

Long noncoding RNA SNHG14 promotes breast cancer cell proliferation and invasion via sponging miR-193a-3p

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Abstract. – OBJECTIVE: Breast cancer (BC) is one of the most ordinary fatal cancers. Recent studies have identified the vital role of long non-coding RNAs (lncRNAs) in the development and progression of BC. In this research, lncRNA SNHG14 was studied to identify how it functioned in the development and metastasis of BC.

PATIENTS AND METHODS: SNHG14 expression in BC tissues was detected by Real Time quantitative Polymerase Chain Reaction (RT-qPCR) in 50 paired patients with BC. And cell proliferation assay, colony formation assay, and transwell assay were enrolled to observe the biological behavior changes of BC cells with gain/loss of SNHG14. In addition, luciferase assay and RNA immunoprecipitation assay (RIP) were performed to discover the potential targets of SNHG14 in BC cells.

RESULTS: SNHG14 expression level in BC samples was higher than that in adjacent ones. Besides, cell growth ability and cell invaded ability of BC cells were inhibited after SNHG14 was silenced, while cell growth ability and cell invaded ability of BC cells were promoted after SNHG14 was over expressed. In addition, miR-193a-3p was upregulated after silence of SNHG14 in BC cells, while miR-193a-3p was downregulated after over expression of SNHG14 in BC cells. Furthermore, luciferase assays and RNA immunoprecipitation assay (RIP) showed that miR-193a-3p was a direct target of SNHG14 in BC.

CONCLUSIONS: Our study uncovers a new oncogene in BC and suggests that SNHG14 could enhance BC cell proliferation and invasion by sponging miR-193a-3p, which provided novel therapeutic target for BC patients.

Keywords:

Long noncoding RNA, SNHG14, Breast cancer, MiR-193a-3p.

Introduction

Breast cancer (BC), accounting for 29% of all cancer diagnoses in women, is the most frequently diagnosed malignancy in female both in China and worldwide. It was estimated that 246,660 new cases were diagnosed of BC and 40,450 cases died due to BC in America in 2016¹. Despite great advances made in the diagnosis and therapeutic treatment in BC, the 5-year survival rate of BC patients remains below 25% because of the high rate of metastasis². However, the mechanism of pathogenesis in BC has not been completely explained. Therefore, it is urgent to have a better understanding of the molecular characteristics of BC.

Long non-coding RNAs (lncRNAs), more than 200 nt in length, have been reported to participate in a diversity of biological progression. For example, by targeting miR-130a-5p/HMGB2, the lncRNA HOXA11-AS promotes glioma cell growth and metastasis³. Cell proliferation and cell migration of ovarian cancer are inhibited after knockdown of lncRNA MNX1-AS1 in ovarian cancer⁴. lncRNA PCAT-1 modulates TP53-miR-215-PCAT-1-CRKL axis and exerts a vital function in tumorigenesis of hepatocellular carcinoma⁵. lncRNA AC132217.4 promotes cell metastasis in oral squamous cell carcinoma by regulation of IGF2 expression⁶. In addition, lncRNA PlncRNA-1 accelerates the progression of colorectal cancer cell *via* PI3K/Akt signaling pathway⁷. However, the clinical role and underlying mechanisms of SNHG14 in the development of BC remain unexplored. In the present study, we performed function and mechanism assays to explore whether SNHG14 functioned in the proliferation and metastasis of BC.

Patients and Methods

Patients and Clinical Samples

50 BC patients who received surgery at our hospital from 2015 to 2018 were enrolled for human tissues. Written informed consent was achieved before the operation. No radiotherapy or chemotherapy was performed before the surgery. All tissues were saved immediately at -80°C . The protocol of the study was approved by the Ethics Committee of Sir Run Run Shaw Hospital, Zhejiang University School of Medicine.

Cell Culture

Human BC cell lines (MCF-7, LCC9, T-47D, SKBR3) and MCF-10A (normal human breast cell line) were got from the Institute of Biochemistry and Cell Biology, Chinese Academy of Science (Shanghai, China). Culture medium consisted of 10% fetal bovine serum (FBS; Life Technologies, Gaithersburg, MD, USA), Dulbecco's modified Eagle's medium (DMEM) (Gibco, Rockville, MD, USA). Besides, cells were cultured in an incubator containing 5% CO_2 at 37°C .

