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ORIGINAL RESEARCH

RETRACTED ARTICLE: Long Noncoding RNA VPS9D1-AS1 Sequesters microRNA-525-5p to Promote the Oncogenicity of Colorectal Cancer Cells by Upregulating HMGA1

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Background: The long noncoding RNA VPS9D1 antisense RNA 1 (VPS9D1-AS1) has emerged as a critical regulator in non-small-cell lung, gastric, and prostate cancers. In this study, we measured the expression levels of VPS9D1-AS1 in colorectal cancer (CRC) and determined the role of VPS9D1-AS1 in regulating the biological activities of CRC cells. In addition, we thoroughly elucidated the molecular mechanism mediating the oncogenic activities of VPS9D1-AS1 in CRC.

Methods: The expression levels of VPS9D1-AS1 in CRC tissues and cell lines were detected via quantitative reverse transcription-polymerase chain reaction. Loss-of-function experiments were performed to detect the effects of VPS9D1-AS1 silencing on CRC cell proliferation, apoptosis, migration, and invasion as well as on tumor growth in vivo. Bioinformatics analysis predicted the potential microRNAs (miRNAs) interacting with VPS9D1-AS1, and this prediction was further confirmed via RNA immunoprecipitation and luciferase reporter assays.

Results: Our results demonstrated the upregulated expression of VPS9D1-AS1 in CRC tissues and cell lines. Functionally, VPS9D1-AS1 interference suppressed CRC cell proliferation, migration, and invasion and promoted cell apoptosis in vitro. In addition, the loss of VPS9D1-AS1 hindered tumor growth in vivo. Mechanistic studies identified VPS9D1-AS1 as a competing endogenous RNA in CRC cells, in which VPS9D1-AS1 acted as a molecular sponge of miR-525-5p and consequently increased the expression of high-mobility group AT-hook 1 (HMGA1). Moreover, rescue experiments revealed that the regulatory effects of VPS9D1-AS1 deficiency on CRC cells were abolished after miR-525-5p inhibition or HMGA1 restoration.

Conclusion: The newly identified competing endogenous RNA pathway involving VPS9D1-AS1, miR-525-5p, and HMGA1 is implicated in the control of CRC progression and may provide an effective target for CRC diagnosis and therapy.

Keywords: VPS9D1 antisense RNA 1, colorectal cancer, competing endogenous RNA model, therapeutic target

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Introduction

Colorectal cancer (CRC) is the third-most common malignant tumor and the second leading cause of cancer-related deaths worldwide.[1] Each year, CRC affects approximately 1.2 million patients and causes 860,000 deaths globally.[2] The treatment

regimens for CRC include surgical resection, radiotherapy, and chemotherapy, which have progressed in the last decade. However, the clinical treatment and long-term survival of patients with CRC remain unknown.[3,4] Tumor development, metastasis, and recurrence are the major contributors to CRC-related deaths; these processes are complex and largely unclear.[5,6] Unfortunately, approximately 25%–30% of patients are diagnosed at advanced stages mainly due to limited effective diagnostic techniques.[7] Accordingly, additional studies investigating CRC genesis and progression are of great significance for the identification of novel diagnostic and therapeutic targets.

Long noncoding RNAs (lncRNAs) have attracted great attention in recent years.[8] lncRNAs are a group of transcripts longer than 200 nucleotides with limited protein-coding ability.[9] lncRNAs function as guides, scaffolds, tethers, and decoys of other molecules and are implicated in the control of biological processes and pathological progression.[10] Many recent studies have reported that lncRNAs are differentially expressed in various human diseases, including cancer.[11–13] Regarding CRC, several lncRNAs have been reported to be dysregulated; these lncRNAs have been confirmed as important mediators in the oncogenesis and progression of CRC. lncRNAs may execute oncogenic or anti-oncogenic actions, thereby thus regulating tumor phenotypes in patients with CRC.[14,15]

microRNAs (miRNAs) are endogenous noncoding short RNA transcripts with a length of approximately 17–25 nucleotides.[16] They target the 3′-untranslated regions (3′-UTRs) of their target genes, resulting in transcriptional repression and mRNA degradation.[17] In particular, approximately one-third of human genes are predicted to be regulated by miRNAs.[18] In recent years, the proposed competing endogenous RNA (ceRNA) theory has received wide recognition.[19] Based on this theory, lncRNAs competitively bind and sequester certain miRNAs, consequently liberating miRNA target genes and increasing the levels of transcription and translation products.[20] Therefore, identifying tumor-associated lncRNAs in patients with CRC and exploring their detailed roles are considered useful strategies to discover promising targets for cancer diagnosis and management.

VPS9D1-AS1 has been reported to control the progression of non-small-cell lung,[21,22] gastric,[23] and prostate[24] cancers. However, the expression status and roles of VPS9D1-AS1 in CRC remain unknown. In this study, we determined the expression levels of VPS9D1-AS1 in CRC tissues and cell lines. In addition, we elucidated the roles of VPS9D1-AS1 in CRC cell proliferation, apoptosis, migration, and invasion using loss-of-function assays. Significantly, we thoroughly investigated the molecular mechanism mediating the oncogenic activities of VPS9D1-AS1 in CRC.

Materials and Methods

Tissue Collection and Cell Culture Conditions

Paired CRC tissues and adjacent non-tumor tissues were obtained from 61 patients with CRC at Jilin Cancer Hospital. These patients had not undergone any previous chemotherapy, radiotherapy, or other anticancer treatments. The collected fresh tissues were immediately snap-frozen in liquid nitrogen and then preserved in liquid nitrogen until use. Our current study was conducted under the approval of Jilin Cancer Hospital (2017.03–-0002) and performed following the Declaration of Helsinki. Furthermore, signed informed consent forms were provided by all participators.

The normal human colon epithelial cell line FHC and CRC cell line HCT116 were obtained from American Type Culture Collection (Manassas, VA, USA). Three additional CRC cell lines, namely HT29, SW480, and SW620, were all purchased from the Institute of Biochemistry and Cell Biology of the Chinese Academy of Sciences (Shanghai, China). DMEM:F12 medium (Gibco; Thermo Fisher Scientific Inc., Waltham, MA, USA) supplemented with 10% fetal bovine serum (FBS; Gibco; Thermo Fisher Scientific, Inc.) and a 1% antibiotic/antimycotic solution (Gibco; Thermo Fisher Scientific, Inc.) was used for FHC cell culture. The culture medium contained added supplements, including 25 mM HEPES, 10 ng/mL cholera toxin, 0.005 mg/mL insulin, 0.005 mg/mL transferrin, 100 ng/mL hydrocortisone, and 20 ng/mL human recombinant epidermal growth factor. HCT116 and HT29 cells were grown in McCoy's 5A medium (Gibco; Thermo Fisher Scientific, Inc.) containing 10% FBS and a 1% antibiotic/antimycotic solution. L-15 medium (Gibco; Thermo Fisher Scientific Inc.) was used to culture SW480 and SW620 cell lines, and the other culture conditions were the same as those used for HCT116 and HT29 cell lines. All cells were cultured at 37°C in a humidified incubator supplied with 5% CO_2 and 95% air.

Transfection

Small interfering RNAs (siRNAs) targeting VPS9D1-AS1 (si-VPS9D1-AS1) and negative control (NC) siRNA (si-NC) were obtained from GenePharma Technology (Shanghai,

China). miR-525-5p mimic and miR-525-5p inhibitor were synthesized by RiboBio Biotechnology (Guangzhou, China) and used to increase and decrease endogenous expression levels of miR-525-5p, respectively. miRNA mimic NC (miR-NC) and NC inhibitor were used as controls. The HMGA1 overexpression plasmid pcDNA3.1-HMGA1 and empty pcDNA3.1 plasmid were designed and generated by Genearray Biotechnology (Shanghai, China). Lipofectamine™ 2000 was used for all cell transfections according to the manufacturer's protocol.

Total RNA Isolation and Quantitative Reverse Transcription-Polymerase Chain Reaction (qRT-PCR)

The TRIzol® reagent (Beyotime; Shanghai, China) was used to isolate total RNA from cultured cells or tissue specimens. The quality and quantity of total RNA were examined via the NanoDrop 2000c spectrophotometer (Invitrogen; Thermo Fisher Scientific, Inc.). For the detection of VPS9D1-AS1 and HMGA1, the PrimeScript™ RT reagent Kit with gDNA Eraser (Takara, Dalian, China) was used to perform reverse transcription. Next, cDNA amplification was conducted using the TB Green Premix Ex Taq (Takara). The expression levels of VPS9D1-AS1 and HMGA1 were normalized to the level of glyceraldehyde 3-phosphate dehydrogenase (GAPDH).

