Correction

DEVELOPMENTAL BIOLOGY. For the article “Requirement of Nanog dimerization for stem cell self-renewal and pluripotency” by Jianlong Wang, Dana N. Levasseur, and Stuart H. Orkin, which appeared in issue 17, April 29, 2008, of Proc Natl Acad Sci USA (105:6326–6331; first published April 24, 2008; 10.1073/pnas.0802288105), the authors note that, as indicated by thin vertical lines, multiple blots from the same experiments were juxtaposed in Fig. 1A, and irrelevant lanes were removed from the same blot in Figs. 1B, 3D, and 4B. In accordance with PNAS editorial policy on the preparation of digital images, the corrected figures and legends appear below. These changes do not affect the conclusions of the article.

Fig. 1. Confirmation of Nanog–Nanog interaction (dimerization). (A) Western blot analysis of gel filtration fractions containing protein complexes using anti-Nanog antibody. Fractions that may contain Nanog homodimers are indicated with a red rectangle (Upper). A close-up of fractions containing potential Nanog dimers and monomers is also presented (Lower). Sample fractions were loaded in four (Upper) and two (Lower) denaturing polyacrylamide gels, respectively, and Western data are presented with thin vertical lines separating the different gels. (B) CoIP in heterologous 293T cells. 293T cells were transiently transfected with constructs indicated, and total lysates were prepared and incubated with anti-M2-FL agarose (Left) or anti-V5 agarose (Right) overnight. Unbound material was washed away; bound material was eluted and subjected to Western blot analyses using the antibodies indicated (Upper). Total lysates as input were also subjected to Western blot analyses with the antibodies indicated (Upper). Total lysates as input were also subjected to Western blot analyses with the antibodies indicated (Upper). Total lysates as input were also subjected to Western blot analyses with the antibodies indicated (Upper). Total lysates as input were also subjected to Western blot analyses with the antibodies indicated (Upper). Total lysates as input were also subjected to Western blot analyses with the antibodies indicated (Upper).

Fig. 4. Tethered Nanog mutants maintain DNA-binding capacity. (A) Schematic depiction of the tethered Nanog dimer (NN) and monomer (NNH) mutants. The 22-aa flexible polypeptide linker is shown. (B) EMSA of mutants’ binding to the Cdx2 (lanes 1–9) and the Gata6 (lanes 10–13) promoter DNA sequences. * indicates specific binding signals; < denotes the supershift bands by anti-Nanog. Wild-type (wt) and vector-transfected COS extracts were used as negative controls. The thin vertical line indicates removal of irrelevant lanes and juxtaposition of lanes relevant for this study.
Fig. 3. Nanog homodimerization is required for its interaction with other pluripotency factors. (A) CoIP of V5his-tagged pluripotency network proteins Sall4, Zfp281, Zfp198, and BirA (control) with dimeric FLbioNanog and monomeric FLbioNanog10WA mutants. (B) CoIP of V5his-tagged Dax1 and BirA (control) with dimeric FLbioNanog and monomeric FLbioNanog10WA mutants. *n.s. indicates a nonspecific signal; * indicates the FLbioNanog signal. Note the much lower input level of FLbioNanog than FLbioNanog10WA and yet a higher IP signal (+) of FLbioNanog than FLbioNanog10WA. (C) CoIP of V5his-tagged Nac1 with dimeric FLbioNanog and monomeric FLbioNanog10WA mutants. (D) CoIP of V5his-tagged Oct4 with dimeric FLbioNanog and monomeric FLbioNanog10WA mutants. The thin vertical lines indicate removal of irrelevant lanes and juxtaposition of the two lanes relevant for this study.
Requirement of Nanog dimerization for stem cell self-renewal and pluripotency

Jianlong Wang*, Dana N. Levasseur*, and Stuart H. Orkin*‡

*Division of Hematology-Oncology, Children’s Hospital and Dana Farber Cancer Institute, Harvard Medical School, Harvard Stem Cell Institute, and Howard Hughes Medical Institute, Boston, MA 02115

Contributed by Stuart H. Orkin, March 6, 2008 (sent for review February 29, 2008)

Pluripotency of embryonic stem (ES) cells is maintained by transcription factors that form a highly interconnected protein interaction network surrounding the homeobox protein Nanog. Enforced expression of Nanog in mouse ES (mES) cells promotes self-renewal and alleviates their requirement for leukemia inhibitory factor (LIF). Understanding molecular mechanisms by which Nanog functions should illuminate fundamental properties of stem cells and the process of cellular reprogramming. Previously, we showed that Nanog forms multiple protein complexes in mES cells. Here, we demonstrate that Nanog dimerizes through its C-terminal domain rather than the homeodomain. Dimerization is required for interaction with other pluripotency network proteins. We also show that enforced expression of the Nanog dimer, but not the monomer, functionally replaces wild-type Nanog to sustain LIF-independent self-renewal of ES cells. Our results demonstrate that Nanog–Nanog homodimerization is a critical aspect of its function promoting stem cell pluripotency.

