Kondo Y, Yamashiki N, Goto T, Shiina S, Omata M, Yoshida H, Koike K	alfa-2a for advanced hepatocellular carcinoma				
Sato M, Tateishi R, Yasunaga H, Horiguchi H, Yoshida H, Matsuda S, Koike K	Mortality and morbidity of hepatectomy, radiofrequency ablation, and embolization for hepatocellular carcinoma: a national survey of 54,145 patients	J Gastroenterol	47(10)	1125-1133	2012
Yoshikawa T, Takata A, Otsuka M, Kishikawa T, Kojima K, Yoshida H, Koike K	Silencing of microRNA-122 enhances interferon-α signaling in the liver through regulating SOCS3 promoter methylation	Sci Rep	2	637	2012
Nakagawa H, Isogawa A, Tateishi R, Tani M, Yoshida H, Yamakado M, Koike K	Serum gamma-glutamyltransferase level is associated with serum superoxide dismutase activity and metabolic syndrome in a Japanese population	J Gastroenterol	47(2)	187-194	2012
Soroida Y, Ohkawa R, Nakagawa H, Satoh Y, Yoshida H, Kinoshita H, Tateishi R, Masuzaki R, Enooku K, Shiina S, Sato T, Obi S, Hoshino T, Nagatomo R, Okubo S, Yokota H, Koike K, Yatomi Y, Ikeda H	Increased activity of serum mitochondrial isoenzyme of creatine kinase in hepatocellular carcinoma patients predominantly with recurrence	J Hepatol	27(2)	330-336	2012
Takata A, Otsuka M, Yoshikawa T, Kishikawa	A miRNA machinery component DDX20	Biochem Biophys Res	420(3)	564-569	2012

T, Kudo Y, Goto T, Yoshida H, Koike K	controls NF-κB via microRNA-140 function	Commun			
Masuzaki R, Tateishi R, Yoshida H, Arano T, Uchino K, Enooku K, Goto E, Nakagawa H, Asaoka Y, Kondo Y, Goto T, Ikeda H, Shiina S, Omata M, Koike K	Assessment of disease progression in patients with transfusion-associated chronic hepatitis C using transient elastography	World J Gastroenterol	18(12)	1385-1390	2012
Kudo Y, Tateishi K, Yamamoto K, Yamamto S, Asaoka Y, Ijichi H, Nagae G, Yoshida H, Aburatani H, Koike K	Loss of 5-hydroxymethylcytosine is accompanied with malignant cellular transformation	Cancer Sci	103(4)	670-676	2012
Goto E, Masuzaki R, Tateishi R, Kondo Y, Imamura J, Goto T, Ikeda H, Akahane M, Shiina S, Omata M, Yoshida H, Koike K	Value of post-vascular phase (Kupffer imaging) by contrast-enhanced ultrasonography using Sonazoid in the detection of hepatocellular carcinoma	J Gastroenterol	47(4)	47(4)	2012
Shiina S, Tateishi R, Arano T, Uchino K, Enooku K, Nakagawa H, Asaoka Y, Sato T, Masuzaki R, Kondo Y, Goto T, Yoshida H, Omata M, Koike K	Radiofrequency ablation for hepatocellular carcinoma: 10-year outcome and prognostic factors	Am J Gastroenterol	107(4)	569-577	2012
Enooku K, Tateishi R, Kanai F, Kondo Y, Masuzaki R, Goto T, Shiina S, Yoshida H, Omata M, Koike K	Evaluation of molecular targeted cancer drug by changes in tumor marker doubling times	J Gastroenterol	47(1)	71-78	2012

Sekiguchi S, Kimura K, Chiyo T, Ohtsuki T, Tobita Y, Tokunaga Y, Yasui F, Tsukiyama-Kohara K, Wakita T, Tanaka T, Miyasaka M, Mizuno K, Hayashi Y, Hishima T, Matsushima K, Kohara M	Immunization with a recombinant vaccinia virus that encodes nonstructural proteins of the hepatitis C virus suppresses viral protein levels in mouse liver	PLoS One.	7(12)	e51656.	2012
Murakami Y, Fukasawa M, Kaneko Y, Suzuki T, Wakita T, Fukazawa H.	Selective estrogen receptor modulators inhibit hepatitis C virus infection at multiple steps of the virus life cycle.	Microbes Infect.	15(1)	45-55.	2013
Saeed M, Gondeau C, Hmwe S, Yokokawa H, Date T, Suzuki T, Kato T, Maurel P, Wakita T.	Replication of hepatitis C virus genotype 3a in cultured cells.	Gastroenterology.	144(1)	56-58.e7	2013
Date T, Kato T, Kato J, Takahashi H, Morikawa K, Akazawa D, Murayama A, Tanaka-Kaneko K, Sata T, Tanaka Y, Mizokami M, Wakita T.	Novel cell culture-adapted genotype 2a hepatitis C virus infectious clone.	J Virol.	86(19)	10805-20.	2012
Suzuki R, Saito K, Kato T, Shirakura M, Akazawa D, Ishii K, Aizaki H, Kanegae Y, Matsuura Y, Saito I, Wakita T, Suzuki T.	Trans-complemented hepatitis C virus particles as a versatile tool for study of virus assembly and infection.	Virology.	432(1)	29-38.	2012
Ando T, Imamura H, Suzuki R, Aizaki H, Watanabe T, Wakita T, Suzuki T.	Visualization and measurement of ATP levels in living cells replicating hepatitis C	PLoS Pathog.	8(3)	e1002561.	2012

	virus genome RNA.				
Date T, Morikawa K, Tanaka Y, Tanaka-Kaneko K, Sata T, Mizokami M, Wakita T.	Replication and infectivity of a novel genotype 1b hepatitis C virus clone.	Microbiol Immunol.	56(5)	308-17.	2012
Tanimoto Y, Tashiro H, Aikata H, Amano H, Oshita A, Kobayashi T, Kuroda S, Tazawa H, Takahashi S, Itamoto T, Chayama K and Ohdan H.	Impact of pegylated interferon therapy on outcomes of patients with hepatitis C virus-related hepatocellular carcinoma after curative hepatic resection.	*Ann Surg Oncol.*	19	418-425	2012
Sainz B, Jr., Barretto N, Martin DN, Hiraga N, Imamura M, Hussain S, Marsh KA, Yu X, Chayama K, Alrefai WA and Uprichard SL.	Identification of the Niemann-Pick C1-like 1 cholesterol absorption receptor as a new hepatitis C virus entry factor.	*Nat Med.*	18	281-285	2012
Ohnishi M, Tsuge M, Kohno T, Zhang Y, Abe H, Hyogo H, Kimura Y, Miki D, Hiraga N, Imamura M, Takahashi S, Ochi H, Hayes CN, Tanaka S, Arihiro K and Chayama K.	IL28B polymorphism is associated with fatty change in the liver of chronic hepatitis C patients.	*J astroenterol.*	47	834-844	2012
Ochi H, Hayes CN, Abe H, Hayashida Y, Uchiyama T, Kamatani N, Nakamura Y and Chayama K.	Toward the establishment of a prediction system for the personalized treatment of chronic hepatitis C.	*J Infect Dis.*	205	204-210	2012

