**SUPPLEMENTAL INFORMATION**

**Supplemental Figure Legends**

**Supplemental Figure S1. Expression and silencing of *NM23-H1* in epithelial cancer cells**

(A) Left panel: Whole-cell lysates from human normal hepatocytes in primary culture (HH), human hepatoma cell lines (HepG2, PLC/PRF/5, Mahlavu), the breast carcinoma cell line MDA-MB-231, and colorectal cancer cell line HCT8/S11 were analyzed by western blotting with polyclonal anti-NM23-H1 that does not cross-react with NM23-H2. Right panel: Cellular invasion assays in native type I collagen were performed for 24h. Data are means±sem of three independent experiments. (B) Differential impact of *NM23-H1* silencing on *NM23-H1* and *NM23-H2* expression. First panel: *NM23-H1* and *NM23-H2* mRNA levels were analyzed by RT-PCR in HepG2 cells upon *NM23-H1* silencing. Second-fourth panel: protein levels were determined by western blotting using anti-NM23-H1 and -H2 specific antibodies in control and silenced HepG2, HCT8/S11, and PLC/PRF/5 cells. Control siRNA (C) and siRNAs targeting *NM23-H1* (Si1 and Si2) were used at 50 nM; cells were analyzed 48h after transfection. (C) Representative fields showing NM23-H1 immunostaining of HepG2 cells transfected with control and *NM23-H1* siRNA (Si1). Scale bar, 20 μm. (D) Total NDPK activity in extracts from HepG2 and HCT8/S11 cells transfected with control and *NM23-H1* siRNA (Si1). NDPK activity was measured 48h post-transfection. Data are means±sem of three independent experiments, each performed in triplicate. Significant at $^{*}P<0.05$ *versus* control cells.

**Supplemental Figure S2. *NM23-H1* silencing induces scattering in epithelial cancer cells**

(A) Phase-contrast (upper panel) and scanning electron (lower panel) microscopy of control and silenced (Si1) HepG2 cells 48, 72 and 96h post-transfection. Silenced cells are scattered and showed cytoplasmic extensions. Similar morphological changes were observed with the Si2 siRNA (not shown). Scale bar, 20 μm. (B) Cell partitions obtained by three geometrical

methods -Voronoï's partition (Voronoï), Delaunay's graph (Delaunay) and Minimum Spanning Tree (MST)- in control and silenced HepG2 cells 48, 72 and 96h post-transfection. Si1-silenced cells exhibited relatively homogeneous Voronoï areas, and Delaunay and MST segment lenghts did not display an important variation, indicating a more dispersed and random spatial distribution of NM23-H1 depleted cells by comparison to control cells. (C) Comparison of parameters calculated from each of geometrical methods in (B). Three graphic models show that when *NM23-H1* was silenced 96h post-transfection, the RFH value (roundness factor homogeneity) slightly increased while the AD value (area disorder) decreased, and that the σ (SD) and disorder index values from Delaunay and MST models decreased. This indicates that NM23-H1 depleted cells have a more dispersed and random spatial distribution than control cells, all of which showing a cohesive cluster distribution ($P$<0.05). (D) Upper panel: Phase-contrast microscopy of control and Si1-silenced HCT8/S11 cells seeded on native type I collagen gel and cultured for 24h. Arrows indicate invasive cytoplasmic extensions. Scale bar, 50 μm. Lower panel: Phase-contrast microscopy of control and Si1-silenced PLC/PRF/5 cells 96h post-transfection. Scale bar, 50 μm.

**Supplemental Figure S3. Time course of *NM23-H1* silencing and recovery**

HepG2 cells were transfected with control and *NM23-H1* siRNA (Si1) before being harvested at various times post-transfection (2-14 days) and analyzed by western blotting for NM23-H1 and -H2.

**Supplemental Figure S4. Expression of the E-cadherin transcriptional repressors Snail, Slug and Twist in control and *NM23-H1*-silenced HepG2 cells**

(A) Total RNA from HepG2 cells transfected with control and *NM23-H1* siRNA (Si1) was subjected to RT-QPCR with primers designated to amplify Slug and Snail. Data represent means±sem from three experiments. (B) Control and *NM23-H1*-silenced (Si1) HepG2 cells

were analyzed by western blotting for Slug, Snail and Twist. NIH3T3 cell extracts were used as a positive control for Slug and Snail.

