Journal of Cancer Research and Clinical Oncology (2026) 152:93
https://doi.org/10.1007/s00432-026-06454-4

RESEARCH

LncRNA-LINC01281 exerts anti-cancer functions via the MYC/VEGF pathway in the progression of cervical cancer

Zhang Shuqian[1] · Chen Zhi[1] · Quratul Ain[1] · Liu Yan[1] · Luo Chengfang[1] · Bai Xiaoxu[1] · Zhang Song[2] · Gao Jiayin[1]

Received: 31 January 2026 / Accepted: 24 February 2026

Abstract

Introduction Cervical cancer is the fourth most common cancer in women and remains a major global health issue. Long non-coding RNAs (lncRNAs) play a crucial role in tumor biology regulation. This study investigates the role of LINC01281 in cervical cancer.

Methods LncRNAs were identified from The Cancer Genome Atlas (TCGA) database, focusing on LINC01281 for detailed analysis. GSEA revealed MYC-mediated VEGF signaling as a potential pathway. Functional assays in HeLa cells assessed the impact of LINC01281 overexpression and knockdown on proliferation, migration, and the MYC-VEGFA pathway.

Results LINC01281 is identified as a unique prognostic marker for cervical cancer. GSEA indicated participation in VEGF signaling through MYC modulation. LINC01281 overexpression inhibited MYC expression, leading to reduced cell proliferation and migration. MYC silencing led to a decreased expression of VEGFA at both transcript and protein levels. LINC01281 encodes a 42-amino acid peptide, highlighting its biological significance.

Conclusion LINC01281 influences cervical cancer progression via the MYC-VEGFA pathway and may serve as a potential biomarker and therapeutic target. The lncRNA and its peptide show promise for use in cervical cancer treatment.

Keywords Bioinformatics analysis · Cervical cnacer · Enrichment analysis · LncRNA · Western blot

Introduction

Cancer has emerged as a significant global public health and economic challenge in the twenty-first century. Cervical cancer (CC) is the most common and deadly of the gynaecological cancers, making it a major global health problem (Bray et al. 2024). Unsettlingly, current patterns suggest that CC is affecting a younger population more and more (He and Li, 2021). Even though comprehensive screening programs and the widespread use of HPV vaccination have decreased incidence rates worldwide, mortality is still disproportionately high in many low- and middle-income nations (Kakotkin et al. 2023; Singh et al. 2023). Due to their invasive nature, CC cells are more likely to metastasise and recur, which usually leads to treatment failure (Liontos et al. 2019). Therefore, investigating the fundamental mechanisms of CC development and creating innovative treatment and preventive approaches continue to be crucial from a clinical standpoint.

Research has traditionally focused mostly on genes that code for proteins, frequently underestimating the potential diagnostic and therapeutic value of long non-coding RNAs (lncRNAs) (Pan et al. 2023). But because to developments in transcriptomics and sequencing technologies, it is now known that many lncRNAs are important modulators of gene expression, refuting the idea that they are just transcriptional noise (Gonzales et al. 2024; Mercer et al. 2009; Wen et al. 2024). LncRNAs can participate in a variety of biological processes by interacting with proteins, other RNA molecules, and DNA. Numerous diseases, including cancer, have been linked to lncRNA dysregulation (Arunkumar, 2024). In the pathogenic processes of CC, for instance, overexpression of LncRNA-C5orf66-AS1 can competitively

Zhang Shuqian, Chen Zhi and Quratul Ain have contributed equally to this work.

✉ Gao Jiayin
gaoguimeizi1@163.com

[1] Department of Obstetrics and Gynecology, The Second Affiliated Hospital of Harbin Medical University, Harbin, Heilongjiang, China

[2] Department of Hospital Record, The First Affiliated Hospital of Harbin Medical University, Harbin, Heilongjiang, China

Published online: 24 April 2026

bind with miR-637, resulting in increased levels of RING1 expression and a dismal prognosis for patients (Xu et al. 2019). It has also been demonstrated that LncRNA SNHG1 inhibits the course of CC through the miR-195/NEK2 axis (Ji et al. 2020). In an effort to slow or stop the cancerous development of CC, this work focusses on clarifying the transcriptional expression and regulatory mechanisms of lncRNAs.

Tumor angiogenesis plays a critical role in the malignant progression of neoplasms, serving as a vital process for tumor growth and metastasis (Song et al. 2021). The activation of the vascular endothelial growth factor (VEGF) signalling pathway is essential to angiogenesis, promoting the development of new blood vessels in the tumour microenvironment (Ferrara, 2010). Additionally, in cervical cancer (CC), tumour cell invasion is significantly linked to the activation of the VEGF pathway (Fu et al. 2020). A multitude of long non-coding RNAs (lncRNAs) have been recognised as regulators of the VEGF signalling pathway in several malignancies, acting as both pro-angiogenic and anti-angiogenic agents (Alharthi et al. 2024; Jin et al. 2020). In the context of preeclampsia, lncRNA MALAT1 has been demonstrated to affect trophoblast activity via modulating the VEGF/VEGFR1 pathway (Song et al. 2022). lncRNA MEG3 downregulates VEGFA, therefore limiting tumour progression in endometrial cancer (Jia et al. 2016).

Historically, lncRNAs were regarded as non-coding entities, lacking the ability to encode proteins (Aswathy and Sumathi, 2023). Recent studies have shown that several lncRNAs contain open reading frames (ORFs) in their sequences, allowing them to encode bioactive peptides and participate in many physiological and pathological processes (Wu et al. 2020). Our study's bioinformatics research indicated that LINC01281 contains an ORF that can encode a 42-amino acid peptide, which we validated by Western blot analysis.

Comprehensive bioinformatics analyses revealed lncRNA LINC01281 as a favourable prognostic marker for patients with cervical cancer. Functional investigations revealed that the overexpression of LINC01281 results in diminished MYC expression, hence blocking the VEGF signalling pathway through the downregulation of VEGFA. Our data suggest that LINC01281 has anti-carcinogenic properties in cervical cancer by modulating the MYC/VEGF signalling axis.

Materials and methods

Data acquisition

The raw transcriptome data and complete pathological features of patients were downloaded from the official website of The Cancer Genome Atlas (TCGA; https://portal.gdc.cancer.gov/) database. The dataset principally comprised comp rehensive patient information including age, clinical stage, neoplasm histologic stage, and the Tumor Lymph Node Metastasis (TNM) staging.

Bioinformatic analysis to screen LINC01281

To identify specific lncRNAs linked to the prognosis of cervical cancer patients, we generated Kaplan–Meier (K-M) curves utilizing the survival R package. Subsequently, we employed univariate and multivariate Cox regression models to evaluate the influence of LINC01281 on the prognosis and clinical characteristics of cervical cancer patients. The receiver operating characteristic (ROC) curve was utilized to assess the prognostic efficacy of the model regarding survival by computing the area under the curve (AUC) with the R package timeROC. This study employed clinical correlation analysis to determine whether the expression level of LINC01281 was related to clinical staging.

