes were designed and synthesized by BersinBio Co. LTD (Guangzhou, China). Briefly, NCM460 and HCT116 cells were fixed with 4% formaldehyde for 15 minutes at room temperature. Then, the fixed cells were permeabilized using 0.5% Triton X-100 for 15 minutes. After prehybridized with hybridized solution, cells were incubated with probes at 42°C overnight. All nuclei were stained with DAPI (32670; Sigma-Aldrich, St. Louis, MO, USA) for 5 minutes at room temperature. Fluorescence images were taken using a fluorescence microscope (Leica, Hilden, Germany).

Luciferase reporter assay

All luciferase reporter vectors (SNHG6-WT, SNHG6-MUT, E2F5-WT, and E2F5-MUT) were generated by RiBo Biological Co. LTD. HEK293T cells were seeded into a 24-well plate and grew till 80% confluence. Cells were then co-transfected with 100 ng luciferase reporters and 50 nM miR-181a-5p mimics or controls using Lipofectamine 2000. After 48 hours of transfection, luciferase activities were measured with a Dual Luciferase Assay Kit (Promega) according to the manufacturer's instructions.

Western blot analysis

The antibodies used for Western blot were as follows: E2F5 (1:1,000, ab176017; Abcam, Cambridge, UK), GAPDH (1:1,000, #5174; Cell Signaling Technology [CST], Danvers, MA, USA), N-cadherin (1:1,000, #4061; CST), vimentin (1:1,000, #5741; CST), and E-cadherin (1:1,000, #3195; CST). Briefly, CRC cells were lysed using RIPA buffer (Thermo Fisher Scientific) to collect total protein. Protein concentration was measured by bicinchoninic acid method. A total of 40 μ g protein was subjected to Western blot by separating on a 10% SDS-PAGE gel and transferred to polyvinylidene fluoride membranes (Sigma-Aldrich). Membranes were first incubated with specific antibodies and then with goat anti-rabbit (1:5,000, ab6721; Abcam) or goat anti-mouse (1:5,000, ab6728; Abcam) secondary antibody and analyzed using an ECL kit (Amersham Pharmacia Biotech, Little Chalfont, UK) with an ImageQuant LAS 4000 Mini Biomolecular Imager (GE Healthcare). GAPDH was used as an internal reference. Western blot quantifications were performed using ImageJ software (NIH).

Flow cytometry for cell cycle and apoptosis

For cell cycle analysis, cells with indicated treatment were collected and fixed in 70% ice-cold ethanol at 4°C for 2 hours. Then, the cells were washed with PBS. After incubation with 0.2 mg/mL RNase A (Sigma-Aldrich) for 1 hour at 37°C, 2 µL propidium iodide (PI, Sigma-Aldrich) was added to the cells and incubated for another 30 minutes at room temperature. Cell cycle distribution was analyzed by a FACScan flow cytometer (Becton Dickinson, Franklin Lakes, NJ, USA). For apoptosis analysis, cells with the indicated treatments were harvested and washed once with PBS. Then, cells were resuspended in 100 µL binding buffer and incubated with 10 µg/mL Annexin V-fluorescein isothiocyanate and 10 µg/mL PI (both Sigma-Aldrich) at room temperature for 30 minutes. Apoptosis analysis was performed using a FACScan flow cytometer (Becton Dickinson).

Xenograft tumor formation assay *in vivo*

Four- to six-week-old BALB/c nude mice were used for the xenograft tumor formation assay. Twelve nude mice were randomly divided into three groups of equal size (four per group) including HCT116-sh-NC group, HCT116-shRNA1 group, and HCT116-shRNA2 group. Stable HCT116-sh-NC, HCT116-shRNA1, and HCT116-shRNA2 cells were screened by G418 at 400 µg/mL (Thermo Fisher Scientific). A total of 1×10^6 HCT116 cells stably transfected with SNHG6-NC, SNHG6-shRNA1, and SNHG6-shRNA2 were suspended in 100 µL PBS and subcutaneously injected into the posterior flank of nude mice. Tumor growth was measured every week for 4 weeks with a caliper. The tumor volume was calculated as $(\text{length} \times \text{width}^2)/2$. The xenograft tumor formation assay was approved by the Institutional Ethics Committee of Weifang People's Hospital. All experiments were performed following the Weifang People's Hospital and national guidelines and regulations.

Immunohistochemistry (IHC)

Xenograft tumor samples were fixed with 4% paraformaldehyde. Then, the samples were embedded in paraffin and cut into 4 µm sections. The sections were dewaxed and rinsed with absolute xylene and rehydrated with graded alcohol. After antigen retrieval and endogenous peroxidase activity blocking, the sections were blocked with 5% FBS–PBS solution for 15 minutes at room temperature. Then, the sections were incubated with primary antibody for E2F5 (1:100, ab176017; Abcam) or Ki67 (1:100, ab15580; Abcam) at 4°C overnight. On the next day, the slides were washed with 1X

PBS for three times and incubated with secondary antibody at room temperature for 15 minutes, followed by color development with diaminobenzidine. The cell nuclei were dyed with hematoxylin. Images were captured with a light microscope.

Statistical analyses

All statistical analyses were performed with SPSS version 20.0 software and GraphPad Prism 5.0. The data are presented as mean \pm SD from at least three independent experiments. The difference between two groups was analyzed by Student's *t*-test or a one-way ANOVA when needed. The clinicopathological features of CRC patients were analyzed using chi-squared test. The correlations between expressions were analyzed by Spearman test. Kaplan–Meier analysis and log-rank test were used for prognostic analyses. Univariate and multivariate Cox proportional hazards regression analyses were used to test for independent prognostic factors. All *P*-values were two-sided, and *P* < 0.05 was considered statistically significant.

Results

SNHG6 is upregulated in CRC tissues and cell lines

To investigate the relevance of SNHG6 in CRC development, we first examined SNHG6 expression in 141 paired CRC tissues and adjacent normal samples by qRT-PCR. Compared with normal tissues, SNHG6 was significantly upregulated in CRC tissues (Figure 1A). Next, SNHG6 expression was determined in two microarray datasets (GSE23878 and GSE9348) from Gene Expression Omnibus database. Consistently, SNHG6 expression was statistically increased in CRC tissues compared with normal samples, as confirmed by the two microarray datasets (Figure 1B and C). The transcription levels of SNHG6 were then detected in a panel of CRC cell lines (HT-29, HCT116, SW480, SW620, and CACO2) and a normal colorectal epithelial cell line, NCM460. As shown in Figure 1D, the expression levels of SNHG6 were higher in the malignant cell lines than that in NCM460 cells. FISH assay confirmed that the expression level of SNHG6 in HCT116 cells was higher than in NCM460 cells, and that SNHG6 was mainly localized in cytoplasm in the two cell lines (Figure 1E).

