

# LINC02476 Promotes the Malignant Phenotype of Hepatocellular Carcinoma by Sponging miR-497 and Increasing HMGA2 Expression

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**Background:** Long noncoding RNAs (lncRNAs) can promote hepatocellular carcinoma (HCC) initiation and progression. In this report, we examined the role of lncRNA LINC02476 in HCC.

**Methods:** The expression levels of different lncRNAs in HCC were explored using the TCGA database and lncRNA LINC02476 was selected for further study. The expression of LINC02476 in HCC tissues was determined by real-time PCR. The clinicopathological characteristics of HCC patients were analyzed relative to the expression of LINC02476. The expression of LINC02476 was downregulated in HCC cells using a lentiviral vector and different assays were performed to study cell growth, proliferation, invasion, apoptosis and the cell cycle. miR-497 was selected as a miRNA that could interact with LINC02476 which was further tested by RNA immunoprecipitation. HMGA2 was selected as a possible target of miR-497, and their interaction was confirmed by a luciferase reporter assay.

**Results:** LINC02476 expression was elevated in HCC cell lines and HCC tissues. When LINC02476 was downregulated, the growth and the invasion of HCC cells decreased in vitro and in vivo. LINC02476 negatively regulated the expression of miR-497 by acting as a sponge. HMGA2 was directly targeted and inhibited by miR-497.

**Conclusion:** The results indicate that LINC02476 functions through the miR-497/HMGA2 axis and that it has a role in the growth and metastasis of HCC cells. Therefore, LINC02476 could be an interesting new molecular target in HCC therapies.

**Keywords:** LINC02476, miR-497, HMGA2, hepatocellular carcinoma

## Introduction

Hepatocellular carcinoma (HCC) is the sixth most common cancer and the second most lethal cancer in the world.<sup>1</sup> HCC patients are often diagnosed at later stages in the progression of the disease and even though patients undergo surgical resection, the overall prognosis is poor due to a high rate of tumor recurrence.<sup>2</sup> Therefore, novel strategies are needed to improve the diagnosis and treatment of HCC patients.

Only a small portion of the human genome is translated into proteins. Most transcripts are noncoding RNAs<sup>3</sup> that are categorized as small (<200 nt) or long (>200 nt) noncoding RNAs.<sup>4</sup> Dysregulation of long noncoding RNAs (lncRNAs) can promote tumor initiation, growth and metastasis.<sup>5</sup> For instance, CRNDE, TUG1 and NEAT1 are three examples of lncRNAs that are often elevated in HCC and are related to worse prognoses.<sup>6–8</sup> MicroRNAs (miRNAs) are a family of small noncoding RNAs<sup>9</sup> that post-transcriptionally control mRNAs by binding to their 3' untranslated regions (UTRs) leading to direct transcript degradation or translational repression.<sup>10</sup> It

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is estimated that miRNAs can modulate more than 70% of human genes. Dysregulation of a single miRNA can therefore have a crucial impact on tumor development and progression.<sup>11</sup> MiRNAs can act as oncogenes or tumor suppressor genes, depending on the target genes that they regulate.<sup>12,13</sup> LncRNAs can interact with miRNAs by acting as molecular sponges. For example, TUG1 interacts with miR-144 and as a result promotes growth and invasion of HCC cells.<sup>7</sup> Furthermore, HOXA11-AS promotes the migration and invasion of HCC cells by inhibiting the expression of miR-124 by binding to EZH2.<sup>14</sup>

In the present study, we explored the expression level of lncRNA LINC02476 in HCC. To determine the role of LINC02476 in HCC we looked for interactions with miRNAs and explored possible proteins that could be involved.

## Methods and Materials

### Cell Culture and Samples Collection

For this study the following cell lines were used; HCC cell lines Bel7402, Hep3B, HepG-2 and Huh7 and the normal liver epithelial cell line LO2 (Institute of Biochemistry and Cell Biology of the Chinese Academy of Sciences, Shanghai, China). Cells were cultured in RPMI-1640 medium supplemented with 10% fetal bovine serum in a humidified 5% CO<sub>2</sub> atmosphere at 37°C.

Formalin-fixed and paraffin-embedded HCC tissues and normal liver tissue samples were obtained from the First Affiliated Hospital of Soochow University and Wenzhou Medical University. All methods were approved by the Clinical Research Ethics Committees of Soochow University and Wenzhou Medical University. All patients provided written informed consent, which was conducted in accordance with the Declaration of Helsinki.

### Cell Transfection, Lentivirus Production and Transfection

The pcDNA3.1-HIV-TA2 and empty pcDNA3.1 vectors were purchased from GeneChem (Shanghai, China). MiR-497,

miR-ctrl, anti-miR-ctrl and anti-miR-497 were purchased from Ruibo (Guangzhou, China). Cells were transfected with oligonucleotides and plasmids using Lipofectamine 2000 (Invitrogen) following the manufacturer's instructions.

