

RETRACTED ARTICLE: Long Noncoding RNA LINC01426 Sequesters microRNA-519d-5p to Promote Non-Small Cell Lung Cancer Progression by Increasing ETS1 Expression

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Jixin Dai¹
Bing Wang²
Yueming Zhao¹
Xuerong Zuo¹
Hongxia Cui¹
Xi Chen²
Xianhong Liu¹

¹Department of Oncology, Jilin Cancer Hospital, Changchun, Jilin 130000, People's Republic of China; ²Department of Radiotherapy, Jilin Cancer Hospital, Changchun, Jilin 130000, People's Republic of China

Purpose: Recent studies have identified important roles for long intergenic non-protein coding RNA 1426 (*LINC01426*) in glioma and clear cell renal cell carcinoma. The present study evaluated the expression profile of *LINC01426* in non-small cell lung cancer (NSCLC) tissues and cell lines. Furthermore, the function of *LINC01426* in NSCLC and the molecular mechanisms involved were extensively studied.

Methods: The abundance of *LINC01426* in NSCLC tissues and cell lines was determined using quantitative reverse transcription-polymerase chain reaction. The cell counting kit-8 assay, flow cytometry, transwell experiments for migration and invasion, and xenograft tumor model were used to assess the function of *LINC01426* in NSCLC cells. Mechanistic studies were performed using luciferase reporter assay and RNA immunoprecipitation.

Results: Significant *LINC01426* upregulation was observed in NSCLC tissues and cell lines. Silencing *LINC01426* inhibited proliferation, migration, and invasion of NSCLC cells and promoted cell apoptosis in vitro. Furthermore, interference of *LINC01426* restricted tumor growth of NSCLC cells in vivo. In addition, *LINC01426* showed the ability to directly bind to microRNA-519d-5p (miR-519d-5p) and act as a molecular sponge for miR-519d-5p in NSCLC cells. Furthermore, the *ETS proto-oncogene 1* (*ETS1*) was identified as a direct target of miR-519d-5p and *LINC01426* could indirectly upregulate *ETS1* expression by sponging miR-519d-5p. Moreover, the cancer-inhibiting activities of *LINC01426* knockdown in NSCLC cells were partially offset by miR-519d-5p inhibition.

Conclusion: *LINC01426* increases *ETS1* expression by sequestering miR-519d-5p, thereby aggravating the malignant progression of NSCLC. The *LINC01426*/miR-519d-5p/*ETS1* competing endogenous RNA pathway may provide a target for designing therapeutic agents for NSCLC treatment.

Keywords: long intergenic non-protein coding RNA 1426, NSCLC, ETS proto-oncogene 1, ceRNA

Introduction

Lung cancer is the most commonly diagnosed cancer and the leading cause of cancer-related mortality worldwide.¹ According to estimates, lung cancer will afflict 228,150 individuals and cause 147,510 deaths annually worldwide.² Non-small cell lung cancer (NSCLC), the most prominent type of lung cancer, accounts for approximately 80%–85% of all lung cancer diagnoses.³ NSCLC comprises several pathological types, including squamous cell carcinoma, adenocarcinoma, and large cell carcinoma.⁴ Over

Correspondence: Xianhong Liu
Department of Oncology, Jilin Cancer Hospital, 1018 Huguang Road, Changchun, Jilin 130000, People's Republic of China
Email liuxianhong_onc@163.com

the past few decades, with progress in diagnostic techniques and therapeutic regimens, the clinical outcome for NSCLC has substantially improved.⁵ However, the prognosis for NSCLC remains dismal as the 5-year survival rate is only 19.7%.⁶ Recurrence, metastasis, and drug resistance lead to poor clinical outcomes for NSCLC.⁷ NSCLC exhibits complicated biological characteristics, involving multiple pathophysiological changes, and gene and molecular pathway dysregulation.⁸ Consequently, the underlying mechanisms remain elusive and require further exploration. Therefore, elucidating the molecular events responsible for NSCLC pathogenesis will be useful for improving diagnosis and treatment.

Long noncoding RNAs (lncRNAs) are transcripts consisting of >200 nucleotides.⁹ They lack protein coding capacity and have attracted increased attention over the past decade.¹⁰ Furthermore, lncRNAs are implicated in the control of several physiological processes, such as genomic imprinting, chromatin organization, immunoregulation, cell cycle, and differentiation.^{11,12} Compelling studies have revealed that numerous lncRNAs are aberrantly expressed in various human malignancies and affect cell biological processes associated with cancer.^{13–15} In NSCLC, lncRNAs have emerged as novel regulators of oncogenesis and cancer progression, and they contribute to the malignant phenotype.^{16–18}

MicroRNAs (miRNAs) are a cluster of highly conserved, single-stranded, short noncoding RNA transcripts composed of 17–25 nucleotides.¹⁹ These molecules are capable of negatively regulating gene expression via base pairing with the 3'-untranslated regions (3'-UTRs) of target mRNAs. This triggers mRNA degradation and translation repression.²⁰ The differentially expressed miRNAs can regulate the oncogenicity of NSCLC by executing tumor-promoting or tumor-inhibiting roles.^{21,22} In recent years, the competing endogenous RNA (ceRNA) theory has been proposed and gradually been adopted.²³ This theory asserts that lncRNAs function as ceRNAs by decoying specific miRNAs, thereby abolishing the miRNA-mediated target mRNA degradation.²⁴ Therefore, elucidating the detailed functions of cancer-associated lncRNAs in NSCLC will contribute to cancer intervention and therapy.

Recent studies have identified the important roles for *LINC01426* in glioma,^{25,26} clear cell renal cell carcinoma,²⁷ and lung adenocarcinoma.²⁸ However, studies on the expression profile and functions of *LINC01426* in NSCLC are limited. Therefore, the main aim of our study was to detect the expression profile for *LINC01426* in NSCLC tissues and cell lines. Furthermore, the function

of *LINC01426* in NSCLC and the related molecular mechanisms involved were investigated.

Materials and Methods

Tissue Sample Collection

A total of 58 pairs of NSCLC tissues and corresponding adjacent normal tissues were obtained from patients at the Jilin Cancer Hospital. None of the patients had previously received preoperative radiotherapy, chemotherapy, or other anticancer treatments, and none experienced any other acute or chronic diseases or cancers. Tissues were stored in liquid nitrogen until further use. The Ethics Committee of Jilin Cancer Hospital (2017-0216) reviewed and approved this study. The study was conducted in accordance with the Declaration of Helsinki, and all tissue samples were obtained with written informed consent.

