To identify the proteins that bind to MEF/ELF4, we performed the TAP procedure and analyzed the amino acid sequence of the protein complex, thereby identifying 25 proteins (including NPM1). NPM1 is essential for embryonic development and is frequently translocated or mutated in hematological malignancies (24). Therefore, we decided to focus on the interaction between NPM1 and MEF/ELF4.

Wt-NPM1 interacts with MEF/ELF4 in vivo and in vitro

To determine if Wt-NPM1 interacts with MEF/ELF4 in human cells, we transfected 293T cells with FLAG-MEF/ELF4 and V5-Wt-NPM1 expression plasmids and performed immunoprecipitations with mouse monoclonal anti-FLAG or anti-V5 antibody. As shown in Fig. 1A, FLAG-MEF/ELF4 protein co-precipitated with V5-Wt-NPM1 by the anti-V5 antibody (lane 1), but not by the isotype-matched control (lane 2). In reciprocal experiments, V5-Wt-NPM1 protein co-precipitated with Flag-MEF/ELF4 protein by the anti-Flag antibody (lane 3). These results showed the *in vivo* interaction between Wt-NPM1 and MEF/ELF4. To ascertain whether Wt-NPM1 protein interacted directly with MEF/ELF4, an *in vitro* association assay with biotin-labeled *in vitro*-translated Wt-NPM1 and bacterially recombinant His-MEF/ELF4 fusion protein was performed (Fig. 1B). Biotin-labeled Wt-NPM1 bound to His-MEF/ELF4 (lane 1), but not to His alone (lane 2). These results demonstrated that His-MEF/ELF4 bound directly to Wt-NPM1.

To characterize the region of Wt-NPM1 that binds MEF/ELF4, five distinct GST-NPM1 proteins were prepared (Fig. 1C). GST pull-down assays (Fig. 1D (a)) and His tag pull-down assays (Fig. 1D (b)) revealed that the N-terminal region of NPM1 (the F1, F2, and F3 fragments that contain the oligomerization domain) bound to His-MEF/ELF4, unlike the C-terminal region of NPM1 (F4 and F5).

Wt-NPM1 interferes with MEF/ELF4 binding to target DNA sequences

To assess the direct role of Wt-NPM1 in MEF/ELF4 action, we undertook EMSA. His-MEF/ELF4 bound to the APET probe (1), but no band was observed with His, GST, or GST-NPM1 (Fig. 2). The shifted band of MEF/ELF4 was diminished when the APET competitor was added to the reaction mixture. When Wt-NPM1 was added to the reaction mixture, the shifted band containing MEF/ELF4 was diminished. These results implied that Wt-NPM1 inhibits the DNA binding of MEF/ELF4 DNA through direct interactions.

Wt-NPM1 inhibits, whereas Mt-NPM1 enhances, MEF/ELF4-dependent

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transcriptional activity

To study the functional relevance of the physical interaction between MEF/ELF4 and Wt-NPM1, we transfected pcDNA/MEF/ELF4 in combination with pcDNA/Wt-NPM1 and examined the activity of the APET promoter construct (1) in 293T cells (Fig. 3A). As reported previously, MEF/ELF4 activated the APET promoter by approximately 159-fold. Co-expression of Wt-NPM1 with MEF/ELF4 led to a significant decrease in luciferase activity. Similar data were obtained by using COS7 cells (Fig. 3B) and a human leukemia cell line, U937 (Fig. 3C).

Having shown that NPM1 expression attenuated the transcriptional activity of MEF/ELF4 in leukemia cells, we next assessed whether the inhibition of Wt-NPM1 expression *in vivo* enhanced MEF/ELF4-dependent transcriptional activity. The siRNA directed against Wt-NPM1 in 293T cells suppressed the expression of Wt-NPM1 protein by 60%-70% (Fig. 3D). Transient transfections were performed by using NPM1-knockdown 293T cells with pcDNA/MEF/ELF4 and PGL4/APET reporter plasmids. A luciferase assay revealed that MEF/ELF4-dependent transcriptional activity was significantly elevated in Wt-NPM1-knockdown cells by 1.8-fold (Fig. 3E). These results implied that Wt-NPM1 functioned as an inhibitor of MEF/ELF4.

Mutated nucleophosmin (Mt-NPM1) has been found in 50% of adult AML patients with normal karyotypes (15). It has been suggested that the mutation is a critical event for leukemogenesis. To determine the effect of Mt-NPM1 on the transcription-activating properties of MEF/ELF4, we transfected pcDNA/MEF/ELF4 in combination with pcDNA/Mt-A-NPM1, pcDNA/Mt-I-NPM1, or pcDNA/Mt-J-NPM1 and then examined the activity of the APET promoter construct in 293T cells (Fig. 3F). Co-expression of Mt-NPM1 with MEF/ELF4 led to a 315-fold increase in luciferase activity. Similar data were obtained with COS7 (Fig. 3G) and U937 (Fig. 3H) cells. To show the effect of the coexistence of both Wt- and Mt-NPM1, we transfected 293T cells with various amounts of plasmids that expressed Wt-NPM1 and Mt-A-NPM1. The expression of Mt-NPM1 enhanced MEF/ELF4-dependent APET promoter activation in a dose-dependent manner, even in the presence of Wt-NPM1 (Fig. 3I). Taken together, our results suggest that Wt-NPM1 has an inhibitory effect, whereas Mt-NPM1 has enhancing effect, on the function of MEF/ELF4.