The shRNA sequence targeting LINC02476 was designed by GeneChem (Shanghai, China). The sequences were cloned into the pGFP-C-shLenti vector (Origene) following the instructions from the manufacturer. The lentiviral packaging plasmid psPAX2 and the envelope plasmid pMD2.G were obtained from Addgene. The viruses were packaged in 293T cells following the standard protocol. Polybrene (6 µg/ml) was used to infect HCC cells with virus particles.

### Quantitative Real-Time PCR (qRT-PCR)

Total RNA extraction was performed with TRIzol reagent (Invitrogen). The first-strand cDNA was synthesized with using PrimeScript<sup>TM</sup> 1st Strand cDNA Synthesis Kit (TaKaRa). Subsequently, the real-time PCR was performed by using SYBR<sup>®</sup> Green PCR kit (TaKaRa). The relative fluorescence units were used to represent units in the study. GAPDH was used for normalization in the assay. Primers are listed in Table 1.

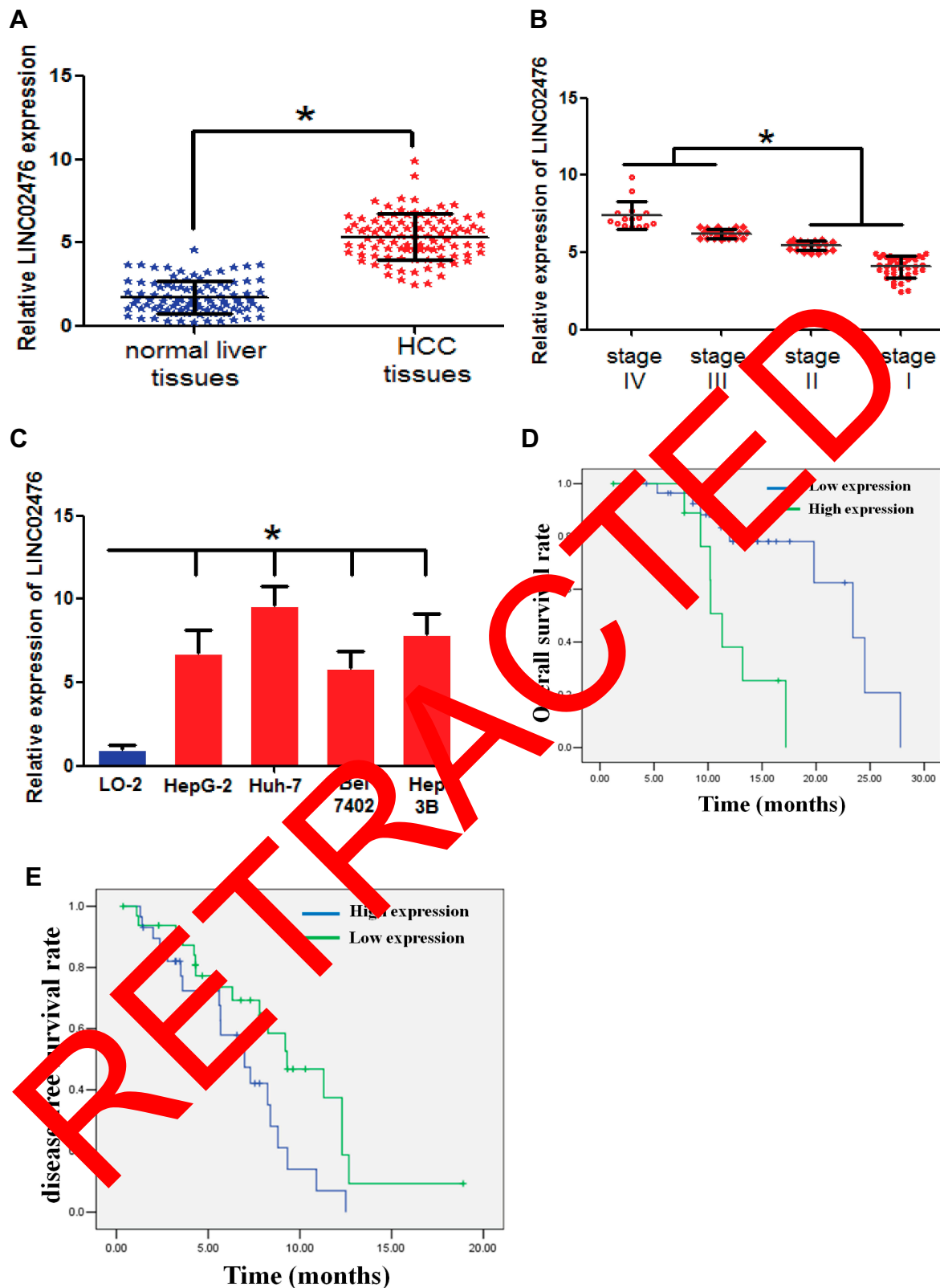
The PARIS Kit (Life Technologies) was used to examine the sub-cellular distribution of LINC02476 in HCC cells. The RNA was extracted from both fractions. Subsequently, qRT-PCR was performed to examine the expression ratios of specific RNA molecules between the nuclear and cytoplasmic fractions.

