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ORIGINAL RESEARCH

LncRNA NEAT1 Promotes Proliferation, Migration And Invasion Via Regulating miR-296-5p/CNN2 Axis In Hepatocellular Carcinoma Cells

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Background: Emerging evidence has revealed that long noncoding RNA nuclear paraspeckle assembly transcript 1 (lncRNA NEAT1) is implicated in the development of various cancers. However, the underlying molecular mechanisms of NEAT1 in hepatocellular carcinoma (HCC) remain unclear.

Methods: The expression of NEAT1, miR-296-5p and Calponin 2 (CNN2) was detected by quantitative real-time polymerase chain reaction or Western blot, respectively. Cell proliferation and apoptosis were analyzed by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay or flow cytometry, respectively. Transwell assay was used to determine cell migration and invasion. The interaction between miR-296-5p and NEAT1 or CNN2 was analyzed by dual-luciferase reporter assay and RIP assay. Huh7 cells transfected with sh-NEAT1 were used to establish the murine xenograft model.

Results: NEAT1 was elevated in HCC tissues and cell lines. Knockdown of NEAT1 significantly inhibited proliferation, migration and invasion of HCC cells in vitro as well as tumor growth in vivo. NEAT1 was a sponge of miR-296-5p and remarkably reduced the level of miR-296-5p in HCC cells. Furthermore, NEAT1 silence significantly decreased the expression of CNN2, which was the direct target of miR-296-5p. Besides that, the tumor suppression caused by NEAT1 silence could be rescued by CNN2 restoration or miR-296-5p inhibition in vitro. Additionally, NEAT1 indirectly regulated CNN2 expression by competing with miR-296-5p in vitro and in vivo.

Conclusion: LncRNA NEAT1 contributes to HCC progression by regulating miR-296-5p/CNN2 axis, providing a novel regulatory mechanism for HCC development and a promising therapeutic target for the HCC treatment.

Keywords: NEAT1, miR-296-5p, CNN2, HCC, progression

Introduction

Hepatocellular carcinoma (HCC) is a common malignancy with high lethality worldwide.[1] Aberrant cell differentiation, early metastasis, and fast infiltrating growth are thehallmarks of HCC development.[2] Although advances in medical, locoregional and surgical therapies, the overall survival rate in HCC remains unsatisfactory.[3] Recently, emerging evidence has indicated that the therapies based on the genomic and immune are transforming the treatment of many tumors and are beginning to be used to improve the prognosis outcome of HCC patients.[4]

Long noncoding RNAs (lncRNAs) are a class of non-coding RNAs with longer than 200 nts in length, and have no potential to encode proteins. Numerous

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evidence has exhibited the significant regulatory rolesof lncRNAs in the development, prognosis, and therapy in diverse cancer types.[5,6] Up to date, various lncRNAs have been identified in HCC to exert roles in diagnosis,[7] cell differentiation, metastasis, growth,[8,9] chemoresistance,[10] therapy outcome prediction[11] and so on. Thus, lncRNAs are thought to be promising targets for HCC therapy with a view to the regulation in HCC pathogenesis. LncRNA nuclear paraspeckle assembly transcript 1(NEAT1) is a cancer-related lncRNA, and aberrantly NEAT1 expressionin a variety of cancers has been investigated.[12] Besides that, the important rolesof NEAT1 in the pathogenesis and progression of several cancers has also been observed, including HCC.[13,14] Nevertheless, the precise molecular mechanism of NEAT1 in HCC is still vague.

Recent findings have also shown many microRNAs (miRNAs) play a central role in the regulation of HCC tumorigenesis and development.[15,16] Among these miRNAs, miR-296-5p was also reported to be down-regulated in HCC tumor tissues and cells and involved in the event of HCC,[17,18] which was a potential candidate for HCC treatment. Calponin 2 (CNN2), encoded by the CNN2 gene, is an actin filament-associated regulatory protein, and is closely associated with cell proliferati and migration.[19,20] Recently, Kang et al claimed CNN deletion suppressed tumor growth and metasta[21] indicating the potential roles of CNN2 in H C mol ular target therapy. Therefore, it is also neces inth opment of HCC treatment to clarify t role a olecular mechanism of miR-296-5p and C in HCC.

In this study, we aimed to investig the expression pattern of NEAT1 in HCC ssues and cell es, explored the biological function well a he underlying molecular mechanismof NEAT1 HC develo ment and growth in vitro and in v

Materia And Methods

Patients An Specimens

Tumor tissues and matched paracancerous tissues from 30 HCC patients were collected at The First Hospital of Jilin University. All HCC tissues were histopathologically diagnosed by two independent pathologists and were immediately preserved in liquid nitrogen until used. Patients and hospital had provided the written informed consent and this was conducted in accordance with the Declaration of Helsinki and this work was approved by Ethics Committee of the First Hospital of Jilin University.

Cell Culture And Transfection

The normal human hepatocyte THLE-2, HCC-derived cell lines (HepG2 and Huh7) and 293T cells were purchased from BioVector NTCC Inc. (Beijing, China). All cells were cultured in Dulbecco's modified Eagle's medium (DMEM; Gibco, Grand Island, NY, USA) harboring with 10% fetal bovine serum (FBS; Gibco) and 1% penicillin/streptomycin at 37°C with 5% CO_2.

The miRNA mimic or inhibitor targeting miR-296-5p (miR-296-5p mimic or miR-296-5p inhibitor) and their corresponding negative control (miRNA NC itor NC) were purchased from RIBOBIO (Guang ou, China). ort hairpin RNA (shRNA) targeting NEAT1 (sh- EAT1), shR A scramble control (sh-NC), small i erfering R (siR A)targeting NEAT1 (si-NEAT1), RNA gative ntrol (si-NC), pcDNA3.1-CNN2 erex on vect (pcDNA-CNN2), pcDNA3.1 emp vector (pc NA-C ntrol) were synthesizedby Gene harma Shanghai, C na). Subsequently, Lipofectamine 2000 reagent (vitrogen, Carlsbad, CA, USA) was used transfect these oligonucleotides or vectors into HepG2 and Huh7 cells fo owing the protocol of the manufacturer.

