Loss of Nucleolar Histone Chaperone NPM1 Triggers Rearrangement of Heterochromatin and Synergizes with a Deficiency in DNA Methyltransferase DNMT3A to Drive Ribosomal DNA Transcription

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Background: NPM1 is a nucleolar histone chaperone mutated in cancer. NPM1-deficient cells display rearrangement of perinucleolar heterochromatin, and simultaneous knockdown of NPM1 and DNMT3A enhances transcription of ribosomal DNA. NPM1 loss disrupts heterochromatin organization around the nucleolus. The nucleolus has emerged as a platform for the organization of chromatin enriched for repressive histone modifications associated with repetitive DNA. NPM1 is a nucleolar protein required for the maintenance of genome stability. However, the role of NPM1 in nucleolar chromatin dynamics and ribosome biogenesis remains unclear. We found that normal fibroblasts and cancer cells depleted of NPM1 displayed deformed nucleoli and a striking rearrangement of perinucleolar heterochromatin, as identified by immunofluorescence staining of trimethylated H3K9, trimethylated H3K27, and heterochromatin protein 1γ (HP1γ/CBX3). By co-immunoprecipitation we found NPM1 associated with HP1γ and core and linker histones. Moreover, NPM1 was required for efficient tethering of HP1γ-enriched chromatin to the nucleolus. We next tested whether the alterations in perinucleolar heterochromatin architecture correlated with a difference in the regulation of rDNA. U1242MG glioma cells depleted of NPM1 presented with altered silver staining of nucleolar organizer regions, coupled to a modest decrease in H3K9 di- and trimethylation at the rDNA promoter. rDNA transcription and cell proliferation were sustained in these cells, indicating that altered organization of heterochromatin was not secondary to inhibition of rDNA transcription. Furthermore, knockdown of DNA methyltransferase DNMT3A markedly enhanced rDNA transcription in NPM1-depleted U1242MG cells. In summary, this study highlights a function of NPM1 in the spatial organization of nucleolus-associated heterochromatin.

Nucleoli are prominent nuclear structures assembled and organized around actively transcribed ribosomal DNA (rDNA). The nucleolus has emerged as a platform for the organization of chromatin enriched for repressive histone modifications associated with repetitive DNA. NPM1 is a nucleolar protein required for the maintenance of genome stability. However, the role of NPM1 in nucleolar chromatin dynamics and ribosome biogenesis remains unclear. We found that normal fibroblasts and cancer cells depleted of NPM1 displayed deformed nucleoli and a striking rearrangement of perinucleolar heterochromatin, as identified by immunofluorescence staining of trimethylated H3K9, trimethylated H3K27, and heterochromatin protein 1γ (HP1γ/CBX3). By co-immunoprecipitation we found NPM1 associated with HP1γ and core and linker histones. Moreover, NPM1 was required for efficient tethering of HP1γ-enriched chromatin to the nucleolus. We next tested whether the alterations in perinucleolar heterochromatin architecture correlated with a difference in the regulation of rDNA. U1242MG glioma cells depleted of NPM1 presented with altered silver staining of nucleolar organizer regions, coupled to a modest decrease in H3K9 di- and trimethylation at the rDNA promoter. rDNA transcription and cell proliferation were sustained in these cells, indicating that altered organization of heterochromatin was not secondary to inhibition of rDNA transcription. Furthermore, knockdown of DNA methyltransferase DNMT3A markedly enhanced rDNA transcription in NPM1-depleted U1242MG cells. In summary, this study highlights a function of NPM1 in the spatial organization of nucleolus-associated heterochromatin.

Nucleoli are the non-membrane-surrounded intranuclear sites of ribosome biogenesis that harbor copies of the ribosomal RNA (rRNA) gene. The ribosomal DNA (rDNA) is arranged in the form of tandemly arranged repeats at the chromosomal nucleolar organizer regions (NORs) located on the short p arms of the five acrocentric chromosomes in humans, chromosomes 13, 14, 15, 21, and 22. The diploid human genome contains around 300–400 copies of the 43-kb rDNA unit (1). Each rDNA unit consists of ~13.3 kb of sequence encoding the 28S, 5.8S, and 18S rRNAs, and a non-coding intergenic spacer that harbors an enhancer, a spacer promoter, and the core promoter of the rDNA unit (2). Not all rDNA units are active, and up to 50% remain epigenetically silenced in normal human cells (1, 2). Upon initiation of rDNA transcription by RNA pol I, additional proteins and RNA molecules are rapidly recruited to the growing nucleolus. The fully mature nucleolus can be subdivided into three distinct compartments known as the fibrillar center (FC), the dense fibrillar component (DFC), and the granular component (GC). Although still a matter of debate, the prevailing view is that pre-rRNA is transcribed from rDNA at the border between the FC and the DFC. The FC is enriched in components of the RNA pol I machinery, such as the transcription factor UBF, whereas the DFC harbors various RNA-modifying enzymes and pre-rRNA processing factors including fibrillarin (3, 4). Surrounding the FC and the DFC is the GC, where pre-ribosome subunit assembly takes place (3, 4). Immediately juxtaposed to the GC is a shell of perinucleolar heterochromatin composed of silent rDNA, repetitive satellite DNA on centric or pericentric chromatin, and heterochromatic regions from non-NOR-bearing chromosomes (5). The formation and spatial organization of heterochromatin around the

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**Significance:** Rearrangement of heterochromatin in NPM1-deficient cells may be of importance in tumor development.

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nucleolus is of importance for the overall stability of the genome (5–9). It is therefore vital to understand the processes involved in structural maintenance of the nucleoli in relation to the organization of chromatin and vice versa.

An abundant nucleolar protein enriched in the GC is NPM1 (also known as B23 or nucleophosmin). NPM1 is essential for the normal development of the mouse embryo and for the stability of the genome (10, 11). Npm1<sup>−/−</sup> mice display aberrant organogenesis and die between embryonic day E11.5 and E16.5 due to anemia. Npm1 is haplo-insufficient for tumor suppression in hematopoietic cells, and allelic loss results in aneuploidy, increased centrosome numbers, and DNA damage checkpoint activation in these cells (11–13). NPM1 is involved in various cellular processes including centrosome duplication, mRNA splicing, ribosome biogenesis, and apoptosis (14). NPM1 interacts directly with many cellular proteins including the p53 tumor suppressor, MDM2, and ARF (15–17). p53 is normally active in the nucleus as a transcription factor and is polyubiquitinated by the MDM2 ubiquitin E3 ligase, a modification that triggers its proteasome-dependent degradation (18). ARF is a nuclear protein that binds and antagonizes MDM2 ubiquitin ligase activity for p53 (19, 20). In turn, NPM1 binds and co-localizes with ARF and protects it from degradation (21). Thus, in the absence of NPM1, ARF is unstable and is less effective in activating p53 (10, 22). NPM1 may promote oncogenesis by interfering with the activation of p53 by ARF (10, 22). On the other hand, NPM1 regulates turnover of c-Myc by acting on the F-box protein Fbw7<sup>γ</sup>, a component of the E<sub>3</sub> ligase complex involved in the ubiquitination and proteasome degradation of c-Myc (23) with the consequence that loss of NPM1 stabilizes c-Myc.

NPM1 may act as a histone chaperone in the nucleolus, as it binds histones and assembles nucleosomes in vitro (24, 25), but the role of NPM1 in chromatin dynamics and ribosome biogenesis remains poorly understood. We designed a series of experiments to better understand the role of NPM1 in the nucleolus, in particular, how altered levels of NPM1 may affect the nucleolar chromatin including the rRNA genes. We found that cells lacking NPM1 displayed one important difference with respect to wild type cells: a profound alteration in the architecture of perinucleolar heterochromatin. In support, we could show that NPM1 associated with components of chromatin including linker histone H1.5 and heterochromatin protein HP1<sup>γ</sup>. Moreover, NPM1 was required for perinucleolar tethering of HP1<sup>γ</sup>-stained chromatin foci. In this context, NPM1 was dispensable for ribosome biogenesis. Only minor changes in rDNA transcription were detected in NPM1-depleted cells, but silencing of the DNA methyltransferase DNMT3A synergized with loss of NPM1 to drive rDNA transcription.

**EXPERIMENTAL PROCEDURES**

**Cell Cultures**—Osteosarcoma cell line U2OS (wild type, WT p53) was purchased from ATCC (Manassas, VA). Glioma cell line U1242MG (mutant p53) was maintained in our laboratory and has been described (26). Glioma cell line U343MGa CI2-6 (WT p53) has also been described and characterized (27). Normal human diploid dermal fibroblasts (NHDF-c, lot 1x0083002.2) derived from juvenile foreskin were purchased from Promocell (Heidelberg, Germany). p53<sup>−/−</sup> and p53<sup>−/−</sup>Npm1<sup>−/−</sup> mouse embryo fibroblasts were provided by O. Sangfelt (Karolinska Institutet, Stockholm) and were originally a gift from E. Colombo (10). WT mouse embryoblasts (PMEF-CFL, lot 2137256-1) were from Millipore (Billerica, MA). Cells were cultured in Iscove’s modified Dulbecco’s medium containing 10% fetal bovine serum, antibiotics (100 μg of penicillin and 50 μg of streptomycin sulfate/ml), and 2 mM glutamine at 37 °C, 5% CO<sub>2</sub>.