Cell Transfection

Lentivirus expressing short-hairpin RNA (shRNA; Biosettia Inc., San Diego, CA, USA) against SNHG14 was synthesized. SNHG14 shRNA (SNHG14/shRNA) and negative control (control) were then used for transfection of T-47D BC cells. 48 h later, Real Time quantitative Polymerase Chain Reaction (RT-qPCR) was used to detect transfection efficiency. Besides, lentivirus (Biosettia Inc., San Diego, CA, USA) against SNHG14 (SNHG14/shRNA) was synthesized and then used for transfection of SKBR3 BC cells. Empty vectors was used as control. 48 h later, RT-qPCR was used to detect transfection efficiency in these cells.

RNA Extraction and RT-qPCR

TRIzol reagent (Invitrogen, Carlsbad, CA, USA) was utilized to separate the total RNA. Trizol reagent Transcription Kit (TaKaRa Bio-technology Co., Ltd., Dalian, China), complementary deoxyribose nucleic acid (cDNA) was then reverse transcribed from total RNA. Thermocycling conditions were as follows: pre-denaturation at 95°C for 5 min, denaturation at 95°C for 10 s, annealing at 60°C for 30 s, a total of 35 cycles. Following are the primers using for RT-qPCR: SNHG14, forward: 5'-GGGTGTTTACGTAGAC-CAGAACC-3' and reverse: 5'-CTTCCAAAAG-

CCTTCTGCCTTAG-3'; β -actin, forward: 5'-CCAACCGCGAGAAGATGA-3' and reverse: 5'-CCAGAGGCGTACAGGGATAG-3'.

Cell Proliferation Assay

Cell proliferation of BC cells in 96-well plates was monitored every 24 h by Cell Counting kit-8 (CCK-8) assay (Dojindo, Kumamoto, Japan). Spectrophotometer (Thermo Scientific, Bedford, IL, USA) was applied for measurement of optical absorbance at 450 nm.

Transwell Assay

8- μm pore size insert was provided by Corning (Corning, NY, USA). 4×10^4 cells in 150 μL serum-free medium were transfected to the top chamber of the insert coated with 50 μg Matrigel (BD, Bedford, MA, USA). The bottom chamber was covered with DMEM + FBS. 48 h later, the top surface of chambers was immersed for 10 min with precooling methanol and was stained in crystal violet for 10 min.

Luciferase Assay and RNA

Immunoprecipitation Assay (RIP)

The 3'-UTR of SNHG14 was cloned into the luciferase reporter (Promega, Madison, WI, USA) as wild type (WT) 3'-UTR. Site-direction mutagenesis of the miR-193a-3p binding site in SNHG14 3'-UTR as mutant (MUT) 3'-UTR was conducted through quick-change site-directed mutagenesis kit (Stratagene, La Jolla, CA, USA). Then, they were used for transfection of BC cells. The luciferase assay was conducted on the dual Luciferase reporter assay system (Promega, Madison, WI, USA). For RIP assay, Magna RIP RNA-Binding Protein Immunoprecipitation Kit (Millipore, Billerica, MA, USA) was performed according to the protocol. Then, the RT-qPCR was used to detect Co-precipitated RNAs. Treated BC cells were collected and lysed using RIP lysis buffer containing protease inhibitor and RNase inhibitor. Cells were incubated with the RIP buffer containing magnetic beads coated with Ago2 antibodies (Millipore, Billerica, MA, USA). IgG acted as a negative control (input group). After incubation for 2 h at 4°C , coprecipitated RNAs were isolated and measured by RT-qPCR analysis.

Statistical Analysis

All statistical analyses were carried out using GraphPad Prism 5.0 (La Jolla, CA, USA). The difference between the two groups was compared by the Student *t*-test. The statistical significance was defined as $p < 0.05$.

Results

SNHG14 Expression Level in BC Tissues and Cells

Firstly, SNHG14 expression was detected *via* RT-qPCR in 50 patients' tissues and 4 BC cell lines. As a result, SNHG14 was significantly up-regulated in BC tissue samples (Figure 1A). The SNHG14 expression level of BC cells was higher than that of MCF-10A (Figure 1B).