High SNHG6 expression is associated with poor prognosis in CRC

The 141 CRC patients enrolled in this study were divided into SNHG6 high (above the median, *n*=71) and SNHG6 low group (below the median, *n*=70) based on the median value

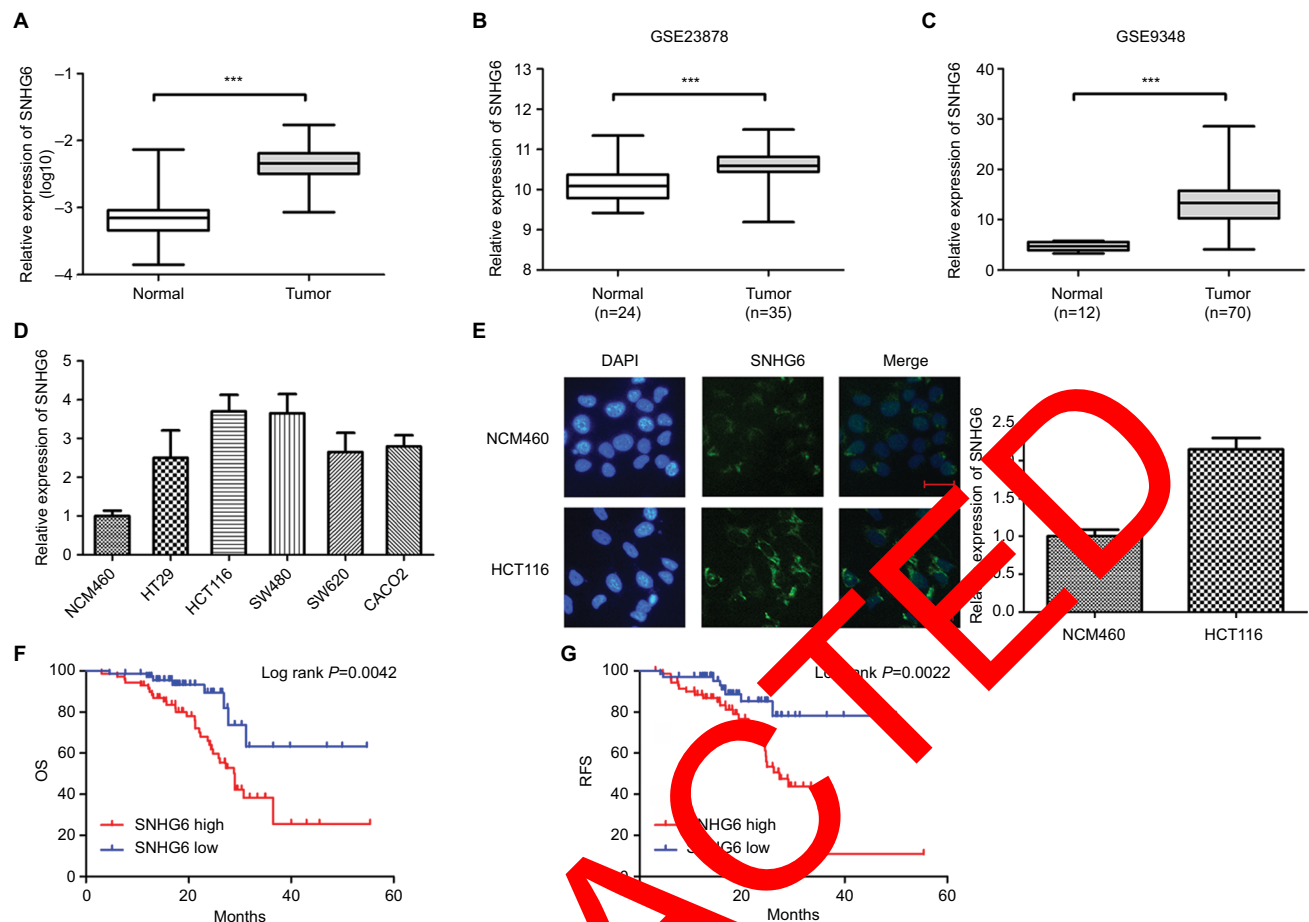


Figure 1 SNHG6 is overexpressed in CRC tissues and cell lines and associated with poor prognosis.

Notes: (A) The relative expression levels of SNHG6 to GAPDH as determined by qRT-PCR in 141 paired clinical CRC and normal tissues. CT values for GAPDH in normal tissues and tumor tissues were 21.3 ± 2.72 and 20.8 ± 3.14 , respectively. CT values are presented as mean \pm SD. (B and C) Expression levels of SNHG6 in CRC and normal tissues from GEO microarray datasets. (D) Expression levels of SNHG6 in a normal colorectal epithelial cell line (NCM460) and CRC cell lines (HT-29, HCT116, SW480, SW620, and CACO2). (E) Representative FISH images showing SNHG6 expression in NCM460 and HCT116 cells. Scale bars = 50 μm. The relative expression of SNHG6 (fluorescent intensity and area) was determined using ImageJ software. Kaplan-Meier analysis and log-rank test were used to analyze the association between SNHG6 expression and (F) OS and (G) RFS in 141 CRC patients. Patients were divided into SNHG6 high and SNHG6 low groups by median value of SNHG6 expression. *** $P < 0.001$. **Abbreviations:** CRC, colorectal cancer; CT, cycle threshold; FISH, fluorescence in situ hybridization; GEO, Gene Expression Omnibus; OS, overall survival; qRT-PCR, quantitative real-time PCR; RFS, relapse-free survival.

of SNHG6 expression to evaluate the correlation between SNHG6 expression and clinicopathological features. The results showed that high expression of SNHG6 was observed more frequently in CRC patients with a large tumor size ($T > 5$ cm, $P < 0.001$), advanced TNM stage (III and IV, $P = 0.002$), and positive distant metastasis ($P = 0.017$), but there was no significant correlation of SNHG6 with age, gender, tumor location, lymphatic invasion, and venous invasion (Table 1). Furthermore, Kaplan-Meier analysis and log-rank test indicated that high expression of SNHG6 was significantly associated with shorter overall survival (OS, $P = 0.004$) and relapse-free survival (RFS, $P = 0.002$) in CRC patients (Figure 1F and G). In addition, the prognostic values of SNHG6 were evaluated by multivariate Cox proportional hazards regression analyses. The results indicated that SNHG6 was an independent prognostic factor

of worse OS (HR = 2.83, 95% CI: 1.20–8.36, $P = 0.018$; Table 2) and RFS (HR = 2.07, 95% CI: 1.17–6.20, $P = 0.020$; Table 3).

Knockdown of SNHG6 inhibits CRC cell proliferation and tumor growth

HCT116 and SW480 cell lines, which expressed relatively high SNHG6 levels, were chosen to investigate the potential roles of SNHG6 in CRC. The SNHG6 expression was effectively silenced by two shRNAs (shRNA1 and shRNA2) targeting SNHG6 in HCT116 and SW480 cells (Figure 2A). Subsequently, the impact of SNHG6 silencing on cell proliferation was examined. As shown in Figure 2B, knockdown of SNHG6 significantly inhibited proliferation. Colony formation assay showed that the numbers of colonies were dramatically decreased by SNHG6 shRNA1 and shRNA2

(Figure 2C). To investigate the role of SNHG6 in tumorigenesis *in vivo*, we injected HCT116 cells stably transfected with SNHG6 shRNA1, shRNA2, and sh-NC into nude mice. The results showed that SNHG6 shRNA1 and shRNA2 significantly suppressed tumor growth compared with sh-NC (Figure 2D and E). The tumor size and weight in shRNA1 and shRNA2 groups were much lower than controls (Figure 2D and F). IHC results showed that the percentage of positive Ki67 cells in sh-NC group was much higher than in shRNA1 and shRNA2 groups (Figure 2G). Furthermore, the impact

of SNHG6 knockdown on cell cycle progression and apoptosis was detected by flow cytometry. SNHG6 knockdown significantly caused G0/G1 arrest and promoted apoptosis in HCT116 and SW480 cells (Figure 3A and B).