R A Extraction And Quantitative eal-Time Polymerase Chain Reaction qRT-PCR)

Trizol reagent (Invitrogen) was used to isolate RNA from HCC tissues and cells following the standard introductions. For mRNA expression analysis, the complementary DNA (cDNA) was synthesized with the PrimeScript RT reagent kit (Takara, Dalian, China). For miRNA expression detection, SuperScript III First-Strand Synthesis System (Invitrogen) was used to generate cDNA. Next, SYBR Premix Ex Taq (Takara) was applied to perform quantitative PCR. The relative expression was calculated using $2^{-\Delta\Delta CT}$ methods with normalization to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) or U6. The primer sequences used in this study were listed as followed: NEAT1 F, 5′-TGGCTAGCT CAGGGCTTCAG-3′ and R, 5′-TCTCCTTGCCAAGCTTC CTTC-3′; CNN2 F, 5′- GGTCAAGGCCATATCCCAATAC-3′ and R, 5′-GGCATAGAAACCACAAACTGCTC-3′; GAP DH F, 5′-AACTTTGGCATTGTGGAAGG-3′ and R, 5′-ACACATTGGGGGTAGGAACA-3′; miR-296-5p F, 5′-TGC CTAATTCAGAGGGTTGG-3′ and R, 5′-CTCCACTCCTG GCACACAG-3′; U6 F, 5′-CTCGCTTCGGCAGCACA-3′ and R, 5′-ACGCTTCACGAATTTGCGT-3′.

Western Blot

Proteins were isolated from cells and tissues with RIPA reagent (Beyotime, Shanghai, China) and then the content was quantified by a bicinchoninic acid method. Equal proteins were separated by 10% sodium dodecyl sulfate polyacrylamide gel electrophoresis and transferred onto nitrocellulose membrane (Millipore, Billerica, MA, USA). Subsequently, the membrane was incubated with primary antibodies against CNN2 or GAPDH, and followed by interaction with the HRP-conjugated secondary antibody after blockage with 5% non-fat milk for 1 h. Protein signaling was visualized using Enhanced Chemiluminescence.

Cell Proliferation Assay

Transfection cells were cultured in 96-well plates at 37°C overnight. Subsequently, each well was interacted with 10 μL 3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) solution (Sigma, St. Louis, MO, USA) for another 4 h, followed by incubation with 150 μL DMSO (Sigma) after removing the supernatants. Finally, the absorbance at 490 nm was analyzed.

Cell Apoptosis Assay

Apoptotic cells were detected with the help of Annexin V-FITC/PI apoptosis detection kit (BD Biosciences, San Jose, CA, USA) following the standard protocol. Briefly, cells were resuspended with binding buffer, and then stained with 10 μL Annexin V-FITC and PI for 15 min in the dark. Finally, the apoptotic cells were analyzed by FlowJo software.

Cell Migration And Invasion

For migration assay, transfection cells resuspended in serum-free DMEM were added into the top of the transwell chambers. After that, the lower chamber was filled with 500 μL DMEM mixed with 10% FBS. After incubation for 24 h at 37°C, migrated cells were stainedand counted with a microscope. For invasion assay, the upper chamber membrane was pre-coated with Matrigel (BD Biosciences) and the other steps were similar to cell migration assay.

Dual-Luciferase Reporter Assay

The WT or MUT NEAT1/CNN2 3′UTR containing with miR-296-5p binding sequences was synthesized and cloned into the pmirGLO Vector (Promega, Shanghai, China). Then 293T cells were co-transfected with constructed vector and miR-296-5p mimics or miRNA NC for 48 h, accordingly. Finally, a dual-luciferase reporter assay kit (Promega) was utilized to analyze the relative luciferase activity.

RNA Immunoprecipitation (RIP) Assay

RNA immunoprecipitation (RIP) assay was performed with the Magna RIP Kit (Millipore). HepG2 and Huh7 cells were lysed in RIP buffer (Millipore), and then the lysate was incubated with magnetic beads coated with human anti-Ago2 or IgG antibody. Subsequently, the enrichment of NEAT1, CNN2 or miR-296-5p was measured by qRT-PCR as described above, respectively.

Murine Xenograft Assay

BALB/c nude mice (male, 4–6 weeks old, N=6, each group for 3 mice) were used for the xenograft assays. The study was permitted by the Animal Research Committee of The First Hospital of Jilin Universityand performed in accordance with the guidelines of the National Animal Care and Ethics Institution. Huh7 cells (2×10^6) transfected with lentivirus harboring sh-NEAT1 or sh-NC were subcutaneously injected into the nude mice. Subsequently, the tumor size was monitored every 7 d and the tumor volume was calculated. After 30 d, all mice were sacrificed and tumor mass was weighted and harvested for subsequent molecular analysis.

Statistical Analysis

Data from at least three independently experiment were indicated as mean ± standard deviation (SD). The differences among different groups were analyzed by Student's *t*-test or one-way analysis of variance (ANOVA). $P < 0.05$ exhibited a statistically significance. All statistical analyses were conducted using the GraphPad Prism 7 software (GraphPad Inc., San Diego, CA, USA).

Results

The Expression Of NEAT1 And CNN2 Is Up-Regulated In HCC Tissues And Cells

The expression of NEAT1 and CNN2 in 30 pairs HCC tissues and normal tissues was investigated using qRT-PCR or Western blot, and results indicated the expression-levels of NEAT1 and CNN2were high in HCC tissues compared with the normal tissues (Figure 1A–C). Similarly, we also observedthe same changes that NEAT1 and CNN2 was up-regulated in HCC cell lines (HepG2 and Huh7) compared to the normal human hepatocyte

