

HMGN1 Modulates Nucleosome Occupancy and DNase I Hypersensitivity at the CpG Island Promoters of Embryonic Stem Cells

Tao Deng,^a Z. Iris Zhu,^b Shaofei Zhang,^a Fenfei Leng,^{a,c} Srujana Cherukuri,^a Loren Hansen,^{b,*} Leonardo Mariño-Ramírez,^b Eran Meshorer,^d David Landsman,^b Michael Bustin^a

Protein Section, Laboratory of Metabolism, Center for Cancer Research, National Cancer Institute, Bethesda, Maryland, USA^a; Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Maryland, USA^b; Department of Chemistry & Biochemistry, Florida International University, Miami, Florida, USA^c; Department of Genetics, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel^d

Chromatin structure plays a key role in regulating gene expression and embryonic differentiation; however, the factors that determine the organization of chromatin around regulatory sites are not fully known. Here we show that HMGN1, a nucleosome-binding protein ubiquitously expressed in vertebrate cells, preferentially binds to CpG island-containing promoters and affects the organization of nucleosomes, DNase I hypersensitivity, and the transcriptional profile of mouse embryonic stem cells and neural progenitors. Loss of HMGN1 alters the organization of an unstable nucleosome at transcription start sites, reduces the number of DNase I-hypersensitive sites genome wide, and decreases the number of nestin-positive neural progenitors in the subventricular zone (SVZ) region of mouse brain. Thus, architectural chromatin-binding proteins affect the transcription profile and chromatin structure during embryonic stem cell differentiation.

Embryonic stem cell (ESC) pluripotency and differentiation are controlled by the coordinated action of multiple epigenetic factors that affect the structure of chromatin and regulate gene expression. These include transcription factors, chromatin remodeling complexes, and additional proteins that alter the properties of chromatin such as linker histone H1 variants and members of the high-mobility-group (HMG) protein superfamily (1–5).

Histone H1 variants and HMG protein are ubiquitously found in the nuclei of all vertebrate cells. These structural proteins bind dynamically to nucleosomes without any known DNA sequence specificity (6, 7), modulate the local and global structures of chromatin, and affect gene expression. Histone H1 represents the most abundant family of chromatin-binding proteins; most nuclei contain sufficient H1 molecules to bind to all the nucleosomes. The interaction of H1 with nucleosomes stabilizes the compact, higher-order chromatin structure (8). Vertebrate nuclei contain 3 families of HMG proteins, named HMGA, HMGB, and HMGN, each of which induces specific alterations in DNA or chromatin structure (9, 10). The dynamic binding of HMGs to nucleosomes reduces the interaction of H1 with chromatin and can counteract the chromatin-condensing activity of H1 (7, 11). Thus, the interplay between H1 and HMG proteins could play a role in chromatin dynamics and function (12). Although extensively studied, the cellular function and mechanism of action of these chromatin architectural proteins, and the extent to which they can affect the properties of ESCs, are not fully elucidated.

Here we examine the role of HMGN1, a major variant of the HMGN protein family, in regulating the chromatin structure and properties of mouse embryonic stem cells (ESCs) during their differentiation along the neuronal pathway. HMGNs could affect chromatin structure and ESC differentiation because they bind specifically to nucleosome core particles (CPs) (13, 14), affect the levels of histone modifications (15), and have been linked to the generation of DNase I-hypersensitive sites (DHS) (16), the hall-

mark of chromatin regulatory sites. HMGNs counteract the activity of certain nucleosome remodeling complexes (17) and thus could affect nucleosome positioning (18, 19). In human T cells, HMGN1 preferentially localizes to chromatin regulatory regions such as promoters, enhancers, and nucleosomes bordering CTCF sites (20); in tissue culture cells, either up- or downregulation of HMGN1 levels alters the cellular transcription profile (21). Furthermore, the expression of HMGN genes is related to differentiation processes such as erythropoiesis, myogenesis, osteoblast differentiation, kidney organogenesis, preimplantation development of early mouse embryo, and *Xenopus* embryogenesis (22). Transient depletion of HMGN proteins from one- or two-cell mouse embryos slowed the progression of preimplantation development (23), and altered HMGN expression during *Xenopus* embryogenesis led to malformed tadpole embryos (24). Taken together, these results suggest a link between regulated expression of HMGN proteins and cellular differentiation.

To test whether HMGN1 could affect ESC differentiation in the biological context of a whole organism, we first verified that the protein is expressed during preimplantation development

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Address correspondence to Michael Bustin, bustin@helix.nih.gov.

* Present address: Loren Hansen, Stanford University, School of Medicine, Department of Pathology, Stanford, California, USA.

T.D. and Z.I.Z. contributed equally to this article.

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(23). We found robust HMGN1 expression throughout all these developmental stages and therefore generated ESCs from *Hmgn1*^{-/-} mice, induced them to differentiate along the neuronal pathway, and compared their chromatin structure and transcription profiles to those of *Hmgn1*^{+/+} ESCs. We found strong preferential binding of HMGN1 to promoters containing CpG islands (CGI), especially when these were transcriptionally active. Significantly, using limiting micrococcal nuclease digests, we detected an unstable nucleosome positioned at the transcription start sites (TSS) of CGI promoters, in a region considered to be “nucleosome depleted” (25–27). The stability of these nucleosomes is related to transcription and affected by HMGN1. Likewise, we found that HMGN1 colocalizes with and affects the hypersensitivity of DHS at the CGI promoters of ESCs. Loss of functional HMGN1 did not noticeably affect ESC differentiation but led to changes in the cellular transcription profiles of neural progenitor cells (NPCs) and neurons. In mouse brain, loss of HMGN1 led to a decrease of nestin-positive NP cells in the subventricular stem cell zone.

Our report provides additional information on the chromatin landscape of ESCs and NPCs and identifies HMGN1 as a protein that affects chromatin structure at the transcription start sites of promoters containing CpG islands of ESCs and that modulates the number of nestin-positive cells in mouse brain.

MATERIALS AND METHODS

ES cell culture and *in vitro* differentiation. *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ESC lines were derived from littermate 3.5-day blastocysts obtained from *Hmgn1*^{+/+} and *Hmgn1*^{+/-} mice matings (28). In *Hmgn1*^{-/-} mice, we deleted exons II to IV, which code for the nucleosome-binding domain of the protein (29). The ES cells were cocultured with mitomycin C-treated primary mouse embryonic fibroblast (MEF) feeders (Millipore) or cultured under feeder-free conditions; they were maintained in Knockout Dulbecco's modified Eagle's medium (KO-DMEM; Invitrogen), with 20% serum replacement (SR; Invitrogen), 0.055 mM β -mercaptoethanol (Sigma), 2 mM L-glutamine (Invitrogen), 0.1 mM MEM nonessential amino acid (Invitrogen), 5,000 U/ml penicillin-streptomycin (Invitrogen), and 1,000 U/ml leukemia inhibitory factor (LIF) (Millipore). Cells were passaged every 2 days using 0.05% trypsin-EDTA. *In vitro* differentiation of ES cells according to neural lineage was performed using a mouse dopaminergic neuron differentiation kit (R&D Systems) according to the manufacturer's instruction.

RNA and cDNA preparation. Equal amounts of cells were used for total RNA isolation by the use of an RNeasy Mini kit (Qiagen) followed by “on-column” DNase I treatment. RNA (500 ng) was used for cDNA synthesis by iScript kit (Bio-Rad). Equal amounts of cDNA were applied for real-time PCRs with Power SYBR green mix (Applied Biosystems). β -Actin served as an internal control. Reactions and measurements were performed using an AB 7900HT Fast real-time PCR system and software.

Antibodies, Western blotting, and immunostaining. Rabbit affinity pure polyclonal anti-mouse HMGN1 antibodies were generated in our laboratory (29). Antiactin antibody was from Sigma (A5316). Anti-Oct3/4 antibody was from Santa Cruz (sc-5279), antinestin antibody was from Millipore (MAB-353), and anti-tyrosine hydroxylase (anti-Th) antibody was from Tel-Freez (P40101). Horseradish peroxidase (HRP)-conjugated secondary antibodies for Western blots were from Pierce. Fluorescence secondary antibodies were Alexa Fluor 488–donkey anti-rabbit IgG and Alexa Fluor 568–donkey anti-mouse IgG (Invitrogen). For Western blots, whole-cell lysates were prepared in 1 \times SDS-PAGE sample buffer (Bio-Rad) supplemented with protease inhibitors (Roche Applied Science). The samples were fractionated on 15% precast Criterion gels, transferred by the semidry method to a polyvinylidene difluoride (PVDF) membrane, blocked with nonfat milk in Tris-buffered saline–Tween 20

(TBST), and probed with antibodies. Chemiluminiscent detection using ECL Plus has been performed according to Amersham recommendations.

