

LncRNA LINC01140 Inhibits Glioma Cell Migration and Invasion via Modulation of miR-199a-3p/ZHX1 Axis

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Yanchao Xin¹
Wuzhong Zhang¹
Chongchong Mao²
Jianxin Li¹
Xianzhi Liu²
Junbo Zhao¹
Junfeng Xue¹
Junqing Li¹
Yonglu Ren¹

¹Department of Neurosurgery, People's Hospital of Jiaozuo City, Jiaozuo City, Henan Province 454002, People's Republic of China; ²Department of Neurosurgery, The First Affiliated Hospital of Zhengzhou University in Henan Province, Zhengzhou City, Henan Province 450052, People's Republic of China

Purpose: Glioma is an aggressive tumor from the nervous system, which causes more than 70% of primary malignant brain tumors. Considering its severe malignancy, there is an urgent need to investigate more practical markers to understand the pathogenesis of glioma, and potential treatment methods for glioma patients. In the paper, we are focused on examining the roles of LINC01140, miR-199a-3p, and ZHX1 in the progression of gliomas, as well as their inner associations and modulation mechanisms.

Methods: qRT-PCR was employed to examine the expression levels of LINC01140 and miR-199a-3p. We measured the expressions of ZHX1 via qRT-PCR and Western blotting. CCK8 assays, migration assays, and invasion assays were carried out to determine the cell viabilities and abilities of migration and invasion. We also conducted in vivo tumor growth experiments to investigate the roles of LINC01140 in glioma developments.

Results: The expressions of LINC01140 were promoted in glioma. Silencing LINC01140 could inhibit glioma cell viabilities, migration, and invasion. In our experiments, miR-199a-3p was inhibited in glioma. LINC01140 negatively regulated the expressions of miR-199a-3p in glioma. MiR-199a-3p could target ZHX1 to inhibit its expression in glioma cells.

Conclusion: LINC01140 could promote glioma developments by modulating the miR-199a-3p/ZHX1 axis.

Keywords: LINC01140, glioma, ZHX1, miR-199a-3p

Introduction

Glioma is a very severe and aggressive tumor from the nervous system, which possesses more than 70% of primary malignant brain tumors.¹⁻³ Despite developments and advancements, such as surgeries, physical irradiations, and chemotherapies,⁴ the five-year survival rates for glioma patients is still unsatisfied, resulting in the fact that glioma is almost not curable.^{5,6} Growing interests have been paid to discover the effective gene functions, as well as molecular interaction networks to develop robust and efficient diagnostic or prognostic biomarkers and therapeutic targets.^{7,8} However, only a few genes and proteins have been investigated to exert possible biological function with the developments of glioma till present.⁹ Due to the above considerations, more studies should be carried out to discover more practical markers and understand the pathogenesis of glioma, as well as the potential treatment methods and directions for glioma patients.

It is well established that complicated genes interactions and molecular networks are participating in the initiations and developments of gliomas.¹⁰⁻¹² Long non-coding RNAs (lncRNAs) are a group of RNAs that have lengths of over 200 nt.¹³ Many

Correspondence: Xianzhi Liu
Department of Neurosurgery, The First Affiliated Hospital of Zhengzhou University in Henan Province, No. 1 Jianshe East Road, Zhengzhou City, Henan Province 450052, People's Republic of China
Tel +86 371-66278517
Email dq3084@163.com

lncRNAs have been demonstrated to have oncogenic or tumor-suppressive roles in glioma developments,¹⁴ such as TUG1,¹⁵ MALAT1,¹⁶ CASC2,¹⁷ and ATB.¹⁸ Various lncRNAs have shown promising effects in the tumorigenesis of gliomas. For instance, Feng et al reported the expressions and roles of re-programming-related lincROR in glioma.¹⁹ Guo also proposed another LincRNA of POU3F3 which was overexpressed in gliomas, and it also contributed to the tumorigenesis of gliomas.²⁰ LncRNA LINC01140 is one of the lncRNAs, which is an essential subtype of lncRNAs.²¹ LncRNA LINC01140 has been demonstrated to exert important functions in breast cancer²² and papillary thyroid cancer.²³ As far as we know, there is very limited information that was revealed regarding LINC01140 in glioma. In this paper, we aim to reveal a novel lncRNA of LINC01140, and investigate its role in glioma developments.

Previous studies have demonstrated that lncRNAs could bind with microRNAs (miRNAs, ~22 nt) and exert their roles to affect the growth of human cancers.²⁴ For example, Cai reported that lncRNA taurine upregulated 1 (TUG1) enhanced tumor angiogenesis by suppressing miR-299 in glioma.²⁵ Accumulative evidence has suggested that miR-199a-3p could suppress glioma cell proliferation.^{26,27} Through our preliminary bioinformatics, it is highly possible that miR-199a-3p may also interact with LINC01140. Human zinc-fingers and homeoboxes 1 (ZHX1) were identified as a protein with up-regulated expressions in many types of human cancers.^{28,29} It has been shown to have associations with ZHX1 in gastric cancer³⁰ and hepatocellular carcinoma.³¹ In this paper, we are focused on examining the roles of LINC01140, miR-199a-3p, and ZHX1 in the progression of gliomas, as well as their inner associations and modulation mechanisms.

Materials and Methods

Cell Line Culture

We obtained the glioma cell lines of U87, U251, SHG-44, and U-118MG, and also human astroglial cell line of HA from Cell Bank of the Chinese Academy of Sciences (Shanghai, China). Cells were kept in high-glucose Dulbecco's Modified Eagle medium (DMEM, Invitrogen, US) with 10% FBS (Invitrogen, US) at 37°C with 5% CO₂.

Cell Transfection

Negative control (NC), miR-199a-3p-mimic, miR-199a-3p-inhibitor, shLINC01140, shNC were provided by Genepharma, US. 5 µL HiPerFect (Qiagen, US) was mixed

with 200 µL growth media without antibiotics, serum or antifungals to prepare the transfection mix. NC, miR-199a-3p-mimic, miR-199a-3p-inhibitor, shLINC01140, or shNC (all from Genepharma) were pipetted to 200 µL transfection mix at a final concentration of 30 nM in 12-well plates for 10 mins at 25 Celsius. Cells (1×10⁵ cells/well) were seeded in 200 µL of growth media and incubated with 37°C, 5% (v/v) CO₂ for a night. On the 2nd day, 800 µL media with 0.1% FBS was pipetted to the wells. The sequences are shNC: 5'-GACGGTAAGTAGGCGA-3'; and shLINC01140-5' TTTAATTGGGCCGTCT-3'.

qRT-PCR

Total RNA was extracted via TRIzol (Invitrogen, US). RNA was reversely transcribed by ReverTra (Toyobo, Japan) and amplified by SYBR (Toyobo, Japan). PCR procedures were at 94°C for 2 min, at 94°C for 30 s, at 54°C for 30 s, at 72°C for 1 min, and performed for 30 cycles, they were at 72°C for 10 min. The expressions of LINC01140, ZHX1, and miR-199a-3p were calculated by the 2^{-ΔΔCT} method. U6 and GAPDH were regarded as reference. The sequences are listed below.

LINC01140 forward: CATCTCATCGGCATGGACCT; Reverse: CAAACTGGACTGACTTTTACCA.

ZHX1 forward: 5'-CAGGTCAGAGAGTGGTTTGC-3'; Reverse: 5'-GTCGTGGAGGTTCCCAAGT-3'.