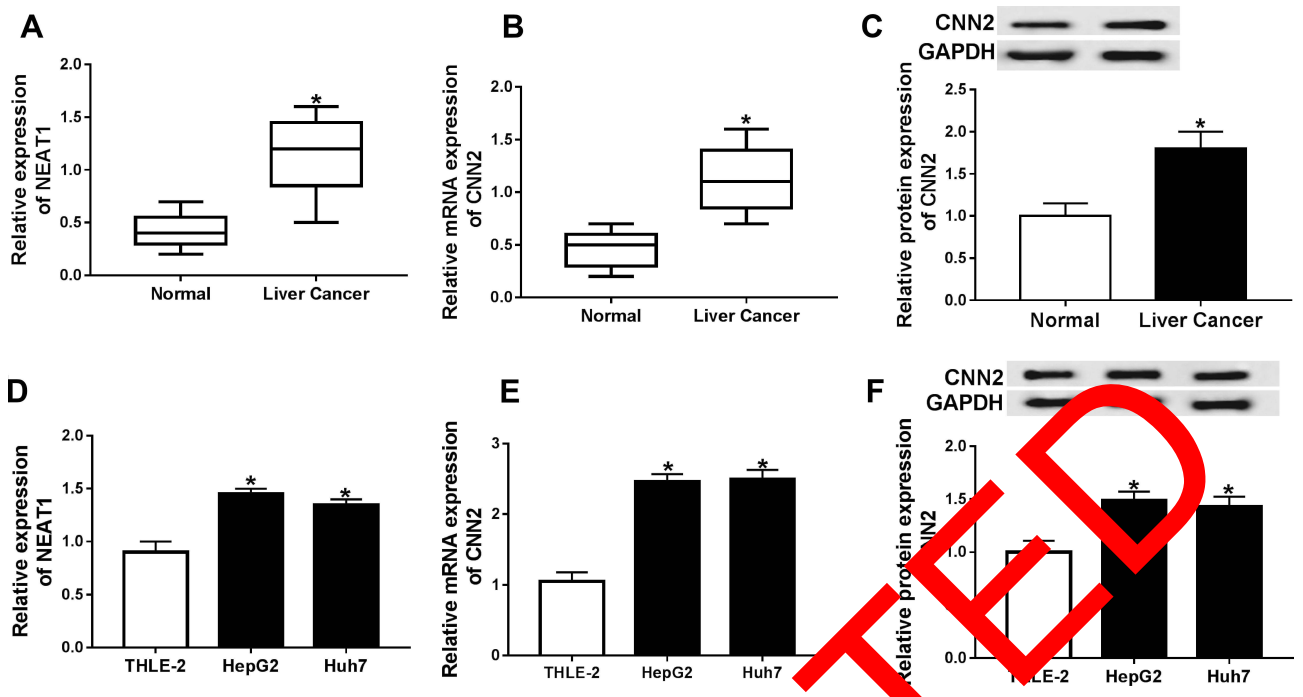

Figure 1 The expression of NEAT1 and CNN2 is up-regulated in HCC tissues and cells. (**A**–**C**) The expression of NEAT1 and CNN2 in HCC and normal tissues was detected using qRT-PCR or Western blot. (**D**–**F**) The expression of NEAT1 and CNN2 in normal human hepatocyte THLE-2 and HCC cell lines (HepG2 and Huh7) was measured by qRT-PCR or Western blot. *P<0.05.

THLE-2 (Figure 1C–F), indicating the potential involvement of NEAT1 and CNN2 in HCC progression and the possible correlation between NEAT1 and CNN2 in HCC.

Besides that, the association between NEAT1 expression levels and HCC patients' progression was analyzed. Based on the statistical analysis results presented in Table 1, it implied that high expression NEAT1 was significantly associated withthe high incidence of tumor size (P=0.0097), TNM stage (P=0.0281) and lymphatic metastasis (P=0.0410). Therefore, NEAT1 might be an important regulator for HCC progression.

NEAT1 Silence Inhibits Cell Proliferation, Migration And Invasion But Induces Apoptosis In HCC

To explore the potential biological functions of NEAT1 in HCC progression, the expression of NEAT1 was down-regulated using siRNA sequences. As expected, an obviously decreased expression of NEAT1 in cells transfected with si-NEAT1 was observed (Figure 2A). After that, MTT assay showed that knockdown of NEAT1 significantly inhibited proliferation of HepG2 and Huh7 cells (Figure 2B and C). Furthermore, compared with the si-NC group, NEAT1 deletion showed an obviously promotion in cell apoptosisfrom 5.86% to 17.43% (total early and late apoptosis) (Figure 2D).

Besides that, transwell assay results exhibited a remarkable inhibition of cell migration and invasion in HCC induced by NEAT1 silence (Figure 2E and F). Taken together, these data

Table 1 Correlation Between NEAT1 Expression And Clinical Clinicopathological Parameters Of HCC

Parameter	Case	NEAT1 Expression		p
		Low (n=15)	High (n=15)	
Age (years)				
≤60	19	14	5	0.56
>60	11	7	4	
Gender				
Female	17	10	7	0.27
Male	13	5	8	
Tumor size				
≤5 cm	16	14	2	*0.0097
>5 cm	14	6	8	
TNM stages				
I-II	14	10	4	*0.0281
III-IV	16	5	11	
Lymphatic metastasis				
Negative	22	5	17	*0.0410
Positive	8	5	3	

Note: *P<0.05.