Embryonic stem cells | homeoprotein

Embryonic stem (ES) cells, derived from the inner cell mass of the early mouse embryo (1, 2), are distinguished by unlimited self-renewal potential and the capacity for multilineage differentiation. An understanding of the molecular underpinnings of these properties requires elucidation of regulatory networks operative in ES cells. Initial efforts in dissecting transcriptional (3–5) and protein interaction (6) networks of mouse and/or human ES cells form a foundation for further mechanistic studies.

Several transcription factors, notably the homeobox proteins Oct4 (7) and Nanog (8, 9), as well as the HMG box containing Sox2 protein (10), play fundamental roles in early development and stem cell pluripotency. These key factors act in combination to sustain pluripotency by activating ES cell critical factors (including themselves) and repressing differentiation-promoting genes. ES cells are sensitive to the dosage of Nanog (11) and Oct4 (12). Enforced expression of Nanog relieves ES cells from their leukemia inhibitory factor (LIF) requirement (9) and promotes transfer of pluripotency after cell fusion (13). In contrast, overexpression of Oct4 drives primitive endoderm differentiation (12), possibly because of direct repression of the Nanog promoter by excessive Oct4 (14). In addition, Sox2 stabilizes ES cells in a pluripotent state by maintaining the requisite level of Oct4 expression (15). Dosage sensitivity suggests that the ES cell state reflects a balance of multiple transcriptional inputs that are likely exerted through association and dissociation of multiprotein complexes. In specifying lineages, Oct4 and Cdx2 counteract each other’s functions to shift the balance between trophectoderm and ICAM fates (16), and Nanog and Gata6 antagonize each other to define epiblast and primitive endoderm lineages (17). The ES cell state, therefore, is likely to be maintained by the continuous and direct interplay of multiple nuclear factors, acting in cooperative and antagonistic modes.

The specific actions of transcriptional regulatory proteins are mediated through their selective association with other protein factors. Previously we showed that Nanog forms multiple protein complexes with apparent molecular sizes of ~150 kDa to several mega-Daltons (6). By protein microsequencing we demonstrated that Nanog associates with numerous other critical factors that, in aggregate, form a tight protein interaction network apparently dedicated to pluripotency (6). Here, we pursue how Nanog functions in this context.

As a divergent homeobox protein, Nanog is most closely related to mouse NK2 family members Nkx2.3 (8) and Nkx2.5 (9). Nkx2.5 has been studied in detail for its direct DNA contacts (18) and homodimerization via the homeodomain (HD) (19). HD proteins often form homodimeric and heterodimeric complexes through their HDs in specifying their transcriptional actions. In some cases, homodimerization may result in cooperative DNA-binding activity (20), whereas in other instances it may result in the inhibition of DNA-binding and/or transcriptional activity (21). Outside of its HD, Nanog shares little homology with NK2 proteins. Prior work suggests that the N-terminal domain (ND) and C-terminal domain (CD) of mouse Nanog possess transactivator function in conventional reporter assays (22), whereas the CD of human Nanog may be functionally dominant in transactivation (23). The CD is distinctive for a prominent tryptophan-rich (WR) subdomain that is highly conserved between mouse and human and acts as a strong transactivator in reporter assays (24).

To study how Nanog functions in the pluripotency network, and how it associates with other network proteins to regulate target gene expression, we have explored the structure–function relationship of the Nanog protein in vivo in mouse ES (mES) cells. We show that the Nanog polypeptide assembles in a homodimer that is mediated by the CD rather than the HD, and Nanog–Nanog homodimerization is necessary for its interaction with other critical factors in the pluripotency network. Finally, we provide functional evidence supporting a requirement of Nanog–Nanog dimerization in stem cell self-renewal and pluripotency.

