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LINC01106 stimulates growth and metastasis of colorectal carcinoma by sponging miR-744-5p

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Abstract: The development of colorectal carcinoma, a prevalent malignancy, remains insufficiently understood. This study examined the role of LINC01106 in colorectal carcinoma progression and elucidated the underlying molecular mechanisms. The expression of LINC01106 was analyzed using data from the database of gene expression profiling interactive analysis and 50 clinical specimens. The prognostic relevance of LINC01106 in colorectal carcinoma was assessed. Functional assays were performed after LINC01106 knockdown to assess changes in proliferation and metastatic capabilities. The expression of LINC01106 was found to be significantly elevated in colorectal carcinoma tissues and was linked to unfavorable overall survival outcomes in patients with colorectal carcinoma. Knockdown of LINC01106 significantly suppressed the proliferation and metastasis of colorectal carcinoma cells. MiR-744-5p was identified as a direct target of LINC01106, exhibiting an inverse correlation with LINC01106 expression. Elevated expression of miR-744-5p hindered the proliferation and metastatic potential of colorectal carcinoma cells—effects that were reversed by co-overexpression of LINC01106. In summary, LINC01106 was highly expressed in colorectal carcinoma and enhanced the proliferation and metastasis of colorectal carcinoma cells by directly interacting with miR-744-5p, highlighting its potential as a therapeutic target.

Keywords: Colorectal carcinoma, LINC01106, miR-744-5p, proliferation, metastasis.

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INTRODUCTION

Colorectal carcinoma (CRC) is a prevalent malignant tumor (Alina *et al.,* 2023). Its global incidence ranks third among all cancers, following lung and breast carcinoma. Each year, approximately 1.8 million people are newly diagnosed with CRC (Murphy and Zaki, 2024). Although therapeutic strategies for CRC – including surgery, chemotherapy, and radiotherapy – have improved, the prognosis remains poor (Poter *et al.,* 2024). Clarifying the molecular mechanisms of CRC is crucial for developing effective therapeutic targets.

Noncoding RNAs account for a large proportion of human genome transcripts (Zhang *et al.,* 2022). Long noncoding RNAs (lncRNAs) are transcripts exceeding 200 nucleotides that lack protein-coding ability but can regulate gene activity at multiple levels, especially post-transcriptionally (Bunch, 2018; Liu *et al.,* 2021; Zuo *et al.,* 2022; Safi *et al.,* 2023; Liu *et al.,* 2022). Notably, lncRNAs play vital roles in human tumors (Gugnoni *et al.*, 2025; Saadh *et al.*, 2025; Suliman *et al*., 2025; Li *et al*., 2025). For example, lncRNA HAND2-AS1 inhibited osteosarcoma proliferation by modulating glucose metabolism (Chen *et al.,* 2019). Knockdown of lncRNA RHPN1-AS1 weakened the proliferative and metastatic abilities of head and neck squamous cell carcinoma cells (Qiu *et al.,* 2019). LINC00460 accelerated nasopharyngeal carcinoma cell invasion and metastasis by targeting miR-30a-3p/Rap1A (Hu *et al.,* 2019). One mechanism by which lncRNAs influenced cancer is by acting as competing endogenous RNAs (ceRNAs) that sponge tumor-suppressive microRNAs (miRNAs), thereby de-repressing the miRNAs' target genes (Yu *et al.,* 2019).

MiRNAs are ~22-nucleotide noncoding RNAs that modulate gene expression by binding to the 3′ UTR of target mRNAs, causing translational repression or mRNA degradation (Smolarz *et al.,* 2022; Chakrabortty *et al.,* 2023; Mok *et al.,* 2024). MiRNAs are highly conserved among species and are extensively involved in tumor development (Al-Hawary *et al.,* 2024). For example, knockdown of miR-877 suppressed proliferative and invasive capacities in cervical cancer cells by targeting MACC1 (Meng *et al.,* 2019). miR-96-5p promoted gastric cancer proliferation by binding to FOXO3 (He and Zou, 2020). miR-7-5p induced growth arrest, cell cycle arrest, and apoptosis in NSCLC by targeting PAK2 (Li *et al.,* 2019).

LINC01106 is an oncogenic lncRNA that has recently drawn attention in CRC research. Initial evidence from bioinformatics studies suggested that LINC01106 could be a potential biomarker and ceRNA in CRC and

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inflammatory bowel disease-related CRC (Sun *et al.,* 2019). Subsequent work demonstrated that LINC01106 drove CRC cell stemness and growth through a positive feedback loop involving Gli transcription factors, in part by sponging miR-449b-5p (Fan *et al.,* 2022). In that study, LINC01106 upregulation was found to promote CRC growth and cancer stemness by increasing GLI1/GLI2/GLI4 signaling (via miR-449b-5p sequestration). However, that mechanism primarily addressed tumor cell self-renewal and did not explore the impact of LINC01106 on invasion and metastasis or identify other miRNA targets. Another lncRNA, MNX1-AS1, was reported to promote colorectal cancer progression by sponging miR-744-5p and inducing epithelial-mesenchymal transition (EMT) (Huang and Sun, 2021). This finding underscored the potential importance of miR-744-5p as a tumor suppressor in CRC. Notably, prior to our work, no study had experimentally confirmed miR-744-5p as a direct target of LINC01106 in CRC or elucidated its functional significance.

In this study, the biological functions of LINC01106 and its interaction with miR-744-5p in regulating CRC progression were investigated. It was shown that LINC01106 was markedly upregulated in CRC and correlated with poor patient survival. Through in vitro loss-of-function and rescue experiments, LINC01106 was demonstrated to directly sponge miR-744-5p, thereby promoting CRC cell proliferation, migration, and invasion. This work identified a novel LINC01106/miR-744-5p axis that contributed to CRC aggravation, distinguishing this mechanism from previously reported pathways and highlighting its potential as a therapeutic target.