**Cell Proliferation Assay**—U2OS and U1242MG cells were transfected with siRNAs at day 0 (0 h) and day 4 (96 h) with a split of cells at day 3 (72 h). At day 6 the cells were split again and seeded in 6-well cell culture dishes in triplicates at a density of 20,000 cells/well in 2 ml of complete medium. Cells were counted using a hemocytometer, and cell numbers were determined at the indicated time points. The mean and standard deviation at each time point were obtained from a triplicate experiment. In the case of normal human diploid fibroblasts (HDFs) we determined the cell numbers at days 4 (96 h), 7, and 10 following siRNA transfection at day 0 (0 h). The number of cells in control siRNA (siCtrl) cultures was set to 100% in each case, and the percentage of cells in siNPM1-treated cultures relative to siCtrl is given.

**Chemicals**—Chemicals were purchased from Sigma-Aldrich. The drugs and their respective stock solutions, stored at −20 °C, were as follows: actinomycin D (1 mM in DMSO), Nutlin-3 (10 mM, DMSO), and 5-fluorouracil (25 mM, DMSO). The final working concentrations of the drugs are given in Figure 1 legend.

**siRNA Transfection**—To transfected cells in 6-well plates with siRNA we used Oligofectamine according to the manufacturer’s instructions (Invitrogen). The dynamics and efficiency of NPM1 depletion by siRNA were tested by the use of a number of different oligonucleotides. To reduce the NPM1 protein level and to eliminate the nucleolar staining, it was necessary to conduct two rounds of siRNA transfections 4 days apart. siCtrl oligonucleotides were purchased from Invitrogen and Dharmacon. A number of NPM1 siRNAs were used, including two separate siRNAs purchased from Applied Biosystems: siNPM1-1 (5′-CCAAAUUCAUCAUUAUGU-3′) and siNPM1-2 (5′-UUAUGAAAAUGAGCACCCAG-3′).

Mostly, we used an On-Target SMARTpool NPM1 siRNA set (Dharmacon), simply denoted as siNPM1, based on the following set of NPM1 siRNA target sequences: 5′-UUAAGGCGCA- CAAAAGAUU-3′, 5′-ACAGAAGUUCCUUAGAAGA-3′, 5′-AAUGCAAGCAAGUAUAGAA-3′, and 5′-GUAAAGACAA-UAAAGCAA-3′. To deplete human DNMT3A we used Stealth siRNA1 DNMT3A HSS176225 (Invitrogen) and Silencer Select DNMT3A siRNA2 S200426 (Invitrogen). The final concentration of siRNA was kept to no more than 40 nM.

**Plasmid DNA Transfection**—Plasmids were transfected using Lipofectamine 2000 reagent (Invitrogen). Myc-tagged WT NPM1-(1–294) and mutated Myc-NPM1-(117–294) in the pCDS3 vector were a gift from Yanping Zhang (28). Expression vectors pEGF-C1-HP1α, -HP1β, and -HP1γ wild type and HP1γ C59R mutant were a gift from Peter Hemmerich and have been characterized previously (29). Empty pEGF-C1 vector was purchased from Clontech.
**Immunoblotting**—For analysis of detergent-soluble proteins we used the Nonidet P-40 lysis buffer composed of 50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 0.5% Nonidet P-40, 50 mM NaF, 1 mM NaVO₃, 1 mM dithiothreitol, 1× protease inhibitor mixture (Roche), and 1 mM phenylmethylsulfonyl fluoride (Sigma-Aldrich). To analyze total NPM1, histones, and histone modifications, we prepared whole cell extracts by scraping cells directly into SDS-containing sample buffer (2% SDS). The cell lysates were sheared through 18-gauge needles and boiled in order to solubilize the chromatin. Chromatin isolation by small-scale biochemical fractionation was carried out as described (30). Protein concentration in Nonidet P-40 lysis buffer extract was determined by Bradford assay (Bio-Rad). In the case of the whole cell extracts, we ran pilot gels and stained them with Ponceau S or Coomassie Brilliant Blue (CBB) to verify equal loading. Proteins were separated by SDS-PAGE. Transfer of proteins from the gels onto nitrocellulose membranes was conducted on a Bio-Rad Turbo transfer machine. For immunoblotting, the PVDF membranes were incubated in blocking solution (5% milk in PBS) with primary antibodies overnight followed by three washes in PBS and subsequent incubation with secondary horseradish peroxidase-conjugated antibody at room temperature for 2 h. After three additional washes in PBS, the proteins were visualized by using ECL reagent (Amersham Biosciences) or West Pico (Pierce).

**Nuclear Complex Co-immunoprecipitation and Mass Spectrometry**—For small-scale co-immunoprecipitation (co-IP), cells were harvested in 0.5% Nonidet P-40 lysis buffer, and the cleared supernatants were transferred to a new tube. Antibodies were added to the lysates and samples incubated overnight at 4 °C with rotation. Protein A/G beads were added for another 2 h, and then the samples with beads were washed three times with cold lysis buffer. Pelleted beads were dissolved in SDS-containing sample buffer and boiled, and the supernatant was analyzed by SDS-PAGE. In the case of large-scale co-IP followed by mass spectrometry, the cells were harvested and prepared according to the nuclear complex co-IP kit instructions using the high stringency buffer option (Active Motif). Immunoprecipitates were separated by SDS-PAGE, and gels were stained with colloidal CBB kit according to the manufacturer’s instructions (Invitrogen). The stained bands unique to the NPM1 antibody lane were cut out and subsequently identified by mass spectrometry (LC-MS/MS) bought as an external service from Alphalyse A/S (Denmark). In brief, the protein samples were reduced and alkylated with iodoacetamide (i.e. carbamidomethylated) and subsequently digested with trypsin. The resulting peptides were concentrated on a ZipTip micro-purification column and eluted onto an AnchorChip target for analysis on a Bruker Autoflex III MALDI TOF/TOF instrument. The peptide mixture was analyzed in positive reflector mode for accurate peptide mass determination. MALDI MS/MS was performed on 15 peptides for peptide fragmentation analysis (partial sequencing). Peptide tolerance was set to 60 ppm with up to one miscleavage allowed. The MS and MS/MS spectra were combined and used for database searching using Mascot software, version 2.2.03. Proteins were identified in NRDB1 database. Accession numbers listed in Table 1 are linked to the UniProt database.

**RNA Isolation and qRT-PCR**—Total cellular RNA was extracted with TRizol reagent (Invitrogen). Real-time quantitative reverse transcriptase-polymerase chain reaction (qRT-PCR) was performed to determine the expression of 47S pre-rRNA transcript. The Power SYBR® Green RNA-to-CT™ One-Step kit (Invitrogen) was used together with an Applied Biosystems 7500 real-time PCR system. 47S pre-rRNA was amplified using the following primers: forward, 5′-TGTCA-GGGTTCCTGCTCTC3′; and reverse, 5′-GAGAGCACGACGT-CACCAC3′. GAPDH was used as the internal standard and amplified using the following primers: forward, 5′-CGACCAC-TTGTCAAGCTCA3′; reverse, 5′-AGGGGAGATTGCTTGGTG3′.

**Immunofluorescence Staining and Microscopy**—Immunofluorescence staining was carried out as described (31). Immunostained cells were analyzed by using a Zeiss Axioplan II microscope equipped with Plan-Apochromat 63×/1.4 and Plan-Neofluar ×100/1.30 objectives controlled by AxioVision 3.1 software. Images were assembled in Adobe Photoshop CS5 or Adobe Illustrator CS5. For analysis of the number, size, and Ag-NOR area of nucleoli, we used the Imagej program.

**Antibodies**—The following antibodies were used: NPM1 (mouse IgG1, Sigma-Aldrich clone FC82291), p53 (mouse, Sigma-Aldrich clone DO1), p21 (rabbit, Abcam), β-actin (mouse IgG1, Sigma-Aldrich clone AC-15), WIG1/ZMAT3 (rabbit, Sigma-Aldrich AV50793), PUMA (rabbit, Abcam ab9643), fibrillarin (rabbit, Abcam ab5821), nucleolin (mouse, Abcam ab13541), RPL11 (mouse IgG1, Invitrogen clone 3a4a7), PCNA (mouse IgG, Santa Cruz Biotechnology clone PC10), α-tubulin (mouse IgM, Santa Cruz Biotechnology clone 10D8), DNMT3A (mouse, Abcam ab13888), DNMT3A (rabbit, Santa Cruz Biotechnology sc-20703), UBF1 (rabbit, Sigma-Aldrich 4503056), BrdU (mouse IgG1, Sigma-Aldrich clone BU33), GFP (mouse IgG1, Roche clone s7.1 and 13.1), GFP (rabbit IgG, Abcam), c-Myc (mouse IgG1, Abcam ab4441), H3 (rabbit IgG, Abcam ab1791), H1 (mouse IgG2a, Santa Cruz Biotechnology sc-8030), H1.5 (rabbit IgG, Abcam ab24175), phospho-histone H2A.X Ser-139 (rabbit, Cell Signaling 2577), phospho-ATM/ATR substrates (rabbit, Cell Signaling 2851), phospho-ATM Ser-1981 (rabbit, Cell Signaling 13050), and CENPA (mouse, Abcam ab13939). The following antibodies were obtained from Active Motif: H3K9me3 (rabbit serum, 39162), H3K9me2 (rabbit IgG, 39240), H4K20me1 (rabbit serum, 39176), H3K27me3 (rabbit IgG, 39175), H3K4me3 (rabbit IgG, 39915), H3K9ac (rabbit IgG, 39917), H3 (rabbit serum, 39164), H4 (rabbit serum, 39270), H3 pan-Ac (rabbit serum, 39140), H4 pan-Ac (rabbit serum, 39244), HP1γ (mouse IgG1, clone 1MOD-1A9), HP1α (mouse IgG1, clone 2MOD-1G6), and HP1β (mouse IgG1, clone 2HP-1H5).