Silence of SNHG14 Inhibited Cell Proliferation and Invasion in T-47D BC Cells

In this study, we chose the T-47D BC cell line for the silence of SNHG14. Then, the SNHG14 expression was detected by RT-qPCR (Figure 2A). Moreover, results of CCK-8 assay and colony formation assay showed that the silence of SNHG14 significantly inhibited the ability of cell growth in BC cells (Figure 2B and 2C). The outcome of the transwell assay also revealed that the number of invaded cells was remarkably decreased after SNHG14 was silenced in BC cells (Figure 2D).

Overexpression of SNHG14 Promoted Cell Proliferation and Invasion in SKBR3 BC Cells

In this study, we chose the SKBR3 BC cell line for the overexpression of SNHG14. Then, the SNHG14 expression was detected by RT-qPCR (Figure 3A). Moreover, results of CCK-8 assay and colony formation assay showed that the

overexpression of SNHG14 significantly promoted the ability of cell growth in BC cells (Figure 3B and 3C). The outcome of the transwell assay also revealed that the number of invaded cells remarkably increased after SNHG14 was overexpressed in BC cells (Figure 3D).

The Interaction Between miR-193a-3p and SNHG14 in BC Cells

DIANA LncBASE Predicted v.2 (http://olona.imis.athena-innovation.gr/diana_tool/web/index.php?r=lna%20index-predicted) was used to find the miRNAs that contained complementary base with SNHG14. We selected miR-193a-3p, which contained binding area of SNHG14 (Figure 4A). RT-qPCR results showed that upregulated miR-193a-3p was observed in sh-SNHG14 group compared with control group (Figure 4B). RT-qPCR results showed that downregulated miR-193a-3p was observed in SNHG14 group compared with empty vector group (Figure 4C). Furthermore, results of luciferase assay showed that luciferase activity was significantly reduced through co-transfection of SNHG14-MUT and miR-193a-3p, while no significant changes of luciferase activity were observed through co-transfection of SNHG14-MUT and miR-193a-3p (Figure 4D). Meanwhile, RIP assay identified that SNHG14 and miR-193a-3p were significantly enriched in Ago2-containing beads compared to input group (Figure 4E). All these data revealed that miR-193a-3p was a direct target of SNHG14.

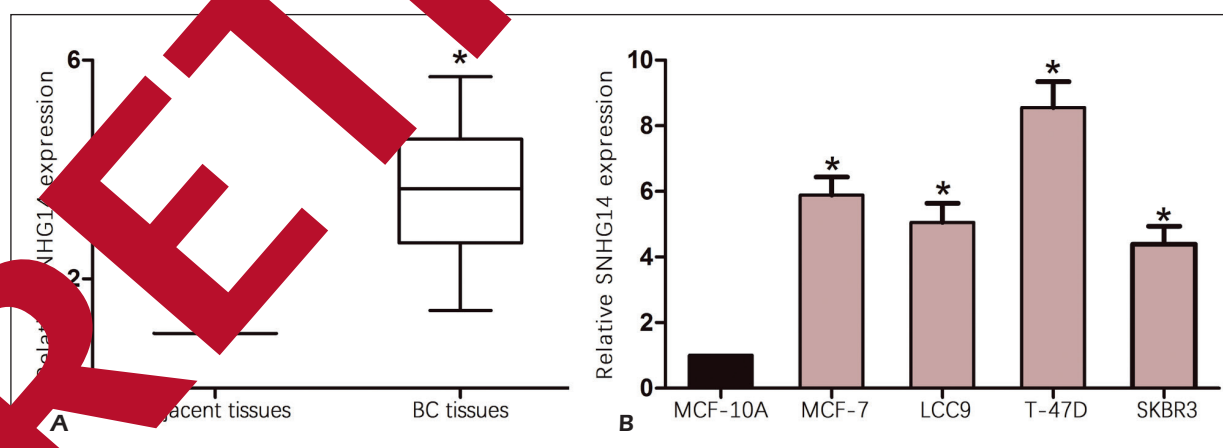


Figure 1. Expression level of SNHG14 was increased in BC tissues and cell lines. **A**, SNHG14 expression was significantly increased in the BC tissues compared with adjacent tissues. **B**, Expression levels of SNHG14 relative to β -actin were determined in the human BC cell lines and MCF-10A (normal human breast cell line) by RT-qPCR. Data are presented as the mean \pm standard error of the mean. * $p < 0.05$.