GAPDH forward: 5'-CCCATCACCATCTTCCAGGA G-3'; Reverse: 5'-CTTCTCCATGGTGGTGAAGACG-3'.

miR-199a-3p forward: 5'-CAATCGCTTTCAAATAG-3'; Reverse: 5'-CAGGAGATGCTGTCATC-3'.

U6: forward 5'-CTCGCTTCGGCAGCACA-3' reverse: 5'-AACGCTTCACGAATTTGCGT-3'.

Western Blotting

Total proteins were lysed by RIPA buffer (Beyotime, China), washed, and centrifugated at 10,000 g for five minutes. The supernatants were utilized for Western blotting. Proteins were measured by BCA (Pierce, US) and had electrophoresis transferred to PVDF membranes (Life Technologies, US). Membranes were treated with TBST and 5% skimmed milk at 25 Celsius for an hour. Then, it was treated with primary antibodies of anti-ZHX1 (1:1000; Abcam, UK) and anti-GAPDH (1:1000; Shangon, Shanghai) at 4°C for a night. The membrane was incubated with the secondary antibody of HRP-linked anti-rabbit IgG (1:200; BM1921, Bosterbio) at 25 Celsius for 1.5 hrs. ECL Plus (Life Technologies, US) was used for quantification. β-actin was the internal control.

CCK-8 Assays

Cell-Counting Kit-8 (CCK-8; Dojindo Molecular Technologies, Japan) was utilized to examine the cell viabilities under different transfection. The cells were plated in 96-well plates for one day. Then, they were transfected and incubated for one day, two days, three days, or 4 days. 10 μ L CCK-8 assay reagent was added to every well. After 2 hrs incubation, the signal was detected by an enzyme immunoassay analyzer (Thermo Fisher Scientific, US).

Dual-Luciferase Assay

LINC01140 was amplified and cloned to the pMIR-REPORT luciferase vector (OBio Biology, China). LINC01140-WT (wild-type) fragment was mutated and cloned into the vector to construct a LINC01140-MUT (mutant). BSG803 cells were then incubated in 48-well plates, co-in transfection by LINC01140-WT or LINC01140-MUT, and either miR-199a-3p-mimic, miR-199a-3p-inhibitors, or negative control. After two days, cells were analyzed by Dual-Luciferase assay (Promega, US).

RNA Immunoprecipitation (RIP)

RNA Immunoprecipitation experiments were performed using the Magna RIP RNA-Binding Protein IP Kit (Millipore, Bedford, MA, USA) and the Ago2 antibody (2897; Cell Signaling, Danvers, MA, USA). Cells were co-transfected with pCMV-MS2, pCMV-LINC01140-MS2 or pCMV-LINC01140-mut-MS2 and pMS2-GFP (Addgene) for 48 hrs. After that, RIP was conducted according to the literature method.³²

Invasion Assays and Migration Assays

The transwell chamber was placed on a 24-well plate with Matrigel (BD, US) and incubated for 15 min at 37 Celsius. After digesting, centrifuging and counting the cells, cells were diluted to 25,000 cells/mL. The cell suspension was seeded in the upper chamber. 500 μ L medium and 10% FBS were utilized in the lower chamber. Cells were fixed by paraformaldehyde and stained by crystal violet for fifteen minutes. Non-invasive cells were removed. After drying, invasive cells on the lower chamber were measured in 4 randomly selected fields ($\times 200$) by a microscope. Cell migration assays were carried out with similar protocols excluding the Matrigel, with a density of 1.5×10^5 cells/well.

In vivo Assay

4 weeks' old female athymic BALB/c nude mice were kept in specific pathogen-free conditions U87 cells were in transfection by sh-LINC01140 or shNC. 10^7 cells were subcutaneously administered to one side of every mouse. We checked the tumor growth every week and calculated the tumor volume according to $V = 0.5 \times D \times d^2$ (V , volume; D , longitudinal diameter; d , latitudinal diameter). The experimental procedures were reviewed and permitted by the first affiliated Hospital of Zhengzhou University in Henan Province Experimental Animal Care Commission and conducted in strict accordance with the national institutes of health guidelines for the care and use of experimental animals.

Statistical Analysis

SPSS 17 was employed to analyze the data, which were expressed as mean \pm standard deviation from three independent replicas. The variations in the 2 groups were analyzed using the *t*-test. Variations in over 2 groups were analyzed by one-way ANOVA.

Results

LINC01140's Expression Was Enhanced in Glioma Cells

Figure 1A shows that the mRNA expressions of LINC01140 were up-regulated in glioma cell lines of SHG44, U251, U-118 MG, U87. Figure 1B demonstrates that the levels of miR-199a-3p were reduced than normal brain cell line HA.

Knockdown of LINC01140 Inhibited the Viabilities, Migration, and Invasion of Glioma Cell Lines

Figure 2A shows the successful knockdown of LINC01140 in glioma cell lines in transfection with shLINC01140. The mRNA of LINC01140 was greatly inhibited in shLINC01140. Figure 2B shows that shLINC01140 significantly reduced the glioma cell viabilities. Figure 2C and D demonstrated that the migrative and invasive activities of glioma cells were apparently inhibited by shLINC01140. It was obvious that knockdown of LINC01140 restrained growth, migration, and invasion abilities of glioma cells.

LINC01140 Directly Sponged miR-199a-3p

Figure 3A searches LncBase v2.0 and observed that miR-199a-3p might have shared binding sequences with LINC01140. Figure 3B demonstrates that mRNA expressions

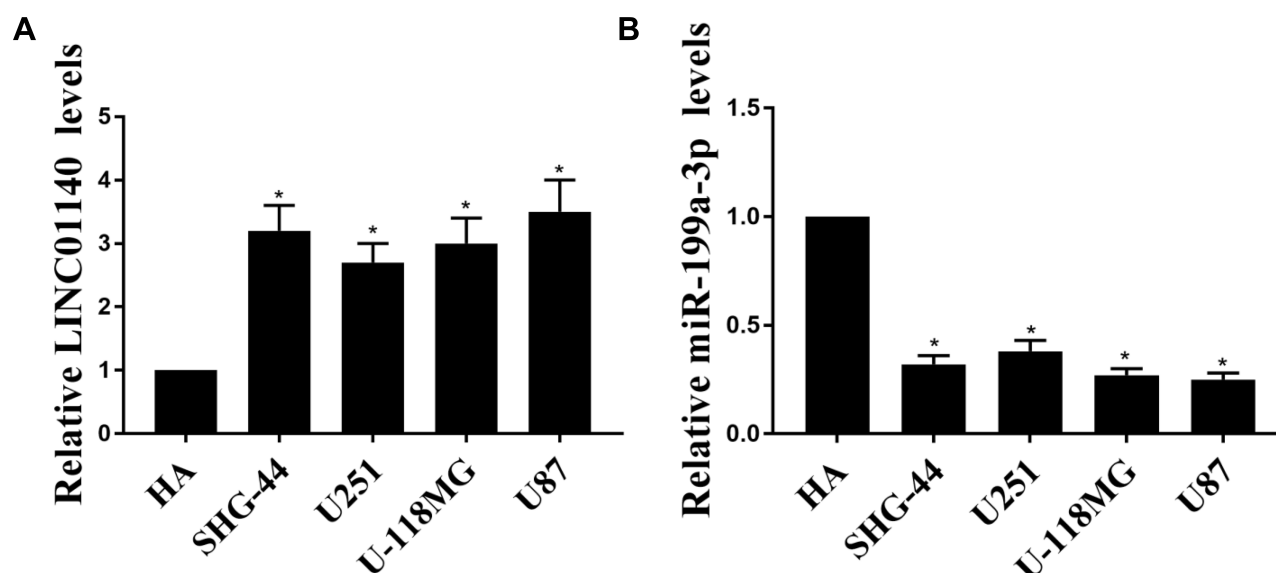


Figure 1 LINC01140's expression was enhanced in glioma cells. **(A)** mRNA expressions of LINC01140 in glioma cells and the normal cells. **(B)** mRNA expressions of miR-199a-3p in glioma cells and the normal cells. *P < 0.05, n=3.

