OncoTargets and Therapy

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ORIGINAL RESEARCH

RETRACTED ARTICLE: Long Intergenic Non-Protein Coding RNA 519 Promotes the Biological Activities of Tongue Squamous Cell Carcinoma by Sponging microRNA-876-3p and Consequently Upregulating MACC1

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Purpose: Long intergenic non-protein coding RNA 519 (*LINC00519*) promotes the development of lung squamous cell carcinoma. In this study, we detected the expression of *LINC00519* in tongue squamous cell carcinoma (TSCC) and examined its clinical significance. Additionally, the regulatory effects of *LINC00519* on behaviors of TSCC tumor cells were explored through functional experiments. Finally, mechanistic studies were performed to elucidate the molecular events underlying the tumor-promoting actions of *LINC00519* in TSCC.

Materials and Methods: The expression of *LINC00519* in TSCC tissues and cell lines was determined using quantitative reverse transcription-polymerase chain reaction. Cell counting kit-8 assay, flow cytometric analysis, cell migration and invasion assays and xenograft tumor model analysis were used to detect TSCC cell proliferation, apoptosis, migration and invasion and in vivo tumor growth, respectively. Mechanistic studies were performed using bioinformatics analysis, RNA immunoprecipitation assay, luciferase reporter assay and rescue experiments.

Results: *LINC00519* was overexpressed in both TSCC tissues and cell lines. A high *LINC00519* level was associated with poor overall survival in patients with TSCC. In vitro, *LINC00519* played cancer-promoting roles in TSCC progression by facilitating cell proliferation, migration and invasion and restraining cell apoptosis. In vivo, *LINC00519* downregulation resulted in decreased TSCC tumor growth. Mechanistically, *LINC00519* acted as a competing endogenous RNA for microRNA-876-3p (miR-876-3p), which directly targets metastasis associated with colon cancer-1 (*MACC1*), in TSCC cells. *LINC00519* upregulated the expression of *MACC1* in TSCC cells by sequestering miR-876-3p. Rescue experiments further affirmed that miR-876-3p inhibition or *MACC1* overexpression mitigated the inhibitory influences of *LINC00519* depletion on cell proliferation, migration and invasion and neutralized the promoting actions of *LINC00519* knockdown on cell apoptosis in TSCC.

Conclusion: *LINC00519* aggravated the oncogenicity of TSCC by regulating the miR-876-3p/MACC1 axis. Our findings suggest that the LINC00519/miR-876-3p/MACC1 pathway may be an underlying therapeutic target in TSCC.

Keywords: competing endogenous RNA pathway, metastasis associated in colon cancer-1, tongue squamous cell carcinoma, miRNAs

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Introduction

Tongue squamous cell carcinoma (TSCC) is the most common form of oral cancer, accounting for approximately 25–40% of all oral cancer cases.[1] The tongue has an abundant lymphatic and vascular supply and frequent movement, which promote local and distal metastasis.[2] Patients with TSCC are prone to high rates of recurrence and lymph node metastasis even after early detection and treatment with first-line therapies, resulting in poor survival.[3] The methods used to diagnose and treat TSCC have undergone extensive development in recent decades. Unfortunately, the clinical outcomes of patients with TSCC remain unsatisfying and are mainly attributed to rapid tumor progression.[4] Despite numerous scientific studies of basic cellular activity in TSCC,[5–7] the detailed molecular events involved in TSCC carcinogenesis and progression are largely elusive. Therefore, a complete recognition of the mechanisms underlying TSCC pathogenesis is urgently needed, as this may be useful in the identification of potential therapeutic targets.

In the human genome, approximately 98% of all transcripts lack an open reading frame and do not encode proteins; these are termed non-coding RNAs.[8] Long non-coding RNAs (lncRNAs) are a group of non-protein coding RNA molecules with lengths of >200 nucleotides.[9] These lncRNAs contribute to almost all physiological processes, including immune responses, growth, differentiation and metabolism.[10,11] Recent studies have identified lncRNAs as drivers of cancer oncogenesis and progression.[12–14] Particularly, an increasing number of literature reports suggest the differential expression of lncRNAs in TSCC.[15–17] Dysregulated lncRNAs exert oncogenic or anti-oncogenic effects and participate in the regulation of multiple cancer-associated biological behaviors in TSCC.[18–20]

MicroRNAs (miRNAs) are a family of short, single-stranded, evolutionarily conserved, non-coding RNA transcripts (17–24 nucleotides). These transcripts can regulate the expression of genes by directly binding to the 3′-untranslated regions (3′-UTRs) of their target genes, thus inducing the RNA induced silencing complex.[21] The number of known miRNAs exhibiting aberrant expression in TSCC is increasing, and these transcripts play critical roles in controlling the malignant behaviors of these tumors.[22–24] Regarding the associated mechanism, Leonardo Salmena proposed a competing endogenous RNA (ceRNA) theory,[25] in which lncRNAs act as miRNA "sponges" and decrease the inhibitory regulatory actions of miRNAs against their target messenger RNAs (mRNAs). Therefore, comprehensive studies of non-coding RNAs and the associated mechanisms may facilitate the development of potential targets for the diagnosis, prognosis and treatment of TSCC.

Long intergenic non-protein coding RNA 519 (*LINC00519*) was previously confirmed to promote the development of lung squamous cell carcinoma.[26] Nevertheless, the expression and role of *LINC00519* in TSCC and the related mechanisms have not been well studied. Therefore, we detected the expression of *LINC00519* in TSCC and examined its clinical significance. Additionally, we explored the regulatory effects of *LINC00519* on TSCC tumor cell behaviors through a series of functional experiments. Finally, we conducted mechanistic studies to elucidate the mechanisms underlying the tumor-promoting actions of *LINC00519* in TSCC.

Materials and Methods

Clinical Specimens

The study protocol was approved by the Research Ethics Committee of Henan Provincial People's Hospital (REC-HNPPH.20140702) and was compliant with the principles of the Declaration of Helsinki. All tissues were obtained after the participants provided written informed consent. A total of 52 TSCC tissues and adjacent normal tissues were collected from patients at Henan Provincial People's Hospital. All clinical specimens were stored in liquid nitrogen until required. None of the patients had received preoperative chemotherapy or radiotherapy or had a history of other malignancies.

Cell Culture and Transfection

Three human TSCC cell lines, SCC-9, SCC-15 and CAL-27, were acquired from American Type Culture Collection (ATCC; Manassas, VA, USA). SCC-9 and SCC-15 cells were grown in a 1:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 medium (Gibco; Thermo Fisher Scientific, Inc., Waltham, MA, USA) containing 10% fetal bovine serum (FBS; Gibco; Thermo Fisher Scientific, Inc.) and 400 ng/mL hydrocortisone. CAL-27 cells were cultivated in Dulbecco's modified Eagle's medium (Gibco; Thermo Fisher Scientific, Inc.) supplemented with 10% FBS and 1% penicillin-streptomycin solution (Gibco;

Thermo Fisher Scientific, Inc.). Normal human gingival epithelial cells (ATCC® PCS-200-014™; ATCC) were cultured in Minimum Essential Medium (Gibco; Thermo Fisher Scientific, Inc.) containing 10% FBS and 1% penicillin-streptomycin solution. All cells were grown at 37°C in a humidified incubator containing 5% CO_2.

Small interfering RNAs (siRNAs) designed to specifically target *LINC00519* (si-LINC00519) and a corresponding scrambled negative control (NC) siRNA (si-NC) were obtained from GenePharma Co., Ltd (Shanghai, China). MiR-876-3p mimic, miRNA mimic control (miR-NC), miR-876-3p inhibitor (anti-miR-876-3p) and miRNA inhibitor control (anti-miR-NC) were produced by Ribobio Co., Ltd (Guangzhou, China). The *MACC1* overexpression plasmid pcDNA3.1-MACC1 (pc-MACC1), *LINC00519* overexpression plasmid pcDNA3.1-LINC00519 (pc-LINC00519) and empty pcDNA3.1 plasmid were designed and constructed by Shanghai Sangon Company (Shanghai, China). Prior to transfection, the cells were inoculated into 6-well plates and incubated at 37°C with 5% CO_2. On the next day, transfection was performed using Lipofectamine® 2000 (Invitrogen; Thermo Fisher Scientific, Inc.).

Quantitative Reverse Transcription-Polymerase Chain Reaction (qRT-PCR)

TRIzol reagent (Invitrogen; Thermo Fisher Scientific, Inc.) was used to isolate total RNA from tissues or cells. The quality and quantity of the total RNA were determined using a NanoDrop 2000c spectrophotometer (Invitrogen; Thermo Fisher Scientific, Inc.). RNAs were subjected to reverse transcription using the miScript Reverse Transcription kit (Qiagen GmbH, Hilden, Germany), after which miR-876-3p expression was measured via quantitative PCR using the miScript SYBR Green PCR kit (Qiagen GmbH). U6 small nuclear RNA was used as the internal control for miR-876-3p expression. To quantify the expression of *LINC00519* and *MACC1*, total RNA was reverse transcribed into cDNA using the PrimeScript™ RT reagent kit with gDNA Eraser (TaKaRa, Dalian, China), after which quantitative PCR was performed using TB Green® Premix Ex Taq™ II (TaKaRa). The expression levels of *LINC00519* and *MACC1* were normalized to that of *GAPDH*. The $2^{-\Delta\Delta Cq}$ method was used to analyze RNA expression data.