Results

Nanog Forms Homodimers in Regulating Stem Cell Activity. To study how Nanog exerts transcriptional regulation on target gene expression, its HD–DNA contact was modeled after mouse Nkx2.5, which predicted two possibilities: Nanog might act on DNA as a monomer and/or a dimer [supporting information (SI) Fig. S1]. These predicted structures presuppose that Nanog, like Nkx2.5, homodimerizes via its HD (19). To ascertain whether Nanog, indeed, forms homodimers in vivo, we performed size exclusion chromatography of ES cell nuclear extracts to fractionate Nanog-containing protein complexes. Results reveal that, in addition to a broad range of Nanog multiprotein complexes as described (6), Nanog also forms a small complex with an apparent size of ~70–80 kDa, approximating that of a

Author contributions: J.W. and S.H.O. designed research; J.W. and D.N.L. performed research; J.W. analyzed data; and J.W. and S.H.O. wrote the paper.

The authors declare no conflict of interest.

Freely available online through the PNAS open access option.

‡To whom correspondence should be addressed. E-mail: orkin@bloodgroup.tch.harvard.edu.

This article contains supporting information online at www.pnas.org/cgi/content/full/0802288105/DCSupplemental.

© 2008 by The National Academy of Sciences of the USA
Nanog dimerization is required for interaction with pluripotency network proteins. Our prior studies defined important roles in stem cell self-renewal and pluripotency for a number of newly identified critical ES cell factors, such as Sall4, Dax1, Zfp281, and Nac1 (6). To address the potential relevance of Nanog dimerization, we asked whether these and other critical factors within the ES cell pluripotency network (6) interact with the Nanog dimer.

We have already shown that Nanog dimers may constitute the core of Nanog protein complexes (Fig. 1). To confirm this, coIP studies were performed to test interaction of Sall4, Zfp281, Zfp198, Dax1, Nac1, and Oct4 with dimeric Nanog and monomeric Nanog10WA (Fig. 3). The results show that Sall4, Zfp281, Zfp198 (Fig. 3A) and Dax1 (Fig. 3B) only interact with FLbioNanog (a dimerizing-competent version of the Nanog protein), but not FLbioNanog10WA (a nondimerizing version of the protein). Nac1, a BTB-POZ domain protein, preferentially associates with dimeric FLbioNanog, and to a much less extent with monomeric FLbioNanog10WA (Fig. 3C). Oct4, a critical factor for ES cell identity, also preferentially interacts with dimeric FLbioNanog (Fig. 3D); note the input of monomeric FLbioNanog10WA is more than dimeric FLbioNanog and yet the fraction of dimeric FLbioNanog immunoprecipitated by Oct4 was much higher). These results suggest that Nanog dimers likely constitute a core for Nanog-containing complexes.

**Forced Nanog Dimer and Monomer Maintain DNA Binding Capacity.** To address whether Nanog homodimerization is necessary and/or sufficient for stem cell pluripotency, we asked whether a forced Nanog dimer and/or monomer can replace endogenous Nanog in ES cells. Our approach is based on a now classical strategy used to assess the role of MyoD and E47 heterodimerization in myogenesis (27). In this method, two transcription factors are tethered together by using the 22-aa flexible polypeptide [GG(S/G)G(S/G)G(S/G)]11. As intramolecular interactions are greatly favored over intermolecular interactions, forced dimers predominate.

Following the same strategy, we constructed two Nanog mutants. By joining two units of wild-type Nanog (N) with the same flexible polypeptide linker, a forced Nanog dimer (NN) was generated (NN; Fig. 4A Upper). A Nanog monomer mutant (NNH) was constructed by joining a wild-type Nanog unit (N) with another Nanog mutant lacking the dimerization-mediating CD domain (NH; Fig. 4A Lower). The NH mutant itself acts solely as a truncated monomer without any dominant negative effects when overexpressed in ES cells (see Fig. S2). This finding ensures the monomeric properties of the NNH mutant driven by the intramolecular interaction between the wild-type Nanog unit and the NH mutant (see Discussion).

To validate the DNA-binding capacity of the tethered Nanog mutants, we did EMSAs using COS extracts of mutant-expressing cells and probes containing a Nanog consensus binding site (8). The proximal promoters of both Cdx2 and Gata6 contain Nanog consensus binding sites and were used for EMSA. The results (Fig. 4B) show that both the tethered Nanog (NN) and monomer (NNH) bind to the Nanog-binding site in the Cdx2 (Fig. 4B, lanes 4 and 6) and the Gata6 (Fig. 4B, lanes 10 and 12) promoter DNAs. The binding specificity was further confirmed by supershift of the binding bands by anti-Nanog antibody (Fig. 4B, lanes 5, 7, 11, and 13). Binding of wild-type Nanog protein to the Cdx2 promoter sequence, as both a dimer and a monomer, served as a positive control (Fig. 4B, lanes 8 and 9).
Untransfected and vector-transfected COS cell extracts were used as negative controls to identify background binding signals (Fig. 4B, lanes 1–3). Our results indicate that the tethered Nanog proteins retain intrinsic DNA binding capacity, a prerequisite for subsequent testing of their biological activities.