of miR-199a-3p were up-regulated by miR-199a-3p-mimic but suppressed by miR-199a-3p-inhibitor. The luciferase data indicated that the luciferase activities of LINC01140-WT were suppressed by miR-199a-3p, but LINC01140-MUT activities did not change (Figure 3C). Figure 3D employs the RIP experiments. We found that miR-199a-3p could upregulate the LINC00140 enrichment significantly. In addition, Figure 3E indicates that the expression of miR-199a-3p was elevated in cells in transfection by shLINC01140. From Figure 3F, the transfection of miR-199a-3p mimic or inhibitor caused the inhibition or elevation of LINC01140.

The Effect of LINC01140 Was Attenuated by miR-199a-3p in Glioma Cells

MiR-199a-3p-inhibitor and shLINC1140 were co-transfected into U87 cells. Figure 4A shows the CCK-8 assays that down-regulation of LINC01140 inhibited the abilities of cell proliferation, but shLINC1140+miR-199a-3p-inhibitor increased these abilities. Moreover, the migrative (Figure 4B and C) and invasive (Figure 4D and E) abilities of glioma cells were suppressed by shLINC1140, but this phenomenon was attenuated by miR-199a-3p-inhibitor.

ZHX1 Was Directly Targeted by miR-199a-3p

Figure 5A identifies that the miR-199a-3p had shared binding sequences with ZHX1, predicted by miRBase and miRanda. Figure 5B shows the reporter assays in U87 cells and

revealed miR-199a-3p-dependent repression of the ZHX1-WT 3'UTR. Figure 5C shows that the ZHX1 mRNA levels for cells were greatly inhibited by miR-199a-3p mimic but enhanced by miR-199a-3p inhibitor. From Figure 5D, shLINC01140 decreased ZHX1 protein levels. The results in Figure 5E were in consistence with the above results; the protein expressions of ZHX1 were reduced by a miR-199a-3p mimic in U87 cell, but elevated by miR-199a-3p-inhibitor. Figure 5F demonstrates that shLINC01140 inhibited the protein expression of ZHX1. It was confirmed that ZHX1 was a direct target of miR-199a-3p.

The Effect of miR-199a-3p Was Attenuated by ZHX1 in Glioma Cells

Figure 6A confirms the successful transfection of shZHX1 by RT-PCR. Figure 6B utilizes CCK 8 assay and found that the cell viability was upregulated by miR-199a-3p inhibitor, but this effect was attenuated by shZHX1. Figure 6C carries out migration assay and invasion assay. It showed that the cell migration ability and cell invasion ability were enhanced by miR-199a-3p, but were attenuated by shZHX1. These data confirmed that the effect of miR-199a-3p was attenuated by ZHX1 in glioma cells.

LINC01140 Promoted Glioma Growth in vivo

Figure 7A–C demonstrated that knockdown of LINC00140 suppressed the tumor growth rate, tumor volume, and tumor

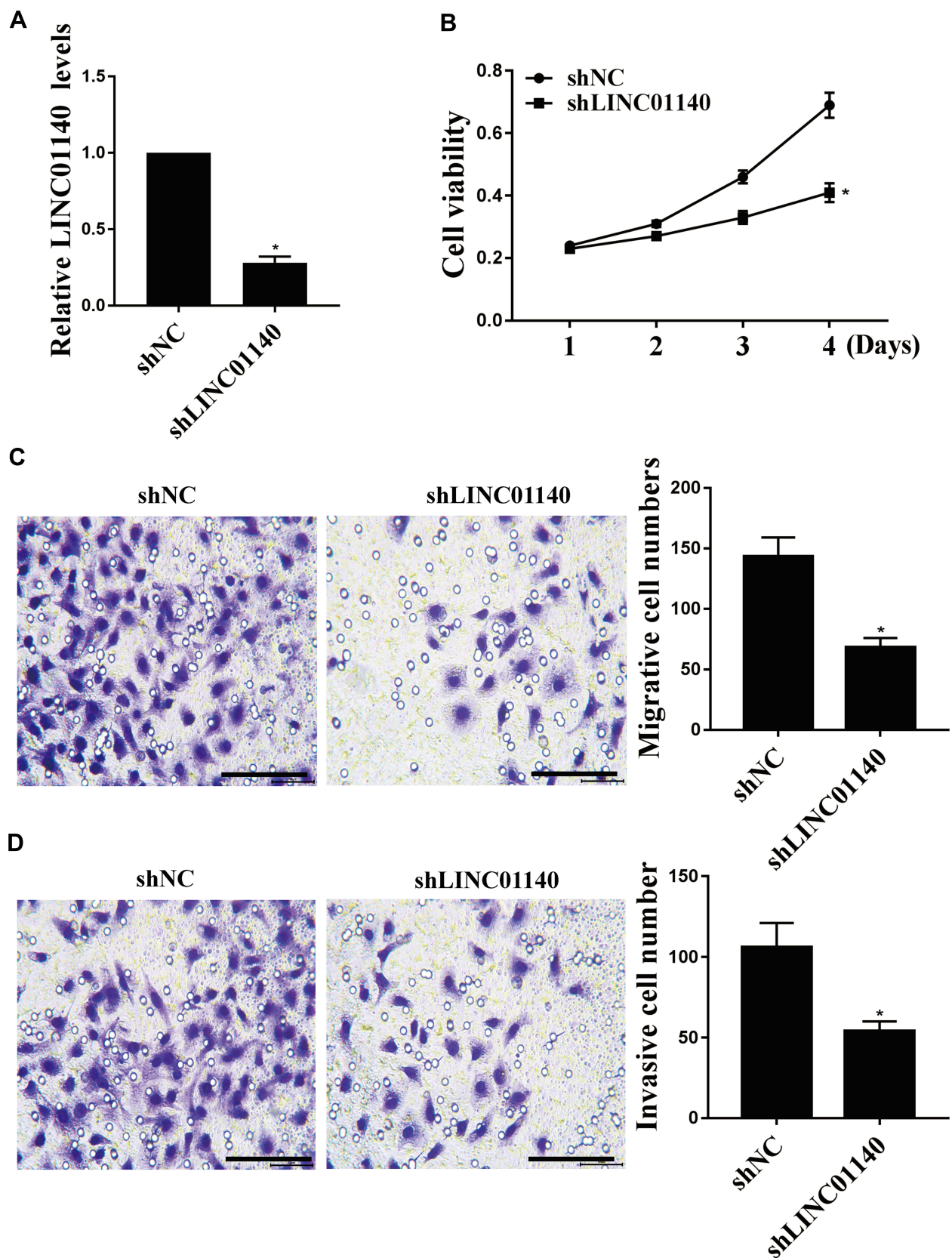


Figure 2 Knockdown of LINC01140 suppressed the viabilities, migration, and invasion of glioma cell lines. **(A)** LINC01140 mRNA level in U87 cell in transfection by shNC and shLINC01140. **(B)** CCK8 assay for cells in transfection by shNC and shLINC01140. **(C)** Migration abilities for cells in transfection by shNC and shLINC01140. **(D)** Invasion abilities for cells in transfection by shNC and shLINC01140. * $P < 0.05$, $n=3$.