For immunostaining, ES cells, neural progenitors, and neurons were grown on coverslips under the conditions described above. Frozen brain sections (30 μ m thick) were prepared from 2-week-old *Hmgn1*^{+/+} and *Hmgn1*^{-/-} mice. Immunofluorescence staining was performed using the corresponding antibodies showed in the figures as previously described (30). The images from cultured cells were taken using a Nikon Eclipse E800 fluorescence microscope and processed using NIS-Elements software (Nikon). The images from the brain sections were taken using a Zeiss LSM 710 confocal system and were processed using Zeiss software.

Dissection of mouse SVZ region. The whole brains of 2-week-old male *Hmgn1*^{+/+} and *Hmgn1*^{-/-} mice were collected. Sections (1 mm thick) were cut using a mouse brain mold and snap-frozen on glass slides on dry ice. The subventricular zone (SVZ) regions from all corresponding sections were dissected using no. 5 tweezers (Dumont) under a dissection microscope and pooled.

Transcription profiling. Microarray expression analysis of total RNA from ES cells, neural progenitors, and neurons was performed using Affymetrix Mouse GeneChips 430 2 (430V2) as described previously (21). Three replicates of *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ESCs, NPCs, and neurons were generated. All analysis was performed using R and BioConductor (31). The quality of the arrays were evaluated with R package version 1.18.0 “affy” (32) and “simpleaffy” (33). Expression levels were derived using the Robust Multichip Average (RMA) protocol (34) with default settings. Differentially expressed genes were identified using an empirical Bayes method implemented in the R package “Limma” (34). *P* values were corrected for multiple testing using a false-discovery-rate method. Genes that have a $|\log_2$ (fold change)| value ≥ 1 and for which the adjusted *P* value is ≤ 0.01 are considered differentially expressed between two conditions (i.e., between *Hmgn1*^{+/+} and *Hmgn1*^{-/-}) or between two differentiation states (i.e., NP versus ES or neuron versus NP).

ChIP-Seq. About 2×10^7 cells (feeder-free ES cells or neural progenitors) were cross-linked directly in culture medium with 1% formaldehyde solution for 10 min at room temperature. Chromatin was fragmented to 200 to 500 bp by sonication (Bioruptor). Chromatin immunoprecipitation (ChIP) experiments were performed using Dynabeads (Invitrogen) and affinity-purified anti-HMGN1. For preparation of sequencing libraries, 20 ng ChIP DNA or input DNA (samples reserved before ChIP) were end repaired using an End-It DNA end repair kit (Epicentre), and then an “A” was added to the 3' end using Klenow (3'-5' exo-) (NEB). After ligation with Illumina adaptors, 200-to-300-bp DNA fractions were size selected on a 2% E-gel (Invitrogen), extracted, and then amplified by 18 cycles of PCR using Illumina primers and Phusion DNA polymerase (NEB). Libraries were purified by the use of Agencourt Ampure beads (Beckman Coulter) and then sequenced on Illumina Genome Analyzer IIx with 36-bp single-end reads.

DNase I hypersensitivity assays. For genome-wide analysis, intact nuclei were isolated from trypsinized cells by incubation on ice for 10 min in buffer containing 0.02% IGEAL CA-630 (Sigma), 1 mM EDTA, 0.5 mM EGTA, 0.5 mM spermidine, and protease inhibitor (Roche Applied Science). DNase I digestion was carried out by incubation of 2×10^7 nuclei with 40 U/ml DNase I (Roche Applied Science) at 37°C for 3 min. After treatment by RNase A and proteinase K, DNA was recovered by phenol-chloroform extraction. DNA fragments with sizes between 150 and 500 bp were isolated by 9% sucrose gradient centrifugation. Construction of libraries and sequencing were performed the same way as described above for the ChIP-Seq samples. DNase I accessibility assays were performed to validate the genome-wide analysis. DNase I digestions were done using 40, 60, or 80 U/ml DNase I. The digested DNA was precipitated, and equal amounts of DNA were analyzed by quantitative real-time PCR as described previously. Primers are available upon request.

Genome-wide nucleosome-positioning assay. Mononucleosomal DNAs from wild-type and *Hmgn1*^{-/-} ES cells and neural progenitors

were isolated by micrococcal nuclease digestion using an EZ Nucleosomal DNA Prep kit (Zymo Research) according to the manufacturer's instruction. In brief, nuclei were isolated from trypsinized cells by incubation on ice for 5 min in Nuclei Prep buffer. Nuclei (1.5×10^6) were then digested using 0.05 to 0.5 unit of micrococcal nuclease in 100 μ l MN Digestion buffer at room temperature for 10 min. Nucleosomal DNA was purified using the columns supplied with the kit and then was then processed on 2% agarose gel to check the size. Mononucleosomal DNA was selected for construction of Illumina sequencing libraries. Library preparation and sequencing were performed as described above for ChIP-Seq.

Bioinformatic ChIP-Seq, DNase I-Seq, and MNase-Seq analyses.

The Mouse Genome 430 2.0 array has 45,101 probe sets associated with 19,824 Mouse Genome Informatics (MGI) gene identifiers. Of these, 17,392 are experimentally validated and are listed in the NCBI RefSeq "NM" gene database. We used these coordinates for TSS analysis. Probe sets were mapped to MGI identifiers using information provided by the Jackson Laboratory (<http://www.informatics.jax.org/>). Unfiltered sequencing reads (from ChIP-Seq, DNase I-Seq, or MNase-Seq) were aligned to the mouse reference genome (NCBI build 37, mm9) using Bowtie (35). Up to 1 mismatch was allowed for each aligned read. Only uniquely aligned reads were collected for further analysis. Binding regions were identified using SICER (36) with the following parameters: effective genome size, 0.787 (78.7% of the mouse genome is mappable); window size, 100 bp for HMGN ChIP-Seq and 50 bp for DNase I-Seq; gap size, 100 bp for HMGN ChIP-Seq and 50 bp for DNase I-Seq. The SICER score in the graph can be viewed as an indication of peak intensity. Calculation of coverage and identification of overlapping binding regions were performed with the "chipseq" and "GenomicRanges" packages in BioConductor (31). Specifically, in analyzing MNase-seq data, since the reads are from the ends of the mononucleosome particle, to best visualize the nucleosome positions, all the reads were shifted to the middle of the corresponding nucleosome core. The average sizes of mononucleosome fragments purified from a 2% agarose gel were determined by Bioanalyzer (Agilent). For normalization, the calculation of coverage at any regions and the comparisons between different data sets were preceded by library size normalization. Control subtraction was carried out in the following way: coverage (exp)/N1 - coverage (control)/N2, in which "exp" is the data set (in .bam format) to be examined, N1 is the library size of the experimental data ("exp"), and N2 is the library size of the control. In this study, input sequences (DNA sequences after sonication only without immunoprecipitation) were used as a control. The function coverage that calculates genome coverage from .bam files is from the "chipseq" package in BioConductor (31).

Microarray data accession numbers. The results of the analysis of the transcription changes during differentiation have been deposited at the Gene Expression Omnibus (GEO) database under accession no. GSE44175. We have deposited the BAM files in the SRA database (accession number SRA066756).

RESULTS

Differentiation of *Hmgn1*^{-/-} embryonic stem cells along the neural lineage. To test whether HMGN1 could affect ESC differentiation, we first reexamined the HMGN1 expression pattern during mouse early embryonic differentiation (23). We found robust HMGN1 expression in oocytes and throughout all preimplantation stages, including the blastocyst stage (Fig. 1A), raising the possibility that HMGN1 affects the chromatin structure and differentiation potential of ESCs. We therefore established ESCs from *Hmgn1*^{+/+} and *Hmgn1*^{-/-} mice. Western blots (Fig. 1C) and immunofluorescence (Fig. 1D) verified that the *Hmgn1*^{-/-} ESCs lacked intact HMGN1 protein. Loss of HMGN1 did not affect the viability or morphology of the ESCs. The *Hmgn1*^{-/-} ESC colonies, just like the *Hmgn1*^{+/+} colonies, remained undifferentiated, as indicated by staining for alkaline phosphatase

(Fig. 1E), immunostaining for Oct3/4 (Fig. 1D), and reverse transcription-PCR (RT-PCR) analysis of *Nanog* levels (Fig. 1H).