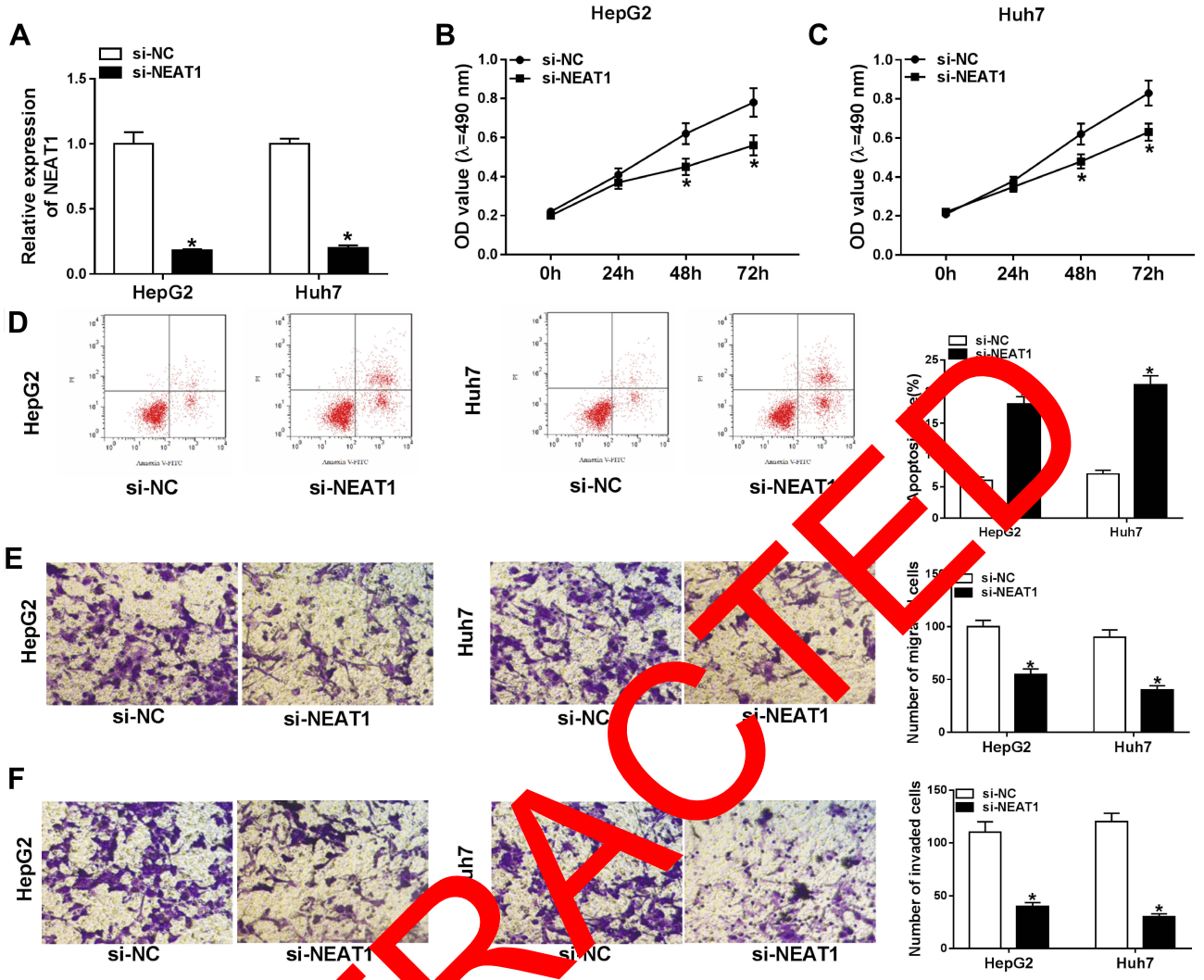

Figure 2 NEAT1 silence inhibits cell proliferation, migration and invasion but induces apoptosis in HCC. HepG2 and Huh7 cells were transfected with si-NEAT1 or si-NC. (**A**) The level of NEAT1 was examined by qRT-PCR. (**B, C**) Cell proliferation was analyzed by MTT assay. (**D**) Flow cytometry was used to analyze cell apoptosis. (**E, F**) The number of migration and invasion cells were detected by transwell assay. *P<0.05.

suggested that NEAT1 silence could inhibit cell progression in HCC.

NEAT1 Silence Suppresses HCC Progression By Regulating CNN2 Expression

When the expression of NEAT1 was inhibited using siRNA sequences in HCC cells, we found a significant reduction of the level of CNN2 at mRNA and protein level, while this decrease could be rescued by following CNN2 overexpressing plasmid transfection (Figure 3A and B). Thus, based on the regulation between NEAT1 and CNN2 in HCC cells, we hypothesized that CNN2might involve in NEAT1 mediated acceleration on HCC progression. We found CNN2 overexpression attenuated NEAT1 deletion-induced cell proliferation inhibition of HepG2 and Huh7 cells (Figure 3C and D). Cell apoptosis was greatly promoted by the depletion of NEAT1, but CNN2 up-regulation obviously weakened NEAT1 silence-mediated cell apoptosis promotion (Figure 3E). Moreover, overexpressed CNN2 also impaired NEAT1 knockdown-induced inhibition in migration and invasion of HepG2 and Huh7 cells (Figure 3F and G). These results indicated NEAT1 promoted HCC progression by regulating CNN2 expression.

NEAT1 Silence Mediates The Inhibition On HCC Progression By Directly Sponging miR-296-5p

To explore how CNN2 participated in NEAT1-mediated regulation on HCC development. The starbase v2.0 program was used to search the potential miRNA targets of NEAT1,