SNHG6 silencing represses CRC cell migration and invasion

Wound healing and transwell assays were performed to determine the effects of SNHG6 depletion on CRC cell migration and invasion in HCT116 and SW480 cells. As shown in Figure 4A and B, the wounds of CRC cells transfected with SNHG6 shRNA1 and shRNA2 healed much slower than controls, indicating that SNHG6 silencing inhibited CRC cell migration. Transwell invasion assays showed that SNHG6 knockdown significantly decreased the number of CRC cells invading through the transwell membrane (Figure 4C and D). EMT plays an essential role in migration and invasion.²⁰ Therefore, the EMT-related markers were detected by Western blot. SNHG6 knockdown significantly decreased the mesenchymal markers N-cadherin and vimentin, while it increased the epithelial marker E-cadherin (Figure 4E). Together, these results suggest that SNHG6 knockdown suppresses CRC cell migration and invasion possibly by regulating EMT.

SNHG6 is a target of miR-181a-5p

Recently, a growing number of lncRNAs have been reported to act as ceRNAs by sponging miRNAs and preventing them from binding functional mRNA targets.²¹ To investigate the underlying mechanisms of SNHG6 in CRC tumorigenesis, bioinformatics tool DIANA lncBase v.2 (22) was used to predict potential lncRNA-miRNA interaction for SNHG6. We identified that SNHG6 held a potential binding site for miR-181a-5p at the region of 173–197 amino acids (Figure 5A). Then, luciferase reporter assay was performed to confirm the bioinformatics prediction. We generated SNHG6 wild-type (SNHG6-WT) luciferase plasmid containing the target

Table 1 Correlation between SNHG6 expression and clinicopathological features in 141 CRC patients

Characteristics	Number of cases	SNHG6		
		Low (n)	High (n)	P-value
Age				
<60	45	23	22	0.858
≥60	96	47	49	
Gender				
Male	72	34	38	0.615
Female	69	36	33	
Tumor size				
≤5 cm	82	59	23	<0.001
>5 cm	69	21	48	
Tumor location				
Rectum	35	16	19	0.697
Colon	106	54	52	
Lymphatic invasion				
No	124	65	59	0.009
Yes	17	5	12	
TNM stage				
I/II	84	51	33	0.002
III/IV	57	19	38	
Distant metastasis				
No	131	69	62	0.017
Yes	10	1	9	
Venous invasion				
No	122	55	65	0.507
Yes	9	3	6	

Note: Bold values represent $P < 0.05$.

Abbreviation: CRC, colorectal cancer.

Table 2 Univariate and multivariate Cox proportional hazards regression analysis of SNHG6 for overall survival in CRC patients

Variants	Univariate analysis			Multivariate analysis		
	HR	95% CI	P-value	HR	95% CI	P-value
Age (≥60 vs <60)	0.90	0.46–1.75	0.755			
Gender (female vs male)	0.86	0.46–1.60	0.640			
Tumor location (rectum vs colon)	0.96	0.47–1.96	0.910			
Distant metastasis (yes vs no)	2.09	0.88–4.98	0.096			
Venous invasion (yes vs no)	1.28	0.40–4.16	0.680			
Tumor size (>5 cm vs ≤5 cm)	2.22	1.16–4.24	0.016	0.87	0.35–2.16	0.763
Lymphatic invasion (yes vs no)	3.81	1.78–8.13	0.001	1.85	0.83–4.12	0.130
TNM stage (III/IV vs I/II)	2.33	1.24–4.36	0.009	3.71	1.65–8.36	0.029
SNHG6 (high vs low)	3.14	1.44–6.83	0.004	2.83	1.20–6.36	0.018

Note: Bold values represent $P < 0.05$.

Abbreviation: CRC, colorectal cancer.

site of miR-181a-5p and SNHG6 mutant (SNHG6-MUT) luciferase plasmid (Figure 5A). As shown in Figure 5B, miR-181a-5p mimics significantly reduced the luciferase activity of SNHG6-WT but not SNHG6-MUT. To further investigate

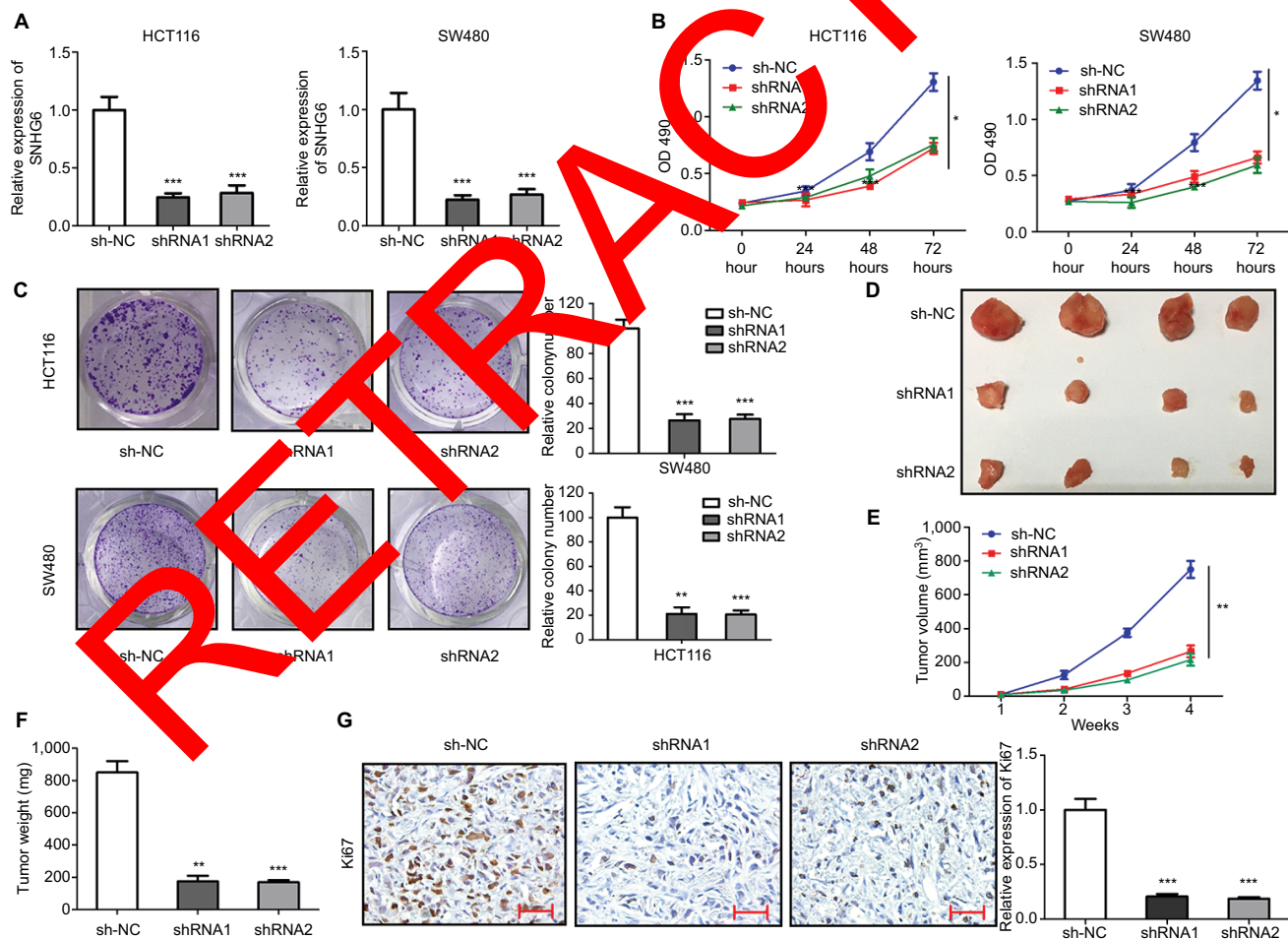
the interaction of SNHG6 and miR-181a-5p, we determined the effect of SNHG6 knockdown on miR-181a-5p expression. The results showed that SNHG6 knockdown increased miR-181a-5p expression in HCT116 and SW480 cells (Figure 5C).