To test whether loss of HMGN1 affects the differentiation potential of the ESCs, we induced differentiation along the neuronal pathway (Fig. 1B). Upon removal of LIF, both the *Hmgn1*^{-/-} and *Hmgn1*^{+/+} ESCs formed embryoid bodies which could be further induced to differentiate into nestin-expressing NPCs as indicated by immunofluorescence and quantitative RT-PCR (Fig. 1F and H). Further differentiation toward dopaminergic neurons resulted in cultures in which most cells developed axons and dendrites, a morphology characteristic of adult neurons (Fig. 1B; see also Fig. S1 in the supplemental material). Immunostaining for tyrosine hydroxylase (TH) revealed that about half of the neurons were dopaminergic neurons (Fig. 1G). The mRNA expression patterns of *Nanog*, *Nestin*, and tropomyosin-related kinase B (*TrkB*), which serve as differentiation markers for ESCs, NPCs, and adult neurons, respectively, further confirmed that the *Hmgn1*^{-/-} ESCs differentiated properly along the neuronal pathway (Fig. 1H).

HMGN1 depletion affects gene expression during ES cell differentiation. Alterations in HMGN levels can affect gene expression, leading to phenotypes that are not immediately obvious (22, 29, 37–39). Therefore, we compared the transcription profiles of *Hmgn1*^{+/+} ESCs, NPCs, and neurons to those of *Hmgn1*^{-/-} cells at the same three differentiation stages. Loss of HMGN1 altered significantly the expression of 19, 169, and 85 genes in ESCs, NPCs, and neurons, respectively (Fig. 2A and B; see also Table S1A in the supplemental material). Quantitative RT-PCR (Q-PCR) analysis of 9 upregulated and 9 downregulated genes (the 3 that were most changed, 3 that were moderately changed, and the 3 that were least changed) at each differentiation stage verified the microarray results (see Table S2 in the supplemental material). Gene ontology analysis performed using DAVID (40) for all the genes with altered expression revealed that genes involved in developmental processes, especially in organ morphogenesis, vasculature development, and tissue development, were the genes most severely affected (see Table S3 in the supplemental material).

Progression through the differentiation stages leading from ESCs to neurons involves major changes in the expression of numerous genes. In both *Hmgn1*^{+/+} and *Hmgn1*^{-/-} cells, close to 4,000 genes showed expression level changes during the switch either from ESCs to NPCs or from NPCs to neurons. Over 85% of these changes involved the same genes in both *Hmgn1*^{+/+} and *Hmgn1*^{-/-} cells. In Table S1B and C in the supplemental material, we list the gene names and their fold change values in both *Hmgn1*^{+/+} or *Hmgn1*^{-/-} cells. In the experiment represented by Fig. 2C, we first sorted the genes based on their fold changes in expression levels in *Hmgn1*^{+/+} cells and then plotted these sorted genes versus the corresponding fold changes in both *Hmgn1*^{+/+} (blue) and *Hmgn1*^{-/-} (red) cells. The differences between red crosses and blue dots indicate that the magnitude of the differentiation-related changes in gene expression was affected by loss of HMGN1 (Fig. 2C). These changes are not due to variations between microarray replicates, because each point represents the fold change calculated from 3 replicates from each cell type, whereas separate control analyses of all the possible versions of the 2 replicates revealed that the variations within the *Hmgn1*^{-/-} or *Hmgn1*^{+/+} groups were very small (see Fig. S2 in the supplemental material). The mean variation between *Hmgn1*^{+/+} and *Hmgn1*^{-/-} cells was more than 4-fold bigger than the variation within duplicates (0.327 versus 0.067 [*P* value < 2.2e-16;

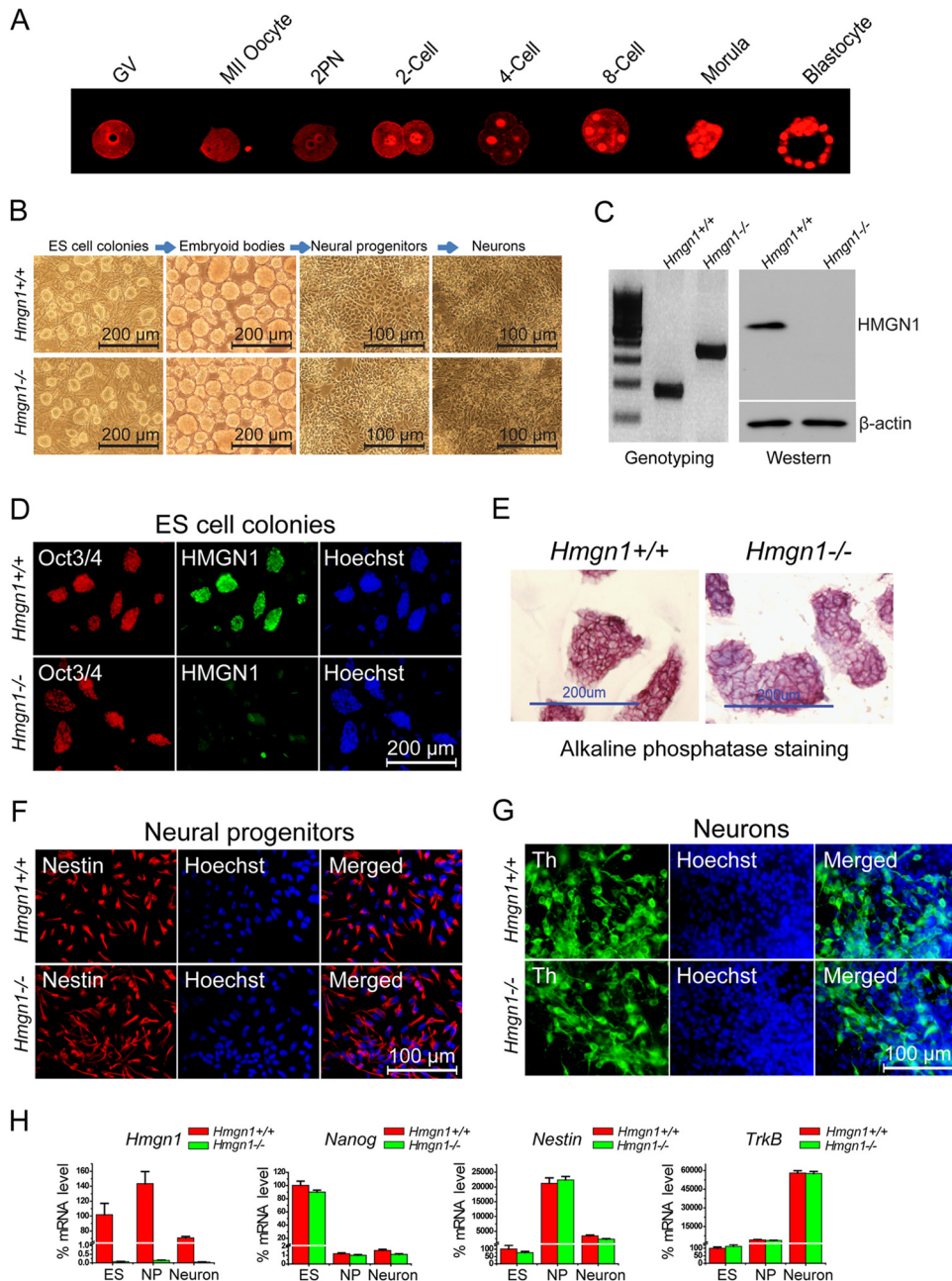


FIG 1 Effects of *Hmgn1* depletion on *in vitro* ES cell differentiation. (A) HMGN1 protein expression during mouse embryonic preimplantation. Immunofluorescence images at the stages indicated above each panel are shown. (B) Morphology of *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ES cell colonies during differentiation along the neuronal pathway. (C) Genotyping (29) and Western analysis of the ES cells used. (D) Immunofluorescence of Oct3/4, an ES cell marker, in the ES cell colonies. (E) Both *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ES cell colonies express the pluripotency marker alkaline phosphatase. (F) Immunofluorescence of the neural progenitor nestin. (G) Immunofluorescence of the dopaminergic neuron marker tyrosine hydroxylase (Th). (H) Quantitative RT-PCR analysis of the expression of *Hmgn1*, *Nanog*, *Nestin*, and tropomyosin-related kinase B (*TrkB*) during *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ES cell neural differentiation. The values obtained in ES cells were set to 100%.

Wilcoxon rank sum test]). Thus, HMGN1 modulates and fine tunes the general fidelity of the cellular transcription profile and does not serve as a specific transcription factor that regulates the expression of a select subset of genes.