**Forced Nanog Dimer, but Not Monomer, Maintains LIF-Independent Self-Renewal.** To test the function of tethered Nanog dimers and monomers for self-renewal and pluripotency, we asked whether enforced expression of the dimer and/or monomer is able to functionally replace endogenous Nanog in ES cells. To this end, an episomal overexpression system (9) was used to achieve enforced expression of wild-type Nanog protein (9). Therefore, these data mimic the colony formation assay of ES cells with enforced expression of wild-type Nanog protein (9). Therefore, our findings argue that the Nanog dimer is the active form of

Untransfected and vector-transfected COS cell extracts were used as negative controls to identify background binding signals (Fig. 4B, lanes 1–3). Our results indicate that the tethered Nanog proteins retain intrinsic DNA binding capacity, a prerequisite for subsequent testing of their biological activities.

**Forced Nanog Dimer, but Not Monomer, Maintains LIF-Independent Self-Renewal.** To test the function of tethered Nanog dimers and monomers for self-renewal and pluripotency, we asked whether enforced expression of the dimer and/or monomer is able to functionally replace endogenous Nanog in ES cells. To this end, an episomal overexpression system (9) was used to achieve enforced expression of wild-type Nanog protein (9). Therefore, these data mimic the colony formation assay of ES cells with enforced expression of wild-type Nanog protein (9). Therefore, our findings argue that the Nanog dimer is the active form of
Nanog protein that serves to replace wild-type Nanog for LIF-independent self-renewal upon overexpression.

Discussion

In this study we have explored how the Nanog protein acts within the pluripotency network (6). Previously, we focused on Nanog-containing protein complexes rather than on the Nanog protein itself. By performing refined size exclusion chromatography, we have now shown that Nanog–Nanog homodimers constitute a major fraction of Nanog protein complexes in ES cells (Fig. 1A).

We confirmed the direct Nanog–Nanog interaction in heterologous cells (Fig. 1B) and delineated the dimerization domain in the Nanog protein (Fig. 2). Moreover, we demonstrated that Nanog homodimerization is required for interaction with a number of critical factors in the network (Fig. 3). Finally, we showed that enforced expression of a Nanog dimer, but not monomer, functionally replaces endogenous Nanog to sustain LIF-independent self-renewal of ES cells (Figs. 4 and 5). Our study confirms and extends the established role of Nanog in stem cell pluripotency and provides insights into the mechanism of Nanog transcriptional regulation for target gene expression in stem cell pluripotency.

As a unique variant HD protein, Nanog bears no obvious relationship with previously characterized proteins, save for modest similarity of its HD with that of the NK2 family of homeoproteins (9). However, unlike NKx2.5, the HD of Nanog is not required for homodimerization (Fig. 2). Besides its presumed role in direct DNA contact, the HD of Nanog has been shown to be required for nuclear localization of the human homolog (28) and interaction with another ES cell critical factor Sall4 in mES cells (29). Quite unexpectedly, we found that the CD of Nanog, particularly the WR subdomain, mediates homodimerization (Fig. 2). The CD has been reported to contain transactivation activity in reporter assays (22, 24), although the in vivo function of this domain remained largely uncharacterized. Our study indicates that an important role of the CD is to mediate Nanog–Nanog homodimerization.