Mt-NPM1 does not interact with MEF/ELF4 in vivo

Since the mutated region of Mt-NPM1 was

located outside the domain responsible for interaction with MEF/ELF4, we hypothesized that Mt-NPM1 might bind to MEF/ELF4. To test this hypothesis, we transfected 293T cells with FLAG-MEF/ELF4 and V5-Mt-A-NPM1 expression plasmids and performed immunoprecipitations with mouse monoclonal anti-FLAG or anti-V5 antibody. Contrary to our expectations, as shown in Fig. 4, FLAG-MEF/ELF4 protein and V5-Wt-A-NPM1 did not co-precipitate with each other (Fig. 4). These results showed that there is little *in vivo* interaction between Mt-A-NPM1 and MEF/ELF4.

Localization of MEF/ELF4 is unaffected by Mt-NPM1

Having shown that Mt-NPM1 enhances the transcriptional activity of MEF/ELF4, we next assessed whether Mt-NPM1 dislocates MEF/ELF4 into the cytoplasm. We transiently co-transfected a MEF/ELF4-GFP fusion protein vector together with the pcDNA/V-Wt-NPM1 or pcDNA/V-Mt-A-NPM1 expression vector into 293T cells. Wt-NPM1 protein and MEF/ELF4 localized to the nucleus (Fig. 5A (a)), whereas Mt-A-NPM1 protein localized to the cytoplasm (Fig. 5A(b)). Contrary to our expectations, the presence of Mt-A-NPM1 did not affect the subcellular distribution of MEF/ELF4. Western blot analysis of MEF/ELF4 and Wt- or Mt-NPM1 in nuclear and cytoplasmic proteins confirmed the nuclear localization of MEF/ELF4 even with Mt-NPM1 (Fig. 5B).

Wt-NPM1 inhibits, whereas Mt-NPM1 enhances, the oncogenic activity of MEF/ELF4

The overexpression of MEF/ELF4 in NIH3T3 cells increases the growth rate, enhances colony formation in soft agar, and promotes tumor formation in nude mice (10). To determine the effects of the interaction of NPM1 with MEF/ELF4 on cell behavior, we assessed the anchorage-independent growth of NIH3T3 cells after co-transfection of MEF/ELF4 with Wt-NPM1 or Mt-A-NPM1. Compared with NIH3T3 transfected with only MEF/ELF4, Wt-NPM1-coexpressing cells showed reduced anchorage-independent growth, whereas Mt-A-NPM1-coexpressing cells exhibited increased growth (Fig. 6).

MEF/ELF4 binds to the HDM2 promoter and activates its expression

In murine cells, MEF/ELF4 binds directly to the Mdm2 promoter, thereby promoting *Mdm2* expression (12). To ascertain whether MEF/ELF4 also directly regulates the promoter activity of *HDM2* (the human analog of Mdm2), we scrutinized the DNA sequence of the *HDM2* gene and found a conserved putative MEF/ELF4 binding site in the P2 promoter (Fig. 7B). To establish the association of MEF/ELF4 with the HDM2

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promoter, we performed a ChIP assay with nuclear lysates from 293T cells expressing FLAG-MEF/ELF4. Immunoprecipitation with the FLAG antibody (but not with the control IgG) and subsequent PCRs revealed the recruitment of overexpressed MEF/ELF4 to the promoter region of the HDM2 gene (Fig. 7A). The luciferase assay revealed that MEF/ELF4 strongly transactivated the wild-type HDM2 promoter (Fig. 7B (a), Fig. 7C) and that the effect was abrogated by mutation of the ETS site (-122 to -82) (Fig. 7B (b), Fig. 7C). Compared with Wt-NPM1, the expression of Mt-A-NPM1 in 293T cells enhanced the association of MEF/ELF4 with the HDM2 promoter as detected by ChIP analysis (Fig. 7D). Taken together, these findings suggest that Mt-NPM1 upregulates HDM2 transcription by increasing the recruitment of MEF/ELF4 to the HDM2 promoter by dislocating Wt-NPM1 that interferes with its binding to the promoter.

Higher levels of HDM2 mRNA in clinical samples from AML patients with Mt-NPM1 and higher MEF/ELF4 expression

To determine the possible clinical relevance of MEF/ELF4, NPM1, and HDM2 in AML patients, we examined the mRNA levels of each in CD34-positive leukemic blasts from 22 AML patients with normal karyotypes. Fourteen patients had Wt-NPM1, and 8 patients had Mt-A-NPM1. There was no significant difference in the clinical characteristics of the Wt-NPM1 group and the Mt-NPM1 group (Table 1). Samples from the Mt-NPM1 group had significantly higher levels of HDM2 expression as compared to the Wt-NPM1 group ($p = 0.009$) (Fig. 8A). In addition, patients with high expression levels of MEF/ELF4 (the MEF/ELF4-H group) had significantly higher HDM2 expression than patients with low expression levels of MEF/ELF4 (the MEF/ELF4-L group) ($p = 0.03$) (Fig. 8B).