MATERIALS AND METHODS

GEPIA dataset

A dataset comprising 275 cases of colon adenocarcinoma (COAD) and 349 normal colon tissue samples was obtained from the GEPIA repository. Additionally, disease-free survival and overall survival data for COAD patients were analyzed to evaluate their correlation with LINC01106 expression levels.

Samples

Fifty CRC tumor samples and their matched normal adjacent tissues were collected and immediately preserved in liquid nitrogen. The following exclusion criteria were applied: patients with distant metastasis or lymph node metastasis at diagnosis, those with concurrent other malignancies, those with severe comorbid conditions (such as significant mental health disorders, recent myocardial infarction, heart failure, or other chronic diseases), and patients with abnormal colorectal function prior to surgery or prior exposure to radiotherapy. TNM staging was determined based on UICC criteria. The Ethics Committee of Nanfang Hospital and Basic Medical College approved this study (23-NF-EC-492), and all participants provided informed consent. The sample size of 50, while moderate, is comparable to similar exploratory studies and was sufficient to detect significant expression differences and survival correlations; however, larger cohorts will be needed for further validation (see Discussion).

Cell culture

The cell lines used in this study (CRC cell lines DLD-1, HCT-116, RKO, SW-480, and the normal intestinal epithelial cell line NCM460) were obtained from the Shanghai Institute of Biochemistry and Cell Biology. Cells were cultured in RPMI-1640 medium supplemented with 10% fetal bovine serum and 1% penicillin-streptomycin, and maintained at 37°C in a humidified atmosphere with 5 % CO_2.

Transfection

Plasmids and oligonucleotides for gene modulation were purchased from RiboBio (Guangzhou, China) and GenePharma (Shanghai, China). These included small interfering RNA targeting LINC01106 (si-LINC01106), an overexpression plasmid for LINC01106 (OE-LINC01106), miR-744-5p mimics, and their respective negative controls. Cells at ~60% confluence in 6-well plates were transfected using Lipofectamine 3000 (Invitrogen) according to the manufacturer's protocol.

qRT-PCR

Total RNA was extracted from cells and tissue samples using TRIzol reagent, and cDNA was synthesized with the PrimeScript RT Reagent Kit. Quantitative real-time PCR (qRT-PCR) was performed using SYBR Green Master Mix (Applied Biosystems) on an ABI PRISM system. Expression levels were normalized to GAPDH (for LINC01106) or U6 snRNA (for miR-744-5p).

The primer sequences were as follows: LINC01106 forward 5′-GTGGTCCGATCCCTAACCAG-3′ and reverse 5′-CGCAAGTCCTCTTTCTCCCT-3′; miR-744-5p forward 5′-TGCGGGGCTAGGGCTAACAGCA-3′ and reverse 5′-TGTCGTGGAGTCGGC-3′; GAPDH forward 5′-CGGAGTCAACGGATTTGGTCGTAT-3′ and reverse 5′-AGCCTCCCATTGGTGGTGAAGA-3′; U6 forward 5′-GCTGAGGTGACGGTCTCAAA-3′ and reverse 5′-GCCTCCCAGTTTCATGGACA-3′. Relative expression was calculated using the 2^-ΔΔCt method (Livak and Schmittgen, 2001).

Colony formation assay

Cells were seeded in 6-well plates at a low density (4 × 10^2 cells per well) and cultured for 10–14 days to allow colony formation. The culture medium was replenished every 3-4 days. At the end of the incubation period, cell colonies were washed with PBS, fixed in 100% methanol for 20 minutes, and stained with 0.1% crystal violet for 20 minutes. The number of visible colonies was then counted from photographs of the stained plates.

CCK-8 Assay

Cell proliferation was assessed using the Cell Counting Kit-8 (CCK-8) assay. Transfected cells were plated into 96-well plates at 4 × 10^2 cells per well. Cell viability was measured at 0, 24, 48, 72 and 96 hours post-seeding by adding CCK-8 reagent (Dojindo, Japan) to each well and incubating for 2 hours, followed by measurement of absorbance at 450 nm using a microplate reader.

Transwell migration and invasion assays

Cell migration and invasion were evaluated using Transwell chamber assays (8 μm pore size; Corning). For the migration assay, 5 × 10^4 cells in serum-free medium were added to the upper chamber, and 500 μl of complete medium was added to the lower chamber as a chemoattractant. After 48 hours of incubation at 37°C, cells that migrated to the underside of the membrane were fixed with methanol for 15 minutes, stained with 0.1% crystal violet for 20 minutes, and counted under a microscope in ten randomly selected fields. For the invasion assay, the procedure was similar except that the Transwell inserts were pre-coated with Matrigel (BD Biosciences) to form a reconstituted basement membrane layer, and 1 × 10^5 cells were seeded in the upper chamber. Invading cells were fixed, stained, and quantified as described for the migration assay.

Dual-Luciferase reporter assay

Bioinformatic tools, TargetScan and miRanda (Agarwal *et al.,* 2015; John *et al.,* 2004), were used to predict potential binding sites for miR-744-5p on the LINC01106 sequence. To experimentally validate the binding, fragments of LINC01106 containing the predicted miR-744-5p binding site (wild-type) and a version with mutated seed-binding sequence (mutant) were cloned into a luciferase reporter vector (pmirGLO). SW-480 and RKO cells were co-transfected with either the wild-type or mutant LINC01106 reporter and miR-744-5p mimics or negative control miRNA. Two days post-transfection, luciferase activity was measured using the Dual-Luciferase Reporter Assay System (Promega), with Renilla luciferase activity used for normalization. A decrease in firefly/Renilla luciferase ratio in the presence of miR-744-5p compared to control was interpreted as successful binding of miR-744-5p to LINC01106's sequence.