### MTT, Colony Formation, Cell Cycle and Boyden Assays

The MTT assay, colony formation assay and cell cycle assay were carried out as previously described.<sup>15-17</sup> To carry out Boyden assay, cells were suspended in serum free DMEM and seeded into the top chamber of Transwell inserts coated with Matrigel. The bottom chambers were used DMEM that contains 10% FBS. The crystal violet was used to stain the migrated cells.

**Table 1** Primers Used in This Study

	Forward	Reverse
LINC02476	5'-GTTGCCGGGTGAAAGCTCTA-3'	5'-CCAGGGGAACAGGAAGCAAT-3'
MiR-497	5'-ACCAGCAGCACACTGTGGTTGT-3'	5'-ATCCAGTGCAGGTCGAGG-3'
GAPDH	5'-AATGGGCAGCCGTTAGGAAA-3'	5'-GCGCCCAATACGACCAATC-3'
HMG2	5'-CAACTCTGATCCCAACCCG-3'	5'-TAAGATTGCCCGGTGGTCC-3'



**Figure 1** LINC02476 expression is upregulated in HCC cell lines and tissues. **(A)** LINC02476 expression is significantly increased in primary HCC tissues. **(B)** The expression level of LINC02476 is upregulated in advanced-stage HCC patients. **(C)** LINC02476 expression is higher in HCC cells compared with a normal liver cell line. **(D)** and **(E)** High-level expression of LINC02476 is associated with a shorter overall survival and disease-free survival time of HCC patients (blue and green curves represent low and high expression of LINC02476, respectively). \*Represents a P value<0.05.

## Western Blot Assay

Protein samples were transferred onto a PVDF membrane which was incubated with a 1:500 dilution of primary antibodies overnight at 4°C. Next, the membrane was incubated with HRP-conjugated rabbit or mouse secondary antibodies at room temperature for 1 hr and developed using a chemiluminescence reagent. The primary antibodies cyclinD1, c-myc, CDK4, MMP-2, MMP-3 and MMP-9 were purchased from Abcam. The primary antibodies E-cadherin, N-cadherin, and Vimentin were purchased from Santa Cruz. All the concentrations of the primary antibodies used in the study were 1:500.

## Luciferase Reporter Assay

Full-length HMGA2 cDNA lacking the 3'-UTR was cloned into the eukaryotic expression vector pcDNA3.1 (Invitrogen). Subsequently, the 3'-UTR of HMGA2 was amplified and cloned downstream of the firefly luciferase gene in the pGL3 vector (Promega). This vector was named WT-HMGA2-3'-UTR (wild type). The GeneTailor™ Site-Directed Mutagenesis System (Invitrogen) was used to perform site-directed mutagenesis in the miR-497 binding site of the HMGA2 3'-UTR. This vector was named MUT-HMGA2-3'-UTR (mutant type). Subsequently, we cotransfected HCC cells with the WT-or MUT-HMGA2-3'-UTR vector and miR-497mimic or inhibitor. The Dual Luciferase Reporter Assay System (Promega) was performed 36 hrs after transfection.

## In vivo Tumor Growth Assay

Sh-ctrl and sh-LINC02476 were injected subcutaneously into the flanks of nude mice, and each group included five mice. After four weeks the xenografts were removed and weighed. The tumor volume was calculated with the following formula:  $4\pi/3 \times (\text{width}/2)^2 \times (\text{length}/2)$ . All procedures involving animals were approved by the Institutional Committee on Animal Care of Soochow University and Wenzhou Medical University and performed in accordance with the National Guidelines for Experimental Animal Welfare (the Ministry of Science and Technology, China).

Immunohistochemistry (IHC) and evaluation of Ki-67 staining.

The Paraffinized sample sections were deparaffinized and dehydrated. Subsequently, 3% H<sub>2</sub>O<sub>2</sub> and goat serum were used to treat the samples, then the samples were incubated with Ki-67, followed by incubated with secondary antibody and visualized using DAB substrate. For statistical analysis, a score  $\leq 6$  indicated low expression, and a score  $> 6$  indicated high expression.

## Statistical Analysis

For statistical analysis SPSS 13.0 and GraphPad Prism 5.0 software were used. Values are shown as the mean  $\pm$  the standard error of the mean (S.E.M). Analyses between groups were performed using one-way ANOVA or the two-tailed Student's *t*-test. A P value  $<0.05$  was considered a statistically significant result.

## Results

### LINC02476 Expression Was Elevated in HCC Tissues and Cell Lines

Among all the lncRNAs that were increased in HCC tissues according to the TCGA database, we focused on LINC02476 as it was one of the most significantly up-regulated lncRNAs (Supplementary Figure 1A).