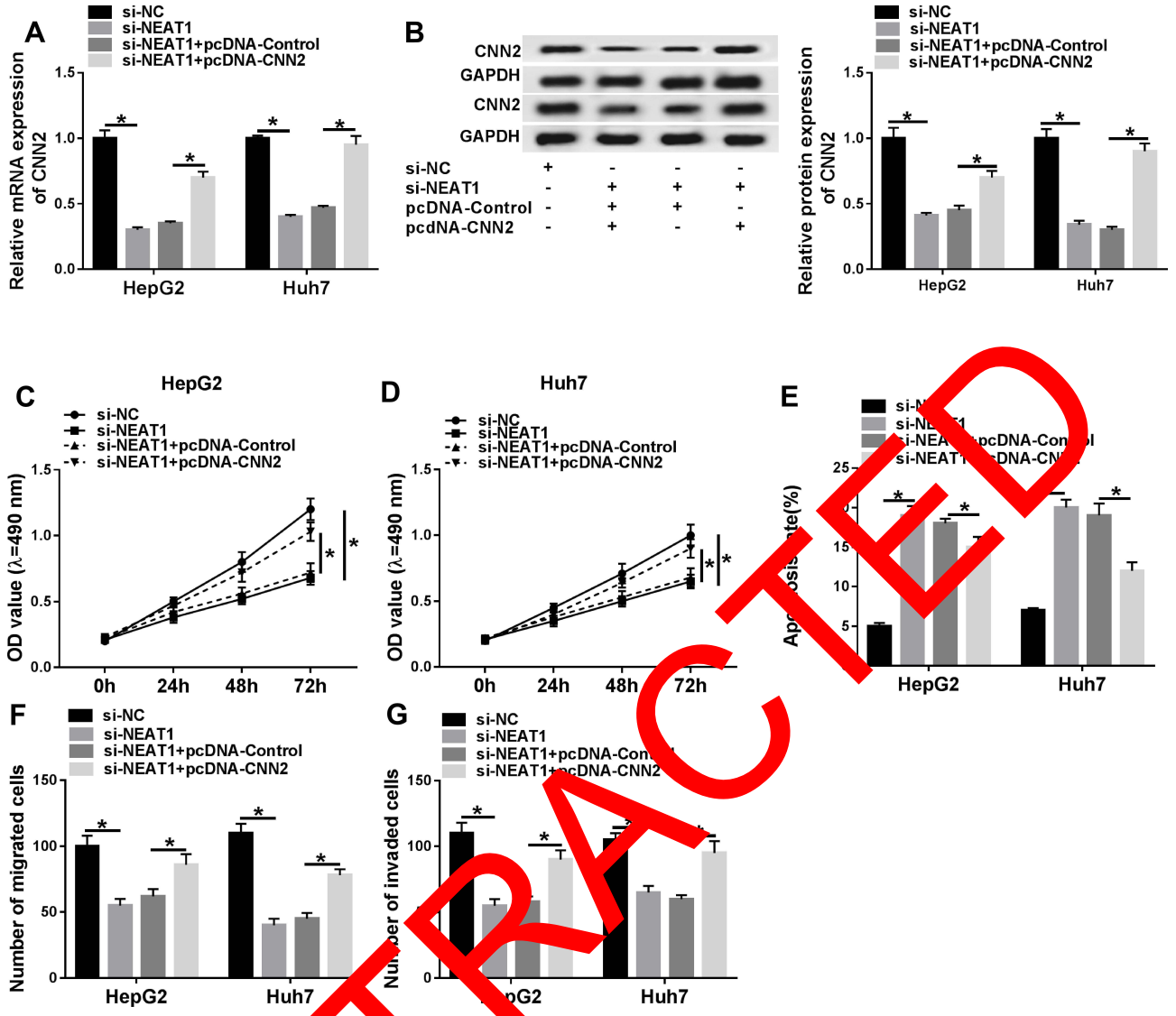

Figure 3 NEAT1 silence suppresses HCC progression by regulating CNN2 expression. HepG2 and Huh7 cells were transfected with si-NC, si-NEAT1, si-NEAT1 + pcDNA-Control, si-NEAT1 + pcDNA-CNN2. (**A, B**) The expression of CNN2 was detected using qRT-PCR or Western blot. (**C, D**) MTT assay was performed to determine cell proliferation. (**E**) The apoptotic cells were measured using flow cytometry. (**F, G**) Transwell assay was applied to examine cell migration and invasion abilities. *P<0.05.

and miR-296-5p were found to contain the binding sites of NEAT1 (Figure 4A). Subsequently, luciferase reporter assay was performed to confirm this predictionand results showed that overexpressed miR-296-5p obviously reduced the luciferase activity of WT-NEAT1 reporter but not MUT-NEAT1 reporter in 293T cells (Figure 4B), and qRT-PCR revealed that down-regulated NEAT1 promoted miR-296-5p expression in HepG2 and Huh7 cells (Figure 4C), indicating that NEAT1 interacted with miR-296-5p and negatively regulated miR-296-5p expression. Furthermore, RIP assay using anti-Ago2 antibody also confirm that NEAT1 interacted withmiR-296-5p in HepG2 and Huh7 cells (Figure 4D and E).

Taken together, we hypothesized miR-296-5p might implicate in NEAT1-mediated regulation on HCC development. To verify this hypothesis, we first detected the level of miR-296-5p and found miR-296-5p was down-regulated in HCC tissues and cell lines (Figure 4F and G), indicating the regulatory roles of miR-296-5p in HCC. Next, miR-296-5p expression was inhibited via the transfection of miR-296-5p inhibitor, anda significant reduction of miR-296-5p was observed (Figure 4H). After that, the HepG2 and Huh7 cells were respectively transfected with si-NC, si-NEAT1, si-NEAT1 + inhibitor NC or si-NEAT1 + miR-296-5p inhibitor to conduct rescue experiments and results showed inhibition