Total RNA was used as a template for cDNA synthesis, which was performed using the MiR X miRNA First Strand Synthesis Kit (Takara), and miR-525-5p expression was quantified using the MiR X miRNA qRT-PCR TB Green® Kit (Takara). U6 snRNA served as the internal reference for miR-525-5p. The $2^{-\Delta\Delta Ct}$ method was used for calculating relative gene expression.

Isolation of Cytoplasmic/Nuclear Cell Fractions

CRC cells in the logarithmic growth period were harvested, and the cytoplasmic and nuclear fractions were separated using the Nuclear/Cytosol Fractionation Kit (Biovision, San Francisco, CA, USA). After total RNA extraction, qRT-PCR was performed to determine the expression levels of VPS9D1-AS1, U6, and GAPDH in each fraction. GAPDH and U6 were used as the cytoplasmic and nuclear internal references, respectively.

Cell Counting Kit-8 (CCK-8) Assay

Single-cell suspensions were prepared at 24 h after transfection, and the cell concentration was adjusted to 2×10^4 cell/mL. Each well of 96-well plates was covered with a 100-μL cell suspension, and cells were cultured for 0, 24, 48, and 72 h. At the indicated time points, 10 μL of CCK-8 reagent (Beyotime) was added into each well and incubated for 2 h at 37°C. Finally, the absorbance was measured at 450 nm using an automatic microplate reader (BioTek, Winooski, VT, USA).

Flow Cytometry

Transfected cells cultured in 6-well plates were collected at 48 h post-transfection and then washed two times with phosphate-buffered saline. Cell apoptosis was measured using the Annexin V-FITC Apoptosis Detection Kit (Beyotime). Briefly, transfected cells were centrifuged, the supernatant was removed, and the cells were resuspended in 195 μL of 1× binding buffer. Next, 5 μL of annexin V-FITC and 10 μL of propidium iodide were added to the cell suspension and the cells were incubated in the dark for 20 min. The apoptosis rate of the cells was analyzed using the FACScan flow cytometer (BD Biosciences, San Jose, CA, USA).

Cell Migration and Invasion Assays

Forty-eight hours after transfection, cells were collected, washed twice with phosphate-buffered saline, and used in the cell migration assay. Following centrifugation, transfected cells were resuspended in FBS-free culture medium, and 1×10^5 cells were plated in the upper chamber (BD Biosciences). In the lower chambers, 500 μL of culture medium supplemented with 20% FBS was added. Twenty-four hours later, the migrated cells were stained with crystal violet (Beyotime) and extensively washed with phosphate-buffered saline. After drying, the stained cells were imaged using a light microscope (Olympus Corporation, Tokyo, Japan) Six randomly selected fields were analyzed. Cell invasion assays were conducted following the same steps, except that the chambers were pre-coated with Matrigel (BD Biosciences).

Xenograft Tumor Model

The short-hairpin RNA (shRNA) targeting VPS9D1-AS1 (sh-VPS9D1-AS1) and NC shRNA (sh-NC) were chemically synthesized by GenePharma Technology and inserted into the pGLVU6/GFP lentivirus plasmid. Next, the generated lentivirus plasmids and lentivirus packaging plasmids were transfected into HEK293T cells. After 3 days, the supernatants containing the sh-VPS9D1-AS1 or sh-NC lentivirus were harvested and used to infect SW480 cells.

The stably-transfected SW480 cells were selected using 0.5 μg/mL puromycin.

In vivo assays were approved by the Institutional Animal Care and Use Committees of Jilin Cancer Hospital (2019.04–1217) and were performed in accordance with the National Institutes of Health's Guide for the Care and Use of Laboratory Animals. Male BALB/c nude mice aged 4–6 weeks were obtained from the Shanghai Experimental Animal Center of the Chinese Academy of Sciences (Shanghai, China) and subcutaneously injected with 2×10^6 SW480 cells stably overexpressing sh-VPS9D1-AS1 or sh-NC. One week after cell injections, the width (W) and length (L) of tumor xenografts were recorded using a Vernier caliper every 4 days, and the volume was calculated using the following equation: volume = $(L \times W^2)/2$. Mice were euthanized 31 days after cell inoculation, and tumor xenografts were harvested for weight measurements.

Bioinformatics Analysis

The putative miRNA targets of VPS9D1-AS1 were predicted using StarBase 3.0 (http://starbase.sysu.edu.cn/) and miRDB (http://mirdb.org/). Three miRNA target prediction databases, namely TargetScan (http://www.targetscan.org/), miRDB, and StarBase 3.0, were used to find the potential targets of miR-525-5p.

RNA Immunoprecipitation (RIP) Assay

The Magna RIP RNA-Binding Protein Immunoprecipitation Kit (Millipore, Bedford, MA, USA) was used for RIP assays. CRC cells were treated with RIP lysis buffer, and the cell extracts were incubated with RIP immunoprecipitation buffer containing magnetic beads conjugated with a human anti-Argonaute2 (Ago2) antibody or normal mouse IgG (Millipore). Following overnight incubation at 4°C, the magnetic beads were harvested and the immunoprecipitated RNA was extracted and analyzed via qRT-PCR.

Luciferase Reporter Assay

The amplified VPS9D1-AS1 and HMGA1 3′-UTR fragments containing the miR-525-5p binding site were inserted into the pmirGLO Dual-Luciferase Reporter Vector (Promega, Madison, WI, USA) to generate wild-type-VPS9D1-AS1 (wt-VPS9D1-AS1) and wt-HMGA1, respectively. The Site-Directed Mutagenesis Kit (Agilent, Santa Clara, USA) was used to perform the site-directed mutation of miR-525-5p binding sites in VPS9D1-AS1 and HMGA1 3′-UTRs. Then, mutant-VPS9D1-AS1 (mut-VPS9D1-AS1) and mut-HMGA1 were synthesized by inserting mutated VPS9D1-AS1 and HMGA1 3′-UTR fragments into the pmirGLO Dual-Luciferase Reporter Vector.

For reporter assays, CRC cells were seeded into 24-well plates. One day later, the reporter plasmids mentioned above, together with miR-525-5p mimic or miR-NC, were cotransfected into CRC cells using Lipofectamine™ 2000. Following 48 h of incubation, transfected cells were collected and subjected to luciferase activity detection using the Dual-Luciferase Reporter System (Promega).

Protein Extraction and Western Blotting

Total protein was extracted from cultured cells using RIPA buffer (Beyotime) and quantified using the BCA Protein Assay Kit (Beyotime). Equivalent proteins were separated via 10% sodium dodecyl sulfate–polyacrylamide gel (SDS–PAGE) electrophoresis, after which the separated proteins were transferred onto polyvinylidene fluoride (PVDF) membranes. Then, the membranes were blocked with 5% nonfat milk powder diluted in TBS with Tween-20 and incubated with primary antibodies targeting HMGA1 (ab202070; Abcam, Cambridge, MA, USA) or GAPDH (ab128915; Abcam) overnight at 4°C. Next, the membranes were washed using TBS in Tween-20 thrice and incubated with an HRP-linked goat anti-rabbit secondary antibody (ab205718; Abcam) at room temperature for 2 h. The ECL Western Blotting Substrate Kit (ab65623; Abcam) was used to detect protein signals.

Statistical Analysis

All experiments were repeated three times. All results were expressed as the mean ± standard deviation (SD). The correlation between VPS9D1-AS1 and miR-525-5p expression was assessed using Pearson's correlation analysis. One-way analysis of variance combined with Tukey's test was used to determine the differences among multiple groups (≥3), whereas comparisons between two groups were analyzed using the Student's *t*-test. SPSS software 22.0 (SPSS, Chicago, IL, USA) was used for all statistical analyses, and statistical significance was set at $P < 0.05$.

