

Long noncoding RNA PROX1-AS1 promoted ovarian cancer cell proliferation and metastasis by suppressing KLF6

L. ZHAO¹, J.-F. LI², X.-J. TONG³

¹Department of Gynecology Center, The First Affiliated Hospital of XinJiang Medical University, Urumqi, China

²Department of Ultrasound, WeiHai Municipal Hospital, WeiHai, China

³Department of Gynecology, Cancer Hospital of China Medical University, Liaoning Cancer Hospital & Institute, Shenyang, China

Abstract. – OBJECTIVE: Recently, the role of long noncoding RNAs (lncRNAs) in tumor progression has attracted much attention worldwide. Numerous studies have identified lncRNA PROX1-AS1 as an oncogene in cancers. Therefore, the aim of this research was to explore the function of PROX1-AS1 in the development of ovarian cancer.

PATIENTS AND METHODS: PROX1-AS1 expression in both ovarian cancer patients and normal subjects was detected by quantitative Real Time-Polymerase Chain Reaction (qRT-PCR). Subsequently, PROX1-AS1 shRNA was constructed and transfected *in vitro*. 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) assay, colony formation assay, transwell assay, and Matrigel assay were utilized to detect the function of PROX1-AS1 in ovarian cancer. In addition, the potential mechanism was explored using qRT-PCR and Western blot assay.

RESULTS: PROX1-AS1 was highly expressed in ovarian carcinoma samples and cell lines ($p < 0.05$). The proliferation, migration, and invasion of ovarian cells were significantly inhibited after PROX1-AS1 was downregulated *in vitro* ($p < 0.05$). Besides, the mRNA expressions of KLF6 were significantly promoted after PROX1-AS1 knockdown. Ovarian cancer cells ($p < 0.05$). Our functional assays showed that KLF6 expression was negatively correlated with PROX1-AS1 expression in ovarian cancer samples.

CONCLUSIONS: PROX1-AS1 enhances the metastasis and proliferation of ovarian cancer cells by suppressing KLF6. Our findings suggest that PROX1-AS1 may be applied as a novel target for therapy of ovarian cancer.

Key words:

Long noncoding RNAs, PROX1-AS1, Ovarian cancer, KLF6.

Introduction

Ovarian cancer remains one of the most fatal and common tumors in women globally, accounting for 5-6% of cancer-related deaths^{1,2}. It has been reported that 22,000 patients are newly diagnosed of ovarian cancer in America in 2017, with 14,100 deaths^{3,4}. Due to the vagueness of symptoms and the lack of early detection tests, 70-80% of patients have already been in advanced stages when first diagnosed⁵. Whereas, almost 50% of the patients may develop resistance to chemotherapy or recurrence after surgery^{6,7}. Therefore, the severe situation underscores the urgency of early detection and the establishment of new therapeutic interventions for ovarian cancer patients.

Long non-coding RNAs (lncRNAs) are a subgroup of non-coding RNAs that do not encode proteins. Currently, lncRNAs have emerged as an important role in tumorigenesis. Multiple studies have found that lncRNAs have the potential to regulate gene expression. By regulating vasculogenic angiogenesis, lncRNA MALAT1 promotes tumorigenicity and metastasis in gastric cancer⁸. LncRNA AC132217.4 promotes the metastasis of oral squamous cell carcinoma by regulating IGF2 expression modulated by KLF8⁹. By sponging miR-124-3p, lncRNA OGFRP1 has been reported to take part in the proliferation of non-small cell lung cancer cells¹⁰. Upregulation of lncRNA LINC01510 has been confirmed negatively associated with the prognosis of colorectal cancer (CRC) patients. Meanwhile, lncRNA LINC01510 may serve as a potential independent prognostic biomarker for CRC¹¹. LncRNA HCCL5 activated by ZEB1 accelerates cell viability, cell migra-

tion, epithelial-mesenchymal transition, and the malignancy of hepatocellular carcinoma¹². However, few studies have uncovered the exact role of PROX1-AS1 in ovarian cancer, as well as the underlying mechanism.

In our study, we found that PROX1-AS1 was remarkably upregulated in ovarian cancer tissues. PROX1-AS1 enhanced the proliferation and metastasis of ovarian cancer *in vitro*. Moreover, KLF6, a tumor suppressor gene, was associated with the function of PROX1-AS1 in ovarian cancer.