Cell Counting Kit-8 (CCK-8) Assay

Transfected cells were detached with trypsin and collected via centrifugation at 24 h post-transfection. The cells were resuspended in a complete culture medium, and a 100 µL volume of suspension containing 2×10^3 cells was inoculated into each well of a 96-well plate. Cell proliferation was evaluated at 0, 24, 48 and 72 h after cell inoculation. At every time point, 10 µL of the CCK-8 reagent (Sigma-Aldrich, St. Louis, MO, USA) was added per well, and the cells were incubated at 37°C with 5% CO_2 for an additional 2 h. Finally, the absorbances at a wavelength of 450 nm were detected using a microplate reader.

Flow Cytometric Analysis of Cell Apoptosis

After a 48-h incubation period, the transfected cells were rinsed with phosphate buffer solution, treated with trypsin and subjected to Annexin V-FITC Apoptosis Detection Kit (Beyotime; Shanghai, China) for cell apoptosis measurement. After centrifugation at 1000 × g for 5 min, the transfected cells were collected and resuspended in 195 µL of Annexin V–FITC binding buffer. Next, 5 µL of Annexin V-FITC and 10 µL of propidium iodide were added to the cell suspension. After an incubated at 20–25°C for 20 min without light, the apoptotic cells were detected using a FACScan flow cytometer (BD Biosciences, Franklin Lakes, NJ, USA).

Cell Migration and Invasion Assays

Cell migration was evaluated according to the Transwell® method in previous publications.[27–29] Transfected cells were washed with phosphate buffer solution and resuspended in FBS-free basal medium. Next, 5×10^4 cells in suspension volume of 200 µL were introduced into each upper chamber of 24-well Transwell insert (Corning Incorporated, Corning, NY, USA). The lower chambers were filled with 600 µL of culture medium supplemented with 20% FBS, which acted as a chemoattractant.

The cells were allowed to pass through the 8 µm pores in the membranes for 24 h, after which the non-migrated cells were gently removed with a cotton swab. The migrated cells were fixed in 4% paraformaldehyde, stained with 0.5% crystal violet and imaged using an inverted light microscope (Olympus Corporation, Tokyo, Japan). Five random fields were selected, and the number of migrated cells was calculated in each field and averaged. To evaluate cell invasion, the upper chambers were

precoated with Matrigel (cat.no 354,234; BD Biosciences). The protein concentration of Matrigel is 9.6 mg/mL. The Matrigel was diluted to 300 ug/mL using FBS-free basal medium. A volume of 100 μL diluted Matrigel was added into the upper chambers and polymerized by cultivating at 37°C for 2 h. The remaining steps were the same as those described for the migration assay.

Xenograft Tumor Model Analysis

Studies involving animals were performed with approval from the Institutional Animal Care and Use Committee of Henan Provincial People's Hospital (ACUC-HNPPH. 20140702), in strict accordance with the NIH guidelines for the care and use of laboratory animals. Short hairpin RNAs (shRNAs) specifically targeting *LINC00519* (sh-LINC00519) and NC shRNA (sh-NC) were synthesized by GenePharma Co., Ltd., and were inserted into the GenePharma Supersilencing Vector. After lentivirus production, CAL-27 cells were transfected with lentiviruses encoding sh-LINC00519 or sh-NC, and the stably LINC00519-silenced CAL-27 cells were selected by incubation with puromycin. Four-week-old BALB/c nude mice were purchased from Shanghai SLAC Laboratory Anim[illegible] Co., Ltd. (Shanghai, China), and injected subcutaneously with CAL-27 cells stably transfected with sh-LINC00519 or sh-NC. From 1 to 4 weeks after cell injection, the width and length of each tumor xenograft was monitored every 4 days, and the tumor volume was calculated using the formula: tumor volume = (length × width^2)/2. Four weeks after implantation, all mice were euthanized by cervical dislocation, and the tumor xenografts were dissected and weighted.

Bioinformatics Analysis

The putative miRNAs of *LINC00519* were determined using the miRDB tool (http://mirdb.org/miRDB/index.html). TargetScan (http://www.targetscan.org/vert_60/) and miRDB online databases were searched for potential targets of miR-876-3p.

Subcellular Fractionation Assay

TSCC cells in the logarithmic growth phase were collected and subjected to nuclear and cytoplasmic fractionation using the Cytoplasmic and Nuclear RNA Purification Kit (Norgen, Thorold, ON, Canada). RNA was extracted from both fractions and subjected to qRT-PCR to test the relative expression of *LINC00519* in both fractions. *GAPDH* and *U6* were used as housekeeping controls in the nuclear and cytoplasmic fractions, respectively.

RNA Immunoprecipitation (RIP) Assay

RIP was performed using the EZ-Magna RIP™ RNA Binding Protein Immunoprecipitation Kit (Millipore, Billerica, MA, USA). TSCC cells were washed twice with phosphate buffer solution, lysed with RIP lysis buffer and centrifuged. The whole-cell extracts were incubated with magnetic beads that had been precoated with a human anti-Argonaute 2 (Ago2) antibody (Millipore) or control IgG (Millipore). An input containing 10% whole-cell extract was used as the positive control. After an overnight incubation at 4°C, the magnetic beads were collected and treated with RNase-free DNase I and Proteinase K to digest the extra DNA and protein. Finally, qRT-PCR was performed to detect the enrichment of *LINC00519* and miR-876-3p in the immunoprecipitated RNA.

Luciferase Reporter Assay

Fragments of *LINC00519* and *MACC1* containing the miR-876-3p binding site were constructed by GenePharma Co., Ltd. and cloned into the psiCHECK-2 luciferase reporter vector (Promega Corporation, Madison, WI, USA) to generate the reporter vectors wild-type-LINC00519 (wt-LINC00519) and wt-MACC1. Site-directed mutations of the miR-876-3p binding sequences in the *LINC00519* and *MACC1* fragments were achieved using a Site-Directed Mutagenesis Kit (Agilent Technologies, Santa Clara, CA, USA). The reporter vectors mutant-LINC00519 (mut-LINC00519) and mut-MACC1 were created by inserting the mutant *LINC00519* and *MACC1* fragments into the psiCHECK™-2 luciferase reporter vector. TSCC cells were seeded into 24-well plates and incubated overnight at 37°C with 5% CO_2, followed by co-transfection with wt or mut reporter vectors and miR-876-3p mimic or miR-NC in the presence of Lipofectamine® 2000. After 48 h, the relative luciferase activity was detected using a Dual-Luciferase Reporter System (Promega).

Western Blotting

For total protein extraction, cultured cells were rinsed with ice-cooled phosphate buffer solution and lysed in RIPA buffer supplemented with protease and phosphatase inhibitors (Beyotime). An enhanced BCA protein assay kit (Beyotime) was used to determine the total protein concentration in each lysate. Equivalent amounts of proteins were loaded onto 10%

SDS-polyacrylamide gels, separated by electrophoresis and transferred onto polyvinylidene difluoride membranes (Millipore). The membranes were blocked in 5% non-fat milk at room temperature for 2 h and were incubated overnight at 4°C with primary antibodies specific for MACC1 (ab226803; Abcam, Cambridge, MA, USA) or GAPDH (ab181602; Abcam). Subsequently, the membranes were probed with a goat anti-rabbit horseradish peroxidase-conjugated secondary antibody (ab205718; Abcam). The labeled proteins on the blots were detected using an ECL Substrate Kit (Abcam). GAPDH served as the loading control.

Statistical Analysis

All experiments were performed in three independently repeats, and all data are presented as means ± standard errors. Student's *t*-test was used to compare the differences between the two groups. Differences in multiple comparisons were examined using a one-way analysis of variance with Tukey's test. A Pearson's correlation analysis was used to evaluate the potential relationships between *LINC00519*, miR-876-3p and *MACC1*. All statistical analyses were performed using SPSS software, version 19.0 (SPSS, Chicago, IL, USA). A P value <0.05 was considered statistically significant.

