The Mre11-Nbs1 Interface Is Essential for Viability and Tumor Suppression

Graphical Abstract

Interaction compromised (Nbs1<sup>mid</sup> mutants)

Complex: • Assembled • Functional • Nuclear

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In Brief
Kim et al. find that Nbs1 promotes the proper assembly and localization of a complex containing Mre11 and Rad50. Nbs1-mediated assembly is required for the function of the complex, and a 108-amino-acid Nbs1 fragment containing the Mre11 interaction domain is sufficient for this essential role.

Highlights
- TALEN editing used to generate Nbs1<sup>mid</sup> mutant mice altered the Mre11 interaction
- The Mre11-Nbs1 interaction is essential for embryonic viability and DDR
- The Nbs1 minimal fragment (108 amino acid) is sufficient to sustain viability
- Nbs1 is required for proper assembly and localization of Mre11 and Rad50

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The Mre11-Nbs1 Interface Is Essential for Viability and Tumor Suppression

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SUMMARY

The Mre11 complex (Mre11, Rad50, and Nbs1) is integral to both DNA repair and ataxia telangiectasia mutated (ATM)-dependent DNA damage signaling. All three Mre11 complex components are essential for viability at the cellular and organismal levels. To delineate essential and non-essential Mre11 complex functions that are mediated by Nbs1, we used TALEN-based genome editing to derive Nbs1 mutant mice (Nbs1mid mice), which harbor mutations in the Mre11 interaction domain of Nbs1. Nbs1mid alleles that abolished interaction were incompatible with viability. Conversely, a 108-amino-acid Nbs1 fragment comprising the Mre11 interface was sufficient to rescue viability and ATM activation in cultured cells and support differentiation of hematopoietic cells in vivo. These data indicate that the essential role of Nbs1 is via its interaction with Mre11 and that most of the Nbs1 protein is dispensable for Mre11 complex functions and suggest that Mre11 and Rad50 directly activate ATM.

INTRODUCTION

The DNA damage response (DDR) is important for maintaining genomic integrity. It comprises pathways that mediate DNA repair, DNA damage signaling, cell-cycle regulation and apoptosis. Impairment of the DDR is associated with diverse human pathologies such as cancer, neurodegenerative disorders, immune deficiency, and premature aging (Ciccia and Elledge, 2010).

The Mre11 complex—Mre11, Rad50, and Nbs1 (Xrs2 in S. cerevisiae)—influences all aspects of the DDR via its role as DNA double-strand break (DSB) sensor as well as its enzymatic and structural roles in DSB repair (Stracker and Petrini, 2011). Each member of the complex has been identified as the underlying basis of chromosome instability syndromes associated with immunodeficiency, radiosensitivity, cell-cycle checkpoint defects, and cancer predisposition (Stracker and Petrini, 2011). These disorders each exhibit decrements in ataxia telangiectasia mutated (ATM) activation or activity, consistent with the idea that the Mre11 complex is required for the activation of ATM. This conclusion is supported by biochemical and genetic analyses in mice, yeast, and human cells (Cerosaletti and Concannon, 2004; Difilippantonio et al., 2005; Schiller et al., 2012; Shull et al., 2009; Stracker et al., 2008; Theunissen et al., 2003; Waltes et al., 2009; Williams et al., 2002).