Nagaoki Y, Aikata H, Kobayashi T, Fukuhara T, Masaki K, Tanaka M, Naeshiro N, Nakahara T, Honda Y, Miyaki D, Kawaoka T, Takaki S, Tsuge M, Hiramatsu A, Imamura M, Hyogo H, Kawakami Y, Takahashi S, Ochi H and Chayama K.	Risk factors for the exacerbation of esophageal varices or portosystemic encephalopathy after sustained virological response with IFN therapy for HCV-related compensated cirrhosis.	*J astroenterol.*			2012
Miki D, Ohishi W, Ochi H, Hayes CN, Abe H, Tsuge M, Imamura M, Kamatani N, Nakamura Y and Chayama K.	Serum PAI-1 is a novel predictor for response to pegylated interferon-alpha-2b plus ribavirin therapy in chronic hepatitis C virus infection.	*J Viral Hepat.*	19	e126-133	2012
Matsuo J, Mizui M, Okita H, Katayama K, Aimitsu S, Sakata T, Obayashi M, Nakanishi T, Chayama K, Miyakawa Y, Yoshizawa H, Tanaka J and for the Hiroshima Hepatitis Study G.	Follow up of the 987 blood donors found with hepatitis C virus infection over 9-18 years.	*Hepatol Res.*	42	637-647	2012
Kumada H, Toyota J, Okanoue T, Chayama K, Tsubouchi H and Hayashi N.	Telaprevir with peginterferon and ribavirin for treatment-naive patients chronically infected with HCV of genotype 1 in Japan.	*J Hepatol.*	56	78-84	2012

Kobayashi M, Suzuki F, Akuta N, Sezaki H, Suzuki Y, Hosaka T, Kawamura Y, Kobayashi M, Saitoh S, Arase Y, Ikeda K, Chayama K, Miyakawa Y and Kumada H.	Association of two polymorphisms of the IL28B gene with viral factors and treatment response in 1,518 patients infected with hepatitis C virus.	*J astroenterol.*	47	596-605	2012
Kawaoka T, Takahashi S, Takaki S, Hiramatsu A, Waki K, Hiraga N, Miki D, Tsuge M, Imamura M, Kawakami Y, Aikata H, Ochi H, Onoe T, Tashiro H, Ohdan H and Chayama K.	Interleukin-28B single nucleotide polymorphism of donors and recipients can predict viral response to pegylated interferon/ribavirin therapy in patients with recurrent hepatitis C after living donor liver transplantation.	*J Gastroenterol Hepatol.*	27	1467-1472	2012
Izumi N, Asahina Y, Kurosaki M, Yamada G, Kawai T, Kajiwara E, Okamura Y, Takeuchi T, Yokosuka O, Kariyama K, Toyoda J, Inao M, Tanaka E, Moriwaki H, Adachi H, Katsushima S, Kudo M, Takaguchi K, Hiasa Y, Chayama K, Yatsuhashi H, Oketani M and Kumada H.	Inhibition of hepatocellular carcinoma by PegIFNalpha-2a in patients with chronic hepatitis C: a nationwide multicenter cooperative study.	*J astroenterol.*			2012
Hayes CN, Imamura M, Aikata H and Chayama K.	Genetics of IL28B and HCV--response to infection and treatment.	*Nat Rev Gastroenterol Hepatol.*	9	406-417	2012

Hayashi N, Okanoue T, Tsubouchi H, Toyota J, Chayama K and Kumada H.	Efficacy and safety of telaprevir, a new protease inhibitor, for difficult-to-treat patients with genotype 1 chronic hepatitis C.	*J Viral Hepat.*	19	e134-142	2012
Chayama K, Takahashi S, Toyota J, Karino Y, Ikeda K, Ishikawa H, Watanabe H, McPhee F, Hughes E and Kumada H.	Dual therapy with the nonstructural protein 5A inhibitor, daclatasvir, and the nonstructural protein 3 protease inhibitor, asunaprevir, in hepatitis C virus genotype 1b-infected null responders.	*Hepatology.*	55	742-748	2012
Chayama K, Hayes CN, Ohishi W and Kawakami Y.	Treatment of chronic hepatitis C virus infection in Japan: update on therapy and guidelines.	*J astroenterol.*			2012
Chayama K, Hayes CN and Imamura M.	Impact of interleukin-28B genotype on in vitro and in vivo systems of hepatitis C virus replication.	*Hepatol Res.*	42	841-853	2012
Okazaki A, Hiraga N, Imamura M, Hayes CN, Tsuge M, Takahashi S, Aikata H, Abe H, Miki D, Ochi H, Tateno C, Yoshizato K, Ohdan H and Chayama K.	Severe necroinflammatory reaction caused by natural killer cell-mediated Fas/Fas ligand interaction and dendritic cells in human hepatocyte chimeric mouse.	*Hepatology.*	56	555-566	2012

Ohishi W and Chayama K.	Treatment of chronic hepatitis B with nucleos(t)ide analogues.	*Hepatol Res.*	42	219-225	2012
Miki D, Ochi H, Hayes CN, Aikata H and Chayama K..	Hepatocellular carcinoma: towards personalized medicine.	*Cancer Sci.*	103	846-850	2012
Matsumoto A, Tanaka E, Suzuki Y, Kobayashi M, Tanaka Y, Shinkai N, Hige S, Yatsuhashi H, Nagaoka S, Chayama K, Tsuge M, Yokosuka O, Imazeki F, Nishiguchi S, Saito M, Fujiwara K, Torii N, Hiramatsu N, Karino Y and Kumada H.	Combination of hepatitis B viral antigens and DNA for prediction of relapse after discontinuation of nucleos(t)ide analogs in patients with chronic hepatitis B.	*Hepatol Res.*	42	139-149	2012
Hayes CN, Akamatsu S, Tsuge M, Miki D, Akiyama R, Abe H, Ochi H, Hiraga N, Imamura M, Takahashi S, Aikata H, Kawaoka T, Kawakami Y, Ohishi W and Chayama K.	Hepatitis B Virus-Specific miRNAs and Argonaute2 Play a Role in the Viral Life Cycle.	*PLoS One.*	7	e47490	2012
Fujimoto A, Totoki Y, Abe T, Boroevich KA, Hosoda F, Nguyen HH, Aoki M, Hosono N, Kubo M, Miya F, Arai Y, Takahashi H, Shirakihara T, Nagasaki M, Shibuya T, Nakano K, Watanabe-Makino K, Tanaka H, Nakamura H, Kusuda J, Ojima H,	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators.	*Nat Genet.*	44	760-764	2012

Shimada K, Okusaka T, Ueno M, Shigekawa Y, Kawakami Y, Arihiro K, Ohdan H, Gotoh K, Ishikawa O, Ariizumi S, Yamamoto M, Yamada T, Chayama K, Kosuge T, Yamaue H, Kamatani N, Miyano S, Nakagama H, Nakamura Y, Tsunoda T, Shibata T and Nakagawa H.					
Akbar SM, Chen S, Al-Mahtab M, Abe M, Hiasa Y, Onji M..	Strong and multi-antigen specific immunity by hepatitis B core antigen (HBcAg)-based vaccines in a murine model of chronic hepatitis B: HBcAg is a candidate for a therapeutic vaccine against hepatitis B virus.	Antiviral Res	96	59-64	2012
Akbar SM, Hiasa Y, Al-Mahtab M, Onji M	Dendritic cell-based immune therapy in liver diseases.	Current Immunology Review	8	28-36	2012
Akbar SM, Chen S, Al-Mahtab M, Abe M, Yoshida O, Iheda Y, Hiasa Y, Onji M.	Suppression of inflammatory mucosal milieu by administration of regulatory dendritic cells in an animal model of primary biliary cirrhosis.increased antigen processing and presentation by dendritic cells.	Euroasian J Heapo-Gastroenterology	2	30-34	2012