Table 3 Univariate and multivariate Cox proportional hazards regression analysis of SNHG6 for relapse-free survival in CRC patients

Variants	Univariate analysis			Multivariate analysis		
	HR	95% CI	P-value	HR	95% CI	P-value
Age (≥ 60 vs <60)	1.43	0.69–2.95	0.340			
Gender (female vs male)	0.88	0.46–1.69	0.700			
Tumor location (rectum vs colon)	0.90	0.43–1.91	0.790			
Distant metastasis (yes vs no)	1.97	0.76–5.08	0.161			
Venous invasion (yes vs no)	1.11	0.27–4.64	0.889			
Tumor size (>5 cm vs ≤ 5 cm)	2.07	1.06–4.05	0.034	1.0	0–2.36	0.820
Lymphatic invasion (yes vs no)	5.20	2.35–11.52	0.000	2.23	1.77–2.80	0.001
TNM stage (III/IV vs I/II)	1.72	0.90–3.28	0.103			
SNHG6 (high vs low)	3.18	1.45–6.98	0.004	2.10	1.05–4.20	0.020

Note: Bold values represent $P < 0.05$.

Abbreviations: CRC, colorectal cancer; RFS, relapse-free survival.



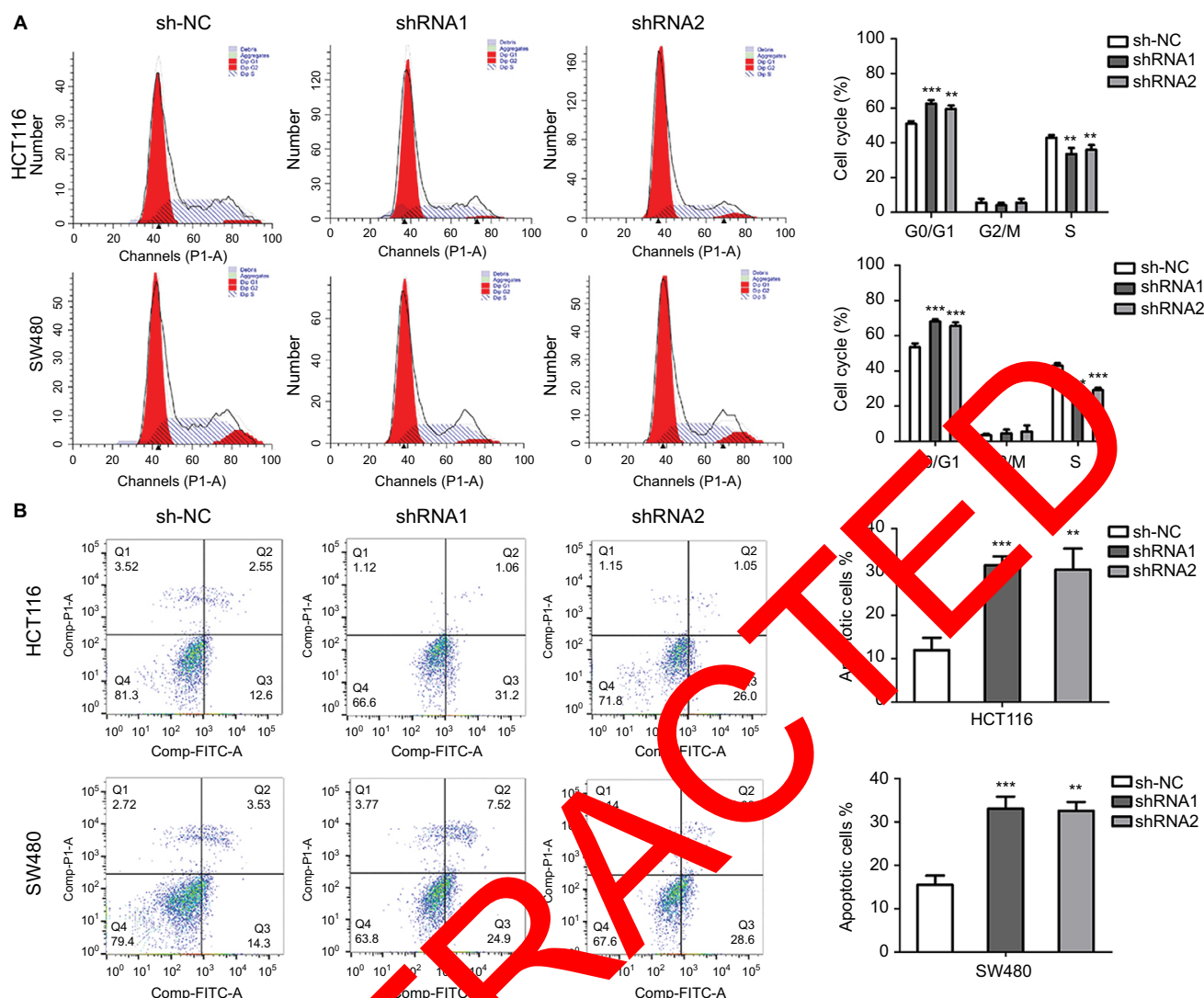


Figure 3 Knockdown of SNHG6 induces CRC cell cycle arrest and promotes cell apoptosis.

Notes: (A) Flow cytometric analysis of the cell cycle progression at 48 hours after transfection of sh-NC, shRNA1, and shRNA2 in HCT116 and SW480 cells. The percentages of cells in G0/G1, S, and G2/M phases are shown. ** $P < 0.01$ and *** $P < 0.001$. (B) Flow cytometric analysis of the cell apoptosis at 48 hours after transfection of sh-NC, shRNA1, and shRNA2 in HCT116 and SW480 cells. ** $P < 0.01$ and *** $P < 0.001$.

Abbreviation: CRC, colorectal cancer.