STATISTICAL ANALYSIS

Data are presented as mean ± standard deviation. Group comparisons were made using Student's *t*-test (for two groups) or ANOVA (for multiple groups), as appropriate. Pearson's correlation analysis was performed to evaluate the association between LINC01106 and miR-744-5p expression levels in tissue samples. A p-value < 0.01 was considered statistically significant. Statistical analyses were carried out using SPSS 22.0 (IBM, USA) and GraphPad Prism 8.0 software.

RESULTS

Upregulation of LINC01106 in CRC

GEPIA database analysis revealed that LINC01106 expression was significantly higher in COAD tumor tissues (n = 275) than in normal colon tissues (n = 349) (fig. 1A). Consistently, in our cohort of CRC patients, LINC01106 was markedly upregulated in tumor tissues compared to adjacent normal tissues (fig. 1B). To assess clinical significance, patient survival data from GEPIA were analyzed: high LINC01106 expression was associated with poorer overall survival in COAD patients (fig. 1C). In contrast, LINC01106 levels did not show a significant correlation with disease-free survival in COAD (fig. 1D). These data suggested that LINC01106 was frequently overexpressed in CRC and might have prognostic value for patient outcomes.

Knockdown of LINC01106 Suppresses CRC Cell Proliferative, Invasive, and Migratory Abilities Next, LINC01106 expression in CRC cell lines was examined. LINC01106 was found to be upregulated in all four CRC cell lines tested (DLD-1, HCT-116, RKO, SW-480) compared to the normal intestinal epithelial cell line NCM460, with RKO and SW-480 showing the highest LINC01106 levels (fig. 2A). SW-480 and RKO cells were selected for loss-of-function studies. Transfection with si-LINC01106 effectively downregulated LINC01106 expression in these cells (fig. 2B). Functional assays indicated that silencing LINC01106 significantly reduced CRC cell growth: CCK-8 assays showed decreased viability in SW-480 and RKO cells after LINC01106 knockdown (fig. 2C), and colony formation assays demonstrated a reduction in the number and size of colonies formed by LINC01106-deficient cells (fig. 2D). Furthermore, Transwell assays revealed that LINC01106 knockdown led to markedly fewer invading cells and migrating cells in both SW-480 and RKO, compared to control-transfected cells (fig. 2E, 2F). These results indicated that LINC01106 actively contributed to the proliferative, migratory, and invasive capacities of CRC cells, supporting an oncogenic role for this lncRNA in CRC.

A Negative interaction between LINC01106 and miR-744-5p

Given that lncRNAs often function by sponging miRNAs, it was investigated whether LINC01106 might interact with specific miRNAs to mediate its effects. Bioinformatic predictions (TargetScan and miRanda) identified a putative binding site for miR-744-5p in the LINC01106 transcript (fig. 3A). To confirm a direct interaction, a dual-luciferase reporter assay was performed. Co-transfection of miR-744-5p mimics significantly reduced the luciferase activity of the wild-type LINC01106 reporter in SW-480 and RKO cells, whereas the mimics had no effect on the mutant reporter lacking the miR-744-5p binding site (fig. 3B). This result demonstrated that miR-744-5p directly bound to

LINC01106. In addition, miR-744-5p expression was measured in CRC specimens and cell lines. miR-744-5p levels were found to be significantly lower in CRC tumor tissues compared to normal tissues (fig. 3C), showing an inverse pattern relative to LINC01106. Consistently, Pearson correlation analysis of the patient samples revealed a strong negative correlation between LINC01106 and miR-744-5p expression levels (fig. 3D). In CRC cell lines, an inverse relationship was also observed: cell lines with higher LINC01106 had lower basal miR-744-5p. Moreover, silencing LINC01106 led to an increase in miR-744-5p levels in SW-480 and RKO cells (fig. 3E), which was consistent with the notion that LINC01106 normally suppressed miR-744-5p by sequestering it. These findings established a negative regulatory interaction between LINC01106 and miR-744-5p in CRC.

LINC01106/miR-744-5p axis drives CRC progression

To determine whether the oncogenic effects of LINC01106 in CRC were mediated through miR-744-5p, rescue experiments were conducted by modulating both molecules. SW-480 and RKO cells were transfected with miR-744-5p mimics to elevate miR-744-5p levels, either alone or in combination with a LINC01106 overexpression plasmid. Transfection efficiencies were confirmed by qRT-PCR: miR-744-5p was significantly upregulated by the mimics, and co-transfection of the LINC01106 expression vector restored LINC01106 levels (fig. 4A). Functionally, increased miR-744-5p alone led to a notable reduction in CRC cell viability (fig. 4B) and markedly impaired cell migration and invasion (fig. 4C, 4D), consistent with miR-744-5p acting as a tumor suppressor. Importantly, co-overexpression of LINC01106 counteracted these suppressive effects: cells co-transfected with LINC01106 and miR-744-5p showed higher viability and greater migratory and invasive capabilities compared to cells with miR-744-5p overexpression alone (fig. 4B–D). The partial "rescue" of the aggressive phenotype by reintroducing LINC01106 indicated that the pro-tumorigenic impact of LINC01106 was at least in part due to its inhibition of miR-744-5p function. Together, these results demonstrated that the LINC01106/miR-744-5p axis was a critical driver of CRC cell proliferation, migration, and invasion.

DISCUSSION

CRC has become the third leading malignancy worldwide, characterized by high mortality and frequent metastasis (Benek and Zengin, 2023). Globally, more than 600,000 people died of CRC each year (Patel and Dominitz, 2024). Surgery offers the best cure for early-stage CRC, but only about 39.6% of CRC cases were diagnosed at an early stage (Willemsen *et al.,* 2023). Consequently, many patients presented with advanced disease, for which the 5-year survival rate was only around 10% (Fan *et al.,* 2023). These statistics highlighted the urgent need to better understand CRC progression and to develop targeted therapies for advanced disease.