Cell Culture

The human non-tumorigenic bronchial epithelial cell line, BEAS-2B, was obtained from the American Type Culture Collection (ATCC; Manassas, VA, USA) and cultured in Bronchial Epithelial Cell Growth Medium (Lonza/Clonetics Corporation, Walkersville, MD, USA). Two NSCLC cell lines, H522 and H460, were also obtained from the ATCC and maintained in RPMI 1640 medium (Gibco; Thermo Fisher Scientific, Inc., Waltham, MA, USA) supplemented with 10% fetal bovine serum (FBS; Gibco; Thermo Fisher Scientific, Inc.) and 1% penicillin/streptomycin (Gibco; Thermo Fisher Scientific, Inc.). The other two NSCLC cell lines, SK-MES-1 and A549, were purchased from the Cell Bank of the Chinese Academy of Sciences (Shanghai, China). A549 cells were cultured in F-12K medium (Gibco; Thermo Fisher Scientific, Inc.) containing 10% FBS, 1% Glutamax, and 1% penicillin/streptomycin. Minimum essential medium (Gibco; Thermo Fisher Scientific, Inc.) containing 10% FBS, 1% Glutamax, 1% Non-essential Amino Acids (Gibco; Thermo Fisher Scientific, Inc.), 1% sodium pyruvate solution (100 mM, Gibco; Thermo Fisher Scientific, Inc.), and 1% penicillin/streptomycin was added to the SK-MES-1 cell culture. All aforementioned cells were grown in a sterilized incubator at 37°C supplemented with 5% CO₂.

Oligonucleotides, Plasmids, and Cell Transfection

The miR-519d-5p mimic, negative control (NC) miRNA mimic (miR-NC), miR-519d-5p inhibitor (anti-miR-519d-5p), and NC inhibitor (anti-NC) were produced by RiboBio

Co., Ltd (Guangzhou, China). The small interfering RNAs (siRNAs) that target *LINC01426* expression (si-LINC01426) and NC expression (si-NC) were designed and synthesized by Genepharma Co., Ltd (Shanghai, China). The *ETSI* over-expressing plasmid, pcDNA3.1-ETSI, was constructed by the Shanghai Sangon Company (Shanghai, China). NSCLC cells were seeded into 6-well plates and grown to 70%–80% confluence before being transiently transfected with oligonucleotides or plasmids using Lipofectamine 2000 (Invitrogen; Thermo Fisher Scientific, Inc.).

RNA Preparation and Quantitative Reverse Transcription–Polymerase Chain Reaction (qRT-PCR)

Total RNA extraction was performed using TRIzol reagent (KeyGEN BioTECH; Nanjing, China). A NanoDrop 2000c spectrophotometer (Invitrogen; Thermo Fisher Scientific, Inc.) was used for determining the quality and quantity of total RNA. Total RNA was reverse transcribed into complementary DNA (cDNA) using a Mir-X miRNA First-Strand Synthesis Kit (Takara, Dalian, China). Quantitative PCR was then performed to detect miR-519d-5p expression using a Mir-X miRNA qRT-PCR RTB Green[®] Kit (Takara). To quantitate *LINC01426* and *ETSI* expression, a QuantiTect Reverse Transcription Kit (Qiagen GmbH, Hilden, Germany) was employed for cDNA synthesis. Thereafter, a QuantiTect SYBR Green PCR Kit (Qiagen GmbH) was used for quantitative PCR. *GAPDH* acted as an endogenous control for *LINC01426* and *ETSI*, whereas miR-519d-5p expression was normalized to that of *U6* small nuclear RNA. All gene expression measurements were calculated using the $2^{-\Delta\Delta Cq}$ method. Each sample was measured in triplicate, and the same experiment was repeated three times.

Cell Counting Kit-8 (CCK-8) Assay

Transfected cells were detached with 0.25% trypsin at 24 h post-transfection, centrifuged, and resuspended in complete culture medium at a density of 2×10^4 cells/mL. Each well of the 96-well plates was administered 100 μ L cell suspension, and 5 replicate wells were established for each group. After cultivating for 0, 24, 48, and 72 h, 10 μ L CCK-8 solution (Dojindo Laboratories, Kumamoto, Japan) was added, and the plates were incubated at 37°C with 5% CO₂ for 2 h. The absorbance at 450 nm was measured using a microplate reader (Tecan Group, Ltd., Mannedorf, Switzerland).

Flow Cytometry

An Annexin V-FITC Apoptosis Detection Kit (Beyotime; Shanghai, China) was used in the assessment of cell apoptosis. Briefly, transfected cells were cultured for 48 h, detached using EDTA-free trypsin, and centrifugated at 1000 \times g for 5 min at 4°C, followed by resuspending in 195 μ L binding buffer. Thereafter, 5 μ L Annexin-V-FITC and 10 μ L PI were added to the cell suspension. After 20-min incubation at 25°C in the dark, cell apoptosis was detected using a flow cytometer (BD Biosciences, Franklin Lakes, NJ, USA). All data were analyzed using a BD FACSCanto™ system software v2.4 (BD Biosciences).

Transwell Experiments for Migration and Invasion

Cell migration and invasion were evaluated in transwell experiments. For the migration assay, 1×10^5 cells were resuspended in serum-free culture medium and plated into the upper compartment of the transwell chambers (BD Biosciences). The lower chambers were loaded with 100 μ L culture medium supplemented with 20% FBS. After 24 h, the cells remaining on the upper surface of the membranes were removed using a cotton swab. The migrated cells were fixed with 4% paraformaldehyde and then stained with 0.1% crystal violet. These cells were visualized using an inverted light microscope (Olympus Corporation, Tokyo, Japan). A total of six fields of view were arbitrarily selected and the cell numbers were counted. The experimental procedure for the invasion assay were the same as the migration assay, except that the transwell chambers were precoated with Matrigel (BD Biosciences).

Tumor Xenografts

All animal experiments were conducted following the NIH guidelines for the care and use of laboratory animals and approved by the Animal Experimental Ethics Committee of Jilin Cancer Hospital (2018–1102). Male BALB/c nude mice (4–6 weeks old) were obtained from the Beijing Vital River Laboratory Animal Technology Co., Ltd. (Beijing, China) and housed under specific pathogen-free conditions. The lentivirus stably expressing short hairpin RNA (shRNA) against *LINC01426* (sh-LINC01426) and NC (sh-NC) were designed and prepared by Genepharma Co., Ltd.

H460 cells were transduced with lentivirus and treated with puromycin to obtain a stable cell line. A total of 6

mice were used in animal experiments, and were randomly divided into groups sh-LINC01426 and sh-NC. H460 cells stably overexpressing sh-LINC01426 were subcutaneously injected into the flanks of nude mice in sh-LINC01426 group, whereas the sh-NC group was subcutaneously injected with H460 cells stably overexpressing sh-NC. Tumor width and length were weekly monitored using a Vernier caliper, and the tumor volume was calculated as follows: tumor volume = $0.5 \times (\text{length} \times \text{width}^2)$. After 4 weeks, the nude mice were euthanized by cervical dislocation, the tumor xenografts were removed, weighed, and used for subsequent assays.