The expression level of LINC02476 was analyzed in a cohort of 97 HCC patients. LINC02476 was upregulated in HCC tissues compared with adjacent normal tissues (Figure 1A). Compared with that at early-stage HCC, the expression level of LINC02476 was higher in advanced-stage HCC (Figure 1B). In HCC cell lines the expression level of LINC02476 was also upregulated compared with

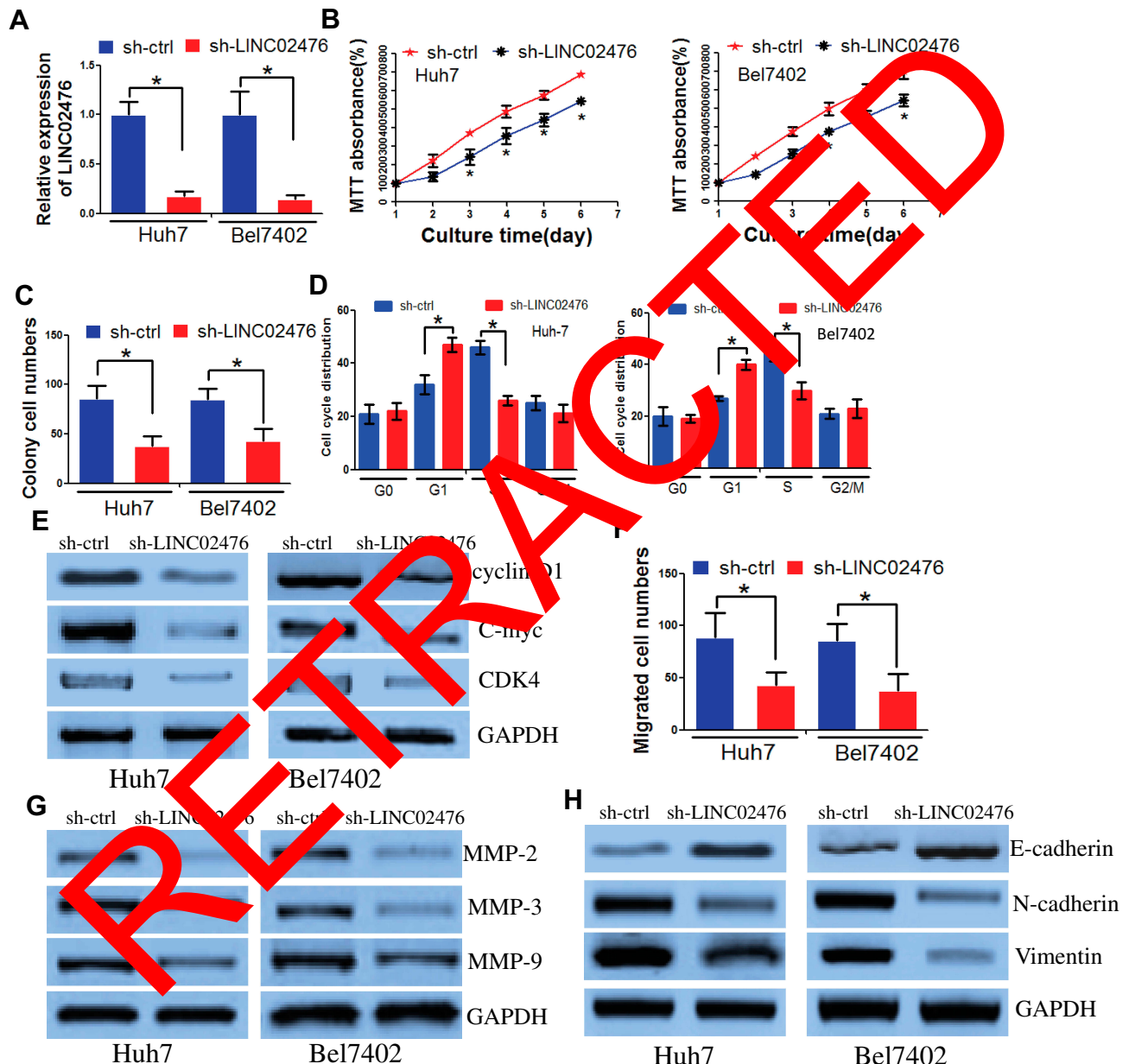
**Table 1** Associations Between lncRNALINC02476 Expression and Patients' Clinicopathological Features

Variable	No. of Patients	LINC02476 Low Expression	LINC02476 High Expression	P value
<b>Age</b>				
<60	50	28	22	0.265
$\geq 60$	47	21	26	
<b>Gender</b>				
Male	49	26	23	0.612
Female	48	23	25	
<b>Tumor size</b>				
<5cm	50	38	12	0.000
$\geq 5$ cm	47	11	36	
<b>Lymph Node Involvement</b>				
Absent(pN0)	50	32	18	0.008
Present (pN+)	47	17	30	
<b>TNM Stage</b>				
I-II	47	29	18	0.033
III-IV	50	20	30	
<b>HBV Infection</b>				
Yes	51	22	29	0.126
No	46	27	19	

the expression in the normal human liver cell line LO2 (Figure 1C). The in vitro translation assay revealed that LINC02476 did not have coding ability (Supplementary Figure 1B). Subcellular fractionation combined with real-time PCR analysis showed that LINC02476 was predominantly located in the cytoplasmic fraction (Supplementary Figure 1C).

## Elevated LINC02476 Expression Was Associated with Unfavorable Prognosis

The associations between LINC02476 expression levels and patient clinicopathological features are shown in Table 2. To separate HCC patients with low expression levels (49/97, 50.5%) from patients with high expression levels (48/97, 49.5%), the median LINC02476 expression value was used.