Patients and Methods

Tissue Specimens

Paired ovarian carcinoma tissues and adjacent normal tissues were sequentially collected from 50 ovarian carcinoma patients undergoing surgery from December 2017 to December 2019 in The First Affiliated Hospital of XinJiang Medical University. The selection of patients was based on the guideline proposed by the Union for International Cancer Control (UICC). This study was approved by The Ethics Committee of The First Affiliated Hospital of XinJiang Medical University. The protocol of the study performed as Declaration of Helsinki Principle required.

Cell Culture

Human ovarian cancer cell lines (A2780, V112D, HO-8910, and SKOV3) and normal ovarian cell line (ISOE80) were cultured in Dulbecco's Modified Eagle's Medium (DMEM; Gibco, Fisher Scientific, Inc., Waltham, MA, USA) consisting of 10% fetal bovine serum (FBS; Thermo Fisher Scientific, Inc., Waltham, MA, USA) and penicillin, and maintained in a humidified atmosphere with 5% CO₂ at 37°C.

Lentivirus Expression of Short-Hairpin RNA and Cell Transfection

Lentivirus expressing short-hairpin RNA (shRNA) directed against PROX1-AS1 were provided by GenePharm (Shanghai, China). The complementary DNA encoding PROX1-AS1 was annealed and inserted into pcDNA3.1 (GenePharm, Shanghai, China). Subsequently, they were infected into ovarian cancer cells, according to the instructions of Lipofectamine 3000 (Invitrogen, Carlsbad, CA, USA). PROX1-AS1 expression in transfected cells was conducted

using quantitative Real Time Polymerase Chain Reaction (RT-qPCR).

RNA Extraction and RT-PCR

Total RNA in tissues and cells was extracted by using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). Subsequently, extracted total RNA was reverse-transcribed to complementary deoxyribose nucleic acids (cDNAs) through Reverse Transcription (Takara, Dalian, China). The reaction conditions were as follows: 30s at 42°C for 40 cycles at 95°C, and 5min at 60°C. 2-ΔΔCt method was utilized for calculating relative expression of genes. The primer sequences used in this study were as follows: PROX1-AS1 forward 5'-CTAGTTAGCAG-GCCTAGCAC-3', PROX1-AS1 reverse 5'-AAGAGAGGCGTGGAAAGAA-3'; β-actin, forward 5'-GATGGAAATCGTCAGAGGCT-3' and reverse 5'-TGGCGTTAGTTGGAAATGC-3'.

Western Blot Analysis

Proteins were collected from cells *via* radioimmunoprecipitation assay (RIPA) buffer and identified by using a protein assay (bicinchoninic acid method; Beyotime, Shanghai, China). Target proteins were separated by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred onto polyvinylidene difluoride (PVDF) membranes. Then, the membranes were incubated with primary antibodies overnight. On the next day, the membranes were incubated with rabbit anti-β-actin (Cell Signaling Technology, Danvers, MA, USA) and rabbit anti-KLF6 (Cell Signaling Technology, Danvers, MA, USA). The Pierce enhanced chemiluminescence (ECL) was utilized for visualizing Western Blotting Substrate Immunoreactive bands (Santa Cruz Biotechnology, Inc., Santa Cruz, CA, USA).

MTT (3-[4,5-Dimethylthiazol-2-yl]-2,5-Diphenyl Tetrazolium Bromide) Assay

MTT (Roche, Basel, Switzerland) assay was used to detect cell proliferation. 200 μL of transfected cells were first seeded into 96-well plates at a density of 2×10³ cells per well. Following the manufacturer's protocol, cell proliferation was assessed every 24 h.

Colony Formation Assay

To detect the long-term effect of PROX1-AS1 on cell proliferation, colony formation assay was conducted. 5×10² cells/well cells were seeded into 6-well plate, and culture medium was replaced

every day. 7 day later, formed colonies were fixed with 75% ethanol for 30 min and stained with 0.2% crystal violet. Finally, colonies were photographed and counted.

Wound Healing Assay

After transfection, the cells were seeded into 6-well plates and incubated in DMEM medium overnight. On the next day, the cells were scratched with a plastic tip and cultured in serum-free DMEM. Each assay was repeated in triplicate independently. Relate distance was viewed under a light microscope (Olympus Corp., Tokyo, Japan) at 48 h.

