NSUN5 promotes progression and predicts poor prognosis in hepatocellular carcinoma

XIAO-WEN ZHANG[1*], LU-YI WU[1*], HUI-RONG LIU[1*], YAN HUANG[1], QIN QI[1], RUI ZHONG[1], LU ZHU[1], CHUN-FANG GAO[1,2], LIN ZHOU[3], JIAN YU[4] and HUAN-GAN WU[1]

[1]Department of Acupuncture and Moxibustion, Yueyang Hospital of Integrated Traditional Chinese and Western Medicine, Shanghai University of Traditional Chinese Medicine, Shanghai 200437; [2]Department of Laboratory Medicine, Eastern Hepatobiliary Surgery Hospital, Naval Medical University, Shanghai 200438; [3]Department of Laboratory Medicine, Changzheng Hospital, Naval Medical University, Shanghai 200003; [4]The Third Department of Hepatic Surgery, Eastern Hepatobiliary Surgery Hospital, Naval Medical University, Shanghai 200438, P.R. China

Received June 10, 2022; Accepted September 16, 2022

DOI: 10.3892/ol.2022.13559

Abstract. The 5-methylcytosine (m5C) RNA methyltransferase NOP2/Sun RNA methyltransferase 5 (NSUN5) has been reported to serve important roles in numerous diseases. However, the functions and clinical significance of NSUN5 in hepatocellular carcinoma (HCC) remain unknown. Clinical information and NSUN5 mRNA sequencing data for 374 patients with HCC were downloaded from The Cancer Genome Atlas (TCGA) database, and NSUN5 mRNA and protein expression levels in 120 patients with HCC (present study cohorts) were assessed using reverse transcription-quantitative PCR, western blotting or immunohistochemistry. The association between NSUN5 mRNA and protein expression levels and the clinical characteristics (or prognosis) of patients with HCC was analyzed using the χ^2 or log-rank test. The functions of NSUN5 in HCC were evaluated using *in vitro* and *in vivo* experiments, and the mechanism by which NSUN5 affected the progression of HCC was assessed using bioinformatics analysis using LinkedOmics. NSUN5 was significantly upregulated and predicted poor prognosis in HCC according to data from both TCGA database and present study cohorts. NSUN5 significantly promoted HCC proliferation and migration *in vitro* and significantly induced HCC tumor growth *in vivo*. Bioinformatics analysis demonstrated that NSUN5 was positively correlated with genes associated with translation in HCC. It was hypothesized that overexpression of NSUN5 strengthened ribosome functions and global protein translation, which may promote the proliferation and migration of HCC. In conclusion, NSUN5 may promote the progression of HCC by enhancing translation, thus making it a potential target for HCC treatment.

Correspondence to: Professor Huan-Gan Wu, Department of Acupuncture and Moxibustion, Yueyang Hospital of Integrated Traditional Chinese and Western Medicine, Shanghai University of Traditional Chinese Medicine, 110 Ganhe Road, Shanghai 200437, P.R. China
E-mail: wuhuangan@shutcm.edu.cn

Dr Jian Yu, The Third Department of Hepatic Surgery, Eastern Hepatobiliary Surgery Hospital, Naval Medical University, 225 Changhai Road, Shanghai 200438, P.R. China
E-mail: 1274432278@qq.com

*Contributed equally

Key words: NSUN5, m5C, hepatocellular carcinoma, RNA methyltransferase

Introduction

Hepatocellular carcinoma (HCC) is a major health problem, which represents the sixth most commonly diagnosed cancer and third most common cause of cancer death worldwide (1). The mortality from HCC is primarily due to its metastasis, complex pathogenesis and postsurgical recurrence (2). Early HCC onset is usually undetected and most patients are in the late stage at diagnosis, which is also an important reason for the poor long-term prognosis (2). Molecularly targeted agents and immune checkpoint inhibitors have been developed; however, the therapeutic effect of such treatments on HCC is still unsatisfactory (3). Drug resistance and limited therapeutic targets are problems to be solved. Therefore, it is critical to study the mechanisms underlying the development and progression of HCC to develop novel therapeutics that may improve the overall survival of patients with HCC across its stages.

Post-transcriptional RNA modifications are crucial regulators of gene expression and are involved in the pathogenesis of numerous diseases, including different types of cancer (4). Notably, 5-methylcytosine (m5C) is an abundant and conserved modification in numerous types of RNA, including transfer RNA, mRNA, ribosomal (r)RNA and other types of noncoding RNA (4). The roles of the RNA m5C modification and its modifying enzymes, defined as writers (proteins upregulating modification level), readers (proteins recognizing modification) and erasers (proteins downregulating modification level), in gene regulation and chromatin organization remain largely unclear (5). NOP2/Sun RNA methyltransferase

5 (NSUN5) is one of the eight evolutionarily conserved m5C RNA methylases (NSUN1-7 and DNA methyltransferase 2) that have been recognized as 'writers' (4,6,7).

Previous studies have reported the role of NSUN5 in human cancer. For example, DNA methylation-associated epigenetic silencing of NSUN5 has been reported to be a hallmark of the long-term survival of patients with glioma (8). In colorectal cancer, NSUN5 has been reported to act as a promotor of tumor development via cell cycle regulation (9). However, to the best of our knowledge, the role of NSUN5 in HCC remains unknown.

In the present study, the clinical significance of NSUN5 expression in patients with HCC was evaluated using The Cancer Genome Atlas (TCGA) database. In addition, the role of NSUN5 in HCC was assessed using *in vitro* and *in vivo* experiments to evaluate whether NSUN5 represented a novel therapeutic target for HCC.

Materials and methods

Patients and samples. Written informed consent was obtained from patients and approval for the present study was obtained from the Ethics Committee of The Eastern Hepatobiliary Surgery Hospital (Shanghai, China; approval no. EHBHKY2 018-02-014). A total of 120 paired HCC and corresponding adjacent noncancerous liver (ANL) tissues were collected from patients undergoing hepatectomy (without preoperative treatment) at The Eastern Hepatobiliary Surgery Hospital. Detailed clinical characteristics are presented in Table SI. Among the samples, 40 pairs (Cohort 1) were collected from April 2021 to July 2021 and assessed using reverse transcription-quantitative (RT-q)PCR and western blotting, and the other 80 pairs (Cohort 2) were collected from February 2014 to November 2015- and assessed using immunohistochemistry (IHC).

RT-qPCR. Total RNA was isolated from human HCC tissues, ANL tissues or HCC cell lines using TRIzol® reagent (cat. no. 1559602. Invitrogen; Thermo Fisher Scientific, Inc.). cDNA was synthesized (15 min at 37˚C; 5 sec at 85˚C and 4˚C) using a cDNA Synthesis Kit (cat. no. RR036A; Takara Biotechnology Co., Ltd.) and qPCR was then performed using a StepOnePlus™ Real-Time PCR System (Applied Biosystems; Thermo Fisher Scientific, Inc.) and TB Green Fast qPCR Mix (cat. no. RR430A; Takara Biotechnology Co., Ltd.). The quantification of NSUN5 was performed using the $2^{-\Delta\Delta Cq}$ method (10) with normalization to β-actin (ACTB). The thermocycling conditions were as follows: Holding stage (95˚C, 3 min), cycling stage (35 cycles; 10 sec at 95˚C, 15 sec at 60˚C and 20 sec at 72˚C), melt curve stage (15 sec at 95˚C, 1 min at 60˚C and 15 sec at 95˚C). The primer sequences used were as follows: NSUN5 forward (F), 5'-CGCTACCATGAGGTC CACTAC-3' and reverse (R), 5'-GCATCTCGCACCACGTCT T-3'; and ACTB F, 5'-CCACCATGTACCCTGGCATTG-3' and R, 5'-TCATCTTGTTTTCTGCGCAAGTTA-3'.