Reduced nestin-positive cells in the SVZ of *Hmgn1*^{-/-} mice. The Allen Brain Atlas database reveals prominent *Hmgn1* expression in the SVZ, in the hippocampus, and in the olfactory bulbs

(Fig. 3A), three regions enriched in neural stem/progenitor cells and active in neurogenesis. Indeed, immunofluorescence staining of brain sections from a 2-week-old mouse indicated that HMGN1 protein was most prominently expressed in the SVZ and the hippocampus, where the cells are tightly packed, as indicated by Hoechst staining (Fig. 3B). Double immunofluorescence analysis of the SVZ regions revealed that nuclei of nestin-expressing

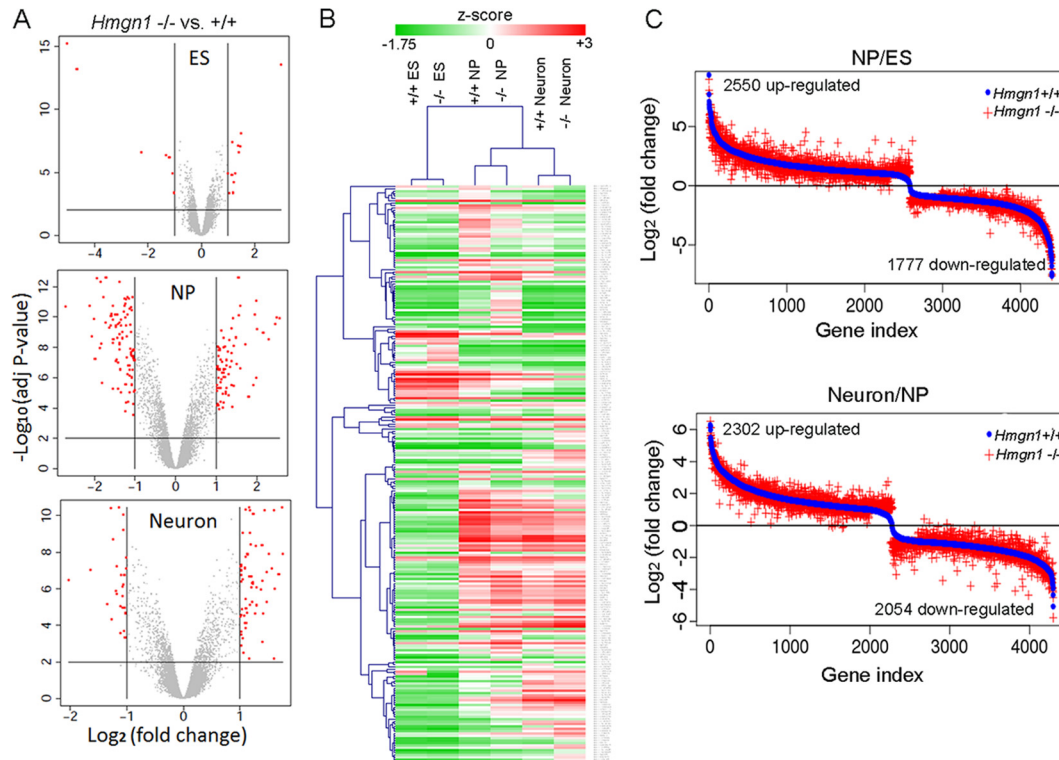


FIG 2 HMGN1 depletion affects gene expression during ES cell differentiation along the neuronal pathway. (A) Transcription analysis of $Hmgn1^{+/+}$ and $Hmgn1^{-/-}$ cells in the ES, NP, and neuron stages. Red dots mark genes (listed in Table S1A in the supplemental material) that were significantly affected by loss of HMGN1. (B) Clustering of genes (represented in panel A) across three differentiation states based on expression values. (C) Comparison of fold changes in gene expression during differentiation processes from ESCs to NPCs or NPCs to neurons in $Hmgn1^{+/+}$ and $Hmgn1^{-/-}$ cells. The difference between red and blue visualizes the effects of HMGN1 loss on gene expression during differentiation.

cells contained significant amounts of HMGN1, an indication that HMGN1 was expressed in mouse NPCs (Fig. 3C).

To test whether loss of HMGN1 affects NPC characteristics in the biological context of the entire organism, we compared the levels of nestin-positive cells in $Hmgn1^{-/-}$ and $Hmgn1^{+/+}$ littermates. Immunofluorescence analysis indicated that loss of HMGN1 reduced the number of nestin-positive cells in the SVZ region (Fig. 3D), and quantitative RT-PCR analysis of RNA isolated from the SVZ regions verified that the expression of *Nestin* mRNA in the $Hmgn1^{-/-}$ SVZ was reduced by 40% compared to that seen in the $Hmgn1^{+/+}$ SVZ (Fig. 3E). Thus, loss of HMGN1 reduces the number of nestin-positive cells in the SVZ region of mouse brain.

HMGN1 preferentially binds to promoters containing CpG islands. To gain insights into the mechanisms whereby HMGN1 affects transcriptional fidelity, we examined the genome-wide distribution of HMGN1 in ESCs and NPCs. Chromatin immunoprecipitation sequencing (ChIP-Seq) failed to yield reliable data on the localization of HMGN1 in ESCs, most likely because their chromatin is hyperdynamic (41, 42) and the chromatin residence time of many nuclear proteins, including HMGN1 (see Fig. S3 in the supplemental material), is relatively short. In NPCs, however, we were able to determine the genome-wide distribution of HMGN1.

In NPCs, 72% of the HMGN1-binding regions were located at gene promoter regions and within gene bodies (Fig. 4A). The HMGN1 peaks in the promoter regions were significantly more

intense (P value $< 2.2 \times 10^{-16}$; Wilcoxon rank sum test), an indication of preferential association with these regions (Fig. 4B). Significantly, we found a striking overlap between HMGN1-binding promoters and CGI-containing promoters. Among all 24,303 annotated promoters in the NCBI Mouse mm9 Refseq database (<http://hgdownload.soe.ucsc.edu/goldenPath/mm9/database/>), there are 15,112 CGI promoters, 10,892 (72%) of which are bound by HMGN1. Conversely, 10,892 (92%) of all 11,881 promoters bound by HMGN1 also contain CGI. In contrast, among the 9,181 non-CGI promoters, only 989 (11%) bind HMGN1 (Fig. 4C).

The Mouse genome transcription arrays contain 45,101 probes which identify 17,392 experimentally validated genes annotated in the Mouse Genome Informatics (MGI) database (43) and listed in the NCBI Refseq database (44). The HMGN1 signal strength at the promoters of the 6,956 most actively transcribed (40% of total genes [Top40]) genes is significantly stronger than at those of the 40% least-transcribed genes (Bot40) (t test P value $< 2.2 \times 10^{-16}$), an indication that HMGN1 preferentially associates with transcriptionally active genes (see Fig. S4 in the supplemental material).

In the Top40 and Bot40 groups, 6,516 (94%) and 3,416 (46%) genes, respectively, contain CGI in their promoters. As shown in Fig. 4D, in the Top40 gene group, the average HMGN1 binding level was 4-fold higher at CGI promoters (black) than at non-CGI promoters (red) (t test P value $< 2.2 \times 10^{-16}$). Furthermore, even in the Bot40 group, the HMGN1 binding to CGI promoters (blue) was 3-fold higher than to the non-CGI promoters (t test P value $<$