Bioinformatics Analysis

The miRDB database (<http://mirdb.org/>) was used to identify miRNAs that may interact with *LINC01426*. The putative targets of miR-519d-5p were predicted using the miRDB (<http://mirdb.org/>) and TargetScan (<http://www.targetscan.org/>) programs.

RNA Immunoprecipitation (RIP) Assay

RIP assay was performed to detect the binding between *LINC01426* and miR-519d-5p using a Magna RIP RNA-Binding Protein Immunoprecipitation kit (EMD Millipore). NSCLC cells were lysed in RIP buffer, and the cell extracts were incubated with magnetic beads conjugated with anti-Ago2 antibody (Millipore) or normal IgG (Millipore). Prior to immunoprecipitation, the magnetic beads were harvested and overnight incubation at 4°C, rinsed with RIP wash buffer, and treated with proteinase K to remove protein. The immunoprecipitated RNA was measured using qRT-PCR.

Nuclear–Cytoplasmic Fractionation Assay

Nuclear and cytoplasmic fractions were separated using the Cytoplasmic and Nuclear RNA Purification Kit (Norgen, Edmonton, Canada, USA). The RNA in both fractions was extracted and subjected to qRT-PCR analysis for determining the distribution of *LINC01426*.

Luciferase Reporter Assay

The *LINC01426* and *ETS1* 3'-UTR fragments containing the miR-519d-5p binding site were amplified and cloned into the pmirGLO luciferase vector (Promega Corporation, Madison, WI, USA). The produced luciferase reporter vectors were termed as LINC01426-wild-type (LINC01426-wt) and ETS1-wt. Mutated *LINC01426* and *ETS1* 3'-UTR fragments with disruption in the putative miR-519d-5p binding sequences

were generated using a QuikChange Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA, USA). Further, the mutated fragments were inserted into the pmirGLO luciferase vector to obtain the LINC01426-mutant (LINC01426-mut) and ETS1-mut reporter vectors. NSCLC cells were seeded into 6-well plates and cotransfected with miR-519d-5p mimic or miR-NC and wt or mut reporter vectors using Lipofectamine 2000. At 48 h after transfection, the Dual Luciferase Reporter Assay System (Promega Corporation) was used to detect the activity of firefly luciferase, which was normalized to that of Renilla luciferase.

Western Blot Analysis

Cultured cells were rinsed with phosphate buffered solution, and total protein was isolated using RIPA buffer (KeyGEN BioTECH). Following quantification using a BCA protein assay kit (KeyGEN BioTECH), equal amounts of protein were separated on 10% sodium dodecyl sulfate polyacrylamide gels. The separated proteins were then transferred to polyvinylidene fluoride membranes (Millipore), blocked with 5% non-fat milk at room temperature for 2 h and incubated overnight with primary antibodies against *ETS1* (ab221861; Abcam, Cambridge, UK) or *GAPDH* (ab181602; Abcam). Goat anti-rabbit IgG-HRP secondary antibody (ab205718; Abcam) was incubated with the membranes. Thereafter, an ECL detection kit (KeyGEN BioTECH) was used for the development of protein signals.

Statistical Analysis

All experiments were repeated thrice, and the data were presented as the means \pm standard deviations. The differences between two groups were determined by a Student's *t*-test. One-way ANOVA, followed by Tukey's post-hoc test, was used to determine the differences among multiple groups. The correlations among *LINC01426*, miR-519d-5p, and *ETS1* expression in the NSCLC tissues were evaluated using Pearson's correlation analysis. All statistical analyses were performed using SPSS19.0 software (SPSS Inc., USA). A P value of <0.05 was considered statistically significant.

Results

LINC01426 is Highly Expressed in NSCLC Tissues and Cell Lines

LINC01426 expression in lung adenocarcinoma (LUAD) and lung squamous cell carcinoma (LUSC) was analyzed using TCGA dataset. The results indicated that *LINC01426* was clearly elevated in LUAD and LUSC (Figure 1A). Further,

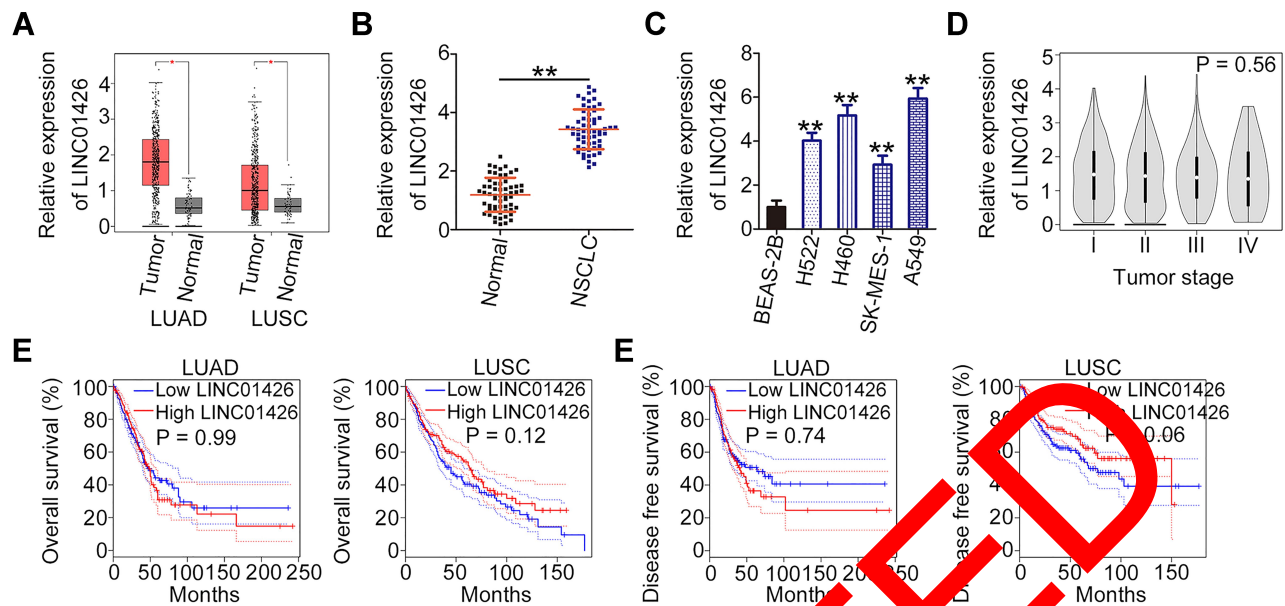


Figure 1 *LINC01426* is highly expressed in NSCLC tissues and cell lines. (A) The TCGA dataset was used to analyze *LINC01426* expression in LUAD and LUSC. (B) *LINC01426* expression in 58 pairs of NSCLC tissues and corresponding adjacent normal tissues was measured using qRT-PCR. (C) *LINC01426* expression in NSCLC cell lines (H522, H460, SK-MES-1 and A549) was measured using qRT-PCR. A human non-tumorigenic bronchial epithelial cell line BEAS-2B was used as control. (D) The correlation between *LINC01426* expression and tumor stage in LUAD and LUSC was analyzed using the TCGA dataset. (E, F) The correlation between *LINC01426* expression and overall survival or disease-free survival in LUAD and LUSC was determined using the TCGA dataset. $P < 0.01$.