Results

VPS9D1-AS1 Exerts Pro-Oncogenic Actions in CRC Cells

To uncover the roles of VPS9D1-AS1 in CRC cells, its expression was first analyzed in TCGA and GTEx

databases. The analysis indicated that VPS9D1-AS1 was highly expressed in both colon adenocarcinoma (COAD) and rectal adenocarcinoma (READ; Figure 1A). In addition, qRT-PCR was used to detect the expression levels of VPS9D1-AS1 61 pairs of CRC tissues and adjacent non-tumor tissues. The expression level of VPS9D1-AS1 was higher in CRC tissues than in adjacent non-tumor tissues (Figure 1B). Consistently, VPS9D1-AS1 was overexpressed in all tested CRC cell lines (HCT116, HT29, SW480, and SW620) compared with normal human colon epithelial cells (FHC) (Figure 1C). TCGA and GTEx databases were also used to determine the clinical relevance of VPS9D1-AS1 expression. However, no correlation was identified between VPS9D1-AS1 expression

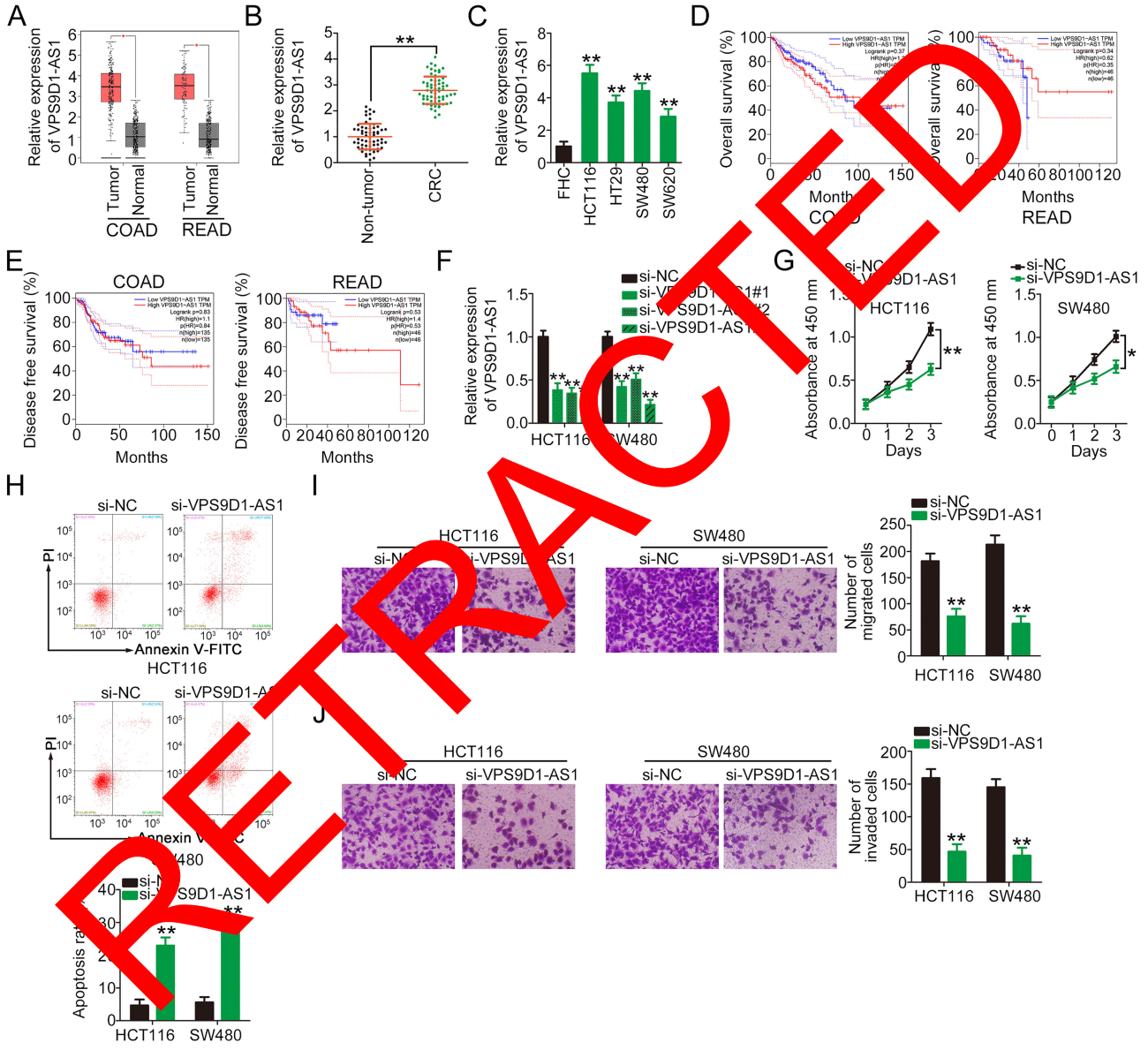

Figure 1 VPS9D1-AS1 depletion attenuates CRC cell proliferation, migration, and invasion and increases cell apoptosis in vitro. (**A**) TCGA and GTEx databases were analyzed to evaluate the expression profile of VPS9D1-AS1 in COAD and READ. (**B**) qRT-PCR analysis of the expression levels of VPS9D1-AS1 in 61 pairs of CRC tissues and adjacent non-tumor tissues. (**C**) qRT-PCR analysis of VPS9D1-AS1 in a panel of CRC cell lines. The normal human colon epithelium cell line FHC was used as a control. (**D, E**) TCGA and GTEx databases were used to analyze the correlation between VPS9D1-AS1 expression and overall survival or disease-free survival in patients with CRC. (**F**) qRT-PCR analysis of HCT116 and SW480 cells transfected with si-VPS9D1-AS1 or si-NC to determine transfection efficiency. (**G**) CCK-8 assays were performed to measure the proliferation of HCT116 and SW480 cells after VPS9D1-AS1 knockdown. (**H**) Flow cytometry assays were performed to test the effect of VPS9D1-AS1 downregulation on CRC cell apoptosis. (**I, J**) Cell migration and invasion assays were performed to determine the migratory and invasive abilities of VPS9D1-AS1-deficient HCT116 and SW480 cells. *P < 0.05 and **P < 0.01.

Abbreviations: COAD, colon adenocarcinoma; READ, rectum rectal adenocarcinoma; CRC, colorectal cancer; VPS9D1-AS1, VPS9D1 antisense RNA 1; si-VPS9D1-AS1, small interfering RNA targeting VPS9D1-AS1; si-NC, negative control small interfering RNA; PI, propidium iodide.

and overall survival (Figure 1D) or disease-free survival (Figure 1E) in patients with CRC.

Next, siRNAs specifically targeting VPS9D1-AS1 (si-VPS9D1-AS1) were used to reduce VPS9D1-AS1 expression in HCT116 and SW480 cells. si-VPS9D1-AS1#3 showed the highest efficiency in silencing VPS9D1-AS1 expression and was selected for further experiments (Figure 1F). CCK-8 assay results revealed that the downregulation of VPS9D1-AS1 evidently suppressed the proliferation of HCT116 and SW480 cells compared with the si-NC group (Figure 1G). Furthermore, transfection with si-VPS9D1-AS1 increased the apoptosis of HCT116 and SW480 cells (Figure 1H). In addition, the effects of VPS9D1-AS1 silencing on the migration and invasion of CRC cells were tested via cell migration and invasion assays. The results showed that VPS9D1-AS1 knockdown impaired the migratory (Figure 1I) and invasive (Figure 1J) abilities of HCT116 and SW480 cells. These results suggest that VPS9D1-AS1 is upregulated in CRC and that it executes tumor-promoting actions during cancer progression.

VPS9D1-AS1 is a miR-525-5p Sponge in CRC Cells

To elucidate the potential mechanism by which VPS9D1-AS1 regulates CRC progression, the subcellular localization of VPS9D1-AS1 was first determined because the specific roles of lncRNAs depend on their subcellular distribution.[25] By isolating cytoplasmic and nuclear cell fractions, VPS9D1-AS1 was found to be mainly enriched in the cytoplasm of HCT116 and SW480 cells (Figure 2A). lncRNAs located in the cytoplasm can operate as ceRNAs by sequestering certain miRNAs and subsequently increasing the expression of their target mRNAs.[26] Therefore, the bioinformatics online tools StarBase 3.0 and miRDB were used to identify the putative miRNAs that may interact with VPS9D1-AS1. In total, six miRNAs, namely miR-331-3p, miR-520a-5p, miR-525-5p, miR-766-5p, miR-2355-5p, and miR-6816-5p, were predicted by both tools to have a high probability of binding to VPS9D1-AS1 (Figure 2B). Because miR-766-5p was previously reported to be upregulated and play an oncogenic role in CRC,[27] it was excluded from this study. qRT-PCR analysis revealed that miR-525-5p expression was markedly increased following the introduction of si-VPS9D1-AS1, whereas the other four miRNAs presented no change (Figure 2C). In tissue specimens from 61 patients with CRC, miR-525-5p expression was obviously reduced (Figure 2D) and inversely correlated with that of VPS9D1-AS1 (Figure 2E; $r = -0.6978$, $P < 0.0001$).