**Supplemental Figure S5. Quantification of the wound healing assay in HCT8/S11 cells**

The mean distance that cells travelled from the edge of the wound was measured at 4, 8 and 24h after wounding. Data are means±sd of three independent experiments. Significant at $^{*}P<0.05$ *versus* control cells.

**Supplemental Figure S6. *NM23-H2* silencing was ineffective to promote invasion**

(A) Impact of *NM23-H2* silencing on NM23-H1 and -H2 protein levels determined by western blotting in control and silenced HepG2 cells. Si1' and Si2' siRNAs targeting *NM23-H2* were used at 5 and 50 nM, respectively; cells were analyzed 48h after transfection. (B) Control siRNA (C) and *NM23-H2*-silenced (Si1', Si2') cells were tested for their ability to invade native type I collagen in the 24h invasion assay. Data are means±sem of three independent experiments. ns: non significant *versus* control cells. (C) Total NDPK activity in extracts from HepG2 and HCT8/S11 cells transfected with control and *NM23-H2* siRNA (Si1'). NDPK activity was measured 48h post-transfection. Data are means±sem of three independent experiments. Significant at $^{*}P<0.05$ *versus* control cells.

**Supplemental Figure S7. *NM23-H1* silencing induces transient Akt activation**

Whole-cell lysates from control and *NM23-H1*-silenced cells were analyzed by western blotting at various times post-transfection with specific antibodies against the phospho-Ser$^{473}$ form of Akt.

**Supplemental Figure S8. Status of Akt in invasive cancer cell lines**

Whole-cell lysates prepared from non invasive (PLC/PRF/5, HepG2, HCT8/S11) and invasive (MDA-MB-231, Malhavu) cancer cell lines were analyzed by western blotting with specific antibodies against Akt, the phosphorylated form of Akt, and tubulin.

**Supplemental Figure S9. Invasion induced by *NM23-H1* silencing is MMP-dependent**

The invasive capacity in native type I collagen of silenced (Si1, Si2) HepG2 (A) and HCT8/S11 (B) cells 48h post-transfection was tested in the presence of the general MMP inhibitor GM6001 (1 and 10 μM). Data are means±sem of three independent experiments. Significant at $^{*}P<0.05$.

**Supplemental Figure S10. NM23-H1/-M1 is dispensable for cancer cell proliferation and liver regeneration, but *NM23-H1* silencing promotes resistance to anticancer drug-induced apoptosis**

(A) The repartition of cells in G1, S and G2/M phases of the cell cycle was determined by flow cytometry of control and Si1-silenced HepG2 and HCT8/S11 cells 48h post-transfection. Note that similar results were observed 72h post-transfection. Data are means±sem of the percentage of cells at each phase in three independent experiments. (B) Control and Si1-silenced HepG2 cells were compared for their ability to form colonies in soft agar after 2 weeks in culture. Representative fields are shown. Arrows show HepG2 colonies. Scale bar, 50 μm. (C) Left panel: Quantification of hepatocyte proliferation was determined by immunostaining for the proliferation marker Ki67 in liver sections after partial hepatectomy of wild-type and *NM23-M1*$^{-/-}$ male mice. Ki67-positive hepatocytes were counted in ten consecutive fields from each liver section. Six to eight mice from each genotype were sacrificed at each time point after hepatectomy. Results are means±sem. Right panel: NM23-M1 and -M2 levels assayed by western blotting of liver samples from wild-type and *NM23-M1*$^{-/-}$ mice during liver regeneration. Three mice from each genotype were analyzed at each time point post-hepatectomy. For each mouse, the pre-operative liver (Time 0h) is indicated. As expected, NM23-M1 was undetectable in liver extracts from *NM23-M1*$^{-/-}$ mice. (D) Control and silenced (Si1, Si2) HepG2 cells 48h post-transfection were treated for 24h with dimethylsulfoxide (DMSO), etoposide (ETP, 1 mM), or camptothecin (CPT, 10 μM). The

percentage of apoptotic cells in the sub-G1 fraction was quantified by flow cytometry. Data are means±sem of three independent experiments. Significant at $^{*}P<0.05$ *versus* controls.