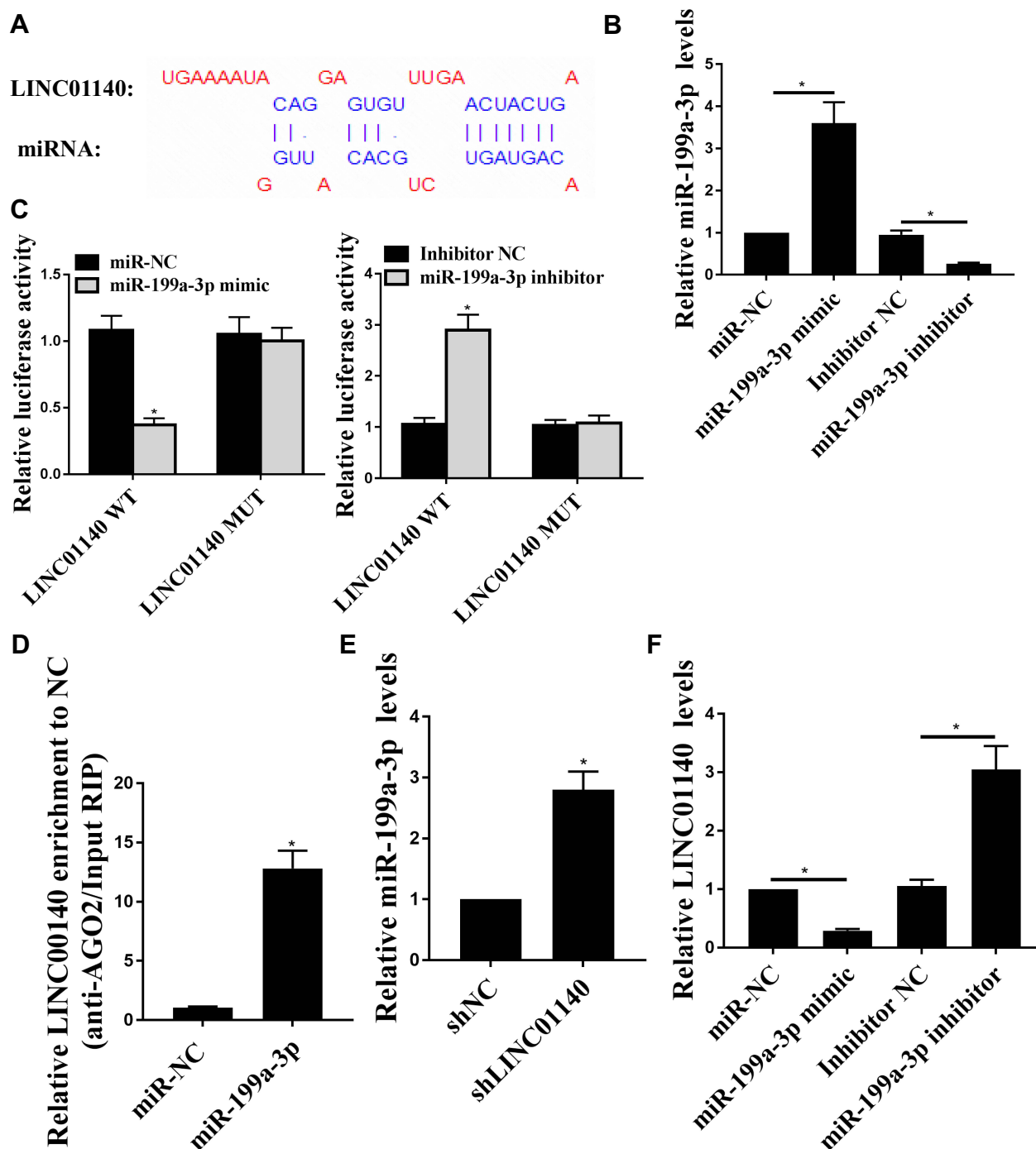


Figure 3 LINC01140 directly sponged miR-199a-3p. **(A)** The shared binding sequences between LINC01140 and miR-199a-3p by LncBase v2.0. **(B)** mRNA expressions of miR-199a-3p in the U87 cell. **(C)** The relative luciferase activity for cells in transfection by miR-NC, miR-199a-3p-mimic, NC inhibitor, or miR-199a-3p-inhibitor. **(D)** RIP experiments for LINC01140 enrichment in cells transfected by miR-199a-3p. **(E)** Expressions of miR-199a-3p in U87 cells in transfection by shNC or shLINC01140. **(F)** Expressions of LINC01140 in U87 cells in transfection by miR-NC, miR-199a-3p mimic, NC inhibitor, or miR-199a-3p-inhibitor. *P < 0.05, n=3.

weight. In addition, Figure 7D shows that the mRNA expressions were inhibited in cells in transfection by shLINC01140. From Figure 7E, the ZHX1 protein level was down-regulated in the shLINC01140 group. Figure 7F illustrates the Ki-67

staining and found that shLINC01140 decreased cell proliferation. We have provided Supplementary Figure 1 to evaluate the effect of linc01140 and MiR-199a-3p on tumor volume and size. ShLINC01140 could inhibit the tumor volume