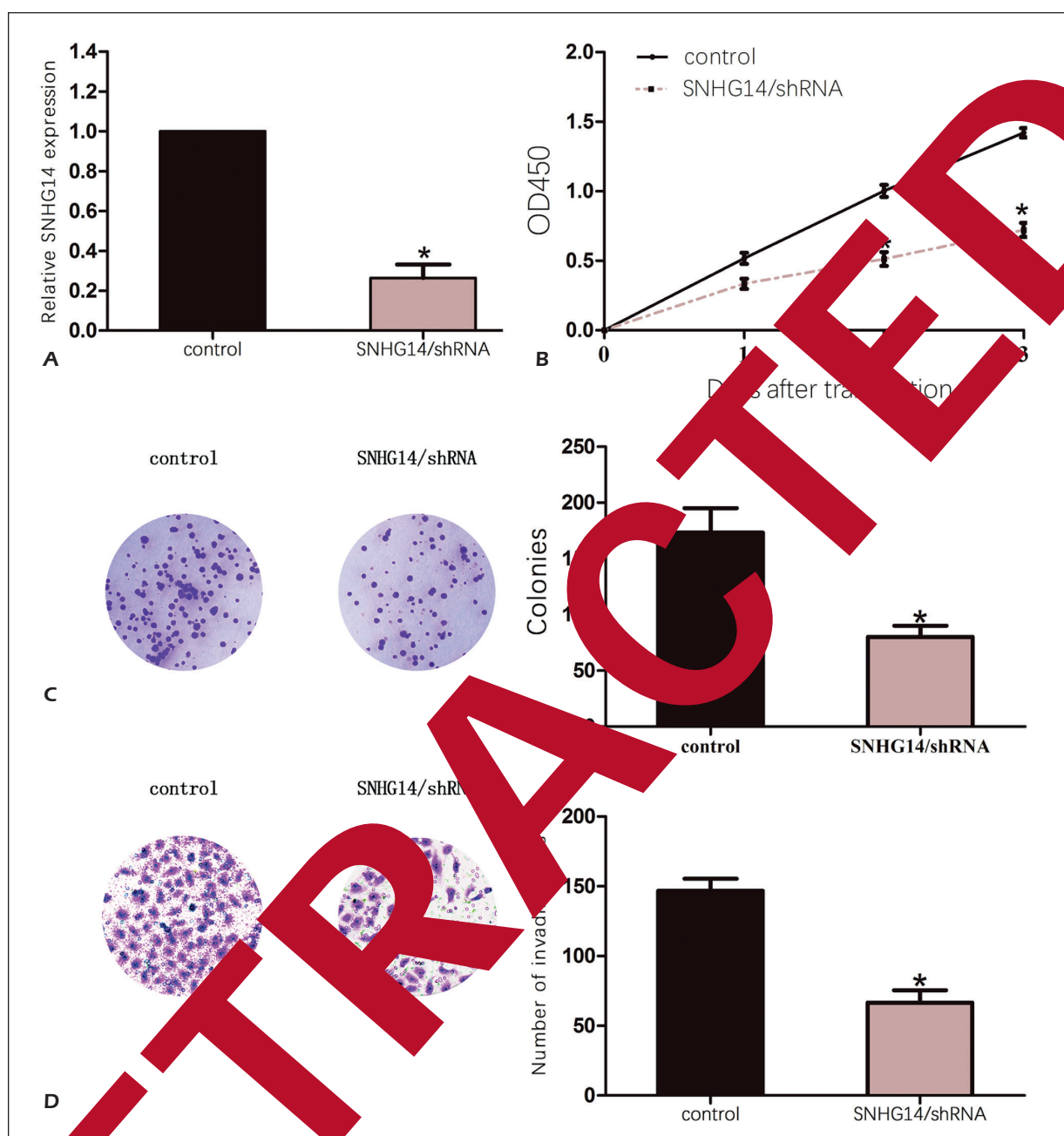


Fig. 7. Silencing SNHG14 inhibited T-47D BC cell proliferation and invasion. **A**, SNHG14 expression in BC cells transfected with SNHG14 shRNA (SNHG14/shRNA) and the negative control (control) was detected by RT-qPCR. β -actin was used as an internal control. **B**, Cell growth assay showed that silence of SNHG14 significantly repressed cell growth ability of BC cells (magnification $\times 100$). **C**, Colony formation assay showed that silence of SNHG14 significantly repressed cell growth ability of BC cells (magnification $\times 100$). **D**, Invasion assay showed that number of invaded cells was significantly decreased via silence of SNHG14 in BC cells (magnification $\times 100$). The results represent the average of three independent experiments (mean \pm standard error of the mean) ($p < 0.05$, as compared with the control cells).

Discussion

Numerous reports have indicated that lncRNAs are important regulators in the development of BC. For instance, lncRNA SNAR facilitates cell

proliferation and metastasis of BC cells and may be a novel therapeutic target⁸. LncRNA UCA1 functioned as an oncogene in BC and modulated cell proliferation and apoptosis by targeting miR-143⁹. LncRNA LINP1 promotes repair of DNA