Al-Mahtab M, Akbar SM, Rahman S, Kamal M, Khan MSI.	Biochemical, virological, immunological and histopathological features of 702 incidentally detected chronic hepatitis B virus carriers in Bangladesh.	Digestion	86	1-5	2012
Hoshino H, Hino K, Miyakawa H, Takahashi K, Akbar SM, Mishiro S.	Inter-genotypic recombinant hepatitis C virus strains in Japan noticed by discrepancies between immunoassay and sequencing.	J Med Virol	84	1018-1024	2012
Khan MSI, Akbar SM, Hossain ST, Mahtab M, Hossain MM, Idris Z.	Possible route of transmission of highly pathogenic avian influenza virus type H5N1 in family poultry at rural Bangladesh.	Pakistan Veterinary Journal	31	112-116	2012
Miyashita K, Kang J-H, Saga A, Takahashi K, Shimamura T, Yasumoto A, Fukushima H, Sogabe S, Konishi K, Uchida K, Fujinaga A, Matsui T, Sakura Y, Tsuji T, Maguchi H, Taniguchi M, Abe N, Akbar SM, Arai M, Mishiro S.	Three Cases of Acute or Fulminant Hepatitis E Caused by Ingestion of Pork Meat and Entrails in Hokkaido, Japan; Zoonotic Food-Borne Transmission of Hepatitis E Virus and Public Health Concerns.	Hepatol Res	42	870-878	2012
Onji H, Koizumi Y, Hanayama M, Akbar SM, Hirooka M, Tokumoto Y, Abe M, Hiasa Y, Aoto M, Mitsuda N, Onji M.	A Case of de novo Hepatitis B Complicated due to Lack of Comprehensive Interventional Approach.	Euroasian Journal of Hepato-Gastroenterology	2	122-125	2012

Hossain MF, Al-Mahtab M, Akbar SM, Rahman S.	Serum aspartate transaminase platelet ratio index (APRI) in patients with non-alcoholic fatty liver disease in Bangladesh.	KMUJ	4(2)	48-52	2012
T Yamashita, M Honda, Y Nakamoto, M Baba, K Nio, Y Hara, SS Zeng, TH Kondo, H Takatori, T Yamashita, E Mizukoshi, H Ikeda, Y Zen, H Takamura, XW Wang, S Kaneko.	Discrete nature of EpCAM(+) and CD90(+) cancer stem cells in human hepatocellular carcinoma.	Hepatology	-	-	(in press)
E Mizukoshi, T Yamashita, K Arai, H Sunagozaka, T Ueda, F Arihara, T Kagaya, T Yamashita, K Fushimi, S Kaneko.	Enhancement of tumor-associated antigen-specific T cell responses by radiofrequency ablation of hepatocellular carcinoma.	Hepatology	-	-	(in press)
A Kitao, O Matsui, N Yoneda, K Kozaka, S Kobayashi, W Koda, T Gabata, T Yamashita, S Kaneko, Y Nakanuma, R Kita, S Arii.	Hypervascular Hepatocellular Carcinoma: Correlation between Biologic Features and Signal Intensity on Gadoxetic Acid-enhanced MR Images.	Radiology	265(3)	780-9	2012
E Mizukoshi, K Fushimi, K Arai, T Yamashita, M Honda, S Kaneko.	Expression of chondroitin-glucuronate C5-epimerase and cellular immune responses in patients with	Liver Int	32(10)	1516-26	2012

	hepatocellular carcinoma.				

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MicroRNA-140 Acts as a Liver Tumor Suppressor by Controlling NF-κB Activity by Directly Targeting DNa Methyltransferase 1 (Dnmt1) Expression

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MicroRNAs (miRNAs) are small RNAs that regulate the expression of specific target genes. While deregulated miRNA expression levels have been detected in many tumors, whether miRNA functional impairment is also involved in carcinogenesis remains unknown. We investigated whether deregulation of miRNA machinery components and subsequent functional impairment of miRNAs are involved in hepatocarcinogenesis. Among miRNA-containing ribonucleoprotein complex components, reduced expression of DDX20 was frequently observed in human hepatocellular carcinomas, in which enhanced nuclear factor-κB (NF-κB) activity is believed to be closely linked to carcinogenesis. Because DDX20 normally suppresses NF-κB activity by preferentially regulating the function of the NF-κB-suppressing miRNA-140, we hypothesized that impairment of miRNA-140 function may be involved in hepatocarcinogenesis. DNA methyltransferase 1 (Dnmt1) was identified as a direct target of miRNA-140, and increased Dnmt1 expression in DDX20-deficient cells hypermethylated the promoters of metallothionein genes, resulting in decreased metallothionein expression leading to enhanced NF-κB activity. MiRNA-140-knockout mice were prone to hepatocarcinogenesis and had a phenotype similar to that of DDX20 deficiency, suggesting that miRNA-140 plays a central role in DDX20 deficiency-related pathogenesis. *Conclusion*: These results indicate that miRNA-140 acts as a liver tumor suppressor, and that impairment of miRNA-140 function due to a deficiency of DDX20, a miRNA machinery component, could lead to hepatocarcinogenesis. (HEPATOLOGY 2013;57:162-170)

Hepatocellular carcinoma (HCC) is the third most common cause of cancer-related mortality worldwide.[1] Although multiple major risk factors have been identified, such as infection with hepatitis viruses B or C, the molecular mechanisms underlying HCC development remain poorly understood, hindering the development of novel therapeutic approaches. Therefore, a better understanding of the molecular pathways involved in hepatocarcinogenesis is critical for the development of new therapeutic options.

Nuclear factor-κB (NF-κB) is one of the best-characterized intracellular signaling pathways. Its activation is a common feature of human HCC.[2-4] It acts as an inhibitor of apoptosis and as a tumor promoter[4,5] and is associated with the acquisition of a transformed phenotype during hepatocarcinogenesis.[6] In fact, studies using patient samples suggest that NF-κB activation in the liver leads to the development of HCC.[7] Although there are conflicting reports,[8] activation of the NF-κB pathway in the liver is crucial for the initiation and promotion of HCC.[4]

Abbreviations: DEN, diethylnitrosamine; Dnmt1, DNA methyltransferase 1; HCC, hepatocellular carcinoma; miRNA; microRNA; miRNP, miRNA-containing ribonucleoprotein; MT, metallothionein; NF-κB, nuclear factor-κB; RT-PCR, reverse-transcription polymerase chain reaction; TNF-α, tumor necrosis factor-α; TRAIL, TNF-related apoptosis-inducing ligand; UTR, untranslated region.

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MicroRNAs (miRNAs) are small RNA molecules that regulate the expression of target genes and are involved in various biological functions.[9-12] Although specific miRNAs can function as either suppressors or oncogenes in tumor development, a general reduction in miRNA expression is commonly observed in human cancers.[13-22] In this context, it can be hypothesized that deregulation of the machinery components involved in miRNA function may be related to the functional impairment of miRNAs and the pathogenesis of carcinogenesis.

In this study, we show that the expression of DDX20, an miRNA-containing ribonucleoprotein (miRNP) component, is frequently decreased in human HCC. Because DDX20 is required for both the preferential loading of miRNA-140 into the RNA-induced silencing complex and its function,[23] we hypothesized that DDX20 deficiency would lead to hepatocarcinogenesis via impaired miRNA-140 function. MiRNA-140 knockout mice were indeed more prone to hepatocarcinogenesis, and we identified a possible molecular pathway from DDX20 deficiency to liver cancer.