Pathway enrichment analysis and functional enrichment analysis

Gene set enrichment analysis (GSEA) and co-expression analysis were performed to identify the cellular signaling pathways and related functions through which LINC01281 participated in regulating the pathological process of cervical cancer. We used the Cluster Profiler package to visualize Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) functional enrichment analysis of 573 specific proteins of LINC01281. A p-value < 0.05 was the standard for significant enrichment.

Cell culture and transfection assay

Cervical cancer cell lines, including HeLa, SiHa, and C-33A, along with human umbilical vein endothelial cells (HUVECs), were obtained from Shanghai Shunran HAKATA Cell Bank. All cell lines were maintained in DMEM medium supplemented with 10% fetal bovine serum (Gibco) and 1% penicillin–streptomycin, cultured in a humidified environment with 5% CO_2 at 37 °C. Prior to transfection, HeLa cells were seeded into 6-well plates at a density of 2×10^5 cells per well. Following the manufacturer's protocol, cells were transfected with either an

overexpression plasmid for LINC01281, LINC01281-specific shRNA, or negative control plasmids using Lipofectamine 2000 (Thermo Fisher/Invitrogen, USA). Positive controls consisted of cells transfected with GAPDH plasmids, while negative controls were cells transfected with scrambled shRNA sequences.

Reverse transcription-quantitative PCR (RT-qPCR)

Quantitative real-time polymerase chain reaction (qRT-PCR) was then conducted using Bestar SYBR Green qPCR Master Mix (DBI, Germany) on an ABI 7500 Fast Real-Time PCR System (ABI, USA). Melting curve analysis was performed for each reaction to verify product specificity and purity, with all reactions showing single peaks confirming specific amplification products without primer-dimer formation (data available upon request). U6 and GAPDH served as internal controls, and data analysis was performed using the 2^−ΔΔCt method.

Cell counting kit-8 (CCK-8) assay

The CCK-8 assay was employed to evaluate the growth and proliferation rates of the transfected cells. Cells were first seeded into 96-well plates at a density of 5×10^3 cells per well and pre-incubated for 24h. Subsequently, 10 µL of CCK-8 reagent was carefully added to each well, ensuring no bubble formation, followed by incubation for 2h at 37 °C. Finally, the absorbance at 450 nm was measured at 0, 24, 48, and 72h using a microplate reader to assess cell viability.

Scratch healing assays

Following transfection, HeLa cells were isolated and prepared as a cell suspension, then seeded into a 6-well plate at a density of 5×10^5 cells per well and cultured to 90% confluence. Vertical scratches were created on the plate surface using a 200 µL pipette tip to simulate a wound. The culture medium was then refreshed with complete medium, and cells were allowed to continue incubation. Cell migration was observed under a microscope at 0 and 24h, capturing images of the same area to document the migration progress.

Western blot (WB) analysis

Total protein was isolated using radioimmunoprecipitation assay (RIPA) buffer, with protein concentration determined via a bicinchoninic acid (BCA) assay kit. Proteins (30 µg per lane) were separated by electrophoresis on 10–12% SDS–polyacrylamide gels and transferred onto a PVDF membrane using the wet transfer method. The membrane was then blocked with 5% non-fat milk at room temperature for 1h before incubation with primary antibodies (anti-MYC, anti-VEGFA, anti-β-actin; all at 1:1000 dilution) at 4 °C overnight. After washing with TBST, the membrane was incubated with a horseradish peroxidase-conjugated secondary antibody (1:5000 dilution) for 1h at room temperature. Protein bands were visualized using an enhanced chemiluminescence (ECL) detection system.

Statistical analysis

Statistical analyses were conducted using GraphPad Prism 8.0 and SPSS Statistics software (version 18.0). All data were presented as mean ± standard deviation (SD). Student's t-test was used for group comparisons, with statistical significance defined as $P < 0.05$.

Results

LINC01281 acted as an independent prognostic risk factor for CC

Transcriptomic data and prognostic follow-up information for 191 cervical cancer patients were obtained from the TCGA database. Kaplan–Meier survival analysis demonstrated that overall survival was significantly higher in the high LINC01281 expression group compared to the low expression group ($P < 0.001$) (Fig. 1A). COX univariate analysis indicated that high LINC01281 expression reduced the risk of poor prognosis in cervical cancer patients ($HR < 1$) (Fig. 1B). Multivariate regression analysis further confirmed that LINC01281 expression level is an independent predictor of overall survival in CC patients ($HR < 1$) (Fig. 1C). Additionally, the ROC curve showed the prognostic diagnostic value of LINC01281 for cervical cancer at three years, with an AUC of 0.767 (Fig. 1D). These findings suggest that lncRNA-LINC01281 is positively correlated with the prognosis of cervical cancer patients, indicating a potential protective role in patient outcomes.

LINC01281 decreased with increasing CC staging

Clinical correlation analysis revealed that LINC01281 expression levels decreased as the T stage advanced and similarly declined with increasing N stage (Fig. 2A, B). Additionally, patients with metastasis exhibited significantly lower LINC01281 expression levels (Fig. 2C). Analyzing the relationship between LINC01281 expression and TNM staging in cervical cancer patients further demonstrated that LINC01281 expression progressively decreased