**Silver Staining of Nucleolus Organizer Regions and Acidic Toluidine Blue O Staining**—Silver staining of NORs (Ag-NOR staining) was conducted as described (32). Cells grown on coverslips were fixed in 2% glutaraldehyde in PBS for 10 min at room temperature, rinsed with PBS and water followed by fixation for 5 min with methanol/acetic acid at a 3:1 ratio, rinsed in water again, and stained (for 45 min) with a mixture of solution A and solution B at a 1:2 ratio, where solution A is composed of 2% gelatin in 1% formic acid and solution B is 50% silver nitrate.
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in ultrapure water. Reactions were terminated by washing the coverslips in ultrapure water and mounting the coverslips on glass slides. Acidic toluidine blue O staining of air-dried unfixed cells was carried out as described (32). A solution of 0.5% toluidine blue O was prepared in 10% ethanol, diluted 1:50 with MacIlvaine’s buffer (0.1 M citric acid, 0.2 M Na₂HPO₄) at pH 5.5. An Olympus microscope equipped with a Leica DFC320 camera and a PlanApo ×40 objective was dedicated to the analysis and documentation of Ag-NOR and toluidine blue O-stained cells.

5-Fluorouridine Labeling—5-Fluorouridine (5-FUrd) is incorporated into mRNA and rRNA. For labeling with 5-FUrd, cells on coverslips were incubated in 2 mM 5-FUrd for 10 min at 37 °C as described (33). Reactions were stopped by washing in ice-cold PBS followed by fixation of cells in 3.7% formaldehyde in PBS for 15 min and subsequent permeabilization in 0.2% Triton X-100. Cells were incubated with primary antibody against BrdU for 1 h followed by three washes and incubation with secondary antibody for 30 min, three additional washes, and mounting of the coverslips onto glass slides.

Ribosomal DNA FISH—The rRNA genes are clustered repeats found close to the centromeres of human chromosomes 13–15, 21, and 22, and these repeats form the NORs. A FISH probe for the NOR was purchased from Chromobios (Nussdorf, Germany). This probe identifies the NOR on each NOR bearing human chromosome. rDNA FISH using cells growing on coverslips was performed as suggested by the manufacturer.

Chromatin Immunoprecipitation and qPCR—Chromatin immunoprecipitation (ChIP) was performed using a ChIP kit according to manufacturer’s protocol (Abcam Ltd., ab500). ChIP DNA samples were analyzed using Power SYBR® Green PCR Master Mix (Invitrogen 4367659) on an Applied Biosystems 7500 real-time PCR system using the standard SYBR® Green 90-min cycling mode. ChIP data were analyzed using the percent input method. Cells were trypsinized, collected, and fixed for 10 min in 1% formaldehyde. Samples were sonicated in a buffer containing protease inhibitors for 10 cycles (30 s on/30 s off) on the high setting using the Diagenode Bioruptor Plus UCD-300 sonication system according to the manufacturer’s recommendation for chromatin sonication. Samples were kept at 4 °C during sonication. A DNA fragment size of around 200–100 base pairs was confirmed using agarose (1.5%) gel electrophoresis. The samples were diluted in ChIP buffer, and an aliquot was stored at −20 °C as input reference. The following antibodies and quantities were used for immunoprecipitation: H3 (5 μg rabbit polyclonal, Abcam ab1791); H3K9me3 (2 μg rabbit polyclonal, Active Motif 39162); H3K9me2 (10 μg rabbit polyclonal Active Motif 39239); and H3K9ac (10 μg rabbit polyclonal Active Motif 39917). Samples were incubated overnight at 4 °C with rotation. Antibody-chromatin complexes were isolated using protein A beads for 60 min with rotation at 4 °C. We used a chromatin sample incubated with protein A beads-only as the negative control. To purify DNA from the samples, a DNA-purifying slurry was added, and the samples were incubated at 98 °C for 10 min, left to cool, incubated with proteinase K at 55 °C for 30 min, and then incubated at 98 °C for 10 min. The samples were resuspended in PCR-grade water and stored at −20 °C for later analysis with quantitative PCR. The following primers (P) were used corresponding to primer pairs A–C: A, P3 forward, AGGTGTCCGGTCCGTGT; A, P3 reverse, GGACAGCTGTACAGCAAAATA; B, P4 forward, TGTAGGGTTTCTGTCCTC; B, P4 reverse, GAGAGCAGCTCGACACAC; C, P5 forward, GAGAGCTCAGTTTATCAGA; and C, P5 reverse, GGGATGAGGGCAGAGTTCG. As control, we used a ChIP primer pair for the γ-actin promoter (ab85783) purchased from Abcam.

Labeling of NewlySynthesized RNA and Protein—rRNA synthesis and processing were analyzed by 1-[methyl-3H]methionine (PerkinElmer Life Sciences) labeling (50 μCi/ml) for 2 h. Total RNA was isolated using TRizol. Isolated RNA was loaded onto 1% agarose-formaldehyde gels, blotted onto Hybond N+ membranes (Amersham Biosciences), sprayed with En3Hance spray (PerkinElmer Life Sciences), and subjected to fluorography for 1–3 days using Biomax MS-1 film and a Biomax translux screen LE (PerkinElmer Life Sciences). To visualize total protein synthesis, cells were cultured in methionine/cysteine-free medium supplemented with 10% (v/v) dialyzed FCS (Invitrogen) for 30 min followed by a 3-h pulse with 50 μCi/ml [35S]methionine/cysteine (PerkinElmer Life Sciences). Whole cell extracts were prepared, and part of the material was resolved by 12% SDS-PAGE followed by autoradiography.

Statistical Analysis—Experiments were usually conducted in three independent experiments, each in triplicate, and the results are presented as the mean ± S.D. Student’s t test was used to evaluate the differences in the data between two groups. Mean, S.D., and t test were calculated in Microsoft Excel. Statistical probability (p) was set at p < 0.05, p < 0.01, and p < 0.001. Means were considered significantly different at p < 0.05.

RESULTS

NPM1 Knockdown Alters the Morphology of Nucleoli—The efficiency and dynamics of NPM1 silencing were evaluated by using a number of different siRNA oligonucleotides that target NPM1. We initially chose to work with the U2OS osteosarcoma and the U1242MG glioma cell lines in which a robust depletion of NPM1 was achieved. Upon visual inspection of cells transfected with NPM1 siRNA, we observed that nucleoli were no longer as phase-dense and compact; they instead appeared distorted and had lost their round shape (Fig. 1A). This nucleolar phenotype occurred in cells transfected with three different siRNA oligonucleotides able to reduce NPM1, but it was not observed in siCtrl-treated cells. Round and compact nucleoli were much less frequent in siNPM1-treated U2OS cells (U2OS: 87.3 ± 3.4% in control versus 12.5 ± 2.4% in siNPM1-treated cells, p < 0.001). This was the case also for U1242MG cells, which presented with 78.4 ± 5.5% round and compact nucleoli in cultures transfected with siCtrl but only 9.1 ± 3.4% round nucleoli in siNPM1-treated cells (p < 0.001). The estimation of nucleolar numbers in NPM1-depleted cells was complicated by the tendency of the elongated nucleoli to not be clearly separated from each other. Nevertheless, counting revealed that there were no significant changes in the number of nucleoli in U2OS and U1242MG cells. The average number of nucleoli in siCtrl-treated U2OS cells was 3.5 ± 1.04/cell, with 3.27 ± 0.90/cell in cells depleted of NPM1, which was not a significant dif-
ference \( p = 0.35, >50 \text{ cells evaluated} \). In U1242MG cells, the
nucleolar number was \( 4.0 \pm 1.31 \) in siCtrl and \( 4.4 \pm 1.44 \) after
siNPM1 treatment \( p = 0.28, >40 \text{ cells evaluated} \). Thus, NPM1
depletion induced deformation of nucleoli but not their
disassembly. In support of these findings, distortion of nucleoli
in HeLa cells depleted of NPM1 has been reported previously
(34).

Nucleoli in NPM1-depleted cells were visualized by immu-
nofluorescence staining for fibrillarin, which served as a marker
for nucleolar DFC regions \( (4, 32) \). In siCtrl cells, NPM1 accu-
culated in the periphery of the nucleolus, whereas the fibril-
larin antibody stained the internal regions of the nucleolus.