The VPS9D1-AS1 sequences containing the miR-525-5p binding site are shown in Figure 2F. The luciferase reporter assay was performed to determine whether miR-525-5p could bind to the predicted target sites within VPS9D1-AS1. The luciferase activity of the wt-VPS9D1-AS1 reporter plasmid was notably decreased in HCT116 and SW480 cells after miR-525-5p upregulation, whereas the luciferase activity of the mut-VPS9D1-AS1 reporter plasmid was unaffected (Figure 2G). Furthermore, RIP assay results showed that VPS9D1-AS1 and miR-525-5p were significantly enriched in Ago2-containing immunoprecipitated RNA isolated from HCT116 and SW480 cells (Figure 2H), indicating that Ago2 could directly bind to VPS9D1-AS1 and miR-525-5p in CRC cells. Taken together, our results suggest that VPS9D1-AS1 inhibits the expression of miR-525-5p in CRC cells by acting as a molecular sponge.

miR-525-5p Directly Targets HMGA1 in CRC Cells

The detailed roles of miR-525-5p in CRC cells remain poorly understood. To address this, miR-525-5p mimic was transfected into HCT116 and SW480 cells (Figure 3A), and its effects on CRC tumor biology were explored. CCK-8 assay and flow cytometry results showed that miR-525-5p upregulation inhibited proliferation (Figure 3B) and promoted apoptosis (Figure 3C) in both cell types. Furthermore, the migratory (Figure 3D) and invasive (Figure 3E) capacities of HCT116 and SW480 cells were obviously hindered by miR-525-5p mimic transfection, as demonstrated by cell migration and invasion assays.

miRNAs perform their roles in human cancers via the transcriptional regulation of their target genes.[28] Therefore, the potential candidates of miR-525-5p were predicted using TargetScan, miRDB, and StarBase 3.0. HMGA1 (Figure 4A) was selected as a candidate target for further investigation because of its known oncogenic roles in CRC tumorigenesis and development.[29–31] To verify whether miR-525-5p was capable of directly binding to the HMGA1 3′-UTR, wt-HMGA1 and mut-HMGA1 reporter plasmids were produced and cotransfected with miR-525-5p mimic or miR-NC into HCT116 and SW480 cells. Ectopic miR-525-5p expression efficiently reduced the luciferase activity of wt-HMGA1 in both cell types, whereas the luciferase activity of mut-HMGA1 was unchanged after

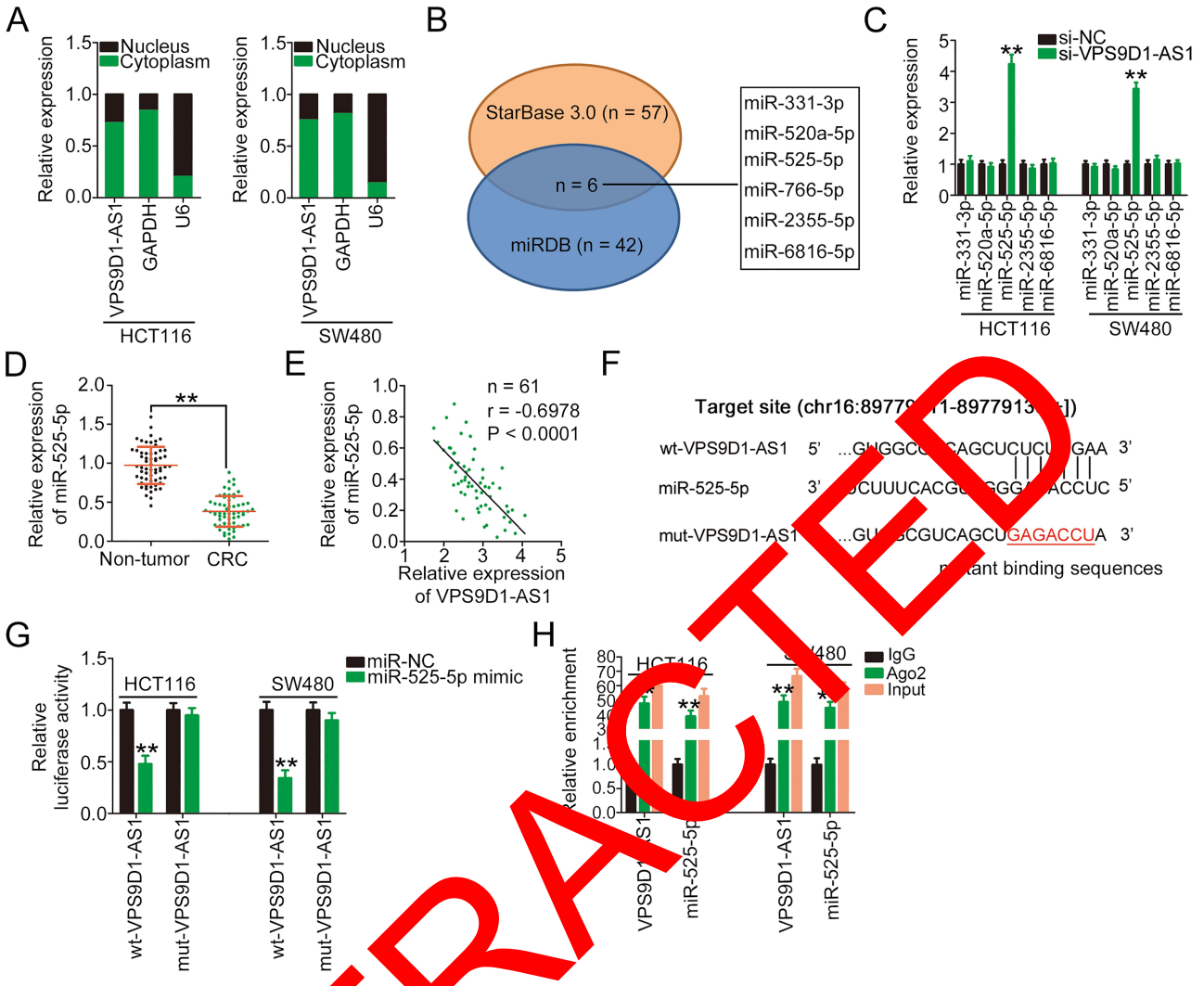

Figure 2 VPS9D1-AS1 functions as a miR-525-5p sponge in CRC cells. (**A**) The isolation of cytoplasmic/nuclear HCT116 and SW480 cell fractions was performed, followed by qRT-PCR to determine the subcellular location of VPS9D1-AS1. (**B**) Schematic illustration of the putative miRNAs interacting with VPS9D1-AS1. (**C**) qRT-PCR was performed to determine the relative expression levels of miR-331-3p, miR-520a-5p, miR-525-5p, miR-2355-5p, and miR-6816-5p in HCT116 and SW480 cells after VPS9D1-AS1 downregulation. (**D**) qRT-PCR was performed to determine miR-525-5p expression in 61 pairs of CRC tissues and adjacent non-tumor tissues. (**E**) Pearson's correlation analysis showed an inverse correlation between VPS9D1-AS1 and miR-525-5p expression in the 61 CRC tissues. (**F**) The wild-type and mutant binding sites of miR-525-5p in VPS9D1-AS1 were presented. (**G**) Luciferase activity of HCT116 and SW480 cells transfected with wt-VPS9D1-AS1 or mut-VPS9D1-AS1 and miR-525-5p mimic or miR-NC. (**H**) RIP assays followed by qRT-PCR analyses were conducted to test miR-525-5p and VPS9D1-AS1 enrichment in HCT116 and SW480 cells associated with Ago2. **P < 0.01.