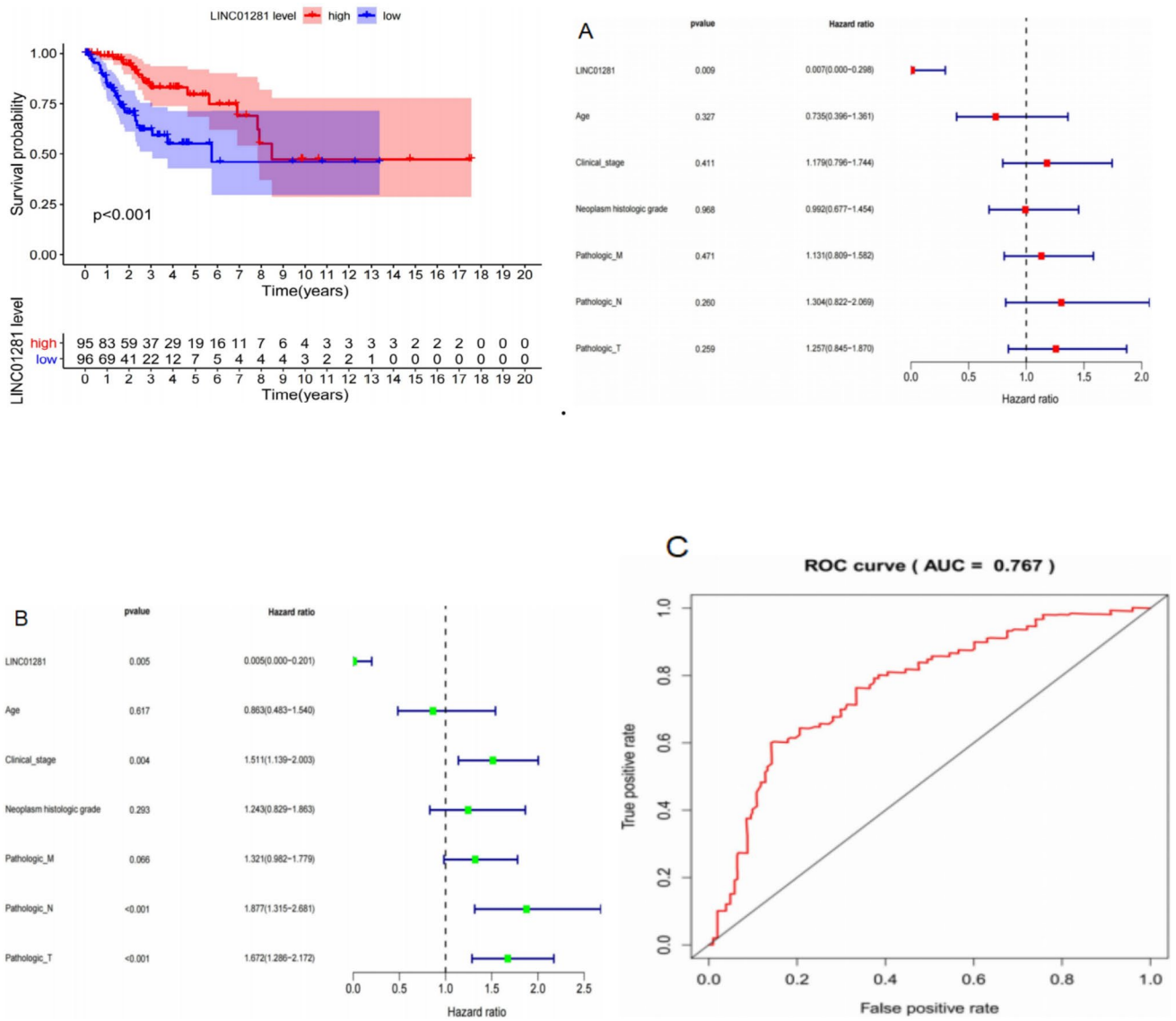

Fig. 1 A.K-M survival analysis. **A** The overall survival of patients in the high expression group of LINC01281 was higher than that in the low expression group. **B** COX univariate analysis: LINC01281 reduce the prognostic risk of cc patients, **B** COX multivariate analysis: LINC01281 reduced the prognostic risk of CC patients. **C** LINC01281 improved the three-year prognosis of CC patients

with advancing clinical stage (Fig. 2D). These findings reinforce the protective role of LINC01281 in cervical cancer progression.

Potential biological processes associated with LINC01281

Gene Set Enrichment Analysis was conducted to explore the pathway activity associated with LINC01281 (Fig. 3A). The results indicated that the VEGF signaling pathway was significantly enriched. To further examine how LINC01281 regulates the VEGF signaling pathway, we performed gene co-expression analysis, revealing a negative correlation between LINC01281 and vascular endothelial growth factor A (VEGFA) ($R = -0.27$, $P = 1.82 \times 10^{-5}$) (Fig. 3B). The upstream regulator of VEGFA was identified using bioinformatics databases UCSC (https://genome.ucsc.edu/), JASPAR (https://jaspar.genereg.net/), and NCBI (https://www.ncbi.nlm.nih.gov/). MYC was selected as a potenti al target, known for its role in the progression of various cancers (Fig. 3C). Co-expression analysis demonstrated a negative correlation between LINC01281 and MYC expression in CC tissue transcriptome data ($R = -0.13$, $P = 0.032$). The binding site between MYC and VEGFA is illustrated in Fig. 3D.

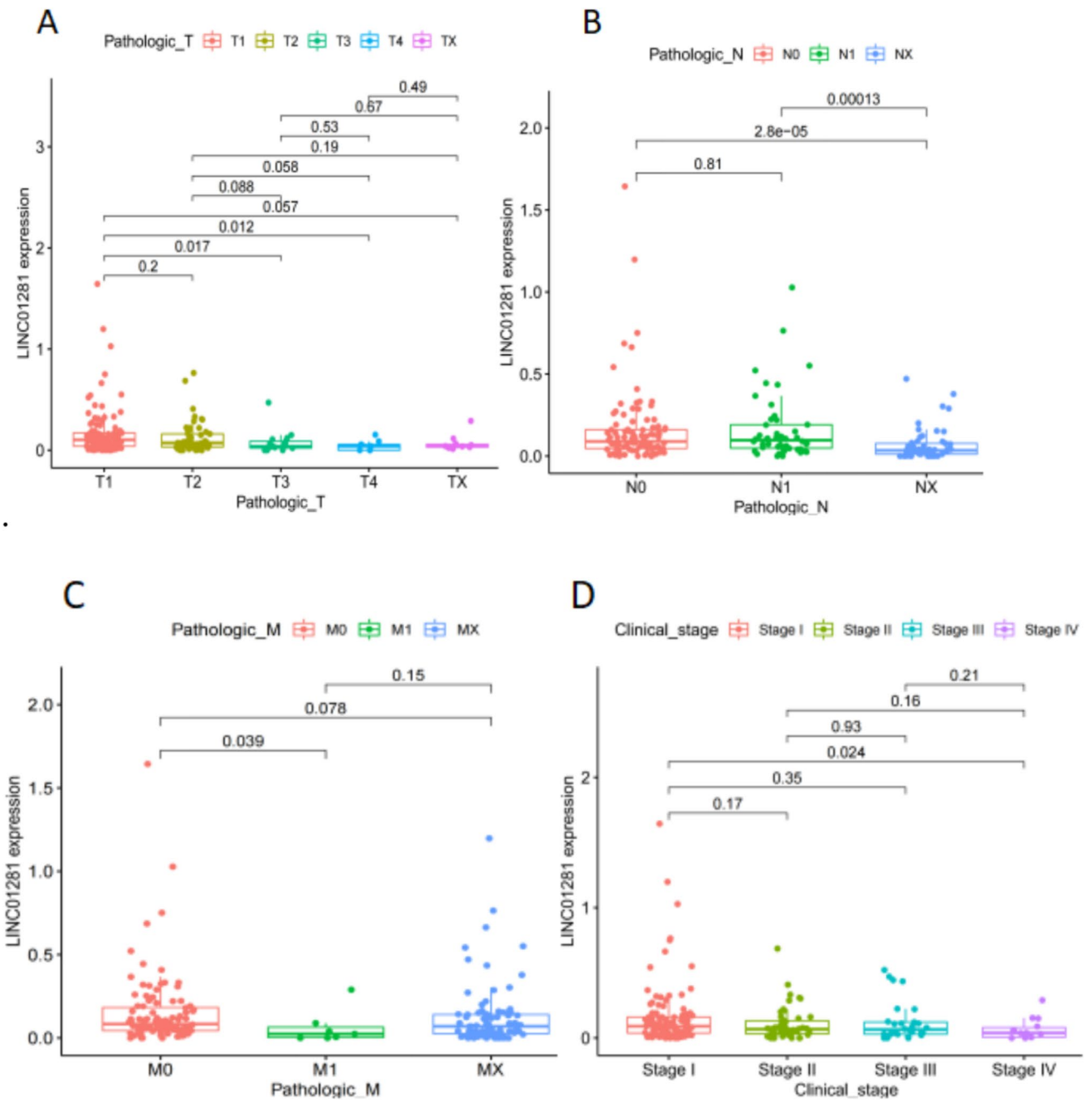

Fig. 2 Clinical correlation analysis, **A–C**.LINC01281 may have a protective effect on the prognosis of CC patients. **D** The clinical staging of CC was negatively correlated with the expression level of LINC01281