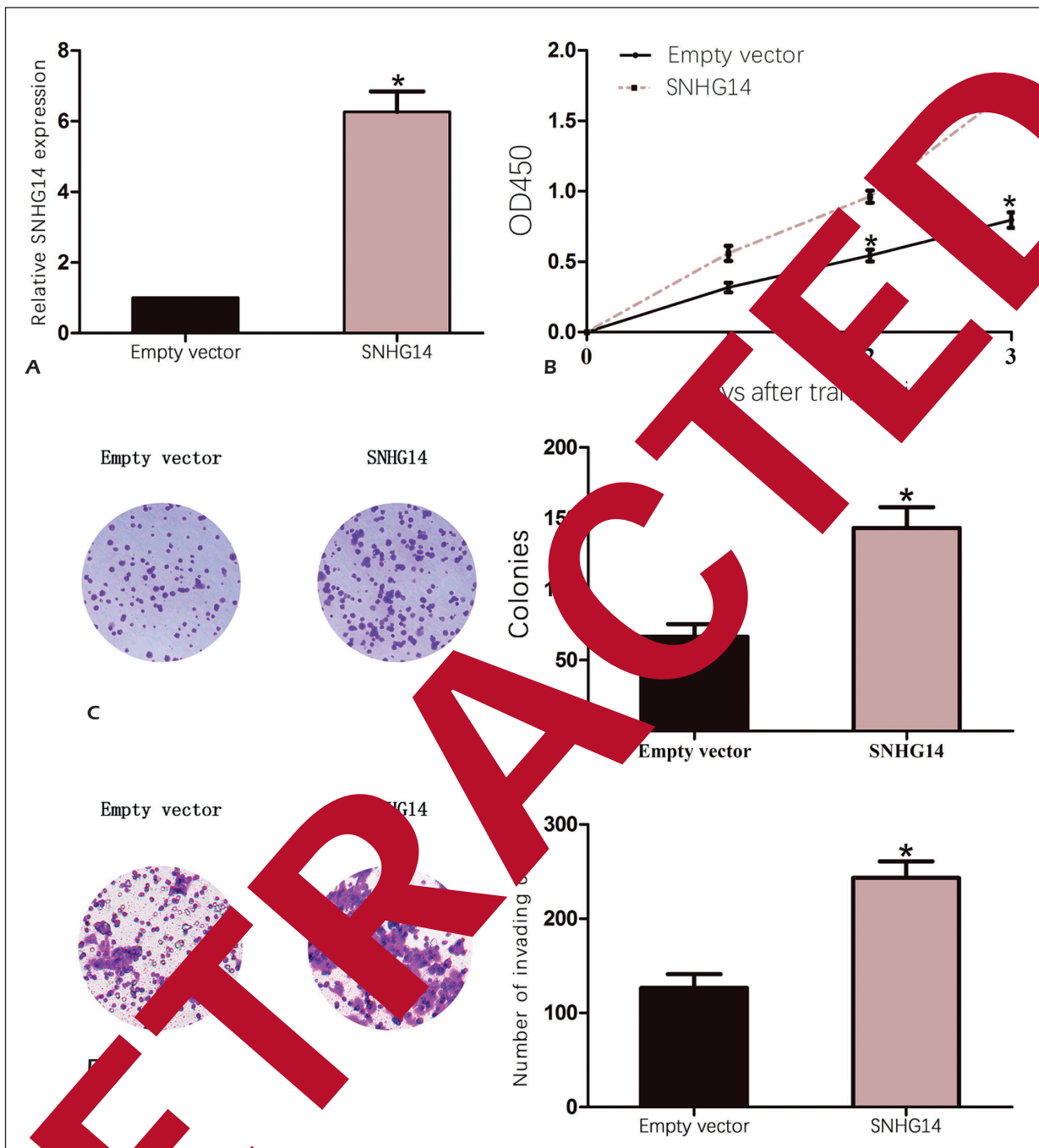


Figure 3 SNHG14 expression promoted SKBR3 BC cell proliferation and invasion. **A**, SNHG14 expression in BC cells transfected with SNHG14 lentivirus (SNHG14) and the empty vector was detected by RT-qPCR. β -actin was used as an internal control. **B**, Cell growth assay showed that overexpression of SNHG14 significantly promoted cell growth ability of BC cells. **C**, Colony formation assay showed that overexpression of SNHG14 significantly promoted cell growth ability of BC cells (magnification: 40 \times). **D**, Transwell assay showed that number of invaded cells was significantly increased via overexpression of SNHG14 in BC cells (magnification: 40 \times). The results represent the average of three independent experiments (mean \pm standard deviation of the mean). * p <0.05.

double-strand breaks and raises the sensitivity of cancer cell to radiotherapy in BC¹⁰. Moreover, lncRNA MEG3 inhibits angiogenesis and invasion

in BC through AKT signal pathway¹¹. Downregulated lncRNA linc-ITGB1 suppresses metastasis and aggressiveness of BC¹².