Moreover, the expression of miR-181a-5p in SNHG6 shRNA1 and shRNA2 xenograft tumors was significantly upregulated compared with sh-NC group (Figure 5D). Meanwhile, miR-181a-5p mimics obviously reduced SNHG6 expression (Figure 5E), and miR-181a-5p inhibitors increased SNHG6 expression (Figure 5F). Then, the expression of miR-181a-5p was detected in CRC cell lines (HT-29, HCT116, SW480, SW620, and CACO2) and NCM460 cells. As shown in Figure 5G, the expression levels of miR-181a-5p were significantly lower in the CRC cell lines than in NCM460 cells. In addition, we found that there was a strongly negative correlation between SNHG6 and miR-181a-5p expression in CRC tissues ($r = -0.37$, $P < 0.001$; Figure 5H). Finally, we investigated whether SNHG6

knockdown inhibited CRC cell proliferation by miR-181a-5p increase. MTT assays showed that miR-181a-5p mimics significantly inhibited cell proliferation, while miR-181a-5p inhibitors significantly promoted the proliferation of HCT116 and SW480 cells (Figure 5I). Furthermore, miR-181a-5p knockdown could effectively reverse the inhibition of cell proliferation caused by SNHG6 silencing (Figure 5J).

SNHG6 regulates CRC cell proliferation via miR-181a-5p/E2F5 axis

TargetScan 7.1 (http://www.targetscan.org/vert_71/) was used to identify the potential targets of miR-181-5 p. There is a potential binding site of miR-181-5 p in E2F5 3'-UTR

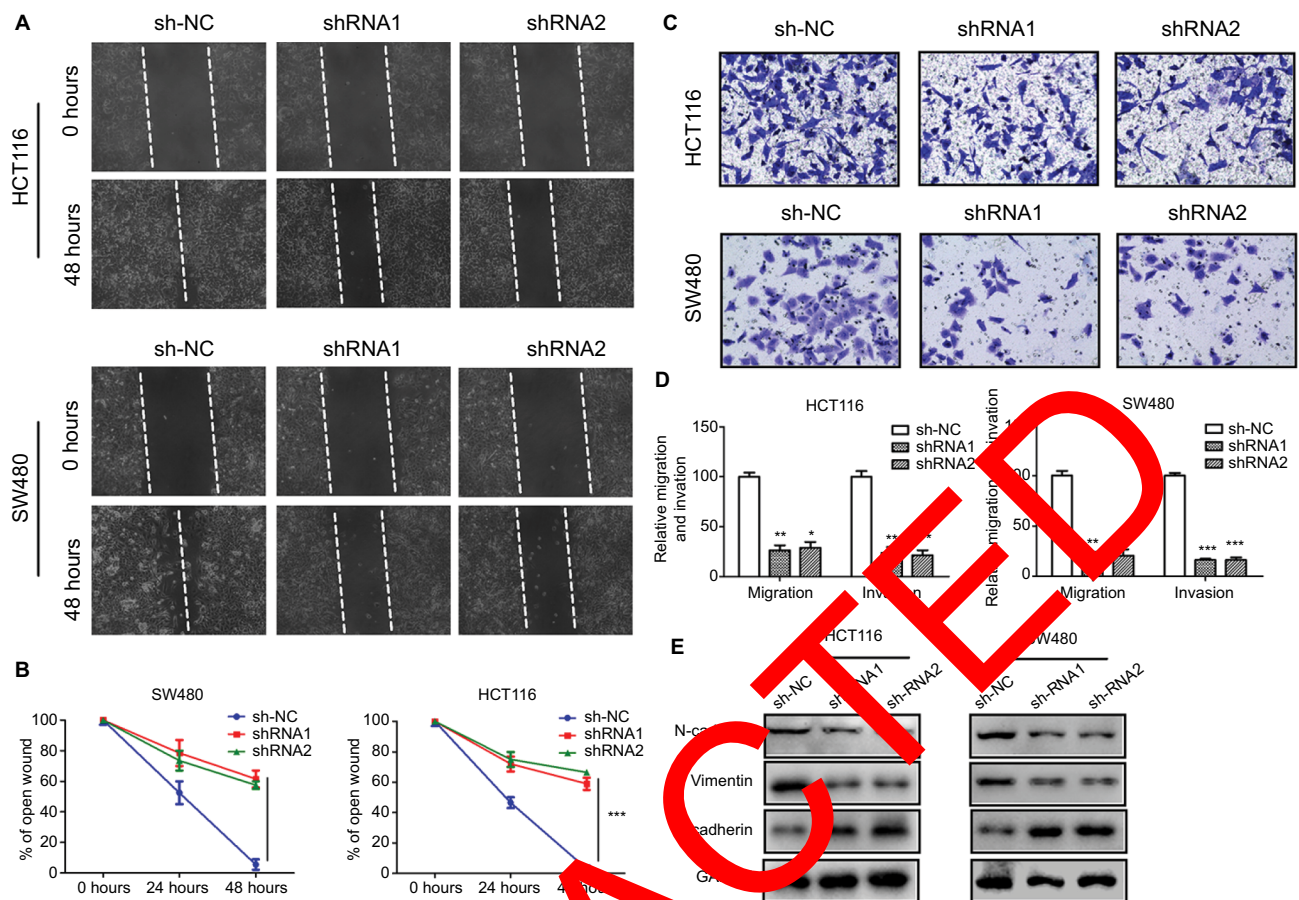


Figure 4 Knockdown of SNHG6 inhibits CRC cell migration and invasion.

Notes: (A) The migration of HCT116 and SW480 cells was examined by wound healing assays. Photographs were captured at 0, 24, and 48 hours. (B) The ratio of wound healing was calculated. $**P<0.01$ and $***P<0.001$. (C) The invasion of HCT116 and SW480 cells was examined by transwell assays. Representative images were taken at 24 hours after seeding. (D) The relative numbers of invaded cells in each group. Data are shown as mean \pm SD. $*P<0.05$, $**P<0.01$, and $***P<0.001$. (E) The protein expression levels of N-cadherin, E-cadherin, and vimentin were detected by Western blot.

Abbreviation: CRC, colorectal cancer.

(Figure 6A). To confirm this prediction, luciferase reporter plasmids of E2F5 3'-UTR wild type and mutant were constructed (Figure 6B). Luciferase reporter assay showed that overexpression of miR-181a-5p significantly inhibited luciferase activity of E2F5 3'-UTR wild type but not E2F5 3'-UTR mutant (Figure 6C). Additionally, overexpression of miR-181a-5p remarkably reduced both mRNA and protein expression levels of E2F5 (Figure 6C and D).

To investigate whether SNHG6 regulated E2F5 via miR-181a-5p, we first detected the relationship between SNHG6 and E2F5 expression in clinical CRC tissues. As shown in Figure 6E, SNHG6 expression was positively correlated with E2F5 ($r=0.52$, $P<0.001$). Knockdown of SNHG6 significantly decreased the mRNA and protein expression levels of E2F5 (Figure 6F and G). Moreover, the expression levels of E2F5 in sh-NC xenograft tumors were significantly higher than in

SNHG6 shRNA1 and shRNA2 tumors (Figure 6H). Overexpression of SNHG6 with SNHG6 wild-type plasmids but not mutant could rescue E2F5 levels in stable SNHG6-knocked down HCT116 and SW480 cells (Figure 7A). Inhibition of miR-181a-5p could also reverse the reduced expression of E2F5 (Figure 7B). To determine whether SNHG6 knockdown inhibited CRC cell proliferation by miR-181a-5p/E2F5 axis, the effects of E2F5 on cell proliferation were determined. As shown in Figure 7C, E2F5 overexpression significantly increased HCT116 and SW480 cell proliferation. Furthermore, E2F5 overexpression could effectively reverse the inhibition of CRC cells proliferation induced by SNHG6 silencing (Figure 7D). Together, these results suggested that SNHG6 may regulate CRC cell proliferation by acting as a ceRNA sponging miR-181a-5p and diminishing miR-181a-5p-mediated repression of E2F5.