Western blotting. Whole-cell lysates were prepared from HCC tissues and cells (Hep3B and SNU387) using RIPA solution (Beyotime Institute of Biotechnology). The concentration of protein in the lysates was determined by BCA protein assay kit (cat. no. P0012; Beyotime Institute of Biotechnology) The lysates (50 μg protein per lane) were then separated by SDS-PAGE on 4-20% gels (SurePAGE™; Bis-Tris; 10x8; 4-20%; gradient, 12 wells; cat. no. M00656; GenScript Biotechnology Co., Ltd.), transferred to a PVDF membrane and blocked using 5% nonfat milk for 1 h at room temperature (~25˚C). Primary antibodies were added after blocking and the membranes were incubated overnight at 4˚C. The next day, the membranes were incubated for 2 h with the appropriate secondary antibody at room temperature. Finally, the protein bands were visualized using enhanced chemiluminescent solution (Beyotime Institute of Biotechnology) and detected using a chemiluminescence system (Bio-Rad Laboratories, Inc.). The primary antibodies used in the present study were NSUN5 (1:1,000; cat. no, 15449-1-AP; Proteintech Group, Inc.) and ACTB (1:5,000; cat. no, 66009-1-Ig; Proteintech Group, Inc.). The secondary antibodies used were goat anti-mouse IgG H&L (HRP) (1:2,000; cat. no. ab6789; Abcam) and goat anti-rabbit IgG H&L (HRP) (1:2,000; cat. no. ab6721; Abcam). Image J (version 1.8.0; Bharti Airtel, Ltd) was used to semi-quantify western blots.

IHC and tissue microarray (TMA) analysis. A TMA was constructed as previously described (11). Briefly, it consisted of collection and selection of tissue blocks (formalin-fixed paraffin-embedded HCC and ANL tissues), design and organization of TMA, punching of TMA and technical cutting of TMA (sections should be ≤5 μm). IHC was performed on the TMA using a two-step immune-peroxidase technique (12) (https://www.abcam.com/ps/pdf/protocols/ihc_p.pdf). Briefly, it consisted of deparaffinization (xylene and ethanol), antigen retrieval (vegetable steamer, 100˚C) and immunohistochemical staining (primary antibody incubated overnight at 4˚C; second antibody incubated for 1 h at room temperature; chromogen, 10 min at room temperature). The primary antibody used was NSUN5 (1:100; cat. no, 15449-1-AP; Proteintech Group, Inc.). The blocking reagent was 0.3% H_2O_2 in TBS (incubated for 15 min at room temperature). The secondary antibody used was goat anti-rabbit IgG H&L (HRP) (1:1,000; cat. no. ab6721; Abcam). TMA scanning was performed using PANNORAMIC DESK II DW scanner (light microscope; 3DHISTECH, Ltd.). IHC scores were assessed for the IHC stains of NSUN5 (13) by three separate observers who had no knowledge of the patient characteristics. The intensity of specific staining was characterized as follows: Not present, 0; weak but detectable above control, 1+; distinct, 2+; and very strong, 3+. For each observed tissue component, a summary value referred to as the H-Score was calculated. This consisted of a sum of the percentages of positively stained cells multiplied by a weighted intensity of staining; H-Score=$\sum$ Pi (i + 1), where 'Pi' was the percentage of stained cells in each intensity category and 'i' was the intensity.

Cell culture. The HCC Hep3B and SNU387 cell lines were purchased from The Cell Bank of Type Culture Collection of The Chinese Academy of Sciences and were authenticated using short tandem repeat profiling. Cells were grown in Dulbecco's modified Eagle's medium (DMEM; Gibco; Thermo Fisher Scientific, Inc.) supplemented with 10% fetal bovine serum (FBS; Gibco; Thermo Fisher Scientific, Inc.) and maintained in a humidified 37˚C incubator containing 5%

CO_2. Using the sequence of NSUN5 mRNA (NM_148956) acquired from the Nucleotide database of National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/ nuccore/NM_148956) and a lentiviral vector (GV492; Ubi-MCS-3FLAG-CBh-gcGFP-IRES-puromycin; Shanghai GeneChem Co., Ltd.), NSUN5 was overexpressed in Hep3B and SNU387 cell lines using the methods previously described (14,15). The viral titer of NSUN5-overexpression (NSUN5-oe) lentivirus and negative control (NC) lentivirus was $4x10^8$ and $3x10^8$ TU/ml, respectively. A total of 48 h after lentivirus transduction, puromycin (2 μg/ml) was added into the culture medium to obtain stably transduced cells. After ~10 days of puromycin selection, the stably transduced cells were collected and subsequent experiments were performed.

In vitro cell behavior assays. For cell proliferation, a Cell Counting Kit-8 (CCK-8) assay (Dojindo Molecular Technologies, Inc.) was performed according to the manufacturer's protocol. Briefly, ~$2x10^3$ cells/well were seeded on a 96-well plate for 24 h and 10 μl CCK-8 solution was added to wells at 0, 1, 2 , 3 or 4 days. The 96-well plate was incubated at 37˚C for 2 h after each addition of CCK-8 solution before measuring the absorbance at 450 nm using a microplate reader (Bio-Rad Laboratories, Inc.).

Cell migration was evaluated using a 12-μm pore polycarbonate membrane Transwell chambers (MilliporeSigma). Cells (10^5) were seeded into the upper Transwell chamber in DEEM (cat no. 11995-065; Gibco; Thermo Fisher Scientific) without FBS and 500 μl DMEM containing 10% FBS was added into the lower chamber. The 24-well plate with Transwell chambers was incubated for 48 h at 37˚C. After incubation for 48 h, the cells were stained using 0.1% crystal violet for 30 min at room temperature (~25˚C). Finally, the upper chambers were observed using a light microscope (Olympus Corporation). These experiments were independently repeated at least three times.

Animal studies. The animal experiments performed in the present study conformed to the guidelines of Animal Research: Reporting of *In Vivo* Experiments (http://www.nc3rs.org.uk/arrive-guidelines) and were approved by the Institutional Animal Care and Use Committee of Shanghai University of Traditional Chinese (Shanghai, China) (approval no. PZ SHUTCM210926007). BALB/c male nude mice (16 mice; age, 5 weeks; weight, ~20 g) used in the present study were purchased from the Laboratory Animal Resources, Chinese Academy of Sciences. All mice were housed in laminar flow cabinets under specific pathogen-free conditions at room temperature (humidity 40-60%) with a 12-h light/dark cycle, and *ad libitum* access to food and water.