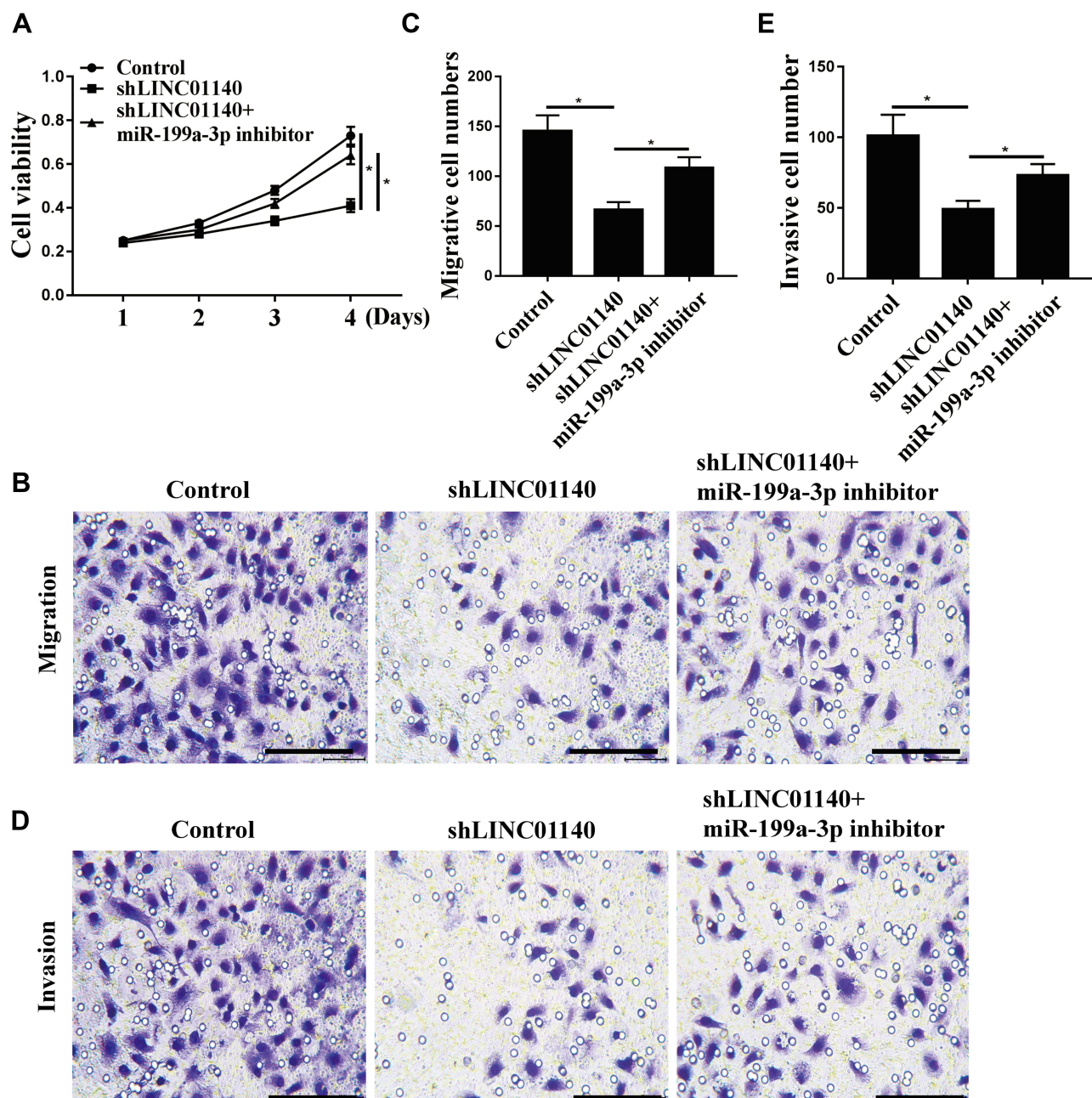


Figure 4 The effect of LINC01140 was attenuated by miR-199a-3p in glioma cells. For glioma cells in transfection by control, shLINC01140, or shLINC01140+ miR-199a-3p inhibitor: (A) CCK8 assay for cell viabilities. (B, C) Transwell for cell migration abilities. (D, E) Transwell for cell invasion abilities. * $P < 0.05$, $n=3$.

(Supplementary Figure 1A) and weight (Supplementary Figure 1B), but miR-199a-3p inhibitor attenuated this effect.

Discussions

Aberrant expressions of lncRNAs and miRNAs are usually closely related to the development, progression, or inhibition of human tumors. LincRNAs have been demonstrated to maintain oncogene properties in a variety of human cancers, such as LincRNA-PCAT-1 for prostate cancer,³³ LincRNA-

ROR for endometrial cancer stem cells,³⁴ LincRNA-ROR for breast cancers.^{35,36} Previous studies have investigated the expressions of LINC01140 in various cancers, including gastric cancer,³⁷ lung cancer,³⁸ and cervical cancer.³⁹ For instance, Song revealed that it was identified to significantly correlated with the overall survival rate.³⁷ Although they did not discuss thoroughly on the expressions of LINC01140, they still gave us a clue about the possible role of LINC01140 in the progression of gastric cancer. As far as we know, we

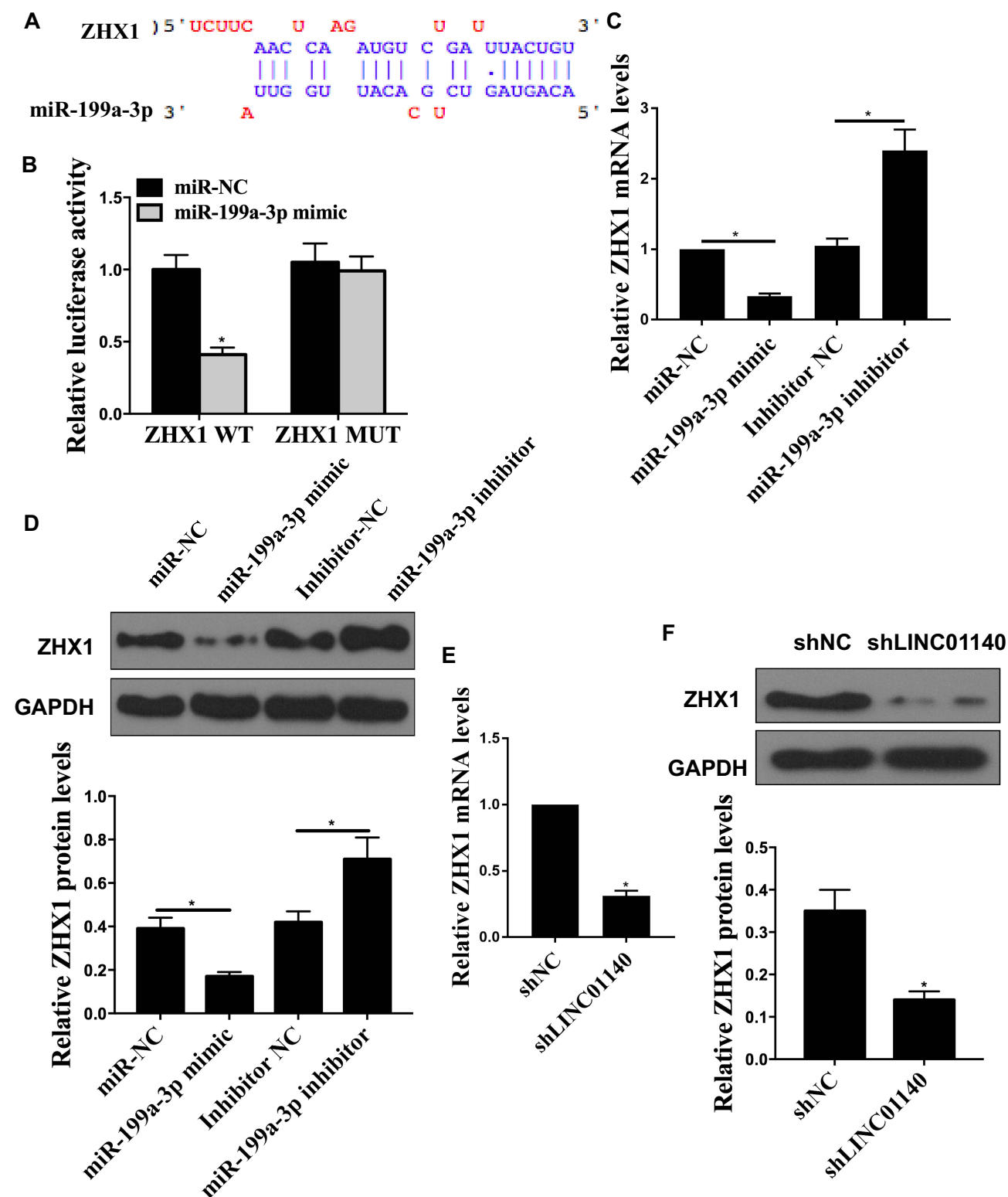


Figure 5 ZHX1 was directly targeted by miR-199a-3p. (A). The commonly shared sequences between miR-199a-3p and ZHX1. (B) The relative luciferase activities for cells in transfection by miR-NC or miR-199a-3p mimic, and ZHX1 WT or ZHX1 MUT. (C) Relative ZHX1 mRNA levels for cells in transfection by miR-NC or miR-199a-3p mimic, inhibitor NC, or miR-199a-3p inhibitor; (D) Western blotting for ZHX1 and GAPDH for cells in transfection by shNC, and shLINC01140. (E). Relative ZHX1 mRNA levels for cells in transfection by shNC or shLINC01140. (F). Western blotting of ZHX1 and GAPDH miR-NC, miR-199a-3p mimic, NC-inhibitor, and miR-199a-3p-inhibitor. *P < 0.05, n=3.