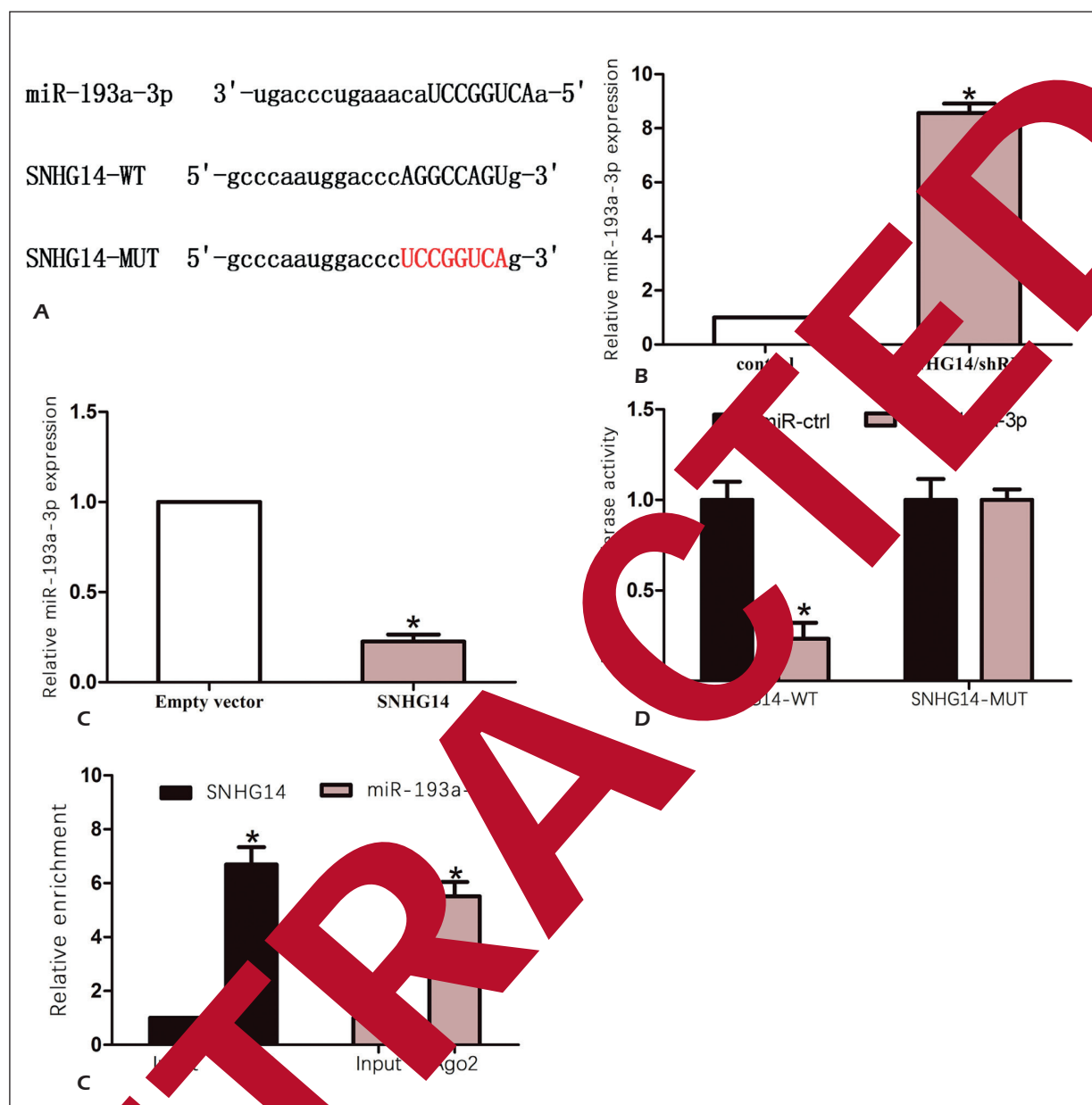


Figure 1. Association between SNHG14 and miR-193a-3p in BC cells and tissues. **A**, The binding sites of miR-193a-3p on SNHG14. **B**, The miR-193a-3p expression was increased in sh-SNHG14 group compared with control group. **C**, The miR-193a-3p expression was increased in SNHG14 group compared with empty vector group. **D**, Co-transfection of miR-193a-3p and SNHG14-WT strongly decreased the luciferase activity, while co-transfection of miR-ctrl and SNHG14-WT did not change the luciferase activity. **E**, RNA pull-down assay showed the enrichment of SNHG14 and miR-193a-3p Ago2-containing beads. The results represent the average of three independent experiments. Data are presented as the mean \pm standard error of the mean. * $p < 0.05$.

Enhanced small nucleolar RNA host gene (SNHG14), as a novel lncRNA, is located on chromosome 11.2. Recent researches¹³⁻¹⁵ have indicated that SNHG14 plays an important role in the progression of tumorigenesis. In our study, SNHG14 was upregulated in BC tissues. Be-

sides, the silence of SNHG14 inhibited cell proliferation and invasion in BC cells, while the overexpression of SNHG14 promoted cell proliferation and invasion in BC cells. Above results indicated that SNHG14 promoted tumorigenesis of BC and might act as an oncogene.