**Supplemental Figure S11. NM23-H1 status during cancer progression in human liver and colon tumors**

(A) Left panel: NM23-H1 and -H2 levels were analyzed by western blotting of liver tissue extracts from human HCC (T) and paired non-tumoral liver tissues (N) of seven patients. HCC were well-differentiated in patients 1, 2, 4-6, and moderately differentiated in patients 3 and 7. Right panel: NM23-H1 and -H2 levels were analyzed by western blotting of liver tissues resected from three control and three cirrhotic patients. (B) Tissue sections from control and cirrhotic liver, and HCC were labeled using specific anti-NM23-H1 antibodies and counterstained with hematoxylin. Asteriskes indicate HCC regions with heterogeneous NM23-H1 labeling. Scale bar, 50 μm. (C) NM23-H1 and -H2 levels assayed by western blotting of human colorectal carcinoma (T) and adjacent tissues (N) from two patients with Dukes's stage A (T1 and T2), two with stages B2 and B2-C (T3 and T4, respectively), one with stage C1 (T5), and five with stage C2 (T6-T10). (D) Immunolabeling of NM23-H1 in tissue sections from human colon carcinoma and adjacent colon mucosa. Arrowheads show the weak NM23-H1 labeling in the non tumoral colon epithelial cells. Scale bar, 50 μm.

**Supplemental Experimental Procedures**

**RNA interference and Transfections**

All siRNA oligonucleotides were synthesized by Ambion (Ambion, Inc., Austin, TX). Two specific siRNAs targeting *NM23-H1* (Si1 5'-GGCUGUAGGAAAUCUAGUU; Si2 5'-GGAUUCCGCCUUGUUGGUC), and *NM23-H2* (Si1' 5'-GCCUAUGGUUUAAGCCUGA; Si2' 5'-GGAUUGAUCAUUCUUUUAU) were used. The siRNA control sequence was 5'-GGCUGUAGAAGCUAUAGUU. Cells were transfected with control or specific siRNA

sequence using the CodeBreaker$^{TM}$ siRNA transfection reagent (Promega Corporation, Madison, WI) for HepG2 cells and the Amaxa Nucleofector technology (Lonza, Cologne, Germany) for HCT8/S11 cells. Where indicated, cells were co-transfected with *NM23-H1* siRNA and expression vectors encoding full lenght MT1-MMP or its catalytic domain mutant form, as described (1).

**Pharmacological inhibitors**

Pharmacological inhibitors of ERK1/2 (PD098059), p38 (SB203580), JNK (SP600125), NF-κB (CAPE), mTOR (rapamycin), PLC (U73122), PKA (KT5720), and MMP (GM6001) were purchased from Calbiochem (San Diego, CA). Inhibitors of PI3K and $G\alpha_0/G\alpha_i$ G-proteins (wortmaninn and pertussis toxin, respectively) were obtained from Sigma-Aldrich (St. Louis, MO). The ROCK inhibitor Y27632 and Clostridium botulinum exoenzyme C3 transferase (abbreviated as C3T) were generous gifts from Yoshitomi Pharmaceutical Industries Ltd (Osaka, Japan) and Dr. Gilles Flatau (INSERM U627, Nice, France), respectively. The src inhibitors PP1 and M475271 were from Biomol Research Laboratories (Le Perray en Yvelines, France) and AstraZeneca (Macclesfield, UK), respectively.

**RT-PCR analysis**

Total RNA was extracted with RNA Plus (Qbiogene, MP Biomedicals, Illkirch, France) and reverse transcribed by extension of random decamer primers using Moloney murine leukemia virus reverse transcriptase (RETROscript, Ambion, Inc., Austin, TX). Complementary DNA was amplified by PCR using *NM23-H1* (5'-CTGCATACAAGTTGGCAGGA and 5'-AGGGAGAACTCACAGCTCCA), *NM23-H2* (5'-GGCCTCTGAAGAACACCTGA and 5'-AATGATGTTCCTGCCAACCT), and *Rac1* (5'-TTCCTATCTCAGCGCCCTGCC and 5'-GGACAGGACCAAGAACGAGGG) primers. Each sample was normalized on the basis of its endogenous *β-actin* mRNA content.