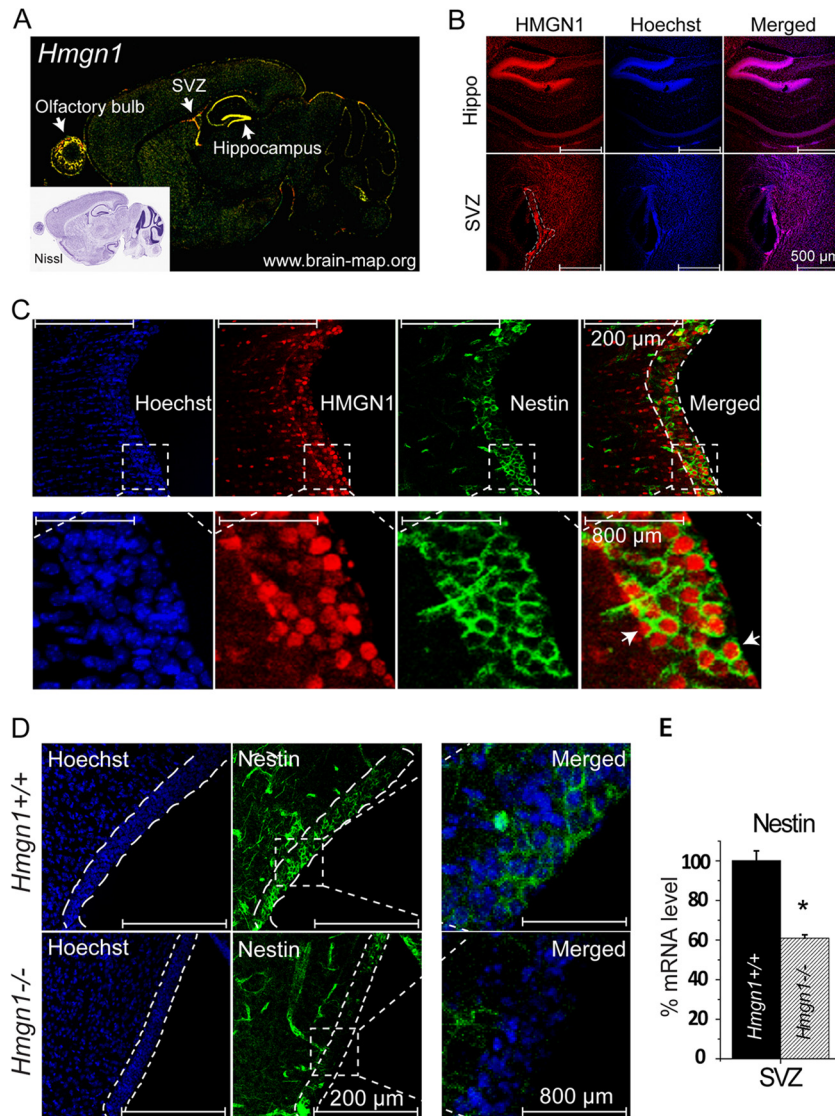


FIG 3 Decreased nestin-positive cells in the brain of *Hmgn1*^{-/-} mice. (A) High *Hmgn1* expression in the subventricular zone (SVZ), hippocampus, and olfactory bulbs of mouse brain (from www.brain-map.org with permission). The inset shows the corresponding Nissl image. (B) Immunofluorescence staining in 2-week-old *Hmgn1*^{+/+} brain reveals high HMGN protein levels in mouse hippocampus and SVZ (outlined by dashes). (C) Double immunofluorescence reveals colocalization of nestin in the cytoplasm of cells expressing HMGN1 in the SVZ region. A magnified image of the area outlined by dashed lines is shown under each panel. (D) Decreased nestin immunofluorescence staining in the SVZ (outlined) of 2-week-old *Hmgn1*^{-/-} mice. (E) Decreased *Nestin* expression in the SVZ of *Hmgn1*^{-/-} mice detected by RT-PCR (*, $P < 0.01$).

2.2e-16). This distribution pattern was not related to transcription level since, in either the Top 40 or the Bot40 group, the gene expression levels were not related to the CGI content in their promoters (Fig. 4D, inset). Thus, the major driving force of HMGN1 binding to promoters is the presence of CGI, rather than the gene expression level. In agreement, HMGN1-binding sites colocalized with H3K4Me3 (Fig. 4E and F), a histone mark associated with transcription initiation at CGI promoters (45).

HMGN1 affects nucleosome organization at TSS of CpG island-containing promoters in ESCs. The organization of nucleosomes in promoters plays an important role in regulating gene expression levels. Given that HMGN1 binds specifically to nucleosomes (13, 14), we mapped the nucleosome organization in *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ESCs and NPCs by deep sequencing of

mononucleosomal DNA isolated from micrococcal nuclease digests. In these digests, the most accessible nucleosomes are released first and then further digested, and the corresponding DNA may not be included in the mononucleosomal fraction of an extensive digest. Therefore, we mapped the genome-wide positions of nucleosomes present in either limited or extensive digests when, respectively, either only ~5% or more than ~80% of the chromatin was converted to mononucleosomes. In these experiments, we ensured that the wild-type and knockout cells were digested to the same extent (Fig. 5A).

The nucleosome positions seen in extensive digestion of both *Hmgn1*^{+/+} ESCs and NPCs were very similar to those seen in other cells and revealed a region depleted of nucleosome at the TSS and flanked by nucleosomes up- and downstream (Fig. 5B).

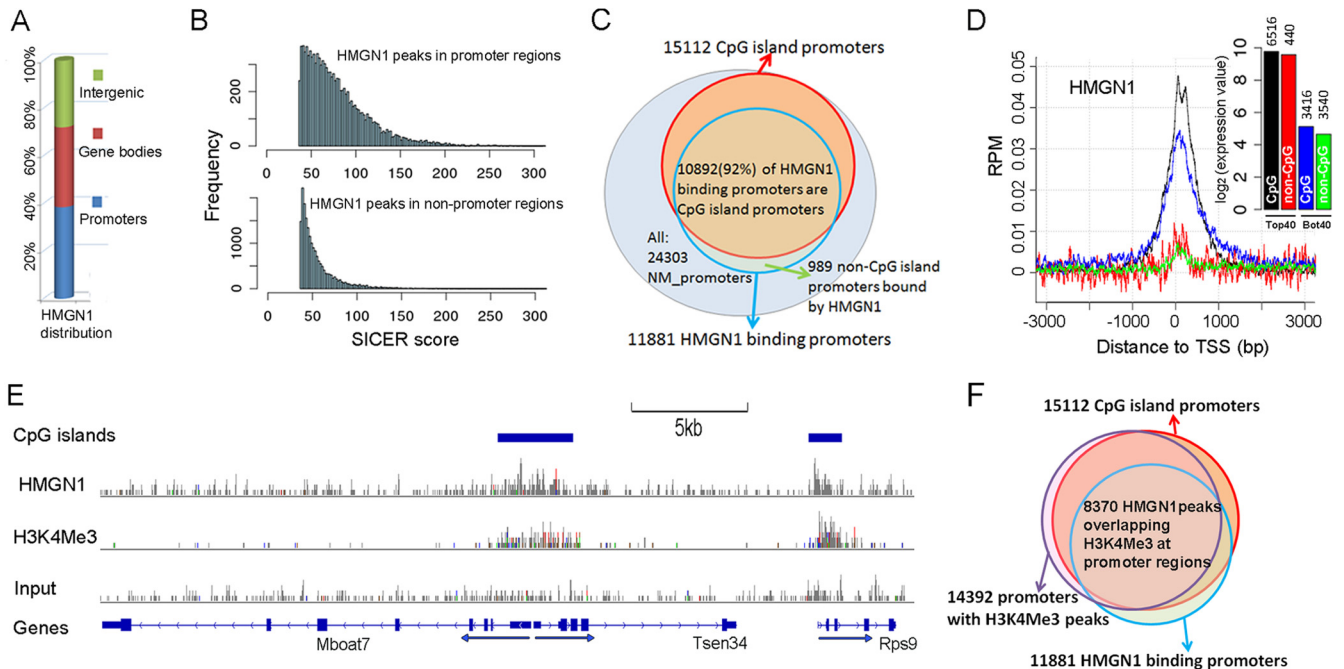


FIG 4 Genome-wide distributions of HMGN1 in neural progenitor cells. (A) Global distribution of HMGN1 throughout the genome. (B) Enhanced HMGN1-binding strength at promoters. (C) HMGN1 binds to promoters containing CpG islands. Note that 92% of the HMGN1-binding promoters are CpG island promoters and that 70% of the CpG island promoters bind HMGN1, regardless of expression levels. (D) Average HMGN1 signals near the transcription start site (TSS) of different groups of genes. Black line, Top40 genes with CpG island promoters; red line, Top40 genes with non-CpG island promoters; blue line, Bot40 genes with CpG island promoters; green line, Bot40 genes with non-CpG island promoters. RPM, reads per million. The inset indicates average expression values (in \log_2) in the four groups of genes. (E) An example of colocalization of HMGN1, CpG island promoters, and H3K4Me3 histone mark. (F) Overlapping of HMGN1-binding promoter and H3K4Me3-positive promoters.

The +1 nucleosome is the best positioned, as manifested by the highest peak at that site. However, analysis of the limited MNase digestions clearly reveals the presence of a nucleosome positioned at the TSS in the “nucleosome-free” regions seen in extensive digestions (arrows, Fig. 5B). The linker DNA regions flanking these nucleosomes are likely the most accessible to the enzyme, and therefore these nucleosomes are the first to be released from the chromatin fiber. Since these nucleosomes may contain histone variants that render them unstable (46), the corresponding DNA fragment is rapidly digested by MNase, resulting in the “nucleosome-free valley” typically seen at the TSS in extensive MNase digests.