The subcutaneous tumor xenograft experiment was performed as previously described (16). A total of eight BALB/C male nude mice were used in the present study. Briefly, for each mouse, NSUN5-oe SNU387 cells ($1.5x10^6$ cells in 150 μl 0.9% sodium chloride) were injected subcutaneously into the armpit of the right forelimb (site approved by the ethics committee) and the same amount of NC SNU387 cells were injected subcutaneously into the armpit of the left forelimb. Tumor development was assessed weekly using a caliper and the tumor volume was calculated as follows: Larger diameter x (smaller diameter)^2/2. The humane endpoints of the xenograft experiment conformed to the Guidelines for the Welfare and Use of Animals in Cancer Research (17). Briefly, immediate humane termination was required when statistically significant effects could be demonstrated, when the mean diameter of the xenograft tumor exceeded ~1.2 cm or when the mice displayed severe symptoms (persistent hypothermia, hind-limb paralysis or weakness). In the present study, the mice were sacrificed by cervical dislocation 4 weeks after implantation, when NSUN5 showed statistically significant growth promotion effects.

LinkedOmics. The 'LinkFinder' module in LinkedOmics (version 4) (18) (http://linkedomics.org/login.php) was used to assess NSUN5-correlated genes in HCC. The 'RNA-seq' platform was chosen for both the 'Search Dataset' and 'Target Dataset', and the 'Spearman Correlation test' was selected as the statistical method. The LinkFinder module of LinkedOmics was used to generate the volcano plots.

NSUN5-correlated genes ('Association Result') were then used to perform enrichment analyses in the 'Link Interpreter-GSEA (Gene Set Enrichment Analysis)' module of LinkedOmics. Biological process, cellular component, molecular function and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways analyses were performed individually. 'Rank Criteria' was chosen as the 'Statistic' ('Spearman correlation' in this situation), 'Minimum Number of Genes' was assigned a value of 3 and 'Simulations' was assigned a value of 500.

TCGA. The URL link for TCGA: https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga. To evaluate the relationship between the expression of NSUN5 and the clinical characteristics of patients with HCC, the clinical information of 374 patients with HCC was downloaded from TCGA liver HCC database (https://portal.gdc.cancer.gov/) (Table SII). NSUN5 mRNA sequencing data for these 374 HCC tissues and 50 ANL tissues (paired with 50 of the 374 HCC tissues) were also downloaded (19) (https://portal.gdc.cancer.gov/) (columns C and D, Table SII).

Statistical analysis. Statistical analyses were performed using SPSS software (version 22.0; IBM, Corp.). Comparisons among continuous variables were performed using paired Student's t-test, unpaired Student's t-test, Mann-Whitney U test or Wilcoxon signed-rank test, whereas comparisons among categorical variables were performed using the Pearson's χ^2 test or Fisher's exact test. The survival curves were generated using the Kaplan-Meier method, and the differences were assessed using a log-rank test. $P<0.05$ (two-tailed) was considered to indicate a statistically significant difference.

Results

NSUN5 is upregulated and predicts poor prognosis in HCC according to TCGA database. The present study demonstrated that the mRNA expression levels of NSUN5 were significantly higher in the 374 HCC tissues compared with those in the 50 ANL tissues (Fig. 1A; $P<0.001$). The mRNA expression levels of NSUN5 in 50 HCC tissues were also significantly higher than those in 50 paired ANL tissues (Fig. 1B; $P<0.001$).

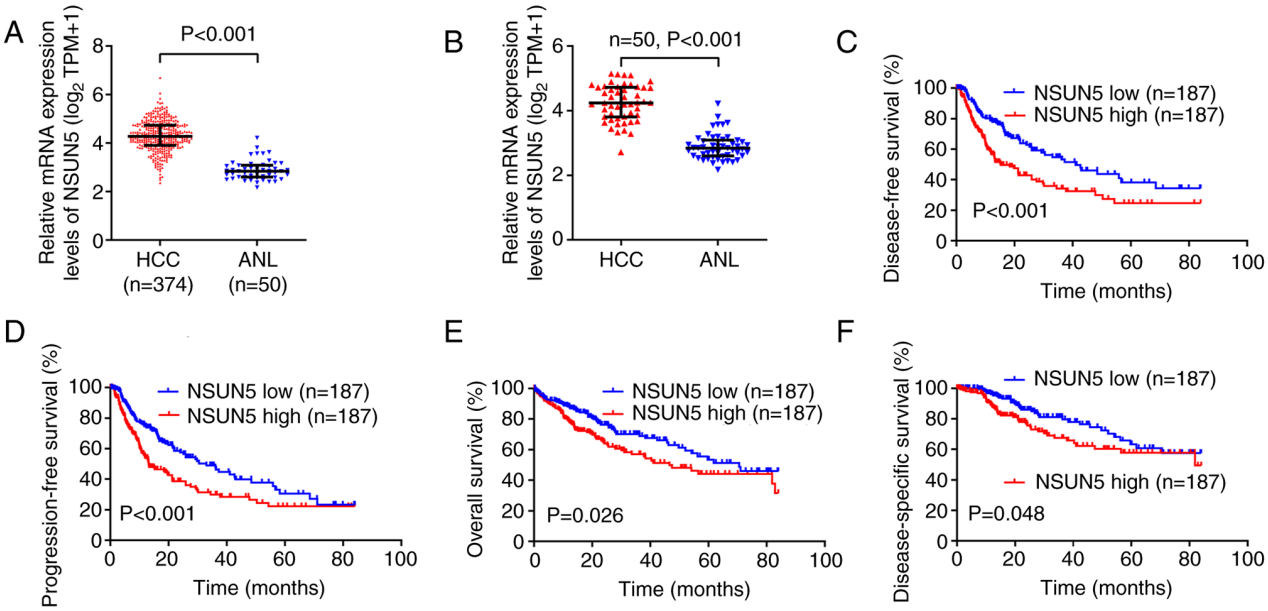

Figure 1. Upregulated NSUN5 predicts poor prognosis in HCC according to The Cancer Genome Atlas database. (A) mRNA expression levels of NSUN5 in 374 HCC and 50 ANL tissues. Mann-Whitney U test was used for statistical comparison. (B) mRNA expression levels of NSUN5 in 50 paired HCC and ANL tissues. The Wilcoxon signed-rank test was used for statistical comparison. Kaplan-Meier survival curves demonstrated the association between NSUN5 expression and (C) disease-free survival, (D) progression-free survival, (E) overall survival and (F) disease-specific survival. The log-rank test was used for statistical comparison. ANL, adjacent noncancerous liver; HCC, hepatocellular carcinoma; NSUN5, NOP2/Sun RNA methyltransferase 5; TPM, transcript per million.