Materials and Methods

Mouse and Liver Tumor Induction. MiRNA-140$^{-/-}$ mice have been described.[24] Recombinant murine tumor necrosis factor-α (TNF-α) (25 μg/kg; Wako, Osaka, Japan) was injected into the tail vein, and the mice were sacrificed 1 hour later. To induce liver tumors, 15-day-old mice received an intraperitoneal injection of diethylnitrosamine (DEN) (25 mg/kg body weight), and were sacrificed 32 weeks later. All animal experiments were performed in compliance with the regulations of the Animal Use Committee of the University of Tokyo and the Institute for Adult Disease, Asahi Life Foundation.

Plasmids. FLAG-tagged human DDX20-expressing plasmids were as described.[23] The pGL3-based reporter plasmid containing Dnmt1 3′ untranslated region (UTR) sequences was provided by G. Marucucci.[25]

Detailed Materials and Methods. The detailed experimental procedures of clinical samples, cells, plasmids, reporter assays, reverse-transcription polymerase chain reaction (RT-PCR) analysis, antibodies, western blotting, cell assays, immunohistochemistry, microarray analysis, methylation analysis, and electrophoretic mobility-shift assay are described in the Supporting Information.

Statistical Analysis. Statistically significant differences between groups were determined using a Wilcoxon rank-sum test. A Wilcoxon signed-rank test was used for statistical comparisons of protein expression levels between HCC and surrounding noncancerous tissues.

Table 1. Cases with Differential Expression Levels of miRNP Components in HCC (n = 10)

Gene ID	Gene Symbol	Decreased	Increased	No Change
23405	Dicer1	2	1	7
27161	EIF2C2 (AGO2)	1	1	8
6895	TARBP2(TRBP2)	2	0	8
11218	DDX20 (GEMIN3)	8	0	2
50628	GEMIN4	1	0	9

The expression levels of each miRNP component were determined via immunohistochemistry.

The numbers indicate the number of cases that had the differential expression levels (decreased, increased, or no change) in HCC tissues compared with those in surrounding liver tissues.

Results

DDX20 Expression Is Frequently Decreased in HCC. The expression levels of proteins reported to be miRNP components (Dicer, Ago2, TRBP2, DDX20 [also known as Gemin3], and Gemin4)[26] were initially determined via immunohistochemistry in HCC and noncancerous background liver tissues from 10 patients. DDX20 expression was lower in HCC tissue compared with the surrounding noncancerous tissue in 8 of 10 cases, whereas expression of the other genes was unchanged (Table 1 and Supporting Fig. 1). Therefore, and because DDX20 was recently identified as a possible liver tumor suppressor in mice,[27] we determined its role as a human HCC suppressor.

DDX20 protein expression was lower in several HCC cell lines, such as Huh7 and Hep3B (Fig. 1A), compared with normal hepatocytes. DDX20 protein levels were also lower in human HCC needle biopsy specimens than in surrounding noncancerous liver tissue (Fig. 1B). Immunohistochemical analysis

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Additional Supporting Information may be found in the online version of this article.

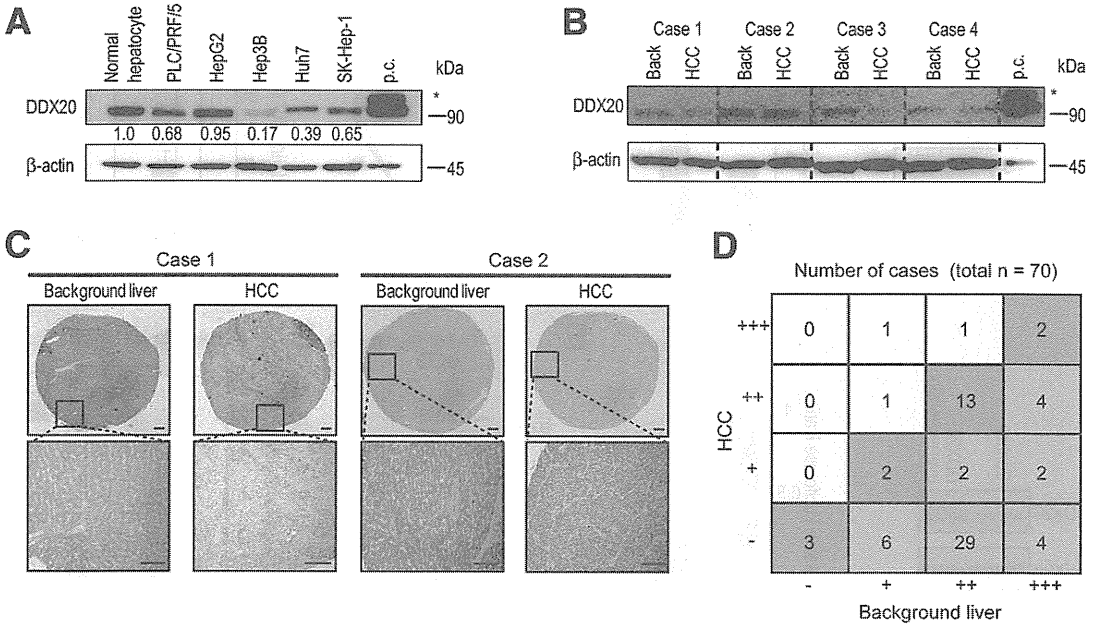

Fig. 1. Reduced DDX20 expression levels in hepatocellular carcinoma. (A) DDX20 protein expression in HCC cell lines. Numbers between the panels indicate DDX20 protein levels normalized to β-actin levels. Lysates of 293T cells transiently transfected with a FLAG-tagged DDX20-expressing plasmid yielded two DDX20 bands corresponding to the endogenous DDX20 protein and the transfected FLAG-tagged DDX20 protein (*) as a positive control (p.c.; far right lane). Data represent the results of three independent determinations. (B) DDX20 protein expression in four HCC needle biopsy specimens and in the surrounding noncancerous background liver tissue (Back). *Positive control. (C) Immunohistochemical analysis of DDX20 protein expression in HCC and surrounding tissues (background liver). Two representative cases are shown. Scale bars, 500 μm. The lower panels display magnified images of the boxed areas in the upper panels. (D) Grid summarizing DDX20 immunohistochemical staining data from 70 cases. In 47 cases (pink shading), DDX20 protein levels were lower in the HCC tissues than in the surrounding tissues ($P < 0.05$; Wilcoxon signed-rank test).

confirmed that DDX20 expression was frequently lower in HCC than in surrounding noncancerous liver tissue (Fig. 1C,D). Specifically, 47 of 70 cases examined showed reduced DDX20 protein expression in HCC versus background noncancerous liver tissue (Fig. 1D and Supporting Table 1). These results indicate that the expression of DDX20, an miRNP component, is frequently reduced in human HCC, and suggest that this reduced DDX20 expression might be involved in the pathogenesis of a subset of HCC cases.