DISCUSSION

In the present study, we identified NPM1 to be a MEF/ELF4-binding protein. Wt-NPM1 inhibited the function of MEF/ELF4 (i.e., DNA-binding and transcriptional activities), whereas Mt-NPM1 augmented its function. Some of these effects of Wt-NPM1 and Mt-NPM1 on MEF/ELF4 were reproducible on the HDM2 promoter (one of the target genes of MEF/ELF4), suggesting that HDM2 expression is influenced by NPM1. Furthermore, we found that the expression of Mt-NPM1 in MEF/ELF4-overexpressing NIH3T3 cells resulted in enhanced malignant transformation. We also found that the mRNA level of HDM2 in primary leukemia cells was higher in patients with NPM1 mutations. Mef/Elf4 directly activates Mdm2 expression (13). Therefore, NPM1 mutation could enhance HDM2 expression through the

increased MEF/ELF4 activity, thereby promoting transformation by inhibiting the p53 pathway.

NPM1 is a multifunctional phosphoprotein that has been implicated in cell proliferation as well as regulation of transcription factors. It appears to repress or stimulate transcription. For example, Wt-NPM1 activates and inhibits p53 function through direct binding (22,25). Interferon regulatory factor-1 (IRF-1), a transcriptional activator, binds to Wt-NPM1, resulting in the inhibition of DNA binding and transcriptional activity (26). Our findings with Wt-NPM1 and MEF/ELF4 are consistent with these observations. Wt-NPM1 interacts directly with c-Myc and regulates the expression of endogenous c-Myc target genes at the promoter, which enhances c-Myc-induced proliferation and transformation (27). In contrast, the present study suggests that Wt-NPM1 inhibits (whereas Mt-NPM1 facilitates) the transformation induced by MEF/ELF4, suggesting that there is a contradiction in terms of NPM1 function. However, the overexpression of Wt-NPM1 without c-Myc activation has only a small effect on proliferation and has no effect on transformation, so Wt-NPM1 may mainly have a role in c-Myc-driven tumors. Interestingly, c-Myc, IRF-1, and MEF/ELF4 are all regulated during the cell cycle, and the levels of these transcription factors are highest in the G1 phase (28,29).

We found that Wt-NPM1 could interfere with the ability of MEF/ELF4 to bind to DNA, resulting in the inhibition of MEF/ELF4-dependent transcriptional activity. The mechanism by which Wt-NPM1 interferes with the DNA binding of MEF/ELF4 is unclear. We previously showed that the 120 amino acids of the N-terminal to the ETS domain in MEF/ELF4 (residues 87-206) are responsible for its binding to AML1 proteins (30); thus, MEF/ELF4 interacts with other proteins outside the DNA-binding domain. As mentioned above, the association of Wt-NPM1 and IRF-1 inhibits the DNA binding of IRF-1. Narayan *et al.* showed that IRF1 binds directly to Wt-NPM1 through a short linear motif in the nuclear localization sequence outside the DNA-binding domain (31). These results suggest that the inhibition of DNA binding by NPM1 may not be through a simple interference with the DNA-binding domain of MEF/ELF4. Determining the protein-binding interface of MEF/ELF4 may help to reveal the mechanism of NPM1-mediated transcriptional regulation.

The heterodimerization domain (residues 186-259) of NPM1 is essential for its interaction with p53 (22), and the c-Myc-binding region is within the NPM1 heterodimerization domain (27). In the case

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of MEF/ELF4 and NPM1, the N-terminal regions of NPM1 (F1, F2, and F3) could bind to His-MEF/ELF4, implying that the oligomerization domain is important for the interaction.

Recently, it has been shown *in vivo* that NPM1 mutants actively contribute to leukemogenesis by conferring a proliferative advantage in the myeloid lineage. In zebrafish, forced expression of mutant NPM1 causes an increase in PU.1-positive primitive early myeloid cells (32). Furthermore, in a transgenic mouse expressing the human NPM1 mutant, although spontaneous AML was not found, myeloproliferation occurred in the bone marrow and spleen (33). Moreover, Vassiliou *et al.* showed that activation of a humanized mouse NPM1 mutant knock-in allele in mouse hematopoietic stem cells caused overexpression of the Hox gene, enhanced self-renewal, and expanded myelopoiesis, resulting in delayed-onset AML in one third of the mice (34). Taken together, these data suggest that NPM1 mutations initiate leukemia by activating a set of proliferative pathways. Mt-NPM1 enhances the transcriptional activity of MEF/ELF4, so the upregulation of HDM2 and subsequent downregulation of p53 may also have a role in leukemogenesis.

In vitro transfection studies and immunohistochemical observations in samples from AML patients have demonstrated that NPM1 mutants recruit Wt-NPM1 from the nucleolus and delocalize it to the nucleoplasm and cytoplasm (18) and that aberrant NPM1 accumulation in the cytoplasm may have a critical role in leukemogenesis. While Wt-NPM1 protein co-localizes with tumor suppressor p19ARF in the nucleolus, Mt-NPM1 delocalizes p19ARF from the nucleolus to the cytoplasm, which results in reduced p19ARF activities (e.g., Mdm2 and $p21^{cip1}$ induction, stimulation of NPM1) (35). Furthermore, by using OCI/AML3 human leukemia cells where mutant NPM1 is localized in the cytoplasm, Bhat *et al.* have recently shown that NPM1 co-localizing nuclear transcription factor, Forkhead box M1 (FOXM1), disappears from the cytoplasm following transient NPM1 knockdown (36). These data suggest that NPM1 may determine the intracellular localization of interacting transcription factors. However, in our experiments, Mt-NPM1 did not interact with MEF/ELF4 in vivo, and the subcellular distribution of MEF/ELF4 was not affected by the presence of Mt-NPM1. It seemed that Mt-NPM1 binds and dislocates Wt-NPM1 into the cytoplasm of leukemia cells, which eventually leads to uncontrolled transactivation of MEF/ELF4. Wt-NPM1 knockdown with siRNA against NPM1 also enhanced MEF/ELF4 activity (Fig. 3E),