a total of 58 pairs of NSCLC tissues and corresponding adjacent normal tissues were collected and analyzed using qRT-PCR to determine *LINC01426* expression. *LINC01426* expression was higher in NSCLC tissues compared with that in the adjacent normal tissues (Figure 1B). Similar to this, *LINC01426* expression in NSCLC cell lines (H522, H460, SK-MES-1 and A549) was significantly upregulated compared with that in the human non-tumorigenic bronchial epithelial cell line BEAS-2B (Figure 1C). Re-analyzing the TCGA dataset along with available survival data revealed no correlation between *LINC01426* expression and tumor stage in either LUAD or LUSC (Figure 1D). Furthermore, a high *LINC01426* expression was not associated with either overall survival (Figure 1E) or disease-free survival (Figure 1F) in patients with LUAD and LUSC. These results indicate that *LINC01426* is upregulated in NSCLC.

LINC01426 Depletion Inhibits NSCLC Cell Proliferation, Migration, and Invasion and Promotes Cell Apoptosis in vitro

LINC01426 expression was most abundant in the cell lines H460 and A549; therefore, they were selected for experimental use. To further elucidate the role of *LINC01426* in NSCLC, si-LINC01426 was transfected into H460 and A549 cells. *LINC01426* expression was decreased in H460 and A549

cells after si-LINC01426 transfection. Of the constructs, si-LINC01426-1 was the most effective and thus selected for functional experiments (Figure 2A). Using CCK-8 assay, our results revealed that *LINC01426* depletion inhibited the proliferation of H460 and A549 cells (Figure 2B). Additionally, *LINC01426* silencing increased apoptosis in H460 and A549 cells (Figure 2C). Furthermore, si-LINC01426 transfection resulted in reduced migration (Figure 2D) and invasion (Figure 2E) of H460 and A549 cells. Overall, *LINC01426* exerts oncogenic activity in NSCLC cells.

LINC01426 Acts as a ceRNA in NSCLC Cells by Sponging miR-519d-5p

To determine the manner in which *LINC01426* affects the oncogenicity of NSCLC cells, lncATLAS (<http://lncatlas.org.eu/>) was used to predict the subcellular localization of *LINC01426*. The results indicated that *LINC01426* was primarily enriched in the cytoplasm (Figure 3A). A nuclear-cytoplasmic fractionation assay coupled with qRT-PCR analysis further confirmed this observation (Figure 3B), suggesting that *LINC01426* is implicated in NSCLC progression via a ceRNA mechanism. A bioinformatics analysis revealed a total of 22 miRNAs that were capable of complementary base pairing with *LINC01426* (Figure 3C). Among these candidates, miR-519d-5p,²⁹ miR-873-3p,^{30,31} miR-377-5p,^{32,33} and miR-548c-3p^{34,35} were selected for experimental