Functional enrichment analysis

TRRUST (https://www.grnpedia.org/trrust/), NCBI ORFinder (https://www.ncbi.nlm.nih.gov/orffinder/), and Detaibio (https://www.detaibio.com/) databases were used to obtain the ORFs encoding peptides in the LINC01281 sequence. The interaction proteins captured from the LINC01281-ORF-Flag group were intersected with the NC group, and 573 proteins unique to the LINC01281-ORF-Flag group were found (Fig. 4A). GO enrichment analysis showed the 573 proteins were enriched in ribonucleoprotein complex biogenesis and ncRNA processing in the biological process category; mitochondrial matrix and cell-substrate junction in the cellular component category; and cadherin binding and structural constituent of ribosome in the molecular function category (Fig. 4B). The enriched KEGG pathways mainly were involved in nucleocytoplasmic transport,

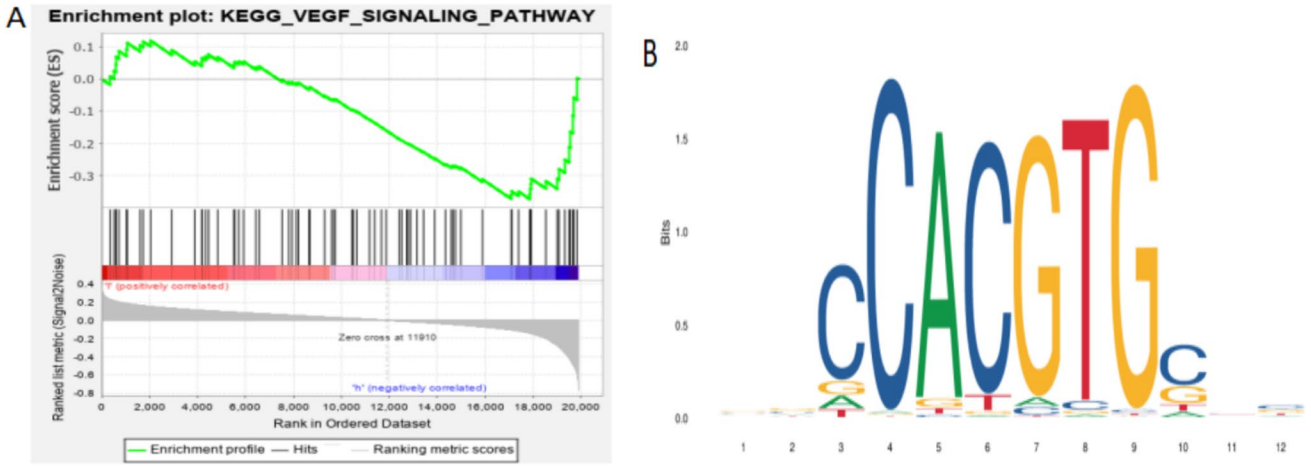

Fig. 3 **A** GSEA pathway enrichment analysis of LINC01281. **B** The correlation between VEGFA and LINC01281. **C** The correlation between MYC and LINC01281. **D** The binding site of MUC and VEGFA