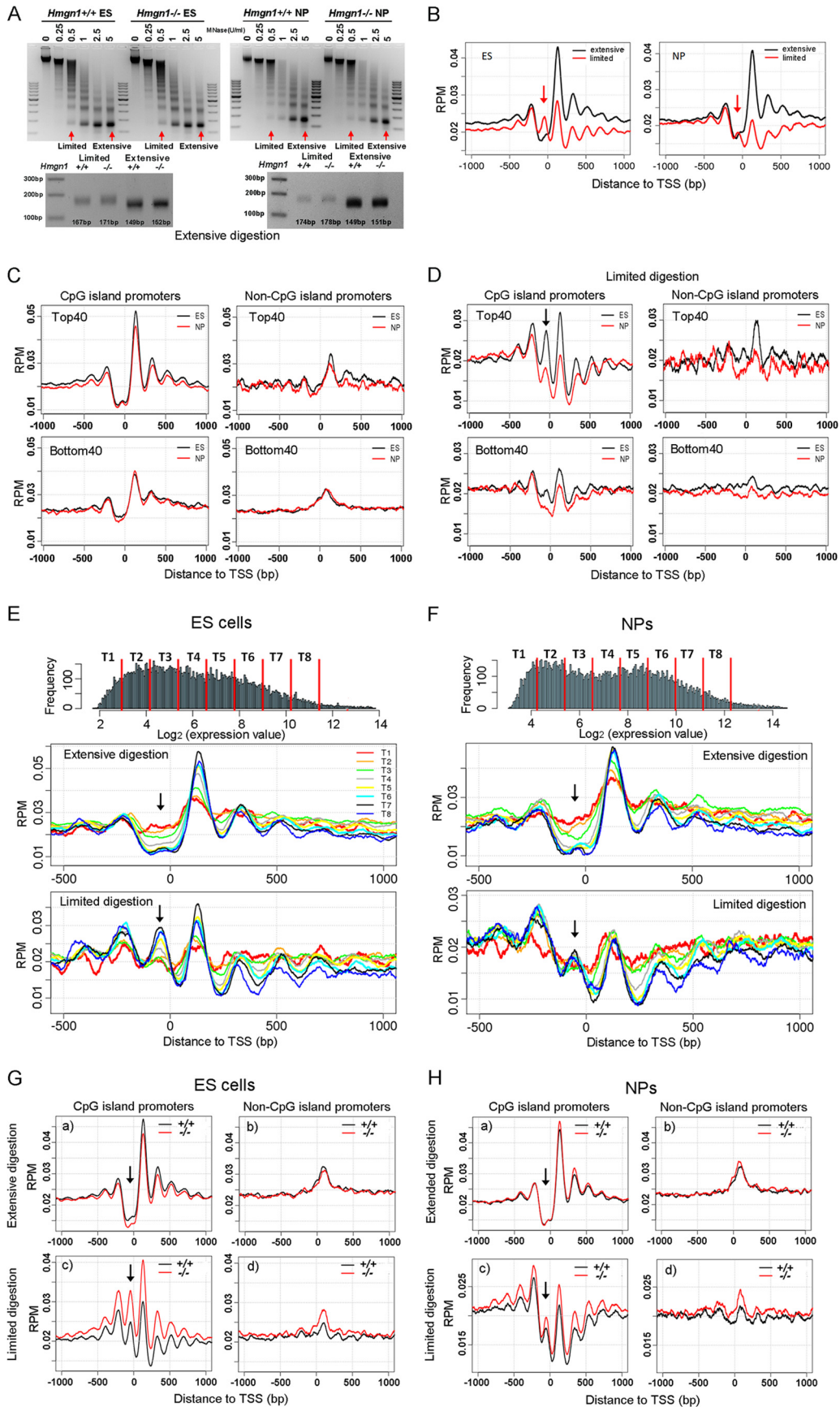
In view of the extensive localization of HMGN1 at CGI promoters, we examined the nucleosome organization at both CGI and non-CGI promoters in the Top40 and Bot40 gene groups. We found that in both ESCs and NPCs, the nucleosomes in the TSS regions containing CGI were significantly better positioned than in non-CGI promoters in both extensive and limited digests (Fig. 5C and D). The nucleosome at the TSS (position 0) is clearly seen in the limited digests but not in the extensive digests of CGI promoters of the Top40 group (Fig. 5D, arrow).

We separated the CGI promoter genes of ESC and NPC into 8 groups based on their expression values and mapped the nucleosome positions around the TSS in each group (Fig. 5E and F). In the least-expressed group (T1; red line) the signal from the unstable nucleosome at TSS was highest in the extensive digestion but lowest in the limited digestion. Conversely, the signal from the most-expressed genes was highest in the limited digestions and lowest in the extensive digestion (Fig. 5E and F), a finding that is

fully compatible with the notion that the DNA signal at this position is related to transcription level. The nucleosome at position +1 became more stable or better positioned as gene expression levels increased. In summary, in TSS regions of the promoters containing CGI, the stability of the nucleosomes is related to transcription levels; enhanced transcription destabilizes the nucleosomes at the TSS (position 0) but stabilizes the nucleosome at the +1 site.

Loss of HMGN1 increased the peak height of all nucleosomes (from -3 to +5) around the TSS of CGI promoters but only in limited digests. The effects were not seen in extensive digests or at non-CGI promoters (Fig. 5G and H). The increased peak height may reflect changes in nucleosome occupancy or accessibility, perhaps due to effects of HMGN1 on chromatin remodeling activities (17) and/or on the binding of linker histone H1 to chromatin (47). Thus, HMGN1 affects the position or stability of the nucleosomes that are most susceptible to micrococcal nuclease digestion, i.e., the nucleosomes located in CGI-containing promoters of transcriptionally active genes.

HMGN1 modulates the DNase I hypersensitivity in the CGI promoters of ESCs. Changes in nucleosome occupancy may affect the locations and strengths of the DNase I-hypersensitive sites (DHS) which are hallmarks of regulatory regions in chromatin. In NPCs, we identified 30,199 DHS and found significant overlap between the locations of DHS and HMGN1 (Fig. 6A and B). The HMGN1-binding signal at HMGN1-DHS overlapping sites was significantly stronger than that at nonoverlapping sites (P value < 2.2×10^{-16} ; Wilcoxon rank sum test) (bar graph, Fig. 6C, panels a and b), and the HMGN1-DHS overlapping sites were preferentially



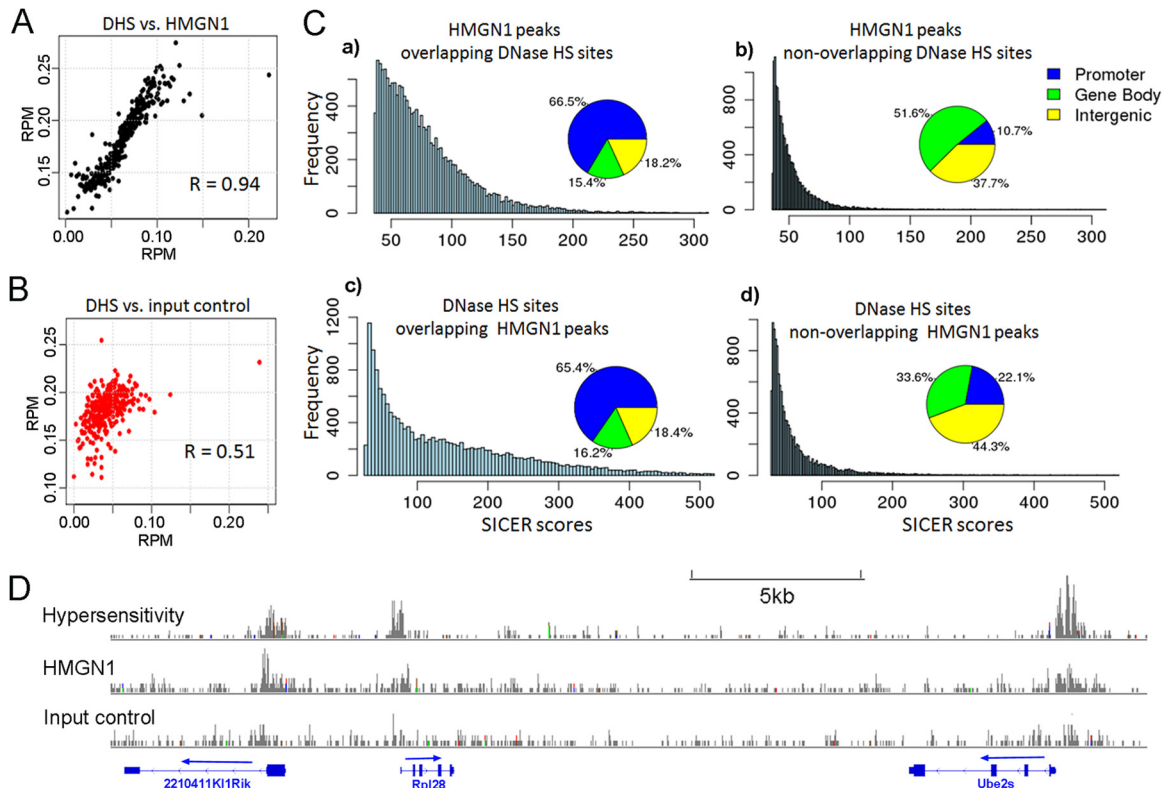


FIG 6 Colocalization of HMGN1 and DNase I hypersensitivity sites (DHS) in neural progenitor cells. (A) Correlation between HMGN1 intensity and DNase I hypersensitivity at all DHS. Average coverage depths (of HMGN1 or hypersensitivity) were calculated at all DNase I-hypersensitive regions. Data, including the corresponding DNase I hypersensitivity data points, were sorted by HMGN1 coverage depth and then grouped into 100 data point bins and averaged. The Pearson correlation coefficient (R) was calculated for the binned data. (B) Correlation between input signal and DNase hypersensitivity at the same regions. (C) Distributions of HMGN1 peaks that either do or do not overlap DNase HS sites (top two panels) and DNase HS sites that either do or do not overlap HMGN1 peaks (bottom). Note that the overlapping regions have stronger signal intensities and are mostly located in gene promoters. (D) An example of colocalization between HMGN1, DNase I hypersensitivity, and gene promoters.

located at promoters (pie chart, Fig. 6C, panels a and b). Thus, 66.5% of the HMGN1 peaks that overlap DHS but only 10.7% of the HMGN1 sites that do not overlap DHS localize to promoters. Likewise, DHS that overlap HMGN1 have significantly more intense peaks (P value $< 2.2e-16$; Wilcoxon rank sum test) and localize to promoter regions with a 3-fold higher frequency (65.4% versus 22.1%) than DHS that do not overlap HMGN1 (Fig. 6C panels c and d).