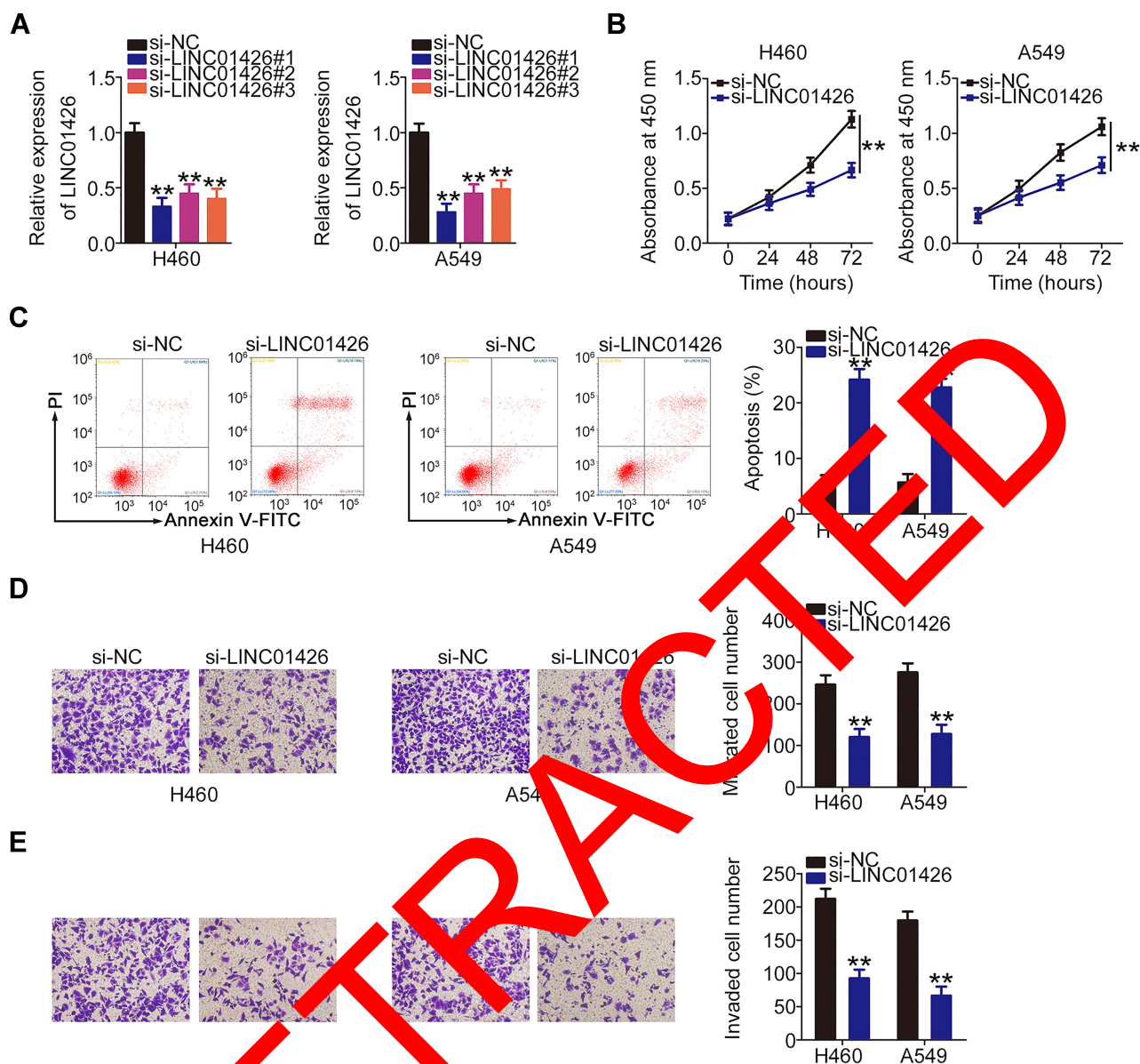


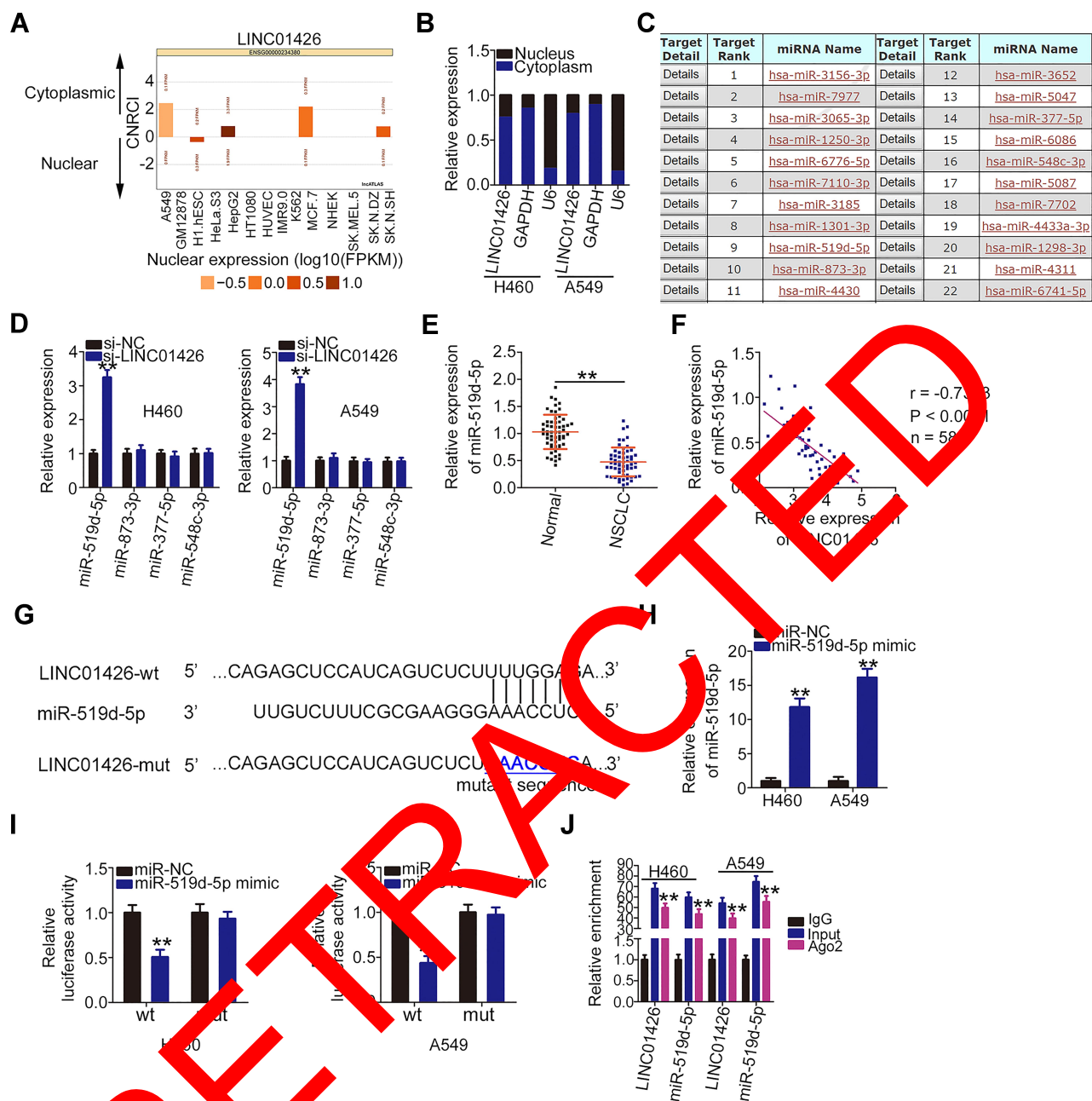
Figure 2 *LINC01426* knockdown inhibits NSCLC cell proliferation, migration, and invasion and promotes cell apoptosis in vitro. **(A)** *LINC01426* expression was measured in H460 and A549 cells using qRT-PCR following si-LINC01426 or si-NC transfection. **(B)** CCK-8 assay was performed to assess the proliferation of *LINC01426*-deficient H460 and A549 cells. **(C)** Flow cytometry was performed to evaluate the effect of *LINC01426* depletion on apoptosis in H460 and A549 cells. **(D, E)** The migratory and invasive capacities of H460 and A549 cells following *LINC01426* silencing were determined by transwell experiments. ** $P < 0.01$.

verification because they played critical functions in various human cancers.

Following *LINC01426* interference, qRT-PCR analysis was performed to detect the expression of the four miRNAs in H460 and A549 cells. It was found that miR-519d-5p expression was significantly increased in *LINC01426* deficient-H460 and -A549 cells (Figure 3D). By contrast, the expression of other three miRNAs remained unchanged following si-LINC01426 transfection. In addition, miR-519d-5p expression was reduced in NSCLC tissues compared with that in the adjacent normal tissues (Figure 3E). Data from

Pearson's correlation analysis revealed an inverse correlation between *LINC01426* and miR-519d-5p levels in the 58 NSCLC tissues (Figure 3F; $r = -0.7313$, $P < 0.0001$).