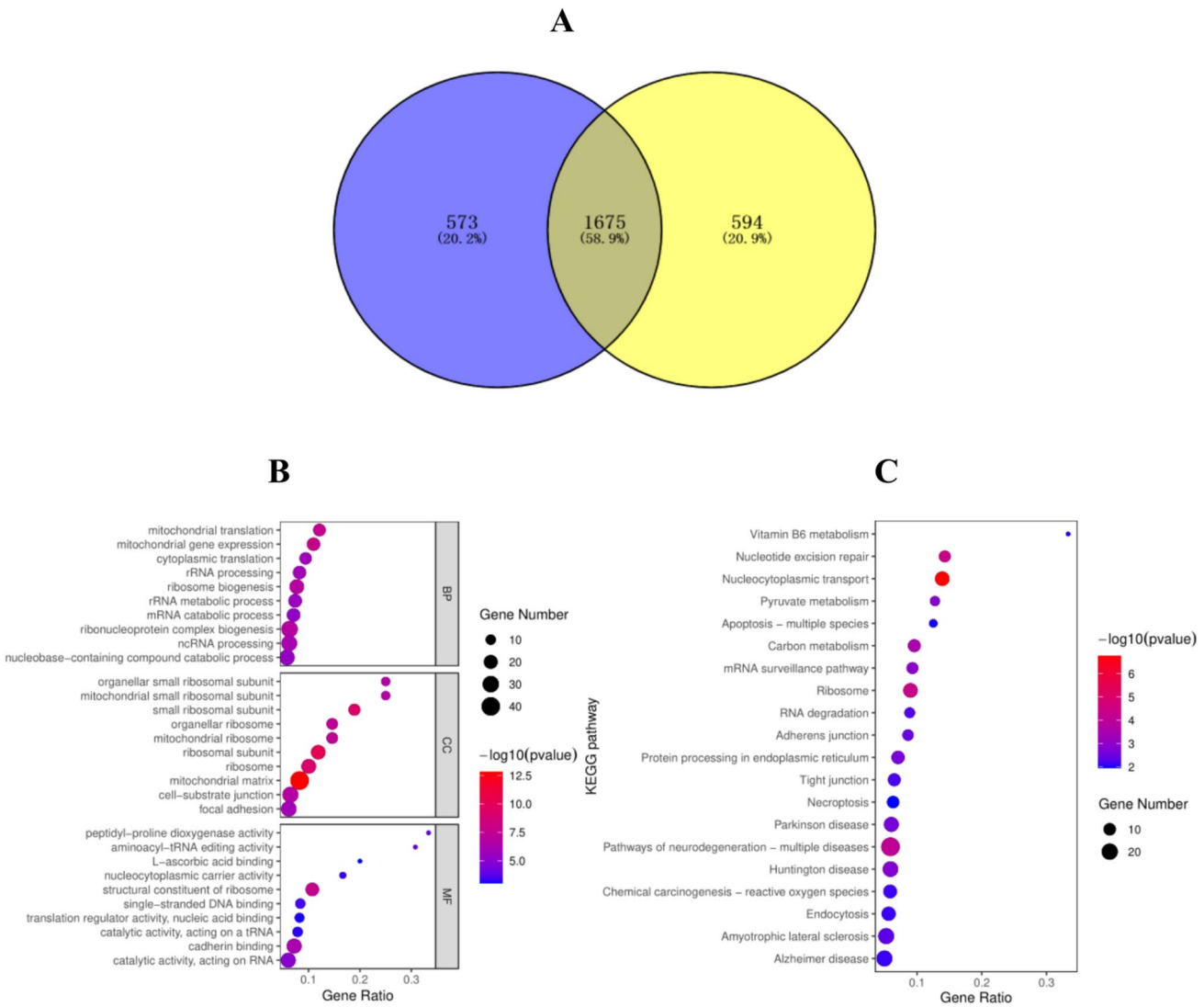

Fig. 4 **A** Venn Diagram of 573 unique proteins. **B** The bubble diagram of enrichment GO analysis(top 10). **C** The results of KEGG pathways analysis of 573 proteins(top 20)

ribosome, and protein processing in endoplasmic reticulum, etc. (Fig. 4C).

LINC01281 functioned as a tumor suppressor in vitro

To determine the physiological role of LINC01281 in cancer, RT-qPCR was conducted in H18, HeLa, SiHa, and C-33A cells to detect their expression levels. The expression of LINC01281 was found to be down-regulated in the above CC cells, with the lowest expression found in HeLa cells, which were thereafter selected for conducting the following experiments (Fig. 5A). We overexpressed LINC01281 by transfection with an overexpression plasmid and knocked down LINC01281 by transfecting with LINC01281-specific shRNA in HeLa cells. In addition, CCK-8 assays were conducted to detect the effect of LINC01281 on HeLa proliferation, and the results showed that overexpression of LINC01281 greatly inhibited cell growth, while LINC01281 knockdown enhanced proliferation (Fig. 5B). Moreover, we used wound healing assay to test whether LINC01281 overexpression affects cell migration. Migration was suppressed by LINC01281 overexpression and enhanced by LINC01281 knockdown (Fig. 5C). These results confirmed that LINC01281 inhibits the proliferation and migration of CC cells.

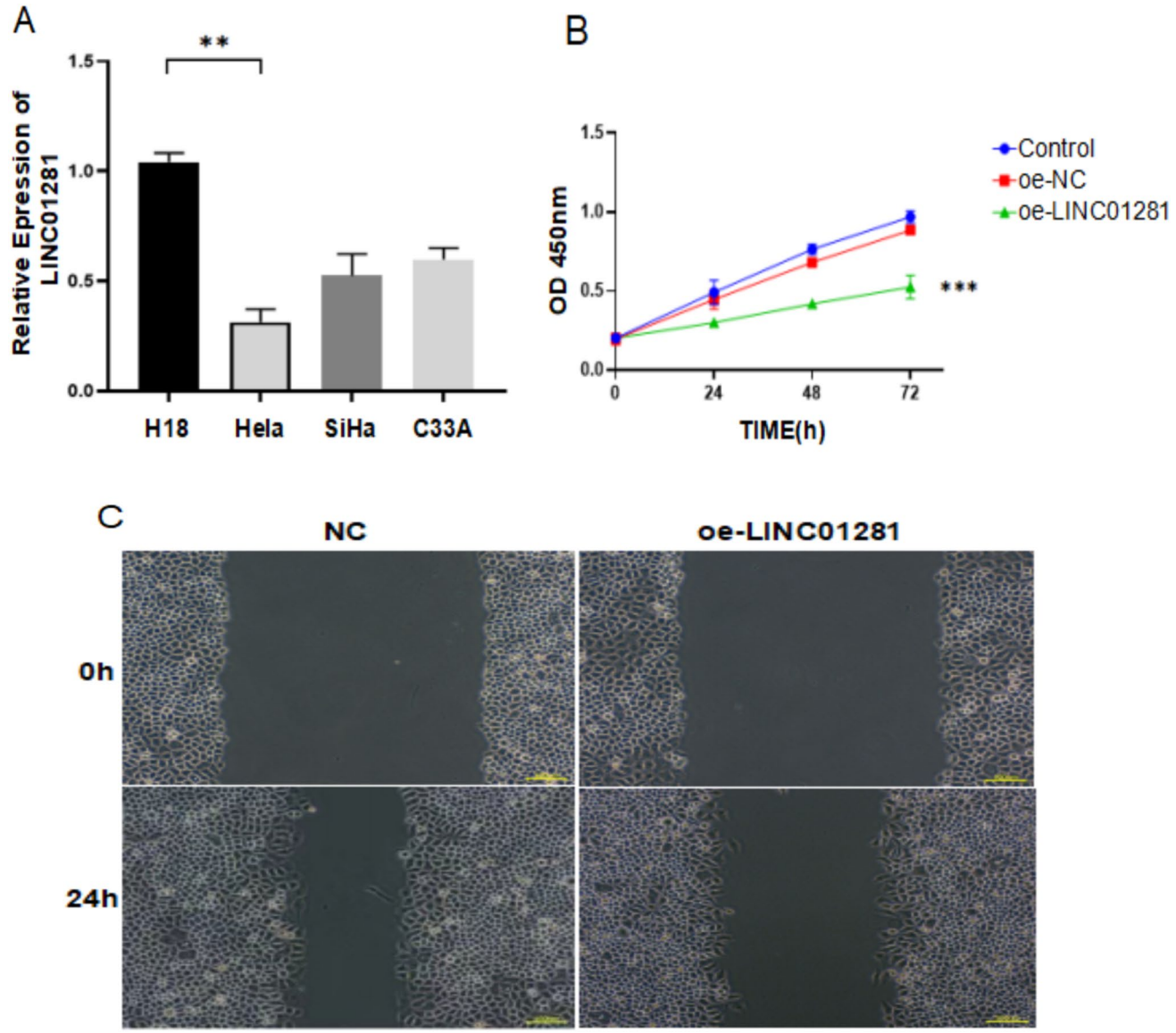

Fig. 5 **A** RT-qPCR was performed to detect LINC01281 expression in cervical cancer cell lines (C-33A, SiHa, and HeLa) and normal cervical cells (H18). **B** CCK-8 assay measured the effects of LINC01281 on the proliferation of HeLa cells that had been transfected with LINC01281 overexpression plasmid or LINC01281-specific shRNA. **C** Wound healing assays of HeLa cells transfected with LINC01281 overexpression plasmid, LINC01281-specific shRNA, or negative controls

LINC01281 affected the VEGFA by negatively regulating MYC

To elucidate the anti-oncogenic mechanism of LINC01281, we stably transfected LINC01281 plasmids into HeLa cells. We observed that LINC01281 overexpression significantly downregulated MYC expression (Fig. 6A). To verify whether VEGFA acts as a downstream target of MYC, we performed MYC knockdown in HeLa cells. RT-qPCR analysis revealed that MYC knockdown reduced the mRNA expression level of VEGFA (Fig. 6B). Additionally, Western blot analysis indicated that VEGFA protein expression decreased following MYC downregulation (Fig. 6C). These findings suggest that LINC01281 may play a crucial role in inhibiting CC progression by modulating the MYC/VEGFA signaling pathway.