NF-κB Activity Is Enhanced by DDX20 Deficiency. Because DDX20 knockout mice are embryonic-lethal,[28] DDX20 has been suggested to have important biological roles. DDX20, a DEAD-box protein,[29] was originally found to interact with survival motor neuron protein.[30] Later, it was identified as a major component of miRNPs,[31] which may mediate miRNA function. As we have reported, DDX20 is preferentially involved in miRNA-140-3p function,[23] acting as a suppressor of NF-κB activity in the liver.[32] DDX20-knockdown PLC/PRF/5 cells exhibit enhanced NF-κB activity[23] (Fig. 2A). Whereas the proliferation rates of DDX20-knockdown cells and control cells were comparable (Fig. 2B), apoptotic cell death after stimulation with TNF-related apoptosis-inducing ligand (TRAIL), which induces both cell apoptosis and NF-κB activation,[33] was significantly reduced in DDX20-knockdown cells (Fig. 2C). Similar results were obtained using DDX20-knockdown HepG2 cells (Supporting Fig. 2A-D). Conversely, NF-κB activity was reduced, but cell proliferation remained unchanged, in Hep3B cells stably overexpressing DDX20 (Fig. 2D,E). Sensitivity to TRAIL-induced apoptosis was restored in these cells (Fig. 2F). Similar results were also obtained using Huh7 cells (Supporting Fig. 2E-H). These data confirm a previous report that DDX20 deficiency enhances NF-κB activity and the downstream events of this pathway.

Metallothionein Expression Is Decreased by DDX20 Deficiency. Next, to investigate the biological consequences of DDX20 deficiency, we examined the changes in transcript levels in DDX20-knockdown cells using microarrays (GEO accession number: GSE28088). The expression of genes driven by NF-κB that are related to carcinogenesis, such as FASLG, IRAK1, CARD9, and Galectin-1, were enhanced significantly in DDX20-knockdown cells, as expected (Table 2). To determine the mechanism underlying the enhanced NF-κB activation in DDX20-deficient cells, we searched for candidate genes and noticed that the

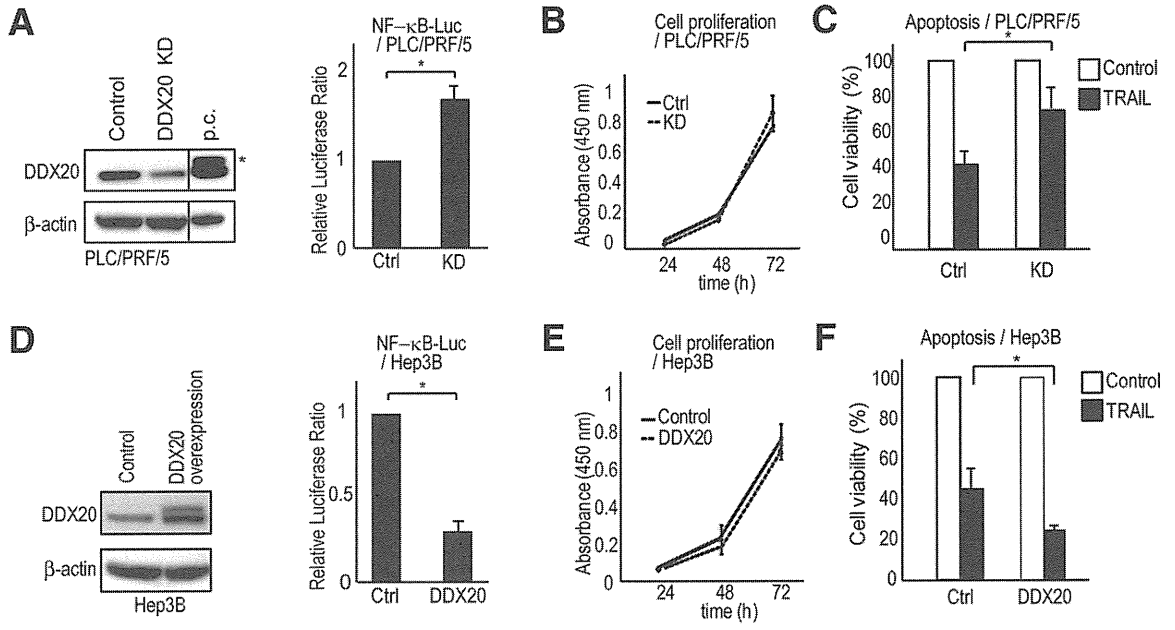

Fig. 2. Modulation of downstream events of the nuclear factor-κB pathway by DDX20. (A) Left: Establishment of stable DDX20-knockdown (DDX20 KD) PLC/PRF/5 cells. *Positive control (p.c.). Right: DDX20 deficiency enhances TNF-α–induced NF-κB activity. NF-κB reporter plasmids were transiently transfected into control (Ctrl) or DDX20-knockdown (KD) PLC/PRF/5 cells. The cells were then treated with TNF-α (5 ng/mL) or vehicle for 6 hours. *$P < 0.05$. Data are presented as the mean ± SD of three independent determinations. (B) Cell proliferation rates were comparable for control (Ctrl) and DDX20-knockdown (KD) PLC/PRF/5 cells. Data are presented as the mean ± SD of three determinations. (C) DDX20 deficiency reduces TRAIL-induced apoptotic cell death. Control (Ctrl) and DDX20-knockdown (KD) PLC/PRF/5 cells were incubated with 25 ng/mL TRAIL. Data represent cell viability after TRAIL stimulation (gray bars) relative to the number of vehicle-treated cells (white bars). *$P < 0.05$. Data are presented as the mean ± SD of triplicate determinations. (D) Left: Establishment of stable DDX20-overexpressing cells. Hep3B cells were infected with control or FLAG-tagged DDX20-overexpressing lentiviruses and selected on puromycin. Western blot analysis confirmed increased expression of DDX20 protein. Right: DDX20 overexpression suppresses TNF-α–induced NF-κB activity. NF-κB reporter plasmids were transiently transfected into Hep3B control (Ctrl) and DDX20-overexpressing (DDX20) cells treated with TNF-α for 6 hours. Data are presented as the mean ± SD of three independent determinations. *$P < 0.05$. (E) Proliferation of control (Ctrl) and DDX20-overexpressing (DDX20) Hep3B cells was measured as described in (B). (F) DDX20 overexpression reduces TRAIL-induced apoptotic cell death. Data for control (Ctrl) and DDX20-overexpressing (DDX20) Hep3B cells are shown. *$P < 0.05$.

Table 2. Increased Expression of NF-κB–Related Genes in DDX20-Knockdown HepG2 Cells Compared with Wild-Type Cells

RefSeq ID	Symbol	Description	Ratio	Representative Gene Function
NM_000639	FASLG	Fas ligand	3.5	NF-κB target, apoptosis
NM_052813	C9orf151	CARD9	2.5	NF-κB cascade, NF-κB target
NM_014959	CARD8	Tumor up-regulated CARD-containing antagonist of CASP9 (TUCAN)	2.2	NF-κB target
NM_131917	FAF1	FAS-associated factor 1 (hFAF1)	1.9	Cytoplasmic sequestering of NF-κB, NF-κB target
NM_020644	TMEM9B	Transmembrane protein 9B precursor	1.9	Positive regulation of NF-κB transcription factor activity
NM_017544	NKRF	ITBA4 protein	1.9	Negative regulation of transcription
NM_006247	PPP5C	Protein phosphatase T	1.8	Positive regulation of NF-κB cascade
NM_020345	NKIRAS1	KappaB-Ras1	1.8	NF-κB cascade
NM_001569	IRAK1	IRAK-1	1.7	Positive regulation of NF-κB transcription factor activity
NM_177951	PPM1A	Protein phosphatase 1A	1.7	Positive regulation of NF-κB cascade
NM_018098	ECT2	Epithelial cell-transforming sequence 2 oncogene	1.6	Positive regulation of NF-κB cascade
NM_002305	LGALS1	Galectin-1 (putative MAPK-activating protein MP12)	1.6	Positive regulation of NF-κB cascade
NM_015093	TAB2	TAK1-binding protein 2	1.6	Positive regulation of NF-κB cascade
NM_004180	TANK	TRAF-interacting protein	1.5	NF-κB cascade
NM_014976	PDCD11	Programmed cell death protein 11	1.5	rRNA processing
NM_015336	ZDHHC17	Putative NF-κB–activating protein 205	1.5	Positive regulation of NF-κB cascade
NM_002503	NFKBIB	IKB-β	1.5	Cytoplasmic sequestering of NF-κB
NM_138330	ZNF675	Zinc finger protein 675	1.5	Negative regulation of NF-κB transcription factor activity

The genes were identified as NF-κB–related based on the Gene Ontology and the GeneCodis Databases.