The 374 patients with HCC were divided into NSUN5-high and NSUN5-low groups according to the median mRNA expression (transcript per million, 18.497) levels of NSUN5 in the 374 HCC tissues. The longest follow-up time assessed in the present study was 7 years (84 months). Kaplan-Meier survival curves demonstrated that higher NSUN5 mRNA expression levels in HCC were associated with significantly lower disease-free survival (Fig. 1C; P<0.001), lower progression-free survival (Fig. 1D; P<0.001), lower overall survival (Fig. 1E; P=0.026) and lower disease-specific survival (Fig. 1F; P=0.048) compared with the NSUN5-low group.

Furthermore, analysis of the association between NSUN5 expression in HCC tissues and the clinical characteristics of patients with HCC demonstrated that higher NSUN5 mRNA expression levels were significantly positively associated with lower weight (P=0.003), lower body mass index (P=0.001), higher serum α-fetoprotein levels (P=0.003), worse tumor node metastasis (TNM) stage (20) (P=0.043), worse histological grade (P=0.004) and vascular invasion (P=0.002) compared with the NSUN5-low group (Table I). These results indicated that NSUN5 may be associated with HCC tumor growth and migration.

Collectively, the bioinformatics analysis of TCGA data demonstrated that NSUN5 was upregulated, associated with worse clinical characteristics and predicted poor prognosis in HCC.

NSUN5 is upregulated and predicts poor prognosis in HCC in cohorts of the present study. To further evaluate the relationship between the expression of NSUN5 and the clinical characteristics of patients with HCC, the mRNA and protein expression levels of NSUN5 were evaluated in the cohorts of the present study (patients with HCC from The Eastern Hepatobiliary Surgery Hospital). RT-qPCR performed in 40 paired HCC and ANL tissues (Cohort 1) demonstrated that the mRNA expression levels of NSUN5 were significantly upregulated in HCC tissues compared with those in the ANL tissues (Fig. 2A; P<0.001). Western blotting in 12 paired HCC and ANL tissues randomly selected from Cohort 1 demonstrated that the protein expression levels of NSUN5 were significantly upregulated in HCC tissues compared with those in the ANL tissues (Fig. 2B and C; P=0.003). Moreover, IHC in Cohort 2 demonstrated that NSUN5 was mainly expressed in the nucleus and indicated that the protein expression levels [indicated by the IHC score (21)] of NSUN5 in 80 HCC tissues was significantly higher than those in the paired ANL tissues (Fig. 2D; P<0.001). The 80 patients with HCC from Cohort 2 were then divided into NSUN5-high and NSUN5-low groups according to the median IHC score (159.029) of NSUN5. Kaplan-Meier survival curves demonstrated that higher NSUN5 expression in HCC was associated with significantly lower recurrence-free survival (Fig. 2E; P=0.002) and lower overall survival (Fig. 2F; P<0.001) compared with the NSUN5-low group.

Furthermore, analysis of the association between the expression of NSUN5 in HCC tissues and the clinical characteristics of patients with HCC demonstrated that higher NSUN5 protein expression levels were positively associated with multiple tumor number (P<0.001), large tumor size (P=0.003), presence of microvascular invasion (P=0.001), worse TNM stage (P<0.001) and worse Barcelona Clinic Liver Cancer stage (22) (P=0.001) compared with the NSUN5-low group (Table II).

In summary, NSUN5 mRNA and protein expression levels were significantly upregulated in HCC, associated with worse clinical characteristics and predictive of poor prognosis in the present study cohorts.

Table I. Clinical characteristics of 374 patients with hepatocellular carcinoma from The Cancer Genome Atlas according to the mRNA expression levels of NSUN5.

Characteristic	NSUN5		P-value
	Low	High	
n	187	187	
Median age, years (IQR)	61 (52-68)	61 (51-69)	0.956[a]
Median height, cm (IQR)	168 (161-175)	167 (161-172)	0.289[a]
Median weight, kg (IQR)	73 (61.5-85.5)	68 (58.0-77.5)	0.003[a]
Median BMI, kg/m^2 (IQR)	25.65 (22.41-29.85)	23.86 (20.80-27.44)	0.001[a]
Median AFP, ng/ml (IQR)	9.5 (4.00-52.25)	26 (4.00-1772.25)	0.003[a]
Median albumin, g/dl (IQR)	4 (3.5-4.3)	4 (3.5-4.3)	0.895[a]
Median prothrombin time, sec (IQR)	1.1 (1.00-9.45)	1.1 (1.00-8.75)	0.302[a]
TNM stage, n (%)			0.043[c]
Stage I	100 (53.5%)	73 (39.0%)	
Stage II	37 (19.8%)	50 (26.7%)	
Stage III	37 (19.8%)	48 (25.7%)	
Stage IV	2 (1.1%)	3 (1.6%)	
Missing	11 (5.9%)	13 (7.0%)	
Sex, n (%)			0.320[b]
Female	65 (34.8%)	56 (29.9%)	
Male	122 (65.2%)	131 (70.1%)	
Residual tumor, n (%)			0.713[c]
R0	166 (88.8%)	161 (86.1%)	
R1	8 (4.3%)	9 (4.8%)	
R2	0 (0.0%)	1 (0.5%)	
Missing	13 (7.0%)	16 (8.6%)	
Histologic grade, n (%)			0.004[b]
G1	34 (18.2%)	21 (11.2%)	
G2	98 (52.4%)	80 (42.8%)	
G3	46 (24.6%)	78 (41.7%)	
G4	6 (3.2%)	6 (3.2%)	
Missing	3 (1.6%)	2 (1.1%)	
Adjacent hepatic tissue inflammation, n (%)			0.835[b]
None	65 (34.8%)	53 (28.3%)	
Mild	52 (27.8%)	49 (26.2%)	
Severe	9 (4.8%)	9 (4.8%)	
Missing	61 (32.6%)	76 (40.6%)	
Child-Pugh grade, n (%)			1.000[c]
A	115 (61.5%)	104 (55.6%)	
B	11 (5.9%)	10 (5.3%)	
C	1 (0.5%)	0 (0.0%)	
Missing	60 (32.1%)	73 (39.0%)	
Fibrosis Ishak score, n (%)			0.088[b]
0	45 (24.1%)	30 (16.0%)	
1/2	13 (7.0%)	18 (9.6%)	
3/4	10 (5.3%)	18 (9.6%)	
5/6	45 (24.1%)	36 (19.3%)	
Missing	74 (39.6%)	85 (45.5%)	
Vascular invasion, n (%)			0.002[b]
No	122 (65.2%)	86 (46.0%)	
Yes	44 (23.5%)	66 (35.3%)	
Missing	21 (11.2%)	35 (18.7%)	

[a]Mann-Whitney U test; [b]Pearson's χ^2 test; [c]Fisher's exact test. AFP, α-fetoprotein; BMI, body mass index; IQR, interquartile range; NSUN5, NOP2/Sun RNA methyltransferase 5; TNM, tumor node metastasis. The missing data in this table were not included in the statistical analyses.