Results

LINC00519 Depletion Inhibits Cell Proliferation, Migration and Invasion and Promotes Cell Apoptosis in TSCC

Because TSCC is a type of head and neck squamous cell carcinoma (HNSC), the *LINC00519* expression profile was analyzed in HNSCs included in The Cancer Genome Atlas (TCGA) dataset. As depicted in Figure 1A, *LINC00519* was expressed strongly in HNSC tissues compared with that in normal tissues. To verify this profile, the expression of *LINC00519* was detected by qRT-PCR in 52 pairs of TSCC tissues and adjacent normal tissues. Consistent with the results of the TCGA dataset analysis, *LINC00519* was overexpressed in TSCC tissues relative to the adjacent normal tissues (Figure 1B). Similarly, higher expression of *LINC00519* was observed in TSCC cell lines (SCC-9, SCC-15 and CAL-27) than in normal gingival epithelial cells (Figure 1C). Next, the prognostic potential of *LINC00519* expression in patients with TSCC was analyzed using the clinical data of TSCC patients. All 52 patients with TSCC were classified into either LINC00519-low or LINC00519-high groups using the median value of *LINC00519* in TSCC tissues as the cutoff point. Patients in the LINC00519-high group had a shorter overall survival duration than those in the LINC00519-low group (Figure 1D, P = 0.028).

To unveil the detailed roles of *LINC00519* in TSCC, this RNA was knocked down or increased in SCC-15 and CAL-27 cells by transfection with si-LINC00519 or pc-LINC00519 (Figure 2A), respectively. Here, si-LINC00519#1 most efficiently silenced LINC00519 expression and was therefore selected for subsequent experiments. CCK-8 assay was used to detect the impact of *LINC00519* on the proliferation of TSCC cells. Transfection with si-LINC00519 suppressed the proliferation of SCC-15 and CAL-27 cells, whereas transfection with pc-LINC00519 promoted cell proliferation (Figure 2B). In addition, flow cytometry analysis indicated that *LINC00519* knockdown resulted in significant increases in the percentages of apoptotic SCC-15 and CAL-27 cells. In contrast, the apoptotic rate was decreased in SCC-15 and CAL-27 cells upon *LINC00519* overexpression (Figure 2C). Cell

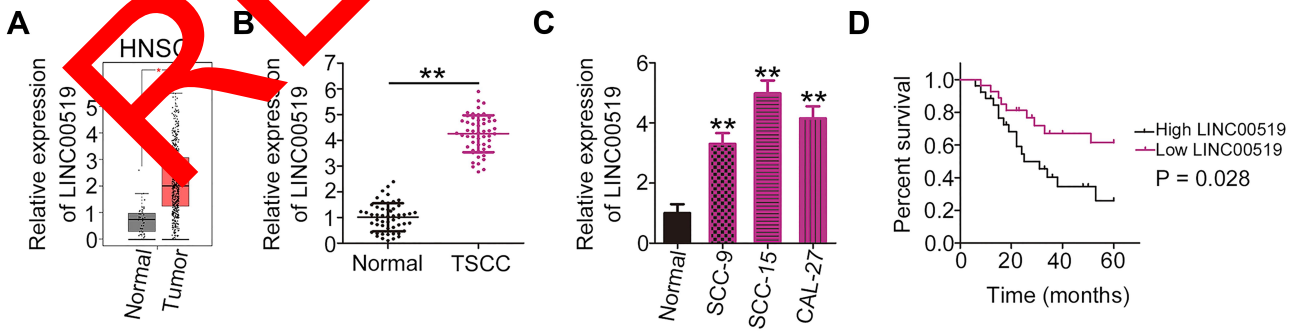

Figure 1 Long intergenic non-coding RNA 519 (*LINC00519*) is overexpressed in tongue squamous cell carcinoma (TSCC). (**A**) *LINC00519* expression was analyzed in head and neck squamous cell carcinoma (HNSC) cases in TCGA. (**B**) Quantitative real-time polymerase chain reaction (qRT-PCR) was performed to detect *LINC00519* expression in 52 pairs of TSCC tissues and adjacent normal tissues. (**C**) *LINC00519* expression in three TSCC cell lines (SCC-9, SCC-15 and CAL-27) and normal gingival epithelial cells was measured by qRT-PCR. (**D**) Overall survival of TSCC patients with high or low *LINC00519* expression was determined by a Kaplan–Meier analysis.**Note:** *P < 0.05 and **P < 0.01.

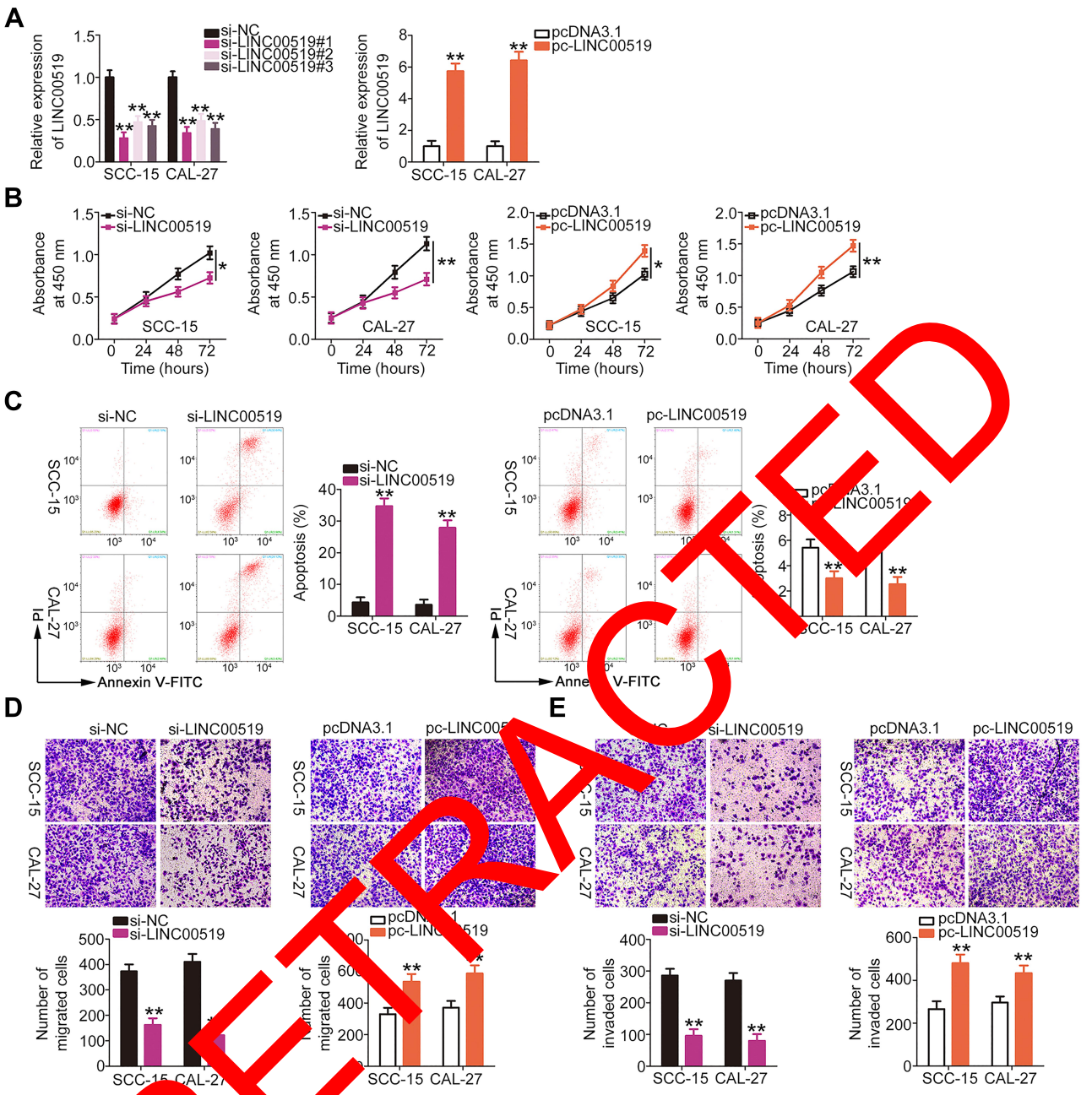

Figure 2 Long in[illegible]genic non[illegible]oding RNA (*LINC00519*) promotes tongue squamous cell carcinoma (TSCC) cell proliferation, migration and invasion and inhibits cell apoptosis. (**A**) [illegible]C-15 and [illegible]L-27 cells were transfected with small interfering RNA specific for *LINC00519* (si-LINC00519) or *LINC00519* overexpression plasmid pcDNA3.1-LINC[illegible]9 ([illegible]INC00519), and *LINC00519* expression was detected by qRT-PCR. (**B**) Cell counting kit-8 assay was performed to detect the proliferation of SCC-15 and CAL-27 [illegible] upon LINC00519 depletion or upregulation. (**C**) Flow cytometry analysis was performed to evaluate apoptosis of in SCC-15 and CAL-27 cells transfected with si-LINC[illegible]519 or pc-LINC00519. (**D** and **E**) The migratory and invasive capacities of SCC-15 and CAL-27 cells were assessed using cell migration and invasion assays after treatm[illegible] with si-LINC00519 or pc-LINC00519, respectively.
Note: *P < 0.05 and **P < 0.01.

migration and invasion assays, respectively, demonstrated that the migratory (Figure 2D) and invasive (Figure 2E) capacities of SCC-15 and CAL-27 cells were considerably hindered by *LINC00519* silencing, but clearly increased by *LINC00519* overexpression. Overall, these results suggest that *LINC00519* acts as an oncogenic lncRNA in TSCC cells.