Transwell Assay and Matrigel Assay

After transfection, 1×10^5 cells in 200 μ L serum-free DMEM were replanted in top chamber (Corning, Inc., Corning, NY, USA) with or without 50 μ g Matrigel (BD, Bedford, MA, USA). Meanwhile, DMEM and FBS were added to the lower chamber. These chambers were then cultured overnight in an incubator supplemented with 5% CO₂ at 37°C. The top surface of chambers was fixed with methanol for 30 min, wiped by cotton swab, followed by staining with crystal violet for 20 min. Five fields were randomly selected for each sample. The number of migrating and invasive cells was finally counted under a Leica DMI4000B microscope (Leica Microsystems, Heidelberg, Germany).

Statistical Analysis

Statistical Product and Solutions (SPSS) 18.0 (SPSS, Chicago, IL, USA) was used for all statistical analysis. The difference between

two groups were compared by t-test. $p < 0.05$ was considered statistically significant.

Results

PROX1-AS1 Was Highly Expressed in Ovarian Cancer Tissues and Cell Lines

PROX1-AS1 expression in 50 pairs of ovarian cancer tissues and adjacent normal tissues was detected via qRT-PCR. PROX1-AS1 was highly expressed in ovarian cancer tissues when compared with adjacent normal tissues ($p < 0.05$, Figure 1A). Moreover, PROX1-AS1 level in ovarian cancer cells was significantly higher than that of normal ovarian cell line ISOE80 ($p < 0.05$, Figure 1B).

Proliferation Was Repressed Via Silence of PROX1-AS1 in Ovarian Cancer

In our study, HO-8910 cells were chosen for knockdown of PROX1-AS1 *in vitro*. qRT-PCR was used for detecting PROX1-AS1 expression (Figure 2A). MTT assay indicated that the growth ability of HO-8910 cells was significantly repressed after PROX1-AS1 was knocked down ($p < 0.05$, Figure 2B). Colony formation assay demonstrated that the number of colonies decreased significantly after PROX1-AS1 was knocked down ($p < 0.05$, Figure 2C).

Cell Migration and Invasion Was Repressed Via Silence of PROX1-AS1 in Ovarian Cancer

Wound healing assay, transwell assay, and Matrigel assay were performed to explore how PROX1-AS1 affected ovarian cancer metastasis.

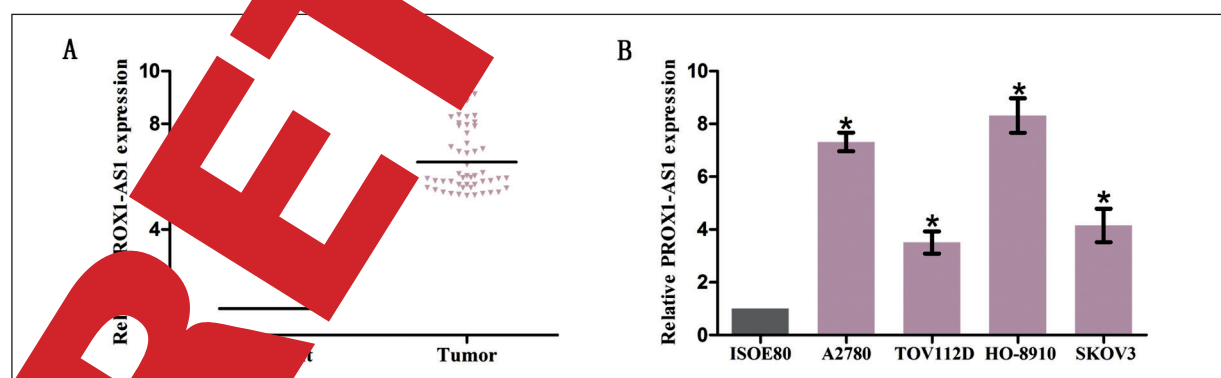


Figure 1 Expression levels of PROX1-AS1 increased significantly in ovarian cancer tissues and cell lines. **A**, QRT-PCR results showed that PROX1-AS1 expression was significantly up-regulated in ovarian cancer tissues compared with adjacent normal tissues. **B**, Expression levels of PROX1-AS1 relative to β -actin were determined in human ovarian cancer cell lines and normal ovarian cell line ISOE80 by qRT-PCR. Data were presented as the mean $\pm$ standard error of the mean. * $p < 0.05$.