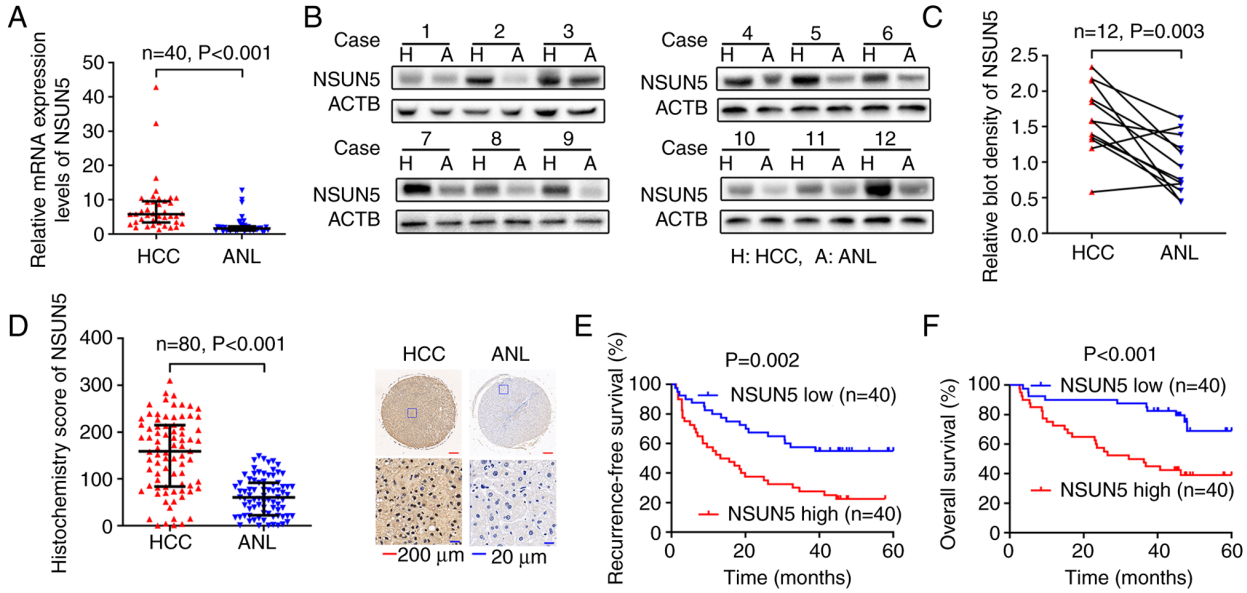

Figure 2. Upregulated NSUN5 mRNA and protein expression levels predict poor prognosis in HCC. (A) mRNA expression levels of NSUN5 were assessed using reverse transcription-quantitative PCR. The Wilcoxon signed-rank test was used for statistical comparison. (B and C) Protein expression levels of NSUN5 were semi-quantified using western blotting in 12 paired HCC and ANL tissues relative to ACTB. Paired Student's t-test was used for statistical comparison. (D) Immunohistochemistry staining of NSUN5, (left) histochemistry score of NSUN5 in 80 paired HCC tissues and ANL tissues, Wilcoxon signed-rank test was used for statistical comparison and (right) representative samples. Kaplan-Meier survival curves presented the association between NSUN5 protein expression levels and (E) recurrence-free survival or (F) overall survival. The log-rank test was used for statistical comparison. ANL, adjacent noncancerous liver; HCC, hepatocellular carcinoma; NSUN5, NOP2/Sun RNA methyltransferase 5; ACTB, β-actin.

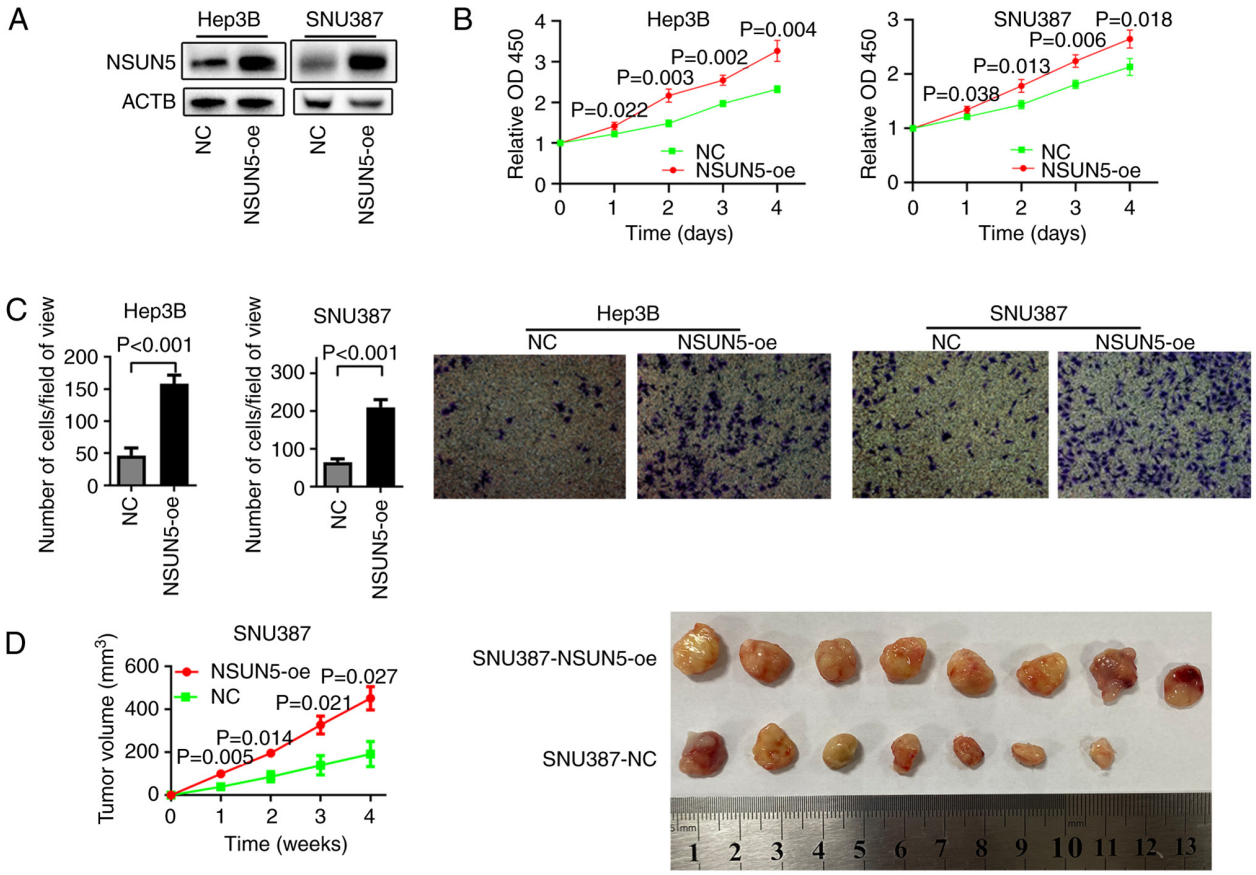

Figure 3. NSUN5 promotes HCC cell proliferation and migration. (A) Protein expression levels of NSUN5 were assessed using western blotting in NSUN5-oe and NC HCC cells. (B) Cell Counting Kit-8 assay results demonstrated that NSUN5-oe promoted the proliferation of HCC cells. (C) Transwell migration assays demonstrated that NSUN5-oe promoted the migration of HCC cells. (B and C) Data are presented as the mean ± SD, n=3; unpaired Student's t-test was used for statistical comparison. (D) Subcutaneous xenografts of HCC SNU387 cells excised from nude mice and tumor volume (n=8). Data are presented as the mean ± SEM and the Mann-Whitney U test was used for statistical comparison. NSUN5, NOP2/Sun RNA methyltransferase 5; HCC, hepatocellular carcinoma; NC, negative control; oe, overexpression.