Figure 3G depicts the binding sequence of miR-519d-5p within the sequence of *LINC01426*. To further validate this prediction, the luciferase reporter assay was conducted to address the binding interaction between *LINC01426* and miR-519d-5p in NSCLC cells. The miR-519d-5p mimic transfection was detected using qRT-PCR. In miR-519d-5p mimic-transfected H460 and A549 cells, miR-519d-5p showed marked overexpression (Figure 3H). The luciferase



activity of *LINC01426*-wt was lower in response to miR-519d-5p upregulation, whereas the activity of *LINC01426*-mut showed no significant change following miR-519d-5p mimic cotransfection (Figure 3I). RIP assay further confirmed this result considering that *LINC01426* and miR-

519d-5p were immunoprecipitated by anti-Ago2 antibody (Figure 3J), indicating the coexistence of *LINC01426* and miR-519d-5p in the same RNA-induced silencing complex. Collectively, these findings suggest that *LINC01426* functions as a ceRNA in NSCLC cells by sponging miR-519d-5p.

miR-519d-5p is an Anti-Oncogenic miRNA That Directly Targets ETS1 in NSCLC Cells

Using bioinformatics tools, *ETS1* (Figure 4A) was identified and selected for further confirmation because of its oncogenic effects in the malignant properties of NSCLC cells.^{36–38} Results of the luciferase reporter assay revealed that miR-519d-5p overexpression significantly inhibited the luciferase activity of ETS1-wt in H460 and A549 cells, whereas the inhibitory effect was abrogated when the binding sequences were mutated (Figure 4B). Moreover, miR-519d-5p upregulation negatively affected *ETS1* mRNA (Figure 4C) and protein (Figure 4D) expression in H460 and A549 cells. Furthermore, *ETS1* was significantly overexpressed in NSCLC tissues compared with that in the adjacent normal tissues (Figure 4E). Importantly, an inverse correlation was observed between the levels of miR-519d-5p and *ETS1* in the 58 NSCLC tissues (Figure 4F; $r = -0.6239$, $P < 0.0001$). In summary, miR-519d-5p directly targets *ETS1* and inhibits NSCLC progression.

LINC01426 Exerts Oncogenic Activity in NSCLC by Regulating the miR-519d-5p/ETS1 Axis

LINC01426 was verified as an miR-519d-5p sponge, and miR-519d-5p directly targeted *ETS1* in NSCLC cells. The above experimental results further suggest that *LINC01426* can regulate *ETS1* expression in NSCLC cells by competitively binding to miR-519d-5p. Accordingly, *ETS1*

mRNA and protein levels in LINC01426-depleted H460 and A549 cells were measured using qRT-PCR and Western blot assays. The results revealed that *ETS1* expression was significantly inhibited in H460 and A549 cells when *LINC01426* was silenced (Figure 5A and B). However, anti-miR-519d-5p (Figure 5C) cotransfection reversed these regulatory effects (Figure 5D and E). The Pearson's correlation analysis revealed a positive correlation between *LINC01426* and *ETS1* mRNA levels in NSCLC tissues (Figure 5F; $r = 0.6636$, $P < 0.0001$). Subsequently, rescue experiments were performed by knocking down miR-519d-5p expression in LINC01426-depleted H460 and A549 cells. Functional experiments demonstrated that miR-519d-5p inhibition abolished the si-LINC01426-mediated effects on cell proliferation (Figure 5G) and apoptosis (Figure 5H) of H460 and A549 cells. Furthermore, although the migratory (Figure 5I) and invasive (Figure 5J) capabilities of H460 and A549 cells were decreased by *LINC01426* downregulation, they were reversed following miR-519d-5p inhibition. Cumulatively, the miR-519d-5p/*ETS1* axis functions as a downstream effector of *LINC01426* in promoting oncogenesis in NSCLC.

LINC01426 Silencing Inhibits NSCLC Cell Growth in vivo

To determine the effect of *LINC01426* on NSCLC cell growth in vivo, a xenograft model was established by injecting H460 cells stably overexpressing sh-LINC01426 or sh-NC into nude mice. The mice in the sh-

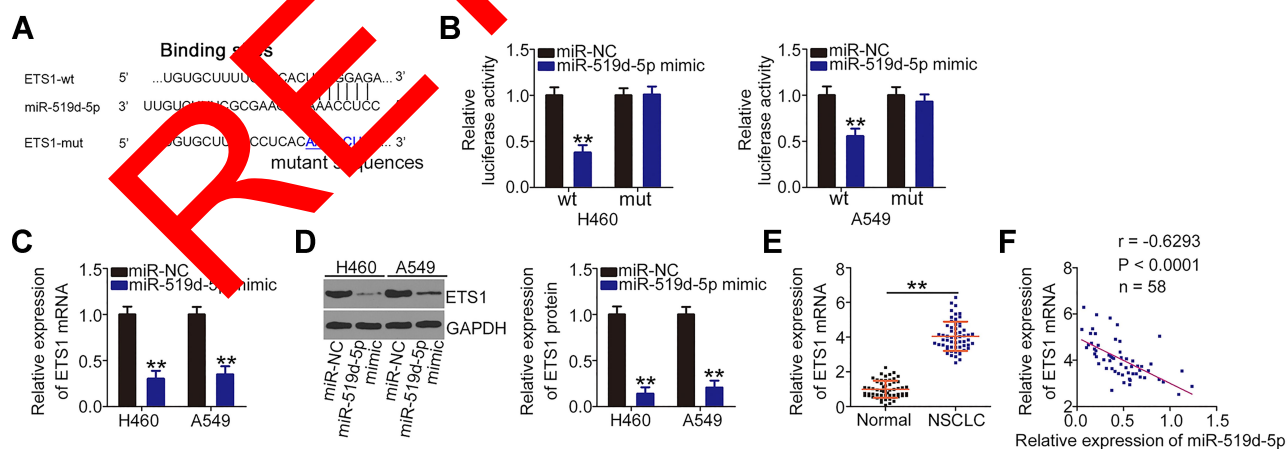


Figure 4 MiR-519d-5p directly targets *ETS1* in NSCLC cells. (A) The predicted miR-519d-5p binding site within the *ETS1* 3'-UTR and corresponding mutated site. (B) ETS1-wt or ETS1-mut and miR-519d-5p mimic or miR-NC were transfected into H460 and A549 cells. Luciferase activity was analyzed after 48-h incubation. (C, D) qRT-PCR and Western blot analysis were performed to measure the *ETS1* mRNA and protein levels, respectively, in miR-519d-5p mimic-transfected or miR-NC-transfected H460 and A549 cells. (E) *ETS1* mRNA expression in 58 pairs of NSCLC tissues and corresponding adjacent normal tissues was measured using qRT-PCR. (F) The correlation between miR-519d-5p and *ETS1* mRNA in 58 NSCLC tissues was analyzed by Pearson's correlation analysis. ** $P < 0.01$.