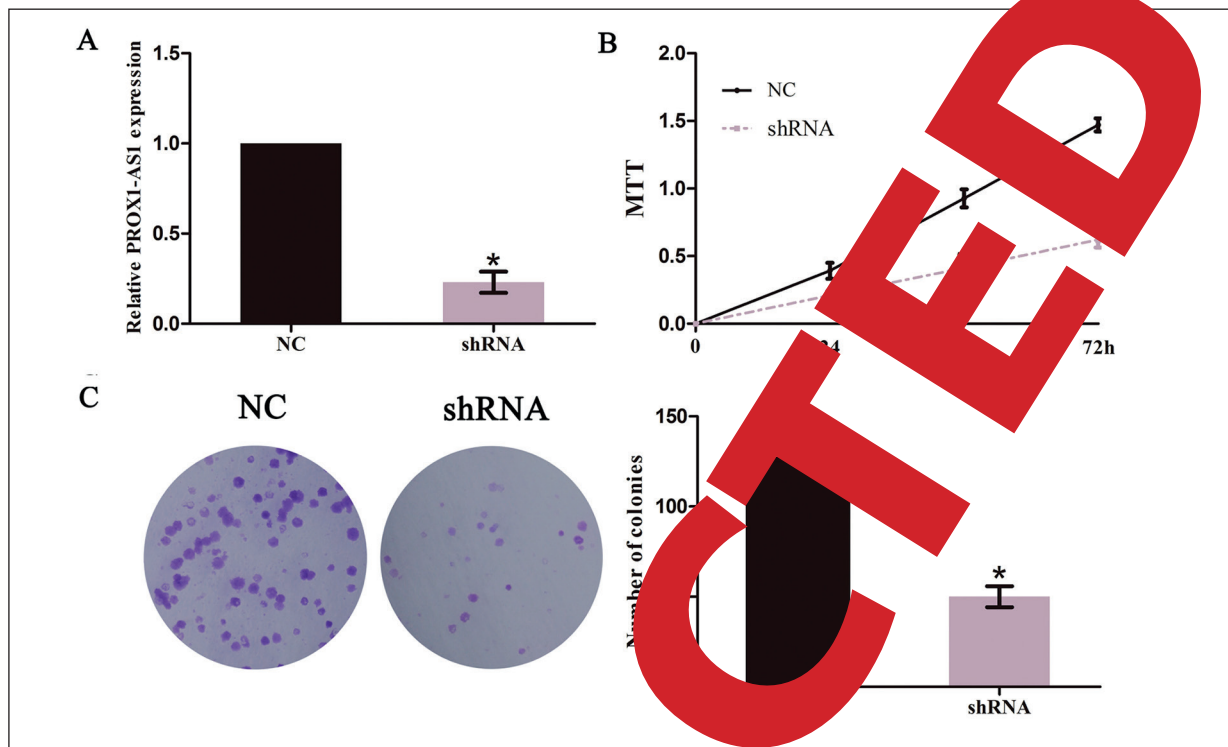


Figure 2. Knockdown of PROX1-AS1 inhibited proliferation. **A**, PROX1-AS1 expression in ovarian cancer cells transduced with PROX1-AS1 shRNA (shRNA) and negative control (NC) was detected by qRT-PCR. β -actin was used as an internal control. **B**, MTT assay showed that knockdown of PROX1-AS1 significantly inhibited the growth of ovarian cancer cells. **C**, Colony formation assay showed that knockdown of PROX1-AS1 significantly reduced the number of colonies in ovarian cancer cells (magnification: 40 $\times$). The results represented the average of three independent experiments (mean $\pm$ standard error of the mean). * $p < 0.05$, as compared with the control cells.

sis *in vitro*. Wound healing assay revealed that the migrated length of ovarian cancer cells was significantly repressed after PROX1-AS1 was knocked down ($p < 0.05$, Figure 3A). Results of transwell assay showed that the migration of ovarian cancer cells was remarkably repressed after PROX1-AS1 knockdown (Figure 3B). Furthermore, Matrigel assay indicated that the number of invasive cells decreased remarkably after PROX1-AS1 was knocked down *in vitro* ($p < 0.05$, Figure 3C).