LINC00519 Competitively Sponges miR-876-3p in TSCC Cells

Next, a series of experiments were carried out to decipher the mechanisms by which *LINC00519* aggravates the oncogenicity of TSCC cells. First, two online predictors of lncRNA subcellular localization, namely lncLocator (http://www.

csbio.sjtu.edu.cn/bioinf/lncLocator/) and lncATLAS (http://lncatlas.crg.eu/), were used to forecast the subcellular location of *LINC00519*. The predictions suggested that *LINC00519* was mostly distributed in the cytoplasm (Figure 3A and B). Next, subcellular fractionation assay confirmed the abundant expression of *LINC00519* in the cytoplasm of SCC-15 and CAL-27 cells (Figure 3C). The accumulated evidence demonstrates that cytoplasmic lncRNA acts as a ceRNA and decoy for certain miRNAs in human cancers.[30–32] Accordingly, a ceRNA model was utilized in the mechanistic studies.

Using the miRDB, 36 miRNAs (Figure 3D) were predicted as potential binding partners of LINC00519. Among these candidates, miR-7-5p, miR-876-3p, miR-216a-5p, miR-450b-5p, miR-890, miR-554, miR-670-3p, miR-30b-3p, miR-891a-3p and miR-215-3p were selected for subsequent assays as their enrollment in tumor genesis and progression. To further filter the results, changes in the expression of these miRNAs were analyzed in SCC-15 and CAL-27 cells after *LINC00519* depletion. qRT-PCR analysis revealed that miR-876-3p expression was increased in LINC00519-deficient SCC-15 and CAL-27 cells, while the expression of other miRNAs did not change in response to si-LINC00519 transfection (Figure 3E). Additionally, miR-876-3p was weakly expressed in TSCC tissues relative to adjacent normal tissues (Figure 3F). Notably, an inverse trend between *LINC00519* and miR-876-3p expression in TSCC tissues was verified using Pearson's correlation analysis (Figure 3G; r = −0.6463, P < 0.0001).

The wild-type and mutant binding sites of miR-876-3p in the sequence of *LINC00519* are presented in Figure 3H. Luciferase reporter assay was performed by co-transfecting wt-LINC00519 or mut-LINC00519 with miR-876-3p mimic or miR-NC into SCC-15 and CAL-27 cells. The upregulation of miR-876-3p eminently decreased the luciferase activity of wt-LINC00519 in both SCC-15 and CAL-27 cells, whereas no obvious change was identified in mut-LINC00519-transfected cells (Figure 3I). Finally, RIP assay revealed that both *LINC00519* and miR-876-3p were greatly enriched in an Ago2 antibody in SCC-15 and CAL-27 cells (Figure 3J), thus suggesting that these RNA elements coexist in the same RNA induced silencing complex. Taken together, the data suggest that *LINC00519* acts as a ceRNA by sponging miR-876-3p in TSCC cells.

MACC1 is a Target of miR-876-3p in TSCC Cells

To explore the effect of miR-876-3p in TSCC cells, miR-876-3p mimic was transfected into SCC-15 and CAL-27 cells. The mimic clearly increased miR-876-3p expression in SCC-15 and CAL-27 cells (Figure 4A). CCK-8 assay implicated that the proliferation capacities of SCC-15 and CAL-27 cells were impaired by the overexpression of miR-876-3p (Figure 4B). In addition, the ectopic expression of miR-876-3p remarkably stimulated the apoptosis of SCC-15 and CAL-27 cells (Figure 4C and D). Cell migration and invasion assays respectively affirmed that miR-876-3p restoration significantly curbed the migratory (Figure 4E) and invasive (Figure 4F) abilities of SCC-15 and CAL-27 cells.

Next, the putative target of miR-876-3p was predicted by bioinformatics analysis. A total of 362 genes were predicted by both TargetScan and miRDB. Among these candidates, the 3′-UTR of *MACC1* contains complementary binding sequences for miR-876-3 (Figure 4G) and was chosen for further confirmation because of its well-known oncogenic actions in TSCC progression.[33] Data from the luciferase reporter assay revealed that the upregulation of miR-876-3p strikingly reduced the luciferase activity of wt-MACC1 in SCC-15 and CAL-27 cells, whereas mutation of the binding site in *MACC1* 3′-UTR counteracted the suppressive action of miR-876-3p on luciferase activity (Figure 4H). Furthermore, *MACC1* was clearly overexpressed in TSCC tissues than in adjacent normal tissues (Figure 4I). Additionally, patients with TSCC characterized by high *MACC1* expression presented shorter overall survival in contrast to patients with low *MACC1* expression (Figure 4J, P = 0.033). There was an inverse expression correlation between miR-876-3p and *MACC1* expression in the TSCC tissues (Figure 4K; r = −0.6188, P < 0.0001). Moreover, transfection with miR-876-3p mimic led to a significant decrease in the expression of *MACC1* mRNA (Figure 4L) and protein (Figure 4M) in SCC-15 and CAL-27 cells. Collectively, miR-876-3p exerts cancer-inhibiting roles and directly targets *MACC1* in TSCC cells.

LINC00519 Regulates MACC1 Expression in TSCC Cells by Sequestering miR-876-3p

LncRNAs can act as ceRNAs by sponging and thereby modulating the targets of miRNAs.[34] After identifying