LINC01281 encoded 42-aa

Initially, the LINC01281 sequence and the open reading frame encoding the 42-amino acid peptide were obtained from the NCBI ORFinder, TRRUST, and Detaibio databases. Based on the sequence, a 42-amino acid peptide antibody was synthesized (Fig. 7A). Following cell state optimization, a Flag-tagged expression vector was constructed by transfecting the full-length LINC01281 and a version of the ORF region with a start codon mutation. Flag expression in the cells was subsequently detected via Western blot analysis, confirming the presence of the 42-amino acid peptide (Fig. 7B).

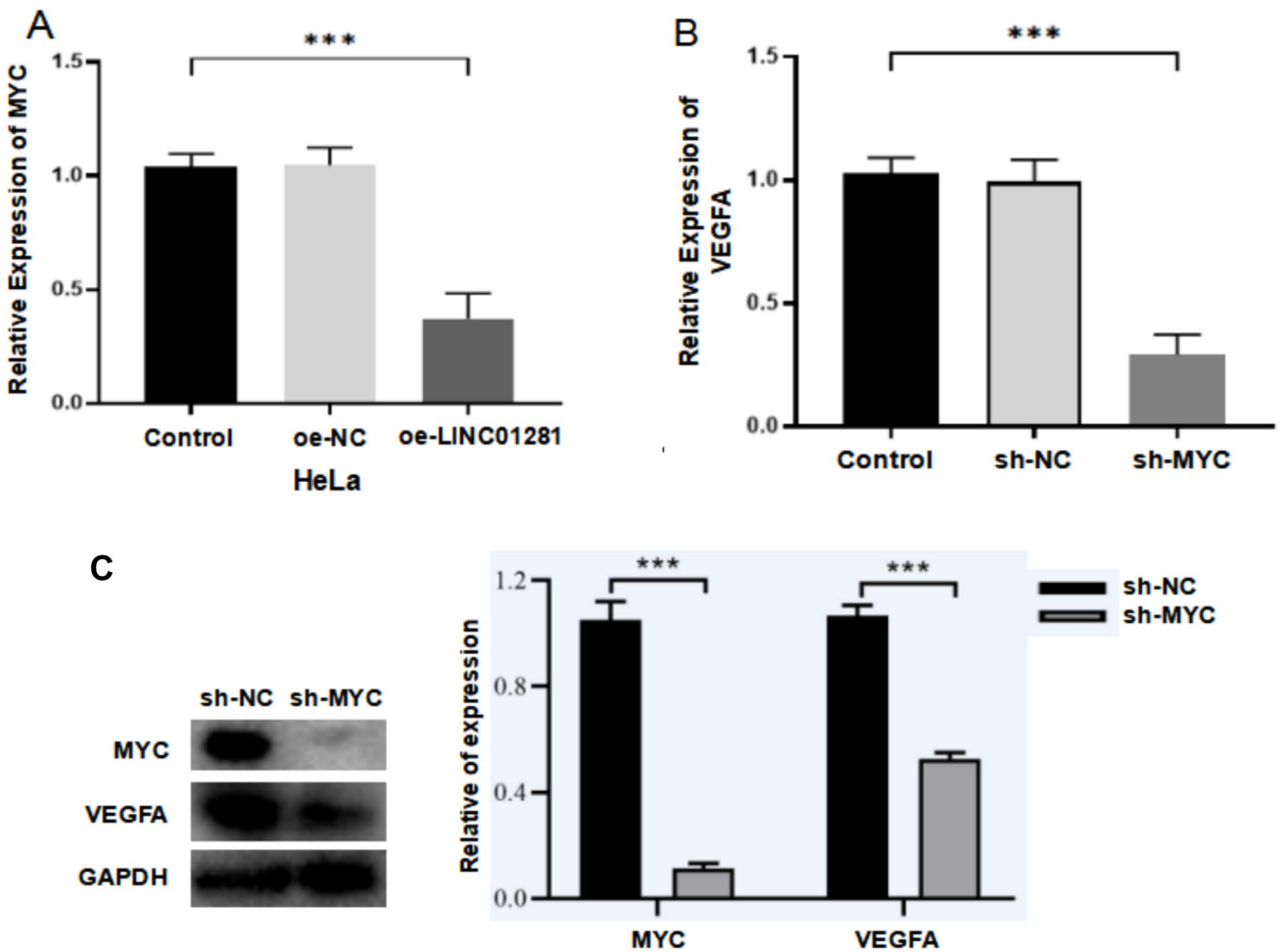

Fig. 6 **A** Overexpression of LINC01281 in HeLa cells could significantly reduce the expression level of MYC by means of RT-qPCR. **B** RT-qPCR analysis was used to detect the mRNA expression of VEGFA in Hela cells transfected with sh-NC or sh-MYC. **C** WB analysis showed that knocking out MYC in HeLa cells significantly reduced the protein expression level of VEGFA