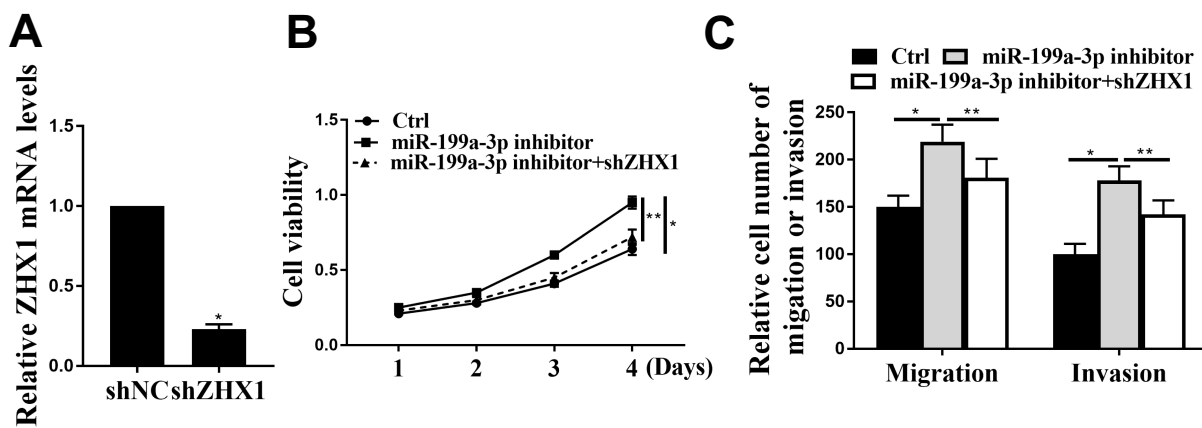


Figure 6 The effect of miR-199a-3p was attenuated by ZHX1 in glioma cells. **(A)**, ZHX1 mRNA levels for cells transfected by shNC or shZHX1. **(B)**, CCK8 assay for cell viabilities transfected by control, miR-199a-3p inhibitor or miR-199a-3p inhibitor+shZHX1. **(C)**, Transwell for cell migration and invasion transfected by control, miR-199a-3p inhibitor or miR-199a-3p inhibitor+shZHX1. * $p < 0.001$, ** $p < 0.05$, $n = 3$.

are the first to report the expressions of LINC01140 in glioma cells. In the qRT-PCR results, we found that mRNA expression of LINC01140 was up-regulated in glioma cell lines of SHG44, U251, U-118 MG, U87, when compared with normal brain cells. In addition, we also noticed that mRNA expressions of miR-199a-3p were reduced in glioma cells than normal brain cell line HA. This may provide useful information in the interactions between LINC01140 and miR-199a-3p.

According to previous findings, the knockdown of an oncogene may hinder the proliferation, growth, migration, and invasion of the corresponding tumor cells. For instance, Yao indicated that the knockdown of lncRNA XIST exerted tumor-suppressive functions in human glioblastoma stem cells by up-regulating miR-152.⁴⁰ In our experiments, we found that shLINC01140 significantly reduced the cell viabilities, the migrative and invasive activities of glioma cells. In consistence with previous findings, we also report that knockdown of LINC01140 restrained growth, migration, and invasion abilities of glioma cells.

In 2015, Shen et al reported that miR-199a-3p suppressed glioma cell proliferation through the regulation of the AKT/mTOR signaling pathway.²⁶ Similar to our results, they also found that the expressions of miR-199a-3p were down-regulated in glioma cell lines. In addition, we noticed that LINC01140 could directly sponge miR-199a-3p in glioma cells. The luciferase results demonstrated that the luciferase activity of LINC01140-WT was suppressed by miR-199a-3p, but LINC01140-MUT activities were not affected by miR-199a-3p. Besides, the expressions of miR-199a-3p were elevated in cells in transfection by shLINC01140, and the

transfection of miR-199a-3p mimic or inhibitor caused the inhibition or elevation of LINC01140. It was evident that miR-199a-3p is a direct target of LINC01140 in glioma cells.

According to CC. Ma in 2016, lncRNA ATB could promote glioma malignancy by negatively regulating miR-200a. The repression of miR-200a restored the sh-ATB induced inhibitory effects on glioma cells. Similarly, our results also revealed that the effect of LINC01140 was attenuated by miR-199a-3p in glioma cells. The CCK-8 assays that down-regulation of LINC01140 inhibited the abilities of cell proliferation, but shLINC01140+miR-199a-3p-inhibitor increased these abilities. In addition, the migration and invasion of glioma cells were suppressed by shLINC01140, but this phenomenon was attenuated by miR-199a-3p-inhibitor.

ZHX1 is a new mouse homeodomain protein containing two zinc-fingers and five homeodomains.⁴¹ It has been widely investigated in its role in human cancers. In 2018, Rui discussed that lncRNA DLG1-AS1 promotes cell proliferation by competitively binding with miR-107 and up-regulating ZHX1 expression in cervical cancer.⁴² In 2017, Guan found that miR-199a-3p inhibited tumorigenesis of hepatocellular carcinoma cells by targeting the ZHX1/PUMA signal pathway.³¹ In our experiments, we firstly found that ZHX1 was directly targeted by miR-199a-3p. The reporter assays in U87 cells revealed miR-199a-3p-dependent repression of the ZHX1-WT 3'UTR. In addition, shLINC01140 decreased ZHX1 protein levels. The protein expressions of ZHX1 were reduced by a miR-199a-3p mimic in the U87 cell but increased by miR-199a-3p-inhibitor. The above findings are in consistence with previous reports. Moreover, we monitored the in vivo growth of glioma tumor. It was found that knockdown of LINC00140 suppressed the tumor growth rate, tumor volume, and tumor