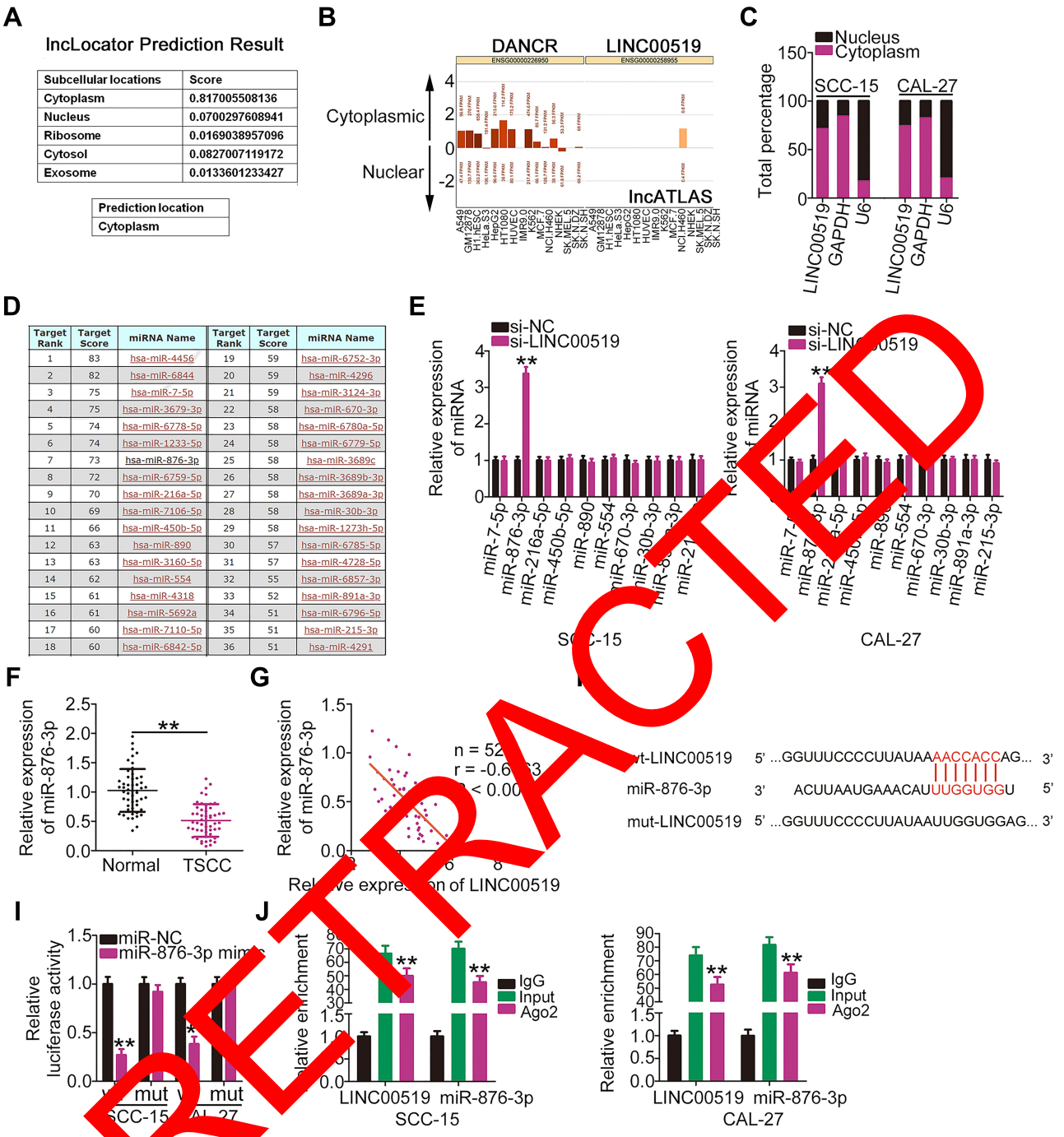

Figure 3 Long intergenic non-coding RNA 519 (*LINC00519*) sponges microRNA (miR)-876-3p in tongue squamous cell carcinoma (TSCC) cells. (**A** and **B**) The distribution of *LINC00519* was predicted using lncLocator and lncATLAS. *DANCR* was used as housekeeping control in the cytoplasmic. (**C**) The subcellular localization of *LINC00519* in SCC-15 and CAL-27 cells was verified using a subcellular fractionation assay. (**D**) Putative miRNAs that could interact with *LINC00519* were obtained from the miRDB. (**E**) Expression levels of miRNAs in LINC00519-depleted SCC-15 and CAL-27 cells were evaluated by quantitative real-time polymerase chain reaction (qRT-PCR). (**F**) qRT–PCR was used to determine the expression status of miR-876-3p in 52 pairs of TSCC tissues and adjacent normal tissues. (**G**) Pearson's correlation analysis revealed an inverse trend in miR-876-3p and *LINC00519* expression levels in TSCC tissues. (**H**) The predicted binding sequences between miR-876-3p and *LINC00519*. The mutant binding sequences are also shown. (**I**) Luciferase reporter assay was used to verify the binding interaction between miR-876-3p and *LINC00519*. Luciferase activity was detected in SCC-15 and CAL-27 cells that were transfected with wild-type (wt)-LINC00519 or mutant (mut)-LINC00519 in the presence of a miR-876-3p mimic or control (miR-NC). (**J**) Enriched miR-876-3p and *LINC00519* via Ago2-specific antibody-mediated bead precipitation were detected using an RNA immunoprecipitation assay.
Note: **P < 0.01.

LINC00519 as a molecular sponge for miR-876-3p, we next attempted to test whether LINC00519 would be implicated in the regulation of *MACC1* expression in TSCC cells. Thus, si-LINC00519 or si-NC was transfected into SCC-15 and CAL-27 cells, and the expression levels of *MACC1* mRNA and protein were measured via

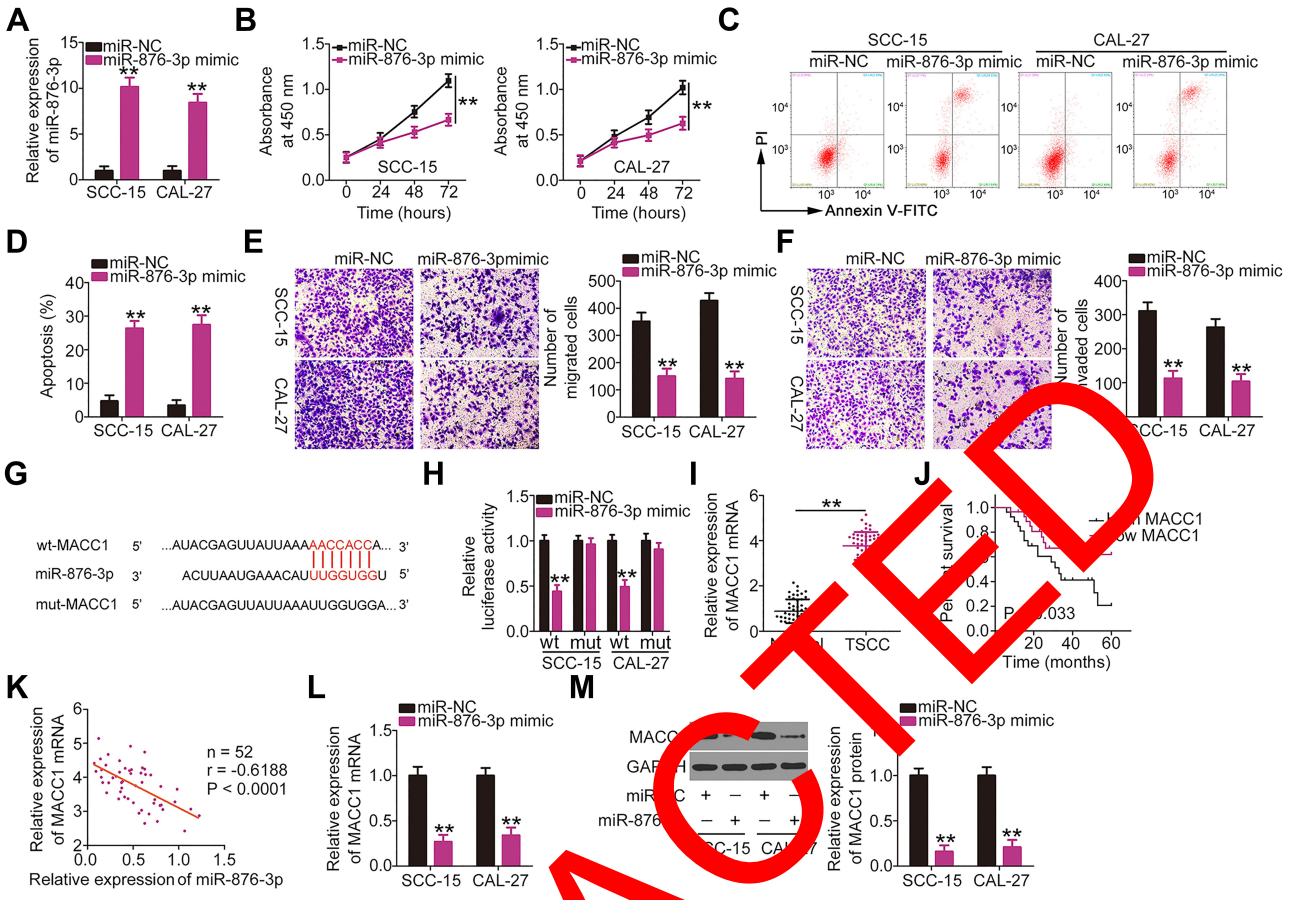

Figure 4 MicroRNA (miR)-876-3p inhibits cancer progression and directly targets metastasis-associated in colon cancer-1 (MACC1) in tongue squamous cell carcinoma (TSCC) cells. (**A**) MiR-876-3p expression was measured by quantitative real-time polymerase chain reaction (qRT-PCR) in SCC-15 and CAL-27 transfected with miR-876-3p mimic or control (miR-NC). (**B**–**D**) The proliferation and apoptosis of miR-876-3p overexpressing SCC-15 and CAL-27 cells were examined using a cell counting kit-8 assay and flow cytometry analysis, respectively. (**E** and **F**) Cell migration and invasion assays were used to determine the migratory and invasive properties, respectively, of SCC-15 and CAL-27 cells upon miR-876-3p overexpression. (**G**) Putative and conserved binding sequences of miR-876-3p within the 3′-UTR of *MACC1*. (**H**) Luciferase reporter assay was conducted to determine the effect of miR-876-3p overexpression on the luciferase activities of wild-type (wt)-MACC1 or mutant (mut)-MACC1 reporter vectors in SCC-15 and CAL-27 cells. (**I**) qRT-PCR was used to analyze *MACC1* mRNA expression in 52 pairs of TSCC tissues and adjacent normal tissues. (**J**) Overall survival of TSCC patients with high or low *MACC1* expression determined by Kaplan–Meier analysis. (**K**) Pearson's correlation analysis was performed to test the correlation between the levels of *MACC1* mRNA and miR-876-3p in the 52 TSCC tissues. (**L** and **M**) SCC-15 and CAL-27 cells were transfected with a miR-876-3p mimic or miR-NC, after which the *MACC1* mRNA and protein levels were evaluated via qRT-PCR and Western blotting.
Note: **P < 0.01.

qRT-PCR and Western blotting, respectively. Interference of *LINC00519* caused prominent decreases in the *MACC1* mRNA (Figure 5A) and protein (Figure 5B) levels in SCC-15 and CAL-27 cells, whereas these regulatory effects were obviously abolished by anti-miR-876-3p (Figure 5C and D). Furthermore, a correlation analysis demonstrated that *LINC00519* expression was positively correlated with *MACC1* expression in TSCC tissues (Figure 5E; r = 0.6645, P < 0.0001). RIP assay further corroborated the coexistence of *LINC00519*, miR-876-3p and *MACC1* in the same RNA induced silencing complex (Figure 5F). In summary, *LINC00519* could decoy miR-876-3p as a molecular sponge in TSCC cells, thus leading to an increase in *MACC1* expression.