Whereas Mre11 and Rad50 orthologs are present in Bacteria, Archaea, and Eukaryota, Nbs1 appears to be restricted to Eukaryota. Accordingly, the protein appears to influence functions that are unique to eukaryotic cells. Unlike Mre11 and Rad50, Nbs1 does not appear to bind DNA, nor does it specify enzymatic activities relevant to DNA repair. Nbs1 primarily influences Mre11 complex function by mediating protein interactions via its N- and C-terminal domains that influence DNA repair, subcellular localization, and ATM-dependent checkpoint and apoptotic functions (Cerosaletti and Concannon, 2003; Desai-Mehta et al., 2001; Larsen et al., 2014; Lloyd et al., 2009; Salto and Kobayashi, 2013; Stracker and Petrini, 2011; Williams et al., 2008). The mechanistic basis for Mre11-complex-dependent ATM activation remains unclear. It is notable that the appearance of Nbs1 in eukaryotes coincides with the Mre11 complex’s role in promoting DNA damage signaling, as does the Mre11 domain with which Nbs1 interacts. The Mre11 interaction interface of Nbs1 is a bipartite structure comprising Mid1 and Mid2 (Mre11 interaction domain) that is conserved among Nbs1 orthologs (Schiller et al., 2012).

Having previously established that the N and C termini alone and in combination are dispensable for ATM activation (Stracker and Petrini, 2011), we undertook mutageneisis of the Mre11-Nbs1 interface with the goal of impairing the Nbs1-Mre11 interaction while leaving the Nbs1 protein otherwise intact in an effort to define the role of Nbs1 in ATM activation. Using transcription activator-like effector nuclease (TALEN)-based genome editing, we created an allelic series in mice consisting of six mutations (Nbs1mid) within Mid2 that impair the interaction between Nbs1 and Mre11 to varying degrees. The most severe mutants abolished the Mre11-Nbs1 interaction, which resulted in the loss of cellular and organismal viability. These data indicate that the Mre11-Nbs1 interaction is essential, and therefore required, for ATM activation.

Complementation of Nbs1-deficient cells with Nbs1 fragments spanning Mid1 and Mid2 rescued the viability of cultured cells...
and hematopoietic cells in vivo. Cells rescued in this manner also exhibited some indices of ATM function. In vitro, the Nbs1 fragments that rescued viability promoted Mre11 dimerization and DNA binding. In addition, they restored the ability of CtIP to activate Mre11 endonuclease activity, a function shown to be dependent on Nbs1. Collectively, these data suggest that the Nbs1-Mre11 interaction is required for proper assembly of the Mre11 complex. Accordingly, that interaction is required for the concerted activities of Mre11 and Rad50 that govern DNA repair and DNA damage signaling and promote viability.

RESULTS

The Evolutionarily Conserved NFKxFxK Motif in Nbs1 Is Essential for Mouse Embryogenesis

The mammalian Nbs1 protein interacts with Mre11 via a bipartite domain near the C terminus, comprising Mid1 and Mid2 (Figure 1A). Mid2 includes a highly conserved NFKxFxK motif, whereas Mid1 is characterized by a single conserved leucine at position 648 of the mouse protein (Figure 1A). We carried out mutagenesis of the NBS1 cDNA to identify alleles that weakened the Nbs1-Mre11 interaction. Mutation of L648 had a minimal effect on the Mre11-Nbs1 interaction, whereas the interaction was severely impaired by mutation of F686 in Mid2 (Figure 1C). On that basis, we carried out TALEN-based gene editing in mice to induce small deletions within Mid2 and thereby compromise the interaction between Mre11 and Nbs1 (Figure S1A).

We generated seven new Nbs1 mutant mice (Nbs1mid1, Nbs1mid2, Nbs1mid3, Nbs1mid4, Nbs1mid5, and Nbs1mid8) in which the NFKxFxK motif of Mid2 is altered (Figure 1B). The genomic sequences of Nbs1 exon 13 from founder mutant lines are listed (Figure S1B). These mutations were modeled in cDNA expression constructs. The ability of the corresponding protein products to interact with Mre11 was assessed by co-immunoprecipitation. Nbs1mid1 was indistinguishable from WT, whereas Mre11 interaction was moderately impaired by mutation of F686 in Mid2 (Figure 1C). On that basis, we carried out TALEN-based gene editing in mice to induce small deletions within Mid2 and thereby compromise the interaction between Mre11 and Nbs1 (Figure S1A).