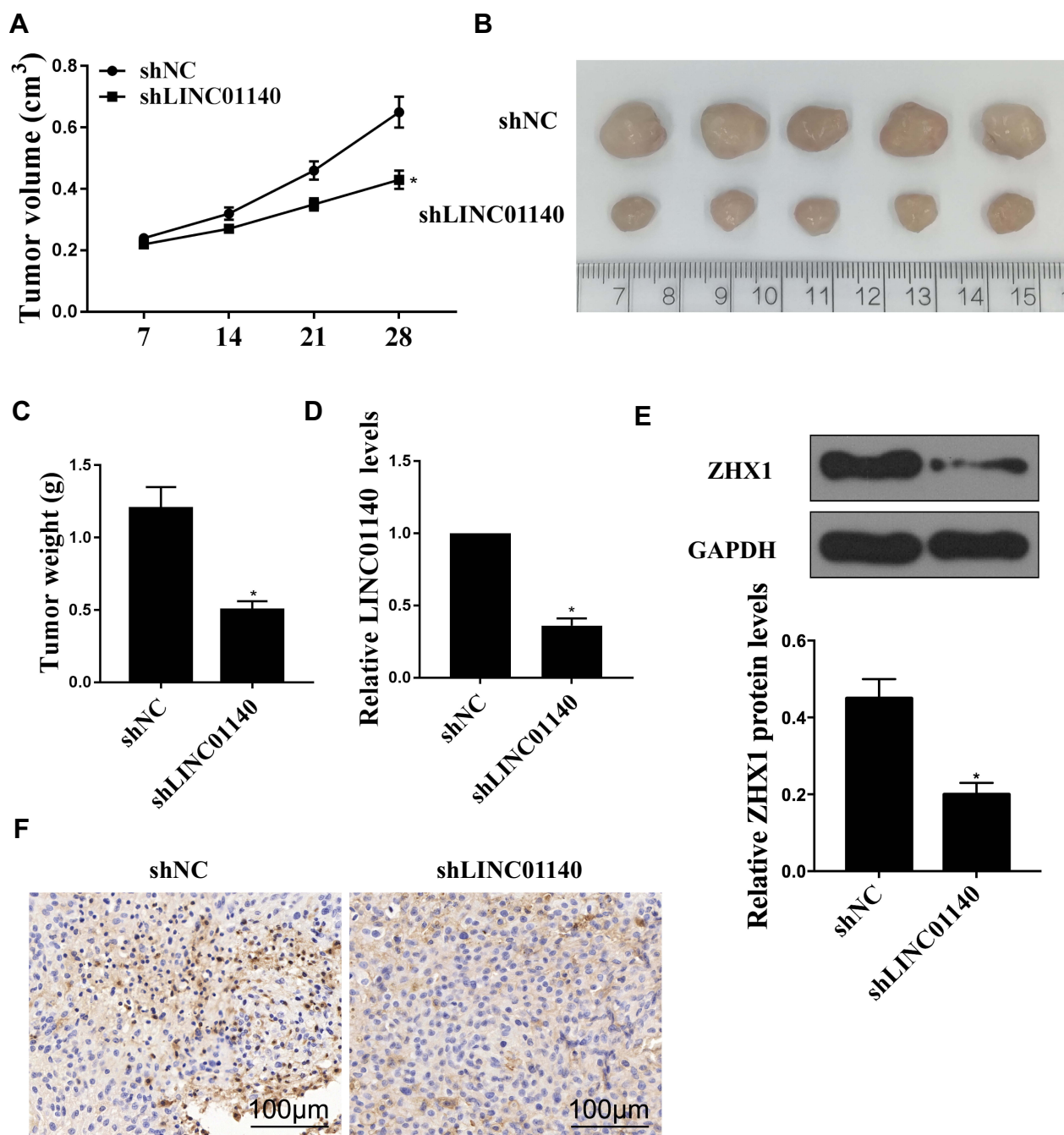


Figure 7 LINC01140 promoted glioma growth in vivo. **(A)** Tumor volumes and growth curves every seven days. **(B)** Tumor size was reduced in the shLINC01140 group compared with the sh-NC. **(C)** Tumor weight in transfection by shNC or shLINC01140. **(D)** The mRNA expressions of LINC01140 in cells in transfection by shNC or shLINC01140. **(E)** Western blotting of ZHX1 proteins in cells in transfection by shNC or shLINC01140. **(F)** Ki-67 staining for cells in transfection by shNC or shLINC01140. * $P < 0.05$, $n=5$.

weight. ZHX1 protein level was down-regulated in the shLINC01140 group, and shLINC01140 decreased cell proliferation. Through these experiments and observations, LINC01140 might exert its biological roles in the promotion of glioma by modulating the miR-199a-3p/ZHX1 axis.

Conclusion

LINC01140 enhanced the developments of by promoting ZHX1 expressions via down-regulating miR-199a-3p. This might provide valuable information for the new therapeutic directions of glioma.

Ethical Approval

All procedures performed in studies involving animals were reviewed and permitted by the First Affiliated Hospital of Zhengzhou University in Henan Province Experimental Animal Care Commission and conducted in strict accordance with the national institutes of health guidelines for the care and use of experimental animals.

Disclosure

The authors report no conflicts of interest in this work.