LncRNAs are increasingly recognized as key regulators in cancer development and progression. They can influence various biological processes including genomic imprinting, X-chromosome inactivation, chromatin modification, and telomere maintenance (Gonzales *et al.,* 2024). In CRC, numerous lncRNAs have been found to play important roles. For instance, lncRNA ZEB1-AS1 promoted CRC carcinogenesis by activating the miR-205/YAP1 axis (Jin and Chen, 2020). LncRNA NEAT1 triggered the onset of CRC by sponging miR-193a-3p (Yu *et al.,* 2019). Overexpression of lncRNA NORAD was associated with enhanced malignancy in CRC (Wang *et al.,* 2018). Consistent with these findings, our study showed that LINC01106 is significantly upregulated in CRC tissues compared to normal tissues, as evidenced by both public database analysis and our patient samples. Furthermore, results showed that elevated LINC01106 expression correlated with worse overall survival in CRC patients, suggesting that LINC01106 could serve as a prognostic marker. Functionally, in vitro experiments demonstrated that LINC01106 promoted CRC cell proliferation, migration, and invasion. Thus, the findings provided strong evidence that LINC01106 acted as an oncogenic lncRNA in CRC.

Our work expanded on prior studies of LINC01106 by identifying a new mechanistic pathway through which it drove CRC progression. Earlier research by Guo *et al.* (2020) showed that LINC01106 can enhance CRC cell growth and stemness via a positive feedback loop involving Hedgehog/GLI signaling, and that LINC01106 acts as a sponge for miR-449b-5p to upregulate GLI4. Another recent study reported that LINC01106 may promote CRC angiogenesis through an m6A-YTHDF1 mediated mechanism and the miR-449b-5p/VEGFA pathway (Ma *et al.,* 2024). These studies underlined the multifaceted oncogenic roles of LINC01106 in CRC. However, neither addressed the role of LINC01106 in cellular invasion/metastasis or the involvement of miR-744-5p. In contrast, our study was the first to establish miR-744-5p as a direct functional target of LINC01106 in CRC. MiR-744-5p had been reported as an important regulator in multiple tumor types. In non-small cell lung cancer, miR-744-5p inhibited cell proliferation and invasion by targeting PAX2 (Chen *et al.,* 2019). In ovarian cancer, miR-744-5p induced apoptosis by directly targeting oncogenic proteins HNRNPC and NFIX (Kleemann *et al.,* 2018). In pancreatic neuroendocrine tumors, miR-744-5p targeted THBS2 and thereby influenced MMP9 via CUX1 (Jiao *et al.,* 2020). Until now, the function of miR-744-5p in CRC remained largely unknown. In this study, miR-744-5p was observed to be frequently downregulated in CRC tissues, aligning with its presumed tumor-suppressive role. Indeed, a recent study confirmed that miR-744-5p was

significantly downregulated in CRC and acted to suppress the malignant phenotype by targeting the oncogene SEPT2 (Zhang *et al.,* 2021). Overexpression of miR-744-5p in CRC cells was shown to inhibit proliferation and induce apoptosis, effects that were reversed by restoring SEPT2 expression. These findings emphasized that miR-744-5p served as a tumor suppressor in CRC by restraining oncogenic targets.

In this study, it was confirmed that miR-744-5p was a direct binding target of LINC01106. The dual-luciferase reporter assay provided clear evidence of a physical interaction: miR-744-5p bound to the wild-type LINC01106 sequence and reduced luciferase activity, whereas mutating the binding site abolished this effect. This result validated that LINC01106 could directly sponge miR-744-5p, acting as a molecular decoy. As a consequence of this sponging, LINC01106 negatively regulated miR-744-5p levels and activity. An inverse correlation between LINC01106 and miR-744-5p expression was demonstrated in CRC specimens, and importantly, when LINC01106 was knocked down, miR-744-5p levels increased in CRC cells. This inverse relationship indicated causality: LINC01106 upregulation likely contributed to CRC progression by repressing miR-744-5p. When miR-744-5p was freed from LINC01106's suppression (either by LINC01106 knockdown or by exogenous miR-744-5p mimics), it could carry out its tumor-suppressive functions, such as downregulating oncogenic target genes (e.g., SEPT2) and thereby inhibiting CRC cell growth and metastasis.

Crucially, the rescue experiments established the LINC01106/miR-744-5p axis as a functional pathway in CRC cells. Ectopic overexpression of miR-744-5p strongly impeded CRC cell proliferation, migration, and invasion, consistent with its suppressive role. Co-overexpression of LINC01106 significantly blunted these effects, demonstrating that LINC01106 could "rescue" cells from miR-744-5p-mediated suppression. This finding moved the understanding beyond mere correlation and showed a direct causal link: LINC01106 promoted CRC malignancy at least in part by antagonizing miR-744-5p. In the absence of LINC01106, miR-744-5p was more available to inhibit its targets and suppress tumor cell aggressiveness; when LINC01106 was abundant, it sequestered miR-744-5p, preventing it from binding target mRNAs, which led to increased expression of pro-tumorigenic genes. Although downstream target genes were not directly measured in this study, it was plausible that LINC01106 sponging of miR-744-5p resulted in upregulation of miR-744-5p target genes like SEPT2, thereby enhancing proliferation and metastasis. Future research should verify these downstream effects by examining the expression of known miR-744-5p targets in the context of LINC01106 manipulation.

While this study provided valuable insights into the role of the LINC01106/miR-744-5p axis in CRC, several limitations should be acknowledged. First, the sample size of 50 clinical tissues was relatively small, which could limit the generalizability of the results. This size was chosen based on feasibility and was in line with other initial studies of lncRNA function; it was sufficient to demonstrate significant differences and correlations, but larger patient cohorts will be necessary to confirm LINC01106's prognostic value and biological effects more robustly. Second, although miR-744-5p overexpression experiments were performed to demonstrate the interplay between LINC01106 and miR-744-5p, the complementary approach of blocking miR-744-5p in the context of LINC01106 knockdown was not tested. Using a miR-744-5p inhibitor or antisense oligonucleotide in LINC01106-silenced cells could further verify that the phenotypic changes were indeed mediated through miR-744-5p. This is proposed as an important follow-up experiment to strengthen the causal link in this axis. Third, no in vivo studies were included in this work. The lack of animal model validation means that the translational relevance of the LINC01106/miR-744-5p axis is not yet confirmed. In vivo experiments (e.g., xenograft models with LINC01106 knockdown or overexpression) would be valuable to verify the effects on tumor growth and metastasis in a physiological context. Finally, the potential off-target effects of the knockdown and overexpression strategies were not extensively addressed. It is possible that some effects observed were partially influenced by off-target or indirect effects. In future studies, using multiple independent siRNAs, CRISPR interference/activation approaches, or rescue constructs with mutated miR-744-5p binding sites could help ensure the specificity of the observed phenomena.