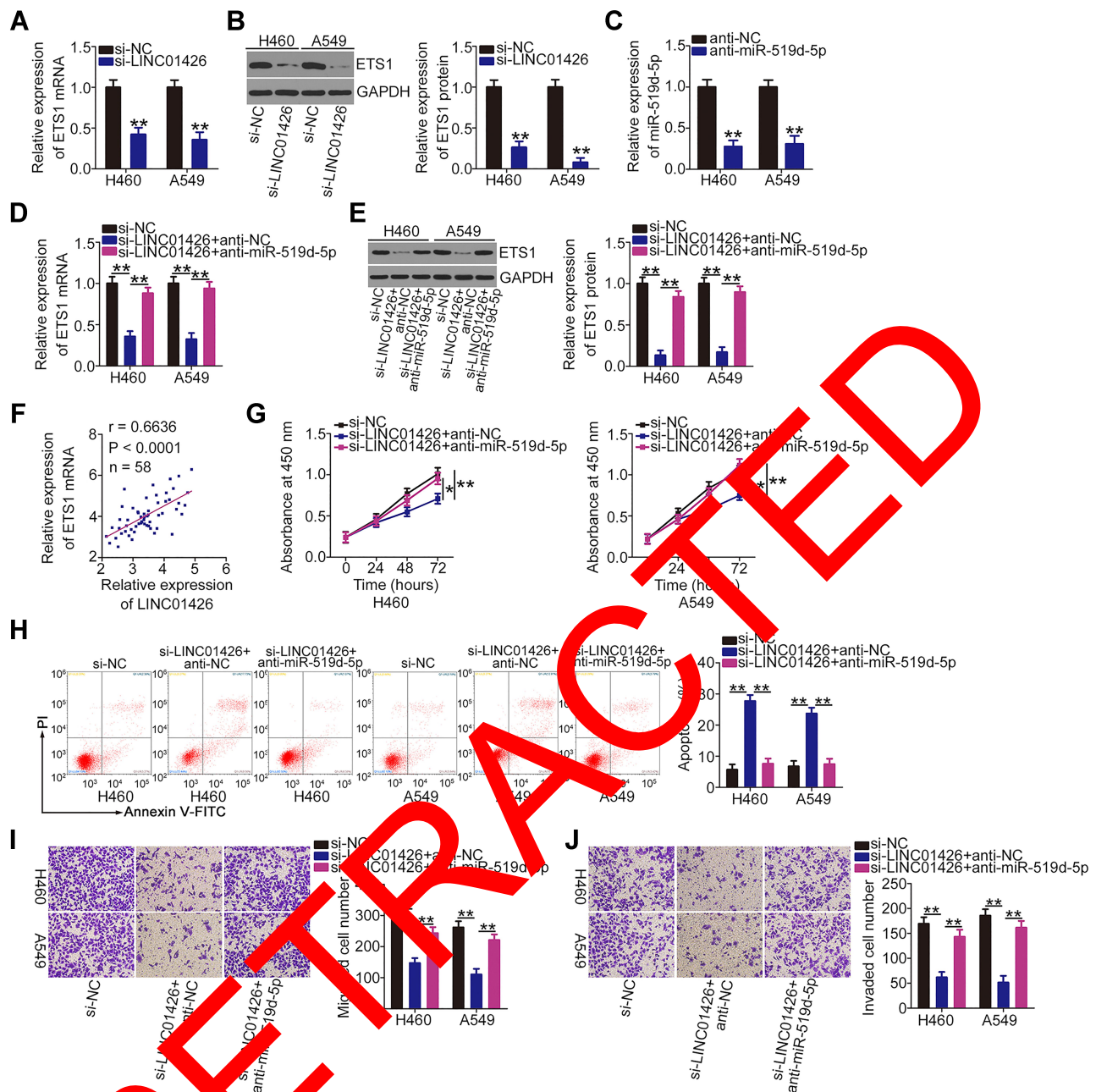


Figure 5 LINC01426 exerts oncogenic activity in NSCLC cells by regulating the miR-519d-5p/ETS1 axis. (A, B) *ETS1* mRNA and protein levels in LINC01426-depleted H460 and A549 cells were determined using qRT-PCR and Western blot analysis, respectively. (C) qRT-PCR was used to assess the transfection efficiency of anti-miR-519d-5p in H460 and A549 cells. (D, E) H460 and A549 cells were transfected with anti-miR-519d-5p or anti-NC in the presence of si-LINC01426. qRT-PCR and Western blot analysis were performed to measure *ETS1* mRNA and protein expression levels, respectively. (F) Pearson's correlation analysis was conducted to assess the relationship between *LINC01426* and *ETS1* expression in 58 NSCLC tissues. (G-J) Anti-miR-519d-5p or anti-NC along with si-LINC01426 was introduced into H460 and A549 cells. The CCK-8 assay, flow cytometry, and transwell experiments for migration and invasion were conducted to determine cell proliferation, apoptosis, and migration and invasion, respectively. * $P < 0.05$ and ** $P < 0.01$.

LINC01426 group exhibited decreased tumor volume (Figure 6A and B) and weight (Figure 6C) compared with the sh-NC group. *LINC01426* and miR-519d-5p expression levels in the tumor xenografts were measured using qRT-PCR. *LINC01426* was downregulated (Figure 6D) and miR-519d-5p was upregulated (Figure 6E) in the

H460 tumor xenografts derived from *LINC01426* knock-down. Furthermore, the *ETS1* mRNA (Figure 6F) and protein (Figure 6G) expression levels were decreased in the LINC01426-depleted tumor xenografts. Collectively, these data indicate that *LINC01426* downregulation suppresses the growth of NSCLC tumors in vivo.