Although LINC02476 expression showed no correlation with age ( $P=0.265$ ), gender ( $P=0.612$ ) or HBV infection ( $P=0.126$ ), increased LINC02476 expression was significantly correlated with tumor size ( $P=0.000$ ), lymph node metastasis ( $P=0.008$ ) and late clinical stage ( $P=0.033$ ). Kaplan-Meier analysis showed that elevated LINC02476 expression was correlated with shorter overall survival and disease-free survival time (Figure 1D and E,  $P<0.05$ ). The median LINC02476 expression value was used as the cut-off between high- and low-LINC02476 group.

## Inhibition of LINC02476 Decreased HCC Cell Proliferation and Invasion

Cell lines Bel7402 and Huh7 were selected for further study as they exhibited the highest expression of LINC02476. Bel7402 and Huh7 cells with stable LINC02476 knock-down were established (sh-LINC02476 cells, Figure 2A). LINC02476 inhibition significantly decreased cell proliferation (Figure 2B) and oncogenic survival (Figure 2C) when compared with sh-ctrl cells. Flow cytometry analysis showed a significantly higher frequency of sh-LINC02476 cells in the G1 phase than in the S phase (Figure 2D). Interestingly, the expression levels of the G1/S phase checkpoint proteins cyclin D1, CDK4 and CDK2

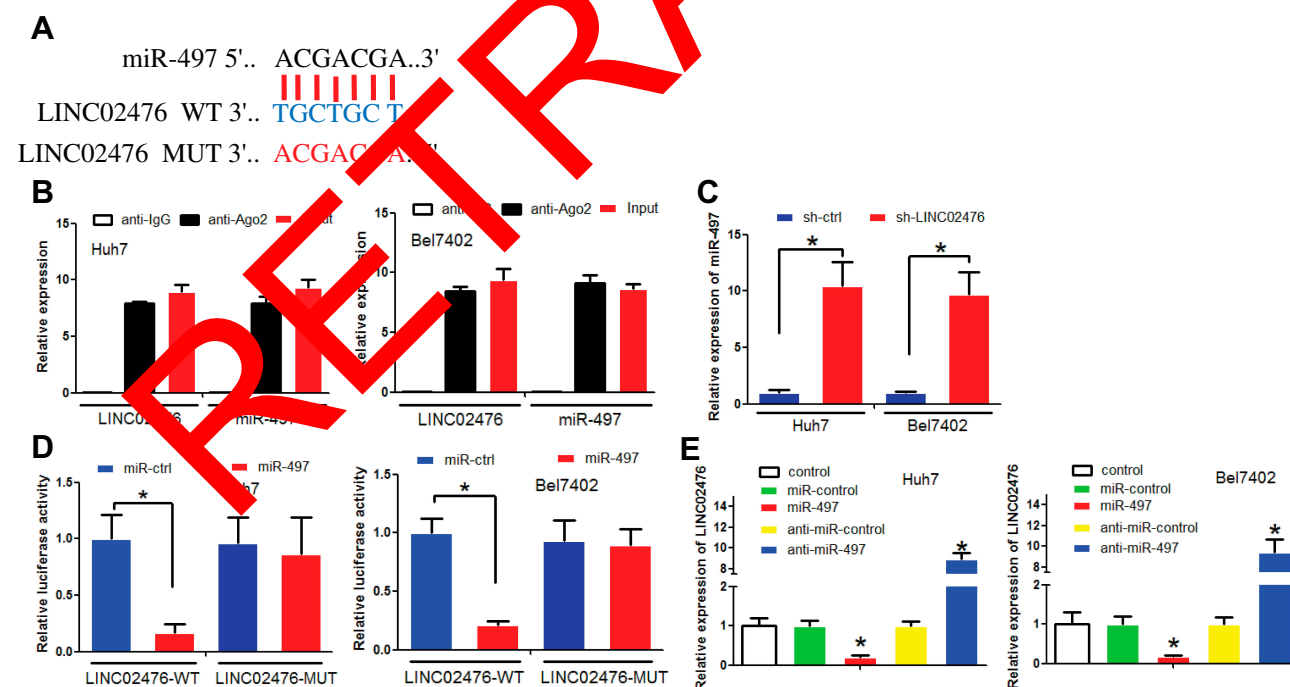
were significantly downregulated in sh-LINC02476 cells (Figure 2E).

Inhibition of LINC02476 decreased HCC cell invasiveness (Figure 2F) and decreased the expression levels of the invasion protein markers MMP-2, MMP-3 and MMP-9 (Figure 2G). The epithelial to mesenchymal transition (EMT) related markers also showed altered expression, whereby E-cadherin was upregulated, while N-cadherin and Vimentin were down-regulated in sh-LINC02476 cells, as determined by the Western blot assay (Figure 2H).

These results suggest that LINC02476 can promote the proliferation and invasion of HCC cells in vitro.