**QPCR**

Quantitative PCR was performed using the Sybr Green PCR Core Reagents Kit (Perkin Elmer Apllied Biosystems, Courtaboeuf, France) on a LightCycler 1.5 (Roche Diagnostics, Mannheim, Germany). The primers used were: 5'-CCCTGAAGATGCATATTCGGAC and 5'-CTTCTCCCCCGTGTGAGTTCTA for *Slug*, 5'-TACAGCGAGCTGCAGGACTCTAAT and 5'-AGGACAGAGTCCCAGATGAGCATT for *Snail*, 5'-GAGCGAAAGCATTTGCCAAG and 5'-GGCATCGTTTATGGTCGGAA for *18S*. Data were collected and analyzed with Roche LightCycler Software 3.5.3 (Roche Diagnostics). Data were expressed as a relative amount ($2^{-\Delta\Delta CT}$) of a control experiment used as a calibrator.

**Immunoblotting**

Cells and tissues were lyzed in RIPA buffer (150 mM NaCl, 1% Nonidet P-40, 0.5% sodium deoxycholate, 0.1% SDS, 50 mM Tris-HCl pH 7.5, 1 mM phenylmethylsulfonylfluoride, 1 mM $Na_3VO_4$ and 10 µg/mL leupeptin). Immunoblotting analysis was performed using specific primary antibodies against NM23-H1, NM23-H2 and their mouse counterparts NM23-M1, NM23-M2, as described previously (2), and the following antibodies:

• anti-E-cadherin mAb 1:2000 (Takara Biomedicals, Gennevilliers, France,)

• anti-vimentin mAb 1:200, anti-CK 18 mAb 1:200, anti-γ-catenin mAb 1:500, anti-tubulin mAb 1:5000, anti-β-actin mAb 1:5000 (Sigma-Aldrich, St-Louis, MO)

• anti-β-catenin pAb 1:2000, anti-phospho-Tyr$^{204}$ ERK1/2 mAb 1:500, anti-ERK1/2 pAb 1:500, anti-twist pAb 1:500 (Santa Cruz Biotechnology Inc., Santa Cruz, CA)

• anti-phospho-Ser$^{473}$ Akt pAb 1:500, anti-Akt pAb 1:500, anti-phospho-Thr$^{389}$ p70 S6 kinase mAb 1:500, anti-p70 S6 kinase pAb 1:250, anti-PTEN pAb 1:500, anti-phospho-Ser$^{9}$ GSK-3β pAb 1:500, anti-GSK-3β mAb 1:1000, anti-phospho-Ser$^{33}$/Ser$^{37}$/Thr$^{41}$ β-catenin pAb 1:500, anti-phospho-Thr$^{183}$/Tyr$^{185}$ JNK mAb 1:500, anti-JNK pAb 1:1000, anti-Snail mAb 1:1000, anti-Slug mAb 1:500 (Cell Signaling Technology Inc., Beverly, MA)

• anti-phospho-Thr$^{180}$/Tyr$^{182}$ p38 pAb 1:500, anti-p38 pAb 1:500 (Calbiochem, San Diego, CA)

• anti-MT1-MMP mAb 1:300 (a gift from M.C. Rio, IGBMC, Illkirch, France).

Membranes were revealed by enhanced chemiluminescence (Amersham Biosciences, Saclay, France) after incubation with a horseradish peroxidase-conjugated anti-rabbit or anti-mouse IgG secondary antibody (Cell Signaling Technology).

**Indirect immunofluorescence analysis**

Cells grown on glass coverslips were fixed with 4% paraformaldehyde, permeabilized with 0.1% Triton X-100 and then incubated with anti-E-cadherin mAb (1:50; Takara Biomedicals), anti-β-catenin pAb (1:500) or anti-γ-catenin mAb (1:100; all from Sigma-Aldrich). The selective polyclonal anti-human NM23-H1 antibodies were used at 1:5000. The actin cytoskeleton was stained with AlexaFluor 594-conjugated phalloidin. The secondary antibodies used were FITC-conjugated goat anti-mouse IgG and AlexaFluor 488-conjugated goat anti-rabbit IgG (both from Molecular Probes, Interchim, Montluçon, France). Nuclei were stained with Dapi (Molecular Probes). Images were obtained by confocal microscopy.

For immunofluorescence analysis of HepG2 cells grown on coverslips coated with a thin layer of gelatin, cells were pre-extracted with 0.3% Triton X-100 in 4% paraformaldehyde, fixed with 4% paraformaldehyde, quenched with 50 mM $NH_4Cl$ and blocked with 5% FCS. Cells were incubated with AlexaFluor-conjugated phalloidin and anti-cortactin mAb (clone 4F11, 1:200, Millipore Corporation, Bedford, MA). The secondary antibody was Cy5-conjugated goat anti-mouse IgG (Jackson ImmunoResearch Laboratories, Baltimore, PA). Cells were imaged with 63x, 1.4NA objectives on a widefield Leica DM6000 B/M microscope equipped with a CoolSNAP HQ CCD camera (Roper scientific, Tucson, AZ) driven by MetaMorph 6 (Molecular Devices Corporation, Sunnyvale, CA).