Abbreviations: GAPDH, glyceraldehyde 3-phosphate dehydrogenase; U6, U6 small nuclear RNA; VPS9D1-AS1, VPS9D1 antisense RNA 1; si-VPS9D1-AS1, small interfering RNA targeting VPS9D1-AS1; si-NC, negative control small interfering RNA; miR-525-5p, microRNA-525-5p; wt, wild-type; mut, mutant; miR-NC, miRNA mimic negative control; Ago2, Argonaute 2; CRC, colorectal cancer.

miR-525-5p overexpression (Figure 4B). To explore whether miR-525-5p regulates HMGA1 expression, HMGA1 mRNA and protein levels were measured in miR-525-5p-overexpressing HCT116 and SW480 cells. The results revealed that miR-525-5p upregulation reduced the mRNA (Figure 4C) and protein (Figure 4D) levels of HMGA1 in HCT116 and SW480 cells. Furthermore, HMGA1 mRNA was highly expressed in CRC tissues (Figure 4E), and an inverse correlation was identified between HMGA1 mRNA and miR-525-5p expression in the 61 CRC tissues (Figure 4F; r = −0.6755, P < 0.0001). Collectively, our results suggest that miR-525-5p directly targets HMGA1 and exhibits anti-oncogenic roles in CRC cells.

VPS9D1-AS1 Facilitates the Oncogenicity of CRC Cells by Regulating the miR-525-5p/HMGA1 Axis

According to the ceRNA theory, lncRNAs can competitively bind to the miRNA response elements of specific miRNAs and thus increase target mRNA expression.[32] Accordingly, a series

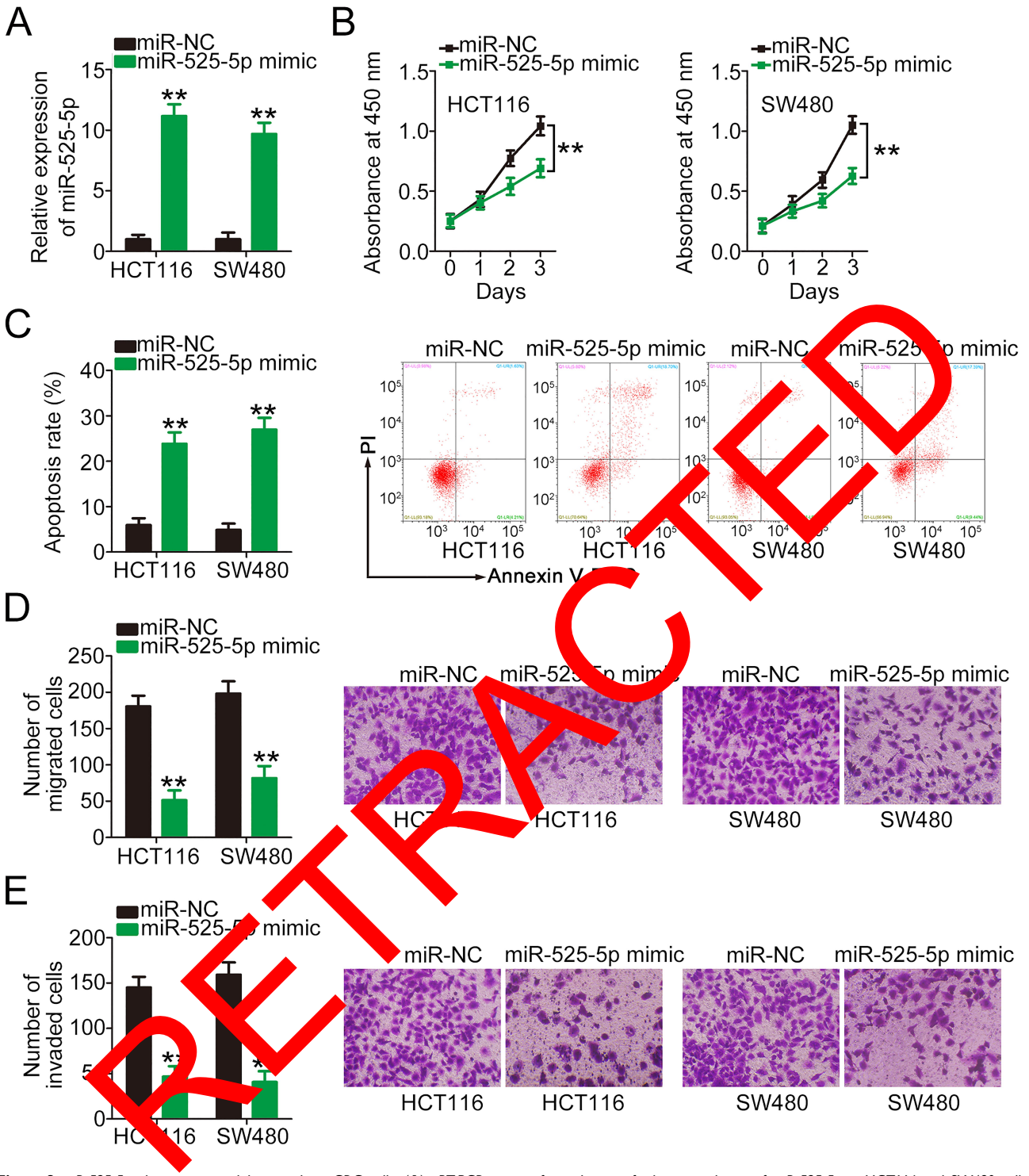

Figure 3 miR-525-5p plays a tumor-inhibiting role in CRC cells. (**A**) qRT-PCR was performed to verify the upregulation of miR-525-5p in HCT116 and SW480 cells transfected with miR-525-5p mimic. (**B, C**) CCK-8 and flow cytometry assays were performed to determine the effects of miR-525-5p overexpression on the proliferation and apoptosis of HCT116 and SW480 cells. (**D, E**) Cell migration and invasion assays were performed to detect the migration and invasion of miR-525-5p mimic-transfected or miR-NC-transfected HCT116 and SW480 cells. **P < 0.01.

Abbreviations: miR-525-5p, microRNA-525-5p; miR-NC, miRNA mimic negative control; PI, propidium iodide.

of experiments were designed to determine whether VPS9D1-AS1 regulates HMGA1 expression in CRC cells. VPS9D1-AS1 knockdown remarkably reduced the mRNA (Figure 5A) and protein (Figure 5B) expression levels of HMGA1 in HCT116 and SW480 cells. Importantly, Pearson's correlation analysis validated a positive correlation between HMGA1 mRNA and VPS9D1-AS1 expression in CRC tissues (Figure 5C; r = 0.6261, P < 0.0001). miR-525-5p inhibitor