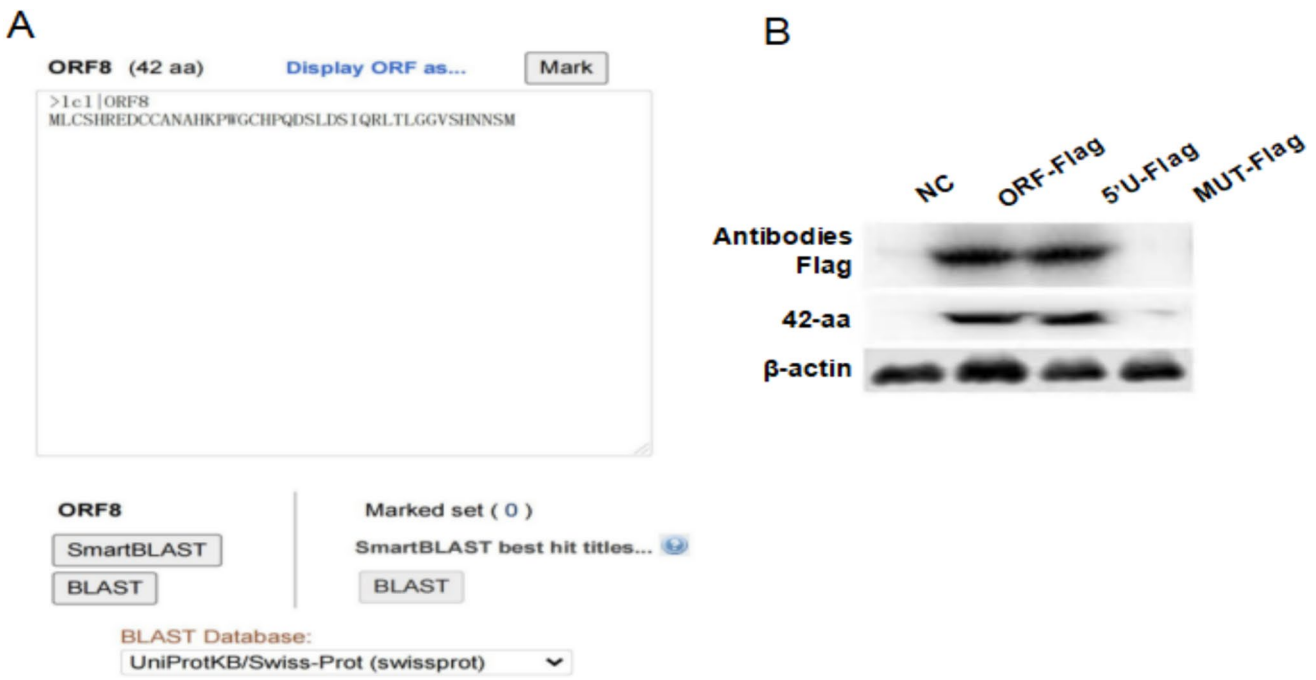

Fig. 7 **A** NCBI orffinder database identified that LINC01281 has the potential to encode 42-aa peptide. **B** Western blot detected 42-aa peptide in cells

Discussion

In 2022, there were about 660,000 new cervical cancer cases and 350,000 deaths globally, according to the International Agency for Research on Cancer (Bray et al. 2024). This statistic highlights the significant impact of the disease. Persistent high-risk HPV infection, mainly HPV 16 and 18, is the primary etiological factor (Wu et al. 2020). The HPV genome's integration into the host genome leads to the dysregulation of E6 and E7 oncogenes, significantly contributing to oncogenesis (Zhi et al. 2023). CC is frequently asymptomatic in early stages and is usually diagnosed at an advanced stage in about two-thirds of patients, underscoring the urgent requirement for new targeted therapies to enhance clinical outcomes (McBride and Warburton, 2017; Zhang et al. 2023).

In CC progression, oncogene activation and tumor suppressor gene inactivation promote malignancy and alter the tumor microenvironment, hindering immune cell function (Sahasrabuddhe, 2024; Li et al. 2019; Xu et al. 2019; Yuan et al. 2021). Grasping these gene regulatory mechanisms at the transcriptional level is essential. Long non-coding RNAs are gaining attention as potential biomarkers in CC (Wang et al. 2021).

This study found a notable downregulation of LINC01281 in CC cell lines. Patients with low LINC01281 expression showed more advanced pathological stages and worse prognoses than those with high expression, indicating that LINC01281 may serve as a protective factor and a potential prognostic marker in cervical cancer. This supports its suggested tumor-suppressive function in other cancers, including laryngeal cancer and lung adenocarcinoma (Yang and Al-Hendy 2022; Zhang et al. 2019). Functional experiments confirmed clinical findings, showing that LINC01281 overexpression significantly inhibits CC cell proliferation and migration, whereas its knockdown enhances these malignant traits.

We investigated the pathways by which LINC01281 exerts its effects. Analysis indicated a significant link between reduced LINC01281 expression and the VEGF signaling pathway. Gene co-expression analysis confirmed a negative correlation between LINC01281 and VEGFA. This contributes to the evidence connecting lncRNAs to tumor angiogenesis; for example, lncRNA MSC-AS1 affects the VEGF pathway in gastric cancer, while MCM3AP-AS1 impacts cell behavior in endometrioid carcinoma through a miRNA/VEGF axis (Liu et al. 2022; Yang et al. 2021). Our study on VEGFA regulation revealed MYC as a crucial transcriptional regulator. A negative correlation was noted between LINC01281 and MYC expression, with MYC knockdown leading to a significant reduction in VEGFA mRNA and protein levels. We propose that LINC01281 influences anti-cervical cancer effects through modulation of the MYC/VEGF signaling axis.

Our study complicates the conventional perspective of lncRNAs as solely non-coding entities. LINC01281 has an open reading frame that can encode a 42-amino acid peptide(Yu et al. 2021; Mezquita et al. 2005; Yoshida 2018).

Our findings contribute to an emerging field where lncRNA-encoded peptides, like DWORF in muscle physiology and HOXB-AS3 in colorectal cancer metabolism, are acknowledged as significant functional entities (Ma et al. 2021; Nelson et al. 2016). This peptide's identification enhances our understanding of LINC01281 function.

Limitations and Future directions.

Our study demonstrates a tumor-suppressive role of LINC01281 in CC, though several limitations must be acknowledged. The exact molecular mechanism by which LINC01281 or its encoded peptide regulates MYC expression is not yet fully understood. Further investigation is needed to determine if this occurs via direct transcriptional repression, post-transcriptional modulation, or protein–protein interaction. Secondly, our functional assays were restricted to in vitro models. Future research should utilize in vivo xenograft models to confirm the anti-tumor effects of LINC01281 and its peptide in a complex tumor microenvironment. The clinical utility of LINC01281 as a biomarker requires validation in larger, prospective patient cohorts. A crucial next step is to determine if the observed biological effects are due to the LINC01281 transcript or its 42-amino acid peptide product, which is vital for creating targeted therapeutic strategies.

Conclusion

This study identifies LINC01281 as a tumor suppressor in cervical cancer for the first time. Our findings show that LINC01281 inhibits malignant cell behaviors, partly by negatively regulating the MYC/VEGF signaling pathway. Our finding that LINC01281 encodes a 42-amino acid peptide challenges the conventional view of lncRNAs and enhances understanding of its biological complexity. This study identifies LINC01281 as a potential prognostic biomarker and therapeutic target, with its encoded peptide offering a new approach for cervical cancer treatment.

Acknowledgements We express our gratitude to all individuals from the at Second Affiliated Hospital of Harbin Medical University and First affiliated Hospital of Harbin medical University who made valuable contributions to our study.

Author contributions Conceptualization: LY, QA and GJY conceived and developed the research idea, formulated the hypothesis, and designed the study. Investigation: QA, GJY conducted the experiments, performed observations, and collected data. Writing: Original Draft Preparation: GJY, ZS, wrote the initial draft of the manuscript, with contributions from GJY, MXX, ZSQ in reviewing and editing the text and preparing figures and tables.

Funding No funding was provided for this research.