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\text{FIGURE 1. NPM1 depletion alters nucleolar morphology. A, phase-contrast (P.C) images of U1242MG cells reveal the morphology of nucleoli in cells transfected with different siRNAs that target NPM1. A number of validated NPM1 siRNAs were used including siNPM1-1 and siNPM1-2. The On-Target SMARTpool NPM1 siRNA was denoted siNPM1. Depletion of NPM1 resulted in deformation of the normally round and phase-dense nucleoli into nonsymmetrical nucleoli with reduced phase contrast. The white arrowheads point at nucleoli in some selected cells. Magnification, ×20. B, U2OS cells were transfected with siCtrl or siNPM1 for 3 and 9 days and subsequently subjected to double immunofluorescence staining for NPM1 (green) and fibrillarin (red). Nuclei were identified by DAPI. Scale bar: 10 μm. C, zoom-in images of representative cells in B. In siCtrl-treated cells, NPM1 preferentially stained the periphery of the nucleolus, whereas the fibrillarin antibody stained the internal regions of the nucleolus (left image). In siNPM1-treated cells, fibrillarin was more concentrated to the smaller foci, and the nucleolar structure was distorted (middle image). D, whole cell protein extracts from U2OS and U1242MG cells treated with siNPM1 or siCtrl were resolved by SDS-PAGE. The levels of NPM1, UBF1, and fibrillarin were determined by IB. Magnification, ×20. E, the effect of NPM1 depletion on cell proliferation was analyzed in U2OS and U1242MG cells that had been depleted of NPM1 \( (\text{siNPM1}) \) or mock-treated \( (\text{siCtrl}) \) for 6 days. To obtain cell proliferation curves, 20,000 cells/treatment were seeded in each well of the 6-well plate. Shown is the mean ± S.D. from a triplicate experiment \( (*, p < 0.05) \). G, NPM1 depletion in U2OS cells affects the p53 response. U2OS cells were transfected with siNPM1 or siCtrl for 6 days followed by exposure to DMSO (control), actinomycin D \( (\text{Act-D}, 5 \text{nM}) \), 5-fluorouracil \( (5\text{-FU}, 5 \text{μM}) \), and Nutlin-3 \( (10 \text{μM}) \) for 18 h. Protein extracts were made from the cells and resolved by SDS-PAGE. Relative levels of NPM1, p53, WIG1 (also known as ZMAT3 or PAG608), PUMA, and p21 were determined by IB. β-Actin and GAPDH served as loading controls. Note that WIG1, PUMA, and GAPDH were developed on a separate blotting membrane.}
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FIGURE 2. Changes in Ag-NOR staining patterns and altered localization of rDNA in NPM1-depleted cells. A, nucleolin immunolocalization (red) in NPM1-depleted and control U2OS cells. Scale bar, 10 μM. B, representative micrographs of Ag-NOR-stained NPM1-depleted U2OS and U1242MG cells. Magnification, ×40. C, Toluidine blue O staining of U2OS cells depleted of NPM1 versus siCtrl. Insets illustrate the perinucleolar white halo in siCtrl cells, lost in siNPM1-treated cells. Magnification, ×40. D, rDNA localization in cells depleted of NPM1. Interphase U2OS cells were subjected to fluorescent in situ hybridization to visualize the localization of the rDNA. The rDNA was hybridized to a probe specific for the NOR region (red), and nuclei were stained with DAPI (blue).

irregular foci (Fig. 1C). At day 6 and onward we obtained a relatively homogenous cell population with very little or no NPM1. Interestingly, nucleoli in these cells were morphologically distorted but seemed intact (Fig. 1C). Depletion of NPM1 did not affect the cellular levels of the nucleolar UBF1 proteins and fibrillarin (Fig. 1D).

We assessed the effect of NPM1 depletion on global protein synthesis by taking the approach of [35S]methionine/cysteine labeling of nascent protein. Silencing of NPM1 did not visibly alter the incorporation of [35S]methionine/cysteine into nascent protein in either U2OS or U1242MG cells during a 3-h pulse labeling (Fig. 1E). We next investigated the cell proliferation rate. We used U2OS and U1242MG cells that had been depleted of NPM1 for 6 days (144 h). We found that proliferation of U2OS cells was significantly decreased (p < 0.05), whereas the proliferation rate of U1242MG cells was not significantly altered when the cells were depleted of NPM1 (Fig. 1F).

Silencing of NPM1 Impairs the p53-dependent Response following Nucleolar Stress—Inhibition of rDNA transcription or defects in rRNA processing induces nucleolar stress and activation of the p53 tumor suppressor (35). Because nucleoli in NPM1-depleted cells displayed a dramatic change in morphology, we tested whether this may have caused nucleolar stress and p53 activation. Interestingly, depletion of NPM1 did not activate p53, and there was no induction of the p53 downstream targets p21, PUMA, and WIG1 (also known as ZMAT3) (Fig. 1G). This lack of p53 stabilization or activation of p53 targets in response to NPM1 depletion in U2OS cells suggests that deformation of nucleoli does not necessarily trigger nucleolar stress and p53 stabilization. U2OS cells transfected with siNPM1 were also incubated in a low concentration of actinomycin D (5 nm) or 5-fluorouracil (50 μM). Actinomycin D will at this concentration mainly act on RNA pol I, thus inhibiting rDNA transcription and triggering a nucleolar stress response, whereas 5-fluorouracil interferes with rRNA processing (35). Additionally, cells were treated with Nutlin-3 (10 μM), which induces p53 by preventing p53-MDM2 interaction, as a control for p53 induction not relying on the nucleolar stress pathway (36). The results showed a clear increase in p53 levels in siNPM1-treated cells just as in siCtrl-treated cells after incubation with actinomycin D, 5-fluorouracil, and Nutlin-3 (Fig. 1G). A deficiency in NPM1 is however known to negatively affect the transcriptional activity of p53 (37, 38). Following stabilization of p53, we detected elevated levels of p21, PUMA, and WIG1. Induction of these proteins was attenuated in siNPM1-treated cells, although the p21 level was relatively unaffected in the case of NPM1-depleted cells treated with Nutlin-3. This result led us to conclude that NPM1 was not required for p53 stabilization in response to nucleolar stress, but still the induction of p21, PUMA and WIG1 was decreased in NPM1 knockdown cells.

Altered Subcellular Distribution of rDNA upon NPM1 Depletion—Given that the change in nucleolar phenotype was an obvious and common alteration in cells with reduced levels of NPM1, we decided to carry out additional structural and functional analyses of the nucleolus. Indirect immunofluorescence staining of nucleolin confirmed the more irregular shape of nucleoli but also confirmed that the nucleolar GC remained intact (Fig. 2A). The NORs are composed of 50–100 rRNA gene copies each. Active NORs include decondensed rDNA at which associated proteins stain intensively with silver (Ag-NORs) and where rDNA transcription is thought to occur, but some NORs remain silent (1, 32). Staining of Ag-NOR proteins with silver nitrate in NPM1-depleted U2OS and U1242MG cells showed that the silver staining was different, and the round nucleolar structure seen in siCtrl-treated cells was lost (Fig. 2B). NPM1 is one among a handful of silver-reactive Ag-NOR proteins (39). A probable explanation for the retained Ag-NOR staining in NPM1-depleted cells could be that it is compensated for by an overall increase in one or several other Ag-NOR proteins and, in combination with the deformed nucleoli, masks any potential loss of NPM1 reactivity with silver. However, the actual contribution of NPM1 to the Ag-NOR signal in situ has not...
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Because the nucleoli in NPM1-depleted cells were no longer clearly seen in the light microscope as phase-dense nuclear bodies, we stained the cells with acidic toluidine blue O. At acidic pH this dye stains RNA and results in prominent nucleolar staining due to the high content of ribosomal RNA in the nucleolus (32). Nucleoli in NPM1-depleted cells could be visualized by this staining, and they clearly remained intact, although their shape was altered (Fig. 2C). Notably, the white rim corresponding to the shell of condensed DNA normally surrounding the nucleolus was missing in NPM1-depleted cells (Fig. 2C, inset). To visualize directly the effect of NPM1 depletion on the localization of the rDNA, in situ hybridization was performed using a fluorescent probe covering the rDNA loci. In control cells, the rDNA was localized within the round nucleoli, whereas in cells depleted of NPM1 the rDNA was unraveled and formed thinner strands extending throughout the nucleus, resembling the fibrillarin and Ag-NOR staining patterns (Fig. 2D).

**Rearrangement of Perinucleolar Heterochromatin in NPM1-depleted Human Cancer Cells—**Nucleoli usually surround themselves with a shell of perinucleolar heterochromatin (1, 5). Nucleoli stain poorly with the fluorescent dye DAPI, whereas perinucleolar heterochromatin stains intensely (1). Depletion of NPM1 led to a loss of dense perinucleolar heterochromatin around the distorted nucleoli as detected by DAPI staining. The chromatin appeared diffuse with no continuous condensation around the nucleoli in U2OS and U1242MG cells depleted of NPM1 (Fig. 3A). Trimethylated H3K9 (H3K9me3) and trimethylated H3K27 (H3K27me3) are considered markers of condensed transcriptionally inactive chromatin, and antibodies to these histone modifications usually stain perinucleolar heterochromatin (7). In NPM1-depleted U2OS cells the H3K9me3/H3K27me3-enriched perinucleolar heterochromatin had collapsed and was instead redistributed within the nucleus and formed irregular foci (Fig. 3B). Trimethylated H3K4 (H3K4me3) and acetylated H3K9 (H3K9ac) are considered markers of transcriptionally active chromatin regions. Nucleoli in U2OS and U1242MG cells were largely devoid of immunofluorescence staining for H3K4me3 and H3K9ac (Fig. 3B). Trimethylation of H3K9 and binding to heterochromatin protein 1 (HP1) are critical events in heterochromatin formation (40). HP1γ isoform localizes to perinucleolar heterochromatin regions surrounding the nucleolus (29), so we evaluated the localization of HP1γ in cells depleted of NPM1. Strikingly, the distinct perinucleolar enrichment of HP1γ was disrupted, and the protein accumulated in irregular foci throughout the nucleus (Fig. 3C). Irregular clusters or clumps of condensed chromatin were also found in the nucleoplasm (Fig. 3C). Given these findings, we conclude that NPM1 maintains the nucleolar chromatin organization by organizing perinucleolar heterochromatin.
the association of NPM1 with histones (24) and the redistribution of H3K9me3 in cells depleted of NPM1, we decided to analyze the total cellular levels of H3 and common posttranslational modifications on H3 as well as H4. By immunofluorescence staining and immunoblotting, we found no evidence of major changes in the total cellular levels of H1, H3, H4, H3K9me3, H3K9ac, H3K27me3, H4K20me1, H4-PanAc, and H3K4me3 following NPM1 depletion in U1242MG cells.