## LINC02476 Acts as a ceRNA to Regulate miR-497 Expression

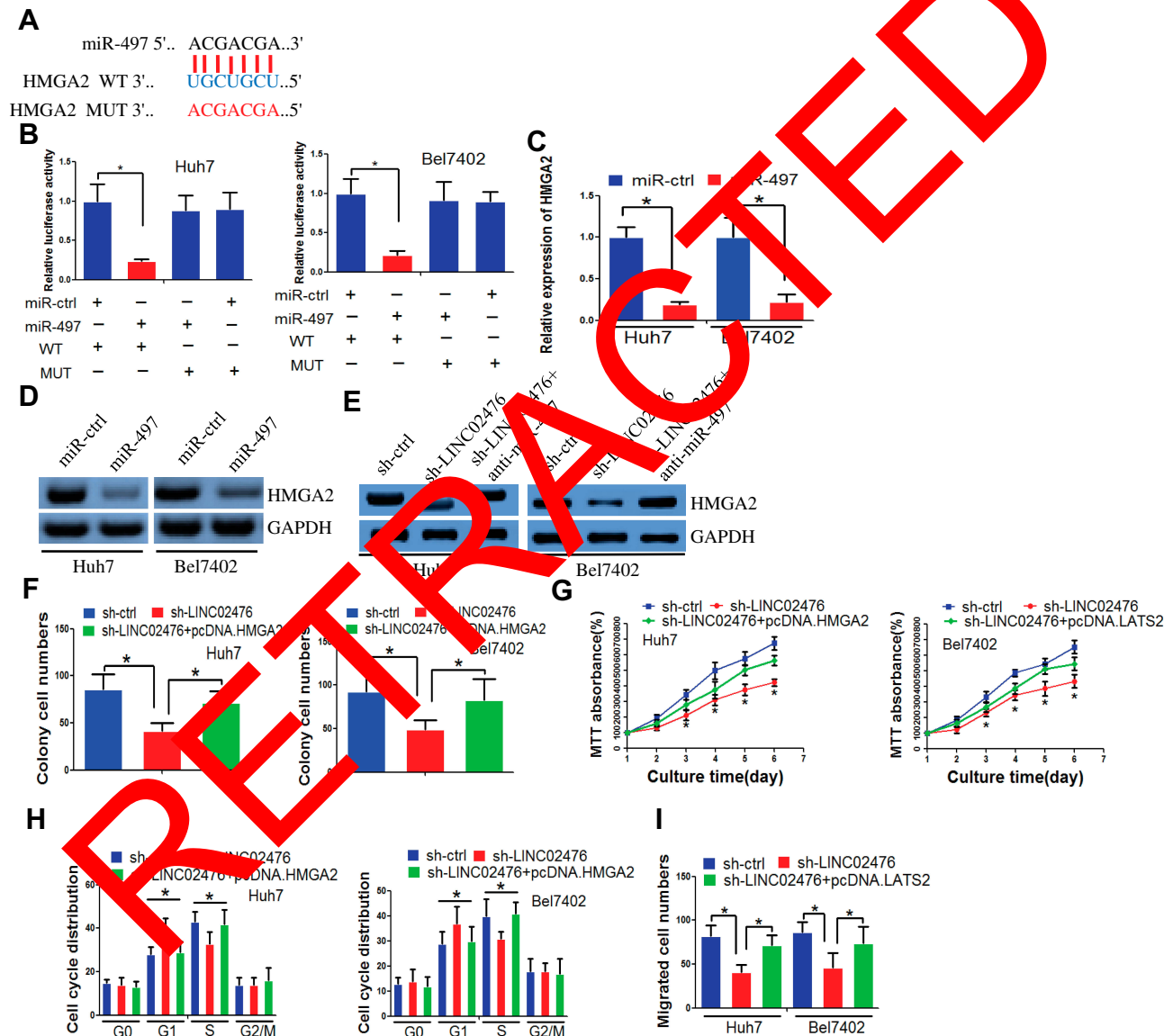
The online software miRDB (<http://mirdb.org/miRDB/index.html>) was used to search for miRNAs with complementary base pairing with LINC02476. Several microRNAs were identified and miR-497 was chosen for further study since it is a well-known tumor suppressor that also functions in HCC.<sup>18</sup> The predicted binding site of miR-497 on LINC02476 is indicated in Figure 3A.<sup>19</sup> The RNA immunoprecipitation assay revealed that LINC02476 and



**Figure 3** LncRNA LINC02476 acts as a ceRNA to regulate HMG2 expression. (A) The binding sites of miR-497 on LINC02476. (B) The RIP assay reveals that LINC02476 and miR-497 are enriched in the same Ago2 immunoprecipitates. (C) MiR-497 expression was increased in sh-LINC02476 cells compared with sh-ctrl cells. (D) Cotransfection of miR-497 and LINC02476-WT strongly decreases the luciferase activity. Cotransfection of miR-ctrl and LINC02476-WT or miR-497 and LINC02476-MUT does not change the luciferase activity. (E) MiR-497 decreases LINC02476 expression, while anti-miR-497 increases LINC02476 expression. \*Means P value  $<0.05$ .