The Interaction between KLF6 and PROX1-AS1 in Ovarian Cancer

The expression level of KLF6 in ovarian cancer cells was higher after PROX1-AS1 shRNA (shRNA) knockdown compared with negative control (control) ($p < 0.05$, Figure 4A). Western blot assay found that the protein expression level of KLF6 was significantly upregulated after PROX1-AS1 was knocked down ($p < 0.05$, Figure 4B). Moreover,

KLF6 expression in ovarian cancer tissues was significantly lower than that of adjacent normal tissues ($p < 0.05$, Figure 4C). These findings all suggested that there was a negative association between KLF6 expression and PROX1-AS1 expression in ovarian cancer (Figure 4D).

Discussion

Many studies¹³⁻¹⁶ revealed the abnormal expression and function of lncRNAs in the development of malignant tumors. They have also been found to directly participate in the proliferation, apoptosis, metastasis, immune regulation, and drug resistance in tumors. Meanwhile, lncRNA is involved in the regulation of various cellular functions, whose disorders are usually associated with human diseases, including malignant tumor.

Reports have indicated that lncRNA is an important regulator in the progression of ovari-

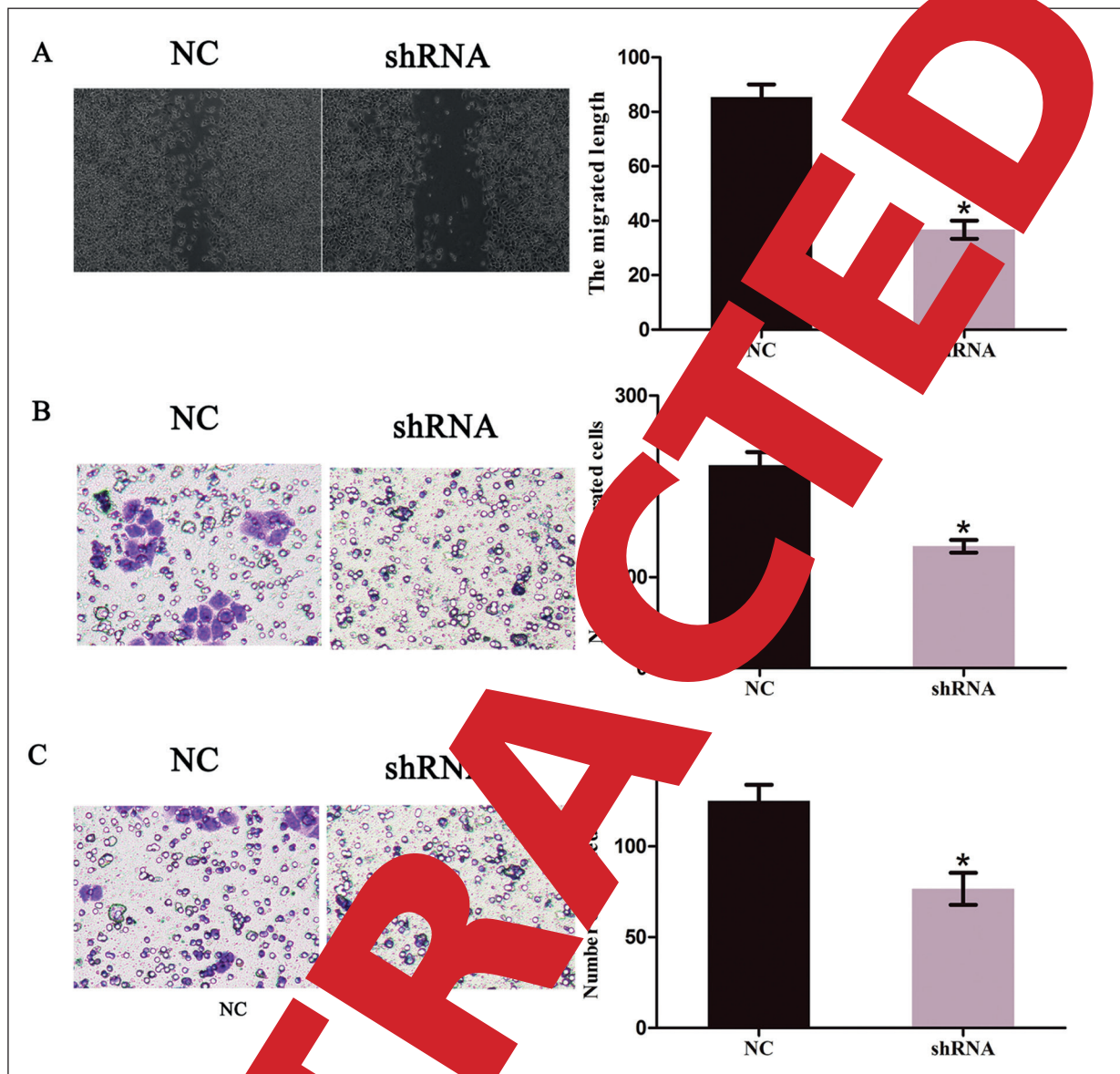