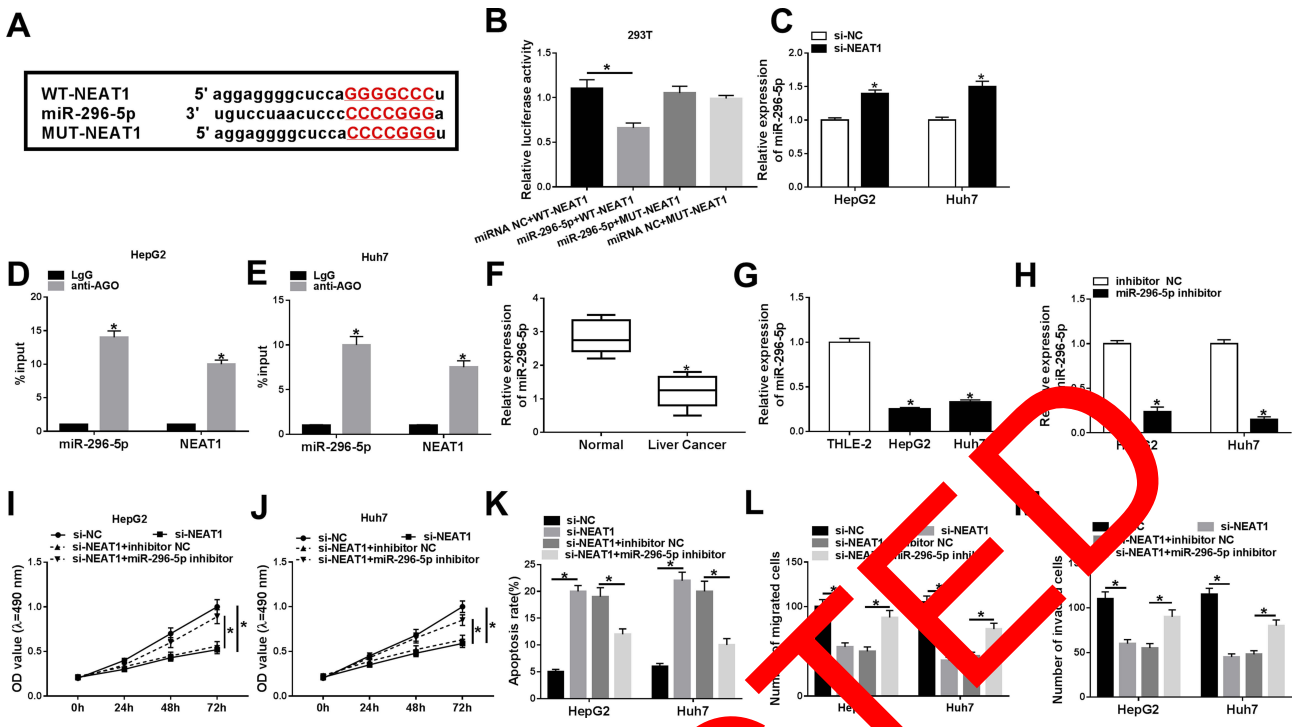

Figure 4 NEAT1 silence mediates inhibition on HCC progression by directly sponging miR-296-5p. (**A**) The binding condition between NEAT1 and miR-296-5p were predicted, and the red bases represented the putative binding sites. (**B**) The Luciferase activity was analyzed in 293T cells co-transfected with WT-NEAT1 or MUT-NEAT1 and miRNA NC, miR-296-5p mimic. (**C**) The expression of miR-296-5p in HepG2 and Huh7 cells transfected with si-NC or si-NEAT1 was measured using qRT-PCR. (**D, E**) The RIP assay was used to determine the interaction between miR-296-5p and NEAT1 in HepG2 and Huh7 cells. (**F**) The expression of miR-296-5p in HCC tissues and normal tissues was detected using qRT-PCR. (**G**) The expression of miR-296-5p in normal human hepatocyte THLE-2 and HCC cell lines (HepG2 and Huh7) was measured by qRT-PCR. (**H**) The expression of miR-296-5p was detected in HepG2 and Huh7 cells after transfection with inhibitor NC or miR-296-5p inhibitor using qRT-PCR. (**I, J**) Cell proliferation was analyzed by MTT assay. (**K**) Flow cytometry was performed to measure apoptotic cells. (**L, M**) The number of migration and invasion cells was analyzed by transwell assay. *P<0.05.

of miR-296-5pmarkedlyreversed NEAT1 deletion-mediated suppression of proliferation (Figure 4I and J), migration (Figure 4L), invasion (Figure 4M) and promotion of apoptosis (Figure 4K) in HepG2 and Huh7 cells. In all, these results implied that NEAT1 silence repressed HCC progression by directly targeting miR-296-5p.

Overexpressed miR-296-5p Suppresses HCC Progression By Directly Targeting CNN2

Using the bioinformatics tools StarBase v2.0 program, CNN2 was found to contain the wild-type or mutant putative binding sites for miR-296-5p (Figure 5A). Afterwards, we constructed luciferase reporters containing the miR-296-5p binding sites on the CNN2 3′UTR, and then observed miR-296-5p overexpression reduced the luciferase activities of the WT-CNN2 reporter vector, but there was no notable change in MUT-CNN2 reporter after overexpression of miR-296-5p in HepG2 and Huh7 cells (Figure 5B). Additionally, we also found miR-296-5p up-regulation reduced the expression of CNN2 at mRNA and proteinlevel in HepG2 and Huh7 cells (Figure 5C and D), indicating the direct interaction between miR-296-5p and CNN2. In the meanwhile, the interaction between miR-296-5p and CNN2 also was confirmed by using RIP assay because of the enrichment of miR-296-5p and CNN2after Ago2 RIP (Figure 5E and F).

Based on the relationship between miR-296-5p and CNN2, we further wanted to know whether miR-296-5p/CNN2 wasresponsible for the progression of HCC. Subsequently, HepG2 and Huh7 cells were transfected with miRNA NC, miR-296-5p mimic, miR-296-5p mimic + pcDNA-Control or miR-296-5p mimic + pcDNA-CNN2, respectively. Then we discovered overexpressed miR-296-5p repressed cell proliferation, while this inhibition could be reversed by CNN2 up-regulation (Figure 5G and H). Cell apoptosis rate was significantly increased when miR-296-5p was increased, whereas CNN2 overexpression induced an opposite result and weakened miR-296-5p mimic-induced cell apoptosis promotion (Figure 5I). Moreover, CNN2 overexpression also partially overturnedmiR-296-5p mimic