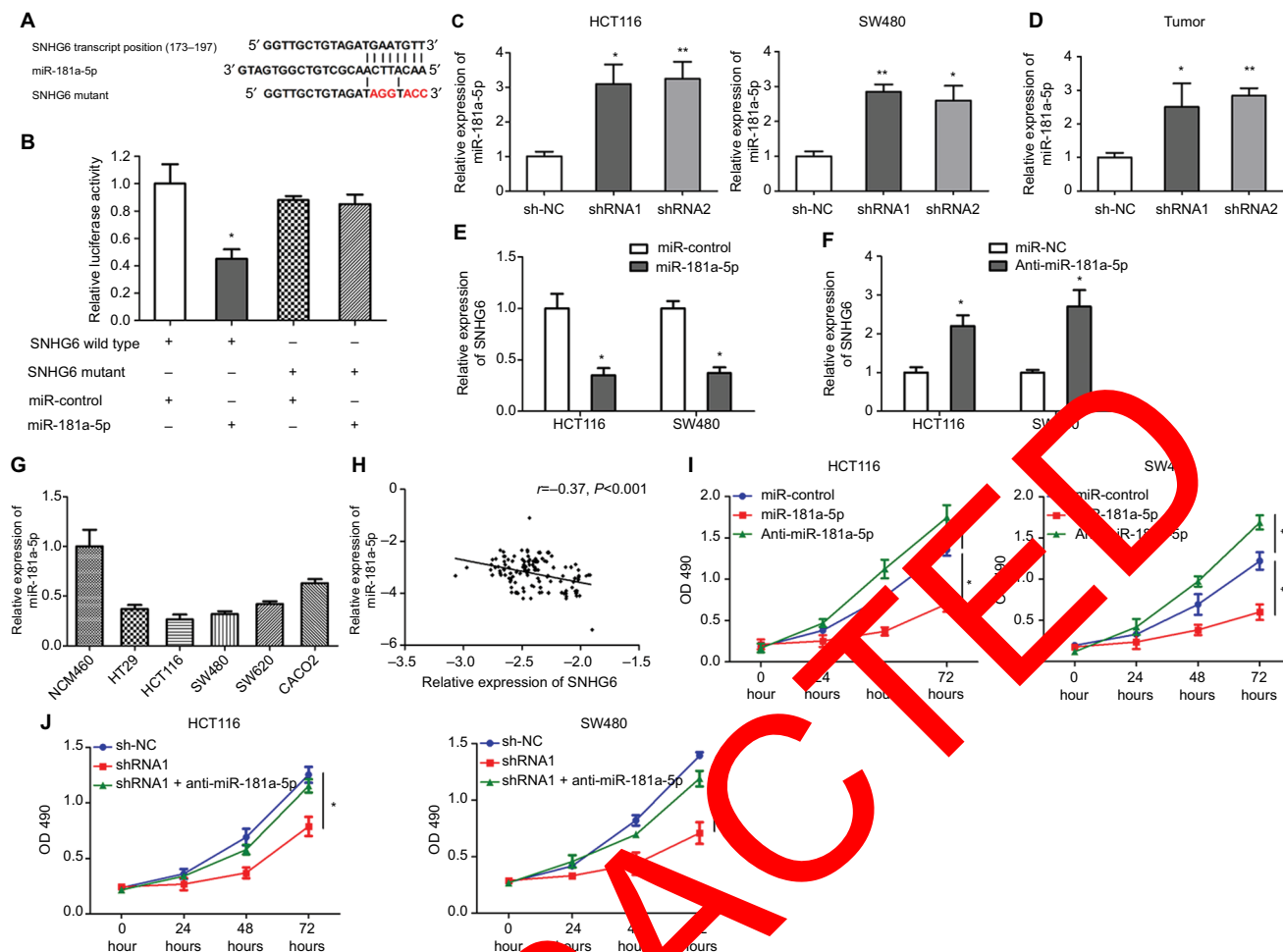


Figure 5 SNHG6 binds to miR-181a-5p.

Notes: (A) The predicted binding site of miR-181a-5p in SNHG6, and mutation of the binding sequence in SNHG6. (B) Luciferase activity assays in 293T cells co-transfected with miR-181a-5p mimics and the indicated SNHG6-WT or SNHG6-MT. (C) The expression of miR-181a-5p was examined by qRT-PCR in HCT116 and SW480 cells transfected with sh-NC or shRNA1 and shRNA2 targeting SNHG6. * $P < 0.05$ and ** $P < 0.01$. (D) The expression of miR-181a-5p was examined by qRT-PCR in SNHG6 sh-NC, shRNA1, and shRNA2 xenograft tumors. * $P < 0.05$ and ** $P < 0.01$. (E) The expression of SNHG6 was examined by qRT-PCR in HCT116 and SW480 cells transfected with miR-control or miR-181a-5p mimics. * $P < 0.05$ and ** $P < 0.01$. (F) The expression of SNHG6 was examined by qRT-PCR in HCT116 and SW480 cells transfected with miR-NC or miR-181a-5p inhibitors. * $P < 0.05$. (G) Expression levels of miR-181a-5p in normal colorectal epithelial cell line (NCM460) and CRC cell lines (HT-29, HCT116, SW480, SW620, and CACO2). (H) The correlation between SNHG6 and miR-181a-5p in 141 CRC tissues. (I and J) Cell proliferation was measured by MTT assays in HCT116 and SW480 cells transfected as indicated. * $P < 0.05$.

Abbreviations: CRC, colorectal cancer; qRT-PCR, quantitative real-time PCR.

Discussion

During the past years, numerous dysregulated lncRNAs have been proved to be implicated in the carcinogenesis and progression of different malignancies.^{4,5} Recently, it has been discovered that SNHG6 was upregulated in GC and HCC and associated with poor prognosis in cancer patients,^{14,15} providing a clue that there may be a potential correlation between SNHG6 and CRC development. In this study, we found that SNHG6 was significantly upregulated in CRC tissues compared with normal tissues, and this result was also confirmed by two microarray datasets. SNHG6 expression was closely correlated with tumor size, advanced TNM stage, and distant metastasis. Survival analysis showed that

high expression of SNHG6 was significantly associated with poor OS and RFS. Consistently, two recent studies with small number of cases also reported that SNHG6 was upregulated in CRC and high expression of SNHG6 predicted worse prognosis for CRC patients.^{17,18} More importantly, we found that SNHG6 was an independent prognostic factor for CRC patients by multivariate Cox proportional hazards regression analyses. Accordingly, these results indicated that SNHG6 might have an important role in CRC.