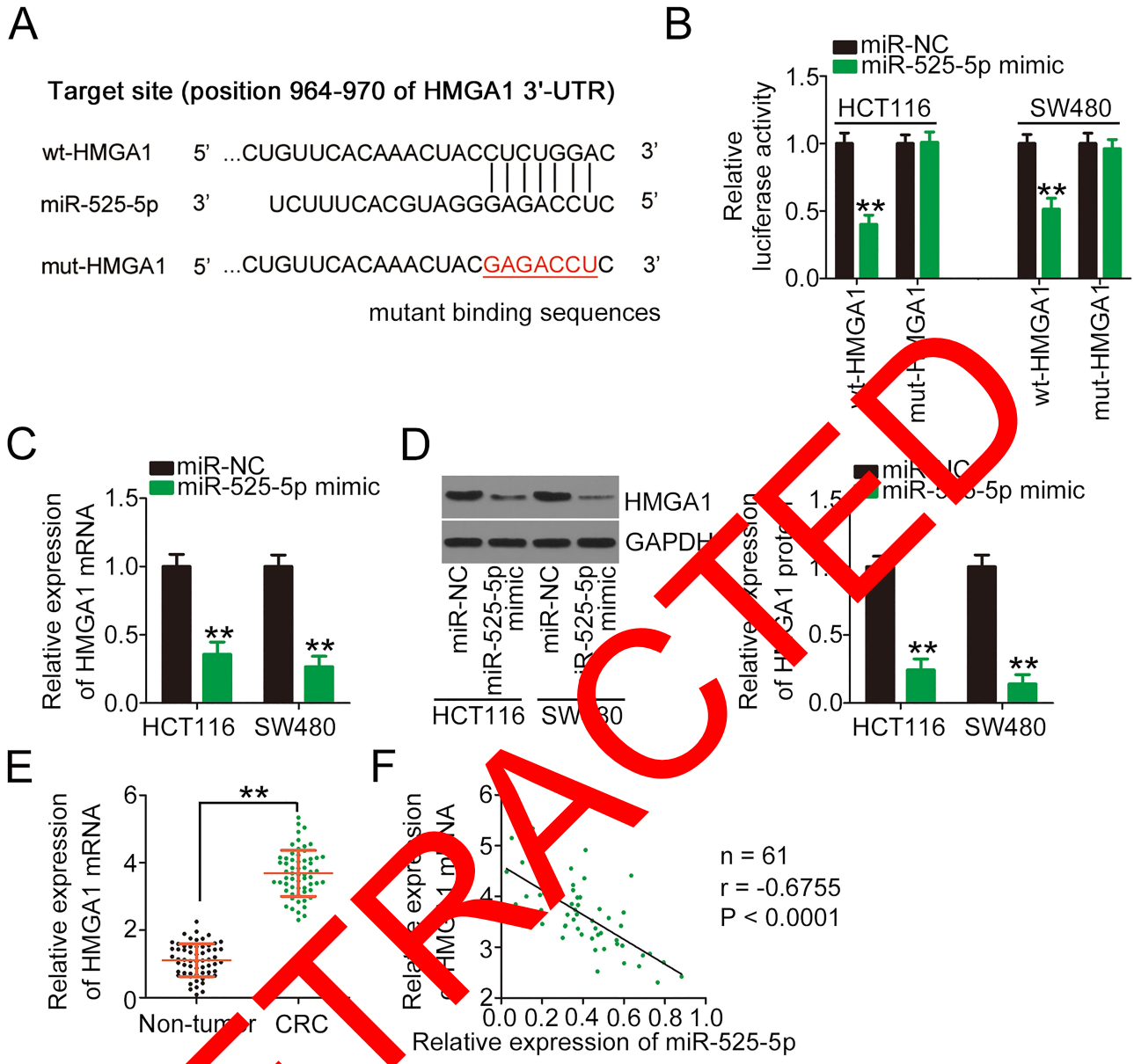

Figure 4 HMGA1 is a direct target of miR-525-5p in CRC cells. (**A**) Bioinformatics analysis predicted that the 3′-UTR of HMGA1 contains a miR-525-5p binding site; the mutated binding sequences were also shown. (**B**) Luciferase activity was determined in HCT116 and SW480 cells cotransfected with wt-HMGA1 or mut-HMGA1 and miR-525-5p mimic or NC. (**C, D**) qRT-PCR and Western blotting were performed to determine the mRNA and protein levels of HMGA1 in HCT116 and SW480 cells in the presence of miR-525-5p mimic or NC. (**E**) qRT-PCR was performed to determine the mRNA level of HMGA1 in 61 pairs of CRC tissues and adjacent non-tumor tissues. (**F**) Pearson's correlation analysis of experimental data presented an inverse correlation between the expression levels of miR-525-5p and HMGA1. **P < 0.01.
Abbreviations: HMGA1, high mobility group AT-hook 1; wt, wild-type; mut, mutant; miR-NC, miRNA mimic negative control; miR-525-5p, microRNA-525-5p; 3′-UTR, 3′-untranslated region; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; CRC, colorectal cancer.

was used in the following assays, and its efficiency in decreasing miR-525-5p expression was detected via qRT-PCR (Figure 5D). VPS9D1-AS1-silenced HCT116 and SW480 cells were further transfected with miR-525-5p inhibitor or NC inhibitor, and changes in the expression levels of miR-525-5p and HMGA1 were measured. As a result, loss of VPS9D1-AS1 substantially increased miR-525-5p expression in HCT116 and SW480 cells, whereas miR-525-5p inhibition counteracted this regulatory effect (Figure 5E). Additionally, cotransfection with miR-525-5p inhibitor restored the HMGA1 mRNA (Figure 5F) and protein (Figure 5G) levels that were decreased by VPS9D1-AS1 knockdown. Furthermore, the results of functional experiments demonstrated that the impacts of VPS9D1-AS1 deficiency on HCT116 and SW480 cell proliferation (Figure 5H), apoptosis (Figure 5I), migration (Figure 5J), and invasion (Figure 5K) were abolished after the introduction of the miR-525-5p inhibitor.

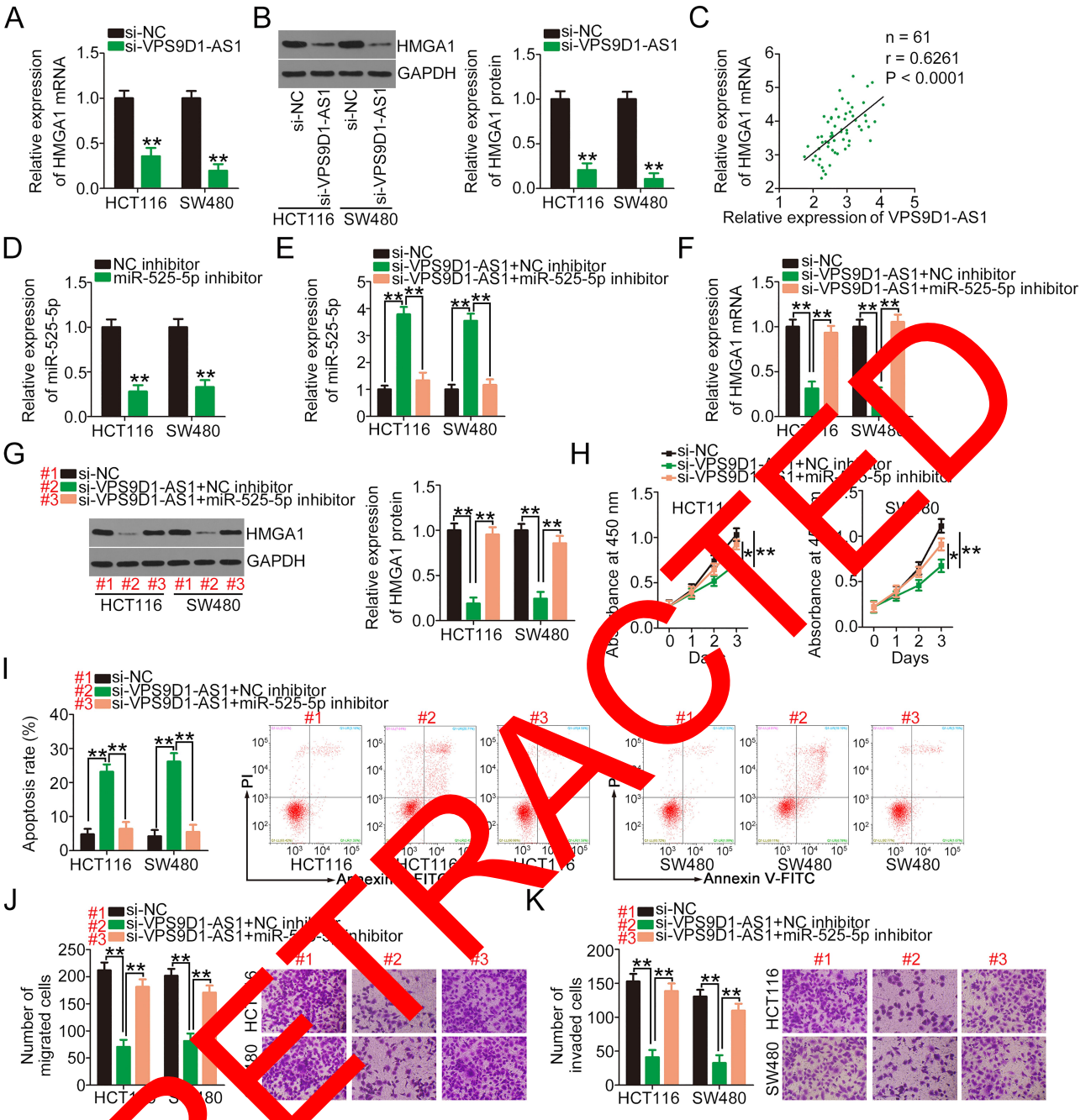

Figure 5 miR-525-5p inhibitor abolishes the inhibitory effects of VPS9D1-AS1 knockdown on CRC cells. (**A, B**) qRT-PCR and Western blotting were performed to detect the mRNA and protein expression of HMGA1 in VPS9D1-AS1-depleted HCT116 and SW480 cells. (**C**) The correlation between VPS9D1-AS1 and HMGA1 mRNA expression in CRC tissues was examined via Pearson's correlation analysis. (**D**) qRT-PCR was performed to determine the efficiency of miR-525-5p inhibitor in decreasing endogenous miR-525-5p expression in HCT116 and SW480 cells. (**E**) HCT116 and SW480 cells were transfected with miR-525-5p inhibitor or NC inhibitor in the presence of si-VPS9D1-AS1, and then changes in the expression of miR-525-5p was analyzed. (**F, G**) RT-qPCR and Western blotting were performed to determine the HMGA1 mRNA and protein levels in the aforementioned cells. (**H–K**) CCK-8, flow cytometry, migration, and invasion assays were conducted to determine the proliferation, apoptosis, migration, and invasion, respectively, of HCT116 and SW480 cells treated as described above. *P < 0.05 and **P < 0.01.