Silencing miR-876-3p or Overexpressing MACC1 Eliminates the Inhibitory Actions of LINC00519 Knockdown on the Progress of TSCC Cells

Rescue experiments were implemented to further elucidate whether *LINC00519* exerted its functions in TSCC cells through the miR-876-3p/MACC1 axis. The efficiency of anti-miR-876-3p as a silencer miR-876-3p expression is depicted in Figure 6A. *LINC00519*-depleted SCC-15 and CAL-27 cells were co-transfected with anti-miR-876-3p or anti-miR-NC. CCK-8 assay revealed that the inhibitory effect of si-LINC00519 on the proliferation of SCC-15 and CAL-27 cells was abolished by co-transfection with

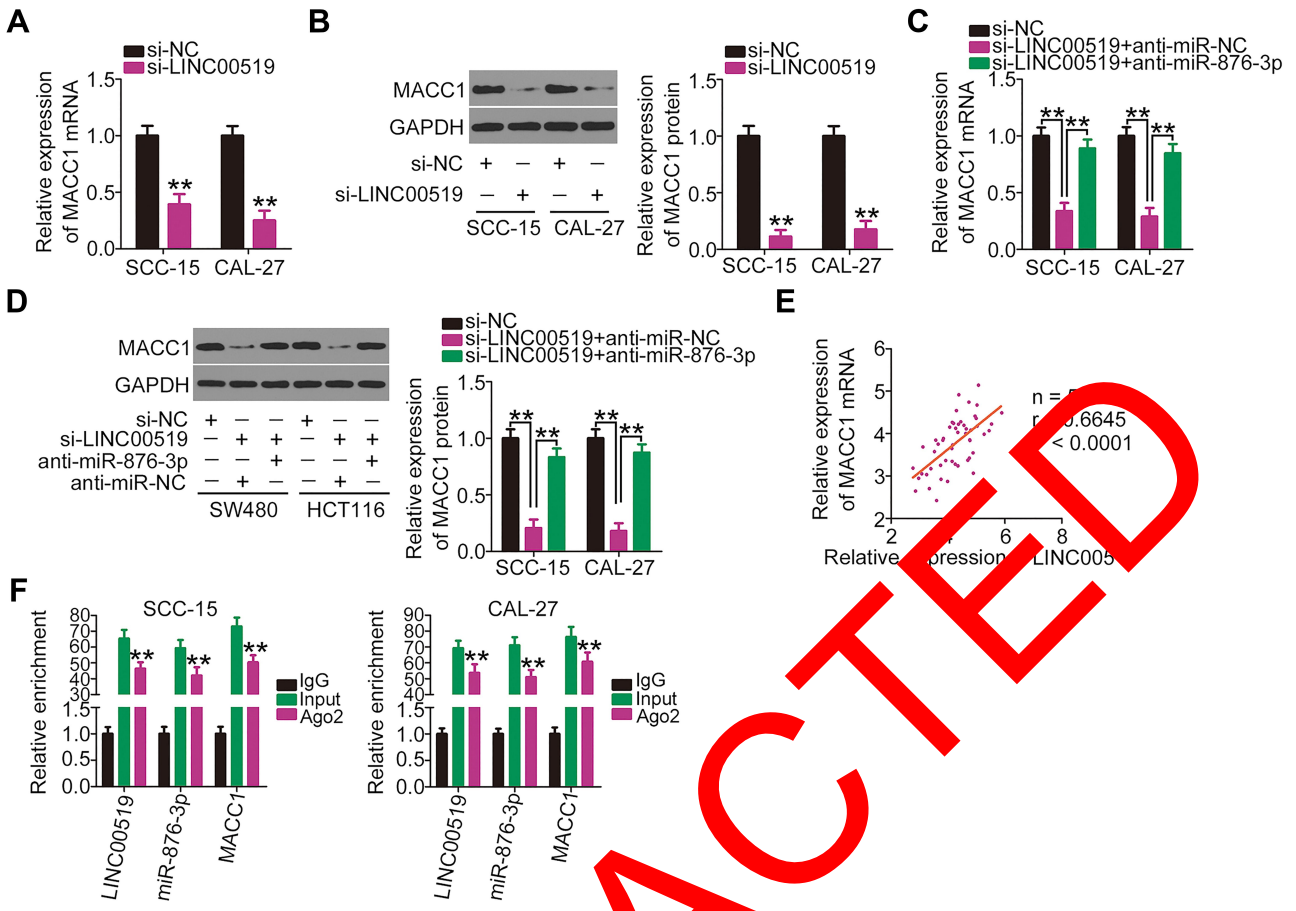

Figure 5 Long intergenic non-coding RNA 519 (*LINC00519*) increases metastasis-associated in colon cancer-1 (*MACC1*) expression by sponging microRNA (miR)-876-3p in tongue squamous cell carcinoma (TSCC) cells. (**A** and **B**) *MACC1* mRNA and protein expression in SCC-15 and CAL-27 cells transfected with small interfering RNA specific for *LINC00519* (si-LINC00519) or a negative control control (NC) were measured by quantitative real-time polymerase chain reaction (qRT-PCR) and Western blotting, respectively. (**C** and **D**) LINC00519-depleted SCC-15 and CAL-27 cells were further transfected with anti-miR-876-3p or anti-miR-NC, after which *MACC1* mRNA and protein expression were measured using qRT-PCR and Western blotting, respectively. (**E**) The correlation between *LINC00519* and *MACC1* mRNA expression in the 52 TSCC tissues was analyzed using a Pearson's correlation analysis. (**F**) Enrichment of *LINC00519*, miR-876-3p and *MACC1* via bead precipitation with Ago2 antibody was detected using an RNA immunoprecipitation assay.
Note: **P < 0.01.

anti-miR-876-3p (Figure 6B). Flow cytometry analysis indicated that the inhibition of miR-876-3p eliminated the increased apoptosis of SCC-15 and CAL-27 cells in response to *LINC00519* knockdown (Figure 6C). In addition, the suppressive effects of *LINC00519* silencing on the migration (Figure 6D) and invasion (Figure 6E) of SCC-15 and CAL-27 cells were clearly reversed by anti-miR-876-3p.

Meanwhile, the *MACC1* overexpression plasmid pc-MACC1 was used in rescue experiments. Western blotting verified that transfection with pc-MACC1 led to increased *MACC1* protein expression in SCC-15 and CAL-27 cells (Figure 7A). SCC-15 and CAL-27 cells were co-transfected with pc-MACC1 or pcDNA3.1 and si-LINC00519, and the influences of these reagents on cell proliferation, apoptosis, migration and invasion were determined by CCK-8 assay, flow cytometry, and cell migration and invasion assays, respectively. The data revealed that interference with *LINC00519* clearly constrained cell proliferation (Figure 7B), promoted cell apoptosis (Figure 7C) and restricted cell migration (Figure 7D) and invasion (Figure 7E), whereas *MACC1* overexpression counteracted these effects. Consequently, these results suggest that *LINC00519* promotes the malignant properties of TSCC cells by regulating the miR-876-3p/MACC1 axis.

Depletion of LINC00519 Restrains TSCC Tumor Growth in vivo

First, *LINC00519* expression was analyzed in CAL-27 cells stably transfected with sh-LINC00519 or sh-NC. qRT-PCR analysis revealed that *LINC00519* expression was remarkably decreased in stably sh-LINC00519-transfected