Figure 3. Knockdown of PROX1-AS1 significantly inhibited ovarian cancer cell migration and invasion. **A**, Wound healing assay showed that knockdown of PROX1-AS1 significantly reduced migrated length in ovarian cancer cells (magnification: 40×). **B**, Transwell assay showed that knockdown of PROX1-AS1 significantly inhibited the migration of ovarian cancer cells (magnification: 40×). **C**, Matrigel assay showed that the number of invaded cells decreased remarkably *via* knockdown of PROX1-AS1 *in vitro* (magnification: 40×). The results represented the average of three independent experiments (mean ± standard error of the mean). * $p < 0.05$ compared with the control cells.

an cancer serving as a potential biomarker and therapeutic target. Overexpression of lncRNA MN1-AS1 suppresses the proliferation and migration of ovarian cancer cells⁴. LncRNA Eln-1-AS1 functions as an oncogene in the proliferation of epithelial OC cells, which is upregulated by estrogen. In addition, knockdown of lncRNA AFAP1-AS1 promotes the proliferation and apoptosis of ovarian cancer cells¹⁸.

PROX1 antisense RNA 1 (PROX1-AS1) is a newly explored lncRNA that has been suggested to promote the progression of papillary thyroid carcinoma¹⁹. Our results showed that PROX1-AS1 expression was significantly upregulated in both ovarian cancer tissues and cells. Multiple lncRNAs have been reported to participate in the development of ovarian cancer, emerging as potential indicators and therapeutic targets. In fact,