Abbreviations: HMGA1, high-mobility group AT-hook 1; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; CRC, colorectal cancer; VPS9D1-AS1, VPS9D1 antisense RNA 1; NC, negative control; miR-525-5p, microRNA-525-5p; si-VPS9D1-AS1, small interfering RNA targeting VPS9D1-AS1; si-NC, negative control small interfering RNA; PI, propidium iodide.

Subsequently, rescue experiments were performed to determine whether HMGA1 contributes to the actions of VPS9D1-AS1 in CRC cells. Western blotting analyses confirmed that transfection with pcDNA3.1-HMGA1 significantly increased the protein level of HMGA1 in HCT116 and SW480 cells (Figure 6A). Functionally, the ectopic expression of HMGA1 in VPS9D1-AS1-depleted HCT116 and SW480 cells clearly restored their cell

proliferation capacity (Figure 6B). Furthermore, flow cytometry analysis revealed that the introduction of pcDNA 3.1-HMGA1 abrogated the promotion of apoptosis induced by VPS9D1-AS1 silencing (Figure 6C). Cell migration and invasion assay results revealed that HMGA1 restoration rescued the inhibitory influences of VPS9D1-AS1 depletion on the migration (Figure 6D) and invasion (Figure 6E) of HCT116 and SW480 cells. In summary, the oncogenic roles of VPS9D1-AS1 in CRC cells are mediated by the miR-525-5p/HMGA1 axis.

VPS9D1-AS1 Interference Attenuates the Tumor Growth of CRC Cells in vivo

To test whether VPS9D1-AS1 controls CRC tumor growth in vivo, a xenograft model was established by subcutaneously injecting stable VPS9D1-AS1 knockdown SW480 cells into nude mice. The tumor volumes (Figure 7A and B) and weights (Figure 7C) of subcutaneous xenografts were strikingly reduced in the sh-VPS9D1-AS1 group compared with the sh-NC group. In addition, total RNA and protein were isolated from tumor xenografts and used for the detection of VPS9D1-AS1, miR-525-5p, and HMGA1 expression. qRT-PCR analysis indicated that VPS9D1-AS1 expression was obviously downregulated (Figure 7D), whereas miR-525-5p was upregulated (Figure 7E) in the sh-VPS9D1-AS1 group. Moreover, Western blotting results showed that the tumor xenografts developed from SW480 cells stably overexpressing sh-VPS9D1-AS1 exhibited decreased HMGA1 protein expression levels (Figure 7F). These results indicate that VPS9D1-AS1 promotes the tumor growth of CRC cells in vivo.

Discussion

With the advancement in sequencing technology in the last decade, an increasing number of lncRNAs have been

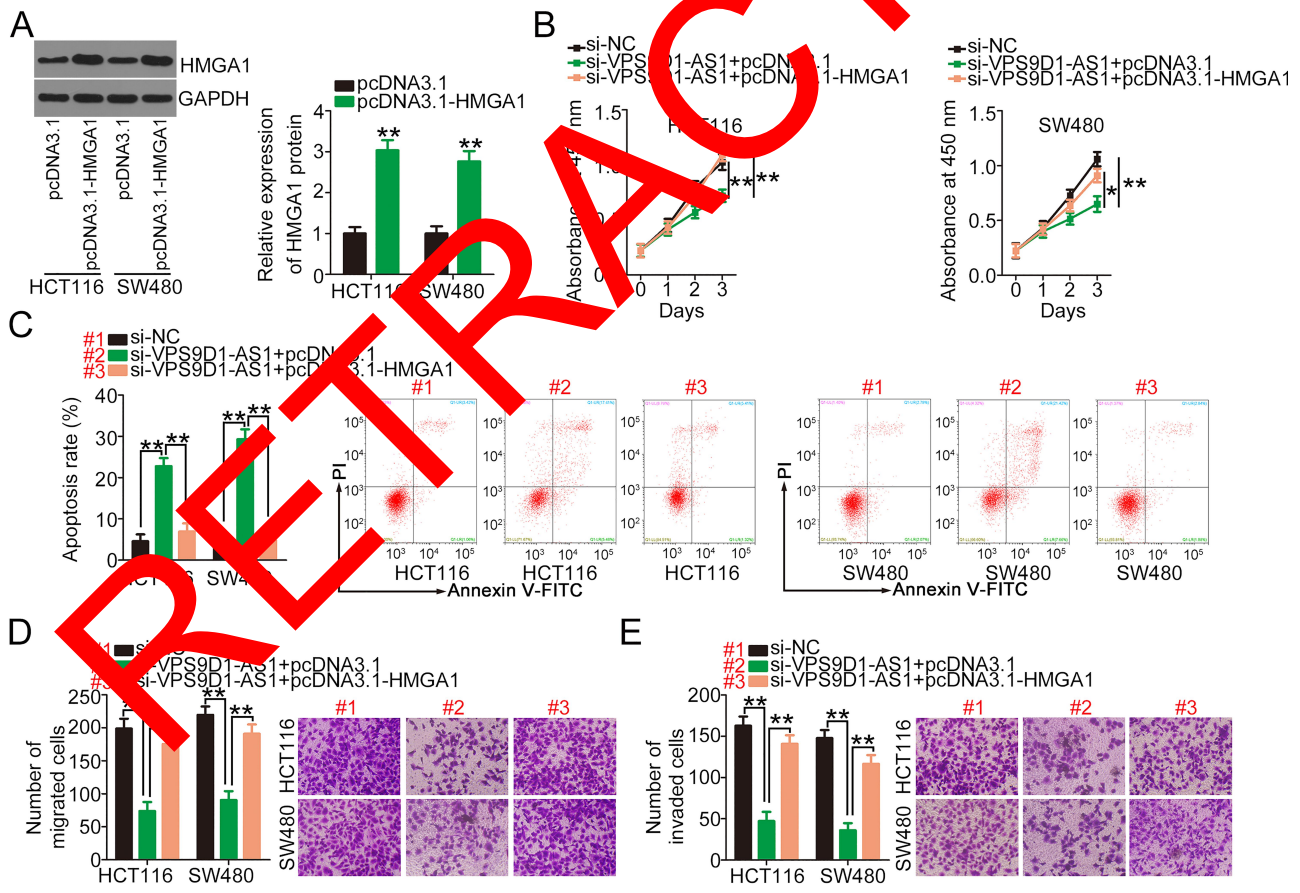

Figure 6 HMGA1 upregulation reverses the impacts of si-VPS9D1-AS1 on CRC cells. (**A**) Western blotting was used to assess the protein level of HMGA1 in HCT116 and SW480 cells after pcDNA3.1-HMGA1 or pcDNA3.1 introduction. (**B, C**) pcDNA3.1-HMGA1 or pcDNA3.1, alongside si-VPS9D1-AS1, was transfected into HCT116 and SW480 cells, followed by the measurement of proliferation and apoptosis using CCK-8 and flow cytometry assays. (**D, E**) Cell migration and invasion assays were performed to determine the migratory and invasive abilities of the cells mentioned above. *P < 0.05 and **P < 0.01.

Abbreviations: HMGA1, high-mobility group AT-hook 1; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; VPS9D1-AS1, VPS9D1 antisense RNA 1; NC, negative control; miR-525-5p, microRNA-525-5p; si-VPS9D1-AS1, small interfering RNA targeting VPS9D1-AS1; si-NC, negative control small interfering RNA; PI, propidium iodide.