miR-497 were both enriched in Ago2 immunoprecipitates when compared with control IgG immunoprecipitates (Figure 3B,  $P<0.05$ ). MiR-497 expression was elevated in sh-LINC02476-treated Bel7402 and Huh7 cells (Figure 3C,  $P<0.05$ ), which suggests that LINC02476 negatively regulates miR-497. Subsequently, the predicted miR-497 binding site on LINC02476 (LINC02476-WT) and a mutated binding site (LINC02476-MUT) were cloned into a reporter plasmid. Cotransfection of miR-497 and LINC02476-WT

decreased luciferase activity, while cotransfection of miR-ctrl and LINC02476-WT or miR-497 and LINC02476-MUT did not change the luciferase activity (Figure 3D,  $P<0.05$ ). Furthermore, miR-497 inhibited the expression of LINC02476 while miR-ctrl did not, and anti-miR-497 increased the expression of LINC02476 while anti-miR-ctrl did not (Figure 3E,  $P<0.05$ ). This suggests that there is a reciprocal interaction between LINC02476 and miR-497.



**Figure 4** HMG2 is a downstream target of miR-497. (A) The binding sites of miR-497 on HMG2. (B) The luciferase assay shows that cells transfected with miR-497 have less luciferase activity than those transfected with miR-ctrl. (C) MiR-497 represses HMG2 mRNA expression in HCC cells. (D) MiR-497 represses HMG2 protein expression in HCC cells. (E) Anti-miR-497 treatment leads to restored HMG2 expression in sh-LINC02476 cells. (F) The MTT assay reveals that sh-LINC02476 cells grow more slowly than the sh-ctrl cells, while overexpression of HMG2 rescues this effect. (G) The colony formation assay shows that sh-LINC02476 cells form smaller and fewer colonies than sh-ctrl cells, which is counteracted by overexpression of HMG2. (H) LINC02476 downregulation affects the cell cycle distribution, which is counteracted by overexpression of HMG2. (I) LINC02476 downregulation inhibits HCC cell invasion ability, which is rescued by overexpression of HMG2. \*Means  $P$  value $<0.05$ .

## LINC02476 Regulated HMGA2 Expression Through miR-497

TargetScan software was used to identify HMGA2, a protein that is known to regulate cancer cell proliferation and invasion, as a downstream target of miR-497. The 3'-UTR of HMGA2 mRNA containing the predicted miR-497 binding site (wild type) or a mutated sequence (mutant type) was subcloned into a luciferase reporter plasmid (Figure 4A). MiR-497 decreased the luciferase activity in the wild type vector but not in the mutant type vector (Figure 4B). In miR-497-treated cells HMGA2 mRNA and protein expression was decreased (Figure 4C and D). This confirms that HMGA2 is a target of miR-497.

Subsequently, we asked whether LINC02476 exerted its function through miR-497 and HMGA2. LINC02476 inhibition was found to decrease HMGA2 expression and this effect was abolished when miR-497 was also inhibited (Figure 4E). The effect of sh-LINC02476 on cell growth, the cell cycle distribution and cell invasion was counteracted by overexpression of HMGA2 (Figure 4F-I).

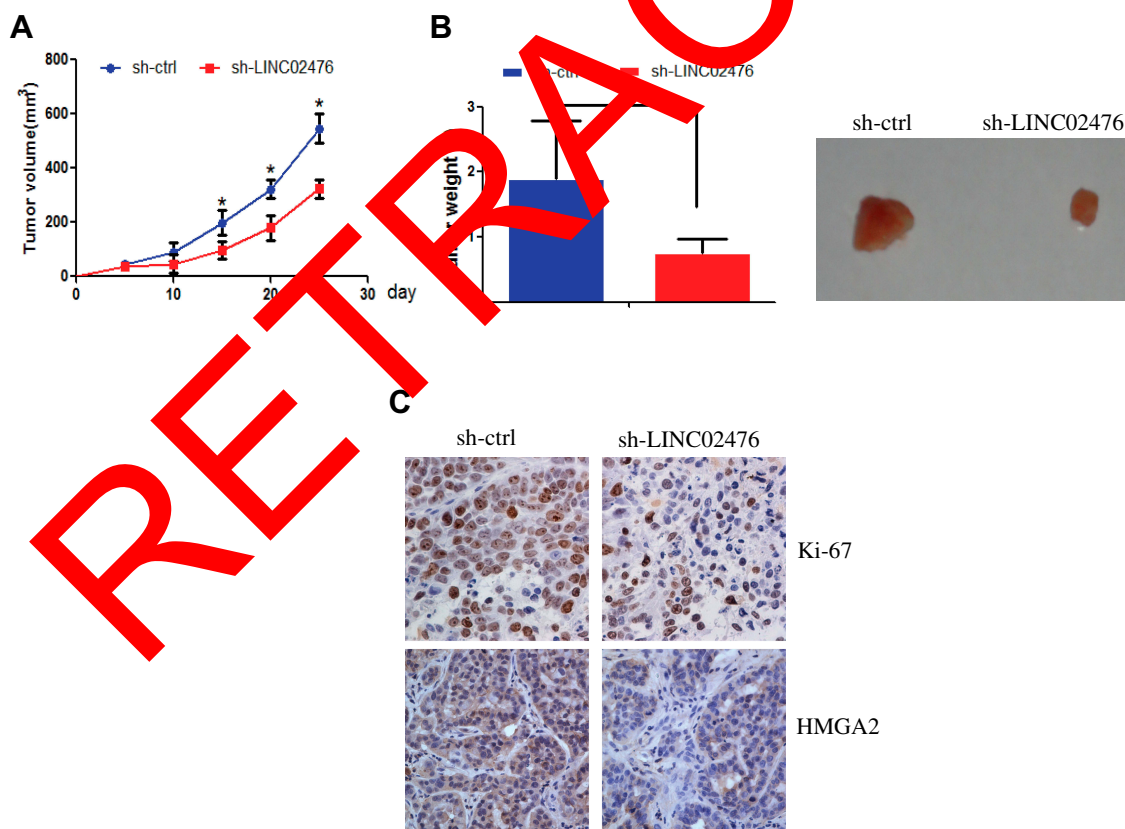
Taken together, these data suggest that LINC02476 functions through the miR-497/HMGA2 axis.