FIGURE 4. NPM1 depletion alters the structure of nucleoli in normal human diploid fibroblasts. A, phase-contrast images of a representative HDF from siCtrl and siNPM1-treated cultures. The white arrowheads point at nucleoli. Magnification, ×20. B, verification of NPM1 knockdown in HDFs. Levels of NPM1, p53, and p21 were determined by IB at day 8 after the first siRNA transfection occasion (day 0). C, detection of NPM1 by immunofluorescence staining in HDF cultures transfected with siCtrl or siNPM1. Nuclei were stained with DAPI. Scale bar: 20 μM. D, HDFs depleted of NPM1 were subjected to double immunofluorescence staining for HP1α and fibrillarin. Insets are zoom-in images of representative nucleoli. Scale bar: 10 μM. E, HDFs depleted of NPM1 were double stained for H3K9me3 and NPM1. Insets are zoom-in images of representative nucleoli. F, morphology of HDFs transfected with siNPM1 or siCtrl indicated no overt changes in gross cell morphology at early time point (day 4). At day 15 the HDF cultures treated with siNPM1 appeared less cell-dense. Magnification, ×20. G, reduced numbers of HDFs were consistently seen in cultures treated with siRNA at days 7 and 10. Shown is the relative cell number at days 4, 7, and 10. The number of cells in siCtrl cultures was set to 100% in each case, and the percentage of cells in siNPM1-treated cultures relative to siCtrl is given. Shown is one representative experiment in triplicate (*, p < 0.05).
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Despite the fact that the cellular distribution of H3K9me3 and H3K27me3 was changed (Fig. 3, B, D, and E). In line with the results in U1242MG cells, neither were there any differences seen in the total cellular levels of H3K9me3, H3K9ac, H3K4me3, and H4K20me1 in U2OS cells depleted of NPM1 (Fig. 3F).

Disruption of Perinucleolar Heterochromatin in NPM1-depleted Human Diploid Fibroblasts—Changes in nucleolar morphology identical to those in U2OS and U1242MG cells were detected in NPM1-depleted normal HDFs. The cells were depleted of NPM1 for 8 days (192 h) prior to analysis by immunofluorescence and immunoblotting. The changes included reduced phase contrast and absence of distinct perinucleolar chromatin (Fig. 4, A–C). H3K9me3 and HP1γ-enriched perinucleolar chromatin was redistributed within the nucleus, forming irregular and scattered foci or clumps in NPM1-depleted HDFs (Fig. 4, D and E). We estimated cell proliferation rates in HDF cultures depleted of NPM1. During the first 4 days, no significant difference in cell number was seen. NPM1 silencing did not significantly impair cell proliferation until 1 week after starting siRNA transfection. On average 25% less cells were found in siNPM1-treated HDF cultures than in siCtrl-treated cultures when measured at day 7 (p < 0.05) as well as at day 10 (p < 0.05) (Fig. 4, F and G). Interestingly, we did not detect an increase in p53 and p21, despite efficient silencing of NPM1 in HDFs as measured at day 8 (Fig. 4B).

We monitored NPM1-depleted HDFs for potential DNA damage by immunofluorescence staining of the cells for DNA damage markers including γ-H2AX, p-ATM, and phosphorylated ATM/ATR substrates but did not detect any increased staining or foci formation in HDFs kept for 2 weeks with reduced NPM1 (data not shown).

Altered Nucleolar Morphology and Scattering of Chromocenters in Npm1-deficient Mouse Embryonic Fibroblasts—Similarly to human cells, nucleoli were altered in p53−/−,Npm1−/− MEFS when compared with WT and p53−/− MEFS. It was not possible to generate Npm1−/− MEFS on a WT p53 background. Importantly, a distorted but more extensive Ag-NOR staining pattern was also observed in p53−/−,Npm1−/− MEFS compared with WT or p53−/− MEFS (Fig. 5A). The mean values for Ag–NOR area per nucleus were 26.2 ± 3.3 μm² for WT MEFS and 38.1 ± 3.0 μm² in the case of p53−/−,Npm1−/− MEFS (p < 0.05, 30 cells evaluated for each genotype) (Fig. 5B). Thus, the Ag–NOR area was significantly expanded in p53−/−,Npm1−/− cells compared with WT MEFS, whereas the difference in mean Ag–NOR area per nucleus comparing WT MEFS and p53−/− MEFS was not statistically significant (Fig. 5B). Given the findings in NPM1-depleted human cells, we analyzed the heterochromatin and the nucleoli in WT, p53−/−, and p53−/−,Npm1−/− MEFS by DAPI, fibrillarin, HP1γ, and H3K9me3 immunofluorescence staining. Analysis of heterochromatin is facilitated in mouse cells in which the satellite repeats are organized in chromo-

FIGURE 5. Altered nucleolar morphology and disrupted heterochromatin organization in p53−/−,Npm1−/− mouse embryonic fibroblasts. A, phase-contrast images of Ag–NOR-stained WT, p53−/−, and p53−/−,Npm1−/− MEFS. Three cells for each genotype are shown. B, average Ag–NOR area representing analysis of 30 cells/genotype (mean ± S.D.; *, p < 0.05). n.s, non-significant. C, whole cell extracts from p53−/−,Npm1−/− and p53−/− MEFS were resolved by SDS-PAGE and transferred to membranes followed by IB with anti-H3, anti-H3K9ac, and anti-H3K9me3 antibodies. D, images of WT, p53−/−, and p53−/−,Npm1−/− MEFS nuclei stained with a mouse monoclonal anti-NPM1 antibody. E, representative images of WT, p53−/−, and p53−/−,Npm1−/− MEFS nuclei stained with a rabbit anti-fibrillarin antibody. F, WT, p53−/−, and p53−/−,Npm1−/− MEFS were double stained for HP1γ and fibrillarin. Scale bar: 10 μm. G, immunofluorescence staining for H3K9me3 in WT, p53−/−, and p53−/−,Npm1−/− MEFS. Cells in D–G were counterstained with DAPI.

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centers, and these chromatons are often juxtaposed to the nucleolus. First, we were able to determine that the total cellular levels of H3K9me3 and H3K9ac remained unchanged in p53−/−,Npm1−/− MEFs when compared with p53−/− MEFs according to immunoblotting (Fig. 5C). Second, we noticed dramatic differences in the nuclear DAPI staining pattern of p53−/−,Npm1−/− MEFs compared with WT and p53−/− MEFs. The chromatons as identified by DAPI, H3K9me3, and HP1γ appeared irregular and smaller, but also more numerous, in the absence of Npm1 (Fig. 5, E–G). Npm1 protein itself was not enriched in chromatons but was restricted to nucleoli and was most distinct in the nucleolar periphery (Fig. 5D). The shell of thin perinucleolar heterochromatin, especially prominent around nucleoli in p53−/− MEFs, was absent around nucleoli in p53−/−,Npm1−/− MEFs (Fig. 5, D and E). Similar to findings human cells, we found that the perinucleolar enrichment of HP1γ was disrupted. Instead, HP1γ was concentrated in irregular smaller structures in contrast to the more symmetrical, round, chromatons present in WT cells (Fig. 5F). Thus, the loss of Npm1 in mouse cells alters the organization of nucleoli and its associated heterochromatin, matching the findings in human cells.

**NPM1 Maintains Nucleolar Chromatin Organization**—We next overexpressed WT and mutant NPM1 in U2OS cells to see whether we could detect an opposite phenotype to that in cells with reduced NPM1. The NPM1 mutant Myc-NPM1-(117–294) lacks the oligomerization domain, is predominantly nucleoplasmic, and is defective in histone binding (41, 42). Overexpression of WT NPM1, but not mutant NPM1, enhanced the features of the already round and compact nucleoli in U2OS cells, in that the surrounding rim of condensed DNA enriched for H3K9me3 and stained intensely with DAPI became much more accentuated (Fig. 6A). This enhancement of the rounded nucleolar structure was not seen in cells transfected with mutant NPM1 or in non-transfected cells serving as internal controls. The effect of additional ectopic NPM1 in U2OS cells was somewhat ambiguous given the abundance of endogenous NPM1 in these cells. Therefore, NPM1 was also ectopically introduced by transfection of the Myc-NPM1 (WT) plasmid into NPM1 was also ectopically introduced by transfection of the Myc-NPM1 (WT) plasmid into WT and p53−/− MEFs. The chromatons as identified by DAPI, H3K9me3, and HP1γ appeared irregular and smaller, but also more numerous, in the absence of Npm1 (Fig. 5, E–G). Npm1 protein itself was not enriched in chromatons but was restricted to nucleoli and was most distinct in the nucleolar periphery (Fig. 5D). The shell of thin perinucleolar heterochromatin, especially prominent around nucleoli in p53−/− MEFs, was absent around nucleoli in p53−/−,Npm1−/− MEFs (Fig. 5, D and E). Similar to findings human cells, we found that the perinucleolar enrichment of HP1γ was disrupted. Instead, HP1γ was concentrated in irregular smaller structures in contrast to the more symmetrical, round, chromatons present in WT cells (Fig. 5F). Thus, the loss of Npm1 in mouse cells alters the organization of nucleoli and its associated heterochromatin, matching the findings in human cells.