Table 3. Decreased Expression Levels of MT Genes in DDX20 Knockdown HepG2 Cells Compared with Wild-Type Cells

Symbol	Description	Ratio
MT1E	Metallothionein-1E	**0.12**
MT1F	Metallothionein-1F	**0.36**
MT1H	Metallothionein-1H	**0.16**
MT1G	Metallothionein-1G	**0.06**
MT1M	Metallothionein-1M	**0.24**
MT1X	Metallothionein-1X	**0.27**
MT2A	Metallothionein-2	**0.28**
MT3	Metallothionein-3	0.84
MTL5	Metallothionein-like 5 (Tesmin)	1.12

Numbers in boldface type indicate values <0.5.

expression levels of a group of metallothioneins (MTs), such as MT1E, MT1F, MT1G, MT1M, MT1X, and MT2A, were all significantly decreased when DDX20 was deficient (Table 3). The decreased expression of MTs in DDX20-knockdown HepG2 and PLC/PRF/5 cells was confirmed via quantitative RT-PCR (Fig. 3a and Supporting Fig. 3). Expression of MT-3, which was not altered in the microarray analysis, was similarly unaltered in quantitative RT-PCR analysis. Notably, it was already known that MTs are frequently silenced in human primary liver cancers.[34-36] In addition, MT knockout mice have enhanced NF-κB activity, likely due to reactive oxygen species, and these mice are more prone to hepatocarcinogenesis.[37] These results suggest that DDX20 deficiency enhances NF-κB activity by decreasing the expression of MTs, which could facilitate the development of liver cancer.

MiRNA-140 Directly Targets Dnmt1. Because MT expression is regulated principally by CpG island methylation in their promoter regions,[38,39] we examined the quantitative methylation status of MT promoters in DDX20-knockdown cells. The CpG islands of the MT1E, MT1G, MT1M, MT1X, and MT2A promoters, and the CpG shores of the MT1F promoters, were significantly more highly methylated under DDX20-deficient conditions, as determined by the comprehensive Illumina Quantitative Methylation BeadChip method (Table 4, Supporting Table 2, and GSE 37633). A crucial step in DNA methylation involves DNA methyltransferase (Dnmt), which catalyzes the methylation of CpG dinucleotides in genomic DNA.[40] The methylation status of MT promoters is mediated specifically by Dnmt1.[41] Because Dnmt1 contains a predicted miRNA-140-3p target site in its 3′ UTR, with a perfect match to its seed sequences (Fig. 3B), and because the effects of miRNA-140-3p activity were impaired in DDX20-knockdown cells,[23] it was hypothesized that whereas miRNA-140 normally targets and suppresses Dnmt1 protein expression, miRNA-140-3p dysfunction due to DDX20 deficiency results in enhanced Dnmt1 expression, leading to hypermethylation of MT promoters. Consistent with this hypothesis, Dnmt1 expression was increased significantly in DDX20-knockdown cells (Fig. 3C). miRNA-140 precursor overexpression suppressed activity of the Dnmt1 3′ UTR reporter construct, the effect of which was lost when two mutations were introduced into its seed sequences (Fig. 3D). MiRNA-140 precursor overexpression suppressed Dnmt1 protein expression (Fig. 3E). These results indicate that miRNA-140 directly targets Dnmt1 and suppresses its expression in the normal state. Consistently, decreased DDX20, increased Dnmt1, and decreased MT expression were detected together in human clinical HCC samples, as determined via immunohistochemistry (Fig. 3F). By contrast, miRNA-140 precursor-overexpressing Huh7 cells showed increased expression of MTs and reduced NF-κB activity *in vitro* (Supporting Fig. 4A,B). Moreover, the increase in the number of spheres formed from PLC/PRF/5 cells due to DDX20 knockdown was antagonized by treatment with an NF-κB inhibitor or a demethylating agent (Supporting Fig. 5). Taken together, these results suggest that the up-regulated Dnmt1 protein expression caused by functional impairment of miRNA-140-3p due to DDX20 deficiency results in decreased expression of MTs *via* enhanced methylation at the CpG sites in their promoters. This may lead to enhanced NF-κB activity and cellular transformation at least *in vitro*.

MiRNA-140 Is a Liver Tumor Suppressor. To further examine the biological consequences of functional impairment of miRNA-140 due to DDX20 deficiency, we determined the phenotypes of miRNA-140 knockout (miRNA-140$^{-/-}$) mice (Fig. 4A). Similar to the *in vitro* DDX20 knockdown results, Dnmt1 expression was increased and MT levels decreased in the liver tissue of these mice (Fig. 4B). NF-κB–DNA binding activity was enhanced in the livers of miRNA-140$^{-/-}$ mice after tail-vein injection of TNF-α, a crucial cytokine that induces NF-κB activity and hepatocarcinogenesis (Fig. 4C). As was found in MT knockout mice, phosphorylation of p65 at serine 276, which is critical for p65 activation, was significantly increased in the livers of miRNA-140$^{-/-}$ mice after DEN exposure, which induces NF-κB activation and liver tumors[37] (Fig. 4D). Notably, the size and number of liver tumors that developed 8 months after DEN exposure were markedly elevated in miRNA-140$^{-/-}$ mice compared with control mice (Fig. 4E,F). These results indicate that miRNA-140$^{-/-}$ mice are indeed