## Knockdown of lncRNA LINC02476 Inhibited Tumor Growth in vivo

Tumor growth of sh-LINC02476 cells was measured in vivo in mice. The mean xenograft tumor weight was lower and tumor growth was slower in the sh-LINC02476 group when compared with the sh-ctrl group (Figure 5A and B). The xenograft tumor proliferation index was determined by Ki-67 staining and was also lower in the sh-LINC02476 group. In addition, the expression level of HMGA2 was decreased in sh-LINC02476 group when compared with that in sh-ctrl group (Figure 5C). These data indicate that LINC02476 promotes tumor growth in vivo.

## Discussion

LncRNAs are known to regulate multiple processes in cancer cell biology, including cell growth and invasion.<sup>20</sup> Recent studies have therefore suggested that lncRNAs can



**Figure 5** LINC02476 inhibition decreases tumor growth and invasion in vivo. (A) Compared with sh-ctrl cell-derived xenograft tumors, sh-LINC02476 cell-derived xenograft tumors grow more slowly. (B) The mean weight of sh-LINC02476 cell-derived xenograft tumors is significantly less compared with sh-ctrl cell-derived xenograft tumors. (C) Knockdown of LINC02476 significantly decreases the percentage of Ki-67-positive cells and HMGA2 expression in tumors when compared with the negative control group. \*Means P value<0.05.



be used as predictive biomarkers and therapeutic targets for the treatment of cancer.

In the present study, the TCGA database was used to search for lncRNAs whose expression levels were increased in HCC. LINC02476 was identified as an oncogene that could be involved in HCC progression. LINC02476 was upregulated in HCC cell lines and patient tissues. When LINC02476 was knocked down in vitro, cell proliferation and colony formation were inhibited. A study in mice showed that LINC02476 downregulation resulted in lower tumor weight and slower tumor growth in vivo. LINC02476 downregulation arrested the cell cycle in the G1 stage and altered the expression of G1/S phase checkpoint proteins. These data suggest that LINC02476 affected cell growth by interfering with the cell cycle. LINC02476 downregulation also inhibited the invasion of HCC cells in vitro. It is well-known that the EMT process plays a vital role in promoting cancer cell invasion.<sup>21</sup> Indeed, LINC02476 downregulation changed the expression of epithelial and mesenchymal markers suggesting that LINC02476 promotes the EMT phenotype leading to HCC cell invasion.

Previous studies have shown that lncRNAs can negatively regulate miRNA expression by acting as endogenous molecular sponges for miRNAs.<sup>22,23</sup> Using online bioinformatic tools, we identified several miRNAs that could interact with LINC02476 and chose miR-497 for further study. Previous studies have shown that miR-497 can act as a tumor suppressor, including in HCC.<sup>24,25</sup> The regulatory relationship between LINC02476 and miR-497 was confirmed by the following data: 1) LINC02476 downregulation increased the expression of miR-497; 2) a luciferase activity assay confirmed the direct binding to the predicted miR-497 binding site on LINC02476; 3) the RIP assay confirmed that LINC02476 and miR-497 were in the same RNA-induced silencing complex. In our study, HMGA2 was identified as a downstream target of miR-497. HMGA2 has been implicated to have a role in tumor growth, tumorigenicity, drug resistance, and metastasis. HMGA2 is therefore a major player in cancer and an important potential therapeutic target. In this study, LINC02476 inhibition decreased the expression of HMGA2 which was abolished when miR-497 was also inhibited. Overexpression of HMGA2 could counteract the effect of LINC02476 on HCC cell growth. This suggests that LINC02476 functions through the miR-497/HMGA2 axis.

In summary, the provided data show that the LINC02476/miR-497/HMGA2 axis is involved in HCC cell growth and invasion. Therapy targeting LINC02476 could improve the treatment of HCC.

## Disclosure

The authors report no conflicts of interest in this work.

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