Looking forward, these findings opened several avenues for further research. Future studies should validate the LINC01106/miR-744-5p axis in larger patient cohorts and evaluate its significance as a prognostic biomarker. Deploying animal models (such as orthotopic CRC models or patient-derived xenografts) will be important to determine whether targeting this axis can suppress tumor growth and metastasis in vivo. Additionally, developing targeted therapeutics against LINC01106 could be of clinical interest. For example, RNA interference or antisense oligonucleotides could be designed to specifically knock down LINC01106 in tumor cells. Given the results of this study, such approaches might reactivate miR-744-5p's tumor suppressor function and inhibit CRC progression. Conversely, one could envision delivering miR-744-5p mimics or preventing its sponging as a therapeutic strategy. Any such therapeutic development would need to assess delivery mechanisms and off-target effects carefully. Furthermore, it would be insightful to explore whether LINC01106 interacted with additional molecular pathways or miRNAs beyond miR-744-5p.

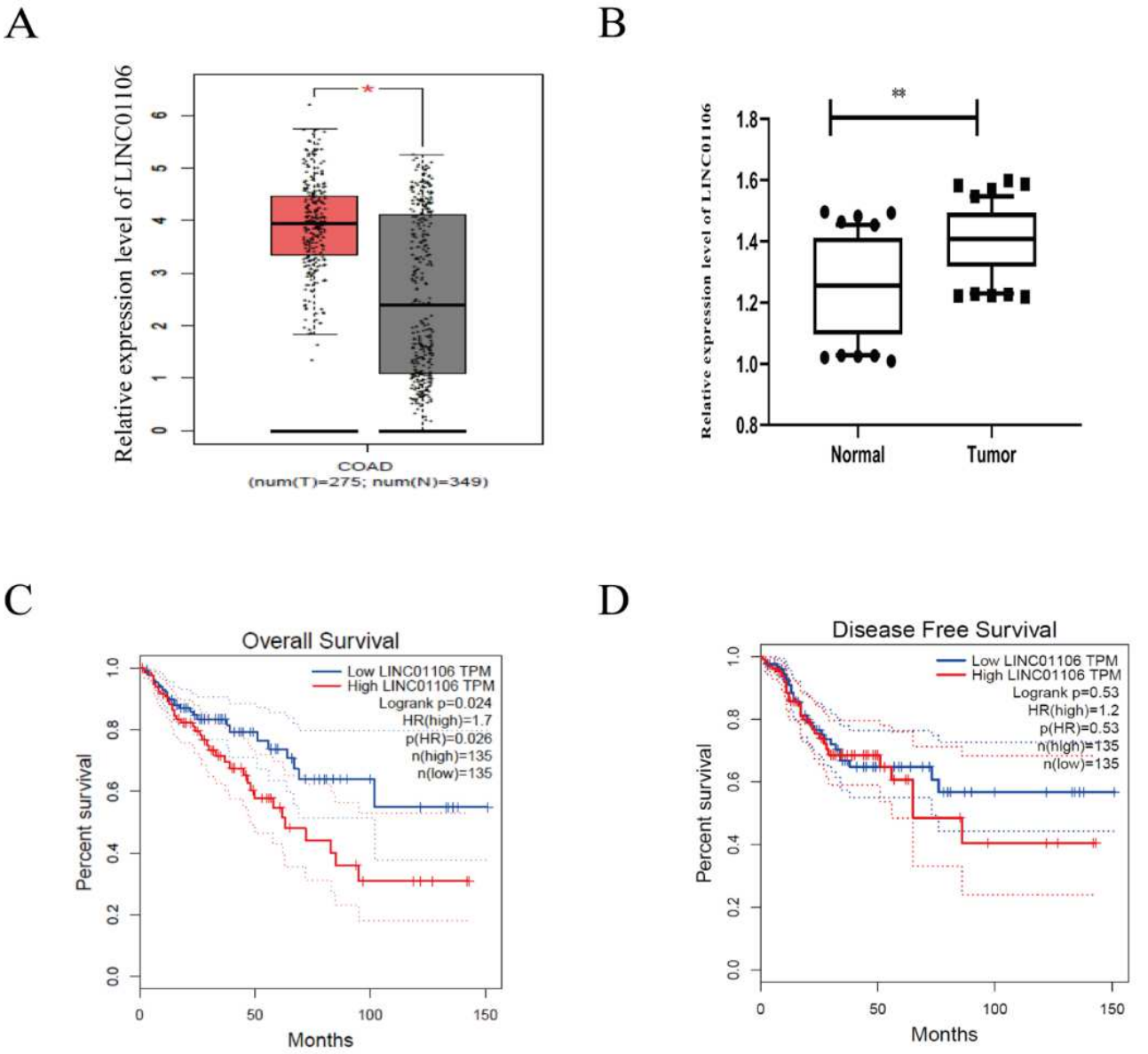

Fig. 1: Upregulation of LINC01106 in CRC. (A) LINC01106 is upregulated in colon adenocarcinoma (A): Gene Expression Profiling Interactive Analysis (GEPIA) database showing significantly higher LINC01106 expression in COAD tumor tissues (n = 275) compared to normal colon tissues (n = 349). (B) High LINC01106 expression in clinical CRC tissues: qRT-PCR analysis of our patient samples indicating that LINC01106 expression is elevated in CRC tumor tissues relative to matched normal tissues. (C) High LINC01106 predicts poor overall survival: Kaplan–Meier curve (GEPIA) demonstrating that CRC patients with higher LINC01106 expression have worse overall survival than those with lower expression. (D) LINC01106 and disease-free survival: No significant difference in disease-free survival was observed between high versus low LINC01106 expression groups in COAD (GEPIA analysis). $p<0.05$, $*p<0.01$ (statistical comparisons in A, B by *t*-test).