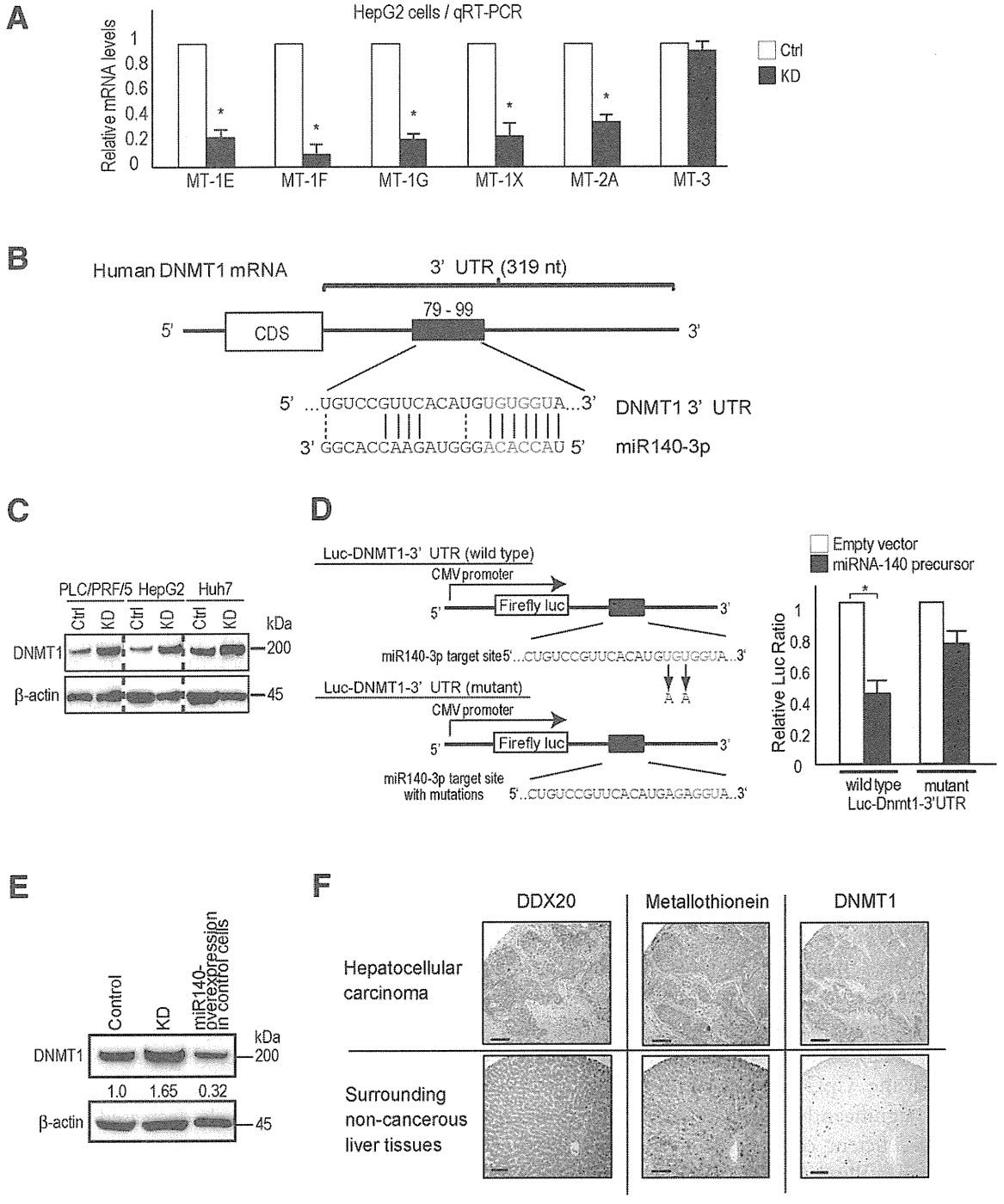

Fig. 3. Targeting of Dnmt1 by miRNA-140-3p and reduced MT expression. (A) The expression levels of MTs were determined using quantitative reverse-transcriptase polymerase chain reaction. The relative expression ratios of the MTs in control (white bars) and DDX20-knockdown (black bars) HepG2 cells were calculated by normalizing control cell values to 1.0. The data represent the mean ± SD of three independent determinations. $*P < 0.05$. (B) Putative miRNA-140-3p target sites in the 3′ UTR of human Dnmt1. Seed sequences are indicated in red. (C) Dnmt1 expression was increased in DDX20-knockdown cells. Ctrl, control cells; KD, DDX20-knockdown cells. (D) Left: Schematic diagrams of wild-type (upper) and mutant (lower) luciferase reporter constructs (Luc-Dnmt1-3′ UTRs) carrying the Dnmt1 3′ UTR region harboring the putative miRNA-140-3p target site. The mutant seed sequence contained two nucleotide substitutions. Right: The Dnmt1 3′ UTR is targeted directly by miRNA-140-3p. Cells were cotransfected with Luc-Dnmt1-3′ UTR (wild-type or mutant) plus either an empty vector (white bars) or a plasmid expressing the miRNA-140 precursor (black bars). Data are the mean ± SD of three independent determinations. (E) Overexpression of miRNA-140 reduces Dnmt1 expression in control cells. Values between the panels indicate Dnmt1 protein levels normalized to those of β-actin. KD, DDX20 knockdown cells. (F) Representative histochemical images showing expression of DDX20, Dnmt1, and MT proteins in HCC (upper three panels) and surrounding tissue (lower panels). Compared with adjacent noncancerous liver tissue, HCCs exhibited decreased DDX20 and MT expression and increased Dnmt1 expression. Note that adjacent sections were stained for each protein. Scale bar, 50 μm.

Table 4. Methylation Levels in CpG Islands of the MT Genes in DDX20-Knockdown HepG2 Cells Compared with Control Cells

Symbol	CpG Island Methylation Ratio	Target ID
MT1E	**1.14**	cg00178359
	1.29	cg06463589
	3.65	cg02512505
	1.02	cg15134649
MT1G	**2.14**	cg16452857
	1.03	cg27367960
	1.00	cg03566142
	0.99	cg07791866
MT1M	**1.16**	cg02132560
	0.98	cg02160530
	1.03	cg04994964
MT1X	**1.24**	cg05596720
	1.05	cg26802333
	1.06	cg09147880
	1.01	cg08872713
MT2A	**2.06**	cg07395075
	0.94	cg20430434

Values were determined using the quantitative Illumina Human Methylation BeadsChip. Boldface values indicate increased methylation levels in DDX20 knockdown cells.

more prone to liver cancer development and suggest that miRNA-140 acts as a liver tumor suppressor, probably by suppressing NF-κB activity, although we cannot completely exclude other molecular mechanisms. Nonetheless, these results also suggest that the impairment of miRNA-140 function due to DDX20 deficiency may lead to hepatocarcinogenesis in humans, as we have observed in miRNA-140$^{-/-}$ mice (Supporting Figs. 6 and 7).

Discussion

Here, we report that miRNA-140$^{-/-}$ mice have increased NF-κB activity and are more prone to HCC development. In addition, we show that DDX20, an miRNP component, is frequently decreased in human HCC tissues. Because DDX20 deficiency preferentially causes impaired miRNA-140 function,[23] the functional impairment of miRNA-140 may result in phenotypes similar to those of miRNA-140$^{-/-}$ mice and may lead to hepatocarcinogenesis. In support of the hypothesis that DDX20 dysfunction is involved in hepatocarcinogenesis, DDX20 is located at 1p21.1-p13.2, a frequently deleted chromosomal region in human HCC,[27] and DDX20 was recently identified as a possible liver tumor suppressor in a functional screen in mice.[27] Although the possibility that intracellular signaling pathways other than miRNA-140 may also be involved in the biological consequences of DDX20 deficiency cannot be denied, we believe that functional impairment of miRNA-140 plays a major role in the phenotypes induced by DDX20 deficiency, based on the phenotypic similarities.

Changes in miRNA expression levels have been reported in various tumors.[7,12,42] However, in this study, we found that reduced expression of an miRNA machinery component might lead to carcinogenesis, at least in part, through functional impairment of miRNAs. Recent studies have shown that components of the RNA interference machinery are associated with the outcome of ovarian cancer patients,[43] and that single-nucleotide polymorphisms in miRNA machinery genes can be used as diagnostic risk markers.[44,45] Therefore, the impairment of miRNA function caused by deregulated miRNA machinery components may also be involved in carcinogenesis.