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suggesting that the depletion of an MEF/ELF4 inhibitor (i.e., Wt-NPM1) in the nucleus is responsible for the transactivation of MEF/ELF4. Taken together, it is likely that NPM1 mutants exert oncogenic functions at least in part through the upregulation of the activities of oncogenic transcription factors such as MEF/ELF4. The correlation between NPM1 mutations and the elevated expression of HDM2 in primary leukemia cells seems to support this theory.

In patients with AML, NPM1 mutations are mutually exclusive of recurrent genetic abnormalities. It can be speculated that the enhanced MEF/ELF4-HDM2-p53 pathway induced by NPM1 mutations may participate in leukemia development, especially in patients with a normal karyotype. The transactivation of MEF/ELF4 by E2F1 is inhibited by p53 (37), suggesting that p53 suppression induced by NPM1 mutation could lead to the activation of E2F1, resulting in the enhanced expression of MEF/ELF4. Our previous data showing the elevated expression of MEF/ELF4 in AML cells with a normal karyotype compared to that of AML cells carrying t(8;21) and t(15;17) seem to support this hypothesis. Our results suggest a new role for NPM1 and MEF/ELF4 in leukemia development.

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FIGURE LEGENDS

Figure 1

NPM1 interacts with MEF/ELF4. (A) 293T cells were transfected with the indicated expression plasmids. After 48 h, cell lysates were immunoprecipitated with anti-FLAG and anti-V5 antibodies. Immunoprecipitates were analyzed by 10% SDS-PAGE and subjected to immunoblotting with anti-V5 antibody (upper row) or anti-FLAG antibody (bottom row). (B) MEF/ELF4 interacts directly with NPM1 *in vitro*. *In vitro* association assays were undertaken by incubating His-MEF/ELF4 fusion protein immobilized by using a His-column with biotin-labeled MEF/ELF4 (lane 1). His alone was incubated with biotin-labeled NPM1 (lane 2) as a control. (C) NPM1 structure and the relative binding of MEF/ELF4 (schematic). HomoD, homodimerization domain, residues 1–117; AD/NLS, acidic domain/nuclear localization domain, residues 117–187; HeteroD, heterodimerization domain, residues 187–259; NBD, nucleic acid binding domain, residues 259–294. (D) The N-terminal portion of NPM1 is the MEF/ELF4-interacting domain. Bacterially expressed and purified GST, GST-NPM1, and GST-NPM1 mutants with deletions were mixed with bacterially expressed and purified His or His-MEF/ELF4 protein. Recombinant proteins were subjected to His or GST affinity columns, followed by immunoblotting with anti-GST or anti-His antibodies. (a): the reactive samples were subjected to analyses in His affinity column followed by immunoblotting with ant-His antibodies (left lower panel) or with anti-GST antibodies (left upper panel). (b): the reactive

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samples were subjected to GST affinity columns, followed by immunoblotting with anti-GST antibodies (right upper panel) or with anti-His antibodies (right lower panel).

Figure 2

EMSA with recombinant His-MEF/ELF4, His, GST, and GST-Wt-NPM1. His-MEF/ELF4 was incubated with GST and GST-Wt-NPM1 at room temperature prior to EMSA by using a biotin-conjugated APET probe (lanes 1-4). An excess amount of unlabeled APET competitor was added to the reaction mixtures (lanes 5 and 6).

Figure 3

Wt-NPM1 inhibits, whereas Mt-NPM1 enhances, MEF/ELF4-dependent APET promoter transactivation. (A) 293T human kidney cell lines, (B) COS7 monkey kidney cell lines, and (C) U937 human hematological cell lines were co-transfected with the luciferase reporter gene of an artificial MEF/ELF4 target promoter (APET) and effecter genes. Target promoter and effecter genes were as follows: lane 1: PGL4/APET; lane 2: PGL4/ETSm-APET; lane 3: PGL4/APET and PcDNA/MEF/ELF4; lane 4: PGL4/APET, pcDNA/MEF/ELF4, and pcDNA/Wt-NPM1; lane 5: PGL4/ETSm-APET and pcDNA/MEF/ELF4; and lane 6: PGL4/APET and pcDNA/Wt-NPM1. Luciferase activity by PGL4/APET alone was assigned a value of 1.0. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*$P < 0.05$). (D) 293T cells transduced with siRNA encoding vector (siWt-NPM1) were harvested 72 h after transduction for Western blotting. Hsp90 is shown as a control. sicNPM1, control siRNA non-relevant to the expression of NPM1; Wild, without transduction. (E) 293T cells were co-transfected with the luciferase reporter plasmid (PGL4/APET), expression plasmid (pcDNA MEF/ELF4), and siWt-NPM1 gene (pcDNA/siRNA-Wt-NPM1) or control. Luciferase activity by PGL4/APET alone was assigned a value of 1.0. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*$P < 0.05$). (F) 293T cells were co-transfected with the luciferase reporter gene of an artificial MEF/ELF4 target promoter and effector genes. Target promoter and effector genes were as follows: lane 1: PGL4/APET; lane 2: PGL4/APET and PcDNA/MEF/ELF4; lane 3: PGL4/APET, pcDNA/MEF/ELF4, and Wt-NPM1; lanes 4, 5 and 6: PGL4/APET, pcDNA/MEF/ELF4, and Mt-A-NPM1, Mt-I-NPM1 or Mt-J-NPM1; and lanes 7, 8, 9 and 10: PGL4/APET and pcDNA/Wt-NPM1, Mt-A-NPM1, Mt-I-NPM1 or Mt-J-NPM1. Luciferase activity by PGL4/APET alone was assigned a value of 1.0. The analysis was performed in

triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*P < 0.05). (G) COS7 cells were co-transfected with the luciferase reporter gene of an artificial MEF/ELF4 target promoter, and effector genes. Target promoter and effector genes were as follows: lane 1: PGL4/APET; lane 2: PGL4/APET and PcDNA/MEF/ELF4; lane 3: PGL4/APET, pcDNA/MEF/ELF4, and Wt-NPM1; lanes 4 and 5: PGL4/APET, pcDNA/MEF/ELF4, and Mt-A-NPM1 or Mt-I-NPM1; and lanes 6, 7, and 8: PGL4/APET and pcDNA/Wt-NPM1, Mt-A-NPM1 or Mt-I-NPM1. Luciferase activity by pcDNA/APET alone was assigned a value of 1.0. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*P < 0.05). (H) U937 cells were co-transfected with the luciferase reporter gene of an artificial MEF/ELF4 target promoter and effector genes. Target promoter and effector genes were as follows: lane 1: PGL4/APET; lane 2: PGL4/APET and PcDNA/MEF/ELF4; lanes 3: PGL4/APET, pcDNA/MEF/ELF4, and Wt-NPM1; lane 4: PGL4/APET, pcDNA/MEF/ELF4 and Mt-A-NPM1; and lanes 5 and 6: PGL4/APET and pcDNA/Wt-NPM1 or Mt-A-NPM1. Luciferase activity by pcDNA/APET alone was assigned a value of 1.0. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*P < 0.05). (I) 293T cells were co-transfected with 0.1 μg of the luciferase reporter gene of an artificial MEF/ELF4 target promoter (lanes 1, 2, 3, 4, 5, 6, 7, 8 and 9) and 0.1 μg of effector genes (PcDNA/MEF/ELF4) (lanes 1, 2, 3, 4, 5 and 6). The effector genes were as follows: lane 1: 0.2 μg of Mt-A-NPM1; lane 2: 0.16 μg of Mt-A-NPM1 and 0.04 μg of Wt-NPM1; lanes 3: 0.1 μg of Mt-A-NPM1 and 0.1 μg of Wt-NPM1; lane 4: 0.04 μg of Mt-A-NPM1 and 0.16 μg of Wt-NPM1; and 5: 0.2 μg of Wt-NPM1; lane 6: none; lane 7: PGL4/APET and 0.2 μg of Mt-A-NPM1; lane 8: PGL4/APET and 0.2 μg of Wt-NPM1; lane 9: PGL4/APET. Luciferase activity by PGL4/APET alone was assigned a value of 1.0. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*P < 0.05).

Figure 4

Mt-A-NPM1 does not interact with MEF/ELF4 in vivo. 293T cells were transfected with the indicated expression plasmids. After 48 h, cell lysates were immunoprecipitated with anti-FLAG and anti-V5 antibodies. Immunoprecipitates were analyzed by 10% SDS-PAGE and subjected to immunoblotting with anti-V5 antibody (upper row) or anti-FLAG antibody (bottom row).

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Figure 5

Localization of MEF/ELF4 was unaffected by the mutation of NPM1. (A) 293T cells were transfected with GFP-MEF/ELF4 fusion protein expression vector and pcDNA/V-Wt-NPM1 (a) or pcDNA/V-Mt-A-NPM1 (b). Forty-eight hours after transfection, cells were fixed and immunofluorescence-stained with anti-V tag antibody. (B) Western blotting of Flag-MEF/ELF4 subcellular distribution in 293T cells co-transfected with pFlag-MEF/ELF4 and pcDNA/V-Wt-NPM1 or pcDNA/V-Mt-A-NPM1. Purity of the subcellular fractions was assessed by blotting with histone H1 (nuclear extraction) and Hsp70 (cytoplasmic extraction).

Figure 6

Mt-NPM1 stimulates MEF/ELF4-induced hyperproliferation and transformation. NIH3T3 cells transfected with various combinations of expression plasmids were plated in soft agar on 60-mm dishes and incubated for 2 weeks. (A) Microscopy of MEF/ELF4-transfected NIH3T3 cells with Wt-NPM1 or Mt-A-NPM1. (B) The average number of colonies of three independent experiments with standard deviation (*$P < 0.05$).