To further investigate the biological role of SNHG6 in CRC, RNA interference approaches were used to silence SNHG6 expression in two CRC cell lines HCT116 and SW480 expressing high levels of SNHG6. As a result,

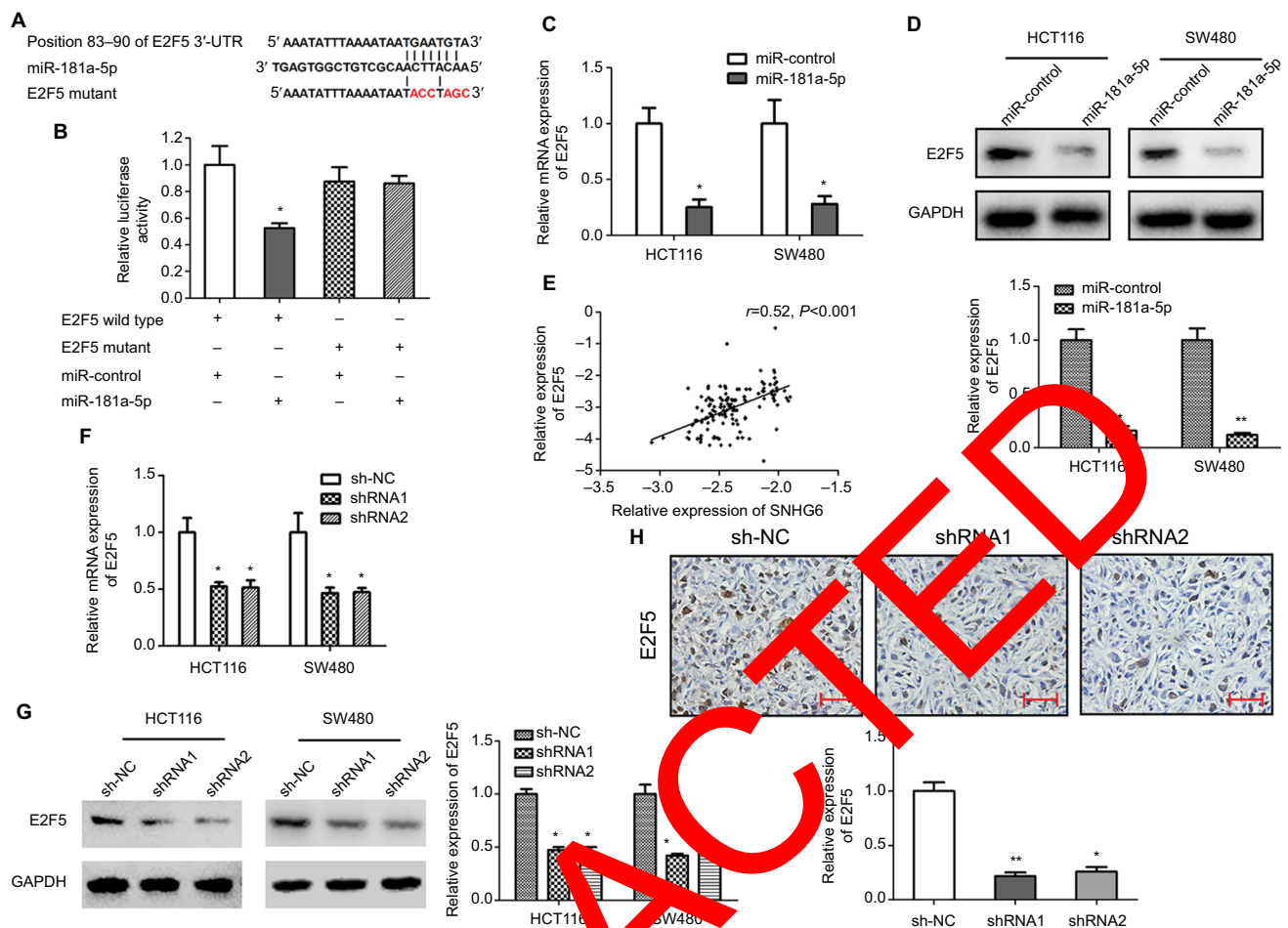


Figure 6 miR-181a-5p targets E2F5.

Notes: (A) The predicted binding site of miR-181a-5p on E2F5 3'-UTR, and mutation of the binding sequence in E2F5 3'-UTR. (B) Luciferase activity in 293T cells co-transfected with miR-181a-5p mimics and the indicated E2F5-WT or E2F5-MUT. * $P < 0.05$. (C) The mRNA expression of E2F5 was examined by qRT-PCR in HCT116 and SW480 cells transfected with miR-control or miR-181a-5p mimics. * $P < 0.05$. (D) The protein expression of E2F5 was examined by Western blot in HCT116 and SW480 cells transfected with miR-control or miR-181a-5p mimics. (E) The correlation between E2F5 and SNHG6 in 141 CRC tissues. (F) The mRNA expression of E2F5 was examined by qRT-PCR in HCT116 and SW480 cells transfected with sh-NC or shRNA1 and shRNA2 targeting SNHG6. * $P < 0.05$. (G) The protein expression of E2F5 was examined by Western blot in HCT116 and SW480 cells transfected with sh-NC or shRNA1 and shRNA2 targeting SNHG6. * $P < 0.05$. (H) Representative images of immunohistochemical staining for E2F5 in xenograft tumors. Scale bars = 50 μ m. * $P < 0.05$, ** $P < 0.01$.

Abbreviations: CRC, colorectal cancer; qRT-PCR, quantitative real-time PCR.

knockdown of SNHG6 significantly inhibited CRC cell proliferation, arrested cell cycle at G0/G1 phase, promoted cell apoptosis, and suppressed cell migration and invasion. In accordance with previous data,¹⁸ SNHG6 silencing could also significantly restrain tumor growth in vivo. It has been demonstrated that many lncRNAs could act as miRNA sponges to interact with various miRNAs and inhibit their posttranscriptional regulatory activities for target genes.^{8,23,24} As for SNHG6, evidence has also revealed that it could function as an endogenous decoy for miR-101-3 p and miR-26a/b to regulate the protein expression of ZEB1 and TAK1, respectively.^{14–16} To fully understand the underlying mechanisms of SNHG6 in CRC, we focused on the mechanism of SNHG6 as a ceRNA.