Our study identified Dnmt1 as a critical target of miRNA-140. The decreased MT expression due to the CpG promoter methylation induced by Dnmt1 resulted in enhanced NF-κB activity. This finding was consistent with the results obtained using MT gene knockout mice, in which enhanced NF-κB activation promoted hepatocarcinogenesis.[37] The decrease in MT expression that results from increased Dnmt1 expression caused by functional impairment of miRNA-140, together with increased NF-κB activation and hepatocarcinogenesis in MT knockout mice,[37] supports the concept that the DDX20/miRNA-140/Dnmt1/MT/NF-κB pathway may play a crucial role in hepatocarcinogenesis. However, we cannot fully exclude the possibility that other intracellular signaling pathways are also involved in the induction of hepatocarcinogenesis by miRNA-140 or DDX20 deficiency, because the precise role of NF-κB in hepatocarcinogenesis has not been clearly defined,[8] although constitutive activation of NF-κB signaling has been frequently detected in human HCCs.[46] The mechanisms by which DDX20 expression is initially decreased and the reason its locus is frequently deleted in HCC remain to be elucidated. However, because DDX20 expression is also regulated by methylation of its CpG promoter,[47] once this pathway is deregulated, decreased DDX20 expression could be maintained by a positive feedback mechanism, even without deletion of its locus.[27]

In conclusion, this study shows that miRNA-140 acts as a liver tumor suppressor. We show that DDX20, an miRNP component, is frequently decreased in human HCC, which may induce hepatocarcinogenesis via impairment of miRNA-140 function. These results suggest the importance of investigations of not only aberrant miRNA expression levels,[12,14,17,48] but also deregulation of miRNP

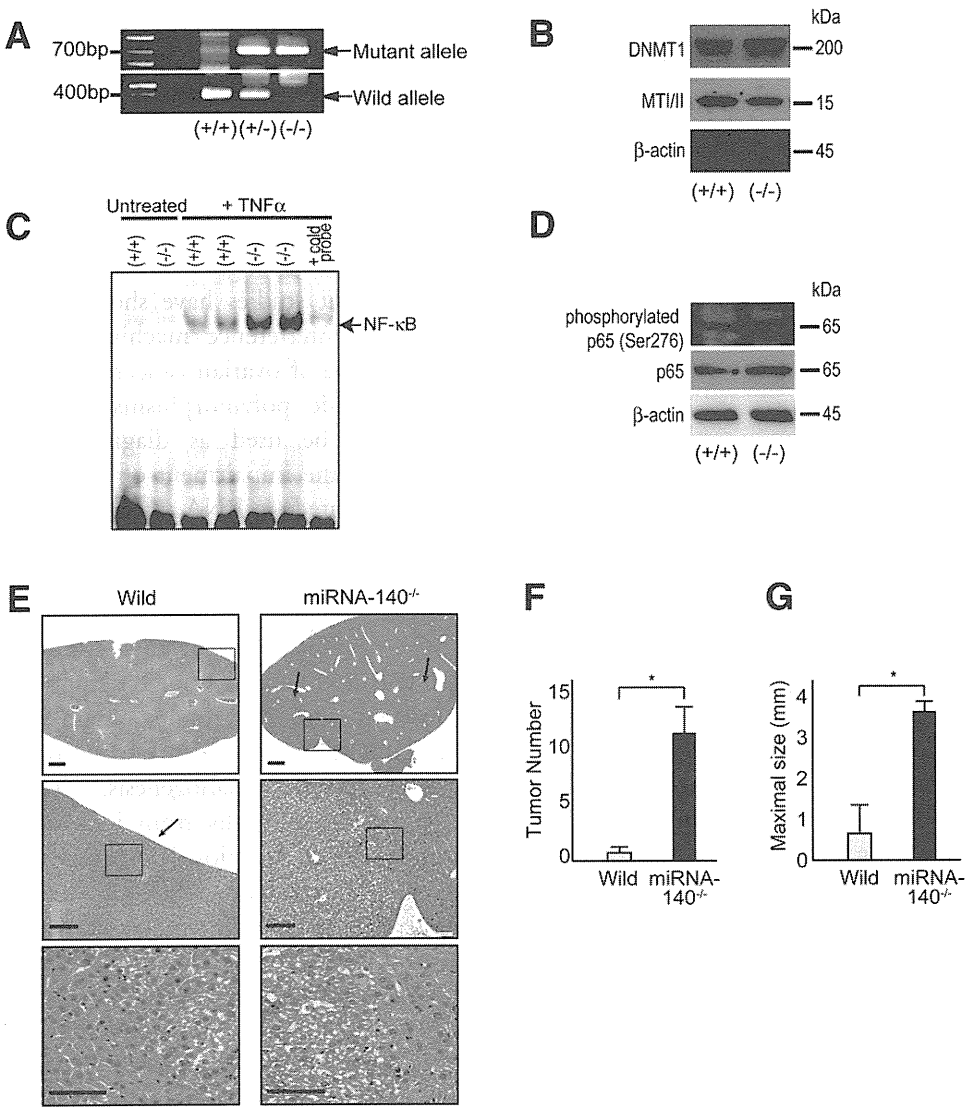

Fig. 4. miRNA-140$^{-/-}$ mice are prone to hepatocarcinogenesis. (A) Representative genotyping of mice with wild-type or mutant alleles. PCR genotyping was performed for miRNA-140 wild-type (419 bp; Wild) and knockout (734 bp; Mutant) alleles. (+/+), wild-type; (+/−), heterozygous; (−/−), knockout. (B) Increased Dnmt1 expression and decreased MTI/II expression in the liver tissues of miRNA-140$^{-/-}$ mice compared with wild-type mice. Western blotting was performed using antibodies against the indicated proteins. (+/+), wild-type; (−/−), miRNA-140$^{-/-}$. The image shown is representative of four independent experiments. (C) NF-κB-DNA binding was assessed via gel-shift assay using equal amounts of liver nuclear extracts from untreated and TNF-α-injected wild-type and miRNA-140$^{-/-}$ mice. (+/+), wild-type; (−/−), miRNA-140$^{-/-}$. Cold probe was added to TNF-α-injected knockout mouse nuclear extract to test assay specificity. A result representative of four independent experiments is shown. (D) Western blotting for phosphorylated p65 expression in the liver at 32 weeks after DEN treatment in miRNA-140$^{-/-}$ mice compared with wild-type mice. A result representative of four independent experiments is shown. (E) Representative histological images of mouse liver at 32 weeks after DEN treatment. Arrows indicate tumors. Higher-magnification images of the highlighted areas in the upper panels are shown in the lower panels. Scale bar, 500 μm. (F) The number (left panel) and size (right panel) of tumors (five random sections per mouse treated with DEN) are presented as the mean ± SD (wild-type mice, n = 8; miRNA-140$^{-/-}$ mice, n = 8). *$P < 0.05$.

components,[22] with subsequent impairment of miRNA function as molecular pathways and possible therapeutic targets for carcinogenesis and other diseases.

References

1. Parkin D, Bray F, Ferlay J, Pisani P. Global cancer statistics, 2002. CA Cancer J Clin 2005;55:74-108.
2. Block T, Mehta A, Fimmel C, Jordan R. Molecular viral oncology of hepatocellular carcinoma. Oncogene 2003;22:5093-5107.
3. Karin M. Nuclear factor-kappaB in cancer development and progression. Nature 2006;441:431-436.
4. Luedde T, Schwabe RF. NF-κB in the liver—linking injury, fibrosis and hepatocellular carcinoma. Nat Rev Gastroenterol Hepatol 2011;8:108-118.
5. Pikarsky E, Porat R, Stein I, Abramovitch R, Amit S, Kasem S, et al. NF-kappaB functions as a tumour promoter in inflammation-associated cancer. Nature 2004;431:461-466.
6. Liu P, Kimmoun E, Legrand A, Sauvanet A, Degott C, Lardeux B, et al. Activation of NF-kappa B, AP-1 and STAT transcription factors is a frequent and early event in human hepatocellular carcinomas. J Hepatol 2002;37:63-71.