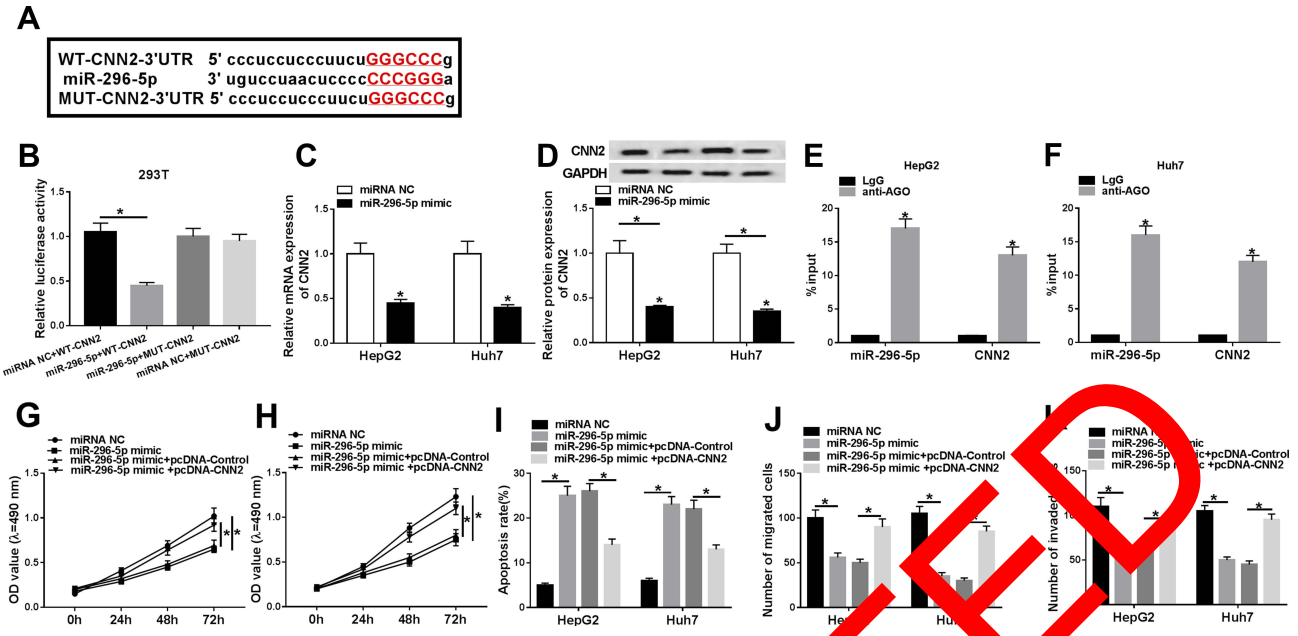

Figure 5 Overexpressed miR-296-5p suppresses HCC progression by directly targeting CNN2. (**A**) The binding condition between CNN2 and miR-296-5p were predicted, and the red bases were the putative binding sites. (**B**) The Luciferase activity was analyzed in 293T cells co-transfected with WT-CNN2 or MUT-CNN2 and miRNA NC, miR-296-5p mimic. (**C, D**) The expression of CNN2 in HepG2 and Huh7 cells transfected with miRNA NC or miR-296-5p mimic was measured using qRT-PCR or Western blot. (**E, F**) The RIP assay was used to determine the interaction between miR-296-5p and CNN2 in HepG2 and Huh7 cells. (**G, H**) MTT assay was utilized to determine cell proliferation. (**I**) The apoptotic cells were examined using flow cytometry. (**J, K**) Transwell assay was performed to determine cell migration and invasion. *P<0.05.

transfection-induced suppression of cell migration and invasion in HCC (Fig. J, K). These data exhibited that CNN2 restoration could overturn miR-296-5p overexpression-induced inhibition on HCC progression.

NEAT1 Indirectly Regulates CNN2 Expression By Competing To miR-296-5p In HCC Cells

To investigate the regulatory relationship among NEAT1, miR-296-5p and CNN2 in HCC cells, HepG2 and Huh7 cells were transfected with si-NC, si-NEAT1, si-NEAT1 + inhibitor NC or si-NEAT1 + miR-296-5p inhibitor. Immediately, we observed that the expression of CNN2 at mRNA and protein level in HepG2 and Huh7 cells was notably inhibited by the silence of NEAT1, but was restored by the inhibition of miR-296-5p (Figure 6A and B), indicating NEAT1 could regulate CNN2 expression by competing to miR-296-5p in HCC cells.

Knockdown Of NEAT1 Inhibits Tumor Growth Of HCC In Vivo

To further elucidate the hepatocarcinogenesis role of NEAT1 in vivo, we established xenograft models using Huh7 cells stably transfected with sh-NEAT1 or sh-NC. After 7 days following the inoculation, we found compared with these in the sh-NC group, tumor volume and

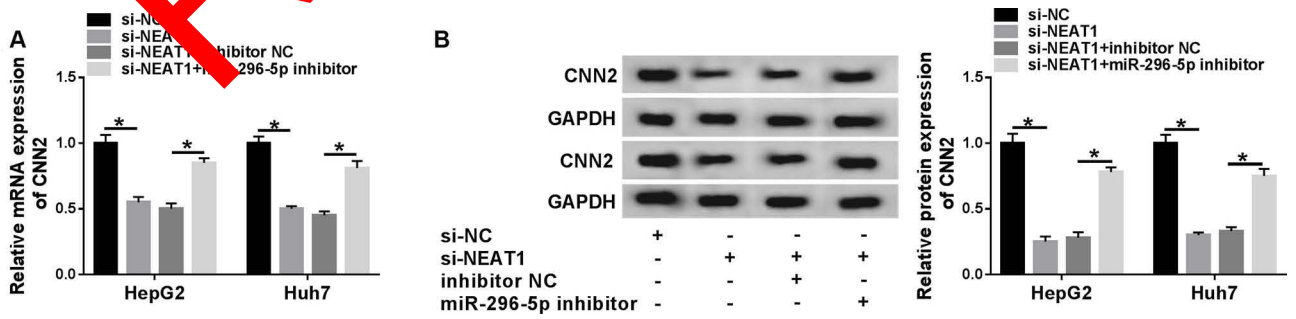

Figure 6 NEAT1 indirectly regulates CNN2 expression by competing for the binding of miR-296-5p in HCC cells. (**A**–**B**) The expression of CNN2 was detected in HepG2 and Huh7 cells transfected with si-NC, si-NEAT1, si-NEAT1 + inhibitor NCor si-NEAT1 + miR-296-5p inhibitor using qRT-PCR or Western blot analysis. *P<0.05.

weight were greatly repressed in the sh-NEAT1 group (Figure 7A and B). Afterwards, qRT-PCR analysis indicated the inhibition of NEAT1 significantly decreased the levels of NEAT1 and CNN2 but increased the expression of miR-296-5p in sh-NEAT1 group compared with that in sh-NC group (Figure 7C–F). Therefore, we demonstrated that NEAT1 silence might inhibit tumor growth by regulating miR-296-5p and CNN2 expression in vivo.

Discussion

Emerging researches have demonstrated that lncRNAs participate in a variety of biological processes and potentially regulate tumor development.[22] LncRNAs may be valuable candidates for the therapyof numerous diseases. Among these lncRNAs, NEAT1 has been reported to be a major driver on the development of many kinds of cancers, such as breast cancer,[23] colorectal cancer,[24] pancreatic cancer,[25] ovarian cancer,[26] non-small cell lung cancer (NSCLC)[27] and so on. Besides that, recent studies also indicated the regulation of NEAT1 in HCC progression. In the current study, a significantly high expression of NEAT1 was observed in HCC tissues and cell lines, indicating the potential involvement of NEAT1 in HCC progression. Immediately, functional experiments were conducted and results suggested NEAT1 deletion obviously inhibited cell proliferation, metastasis but stimulated cell apoptosis in vitro. Additionally, NEAT1 deletion also suppressed tumor growth in vivo. Hence, we validated that NEAT1 silence could repress HCC progression in vivo and in vitro.