Figure 7

MEF/ELF4 transactivates the HDM2 promoter. (A) MEF/ELF4 binds to the HDM2 promoter *in vivo*. Flag-MEF/ELF4-bound DNA from 293T cells was immunoprecipitated with Flag antibody or normal mouse IgG. RQ-PCR amplification was performed on the corresponding templates by using primers for HDM2. (B) Structure of the HDM2 promoter region (-82 to -122) (schematic). (C) 293T cells were transfected with HDM2 promoter-driven luciferase reporter plasmid encoding wild-type [7B (a)] or mutant [7B (b)] protein. Luciferase activity by pcDNA alone was assigned a value of 1.0. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD. (D) 293T cells were co-transfected with pFlag/MEF/ELF4 and pcDNA/Wt-NPM1 or pcDNA/Mt-A-NPM1. RQ-PCR amplification was undertaken on corresponding templates using primers for HDM2. The analysis was performed in triplicate assays, and the results were reproducible. The results are shown as the mean ± SD (*$P < 0.05$).

Figure 8

Expression of Mt-NPM1 and higher expression of MEF/ELF4 are associated with the elevated expression of HDM2 in CD34-positive AML cells. Total RNA isolated from 22 AML patients (CD34-positive leukemia cells) was analyzed for the expression of HDM2 by RQ-PCR. Stratified by the presence of the NPM1 mutation (A) and by the level of ELF4/MEF (B). *P < 0.009 against Wt -NPM1; **P < 0.03 against MEF/ELF4-L, assessed by ANOVA followed by Scheffe's multiple comparison test.

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Table 1. Clinical and laboratory characteristics of patients

	Wt-NPM1	Mt-NPM1	P
No. of patients	14	8	
Sex			
Male	5	5	
Female	9	3	0.60
Median age, years	54.5	62	
(range)	(18–78)	(44–76)	
FAB classification			
M0	1	0	
M1	2	2	
M2	4	2	
M4	2	2	
M5	2	2	
M6	3	0	0.50
TLD+	6	4	0.50
Median WBC count, /μL	7,300	47,500	
(range)	(1300–556000)	(1700–114700)	0.10
Median LDH level	647	669	
(range)	(203–5325)	(270–2391)	0.07
Median BM count, /μL	337,000	475,000	
	(9000–738000)	(34,900–769000)	0.10