**Analysis of cell morphology by electron microscopy analysis**

Cells grown on glass coverslips were fixed with 2% paraformaldehyde and immersed in 1% osmium tetroxide for 1h at room temperature. Cells were dehydrated through a graded alcohol series. After drying with hexamethyldisilazane, cells were coated on a 40-nm thick gold layer with a sputter-coatter. Specimens were observed with a S 260 Cambridge scanning electron microscope operating at 10 kV.

**Analysis of filopodia by scanning electron microscopy**

Samples were fixed with 2.5% glutaraldehyde in 0.1 M cacodylate buffer (pH 7.4). Preparations were then washed in 0.2 M cacodylate buffer (pH 7.4), post-fixed in 1% osmium tetroxide in 0.2 M cacodylate buffer (pH 7.4), and dehydrated through a graded series of ethanol. Samples were transferred in acetone and subjected to critical point drying with $CO_2$ in a Balzers CPD 030. Dried specimens were sputter coated with gold using a BALTEC MED 010 evaporator and were examined with a JEOL JSM 6700F field emission scanning electron microscopy operating at 10 kV.

**Luciferase reporter gene assay**

Cells treated with control siRNA or *NM23-H1* siRNA for 48h were transfected with 1 µg of the pTOPFLASH plasmid reporter using Lipofectamine 2000 (Invitrogen Life Technologies, Carlsbad, CA) according to the procedure described by the manufacturer. As a control, cells were transfected with 1 µg of pFOPFLASH reporter. Cells were serum-deprived for 24h and assayed for luciferase activity. LEF/TCF-dependent luciferase activity was defined as the pTOPFLASH activity *minus* the activity devoted to pFOPFLASH.

**MMP antibody arrays**

MMP levels were determined in cell lysates and conditioned media by using the Quantibody human MMP array (Raybiotech Inc., Norcross, GA), which is a multiplex sandwich enzyme-linked immunosorbent assay for simultaneous and quantitative measurement of different MMPs and TIMPs. Cell lysates were processed in parallel with six-point serial MMP

standards. Non-specifically bound proteins were removed and the array was subsequentially incubated with a mix of biotin-MMP antibodies and streptavidin-conjugated fluorescence dye according to the manufacturer's protocol. The signal was detected with an Axon 4000B laser scanner and analyzed with the GenePix 6 software. Quantibody Q_Analyzer software was used for calculating the final MMP level.

**NDPK activity measurement**

NDPK activity in cell lysates was measured using a spectrophotometric pyruvate kinase-lactate deshydrogenase coupled assay as previously described (2).

**Proliferation assays**

Anchorage-dependent growth was evaluated by flow cytometry. Briefly, cells were fixed in ice-cold 70% ethanol at -20°C and stained with 20 µg/mL propidium iodide for 30 min at 37°C in the dark. DNA content was analyzed by flow cytometry.

To analyze anchorage-independent growth, 1 x $10^4$ cells were suspended in 1 mL DMEM containing 10% FBS and 0.27% SeaPlaque low-melting-temperature agarose. The cells were plated in a 35-mm dish over a 1 mL layer of solidified DMEM containing 10% FBS and 0.6% agarose. The cells were fed every 3 to 4 days by adding 200 µL of DMEM containing 10% FBS. Colonies were photographed at x4 and x10 magnification after two weeks.

**Flow cytometric assessment of apoptosis**

Both adherent and floating cells were collected, fixed in ice-cold 70% ethanol at -20°C, and stained with 20 µg/mL propidium iodide in the presence of 100 µg/mL ribonuclease A for 30 min at 37°C in the dark. DNA content was analyzed by flow cytometry. Apoptotic cells with hypodiploid DNA staining were found in the 'sub-G1' peak.

**Preparation of conditioned medium**

Forty-eight hours after transfection with control siRNA or *NM23-H1* siRNA, cells were incubated for 24-48h in serum-free medium. This medium was harvested, passed through a 0.22 µm filter and stored at -80°C.