Data availability All bioinformatics tools, databases, and web servers used in this study are accessible at the following links: TCGA: https://portal.gdc.cancer.gov/. UCSC: https://genome.ucsc.edu/. JASPAR: https://jaspar.genereg.net/. NCBI: https://www.ncbi.nlm.nih.gov/. NCBI ORFinder: https://www.ncbi.nlm.nih.gov/orffinder/. TRRUST: https://www.grnpedia.org/trrust/. Detaibio: https://www.detaibio.com/.

Declarations

Conflict of interest The authors declare no conflict of interest.

Ethical approval The data utilized in this study was acquired exclusively from publicly accessible databases, and no human subjects were involved in the research process. Thus, ethical approval was not required.

Consent for publication Not applicable.

References

Alharthi NS, Al-Zahrani MH, Hazazi A et al (2024) Exploring the lncRNA-VEGF axis: Implications for cancer detection and therapy. Pathol Res Pract 253:154998

Arunkumar G (2024) LncRNAs: the good, the bad, and the unknown. Biochem Cell Biol 102:9–27

Aswathy R, Sumathi S (2023) Defining new biomarkers for overcoming therapeutical resistance in cervical cancer using lncRNA. Mol Biol Rep 50:10445–10460

Bray F, Laversanne M, Sung H et al (2024) Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA Cancer J Clin 74:229–263

Ferrara N (2010) Pathways mediating VEGF-independent tumor angiogenesis. Cytokine Growth Factor Rev 21:21–26

Fu K, Zhang L, Liu R et al (2020) MiR-125 inhibited cervical cancer progression by regulating VEGF and PI3K/AKT signaling pathway. World J Surg Oncol 18:115

Gonzales LR, Blom S, Henriques R et al (2024) LncRNAs: the art of being influential without protein. Trends Plant Sci 29:770–785

He WQ, Li C (2021) Recent global burden of cervical cancer incidence and mortality, predictors, and temporal trends. Gynecol Oncol 163:583–592

Ji YY, Meng M, MIAO Y (2020) lncRNA SNHG1 Promotes Progression of Cervical Cancer Through miR-195/NEK2 Axis. Cancer Manag Res 12:11423–11433

Jia P, Cai H, Liu X et al (2016) Long non-coding RNA H19 regulates glioma angiogenesis and the biological behavior of

glioma-associated endothelial cells by inhibiting microRNA-29a. Cancer Lett 381:359–369
Jin KT, Yao JY, Fang XL et al (2020) Roles of lncRNAs in cancer: focusing on angiogenesis. Life Sci 252:117647
Kakotkin VV, Semina EV, Zadorkina TG et al (2023) Prevention strategies and early diagnosis of cervical cancer: current state and prospects. Diagnostics. https://doi.org/10.3390/diagnostics13040610
Li L, Liu M, Zhang Z et al (2019) Derlin1 functions as an oncogene in cervical cancer via AKT/mTOR signaling pathway. Biol Res 52:8
Liontos M, Kyriazoglou A, Dimitriadis I et al (2019) Systemic therapy in cervical cancer: 30 years in review. Crit Rev Oncol Hematol 137:9–17
Liu Y, Zhang X, Cheng X et al (2022) Characterization of fatty acid metabolism-related lncRNAs in lung adenocarcinoma identifying potential novel prognostic targets. Front Genet 13:990153
Ma H, Han F, Yan X et al (2021) PBK promotes aggressive phenotypes of cervical cancer through ERK/c-Myc signaling pathway. J Cell Physiol 236:2767–2781
McBrideWARBURTON A AA (2017) The role of integration in oncogenic progression of HPV-associated cancers. PLoS Pathog 13:1006211
Mercer TR, Dinger ME, MATTICK JS (2009) Long non-coding RNAs: insights into functions. Nat Rev Genet 10:155–159
Mezquita P, Parghi SS, Brandvold KA et al (2005) Myc regulates VEGF production in B cells by stimulating initiation of VEGF mRNA translation. Oncogene 24:889–901
Nelson BR, Makarewich CA, Anderson DM et al (2016) A peptide encoded by a transcript annotated as long noncoding RNA enhances SERCA activity in muscle. Science 351:271–275
Pan X, Li C, FENG J (2023) The role of LncRNAs in tumor immunotherapy. Cancer Cell Int 23:30
SAHASRABUDDHE V V, (2024) Cervical Cancer: Precursors and Prevention. Hematol Oncol Clin North Am 38:771–781
Singh D, Vignat J, Lorenzoni V et al (2023) Global estimates of incidence and mortality of cervical cancer in 2020: a baseline analysis of the WHO Global Cervical Cancer Elimination Initiative. Lancet Glob Health 11:e197–e206
Song X, Guo Y, Song P et al (2021) Non-coding RNAs in regulating tumor angiogenesis. Front Cell Dev Biol 9:751578
Song J, Ge Y, Sun X et al (2022) Noncoding RNAs related to the Hedgehog pathway in cancer: clinical implications and future perspectives. Mol Cancer 21:115
Wang Y, He M, Zhang G et al (2021) The immune landscape during the tumorigenesis of cervical cancer. Cancer Med 10:2380–2395
Wen Y, Lei W, Zhang J et al (2024) Advances in understanding the role of lncRNA in ferroptosis. PeerJ 12:e17933
Wu P, Mo Y, Peng M et al (2020) Emerging role of tumor-related functional peptides encoded by lncRNA and circRNA. Mol Cancer 19:22
Xu J, Xu S, Fang Y et al (2019) Cyclin-dependent kinase 9 promotes cervical cancer development via AKT2/p53 pathway. IUBMB Life 71:347–356
Yang Q, Al-Hendy A (2022) The regulatory functions and the mechanisms of long non-coding RNAs in cervical cancer. Cells. https://doi.org/10.3390/cells11071149
Yang W, Ge F, Lu S et al (2021) LncRNA MSC-AS1 is a diagnostic biomarker and predicts poor prognosis in patients with gastric cancer by integrated bioinformatics analysis. Front Med 8:795427
Yoshida GJ (2018) Emerging roles of Myc in stem cell biology and novel tumor therapies. J Exp Clin Cancer Res 37:173
Yu J, Fan Q, Li L (2021) The MCM3AP-AS1/miR-126/VEGF axis regulates cancer cell invasion and migration in endometrioid carcinoma. World J Surg Oncol 19:213
Yuan Y, Cai X, Shen F et al (2021) HPV post-infection microenvironment and cervical cancer. Cancer Lett 497:243–254
Zhang G, Fan E, Zhong Q et al (2019) Identification and potential mechanisms of a 4-lncRNA signature that predicts prognosis in patients with laryngeal cancer. Hum Genomics 13:36
Zhang H, Wang X, Ma Y et al (2023) Review of possible mechanisms of radiotherapy resistance in cervical cancer. Front Oncol 13:1164985
Zhi W, Wei Y, Lazare C et al (2023) HPV-CCDC106 integration promotes cervical cancer progression by facilitating the high expression of CCDC106 after HPV E6 splicing. J Med Virol 95:e28009