Table II. Clinical characteristics of 80 patients with hepatocellular carcinoma according to the protein expression levels of NSUN5.

	NSUN5		
Variable	Low	High	P-value
n	40	40	
Age, years			0.653[a]
≤50	23	21	
>50	17	19	
Sex			0.793[a]
Female	9	10	
Male	31	30	
HBsAg			1.000[b]
Negative	3	2	
Positive	37	38	
Liver cirrhosis			0.633[a]
Without	12	14	
With	28	26	
AFP, μg/l			0.143[a]
≤20	15	9	
>20	25	31	
Pathological satellite			0.179[a]
Absent	24	18	
Present	16	22	
Tumor number			<0.001[a]
Solitary	39	27	
Multiple	1	13	
Edmondson's grade			0.363[a]
I + II	8	5	
III + IV	32	35	
Tumor size, cm			0.003[a]
≤5	24	11	
>5	16	29	
Microvascular invasion			0.001[a]
Absent	31	16	
Present	9	24	
Encapsulation			1.000[a]
Complete	14	14	
Incomplete	26	26	
TNM stage			<0.001[a]
I	39	25	
I + II	1	15	
BCLC stage			0.001[a]
0 + A	39	28	
B + C	1	12	

Statistical comparisons were performed using [a]Pearson's χ^2 test or [b]Fisher's exact test. HBsAg, hepatitis B surface antigen; AFP, α-fetoprotein; TNM, Tumor Node Metastasis; BCLC, Barcelona Clinic Liver Cancer.

NSUN5 promotes the proliferation and migration of HCC cells. To assess the role of NSUN5 in HCC progression, NSUN5 was overexpressed in Hep3B and SNU387 HCC cells (Fig. 3A). CCK-8 and Transwell migration assay results demonstrated that overexpression of NSUN5 significantly promoted the proliferation (Fig. 3B) and migration (Fig. 3C) of HCC cells compared with in the NC group. To assess the function of NSUN5 *in vivo*, a subcutaneous tumor xenograft experiment was performed, which demonstrated that the NSUN5-oe SNU387 xenograft grew significantly faster than the negative control (Fig. 3D). Notably, the NSUN5-NC cells injected into one of the mice did not develop into a tumor.

These results indicated that NSUN5 could promote the proliferation and migration of HCC *in vitro*, and induce the tumor growth of HCC *in vivo*.

NSUN5 is positively correlated with translation in HCC. To evaluate the mechanism by which NSUN5 promoted the progression of HCC, a bioinformatics analysis of NSUN5-correlated genes was performed using LinkedOmics. Among the 19,922 genes analyzed in Table SIII, 4,212 genes were positively correlated and 5,981 genes were negatively correlated with NSUN5 in HCC (P<0.01; Table SIII). The volcano plot showing the correlated genes is presented in Fig. 4A. The top 50 NSUN5 positively and negatively correlated genes are presented in Fig. 4B. Furthermore, Gene Ontology (biological process, cellular component, molecular function) and KEGG pathway analyses of the NSUN5-correlated genes were performed (Fig. 4C-F). Among the 10 biological processes in which NSUN5-positively correlated genes were enriched, five ('protein localization to endoplasmic reticulum', 'ribonucleoprotein complex biogenesis', 'translational elongation', 'protein transmembrane transport' and 'protein folding') were associated with translation (Fig. 4C). Among the seven cellular components in which NSUN5-positively correlated genes were enriched, two ('spliceosomal complex' and 'small nucleolar ribonucleoprotein complex') were associated with translation (Fig. 4D). Among the nine molecular functions in which NSUN5-positively correlated genes were enriched, three ('rRNA binding', 'unfolded protein binding' and 'translation factor activity, RNA binding') were associated with translation (Fig. 4E). Among the 10 KEGG pathways in which NSUN5-positively correlated genes were enriched, three ('ribosome', 'spliceosome' and 'ribosome biogenesis in eukaryotes') were associated with translation (Fig. 4F).

Taken together, these results indicated that NSUN5 was positively correlated with translation in HCC.

Discussion

HCC has a high mortality-to-incidence ratio (23) and the treatment options are severely limited (24); therefore, new treatment approaches are urgently needed. Although emerging immunotherapies (such as immune checkpoint inhibitors) can prolong the survival time of certain patients, the therapeutic effect is limited (25,26). Identifying novel mechanisms may aid the design of new targeted therapies. To the best of our knowledge, the present study is the first to report NSUN5 as a promising molecular target for HCC treatment.

Previous studies on NSUN5 have mostly focused on nervous system diseases. For example, NSUN5 has been reported to contribute to the pathology of Williams-Beuren syndrome (WBS) (27), a neurodevelopmental disorder caused