**Rac1 activation assays**

Rac1 activity was determined in extracts of control and *NM23-H1* siRNA-treated cells by using the luminescence-based G-LISA™ Rac1 activation assay kit (Cytoskeleton, Inc., Denver, CO) according to the manufacturer's instructions. Extracts were prepared 24, 48, and 72h post-transfection by using the provided cell lysis buffer, and 'snap-frozen' until the time of assaying. Lysates were clarified by centrifugation at 13,000 rpm at 4°C for 10 min. Protein concentration was determined according to the manufacturer's protocol, and cell extracts were equalized to contain the same protein concentration for the assay. Luminescence was detected as suggested by the manufacturer.

**Partial hepatectomy and Ki67 immunolabeling**

Wild-type and transgenic *NM23-M1* null mice (3), with the 129/Sv genetic background (3-4 months old), were subjected to two-third hepatectomy. Mice were sacrified at various times after hepatectomy and the regenerating livers were harvested, fixed in formalin and embedded in paraffin or snap-frozen in liquid nitrogen and stored at -80°C until use. Animal experiments were conducted in accordance with national ethical guidelines for the care and use of laboratory animals. Hepatocyte proliferation was assessed by immunolabeling of Ki67 in liver sections by using a SuperSensitive Link-Label Immunohistochemistry detection system (Biogenex, San Ramon, CA) with an anti-Ki67 antibody (1:100, Novocastra Laboratories, Newcastle, UK). Ki67-positive hepatocyte nuclei were counted in 10 consecutive fields from each liver section (0.96 $mm^2$). Six to eight animals were analyzed at each time point.

**Tissue specimens and Immunohistochemistry**

Tumoral and non-tumoral liver tissues were collected from seven patients with HCC who underwent partial hepatectomy without previous anti-tumoral treatment. Patients (six men and one woman) were aged 51-77 years (mean, 61 years). Histological analyses of non-tumoral liver tissues showed no fibrosis in three cases (patients 1-3), cirrhosis in three cases (patients 4-6) and periportal fibrosis without fibrous septa or bridging in one case (patient 7). Chronic liver disease was related to hepatitis C virus infection in three cases (patients 5-7) and to hepatitis B virus infection in one case (patient 4). According to the World Health Organization classification of tumors (4), HCC was well-differentiated in patients 1, 2, 4-6 and moderately differentiated in patients 3 and 7. Control liver tissues were obtained from the hepatectomized liver of two patients with metastatic cancer in the liver and of one patient with liver focal hyperplasia. Primary colorectal cancers, adenomatous polyps, and their matched corresponding adjacent tissues were collected from ten patients who underwent curative resection. Patients (4 men and 6 women) were aged 38-85 years (mean, 60 years). Primary tumors were classified as Dukes's stages A (patients 1 and 2), B2 (patient 3), B2-C (patient 4), C1 (patient 5), and C2 (patients 6-10). French ethical rules for the use of human tissues for research were satisfied.

Immunolabeling was performed using a SuperSensitive Link-Label Immunohistochemistry detection system (Biogenex, San Ramon, CA) according to the manufacturer's protocol with specific antibodies against NM23-H1, as described previously (2), β-catenin (1:300, Santa Cruz Biotechnology, Inc., Santa Cruz, CA), and E-cadherin (1:100, Zymed Laboratories, San Francisco, CA). Microwave antigen retrieval in 10 mM citrate buffer (pH 6) was performed before β-catenin and E-cadherin immunostaining. Peroxidase activity was revealed with 3-amino-9-ethyl-carbazole or 3-3' diaminobenzidine. Slides were counterstained with hematoxylin.

**Supplemental References**

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3. Arnaud-Dabernat S, Bourbon PM, Dierich A, Le Meur M, Daniel JY. Knockout mice as model systems for studying nm23/NDP kinase gene functions. Application to the nm23-M1 gene. J Bioenerg Biomembr 2003; 35: 19-30.

4. Hamilton S, Aaltonen L. Tumours of the liver and intrahepatic bile ducts. In: Hamilton S, Aaltonen L, editors. World Health Organization Classification of Tumors; Pathology and Genetics of Tumours of the Digestive System: IARC Press; 2000. p. 157-202.

**Supplemental Multimedia Files**

**Movie S1. Motility of control HepG2 cells by videomicroscopy**

**Movies S2. Motility of *NM23-H1* silenced HepG2 cells by videomicroscopy**