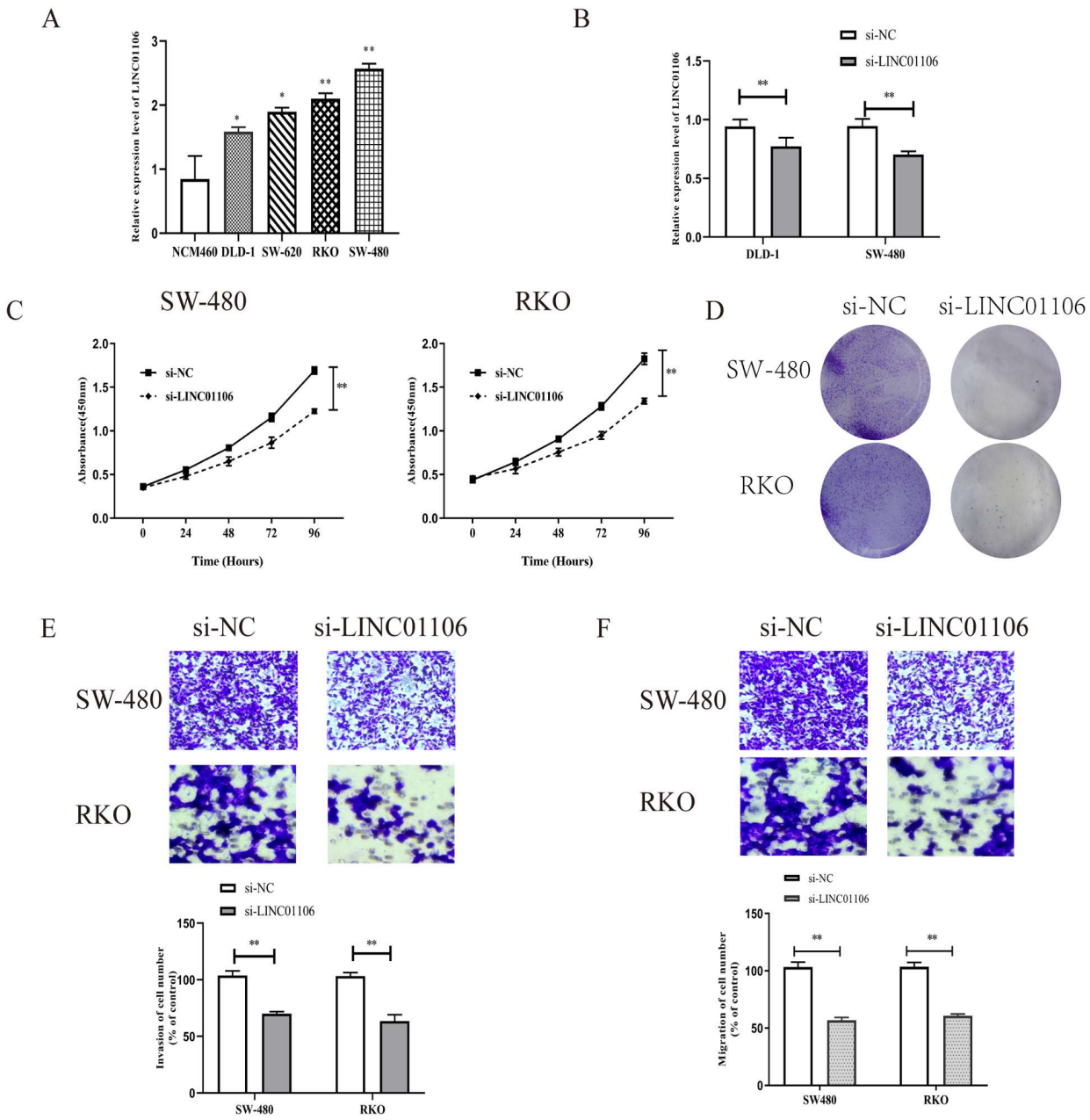

Fig. 2: Knockdown of LINC01106 suppresses CRC cell proliferation, invasion, and migration. (A) LINC01106 is upregulated in CRC cell lines: Relative LINC01106 expression levels in four CRC cell lines (DLD-1, HCT-116, RKO, SW-480) compared to the normal intestinal epithelial cell line NCM460 (by qRT-PCR). (B) siRNA-mediated LINC01106 knockdown: Transfection of si-LINC01106 significantly reduced LINC01106 expression in SW-480 and RKO cells (qRT-PCR, confirming knockdown efficiency). (C) Reduced cell viability upon LINC01106 knockdown: CCK-8 assay showing that SW-480 and RKO cells with LINC01106 silencing have lower viability over 4 days compared to control cells. (D) Reduced colony formation upon LINC01106 knockdown: Representative images and quantification of colony formation assays for SW-480 and RKO cells transfected with si-LINC01106 versus control; far fewer colonies formed in LINC01106-silenced cells (crystal violet staining, image at 10× magnification). (E) LINC01106 knockdown impairs invasion: Transwell invasion assays showing that the number of invading SW-480 and RKO cells is significantly decreased after LINC01106 knockdown (images at 200× magnification). (F) LINC01106 knockdown impairs migration: Transwell migration assays showing reduced migratory SW-480 and RKO cell numbers following LINC01106 silencing (200× magnification). $p<0.05$, $*p<0.01$ for comparisons of si-LINC01106 vs. control (error bars indicate SD of three independent experiments).