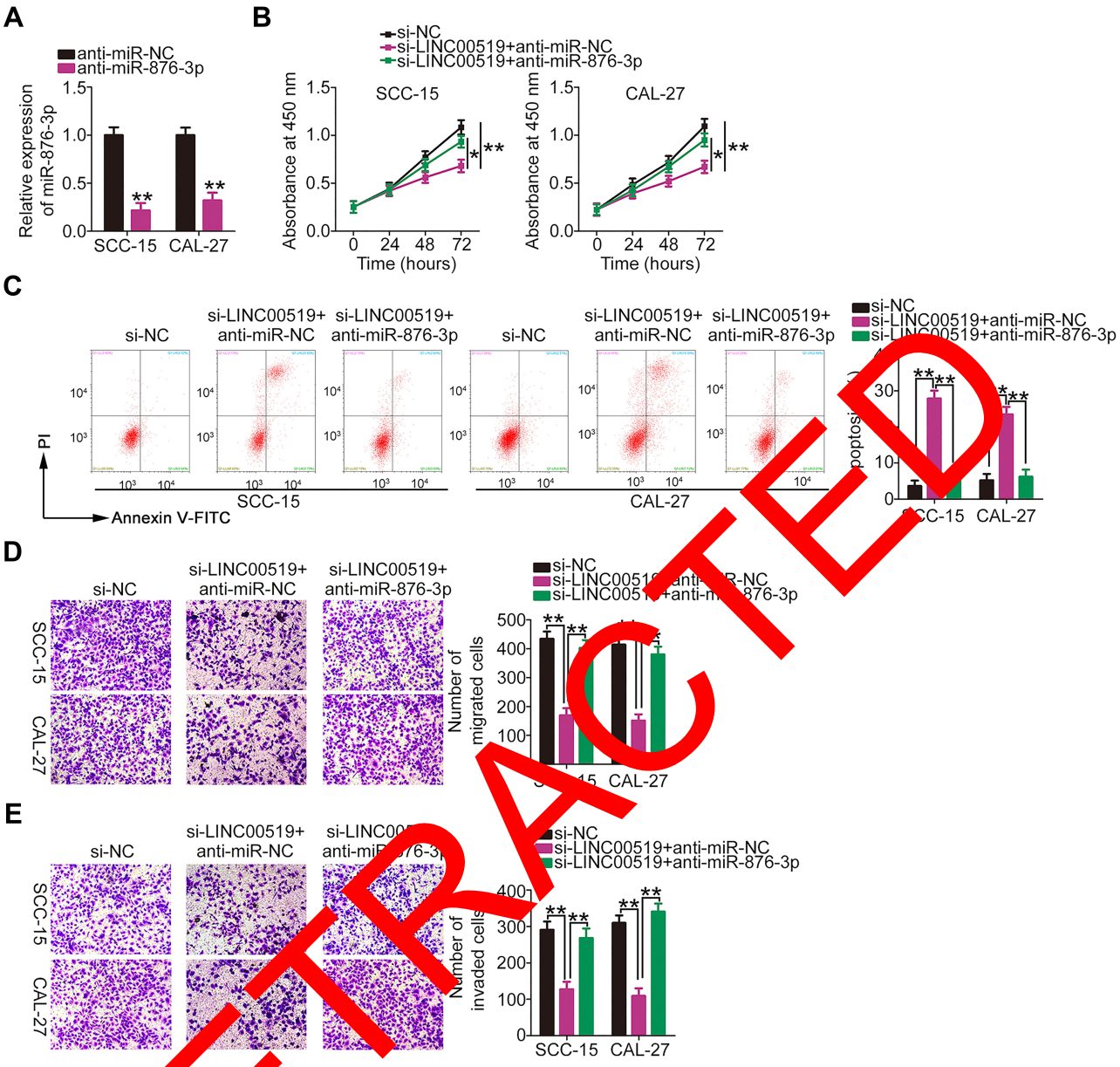

Figure 6 MicroRNA (miR) -3p inhibition eliminates the inhibitory actions of small interfering RNA specific for long intergenic non-coding RNA 519 (si-LINC00519) on SCC-15 and CAL-27 cells. (**A**) ntitative re me polymerase chain reaction (qRT-PCR) was used to assess the expression of miR-876-3p in SCC-15 and CAL-27 cells transfected wit 876-3p nti-mi NC. (**B** and **C**) SCC-15 and CAL-27 cells were transfected with si-LINC00519 in combination with anti-miR-876-3p or anti-miR-NC. A counting t-8 assay a w cytometry analysis were used to detect cell proliferation and apoptosis, respectively. (**D** and **E**) The migration and invasion of SCC-15 a CAL-27 c treated as above described was determined by cell migration and invasion assays, respectively.
Note: *P 05 an

CAL-27 cells relative to sh-NC-transfected cells (Figure 8A), suggesting that sh-LINC00519 lentivirus-infected CAL-27 cells could be used in xenograft tumor model analysis. To investigate the effects of *LINC00519* on tumor growth in vivo, xenograft models were constructed by subcutaneously injecting nude mice with CAL-27 cells stably transfected with sh-LINC00519 or sh-NC. The volumes (Figure 8B and C) and weights (Figure 8D) of the xenograft tumors were strikingly lower in the sh-*LINC00519* group than in the sh-NC group. Molecular analysis revealed that xenograft tumors derived from mice injected with stable LINC00519-knockdown cells contained decreased *LINC00519* (Figure 8E) and increased miR-876-3p (Figure 8F) levels. Furthermore, the decreased *MACC1* mRNA (Figure 8G) and protein (Figure 8H) levels were also confirmed in *LINC00519* depleted-tumor xenografts. These results further supported the cancer-promoting effects of *LINC00519* in TSCC tumorigenesis in vivo.

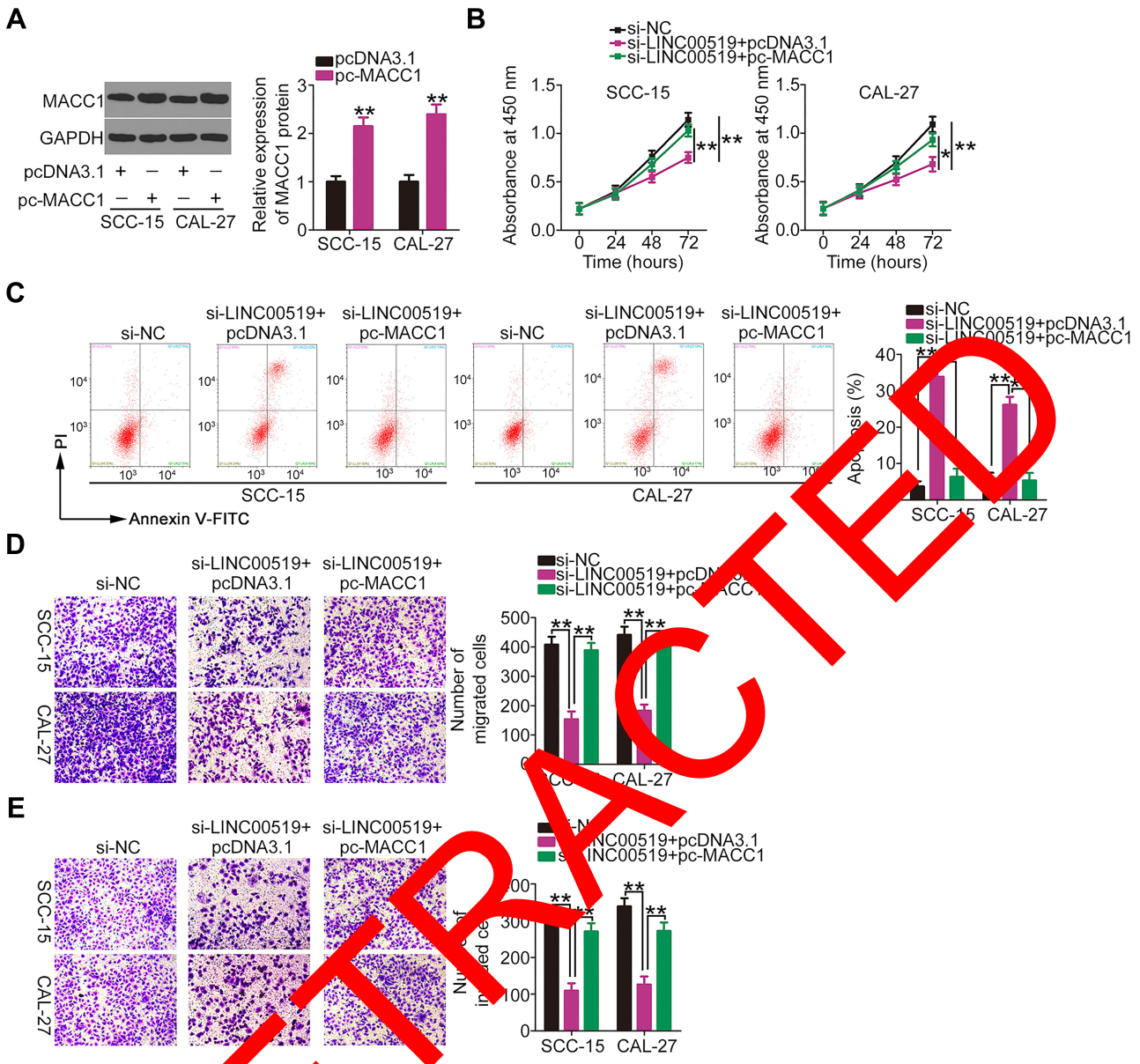

Figure 7 Increased metastasis-associated lung adenocarcinoma transcript 1 (*MACC1*) expression reverses the effect of long intergenic non-coding RNA 519 (*LINC00519*) knockdown on the proliferation, apoptosis, migration and invasion of SCC-15 and CAL-27 cells. (**A**) *MACC1* protein expression was measured by Western blotting after transfection with a *MACC1* overexpression plasmid (pc-MACC1) or empty vector (pcDNA3.1) into SCC-15 and CAL-27 cells. (**B**–**E**) The pc-MACC1 or pcDNA3.1 were co-transfected with siRNA specific for *LINC00519* (si-LINC00519) in SCC-15 and CAL-27 cells. Cell proliferation, apoptosis, migration and invasion were determined using a cell counting kit-8 assay, flow cytometry analysis and cell migration and invasion assays, respectively.
Note: *P < 0.05 and **P < 0.01.

Discussion

The importance of lncRNAs in cancer genesis and progression has recently received considerable attention. Several studies have revealed the dysregulation of lncRNAs in TSCC.[35–37] Abnormally expressed lncRNAs may exert tumor-promoting or tumor-inhibiting effects and could participate in the regulation of tumor properties in TSCC.[38,39] Thus, lncRNAs may be novel auxiliary diagnostic and therapeutic targets in TSCC. However, the detailed roles of most lncRNAs in TSCC and the related molecular mechanisms largely remain unclear. In this study, we attempted to investigate the expression status and regulatory effect of L*INC00519* TSCC. We also explored the molecular mechanisms by which *LINC00519* executes its oncogenic role in TSCC in detail.