Figure 1A

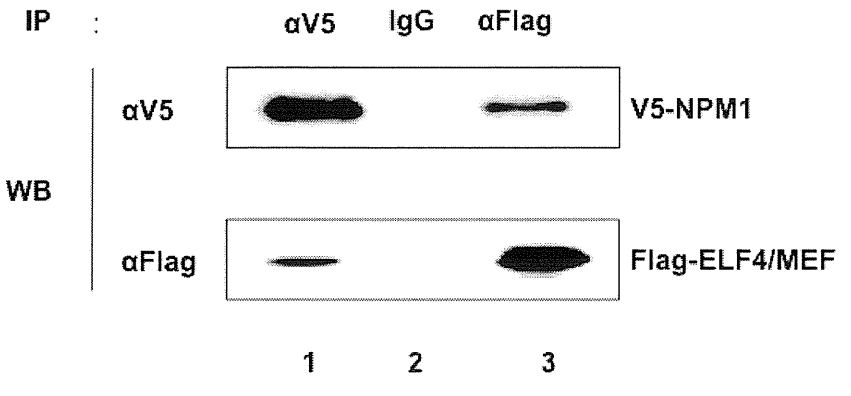

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Figure 1B

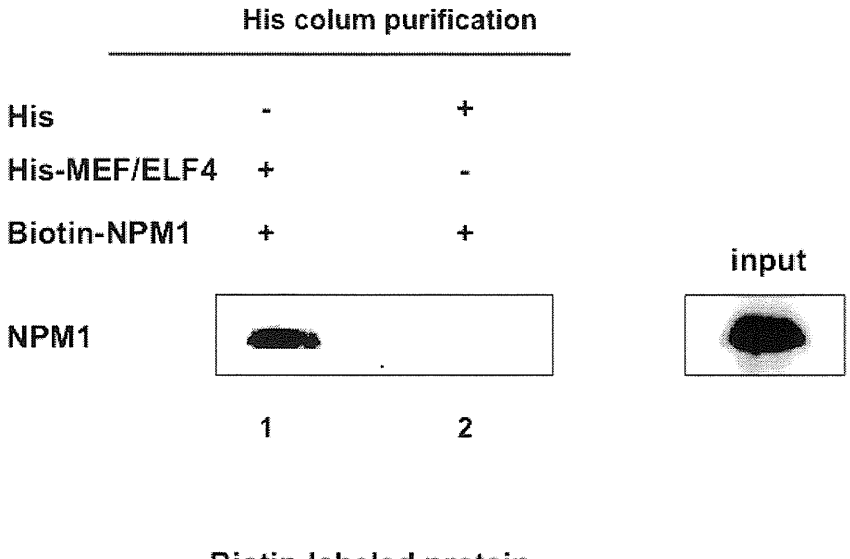

Figure 1C

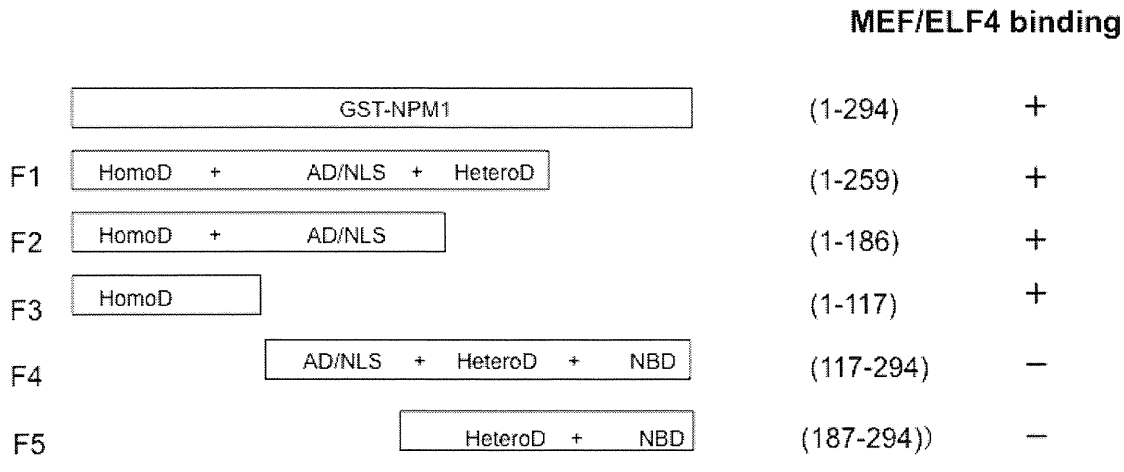

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Figure 1D

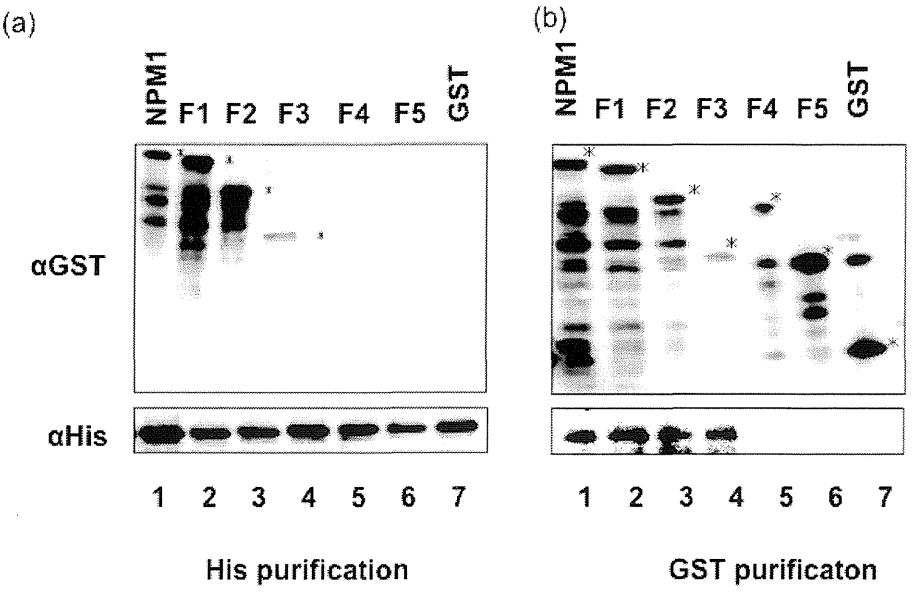

Figure 2

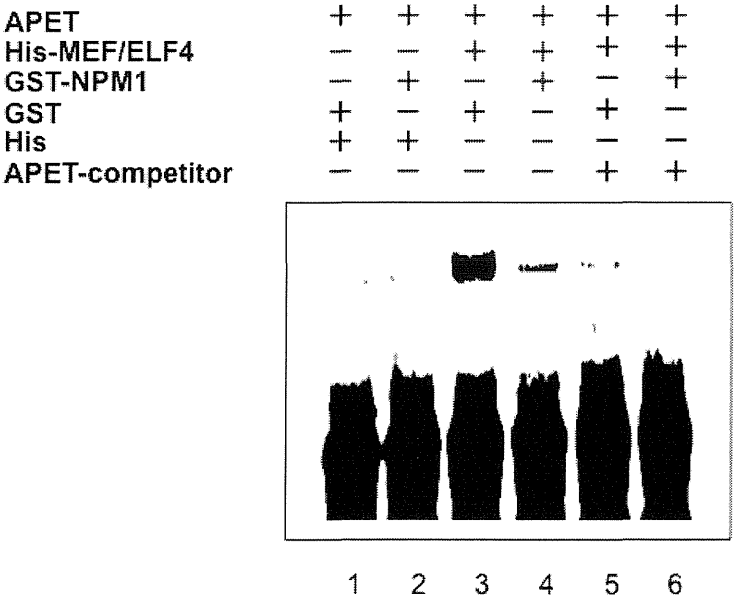