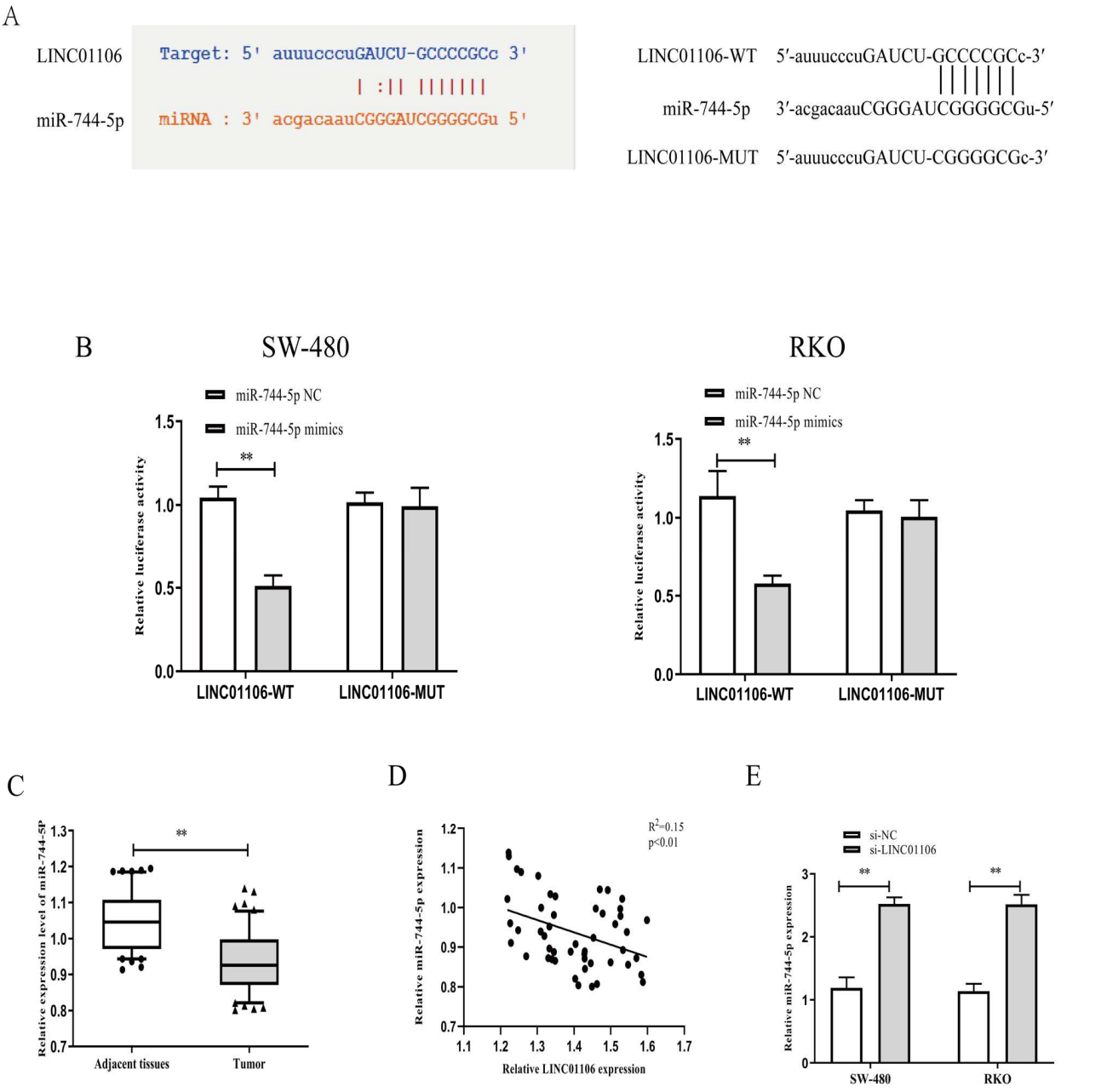

Fig. 3: A negative interaction between LINC01106 and miR-744-5p. (A) Predicted binding site: Schematic of the predicted miR-744-5p binding site in the LINC01106 sequence (complementary base pairing indicated). The seed region of miR-744-5p aligns with nucleotides in LINC01106; a mutant LINC01106 sequence was designed with point mutations (red X) in the seed-binding region. (B) Dual-luciferase reporter assay: Co-transfection of miR-744-5p mimics significantly decreased the relative luciferase activity of the wild-type (WT) LINC01106 reporter in SW-480 and RKO cells, whereas it had no effect on the mutant (Mut) reporter, confirming direct binding between miR-744-5p and LINC01106. (C) miR-744-5p is downregulated in CRC tissues: qRT-PCR showing that miR-744-5p expression is lower in CRC tumor tissues compared to adjacent normal tissues (n = 50 pairs). (D) Inverse correlation in patient samples: Pearson correlation analysis of 50 CRC specimens indicating a significant negative correlation between LINC01106 and miR-744-5p expression levels (each point represents one patient sample). (E) Effect of LINC01106 knockdown on miR-744-5p: qRT-PCR showing that transfection of si-LINC01106 leads to upregulation of miR-744-5p in SW-480 and RKO cells, consistent with the loss of a sponge. $p<0.05$, $*p<0.01$ (for B, comparisons of mimic vs. control; for C and E, comparisons of indicated groups).