**NPM1 Levels Dictate the Structure of the Nucleolus and Its Surrounding Chromatin**—We next overexpressed WT and mutant NPM1 in U2OS cells to see whether we could detect an opposite phenotype to that in cells with reduced NPM1. The NPM1 mutant Myc-NPM1-(117–294) lacks the oligomerization domain, is predominantly nucleoplasmic, and is defective in histone binding (41, 42). Overexpression of WT NPM1, but not mutant NPM1, enhanced the features of the already round and compact nucleoli in U2OS cells, in that the surrounding rim of condensed DNA enriched for H3K9me3 and stained intensely with DAPI became much more accentuated (Fig. 6A). This enhancement of the rounded nucleolar structure was not seen in cells transfected with mutant NPM1 or in non-transfected cells serving as internal controls. The effect of additional ectopic NPM1 in U2OS cells was somewhat ambiguous given the abundance of endogenous NPM1 in these cells. Therefore, NPM1 was also ectopically introduced by transfection of the Myc-NPM1 (WT) plasmid into p53−/− MEFs. This resulted in the emergence of rounded nucleoli that were encircled by perinucleolar chromatin marked by H3K9me3 and more concentrated DAPI staining (Fig. 6C) as well as more concentrated and distinct fibrillarin staining (Fig. 6B). The effect of ectopic NPM1 was dependent on the protein level. Low levels of NPM1, similar to that obtained by knockdown of NPM1 by siRNA in WT cells, failed to restore the disrupted nucleolar morphology to wild type (Fig. 6, B and C). The NPM1 mutant Myc-NPM1-(117–294) failed to restore nucleolar morphology in p53−/−,Npm1−/− MEFs (Fig. 6D). Hence, the structure of the nucleolus correlates closely with NPM1 levels.

**NPM1 Associates with Core and Linker Histones**—Given that the perinucleolar rim of condensed DNA was disorganized in NPM1-depleted cells, we sought to gain further insights into the cause of this phenotype. We first determined the amount of NPM1 in the chromatin fraction. A high level of NPM1 was present in the chromatin fraction (Fig. 7A). Analysis of the distribution of α-tubulin, β-actin, p53, and histone H3 confirmed the accuracy of the chromat fractionation. We had previously identified numerous ribosomal proteins and different RNA helicases as NPM1-associated proteins in the Nonidet-P40 (detergent)-soluble fraction (43). To identify proteins that associate with endogenous NPM1 in the nucleus, including chromatin, we isolated U1242MG cell nuclei and digested the chromatin with Benzonase. The nuclear lysate was used for co-IP

**FIGURE 6. NPM1 levels dictate the structure of the nucleolus.** A, U2OS cells were transfected with WT NPM1 (Myc-NPM1) and mutant NPM1 (Myc-NPM1-(117–294)). Two days post-transfection, the cells were fixed and immunofluorescence-stained for the Myc tag using the 9E10 mAb and H3K9me3 by using a rabbit polyclonal antibody. Nuclei were stained with DAPI. The DAPI and H3K9me3 staining of representative cell nuclei indicated that the perinucleolar heterochromatin had become more dense and accentuated in wild type Myc-NPM1-expressing cells than in cells transfected with mutant Myc-NPM1-(117–294). B and C, exogenous expression of WT Myc-NPM1 in p53−/−,Npm1−/− MEFs restored nucleolar morphology to WT. p53−/−,Npm1−/− MEFs were transfected with Myc-NPM1, and after 2 days the cells were fixed and stained for NPM1 and fibrillarin (B) or NPM1 and H3K9me3 (C). D, failure of mutant NPM1 to restore nucleolar morphology in p53−/−,Npm1−/− MEFs to WT. Cells were transfected with Myc-NPM1-(117–294) mutant and stained for the Myc tag and H3K9me3.
with a highly specific mouse monoclonal NPM1 antibody. The nuclear complex co-immunoprecipitates were then resolved by SDS-PAGE, and gels were stained with silver or CBB. IgH, immunoglobulin heavy chain; IgL, immunoglobulin light chain; $M_w$, molecular weight (kDa). Positions of IgH, IgL, and NPM1 are indicated. C, proteins extracted using the nuclear complex co-IP kit were immunoprecipitated with mouse monoclonal anti-NPM1 antibody overnight or an isotype IgG control antibody (IP Ctrl), and the material bound to beads was analyzed by SDS-PAGE followed by immunoblotting using anti-NPM1, anti-H3, anti-H3K9me3, anti-H3K9ac, anti-H1.5, and anti-HP1.

### TABLE 1

| Protein       | UniProtKB accession No. | Molecular mass Da | Mascot score | Sequence cover (%) | Unique peptides |
|---------------|-------------------------|-------------------|--------------|--------------------|----------------|
| MAGED2        | Q9UNF1                  | 59,660            | 99           | 26                 | 16             |
| NPM1          | P06748                  | 31,090            | 130          | 42                 | 11             |
| Annexin A2    | P07355                  | 36,631            | 90           | 27                 | 7              |
| HNRNPA2B1     | P22626                  | 36,041            | 194          | 44                 | 11             |
| HNRNPD1       | Q14103                  | 27,546            | 117          | 19                 | 6              |
| HNRNPA1       | P09651                  | 34,273            | 119          | 33                 | 9              |
| Histone H1.5  | P16401                  | 22,566            | 149          | 24                 | 6              |
| RPL23         | P62829                  | 16,730            | 182          | 51                 | 10             |
| RPS7          | P62081                  | 22,115            | 67           | 16                 | 6              |
| Histone H2B.1 | P53778                  | 13,950            | 199          | 50                 | 13             |
| RPL35         | P42766                  | 14,543            | 105          | 30                 | 6              |
| RPS20         | P60866                  | 13,478            | 203          | 46                 | 8              |
| Histone H2A   | Q96V66                  | 14,225            | 92           | 44                 | 5              |

* UniProt Knowledgebase.

* Mascot scores of 95 or greater are considered significant.

* Coverage of the protein by identified and matching peptides (%).

* Number of peptides that match the theoretical digest of the primary protein identified.

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### FIGURE 7

Identification of linker histone H1.5 isoform and HP1γ as NPM1-associated proteins. A, biochemical fractionation of proteins revealed that NPM1 is abundant in the chromatin fraction. Protein content in whole cell extracts (W) was compared with that obtained in a biochemical fractionation procedure using the same number of cells. Detergent-soluble proteins (Np), low-salt extracted nucleoplasmic proteins (Nu), and remaining chromatin (C) bound proteins were separated. Histone H3 served as a marker for the chromatin fraction, and α-tubulin was used for the detergent-soluble protein fraction. B, U1242MG cells corresponding to 10 subconfluent p100 plates were subjected to nuclear complex co-IP. The immunoprecipitates were separated by SDS-PAGE, and the gels were subsequently stained with silver or CBB. IgH, immunoglobulin heavy chain; IgL, immunoglobulin light chain; $M_w$, molecular weight (kDa). Positions of IgH, IgL, and NPM1 are indicated. C, proteins extracted using the nuclear complex co-IP kit were immunoprecipitated with mouse monoclonal anti-NPM1 antibody overnight or an isotype IgG control antibody (IP Ctrl), and the material bound to beads was analyzed by SDS-PAGE followed by immunoblotting using anti-NPM1, anti-H3, anti-H3K9me3, anti-H3K9ac, anti-H1.5, and anti-HP1γ.

### TABLE 1

| Protein     | UniProtKB accession No. | Molecular mass Da | Mascot score | Sequence cover (%) | Unique peptides |
|-------------|-------------------------|-------------------|--------------|--------------------|----------------|
| NPM1        | P06748                  | 31,090            | 130          | 42                 | 11             |
| Histone H3  | P67466                  | 16,730            | 182          | 51                 | 10             |
| Histone H2B | P62081                  | 22,115            | 67           | 16                 | 6              |
| RPL23       | P42766                  | 14,543            | 105          | 30                 | 6              |
| RPS20       | P60866                  | 13,478            | 203          | 46                 | 8              |
| Histone H2A | Q96V66                  | 14,225            | 92           | 44                 | 5              |

* UniProt Knowledgebase.

* Mascot scores of 95 or greater are considered significant.

* Coverage of the protein by identified and matching peptides (%).

* Number of peptides that match the theoretical digest of the primary protein identified.

NPM1 (46). Taken together, several chromatin proteins were identified as associated with NPM1.