Figure 3A

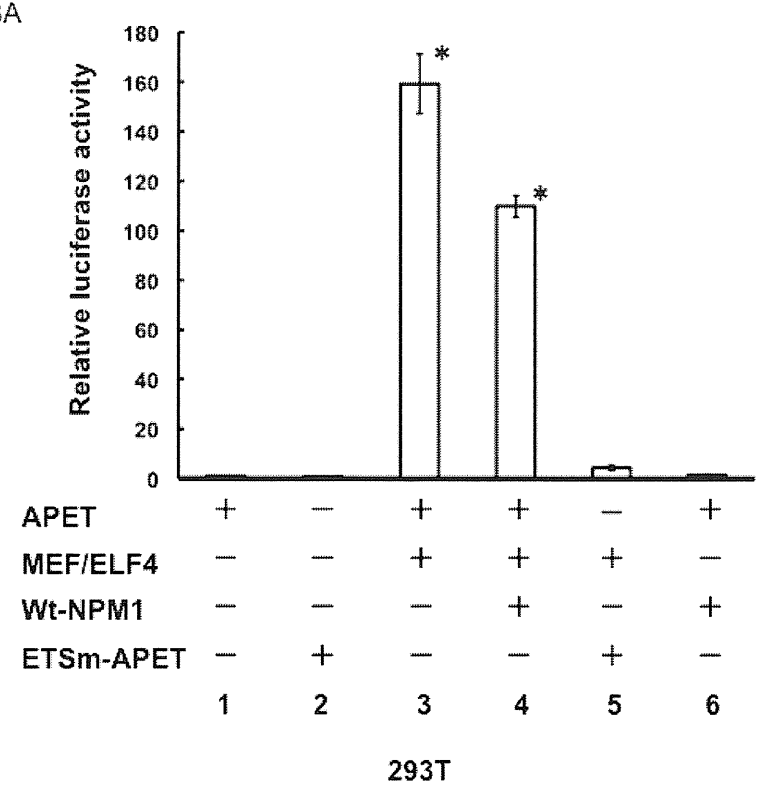

Figure 3B

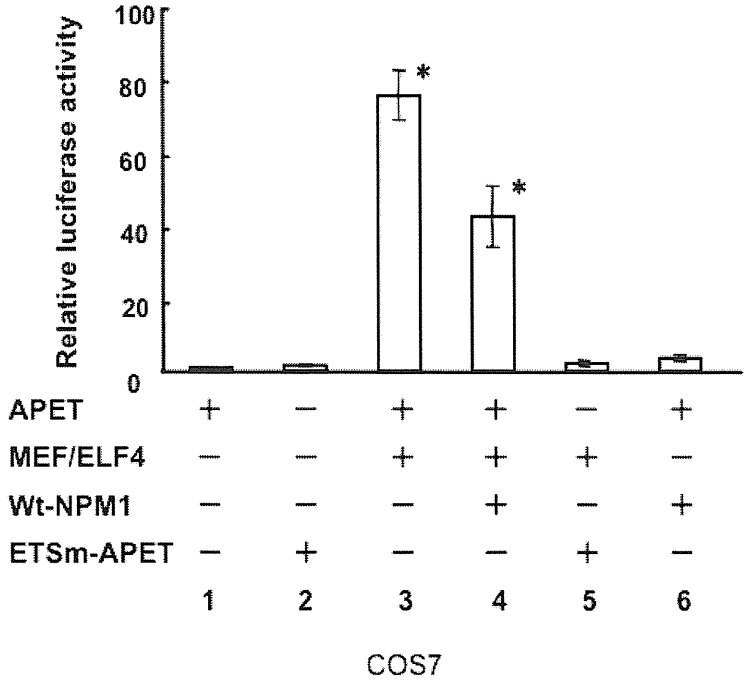

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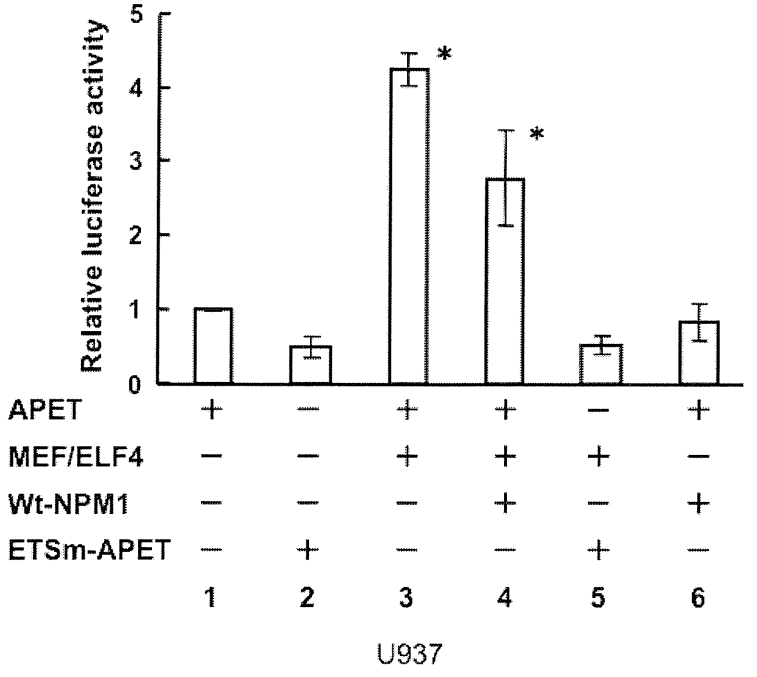
Figure 3C



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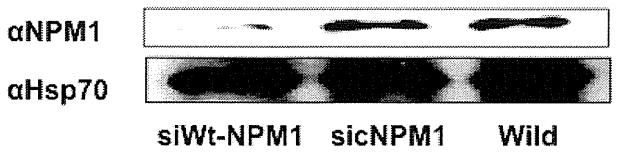

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