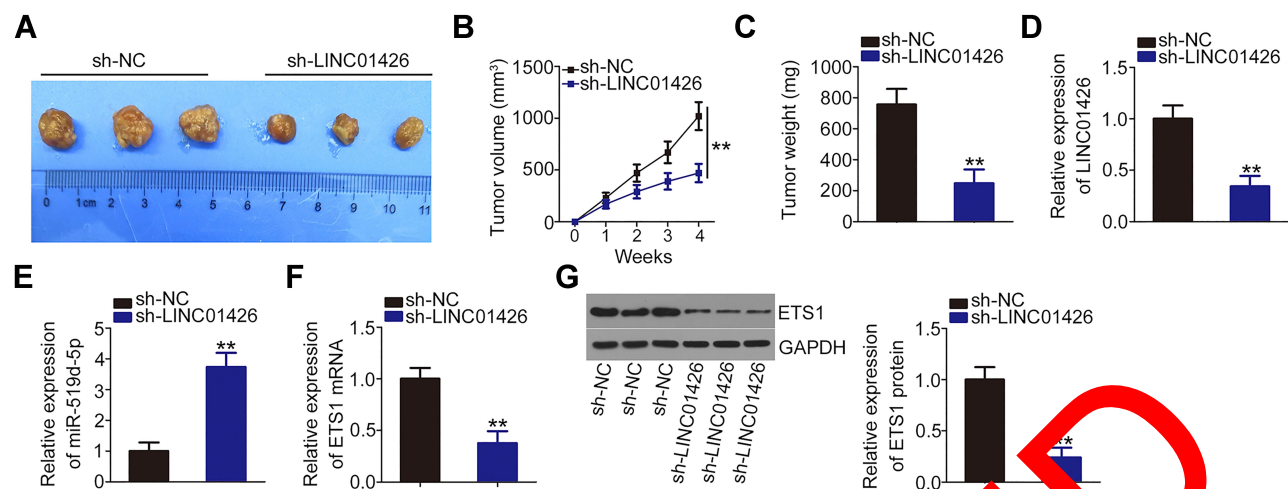


Figure 6 *LINC01426* knockdown inhibits the growth of NSCLC tumors in vivo. (A) After 28 days post-inoculation, mice were euthanized and tumor xenografts were dissected and photographed. (B) Tumor volume was weekly recorded and growth curves were plotted. (C) Tumor xenografts from sh-LINC01426 and sh-NC groups were weighed after removal. (D) *LINC01426* expression in the tumor xenografts was measured using qRT-PCR. (E, F) miR-519d-5p and *ETS1* mRNA expression levels were measured using qRT-PCR. (G) Western blot analysis of *ETS1* protein expression in tumor xenografts obtained from the sh-LINC01426 and sh-NC groups. ** $P < 0.01$.

Discussion

A significant body of evidence has indicated that lncRNAs are aberrantly expressed in NSCLC, which results in cancer progression, unlimited growth, and metastasis.^{39–41} Moreover, lncRNAs have been identified as contributors to NSCLC etiology and development.^{42,43} Therefore, investigating the regulatory activities of lncRNAs in NSCLC may lead to the identification of diagnostic markers and therapeutic targets for this fatal disease. However, the expression profile, detailed function, and regulatory mechanism for most lncRNAs in NSCLC have not been elucidated. In the present study, we determined whether *LINC01426* is dysregulated in NSCLC and whether it could regulate NSCLC progression.

The expression and function of *LINC01426* in human cancers have recently attracted considerable interest. *LINC01426* is upregulated in glioma,²⁵ clear cell renal cell carcinoma,²⁷ and lung adenocarcinoma,²⁸ and elevated *LINC01426* expression is associated with adverse clinicopathological characteristics.^{27,28} In addition, *LINC01426* is reportedly an independent predictor of prognosis in glioma.²⁵ Functionally, *LINC01426* exerts pro-oncogenic activities in glioma,^{25,26} clear cell renal cell carcinoma,²⁷ and lung adenocarcinoma,²⁸ and it is implicated in the regulation of multiple tumor biological phenotypes. Therefore, the effect of *LINC01426* on the malignant phenotype of NSCLC warranted investigation. In the present study, significant *LINC01426* upregulation was observed in NSCLC tissues and cell lines. Functional experiments showed that *LINC01426* knockdown markedly inhibited

the proliferation, migration, and invasion of NSCLC cells and promoted cell apoptosis in vitro. Furthermore, *LINC01426* interference restricted the growth of NSCLC tumors in vivo. These results suggest that *LINC01426* is a useful diagnostic and therapeutic target for NSCLC. But, *LINC01426* expression presented none correlation with tumor stage, overall survival or disease free survival in patients with NSCLC, implying that *LINC01426* may have no potential to be developed as a prognostic biomarker.

The subcellular localization of lncRNAs determines their mechanisms of action.⁴⁴ To elucidate the mechanisms involved in *LINC01426*-mediated control of NSCLC malignant behavior, the subcellular distribution of *LINC01426* was examined. Our study confirmed that *LINC01426* was primarily localized in the cytoplasm of NSCLC cells. Cytoplasmic lncRNAs are capable of sequestering miRNAs and decreasing their inhibitory effects on target genes.⁴⁵ Bioinformatics analysis was performed and the findings validated the relationship between miR-519d-5p and *LINC01426* by revealing that miR-519d-5p was significantly overexpressed in response to *LINC01426* depletion. Furthermore, an inverse correlation existed between *LINC01426* and miR-519d-5p expression in NSCLC tissues. In addition, the luciferase reporter and RIP assays revealed that *LINC01426* showed the ability to directly bind to miR-519d-5p and act as a molecular sponge for miR-519d-5p in NSCLC cells.

Further, mechanistic experiments revealed that *ETS1* is a direct target gene of miR-519d-5p in NSCLC cells.

According to the ceRNA theory, lncRNAs can compete for miRNA binding and consequently increase the target mRNA expression.²³ We evaluated the regulatory effect of *LINC01426* on *ETS1* expression in NSCLC cells. Our results indicated that *LINC01426* positively regulated *ETS1* expression in NSCLC cells by sequestering miR-519d-5p. These findings evidently demonstrate that a *LINC01426*/miR-519d-5p/*ETS1* ceRNA pathway exists in NSCLC.

ETS1, a member of the ETS family of transcription factors, was shown to be the downstream target of miR-519d-5p. *ETS1* is a known oncogene that reportedly facilitates oncogenesis and development in NSCLC by attenuating several processes including proliferation, cell cycle, apoptosis, migration, invasion, tumor formation, chemosensitivity, angiogenesis, and epithelial-mesenchymal transition.^{36–38} In the present study, mechanistic studies revealed a novel regulatory mechanism of the *LINC01426*/miR-519d-5p axis with respect to *ETS1*. MiR-519d-5p functions as a molecular bridge between *LINC01426* and *ETS1*, and the regulatory effect of *LINC01426* on *ETS1* expression is eliminated by miR-519d-5p. Moreover, the anti-oncogenic actions of *LINC01426* deficiency were offset by miR-519d-5p inhibition in NSCLC cells. Therefore, *LINC01426* can induce *ETS1* expression by sequestering miR-519d-5p, thereby aggravating malignant NSCLC progression.

In our study, we did not observe the metastasis in nude mice. It may be due to injection method and inadequate experiment period. Our study used subcutaneous injection. In the near future, we will employ the tail vein injection and longer experiment period to explore whether *LINC01426* can promote the metastasis of NSCLC cells in vivo.

Conclusion

The present study demonstrated the aberrantly high expression of *LINC01426* in NSCLC tissues and cell lines. *LINC01426* knockdown suppressed the tumorigenicity of NSCLC cells in vitro and in vivo. Preliminary experiments identified a *LINC01426*/miR-519d-5p/*ETS1* ceRNA pathway in NSCLC cells, and *LINC01426* exerted oncogenic activity via the miR-519d-5p/*ETS1* axis. The discovery of the *LINC01426*/miR-519d-5p/*ETS1* pathway may lead to the identification of effective therapeutic targets for managing NSCLC.

Consent for Publication

Not applicable.

Disclosure

The authors report no conflicts of interest for this work.

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