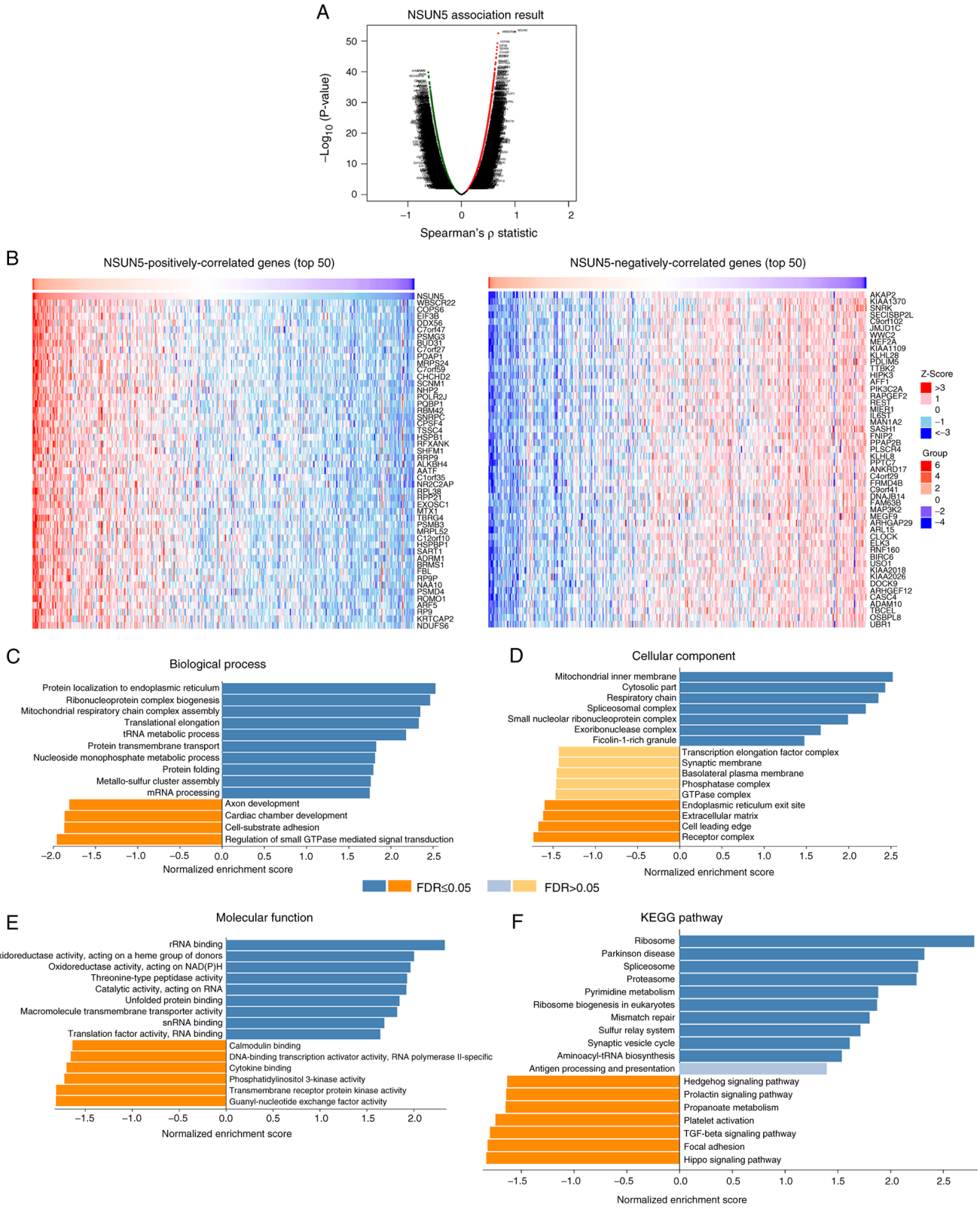

Figure 4. Bioinformatics analysis of NSUN5-correlated genes using LinkedOmics. (A) Spearman's correlation test was performed to assess the correlations between NSUN5 and differentially expressed genes in HCC. (B) Heatmaps presented the top 50 genes that were positively and negatively correlated with NSUN5 in HCC. (C) Biological process, (D) cellular component, (E) molecular function and (F) KEGG pathway analyses of NSUN5-correlated genes in HCC. Blue indicated a positive correlation and orange indicated a negative correlation. NSUN5, NOP2/Sun RNA methyltransferase 5; HCC, hepatocellular carcinoma; FDR, false discovery rate; KEGG, Kyoto Encyclopedia of Genes and Genomes.

by microdeletions of 28 genes, and characterized by cognitive disorders and hypertrophy of the corpus callosum (28,29). The NSUN5 gene is deleted in ~95% of patients with WBS (28). NSUN5-knockout mice have been reported to exhibit spatial cognition deficits, impaired cerebral cortex development and corpus callosum agenesis (5,28,29).

In recent years, the role of NSUN5 in human cancer has been reported. For example, Jiang *et al* (9) reported that NSUN5 promoted the proliferation of colorectal cancer via regulation of the cell cycle. In addition, Janin *et al* (8) reported that NSUN5 inhibited the growth of glioma tumors *in vivo*. In the present study, it was demonstrated that NSUN5, which is mainly expressed in the nucleus, was upregulated in HCC, and this was associated with worse clinical characteristics and was predictive of poor prognosis in HCC, according to TCGA database and the present study cohorts. The results of the present study also indicated that NSUN5 could promote the proliferation and migration of HCC *in vitro* and induce the growth of HCC tumors *in vivo*. As NSUN5 may serve contradictory roles in different organs, potential drugs targeting NSUN5 in HCC should be hepatocyte specific. It has been reported that N-acetylgalactosamine or apolipoprotein-modified nanoparticles can selectively deliver small interfering (si)RNAs to HCC cells (30). Therefore, siRNAs against NSUN5 could be developed as a drug to treat HCC using this method in the future.

Heissenberger *et al* (27) reported that NSUN5 is an rRNA methyltransferase that can mediate the m5C modification of the C3782 position of 28S rRNA in humans and the C3438 position of 28S rRNA in mice. Notably, in this previous study, NSUN5 knockout inhibited the proliferation of human cervical carcinoma HeLa cells and knockout of Nsun5 in the whole mouse body reduced mouse body weight (27). Mechanistically, the loss of NSUN5 was reported to have generated a lower m5C level of 28S rRNA, which impaired the functions of ribosomes and translation of global proteins, thereby decreasing cell proliferation and size (27). In the present study, the bioinformatics analysis demonstrated that NSUN5 was significantly positively correlated with genes associated with ribosomes and translation in HCC. Therefore, it could be hypothesized that overexpression of NSUN5 in HCC would upregulate the m5C level of 28S rRNA; therefore, strengthening the functions of ribosomes and translation of global proteins, and promoting the growth and migration of HCC. Further experiments need to be performed to evaluate this hypothesis in the future.

In conclusion, to the best of our knowledge, the present study was the first to demonstrate that NSUN5 promoted the development of HCC. Therefore, it could be hypothesized that NSUN5 may represent a potential therapeutic target in HCC.

Acknowledgements

Not applicable.

Funding

The present study was supported by grants from the National Natural Science Foundation of China (grant nos. 82002458 and 82102482), the Shanghai Sailing Program (grant no. 19YF1459600) and the Shanghai Clinical Research Center for Acupuncture and Moxibustion (grant no. 20MC1920500).

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

XWZ, HRL, YH and LYW performed the experiments. LYW, HRL and CFG designed the experiments. QQ, CFG and LiZ collected the clinical data. LuZ and RZ performed the statistical analysis. LYW and JY wrote the manuscript. JY, LiZ and HGW conceived the project. XWZ and JY confirm the authenticity of all the raw data. All authors read and approved the final version of the manuscript.

Ethics approval and consent to participate

The present study using human tissues was approved by the Ethics Committee of Eastern Hepatobiliary Surgery Hospital (approval no. EHBHKY2018-02-014). Written informed consent was obtained from each patient according to the policies of the committee. The animal experiments in this study conformed to the Animal Research: Reporting of In Vivo Experiments guidelines (http://www.nc3rs.org.uk/arrive-guidelines) and were approved by the Institutional Animal Care and Use Committee of Shanghai University of Traditional Chinese Medicine (approval no. PZSHUTCM210926007).