In *Hmgn1*^{+/+} ESCs, we identified 56,156 DHS; 67% of these overlapped with the sites in CJ7 mouse ES cells mapped by the Mouse Encode Project (see Fig. S5 in the supplemental material). In *Hmgn1*^{-/-} ESCs, however, we identified only 17,017 sites; 12% of the DHS are new and were not detected in *Hmgn1*^{+/+} ESC, and 88% (15,042) of the sites overlapped the sites detected in wild-type ESCs (Fig. 7A). The DHS retained in *Hmgn1*^{-/-} ESCs were preferentially located in CGI promoters: 58% of the 15,022 DHS that were located in the CGI promoters in *Hmgn1*^{+/+} ESCs were re-

tained in *Hmgn1*^{-/-} ESCs. In contrast, only 15% of 41,156 DHS that were not in CGI promoters were retained. Importantly, the intensity of the DHS retained in *Hmgn1*^{-/-} ESCs was significantly lowered (t test P value $< 2.2e-16$) (Fig. 7B and H), especially at the sites located in CGI promoters (Fig. 7C). Quantitative PCR analysis of the kinetics of DNase I digestion of 5 promoters verified that loss of HMGN1 decreases the DNase I hypersensitivity of these regions (Fig. 7G; see also Table S4 in the supplemental material). The DNase I hypersensitivity of two (*Actb* and *Gapdh*) housekeeping gene promoters, which served as controls, was not affected by loss of HMGN1. In NPC, we found that loss of HMGN1 reduced the number of DHS from 30,199 to 23,320 (Fig. 7D). Within the 23,320 DHS identified in *Hmgn1*^{-/-} NPCs, 11% were new and 89% overlapped the sites present in *Hmgn1*^{+/+}. Loss of HMGN1 did not significantly alter the DHS sensitivity of the retained, overlapping sites (Fig. 7E and F).

Thus, loss of HMGN1 affects the structure of the hyperdy-

FIG 5 Nucleosome positioning at gene transcription start sites (TSS) in ES and NP cells. (A) MNase digestions of ESCs and NPCs; the sizes of the isolated monomers from limited and extensive digests are shown in the bottom panels. (B) Occupancy of nucleosome isolated from limited and extensive digests at the TSS. (C and D) Nucleosome occupancy at TSS of Top40 and Bot40 (Bottom40) genes that either do or do not contain CpG islands after extensive digestion (C) and limited digestion (D). (E and F) Correlation between nucleosome positioning at TSS and gene expression levels at ESCs (E) and NPCs (F). Genes were divided into 8 groups based on expression values (\log_2) as shown at the top of panels E and F. (G and H) Effects of HMGN1 depletion on nucleosome occupancy in the promoters of ESCs and NPCs. Arrows point to the position of the 0 nucleosome, located just upstream of the TSS.

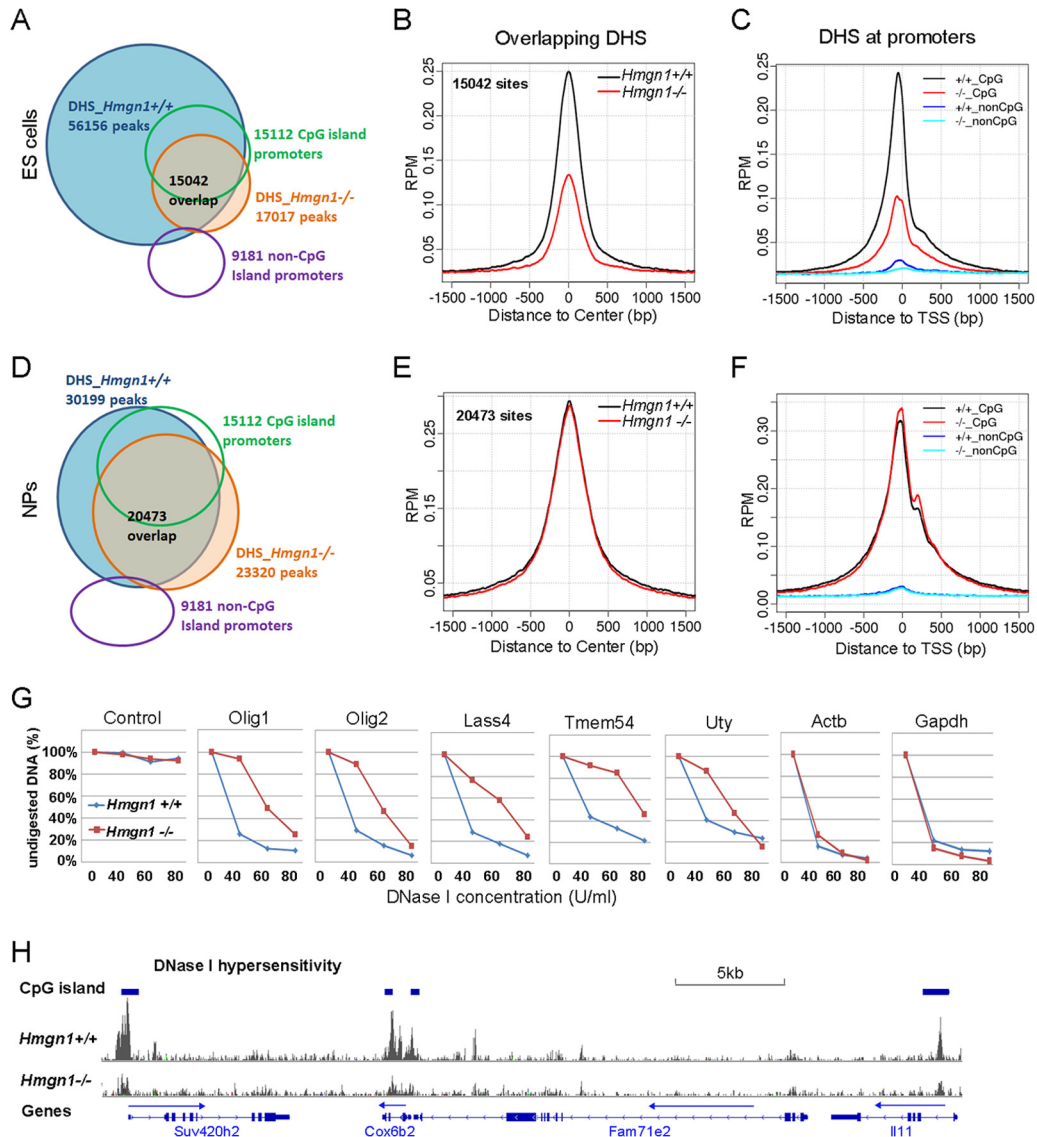


FIG 7 Reduced DNase I hypersensitivity in *Hmgn1*^{-/-} ES cells. (A) DHS in *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ESCs. (B) Decreased DNase I in *Hmgn1*^{-/-} ESCs. Data represent intensities measured at sites that overlap that are present in both *Hmgn1*^{+/+} and *Hmgn1*^{-/-} cells. (C) Loss of HMGN1 decreases the DNase I sensitivity at CpG promoters of ESCs. (D) DHS in *Hmgn1*^{+/+} and *Hmgn1*^{-/-} NP cells. (E) HMGN1 does not affect the DHS in NP cells. (F) HMGN1 does not affect the DHS at the CpG promoters in NP cells. (G) Quantitative PCR validation of DNase I-seq results in ES cells. The results determined with a control taken from a region that is not digested by DNase I verify that equal amounts of DNA were loaded for *Hmgn1*^{+/+} and *Hmgn1*^{-/-} cells. (H) A genome browser view of DNase I hypersensitivity of *Hmgn1*^{+/+} and *Hmgn1*^{-/-} ES cells.

namic chromatin of ESCs to a larger extent than that of the developmentally committed chromatin of NPC, a finding fully compatible with increased nucleosome occupancy seen in limited micrococcal nuclease digests in ESCs. Loss of HMGN1 reduces the DHS located in intergenic region and gene bodies to a larger extent than the sites located at CGI promoters, providing a partial explanation for the moderate effects on transcription levels.