NPM1 Is Required for Efficient Nucleolar Tethering of HP1γ-enriched Foci—By testing the NPM1 nuclear complex co-immunoprecipitate for additional interacting proteins, we found that NPM1 associated with histone H3. Importantly, the pool of H3 bound to NPM1 was not modified at residue Lys-9 with me-3 or monocetyl groups (Fig. 7C). Trimethylation of H3K9 and binding to HP1 is a critical event in heterochromatin formation (40). NPM1 also associated with HP1γ (CBX3) (Fig. 7C). The association appeared specific to HP1γ, as no binding to HP1α and HP1β was detected (Fig. 8A and data not shown). To further investigate the NPM1-HP1γ association, we conducted co-localization and co-IP experiments. Transfected EGFP-tagged HP1γ localized throughout the nucleoplasm but was also detected at perinucleolar heterochromatin regions surrounding the nucleolus as shown previously (29) (Fig. 8B). This localization pattern of ectopic EGFP-HP1γ was similar to that of endogenous HP1γ. The EGFP-HP1γC59R mutant does not accumulate in heterochromatin-rich regions, due to its failure to bind H3K9me3 and DNA (29). EGFP-HP1γ partially co-localized with NPM1, but transfected EGFP-HP1γC59R failed to bind endogenous NPM1 and did not co-localize with endogenous NPM1 in perinucleolar areas (Fig. 8, A and B). Recall that in cells devoid of NPM1, the distinct perinucleolar enrichment of HP1γ was disrupted and HP1γ was instead dispersed from the nucleolar periphery. We next sought to determine how the absence of NPM1 would influence the localization of exogenously introduced EGFP-HP1γ. We also addressed whether exogenously introduced NPM1 could affect localization of EGFP-HP1γ. To this end, we transfected EGFP-HP1γ and MYCNPM1 into WT, p53−/−, and p53−/−Npm1−/− MEFs. Fluorescence microscopy revealed that there was a striking difference in the localization of EGFP-HP1γ depending on the status of NPM1 (Fig. 8C). EGFP-HP1γ displayed a striking enrichment in perinucleolar foci in p53−/−Npm1−/− MEFs, but this pattern was disrupted in p53−/−, Npm1−/− MEFs (Fig. 8, C and D). In contrast, co-expression of NPM1 and EGFP-HP1γ pro-
moted the localization of EGFP-HP1γ into round perinucleolar foci (Fig. 8, C and D). We concluded that NPM1 is required for efficient tethering of HP1γ to the nucleolus. Whether NPM1 can tether HP1γ to nucleoli independently of other nucleolar components remains to be determined.

Reduced Levels of Repressive Histone H3 Modifications in the rDNA Promoter Region following NPM1 Depletion—Next we addressed whether the altered organization of nucleolar chromatin was accompanied by changes at the rDNA. We performed ChIP analysis aimed at determining changes in histone modifications at rDNA chromatin. A schematic representation of the rDNA locus in humans is shown in Fig. 9A. Using U1242MG cells that had been depleted of NPM1 for 6 days, we analyzed H3K9ac and two modifications generally associated with transcriptional repression (H3K9me2 and H3K9me3) at the rDNA. As a comparison we used the RNA pol II-transcribed nuclear γ-actin gene promoter region. We detected H3K9ac at the rRNA gene promoter, although this mark was 7-fold more abundant on the γ-actin gene promoter (Fig. 9B). In contrast, the basal levels of H3K9me3 and H3K9me2 were higher at the rRNA genes than at the γ-actin gene promoter region. Depletion of NPM1 led to a modest decrease in the levels of
H3K9me3 and H3K9me2 at rDNA, and the reduction in
H3K9me2 was most robust in the promoter region, whereas
these marks remained relatively unchanged at the
\(\beta\)-actin promoter. There were relatively minor changes in the low
levels of H3K9ac at the rDNA; however a reduction was seen
at the \(\beta\)-actin promoter. The reduction in H3K9me2 in the
promoter region was significant \((p<0.05)\), whereas the
changes in H3K9me3 and H3K9ac did not reach a signifi-
cance level. Taken together, the silencing of NPM1 resulted
in a modest reduction of repressive histone H3 modifications
at the rDNA.

We next sought to explore whether NPM1 depletion
would result in a defective ribosome biogenesis that in turn
may have affected the organization of perinucleolar chroma-
tin. To investigate rDNA transcription, we first used fluo-
rine-conjugated UTP (FUrd) labeling as a method of semi-
quantitative analysis of RNA pol I/RNA pol II transcription
(33). Here, FUrd was efficiently incorporated in NPM1-de-
pleted U1242MG cells (siNPM1 96% versus siCtrl 97% +.ve
cells, 200 cells counted/siRNA and cell type) (Fig. 10A). FUrd
was also efficiently incorporated in NPM1-depleted U2OS cells
after a FUrd pulse of 10 min (Fig. 10A). Actinomycin D is a
potent inhibitor of RNA pol I in the range of 2 to 10 nm and at
higher concentrations (>100 nm) also of RNA pol II (47). When
U2OS cells were exposed to the drug at a concentration of 10
nm for 2 h, it resulted in efficient inhibition of FUrd incorpora-
tion in U2OS cells (3% +.ve cells, 200 cells counted) (Fig. 10B).
No major difference in FUrd labeling was observed when com-
paring \(p53^{-/-}\) and \(p53^{+/-}\) or \(Npm1^{-/-}\) MEFS (Fig. 10C). Double
immunofluorescence staining confirmed that the strongest
FUrd signals were seen within nucleoli as evidenced by co-
localization with fibrillarin (Fig. 10C).

To investigate the role of NPM1 in rRNA processing, U2OS
cells transfected with siCtrl or siNPM1 were incubated with
\(\mathrm{L}^{-}[\mathrm{methyl}^{-3} \mathrm{H}] \text{methionine to label newly synthesized and pro-
cessed rRNA. Knockdown of NPM1 using two different siRNAs
revealed that the production of 47S pre-rRNA was maintained
and that the processing of 18S and 28S rRNA remained intact
(Fig. 10D)). Similar results were obtained in another cell line,
glioma U343MGa CI2:6, indicating no major differences
between siNPM1 and siCtrl-treated cells in terms of rRNA syn-
thesis and processing (Fig. 10D). In contrast, the depletion of
ribosomal protein S9 (RPS9) in U2OS cells severely impaired
the processing of 47S into mature 18S rRNA. In summary,
NPM1 silencing had only minor effects on rRNA synthesis in
the present experimental settings.

FIGURE 9. Reduced silencing of rDNA in NPM1-depleted U1242MG glioma cells. A, schematic representation of the rRNA gene locus in human. Each rDNA
repeat unit consists of a conserved rRNA coding sequence transcribed by pol I and a divergent intergenic spacer region. The mature 18S, 5.8S, and 28S rRNAs
are derived from a polycistronic rRNA precursor transcript (47S pre-rRNA) by separation from externally and internally transcribed spacers. The rRNA gene was
targeted with three different primer pairs, A, B, and C, binding to different regions of the gene. Primer pair A binds the upstream promoter, B binds in the initial
promoter segment, and C binds the 18S region. B, quantitative ChIP analysis of the rDNA in cross-linked chromatin from U1242MG cells depleted of NPM1 and
precipitated with anti-H3K9me2, anti-H3K9me3, and anti-H3K9ac antibodies. The \(\beta\)-actin gene promoter region served as an internal control. Protein A beads
alone were used as a negative control. Shown is the mean \pm S.D. from three independent experiments (biological replicates), each performed in triplicate (*, 
\(p<0.05\)).
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**FIGURE 10. rDNA transcription and processing in NPM1-depleted cells.** A, 5-FUrd incorporation in NPM1-depleted U1242MG and U2OS cells. The cells were incubated in 2 mM 5-FUrd for 10 min. Scale bar: 20 μM. B, control reactions for 5-FUrd labeling included no primary antibody control and 5-FUrd labeling in actinomycin D-treated U2OS cells (10 nm actinomycin D (Act D) for 2 h) resulting in a much reduced signal. As a comparison, 5-FUrd labeling is also shown in siNPM1- and siCtrl-treated U2OS cells. Scale bar: 10 μM. C, 5-FUrd incorporation in p53+/− and p53−/− Npm1+/− cells. The cells were incubated in 2 mM 5-FUrd for 10 min. Incorporation of 5-FUrd into newly made RNA in A–C was detected by a primary antibody against BrdU followed by a secondary FITC-conjugated anti-mouse antibody. In C, cells were also stained for fibrillarin, revealing co-localization of 5-FUrd and fibrillarin in nucleoli. Scale bar: 10 μM. D, synthesis and processing of rRNA. U2OS cells (lanes 7–10) or U343MGa Cl2:6 cells (lanes 1–6) were transfected with siRNA oligonucleotides as indicated. Lanes 4–6 are a replicate experiment of lanes 1–3. Knockdown and control cells were labeled with [methyl-3H]methionine for 2 h. Ribosomal protein S9 (RPS9) siRNA served as a positive control for disrupted processing of rRNA (31). Newly synthesized 47S, 28S, and 18S rRNA species are indicated (upper panel), and the total 28S and 18S rRNA transferred to the membrane was visualized by methylene blue (lower panel).