The functional significance of Nanog homodimerization is suggested by association of a number of pluripotency network proteins with Nanog dimers, as opposed to monomers (Fig. 3). This observation is consistent with the notion that, on average, homodimers have twice as many interaction partners as nonself-interacting proteins in protein–protein interaction networks (30). Although we stress the relevance of Nanog dimers in
regulating stem cell activity, we cannot formally exclude a possible role of Nanog monomers in target gene regulation, particularly in light of enhanced self-renewal of monomer (NNH)-expressing cells in the presence of LIF (Fig. 5D). Two possible explanations may account for enhanced self-renewal by the Nanog monomeric mutant (NNH). First, the Nanog monomer and dimer might regulate distinct sets of target genes for stem cell self-renewal. In this case, an increase of monomers in the presence of steady-state levels of Nanog dimers and monomers would presumably enhance self-renewal. Alternatively, enhanced self-renewal might result from an increase in dimer formation upon overexpression of NNH in cells grown in the presence of LIF. In this case, an intermolecular, functional Nanog dimer might be formed between wild-type Nanog and the NNH mutant in the presence of steady-state levels of wild-type Nanog. This possibility is supported by in vitro coIP data showing that NNH can still interact with Nanog (data not shown). However, such intermolecular dimer formation was not favored upon LIF withdrawal and subsequent depletion of endogenous Nanog.

Interpretation of the functional data relies on the authenticity of the mutants generated by the tethering strategy (27) in relation to the endogenous protein. Although direct protein structure data are lacking, the strategy has been successfully applied for studies on the heterodimerization of myogenic transcription factors MyoD-E47 (27) and the heterodimerization of hematopoietic transcription factor NF-E2 subunits p18–p45 (31). We have carefully addressed the relevance of the mutants to the functional data by ensuring their intact intrinsic DNA-binding capacity (Fig. 4) and using two complementary strategies to provide biological readouts (Fig. 5). In addition, we have noted that the NH-truncated mutant used to construct the tethered, monomeric Nanog (NNH) is inactive in ES cells (see Fig. S2). This observation ensures that the monomeric version of the Nanog protein (NNH; Fig. 4A) is free of any dominant negative effect and serves as a better monomer mutant than NanogTWA itself (which may have additional effects resulting from the sequence change). Interestingly, it has been reported that the same NH mutant behaves in a dominant negative fashion in F9 embryonic carcinoma cells (32). This finding may be explained by the much weaker pluripotency network in F9 cells than that in ES cells, such that a subtle imbalance between the endogenous Nanog and the NH mutant (when overexpressed) drives cells toward the primitive endodermal lineage. In contrast, ES cells that express high levels of Nanog and possess a robust network are resistant to effects of the NH mutant.

The importance of the Nanog protein for pluripotency is underscored in factor-based reprogramming experiments (reviewed in ref. 25) that demonstrate the utility of selection for Nanog expression (33–35) and direct participation of Nanog (36) for the generation of high-quality induced pluripotency stem cells. In addition, Nanog has been shown to facilitate transfer of pluripotency after cell fusion (13). These data suggest that Nanog may act as a master transcriptional organizer that entrains the hierarchy of pluripotent gene expression after erasure of the differentiated epigenome. How Nanog functions in this process is not well understood. In this study, we provided one aspect of Nanog transcriptional regulation, i.e., homodimerization, which is necessary for its function in promoting stem cell pluripotency.
Materials and Methods

Cell Culture, Total Lysate and Nuclear Extract Preparation, and Size Exclusion Chromatography (Gel Filtration). ES cell lines (J1 and E14T) were maintained on gelatin-coated plates without feeders as described (25). 293T and COS cells were maintained in DMEM (low glucose) supplemented with 10% FCS and 50 units/ml penicillin/streptomycin. These cells were split every other day to maintain 50–70% confluence for optimal transfection.

ColP and Western Blot Analysis. ColP in 293T cells and Western blot analyses using total lysates or nuclear extracts were performed as described (25).

Plasmid Construction. Truncated Nanog mutants were constructed by using a PCR strategy. Briefly, PCRs were performed with the primers in the 5' and 3' ends of Nanog cDNA and the primers with progressive deletion of the HD from 3' to 5' (mutants A to E) and 5' to 3' (mutants F to J), respectively. The mutant K was constructed by using the primers spanning the HD. The LFlbNanog100A1 mutant was constructed by using a site-directed mutagenesis (Stratagene) kit, the template plasmid LFlbNanog as described (6), and two primers containing the alterations of 10 tryptophan residues to alanine. The tethered Nanog dimer and monomer mutants were constructed with three subcloning steps. First, a wild-type unit of Nanog was joined 5' terminally to the full-length 22-aa polypeptide linker by annealing Nanog cDNA and the polypeptide linker containing overlapping the Nanog 3' end cDNA sequence followed by PCR with the two outmost primers. The resulting PCR product containing a XhoI site before the 5' end of Nanog cDNA and a BamHI site in the polypeptide linker was then cloned into XhoI and BamHI sites of the pBluescript SK vector; second, either a wild-type unit or truncated NH unit of Nanog was joined 3' terminally to the full-length 22-aa polypeptide linker by annealing Nanog cDNA and the polypeptide linker containing overlapping Nanog 5' end cDNA sequence followed by PCR with the two outmost primers. The resulting PCR product containing a BamHI site in the polypeptide linker and a NotI site after the 3' end of Nanog cDNA was then cloned into BamHI and NotI sites of the pBluescript SK subclone from step 1; third, the XhoI and NotI fragment from the subclone in step 2 was released and cloned into pPyCAGIZ vectors previously digested with XhoI and NotI.