DISCUSSION

Our studies of ESC chromatin reveal that HMGN1, one of the few nuclear proteins that bind specifically to nucleosome cores but not to isolated histones or DNA, affects the organization of nucleosomes and the DNase I hypersensitivity at active pro-

motors containing CGI. Loss of HMGN1 has only slight effects on the ESC cellular transcription profile and their potential to differentiate into neuronal cells; however, in the brain of *Hmgn1*^{-/-} mice, the levels of neural progenitors in the SVZ region are reduced.

Nucleosome positioning around the TSS of active promoters plays a key role in gene expression. In limited micrococcal nuclease digests, in which only 5% of the genome is converted to nucleosome core particles (CPs), we detect a well-positioned nucleosome at the TSS in a region considered to be nucleosome depleted. The presence of this nucleosome is especially obvious in the CGI promoters of transcriptionally active genes in ESCs (Fig. 5D). The nucleosomes at the TSS of transcribed genes are

likely to be relatively unstable (46) and most accessible to micrococcal nuclease; they are rapidly released and then further digested, leading to nucleosome-free regions which are most clearly delineated at TSS of genes containing CGI (25). Our analysis of the limit digests reveals a correlation between transcription levels and nucleosome occupancy at the TSS. The occupancy is highest in the most transcribed genes and lowest in the least transcribed genes, suggesting that the nucleosomes from the most transcriptionally active genes are the most rapidly released during digestion. However, once released, these nucleosomes, which may contain H2Az variants, are unstable; they are rapidly digested and, therefore, in the extensive micrococcal nuclease digests, the promoters of the most active genes show the most prominent nucleosome-free region. Thus, our studies reveal that the stability of nucleosomes at the TSS is inversely related to transcription levels, since the nucleosomes from the most active genes are most abundant in limit digests and least abundant in extensive digests, while the nucleosomes from the least transcribed genes are most abundant in extensive digests and least abundant in limit digests (compare T1 to T8 in Fig. 5E and F).

Loss of HMGN1, which preferentially binds to TSS containing CGI (Fig. 4), stabilizes the position of the nucleosomes at these TSS—an unexpected finding, since HMGN proteins stabilize the structure of isolated nucleosomes (48) and loss of the protein would therefore be expected to sensitize the released nucleosomes to further digestion. Several mechanisms could account for the effects of HMGN1 on nucleosome positioning and stability. First, because HMGN1 competes with histone H1 (47), loss of HMGN1 would increase H1 binding, thereby decreasing the ability of micrococcal nuclease to access its initial digestion sites in the linker DNA (8) and subsequently further degrade the released nucleosome (49). Second, because HMGN1 reduces the chromatin interaction of nucleosome remodeling complexes (17), loss of HMGN1 could enhance the ability of these complexes to position nucleosomes at the TSS. Third, HMGN1 can transiently enhance the levels of histone acetylation and destabilize nucleosomes during transcription activation (50); therefore, its loss could enhance the stability of a nucleosome at the TSS. Fourth, because HMGN1 is found in metastable multiprotein complexes (51) and interacts with chromatin modifiers such as PCNA (52) and procylic acidic repetitive protein 1 (PARP1) (53), loss of HMGN1 could affect the binding of these proteins to chromatin. Since nucleosome positioning is determined by the coordinated action of several factors, including DNA-binding proteins (18), it remains to be seen whether one or several of these factors are most specifically affected by HMGN1.

A possible link between the presence of HMGN and the generation of DHS in globin genes has been previously suggested (16); however, the extent to which HMGN proteins shape regulatory sites in chromatin is not known. We now find that in NPCs, HMGN1 colocalizes extensively with DHS genome wide in a fashion similar to that seen in human T cells (20). In both NPCs and human T cells, the hypersensitivity of the DHS that colocalize with HMGN1 is stronger than that of the sites that do not colocalize with HMGN1 (Fig. 6). Furthermore, in both NPCs and T cells, the positional overlap of HMGN1 with DHS is especially striking in the promoter region. In NPCs, 65% of the DHS that overlap HMGN1 but only 22% of the sites that do not overlap are located in the promoter region (Fig. 6C, panels c and d). Likewise, in the

promoter region of human T cells, the frequency of DHS that overlap HMGN1 is 3-fold higher than that of sites that do not overlap HMGN1 (28% versus 10%) (20). The preference for HMGN1 to colocalize with the DHS in promoters is even more striking. In NPCs, 66% of the HMGN1 sites that overlap DHS but only 11% of the sites that do not overlap DHS localize to promoter regions. In T cells, the ratio is 32% versus 2% (20). These studies raise the possibility that preferential colocalization of HMGN1 with DHS in promoter regions is a general characteristic of vertebrate chromatin.

Loss of HMGN1 leads to a significant reduction in DHS, especially in the hyperdynamic chromatin of ESCs, where the number of sites is reduced from 56,156 in *Hmgn1*^{+/+} to 17,017 in *Hmgn1*^{-/-} ESCs. The DHS retained in *Hmgn1*^{-/-} ESCs preferentially localize at promoters containing CGI, providing a partial explanation for the relative small changes in transcription seen in these cells. Loss of HMGN1 reduces not only the number but also the hypersensitivity of the retained DHS (Fig. 7B), suggesting that HMGN1 plays a role in maintaining their DNase I sensitivity. Likewise, in NPCs, loss of HMGN1 reduces the number of DHS (Fig. 7D), an expected finding given their extensive colocalization and the observation that the presence of HMGN1 at a site affects its DNase I sensitivity (Fig. 6). Similarly to ESCs, the retained sites localize to CGI promoters; however, in contrast to ESCs, the DNase I hypersensitivity at these sites is not markedly changed, perhaps because their chromatin is less malleable.

Thus, loss of HMGN1 in ESCs affects two important aspects of chromatin organization: nucleosome positioning at the TSS and DNase I hypersensitivity. These effects are moderate, perhaps because HMGN1 functions within a dynamic framework of chromatin-binding proteins that compete for similar sites on nucleosomes. Thus, the absence of HMGN1 could facilitate the binding of another HMGN variant, especially to sites with high affinity for HMGN proteins, thereby minimizing changes in chromatin structure and activity. Indeed, preliminary experiments suggest that loss of HMGN1 induces reorganization in the chromatin binding of the closely related variant HMGN2.

Given that HMGN1 is expressed in most vertebrate cells, binds specifically to nucleosomes, localizes to DHS, and affects the binding of linker H1 to chromatin, its loss would be expected to have significant effects on transcription and the cellular phenotype. Yet our present experiments and analysis of MEFs from mice lacking HMGN variants indicate that loss of a single HMGN has only minor effects on the cellular transcription profile (21). As elaborated above, functional redundancy among HMGN variants and other compensatory events in chromatin may minimize the deleterious effects of a lack of any specific variant, including HMGN1. Yet several types of experiments, including analysis of *Hmgn*^{-/-} mice, reveal that lack of a single HMGN variant may lead to specific phenotypes. Thus, *Hmgn3*^{-/-} mice are diabetic (54) and *Hmgn1*^{-/-} mice are hypersensitive to DNA damage and have an increased incidence of certain cancers (29, 55). The emerging data suggest that each HMGN variant contributes to the maintenance of the fidelity of the cellular transcription profile and that loss of a variant is deleterious, especially under stress condition such as exposure to heat shock (50) or DNA-damaging agents (29, 53, 55). Indeed, we now find that even though the *Hmgn1*^{-/-} ESCs seem to grow and differentiate normally, they are hypersensitive to the DNA-damaging agent doxorubicin (Adriamycin) (see Fig. S6 in the supplemental material). Likewise, the decrease in nestin-pos-

itive cell numbers in the SVZ region of *Hmgn1*^{-/-} mice suggests that while the *Hmgn1*^{-/-} ESCs are not visibly affected in tissue culture, in the context of the entire organism, loss of HMG1 impedes the differentiation or the survival of NP cells. Loss of HMG1 also alters the behavior of mice, most likely by changing expression of MeCp2, a protein that is highly expressed in neurons (37). Our studies link these phenotypic changes to HMG1-mediated alterations in chromatin structure.

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