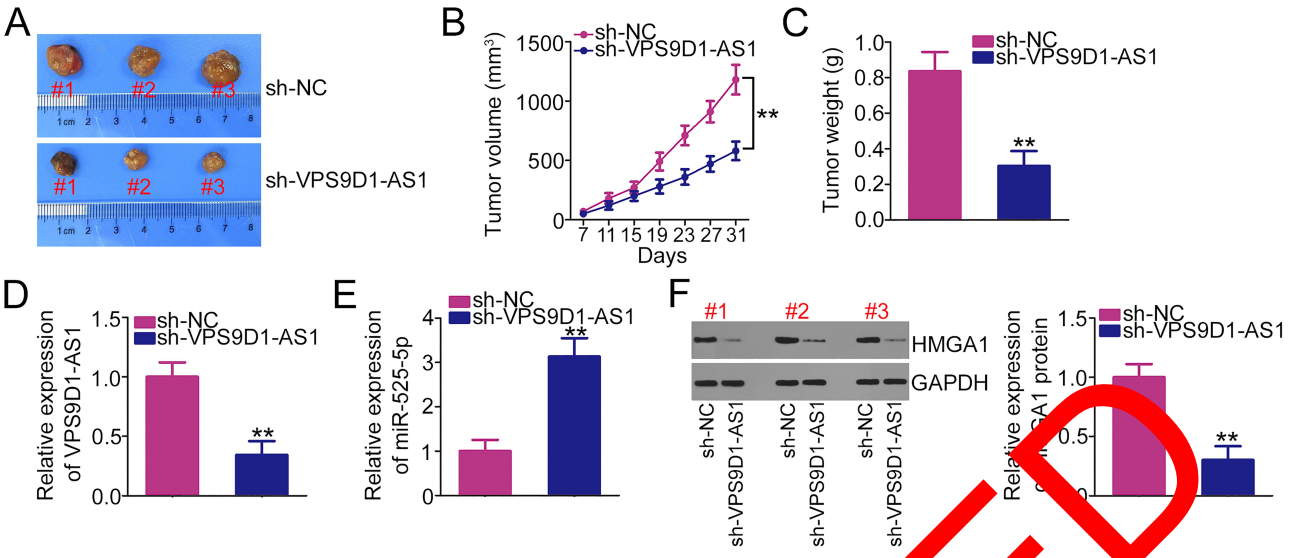

Figure 7 VPS9D1-AS1 downregulation suppresses tumor growth in vivo. (**A**) Representative images of tumor xenografts that originated from SW480 cells stably overexpressing sh-VPS9D1-AS1 or sh-NC. (**B**) The volume of the tumor xenografts was monitored every 4 days after cell injection. (**C**) The weights of the tumor xenografts in sh-VPS9D1-AS1 and sh-NC groups. (**D, E**) qRT-PCR was used to analyze the expression levels of VPS9D1-AS1 and miR-525-5p in tumor xenografts after treatment with SW480 cells stably overexpressing sh-VPS9D1-AS1 or sh-NC. (**F**) Western blotting was performed to determine the protein level of HMGA1 in tumor xenografts after injection with sh-VPS9D1-AS1 or sh-NC. **P < 0.01.

Abbreviations: HMGA1, high-mobility group AT-hook 1; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; VPS9D1-AS1, VPS9D1 antisense RNA 1; miR-525-5p, microRNA-525-5p; sh-VPS9D1-AS1, short -hairpin RNA targeting VPS9D1-AS1; sh-NC, negative control short -hairpin RNA.

identified.[33] In addition, accumulating studies have reported that several lncRNAs are implicated in the control of CRC tumorigenesis and progression.[34–36] Therefore, therapies targeting lncRNAs may be a promising approach for CRC therapy. Although lncRNAs have been widely studied in CRC, the expression pattern and detailed functions of most lncRNAs have not been elucidated. In this work, VPS9D1-AS1 expression was measured in CRC tissues and cell lines. Furthermore, the roles and underlying mechanism of VPS9D1-AS1 in the biological regulation of CRC cells were investigated in detail.

VPS9D1-AS1 is upregulated in non-small-cell lung cancer and shows a close relationship with tumor size, TNM stage, and lymph node metastasis.[21,22] Patients with non-small-cell lung cancer exhibiting high VPS9D1-AS1 expression showed shorter overall survival periods compared with those with low VPS9D1-AS1 expression.[21,22] Overexpressed VPS9D1-AS1 has also been confirmed in patients with gastric[23] and prostate[24] cancers. Functionally, VPS9D1-AS1 performs oncogenic actions in non-small-cell lung,[21,22] gastric,[23] and prostate[24] cancers. However, whether VPS9D1-AS1 is differentially expressed in CRC and whether it regulates cancer progression require further investigation. Our results revealed the high expression of VPS9D1-AS1 in CRC tissues and cell lines. After VPS9D1-AS1 silencing, CRC cell proliferation, migration, and invasion were suppressed, whereas cell apoptosis was promoted in vitro. Additionally, VPS9D1-AS1 knockdown decreased tumor growth in vivo. Therefore, VPS9D1-AS1 might be an attractive target for CRC diagnosis and therapy.

The cellular distribution of lncRNAs is a key element that determines their roles by offering lncRNAs different approaches to interact with various molecules.[11] lncRNAs located in the nucleus regulate cellular processes via chromatin interactions, transcriptional regulation, and RNA processing.[37] Regarding cytoplasmic lncRNAs, the most accepted theory is that they function as ceRNAs to sequester miRNAs from target mRNAs, thereby increasing the levels of transcription and translation products.[20] To uncover the mechanism responsible for the pro-oncogenic actions of VPS9D1-AS1, the bioinformatics tools StarBase 3.0 and miRDB were used to identify miRNAs potentially interacting with VPS9D1-AS1. Among these candidates, miR-525-5p was the only miRNA that showed increased expression following VPS9D1-AS1 knockdown. Additionally, a negative correlation was identified between VPS9D1-AS1 and miR-525-5p levels in CRC tissues. Furthermore, the luciferase reporter and RIP assays revealed that miR-525-5p could directly bind to and interact with VPS9D1-AS1 in CRC cells.

miR-525-5p is differentially expressed in many human cancer types, including CRC.[38–40] To assess the regulatory roles of miR-525-5p in CRC, we conducted a series of

functional assays. Ectopic miR-525-5p expression led to a significant reduction in cellular proliferation, migration, and invasion as well as in an increase in apoptosis in CRC cells. HMGA1 was verified as a direct target of miR-525-5p in CRC and under the control of VPS9D1-AS1 by sequestering miR-525-5p. Notably, a positive correlation between VPS9D1-AS1 and HMGA1 expression was validated in CRC tissues. Taken together, our results identify a novel ceRNA model involving VPS9D1-AS1, miR-525-5p, and HMGA1 in CRC. A comprehensive and detailed understanding of the VPS9D1-AS1/miR-525-5p/HMGA1 ceRNA pathway may be helpful for the identification of new therapeutic techniques targeting CRC. However, other working way may be involved in the mechanisms underlying the tumor-promoting actions of VPS9D1-AS1 in CRC. We will resolve it in the near future.

HMGA1 is a member of the HMGA protein family and is involved in the regulation of the chromatin structure by directly binding to the A/T-rich DNA sequences located in the promoter and enhancer regions of multiple human genes.[41] It is highly expressed in CRC and contributes to the pathology of tumors by regulating numerous biological activities.[29–31] In the present study, HMGA1 was regulated by the VPS9D1-AS1/miR-525-5p axis. Rescue experiments further confirmed that miR-525-5p inhibition or HMGA1 restoration could effectively reverse the tumor-suppressing effects of VPS9D1-AS1 knockdown on CRC cells. Together, VPS9D1-AS1, miR-525-5p, and HMGA1 form an interactive regulatory network that promotes the aggressiveness of CRC cells in vitro and in vivo.

Conclusion

In summary, our results provided convincing evidence that VPS9D1-AS1 increases HMGA1 expression by sponging miR-525-5p in CRC and subsequently promotes cell proliferation, migration, and invasion in vitro and tumor growth in vivo. Therefore, the VPS9D1-AS1/miR-525-5p/HMGA1 pathway may be a promising target to improve the management of CRC.

Disclosure

The authors declare that they have no competing interests.

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