References

- Furnari FB, Fenton T, Bachoo RM, et al. Malignant astrocytic glioma: genetics, biology, and paths to treatment. *Genes Dev.* 2007;21(21):2683–2710. doi:10.1101/gad.1596707
- Schwartzbaum JA, Fisher JL, Aldape KD, Wrensch M. Epidemiology and molecular pathology of glioma. *Nature Rev Neurol.* 2006;2(9):494.
- Friedman HS, Kerby T, Calvert H. Temozolomide and treatment of malignant glioma. *Clin Cancer Res.* 2000;6(7):2585–2597.
- Group GM-aTG. Chemotherapy in adult high-grade glioma: a systematic review and meta-analysis of individual patient data from 12 randomised trials. *Lancet.* 2002;359(9311):1011–1018. doi:10.1016/S0140-6736(02)08091-1
- Stupp R, Hegi ME, Mason WP, et al. Effects of radiotherapy with concomitant and adjuvant temozolomide versus radiotherapy alone on survival in glioblastoma in a randomised Phase III study: 5-year analysis of the EORTC-NCIC trial. *Lancet Oncol.* 2009;10(5):459–466. doi:10.1016/S1470-2045(09)70025-7
- Sanai N, Polley M-Y, Berger MS. Insular glioma resection: assessment of patient morbidity, survival, and tumor progression. *J Neurosurg.* 2010;112(1):1–9. doi:10.3171/2009.6.JNS0952
- Freije WA, Castro-Vargas FE, Fang Z, et al. Gene expression profiling of gliomas strongly predicts survival. *Cancer Res.* 2004;64(18):6503–6510. doi:10.1158/0008-5472.CAN-04-0452
- Nutt CL, Mani D, Betensky RA, et al. Gene expression-based classification of malignant gliomas correlates better with survival than histological classification. *Cancer Res.* 2003;63(7):1602–1607.
- Amano S, Li S, Gu C, et al. Use of genetically engineered bone marrow-derived mesenchymal stem cells for glioma gene therapy. *Int J Oncol.* 2009;35(6):1265–1270. doi:10.3892/ijo_00000443
- Weller M, Felsberg J, Hartmann C, et al. Molecular predictors of progression-free and overall survival in patients with newly diagnosed glioblastoma: a prospective translational study of the German Glioma Network. *J Clin Oncol.* 2009;27(34):5743–5750. doi:10.1200/JCO.2009.23.0805
- Huse JT, Holland EC. Targeting brain cancer: advances in the molecular pathology of malignant glioma and medulloblastoma. *Nature Rev Cancer.* 2010;10(5):319. doi:10.1038/nrc2818
- Huang PH, Xu AM, White FM. Oncogenic EGFR signaling networks in glioma. *Sci Signal.* 2009;2(87):re6–re6. doi:10.1126/scisignal.287re6
- Shi Y, Wang Y, Luan W, et al. Long non-coding RNA H19 promotes glioma cell invasion by deriving miR-675. *PLoS One.* 2014;9(1):e86295. doi:10.1371/journal.pone.0086295
- Zhang X, Sun S, Pu JKS, et al. Long non-coding RNA expression profiles predict clinical phenotypes in glioma. *Neurobiol Dis.* 2012;48(1):1–8. doi:10.1016/j.nbd.2012.06.004
- Li J, Zhang M, An G, Ma Q. LncRNA TUG1 acts as a tumor suppressor in human glioma by promoting cell apoptosis. *Exp Biol Med.* 2016;241(6):644–649. doi:10.1177/1535370215622708
- Ma K-X, Wang H-J, Li X-R, et al. Long noncoding RNA MALAT1 associates with the malignant status and poor prognosis in glioma. *Tumor Biol.* 2015;36(5):3355–3359. doi:10.1007/s13277-014-2969-7
- Liao Y, Shen L, Zhao H, et al. LncRNA CASC2 interacts with miR-181a to modulate glioma growth and resistance to TMZ through PTEN pathway. *J Cell Biochem.* 2017;118(7):1889–1899. doi:10.1002/jcb.25910
- Ma -C-C, Xiong Z, Zhu G-N, et al. Long non-coding RNA ATB promotes glioma malignancy by negatively regulating miR-200a. *J Exp Clin Cancer Res.* 2016;35(1):90. doi:10.1186/s13046-016-0367-2
- Feng S, Yao J, Chen Y, et al. Expression and functional role of reprogramming-related long noncoding RNA (lincRNA-ROR) in glioma. *J Mol Neurosci.* 2015;56(3):623–630. doi:10.1007/s12031-014-0488-z
- Guo H, Wu L, Yang Q, Ye M, Zhu X. Functional linc-POU3F3 is overexpressed and contributes to tumorigenesis in glioma. *Gene.* 2015;554(1):114–119. doi:10.1016/j.gene.2014.10.038
- Hadjicharalambous MR, Roux BT, Csomor E, et al. Long intergenic non-coding RNAs regulate human lung fibroblast function: implications for idiopathic pulmonary fibrosis. *Sci Rep.* 2019;9(1):6020. doi:10.1038/s41598-019-42292-w
- Li D, Li L, Cao Y, Chen X. Downregulation of LINC01140 is associated with adverse features of breast cancer. *Oncol Lett.* 2020;19:1157–1164.
- You X, Zhao Y, Sui J, et al. Integrated analysis of long noncoding RNA interactions reveals the potential role in progression of human papillary thyroid cancer. *Cancer Med.* 2018;7(11):5394–5410. doi:10.1002/cam4.2018.7.issue-11
- Gabrieli G, Wurdinger T, Kesari S, et al. MicroRNA 21 promotes glioma invasion by targeting matrix metalloproteinase regulators. *Mol Cell Biol.* 2008;28(17):5369–5380. doi:10.1128/MCB.00479-08
- Cai H, Liu X, Zheng J, et al. Long non-coding RNA taurine upregulated 1 enhances tumor-induced angiogenesis through inhibiting microRNA-299 in human glioblastoma. *Oncogene.* 2017;36(3):318. doi:10.1038/ncr.2016.212
- Shen L, Sun C, Li Y, et al. MicroRNA-199a-3p suppresses glioma cell proliferation by regulating the AKT/mTOR signaling pathway. *Tumor Biol.* 2015;36(9):6929–6938. doi:10.1007/s13277-015-3409-z
- Chai C, Song L, Yang B, Han S, Li X, Li M. Circulating miR-199a-3p in plasma and its potential diagnostic and prognostic value in glioma. *Eur Rev Med Pharmacol Sci.* 2016;20:4885–4890.
- Yamada K, Printz RL, Osawa H, Granner DK. Human ZHX1: cloning, chromosomal location, and interaction with transcription factor NF-Y. *Biochem Biophys Res Commun.* 1999;261(3):614–621. doi:10.1006/bbrc.1999.1087
- Yamada K, Kawata H, Matsuura K, et al. Functional analysis and the molecular dissection of zinc-fingers and homeoboxes 1 (ZHX1). *Biochem Biophys Res Commun.* 2002;297(2):368–374. doi:10.1016/S0006-291X(02)02203-9
- Wang Z, Ma X, Cai Q, et al. MiR-199a-3p promotes gastric cancer progression by targeting ZHX1. *FEBS Lett.* 2014;588(23):4504–4512. doi:10.1016/j.febslet.2014.09.047
- Guan J, Liu Z, Xiao M, et al. MicroRNA-199a-3p inhibits tumorigenesis of hepatocellular carcinoma cells by targeting ZHX1/PUMA signal. *Am J Transl Res.* 2017;9(5):2457.
- Shang C, Guo Y, Hong Y, Xue Y-X. Long non-coding RNA TUSC7, a target of miR-23b, plays tumor-suppressing roles in human gliomas. *Front Cell Neurosci.* 2016;10:235. doi:10.3389/fncel.2016.00235
- Prensner JR, Iyer MK, Balbin OA, et al. Transcriptome sequencing across a prostate cancer cohort identifies PCAT-1, an unannotated lincRNA implicated in disease progression. *Nat Biotechnol.* 2011;29(8):742. doi:10.1038/nbt.1914
- Zhou X, Gao Q, Wang J, Zhang X, Liu K, Duan Z. Linc-RNA-RoR acts as a “sponge” against mediation of the differentiation of endometrial cancer stem cells by microRNA-145. *Gynecol Oncol.* 2014;133(2):333–339. doi:10.1016/j.ygyno.2014.02.033

35. Hou P, Zhao Y, Li Z, et al. LincRNA-ROR induces epithelial-to-mesenchymal transition and contributes to breast cancer tumorigenesis and metastasis. *Cell Death Dis.* **2014**;5(6):e1287. doi:10.1038/cddis.2014.249
36. Eades G, Wolfson B, Zhang Y, Li Q, Yao Y, Zhou Q. lincRNA-RoR and miR-145 regulate invasion in triple-negative breast cancer via targeting ARF6. *Mol Cancer Res.* **2015**;13(2):330–338. doi:10.1158/1541-7786.MCR-14-0251
37. Song P, Jiang B, Liu Z, Ding J, Liu S, Guan W. A three-lincRNA expression signature associated with the prognosis of gastric cancer patients. *Cancer Med.* **2017**;6(6):1154–1164. doi:10.1002/cam4.2017.6.issue-6
38. Qiao F, Li N, Li W. Integrative bioinformatics analysis reveals potential long non-coding RNA biomarkers and analysis of function in non-smoking females with lung cancer. *Med Sci Monitor.* **2018**;24:5771. doi:10.12659/MSM.908884
39. Yuan LY, Qin X, Li L, et al. The transcriptome profiles and methylation status revealed the potential cancer-related lncRNAs in patients with cervical cancer. *J Cell Physiol.* **2019**;234(6):9756–9763. doi:10.1002/jcp.27661
40. Yao Y, Ma J, Xue Y, et al. Knockdown of long non-coding RNA XIST exerts tumor-suppressive functions in human glioblastoma stem cells by up-regulating miR-152. *Cancer Lett.* **2015**;359(1):75–86. doi:10.1016/j.canlet.2014.12.051
41. Barthelemy I, Carramolino L, Gutiérrez J, Barbero JL, Márquez G, Zaballos A. zhx-1: a novel mouse homeodomain protein containing two zinc-fingers and five homeodomains. *Biochem Biophys Res Commun.* **1996**;224(3):870–876. doi:10.1006/bbrc.1996.1114
42. Rui X, Xu Y, Huang Y, Ji L, Jiang X. lncRNA DLG1-AS1 promotes cell proliferation by competitively binding with miR-107 and up-regulating ZHX1 expression in cervical cancer. *Cell Physiol Biochem.* **2018**;49(5):1792–1803. doi:10.1159/000493625

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