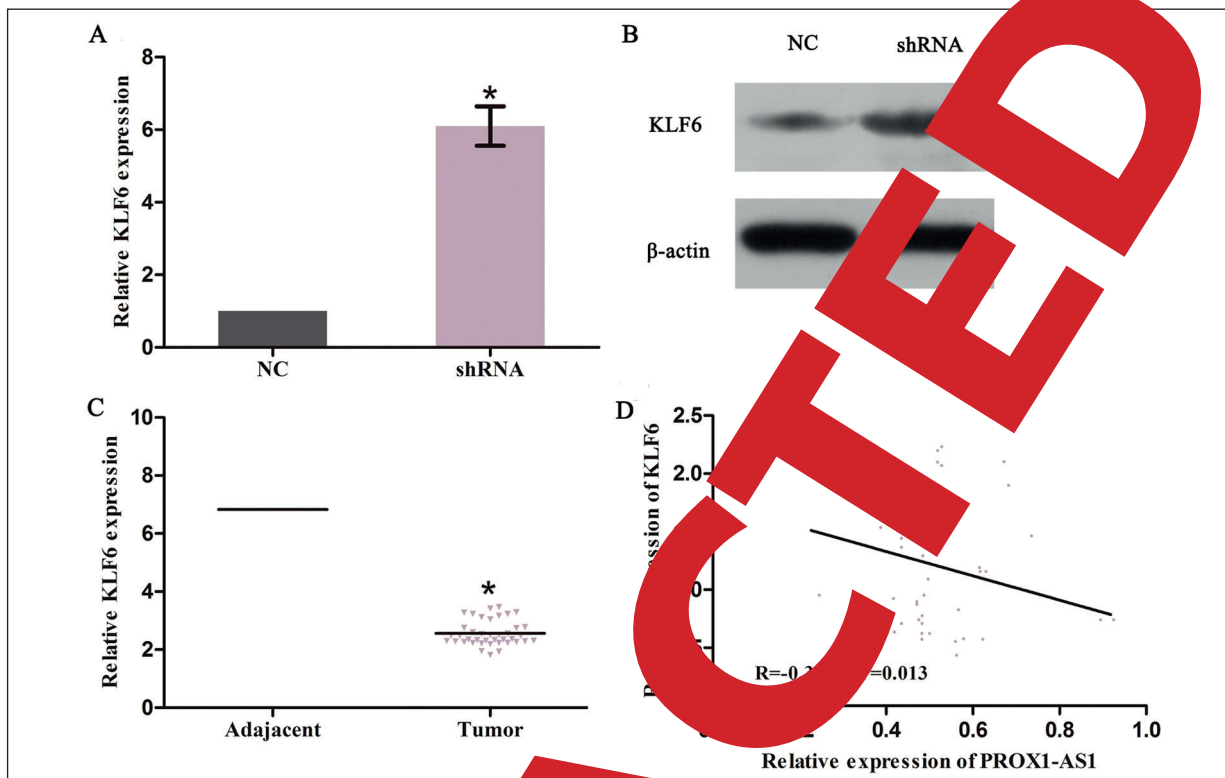


Figure 4. Interaction between PROX1-AS1 and KLF6 in ovarian cancer tissues and cells. **A**, RT-qPCR results showed that KLF6 expression was significantly higher in PROX1-AS1 shRNA (shRNA) group compared with NC group. β -actin was used as an internal control. **B**, Western blot assay revealed the protein expression of increased in PROX1-AS1 shRNA (shRNA) group compared with NC group. **C**, KLF6 was significantly downregulated in ovarian cancer tissues when compared with adjacent normal tissues. **D**, The linear correlation between expression level of KLF6 and PROX1-AS1 in ovarian cancer tissues. The results represented the average of three independent experiments. Data were presented as the mean $\pm$ standard error of the mean. * $p < 0.05$.

lncRNA SNHG14 facilitates the progression of cervical cancer by regulating miR-200a/200b signaling pathway²⁰. Through regulation of epithelial-mesenchymal transition, downregulation of lncRNA SPRY4-IT1 inhibits the metastasis of ovarian cancer²¹. LncRNA ENTP2, activated by estrogen, functions as an oncogene in epithelial ovarian cancer cells¹⁷. In the present study, PROX1-AS1 was first knocked down in ovarian cancer cells, which indicated that the proliferation of ovarian cancer cells was significantly inhibited after PROX1-AS1 was knocked down *in vitro*. Moreover, cell migration and invasion were also remarkably inhibited after PROX1-AS1 downregulation. Above results indicated that PROX1-AS1 was associated with the development of ovarian cancer.

Next, we explored the potential target proteins of PROX1-AS1 using bio-informative methods. The results showed that the potential

target protein, Krüppel-like factor 6 (KLF6), was significantly downregulated in ovarian cancer tissues. Known as a tumor suppressor, KLF6 takes part in the regulation of a variety of biological processes in many carcinomas. KLF6 is deleted glioblastomas, which is related to poor prognosis of patients by targeting KLF6²². KLF6 constrains the progression of hepatocellular carcinoma dissemination by regulating the VAV3-RAC1 signaling axis²³. Meanwhile, KLF6 accelerates cell proliferation and invasion in epithelial ovarian cancer²⁴. In the present study, the mRNA and protein expressions of KLF6 were both significantly upregulated after the knock-down of PROX1-AS1. Moreover, KLF6 expression was negatively correlated with PROX1-AS1 expression in ovarian cancer tissues. All these results suggested that PROX1-AS1 might promote tumorigenesis of ovarian cancer *via* suppressing KLF6.

Conclusions

The above results demonstrated that PROX1-AS1 was highly expressed in both ovarian cancer tissues and cells. Besides, PROX1-AS1 enhanced ovarian cancer cell proliferation, migration, and invasion by targeting KLF6. The novelty of this study was that PROX1-AS1 might contribute to therapy for ovarian cancer as a candidate target.

Conflict of Interest

The Authors declare that they have no conflict of interests.

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