We generated seven new Nbs1mid mutant mice (Nbs1mid1, Nbs1mid2, Nbs1mid3, Nbs1mid4, Nbs1mid5, and Nbs1mid8) in which the NFKxFxK motif of Mid2 is altered (Figure 1B). The genomic sequences of Nbs1 exon 13 from founder mutant lines are listed (Figure S1B). These mutations were modeled in cDNA expression constructs. The ability of the corresponding protein products to interact with Mre11 was assessed by co-immunoprecipitation. Nbs1mid1 was indistinguishable from WT, whereas Mre11 interaction was moderately impaired by mutation of F686 in Mid2 (Figure 1C). The binding of Nbs1mid was similar to that of wild-type protein (data not shown). Whereas Nbs1mid1mid1, Nbs1mid2mid2, Nbs1mid3mid3, and Nbs1mid4mid4 mice were born at expected Mendelian frequencies, homozygosity for either Nbs1mid or Nbs1mid mutations was lethal, indicating that the Mre11-Nbs1 interaction is essential for embryonic viability (Figure 1D).

Figure 1. The NFKxFxK Motif in Nbs1 Is Essential for Mouse Embryogenesis

(A) Schematic structure of mammalian Nbs1 protein and sequence alignment of Mre11-interacting domain 1 and 2 among different species. Invariable residues are shown in black boxes. FHA, BRCT, and AIM denote forkhead-associated domain, BRCA1 C-terminal domain, and ATM-interacting motif, respectively.

(B) Sequence of Nbs1 mutants created by TALEN-mediated gene editing. Nbs1mutmid is a truncated mutant allele.

(C) Nbs1 mutation of different Nbs1mid mutants was assessed by immunoprecipitation (IP) by FLAG antibodies followed by western blot for Mre11. FLAG-tagged WT or mutant full-length Nbs1 was transiently expressed in MEFs. FLAG peptide (100 μg/mL) was added to the WT sample during IP for a FLAG IP control.

(D) Intercrosses of heterozygous Nbs1mid mutants. Numbers of pups born are indicated and expected numbers are shown in parenthesis.
the effects of Nbs1<sup>mid</sup> mutations on ATM activation by examining phosphorylation of the ATM substrates Kap1 (S824) and Chk2, which are ATM substrates. Note that Chk2 migrates slowly when hyperphosphorylated.

(B) Mouse tumor free survival. Each data point represents the percent survival of mice with each genotype at a given age. N denotes total number of mice for each genotype and the average age in death is shown. p value of double mutants compared to p53<sup>−/−</sup> was determined by Wilcoxon rank sum test (**p < 0.01 and ***p < 0.001).

(C) ATM signaling in Nbs1<sup>−/−</sup> MEFs was assessed by western blot for phospho-ATM (S1981) and the phosphorylation of ATM substrates, Kap1 (S824), and Chk2. The asterisk indicates nonspecific band.

(D) Colony-formation assay to assess cell viability of Nbs1<sup>−/−</sup> and Nbs1<sup>−/−</sup> alleles in MEFs.

(E) Nuclei were stained with DAPI (4',6-diamidino-2-phenylindole).

(F) The percentage of nuclei with micronuclei was counted from randomly taken images (mean ± SD, 100 < number [N] from seven images). p value was determined by unpaired t test (**p < 0.001).

(G) Representative chromosome metaphase images of Nbs1<sup>−/−</sup> and Nbs1<sup>−/−</sup> MEFs.