Based on the ceRNA hypothesis, lncRNAs may act as competing endogenous RNAs (ceRNAs) to compete with other genes for miRNAs binding, thereby inversely regulating miRNA-mediated inhibition of the target mRNAs.[28] The lncRNA-miRNA-mRNA function network has been indicated to exert important effects on various biological processes, which may involve in the development of many diseases, including cancers.[29,30] Until now, it has been documented that NEAT1 is closely related to a variety of cancers through serving as a ceRNA. For example, NEAT1 promoted breast cancer growth by miR-101 dependent EZH2 regulation.[31] NEAT1 functioned as a ceRNA for miR-194 to up-regulate ZEB1 expression, thereby contributing to paclitaxel resistance in ovarian cancer cells.[32]

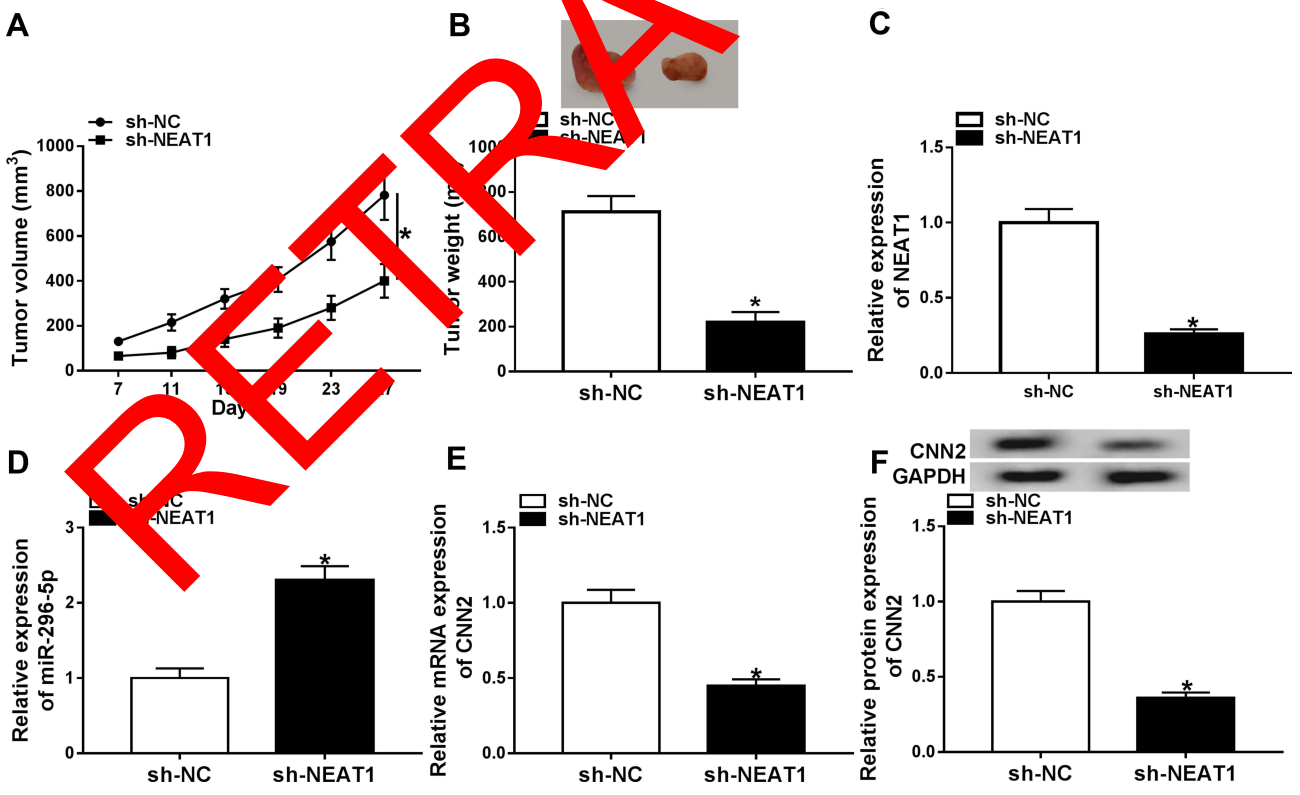

Figure 7 Knockdown of NEAT1 inhibits tumor growth of HCC in vivo. Huh7 cells stably transfected with sh-NEAT1 was used to establish xenograft models. (**A**) Tumor volume was calculated every week. (**B**) Mice were killed and tumor weight was analyzed in each group. (**C**–**F**) The levels of NEAT1, miR-296-5p and CNN2 were measured in two groups by qRT-PCR or Western blot. *P<0.05.

Thus, we hypothesized NEAT1 might implicate in this network by acting as a sponge for miRNAs to regulate the expression of targeted genes in HCC.

In this study, NEAT1 was predicted and confirmed to be a sponge of miR-296-5p and negatively modulated miR-296-5p expression in HCC cells. MiR-296-5p has been documented to function as a tumor suppressor to regulate cell progression by interacting with targeted genes or downstream signaling pathway in many types of cancers. For instances, miR-296-5p inhibited cell progression by directly targeting PLK1 in NSCLC.[33] MiR-296-5p functioned as a tumor suppressor to repress cell metastasis of esophageal squamous cell carcinoma via negatively regulating STAT3 signaling.[34] Thus, we further explored the potential targets of miR-296-5p in HCC and results indicated that miR-296-5p directly targeted CNN2 and suppressed CNN2 expression in HCC cells. After that, co-expression analysis was performed to investigate the regulatory relationship among NEAT1, miR-296-5p and CNN2, and we demonstrated that NEAT1 indirectly regulated CNN2 expression by serving as a sponge for miR-296-5p in vitro and in vivo. Thus, the NEAT1/miR-296-5p/CNN2 regulatory network was identified in HCC cells. Afterwards, rescue experiments were conducted and we found the inhibitory effects mediated by NEAT1 silence on cell progression of HCC could be reversed by CNN2 restoration or miR-296-5p inhibition. In addition, CNN2 restoration also dramatically counteracted the inhibition on HCC cell progression mediated by miR-296-5p overexpression.

Conclusion

In sum up, we observed that NEAT1 deletion or miR-296-5p overexpression could inhibit cell proliferation and metastasis. Mechanistic analysis further demonstrated the involvement of the NEAT1/miR-296-5p/CNN2 regulatory network in the regulation of HCC development, which may shed new light on the regulatory mechanisms and provide a promising therapeutic approach for HCC.

Disclosure

The authors report no conflicts of interest in this work.

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