All PCR products described above were subcloned into pCRII-TOPO vector (Invitrogen) for sequence verification (performed by the Mental Retardation Research Center at Children's Hospital Boston) followed by cloning into the respective expression vectors (pEFlv1S8s from Invitrogen; pPyCAGIZ vectors kindly provided by Ian Chambers, University of Edinburgh, Edinburgh). Sequences for oligonucleotides used in this study are available on request.

EMSA. The sense and antisense oligonucleotides for probes were synthesized with a 5' single nucleotide “G” overhang for labeling with [32P]-dCTP (Amersham) by Klenow enzyme (New England Biolabs) fill-in reaction. The probe sequences are as follows: Cdx2 probe sense, 5'- GTGTTTTAATTAAATTTGAATTTATAATTATTTTA-3'; Cdx2 antisense, 5'-CGAAAATAATATTAAAGACTTATT-AGTTTTAAAAAG-3'; Gata6 sense, 5'-GAGAATAAACTTTGACACTTTAAGG-3'; GAGGGTGGGCCTCA-3', antisense, 5'-TGAGGGCACCACACTACGATTATCCCTTTATTTTTT-3'. The sense and antisense oligonucleotides were annealed before being labeled with Klenow enzyme and [32P]-dCTP. EMSA was performed as described (37).

Serial Passage, Colony Formation Assays, and ES Cell Growth Assay. For serial passage, ES cells were grown in the presence (1,000 units/ml) and absence of LIF, split every other day to maintain 50–80% confluence. After 8 days of serial splitting and passage, cells were subjected to AP staining (Sigma) per the manufacturer's instructions. Colony formation assays were performed as described (9), except that 1,200 cells were grown on a 10-cm plate, and ES cell growth assay were performed as described (8).

Acknowledgments. We thank Vijay Sankaran for modeling the Nanog HD–DNA contacts, Dr. Lingyi Chen for bioinformatics on the Cdx2 promoter, and Drs. Ian Chambers and Austin Smith (Wellcome Trust Center for Stem Cell Research, Cambridge, U.K.) for pPyCAGIZ vectors and E14T ES cells. This work is supported by a Seed Grant from the Harvard Stem Cell Institute Cell Reprogramming Program (to J.W.). H.O. is an Investigator of Howard Hughes Medical Institute.

Fig. S1. Modeling of Nanog homeodomain–DNA contact. (A) Protein structures of mouse NKx2.5 and Nanog. NKx2.5 homeodomain (HD) share 50% homology with that of Nanog. The distinct subdomains associated with NKx2.5 (TN domain and NK2 domain) and Nanog (tryptophan-rich WR domain) are shown. (B) Predicted Nanog monomer and dimer in contact with DNA double helix modeled after NKx2.5. The HD–DNA contact is indicated, and the HD of Nanog is assumed to mediate homodimerization like NKx2.5.
Fig. S2. The truncated NH mutant is inactive in ES cells. (A) The construct of pPyCAG-NH-IRESpuro (IP). (B) Expression of the NH mutant in E14T ES cells. E14T ES cells were transfected with the empty pPyCAG-iP (0) and pPyCAG-NH-iP (NH) and selected with 2 μg/ml puromycin. Stable clones were picked and expanded to obtain total lysate (TL) and nuclear extracts (NE) for Western blot analysis with anti-Nanog antibody. (C) Morphology of control ES cells (0) and ES cells stably expressing the NH mutant (NH). ES cells were serially split and passaged for 8 days, and pictures were taken at day 8. (D) Comparable growth of ES cells expressing the NH mutant and parental E14T cells. A total of 1 × 10⁴ cells were plated in 24-well plates. Nine wells per sample were plated, representing triplicates at three time points (days 2, 4, and 6). The cells were counted every other day, and data of mean ± SD are presented. Data from three representative clones (nos. 1, 13, and 23) were used for cell growth analysis.