(H) Percentage of metaphases with aberrations (**p < 0.001, Fisher’s exact test, more than 40 metaphases).
We were unable to establish embryonic fibroblasts homozygous for the Nbs1<sup>mid3</sup> or Nbs1<sup>mid8</sup> alleles. To define the cellular phenotypes of Nbs1<sup>mid3</sup> and Nbs1<sup>mid8</sup>, these mice were crossed with Nbs1<sup>f</sup> mice in which Cre expression inactivates NBS1 (Demuth et al., 2004). Following transduction of a tamoxifen (4-OHT)-regulated Cre recombinase into immortalized mouse embryonic fibroblasts (MEFs) from Nbs1<sup>mid3</sup> and Nbs1<sup>mid8</sup> mice, 4-OHT was added to the media for 24 hr. Cre-mediated deletion of Nbs1<sup>f</sup> was evident within 24–48 hr (data not shown), and the remaining Nbs1<sup>mid3</sup> and Nbs1<sup>mid8</sup> proteins were present at markedly reduced levels, whereas Mre11 and Rad50 levels were unchanged (Figures 2C and 2S). Colones of Nbs1<sup>−−mid3</sup> or Nbs1<sup>−−mid8</sup> MEFs were not recovered (Figure 2D), indicating that as in the case of mouse embryos, the Mre11-Nbs1 interaction is essential. 4 days following the induction of Cre activity (prior to cell death), indices of genome destabilization were evident in both Nbs1<sup>−−mid3</sup> or Nbs1<sup>−−mid8</sup> alleles, including micronuclei and chromosome aberrations (Figures 2E–2H). These outcomes resemble those observed upon genetic ablation of RAD50, MRE11, or NBS1 (Adelman et al., 2009; Buis et al., 2008; Reina-San-Martín et al., 2005).

ATM activation was assessed in Nbs1<sup>−−mid3</sup> and Nbs1<sup>−−mid8</sup> cells at 4 days following Cre. IR-induced Kap1 S824 and Chk2 phosphorylation were nearly undetectable in Nbs1<sup>−−mid3</sup> (Figure 2C) and severely attenuated in Nbs1<sup>−−mid8</sup> cells (Figure 2S), suggesting that impairing the Mre11-Nbs1 interaction compromised ATM activation. Accordingly, IR-induced ATM S1987 autophosphorylation, a direct index of ATM activation (Bakkenist and Kastan, 2003; Paull, 2015), was also sharply decreased in Nbs1<sup>−−mid3</sup> cells relative to Nbs1<sup>f</sup> controls (Figure 2C). As expected, both Nbs1<sup>mid3</sup> and Nbs1<sup>mid8</sup> alleles exhibit defects in the G2/M checkpoint that were considerably more severe than those observed in Nbs1<sup>mid3mid3</sup> or Nbs1<sup>mid3mid8</sup> alleles (Figure S2D). These assessments may underestimate the severity of the Nbs1<sup>−−mid3</sup> and Nbs1<sup>−−mid8</sup> phenotypes due to the possible presence of residual Nbs1 protein.

The Nbs1 Minimal Fragment Rescues Nbs1 Deficiency

Previously, a C-terminal truncation of 100 amino acids of human Nbs1 that included Mid1 and Mid2 was unable to rescue viability of Nbs1-deficient mouse cells (Difilippantonio et al., 2005). Data presented here indicate that the presence of an essentially complete Nbs1 protein that is unable to interact with Mre11 was not sufficient for viability or ATM activation. Given that the N and C termini are dispensable, singularly or in combination, for cell viability and ATM activation (Stracker and Petрини, 2011) (data not shown), we used deletional mutagenesis to define the “minimal Nbs1” required to support viability.

Three Nbs1 gene segments encoding N-terminal truncation fragments, all of which also lacked the C-terminal 24 amino acids of Nbs1, were constructed in a retroviral expression vector. The constructs encoded fragments of 388, 188, and 108 amino acids (F2, F3, and F4, respectively) fused to a FLAG epitope and SV40 nuclear localization signal (NLS) at their N termini for nuclear localization (Figure 3A). The Nbs1 gene segments were transduced into Nbs1<sup>f/f</sup> MEFs, and the ability of the encoded fragments to interact with Mre11 was assessed via FLAG immunoprecipitation. All fragments co-immunoprecipitated with Mre11 and Rad50 (Figure 3B). Moreover, F4 which spans just 108 amino acids inclusive of Mid1 and Mid2 displaced full-length Nbs1 from Mre11 and Rad50, arguing that Nbs1 is unlikely to interact with other domains of the Mre11 complex (Figure 3B).