Bioinformatics analysis was applied to further determine whether SNHG6 could act as an endogenous sponge by targeting some other miRNAs and miR-181a-5p was identified to be a potential target of SNHG6. Consistent with our prediction, studies have shown that miR-181a-5p was particularly upregulated in several cancers, including CRC.^{25–27} Within CRC clinical tissues, we found that there was a negative correlation between the SNHG6 and miR-181a-5p expression. Moreover, luciferase assay demonstrated that miR-181a-5p mimics significantly reduced luciferase activity of SNHG6-WT but not SNHG6-MUT. SNHG6 silencing increased miR-181a-5p expression. Additionally, SNHG6 expression was also downregulated and upregulated by miR-181a-5p

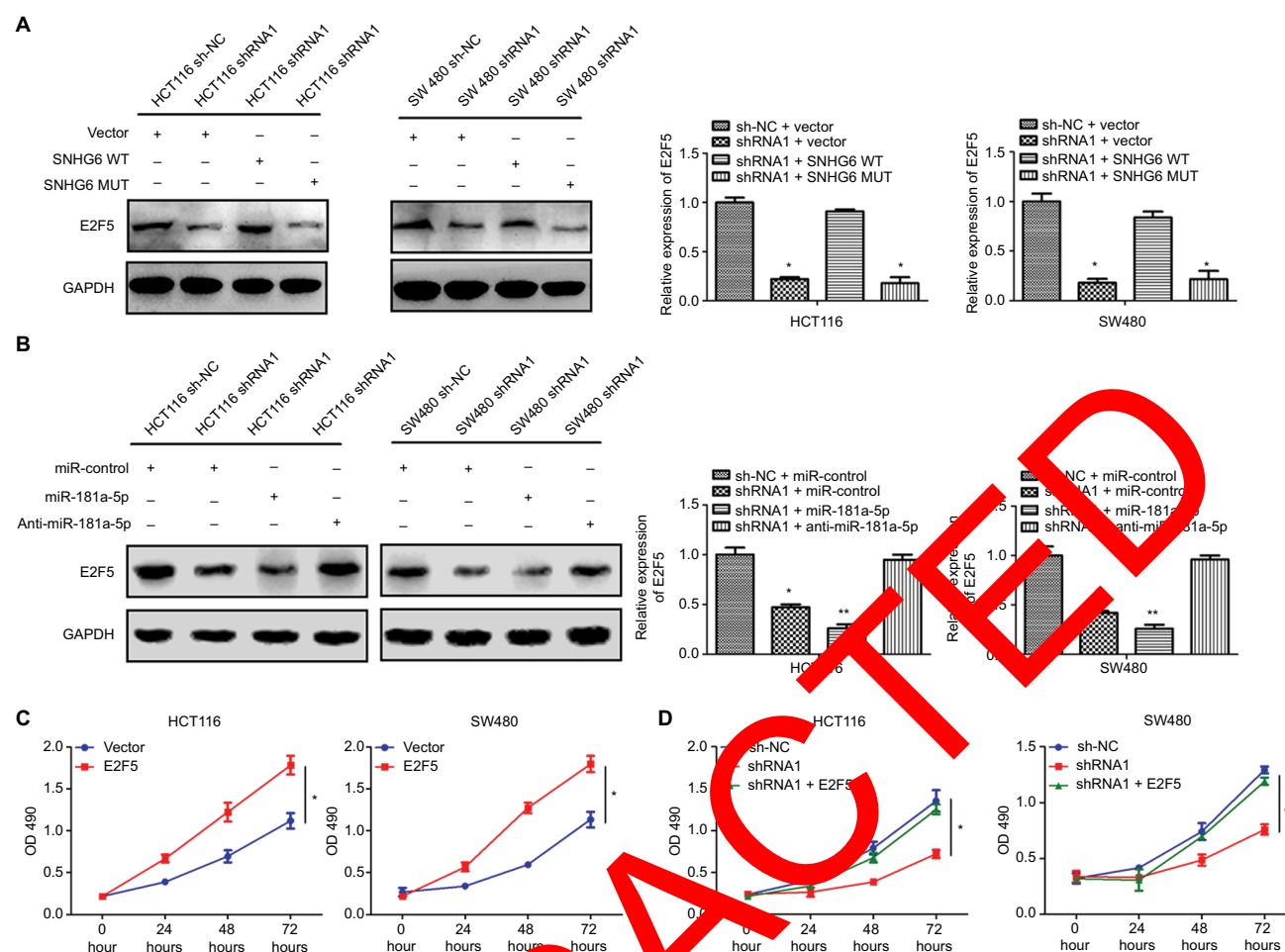


Figure 7 SNHG6 functions as a ceRNA by competitively sponging miR-181a-5p to regulate E2F5 expression.

Notes: (A) The protein expression of E2F5 was examined by Western blot in HCT116 and SW480 cells transfected as indicated. * $P < 0.05$ and ** $P < 0.01$. (B) The protein expression of E2F5 was examined by Western blot in HCT116 and SW480 cells transfected as indicated. * $P < 0.05$ and ** $P < 0.01$. (C) Cell proliferation was measured by MTT assays in HCT116 and SW480 cells transfected as indicated. * $P < 0.05$. (D) Cell proliferation was measured by MTT assays in HCT116 and SW480 cells transfected as indicated. * $P < 0.05$.

Abbreviation: ceRNA, competing endogenous

overexpression and knockdown, respectively. Furthermore, miR-181a-5p inhibition significantly reversed the suppression of cell proliferation caused by SNHG6 silencing. Together, these results strongly suggest that SNHG6 may serve as an endogenous sponge for miR-181a-5p.

On the other hand, bioinformatics analysis was performed to predict the target genes of miR-181a-5p. We identified that E2F5 was a potential target of miR-181a-5p. It has been reported that E2F5 was usually upregulated in different cancers and played important roles in multiple biological processes such as cell proliferation, cell cycle progression, and cell migration and invasion.^{28,29} Subsequently, we confirmed that E2F5 is a direct target of miR-181a-5p by luciferase assay. miR-181a-5p mimics could inhibit the luciferase activities of wild-type E2F5 3'-UTR, but had no effect on the activities of

the mutant E2F5 3'-UTR. In addition, both mRNA and protein expression levels of E2F5 were regulated by miR-181a-5p. Consistent with our observation, a previous study has demonstrated that E2F5 was a target of miR-181a-5p and involved in miR-181a-5p-mediated proliferation of HCC cells.³⁰ Therefore, we speculated that SNHG6 might function as a ceRNA to regulate E2F5 expression by sponging miR-181a-5p.

Then, we determined the relationship between SNHG6 and E2F5 expression. SNHG6 was positively correlated with E2F5 expression in CRC tissues. Moreover, SNHG6 knockdown decreased mRNA and protein levels of E2F5, while overexpressing SNHG6 in stable SNHG6-silenced cells could rescue E2F5 expression. Importantly, the effect of SNHG6 silencing on E2F5 expression could be enhanced by miR-181a-5p mimics and attenuated by miR-181a-5p inhibitors.

Finally, we overexpressed E2F5 in stable SNHG6-silenced CRC cells and found that the suppressed cell proliferation was significantly reversed. These results revealed that there may be a directly competitive correlation between SNHG6 and E2F5 for binding miR-181a-5p.

In summary, our study clarified that SNHG6 was upregulated in CRC tissues and cell lines and was significantly associated with poor OS and RFS in CRC patients. Knockdown of SNHG6 inhibited cell proliferation, arrested cell cycle at G0/G1 phase, promoted apoptosis, and suppressed cell migration and invasion in vitro, and attenuated tumor growth in vivo. More importantly, to the best of our knowledge, this is the first report to show that SNHG6 could function as a ceRNA by sponging miR-181a-5p to regulate E2F5 expression. Thus, our findings provide novel insights into the molecular mechanisms of SNHG6 in promoting CRC tumorigenesis and SNHG6 may serve as an independent prognostic indicator for clinical outcomes of CRC. Moreover, targeting SNHG6 is a promising therapeutic strategy for CRC.

Disclosure

The authors report no conflicts of interest in this work.

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