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

References

1. Cao W, Chen HD, Yu YW, Li N and Chen WQ: Changing profiles of cancer burden worldwide and in China: A secondary analysis of the global cancer statistics 2020. Chin Med J (Engl) 134: 783-791, 2021.
2. Llovet JM, Kelley RK, Villanueva A, Singal AG, Pikarsky E, Roayaie S, Lencioni R, Koike K, Zucman-Rossi J and Finn RS: Hepatocellular carcinoma. Nat Rev Dis Primers 7: 6, 2021.
3. Puisieux MF, Pellat A, Assaf A, Ginestet C, Brezault C, Dhooge M, Soyer P and Coriat R: Therapeutic management of advanced hepatocellular carcinoma: An updated review. Cancers (Basel) 14: 2357, 2022.
4. Gao Y and Fang J: RNA 5-methylcytosine modification and its emerging role as an epitranscriptomic mark. RNA Biol 18: 117-127, 2021.
5. Cheng JX, Chen L, Li Y, Cloe A, Yue M, Wei J, Watanabe KA, Shammo JM, Anastasi J, Shen QJ, *et al*: RNA cytosine methylation and methyltransferases mediate chromatin organization and 5-azacytidine response and resistance in leukaemia. Nat Commun 9: 1163-1163, 2018.
6. Selmi T, Hussain S, Dietmann S, Heiß M, Borland K, Flad S, Carter JM, Dennison R, Huang YL, Kellner S, *et al*: Sequence- and structure-specific cytosine-5 mRNA methylation by NSUN6. Nucleic Acids Res 49: 1006-1022, 2021.
7. Frye M, Harada BT, Behm M and He C: RNA modifications modulate gene expression during development. Science 361: 1346-1349, 2018.
8. Janin M, Ortiz-Barahona V, de Moura MC, Martínez-Cardús A, Llinàs-Arias P, Soler M, Nachmani D, Pelletier J, Schumann U, Calleja-Cervantes ME, *et al*: Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. Acta Neuropathol 138: 1053-1074, 2019.
9. Jiang Z, Li S, Han MJ, Hu GM and Cheng P: High expression of NSUN5 promotes cell proliferation via cell cycle regulation in colorectal cancer. Am J Transl Res 12: 3858-3870, 2020.

10. Livak KJ and Schmittgen TD: Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) method. Methods 25: 402-408, 2001.
11. Hu L, Lau SH, Tzang CH, Wen JM, Wang W, Xie D, Huang M, Wang Y, Wu MC, Huang JF, *et al*: Association of Vimentin overexpression and hepatocellular carcinoma metastasis. Oncogene 23: 298-302, 2004.
12. Tao QF, Yuan SX, Yang F, Yang Y, Yuan JH, Wang ZG, Xu QG, Lin KY, Cai J, Yu J, *et al*: Aldolase B inhibits metastasis through Ten-Eleven Translocation 1 and serves as a prognostic biomarker in hepatocellular carcinoma. Mol Cancer 14: 170, 2015.
13. Budwit-Novotny DA, McCarty KS, Cox EB, Soper JT, Mutch DG, Creasman WT, Flowers JL and McCarty KS Jr: Immunohistochemical analyses of estrogen receptor in endometrial adenocarcinoma using a monoclonal antibody. Cancer Res 46: 5419-5425, 1986.
14. Hou G, Chen L, Liu G, Li L, Yang Y, Yan HX, Zhang HL, Tang J, Yang YC, Lin X, *et al*: Aldehyde dehydrogenase-2 (ALDH2) opposes hepatocellular carcinoma progression by regulating AMP-activated protein kinase signaling in mice. Hepatology 65: 1628-1644, 2017.
15. Tandon N, Thakkar KN, LaGory EL, Liu Y and Giaccia AJ: Generation of stable expression mammalian cell lines using lentivirus. BIO Protoc 8: e3073, 2018.
16. Liu F, Yuan JH, Huang JF, Yang F, Wang TT, Ma JZ, Zhang L, Zhou CC, Wang F, Yu J, *et al*: Long noncoding RNA FTX inhibits hepatocellular carcinoma proliferation and metastasis by binding MCM2 and miR-374a. Oncogene 35: 5422-5434, 2016.
17. Workman P, Aboagye EO, Balkwill F, Bruder G, Chaplin DJ, Double JA, Everitt J, Farningham DAH, Glennie MJ, Kelland LR, *et al*: Guidelines for the welfare and use of animals in cancer research. Br J Cancer 102: 1555-1577, 2010.
18. Vasaikar SV, Straub P, Wang J and Zhang B: LinkedOmics: Analyzing multi-omics data within and across 32 cancer types. Nucleic Acids Res 46: D956-D963, 2018.
19. Cancer Genome Atlas Research Network. Electronic address: wheeler@bcm.edu; Cancer Genome Atlas Research Network: Comprehensive and integrative genomic characterization of hepatocellular carcinoma. Cell 169: 1327-1341.e23, 2017.
20. Liao X and Zhang D: The 8th edition american joint committee on cancer staging for hepato-pancreato-biliary cancer: A review and update. Arch Pathol Lab Med 145: 543-553, 2021.
21. Yu J, Xu QG, Wang ZG, Yang Y, Zhang L, Ma JZ, Sun SH, Yang F and Zhou WP: Circular RNA cSMARCA5 inhibits growth and metastasis in hepatocellular carcinoma. J Hepatol 68: 1214-1227, 2018.
22. Reig M, Forner A, Rimola J, Ferrer-Fàbrega J, Burrel M, Garcia-Criado A, Kelley RK, Galle PR, Mazzaferro V, Salem R, *et al*: BCLC strategy for prognosis prediction and treatment recommendation: The 2022 update. J Hepatol 76: 681-693, 2022.
23. Nelson ME, Lahiri S, Chow JDY, Byrne FL, Hargett SR, Breen DS, Olzomer EM, Wu LE, Cooney GJ, Turner N, *et al*: Inhibition of hepatic lipogenesis enhances liver tumorigenesis by increasing antioxidant defence and promoting cell survival. Nat Commun 8: 14689-14689, 2017.
24. Wilson CL, Mann DA and Borthwick LA: Epigenetic reprogramming in liver fibrosis and cancer. Adv Drug Deliv Rev 121: 124-132, 2017.
25. Thomas MB, Morris JS, Chadha R, Iwasaki M, Kaur H, Lin E, Kaseb A, Glover K, Davila M and Abbruzzese J: Phase II trial of the combination of bevacizumab and erlotinib in patients who have advanced hepatocellular carcinoma. J Clin Oncol 27: 843-850, 2009.
26. Sun HC, Zhu XD, Huang C, Shen YH and Fan J: Initially unresectable hepatocellular carcinoma treated by combination therapy of tyrosine kinase inhibitor and anti-PD-1 antibody followed by resection. J Clin Oncol 38: e16690-e16690, 2020.
27. Heissenberger C, Liendl L, Nagelreiter F, Gonskikh Y, Yang G, Stelzer EM, Krammer TL, Micutkova L, Vogt S, Kreil DP, *et al*: Loss of the ribosomal RNA methyltransferase NSUN5 impairs global protein synthesis and normal growth. Nucleic Acids Res 47: 11807-11825, 2019.
28. Chen P, Zhang T, Yuan Z, Shen B and Chen L: Expression of the RNA methyltransferase Nsun5 is essential for developing cerebral cortex. Mol Brain 12: 74, 2019.
29. Yuan Z, Chen P, Zhang T, Shen B and Chen L: Agenesis and hypomyelination of corpus callosum in mice lacking Nsun5, an RNA methyltransferase. Cells 8: 552, 2019.
30. Hajiasgharzadeh K, Somi MH, Shanehbandi D, Mokhtarzadeh A and Baradaran B: Small interfering RNA-mediated gene suppression as a therapeutic intervention in hepatocellular carcinoma. J Cell Physiol 234: 3263-3276, 2019.