To further identify the underlying mechanism of how SNHG14 affects BC cell proliferation and invasion, we predicted and picked miR-193a-3p as the potential binding miRNA of SNHG14 by using bioinformatic analysis and experimental verification. MiR-193a-3p is widely known as a tumor suppressor in many carcinomas which regulates diverse biological processes. For example, miR-193a-3p promotes the development of colorectal cancer *via* targeting KRAS¹⁶. MiR-193a-3p suppresses metastasis of renal cell carcinoma through regulating PTEN¹⁷. MiR-193a-3p inhibits the aggressive ability of osteosarcoma cells *via* targeting Rab27B¹⁸. Yu et al¹⁹ showed that miR-193a-3p modulates the development of BC. In the present work, the miR-193a-3p expression could be upregulated after knockdown of SNHG14, while the miR-193a-3p expression could be down-regulated after overexpression of SNHG14. Moreover, miR-193a-3p could directly bind to SNHG14 through a luciferase assay, and miR-193a-3p was significantly enriched by SNHG14 RIP assay. All the results above suggested that SNHG14 might promote tumorigenesis of BC *via* sponging miR-193a-3p.

Conclusions

We found that SNHG14 was significantly up-regulated in BC patients. Besides, SNHG14 could facilitate cell proliferation and invasion in BC through sponging miR-193a-3p. These results suggest that SNHG14 may contribute to the therapy of BC as a candidate target.

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Conflict of Interest

The authors declare that they have no conflict of interest.

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