**DISCUSSION**

NPM1 is the most diversified member of the nucleoplasmin family of histone chaperones, which also includes mammalian NPM2 and NPM3, *Drosophila* nucleoplasmin-like protein (dNLP), and the founding member nucleoplasmin, expressed only in the oocytes of amphibians and homologous to NPM2 (54). We found that even a partial reduction in NPM1 levels resulted in a distortion of the rounded nucleolar structure both in normal and cancer cells. Moreover, we found that perinucleolar heterochromatin was rearranged in NPM1-deficient cells, which may have contributed to the structural changes of

**Down-regulation of DNMT3A and NPM1 Enhances rDNA Transcription—**DNA methyltransferases DNMT3A and DNMT3B are the key enzymes for de novo DNA methylation. They play important roles in epigenetic control of gene expression patterns. Among the pairwise relationships between gene mutations in acute myeloid leukemia, one of the most striking was the co-occurrence of mutations in DNMT3A and NPM1 (48). DNMT3A may play a dynamic role in the epigenetic regulation of cancer cell genomes (49–51). DNMT3A localizes to nucleolar foci in resting fibroblasts, indicating a role for de novo DNA methylation in rDNA silencing (52). Biochemicalfractionation showed that DNMT3A is associated with inactive rDNA in the nucleolus (53). We hypothesized that reduced levels of both NPM1 and DNMT3A may affect the regulation of rDNA transcription directly or indirectly. Expression and knockdown of DNMT3A in U1242MG cells were confirmed by immunoblotting (Fig. 11A). To better estimate rDNA transcription in these cells, we performed qRT-PCR for human 47S pre-rRNA transcript levels. The level of 47S was marginally reduced in cells depleted of NPM1 (Fig. 11B). Actinomycin D efficiently prevented RNA pol I transcription and dramatically reduced the levels of 47S. Although depletion of DNMT3A alone had a tendency toward increasing the levels of 47S pre-rRNA, it was not a significant difference compared with siCtrl or untreated cells. In contrast, the levels of 47S pre-rRNA were elevated in DNMT3A and NPM1 co-depleted U1242MG cells (~2-fold increase in the case of siDNMT3A-1/siNPM1 versus siNPM1 alone, p < 0.05). Thus, depletion of both NPM1 and DNMT3A enhanced rDNA transcription. In agreement with the increase in rDNA transcription, we noted that nucleoli in glioma cells co-depleted of DNMT3A and NPM1 had become more phase-dense and rounded compared with NPM1-depleted cells (Fig. 11C). Note also that the nucleolar morphology in DNMT3A single knockdown cells appeared similar to the control (Fig. 11C). Furthermore, the expression and knockdown of DNMT3A were also confirmed in U2OS cells by immunoblotting (data not shown). Immunofluorescence staining revealed that the fibrillarin signal appeared more intense when DNMT3A was co-depleted with NPM1 in U2OS cells (Fig. 11D). Corresponding DAPI images showed that in DNMT3A/NPM1 co-depleted cells, distinct and condensed heterochromatin was partially missing around the majority of the nucleoli. We concluded that although DNMT3A depletion enhanced rDNA transcription in the context of reduced NPM1, it failed to restore the architecture of perinucleolar chromatin to that observed in siCtrl transfected cells.
nucleoli (Fig. 12). Interestingly, the nucleolar phenotype in NPM1-depleted human cells and Trp53⁻/⁻, Npm1⁻/⁻, MEFs was similar to that observed in oocytes from Npm2⁻/⁻ mice. Nucleoli in Npm2⁻/⁻ oocytes lack the surrounding heterochromatin, and fibrillarin staining revealed dispersed nucleolar-like bodies, whereas usually only one single round nucleolus is seen in wild type oocytes (55). Thus, loss of NPM1, similar to the loss of NPM2, affects the organization of the perinuclear chromatin. We compared the phenotype of NPM1-depleted cells with cells depleted of nucleolin, a major nucleolar protein. We found that nucleolin depletion resulted in much smaller, slightly deformed nucleoli with retained phase contrast and distinct perinuclear chromatin (data not shown). The reduced nucleolar size seen in nucleolin-depleted cells would be consistent with a role of nucleolin in RNA pol I transcription (56, 57).

In principle, (i) the effect on perinucleolar chromatin could be attributed to a possible role of NPM1 in the establishment and maintenance of nucleolus-chromatin domain interactions (5), (ii) but it may also reflect a complex integration of the ribosome biogenesis machinery with the surrounding chromatin, indirectly affecting the heterochromatin; (iii) inhibition of heterochromatin formation per se may also contribute to the phenotype observed in NPM1-deficient cells. Below we present these different options in more detail, and we discuss our data that supports the first model (i), that is, a role of NPM1 in tethering of heterochromatin to the nucleolus.

NPM1 interacts with a number of different proteins that may be involved in the organization of chromatin. In addition to the core histones, we identified linker histone H1.5 as bound to NPM1, confirming previous studies (58, 59). Linker histone H1 isoforms are best known for their ability to stabilize condensed,

**FIGURE 11. Knockdown of NPM1 and DNMT3A enhances rDNA transcription.** A, U1242MG cells were transfected with siCtrl, siNPM1, siDNMT3A-1, siDNMT3A-2, or combinations thereof. Protein extracts were made from the cells and resolved by SDS-PAGE. Relative levels of NPM1 and DNMT3A were determined by IB. β-Actin served as a loading control. B, real-time qRT-PCR was used to measure the levels of 47S pre-rRNA in U1242MG cells depleted of NPM1, DNMT3A, or both NPM1 and DNMT3A. Shown is the mean ± S.D. of a triplicate experiment (biological replicates) in which the untreated cell population was set to 1 (arbitrary units). Actinomycin D (Act D) included as a control, was used at a concentration of 5 nM. The difference between siNPM1-depleted cells and cells co-depleted of NPM1 and DNMT3A was significant (p < 0.05). C, phase-contrast (P.C) images of U1242MG cells reveal the morphology of nucleoli in cells transfected with different siRNAs that target NPM1 or DNMT3A. The arrows point at nucleoli. D, U2OS cells were transfected with siCtrl, siNPM1, siDNMT3A-2, or a combination of siNPM1 and siDNMT3A-2 and subsequently were subjected to immunostaining for fibrillarin (red) after 6 days. Nuclei, identified by DAPI, are visualized in black-and-white mode. Scale bar: 10 μM.
higher order chromatin structures. Recently, H1 was shown to interact with a large network of nucleolar proteins (60). In *Drosophila* salivary gland polytene chromosomes, H1 is required for the structural integrity of heterochromatin and the maintenance of pericentric heterochromatin-associated histone marks including H3K9me2 (61). Herein, we also identified HP1γ as a novel NPM1-associated protein. HP1γ is localized to both euchromatin and heterochromatin and is enriched in perinucleolar chromatin (29). We observed HP1γ-NPM1 co-localization in the perinucleolar region, and interestingly, NPM1 was required for the efficient tethering of HP1γ to the nucleolus. It should be pointed out that loss of HP1γ function may negatively affect centromere clustering and cohesion processes (62–64). In fact, the loss of HP1γ in *Drosophila* resulted in nucleolar deformation and fragmentation.

It is conceivable that other NPM1-binding partners also contribute to the organization of perinucleolar heterochromatin. One interaction partner of NPM1 is CTCF, a sequence-specific DNA-binding protein that delimits the juxtaposed domains of active and inactive chromatin (65, 66). CTCF loss resulted in nucleolar fragmentation and reduced rDNA silencing in HeLa cells (67) as well as in *Drosophila* (68). Importantly, CTCF associates with NPM1, and both proteins are present at insulator sites in HeLa cells (65). The nucleoplasmic homolog dNLP mediates centromere clustering by binding to CENPA and anchoring to the nucleolus in a complex together with CTCF and nucleolin in *Drosophila* (9, 69). In the cell lines that we investigated, centromeres were not truly clustered around nucleoli, meaning that CENPA staining was not very useful for describing the rearrangement of perinucleolar chromatin (data not shown).

The morphology of NPM1-depleted nucleoli could potentially also be explained by changes in the formation of heterochromatin. In fact, the formation of heterochromatin is crucial for maintaining nucleolar structure and the integrity of rDNA (70). For example, H3K9 methylation and RNA interference regulate nucleolar stability, and the loss of H3K9 methylation induces fragmentation of the nucleolus due to illegitimate recombination of repetitive DNA sequences (8). A review of the literature revealed that depletion of a number of proteins involved in rDNA silencing and/or heterochromatin formation induces alterations in the nucleolar structure similar to those observed in the case of NPM1 depletion. Among these proteins have been reported DNMT1, HP1, SIRT1, and the histone H3K9 methyltransferase SUV39H1 (8, 71–73). For example, human cells with mutated DNA methyltransferase 1 (DNMT1) presented with a severe decrease in rDNA methylation concomitant with abnormal transcription of rDNA copies and disorganized nucleoli (71). Interestingly, NPM1 is not localized to the fibrillarin-rich regions of nucleoli, where active rDNA transcription and rRNA processing take place. NPM1 is enriched, and juxtaposed, to heterochromatin in the nucleolar periphery marked by H3K9me3/HP1γ (this study). We found that NPM1 depletion led to a decrease in the levels of H3K9me3 and H3K9me2 at the rDNA promoter. Importantly, however, the reduction was relatively modest, and the total cellular levels of these heterochromatin markers remained similar in NPM1-deficient versus control cells. We therefore consider it less likely that changes in heterochromatin formation contributed to the altered nucleolar morphology seen in NPM1-deficient cells.

Disruption or altered organization of the heterochromatin that surrounds nucleoli has been described in cells depleted of ribosomal proteins, indicating the existence of molecular connections among rRNA processing, pre-ribosome export, and nucleolar chromatin organization (74). Any defects in ribosome biogenesis in NPM1-depleted cells may therefore potentially alter the nucleolar chromatin structure. NPM1 has been found to be critical for rDNA transcription in HeLa cells (75), in contradiction to reports of increased rDNA transcription upon acute depletion of NPM1 in *Arf*−/− MEFs (76) and in HeLa cells.

![FIGURE 12. Effects of NPM1 on nucleolar structure.](image-url)
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