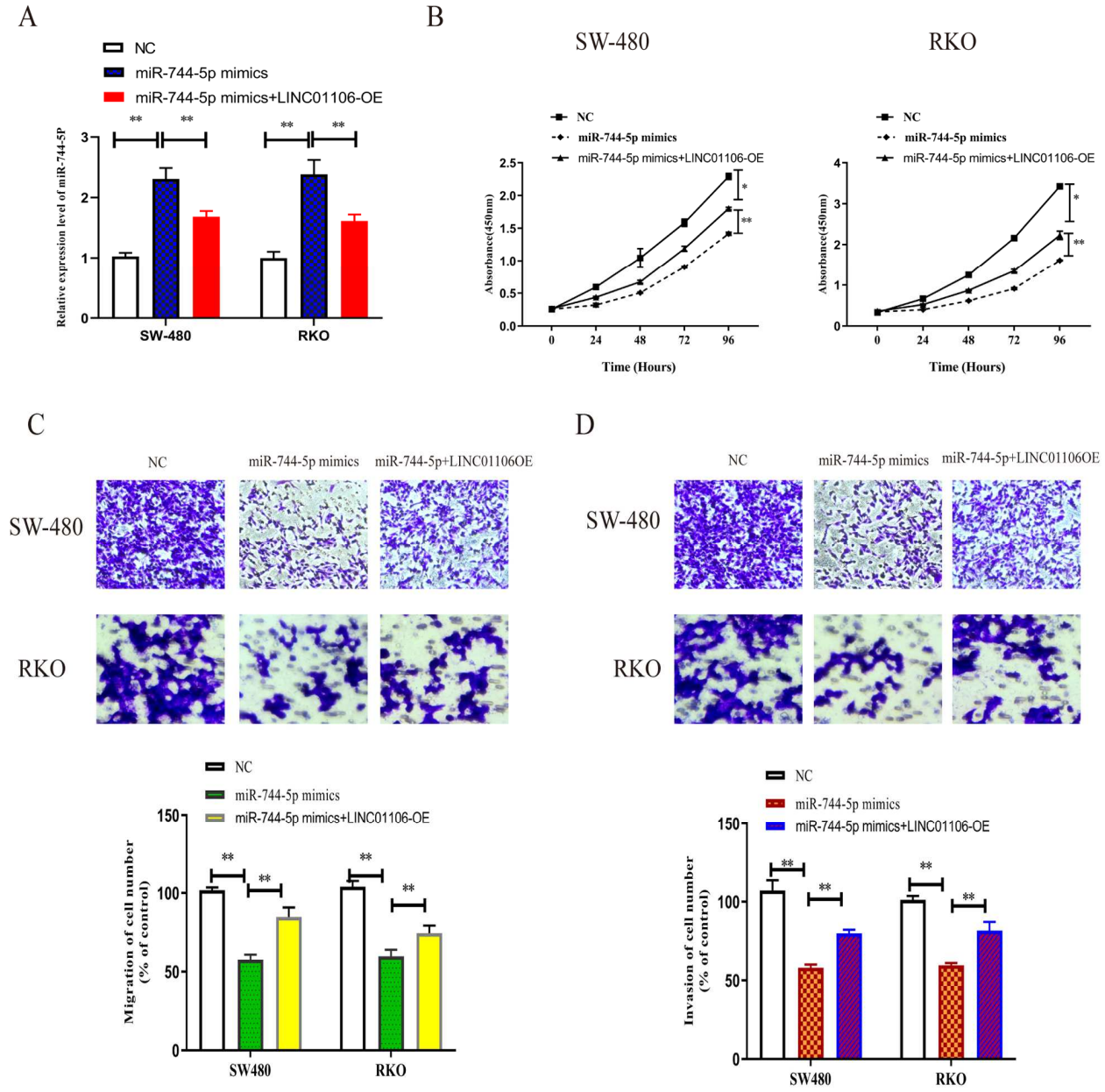

Fig. 4: LINC01106/miR-744-5p axis drives CRC progression (rescue experiments). (A) Transfection efficiency: qRT-PCR confirming successful overexpression of miR-744-5p (using miR-744-5p mimics) and LINC01106 (using LINC01106 overexpression plasmid, "LINC01106-OE") in SW-480 and RKO cells. Groups: control (Ctrl), miR-744-5p mimic (miR-744-5p), LINC01106 overexpression (LINC01106), and co-transfection of miR-744-5p mimic + LINC01106-OE (miR-744-5p + LINC01106). (B) Cell viability rescue: CCK-8 assay results showing that miR-744-5p overexpression alone significantly reduces viability of SW-480 and RKO cells at 48–72 h, whereas co-expression of LINC01106 partially restores cell viability. (C) Migration rescue: Transwell migration assays showing that miR-744-5p overexpression markedly inhibits cell migration; this effect is attenuated when LINC01106 is co-overexpressed (images at 200×). (D) Invasion rescue: Transwell invasion assays showing reduced invasive ability with miR-744-5p overexpression, with partial recovery of invasion upon LINC01106 co-overexpression (200× images). These rescue experiments indicate that the pro-proliferative and pro-metastatic effects of LINC01106 are mediated through miR-744-5p. $p<0.05$, *$p<0.01$ for comparisons: miR-744-5p vs. Ctrl, and miR-744-5p + LINC01106 vs. miR-744-5p alone (error bars represent SD, $n = 3$).

CRC was a complex disease, and LINC01106 might be part of a broader regulatory network. For instance, investigating other miRNAs (Sun *et al.,* 2019) or examining if LINC01106 affected classical signaling pathways (Wnt/β-catenin, EGFR/MAPK, etc.) could uncover novel mechanisms by which this lncRNA drove CRC progression or therapy resistance.

CONCLUSION

In summary, this study identified LINC01106 as a novel oncogenic driver in CRC that promoted tumor cell proliferation, migration, and invasion by sponging miR-744-5p. Evidence was provided that high LINC01106 expression was associated with poor patient survival and that LINC01106 directly bound to and downregulated miR-744-5p, releasing CRC cells from miR-744-5p-mediated growth suppression. Targeting the LINC01106/miR-744-5p axis represented a promising therapeutic strategy for CRC. These findings not only improved the understanding of CRC pathogenesis by adding a new lncRNA-miRNA regulatory axis, but also highlighted LINC01106 as a potential molecular target for innovative CRC treatments.

Conflict of interest

The authors declared no conflict of interest.

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