LINC00519 expression is upregulated in lung squamous cell carcinoma.[26] High *LINC00519* expression is closely associated with an unsatisfactory prognosis in

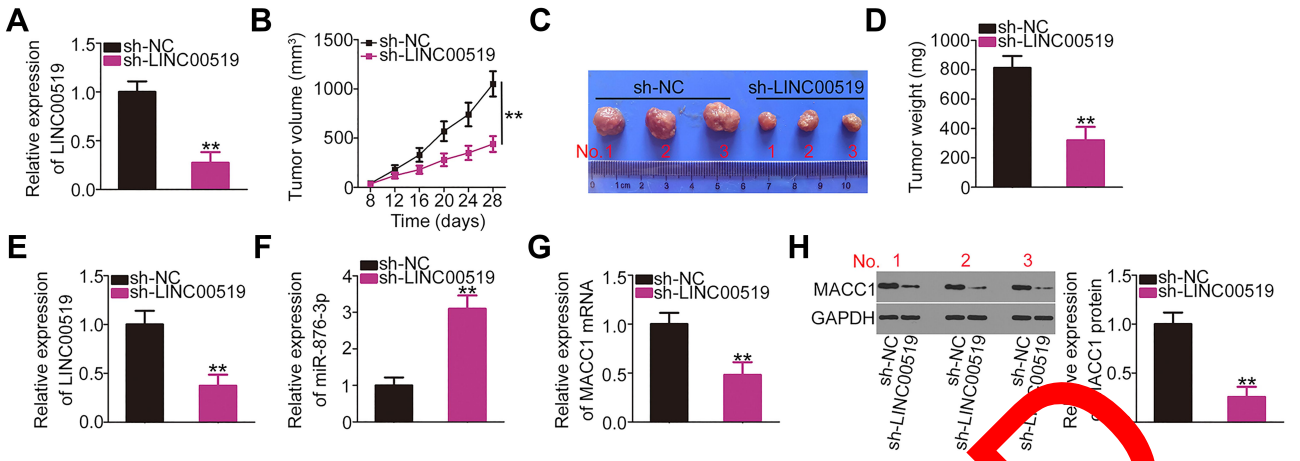

Figure 8 Loss of long intergenic non-coding RNA 519 (*LINC00519*) hinders the growth of tongue squamous cell carcinoma (TSCC) xenograft tumors in vivo. (**A**) The silencing efficiency of short hairpin RNA specific for *LINC00519* (sh-LINC00519) against *LINC00519* was analyzed by quantitative real-time polymerase chain reaction (qRT-PCR). (**B**) One week after cell injection, the tumor volumes was monitored every 4 days and tumor growth curves were plotted. (**C**) Photographs of tumor xenografts resected from nude mice. (**D**) Tumor xenografts were resected and weighted. (**E** and **F**) The expression of *LINC00519* and miR-876-3p in the tumor xenografts was detected by qRT-PCR. (**G** and **H**) qRT-PCR and Western blotting were performed to measure metastasis associated in colon cancer 1 (*MACC1*) mRNA and protein expression in tumor xenografts, respectively.
Note: **P < 0.01.

patients with lung squamous cell carcinoma.[26] Functionally, *LINC00519* exerts pro-oncogenic roles in lung squamous cell carcinoma cells.[26] In contrast, the expression profile and biological functions of *LINC00519* in TSCC have rarely been documented. In this study, *LINC00519* was highly expressed in TSCC from both the TCGA database and our own database. Importantly, patients with high *LINC00519* expression had shorter overall survival durations than those with low *LINC00519* expression. *LINC00519* depletion attenuated TSCC cell proliferation, migration and invasion and promoted cell apoptosis in vitro.

Matrigel is a soluble basement membrane component isolated from Engelbreth-Holm-Swarm mouse sarcoma.[40] It is in a liquid state at 4°C and polymerizes into a physiologically active gel state at a physiological state (24~37°C). It mainly consisted of laminin, type IV collagen, nestin, heparin sulfate glycoprotein, matrix metalloproteinases and various cytokines. In tumors, the basement membrane matrix still presents biological activity in different cells.[41] Matrigel can provide a favorable tumor microenvironment for tumor cell invasion, migration, luminal structure formation, cell biochemical function, and tumor growth in vivo.[42] In our study, a total of 1×10^6 TSCC cells in 100 μL phosphate buffer saline together with an equal volume of Matrigel basement (9.6 mg/mL) membrane matrix were used in xenograft tumor model analysis, and subcutaneously injected into the mice. The results showed that loss of *LINC00519* impaired tumor growth in vivo. These results suggest that *LINC00519* is a potential prognostic biomarker and therapeutic target for TSCC.

Increasing studies have corroborated the roles of lncRNAs in a wide range of processes through various mechanisms.[43] Mechanistically, lncRNAs can modulate gene expression at the pre-transcriptional, transcriptional and post-transcriptional levels, and the subcellular distribution of lncRNAs decides the level of regulation to a great degree.[44] Cytoplasmic lncRNAs always act as molecular sponges for miRNAs, thereby hindering the inhibitory actions of miRNA against target mRNA.[25] Herein, online lncRNA subcellular localization predictors and subcellular fractionation assays were used to determine that *LINC00519* was mostly located in the cytoplasm of TSCC cells, suggesting that this lncRNA may exert its oncogenic actions by sequestering miRNA. Therefore, bioinformatics tool was applied to identify candidate miRNAs that may target *LINC00519*. Using qRT-PCR, luciferase reporter and RIP assays, we revealed that *LINC00519* could act as a miR-876-3p sponge in TSCC cells.

MiR-876-3p is differentially expressed in multiple human cancers and contributes to the tumorigenic processes.[45–47] However, few reports have described the expression and functions of miR-876-3p in TSCC. In this study, we demonstrated the downregulation of miR-876-3p in TSCC. Functionally, miR-876-3p upregulation restricted TSCC growth and metastasis in vitro.

MiRNAs exert regulatory functions by directly binding to the 3′-UTR downstream targets.[48] Hence, we elucidated the direct target gene that contributes to the anti-oncogenic activities of miR-876-3p in TSCC cells. The *MACC1* 3′-UTR contains a highly conserved binding site for miR-876-3p, which was further confirmed by a luciferase reporter assay. Additionally, *MACC1* turned out to be negatively regulated by miR-876-3p in TSCC cells. After identifying *MACC1* as a direct target of miR-876-3p, the association between *LINC00519*, miR-876-3p and *MACC1* in TSCC was unveiled. Our study revealed that *LINC00519* promoted *MACC1* expression in TSCC by decoying miR-876-3p. Additionally, RIP assay affirmed the coexistence of *LINC00519*, miR-876-3p and *MACC1* in the same RNA induced silencing complex. These results provide sufficient evidence supporting the existence of a novel ceRNA pathway involving *LINC00519*, miR-876-3p and *MACC1* in TSCC.

MACC1, which is located on human chromosome 7 (7p21.1),[49] is upregulated in TSCC and is closely associated with lymphatic metastasis.[50] In TSCC patients, increased *MACC1* expression tends to be associated with worse clinical outcomes.[50] *MACC1* is considered the main regulator of tumor progression in TSCC, in which it affects a number of malignant processes.[33,50] *MACC1* affected cancer progression through different mechanisms. For example, *MACC1* improves the cisplatin resistance partially in lung cancer via the PI3K/AKT pathway, whereas its depletion suppresses lung cancer cell proliferation and causes cell apoptosis through the β-catenin pathway.[52] Furthermore, *MACC1* is implicated in the control of HGF/Met and MEK/ERK pathways in ovarian cancer,[53] Akt/β-catenin pathway in nasopharyngeal carcinoma,[54] and HGF/c-Met/AKT pathway in hepatocellular carcinoma.[55] Our study did not explore the effects of *LINC00519* on these signaling pathways that were under the control of *MACC1*. We will resolve it in the near future.

In this study, our results also indicate that *MACC1* is controlled by the LINC00519/miR-876-3p axis in TSCC cells. Meanwhile, rescue experiments revealed that the inhibition of miR-876-3p or overexpression of *MACC1* mitigated the inhibitory influences of *LINC00519* depletion on cell proliferation, migration and invasion and neutralized the exacerbating actions of *LINC00519* knockdown on the apoptosis of TSCC cells. In summary, in TSCC cells, *LINC00519* competes with miR-876-3p to act as a ceRNA and thus activates *MACC1* and aggravates tumor oncogenicity.

Conclusion

LINC00519 expression was upregulated in TSCC, and this long non-coding RNA exerted a tumor-promoting role and thus facilitated TSCC progression. Mechanistically, *LINC00519* acted as a ceRNA for miR-876-3p in TSCC, thus enhancing the expression of *MACC1*. Our current study findings enhance our understanding of the mechanism underlying TSCC pathogenesis and may promote the development of potential targeted therapies for TSCC.

Disclosure

The authors declare that they have no competing interests.

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