Subsequently, Cre activity was induced with 4-OHT, and the ability of fragment-containing cells to form colonies was assessed. Whereas no colonies formed from control (vector-transduced) cells, all of the cells expressing F2, F3, and F4 were able to form colonies after 10 days in culture. PCR genotyping and western blot confirmed that the introduced fragments were the sole source of Nbs1 protein remaining in the Nbs1<sup>−−</sup> cells—the fragments are hereafter designated “rescue fragments” (Figures S3A–S3C). By cloning the cells in this manner and by propagation in culture over the course of several weeks, any contribution from residual Nbs1-proficient (Nbs1<sup>f</sup>) cells to colony formation or subsequent phenotypic assessments was excluded. These data indicated that as few as 108 amino acids of Nbs1 spanning the Mre11-Nbs1 interaction interface are sufficient to sustain the viability of cultured cells.

In addition to sustaining viability, the rescue fragments were able to promote ATM activation in Nbs1<sup>−−</sup> cells. The phenotypes of Nbs1-fragment-expressing cells were compared to a culture of Nbs1<sup>f/f</sup> cells at 4 days after Cre induction. Whereas Kap1 S824 phosphorylation was sharply reduced at 0.5 hr after 5 Gy IR in Nbs1<sup>−−</sup>, it was readily evident in F2- and F3-containing cells and, to a lesser extent, in F4 cells (Figure 3C). IR-induced Kap1 S824 phosphorylation of F4 cells was confirmed as ATM-dependent activity by pretreatment with an ATM inhibitor (Figure S3D). Those complemented cells exhibited restoration of the G2/M checkpoint. After 1 hr following treatment with 3 Gy IR, the mitotic index of F2-, F3-, and F4-containing cells decreased by 68%, 66%, and 44%, respectively, while the decrease was only 14% for ATM<sup>−−</sup> cells (Figure 3D). These data indicate that a substantial degree of ATM-dependent checkpoint function was retained in rescue-fragment-expressing cells. A fragment of human Nbs1 spanning residues 401–754 was previously shown to suppress ATM activation and nuclear localization defects in Nijmegen breakage syndrome (NBS) patient cells (Cerosaletti and Concannon, 2004).

To obtain a quantitative assessment of DDR function in rescue-fragment-containing cells, the frequency of spontaneous chromosome aberrations was assessed. 100% of Nbs1<sup>−−</sup> cells exhibit widespread chromosome fragility, with more than three aberrations per metaphase spread (Figures 3E and 3F). In contrast, fewer than 21% of F2-, F3-, and F4-containing cells exhibited three or more aberrations (Figure 3F), indicating a substantial degree of residual function.

Nevertheless, rescue-fragment-expressing cells did not phenocopy cells expressing wild-type Nbs1. We observed sharply reduced nuclear localization of Mre11 in F4-containing cells relative to F2 or F3-containing cells (Figure 3G), likely accounting for reduced Kap1 phosphorylation in F4-containing cells. Data from budding yeast and human cells indicate that Xrs2 and Nbs1 are required for nuclear localization of Mre11 and Rad50 (Cerosaletti and Concannon, 2004; Cerosaletti et al., 2006), and enforced nuclear localization of Mre11 in S. cerevisiae partially restored function to xrs2Δ mutants (Oh et al., 2016; Tsukamoto et al., 2005). F4-containing cells were more sensitive to IR than F2 cells.
Figure 3. The Nbs1 Minimal Fragment Rescues Nbs1 Deficiency

(A) Structure of Nbs1 fragments used in rescue experiments. Domains are indicated in Figure 1A.

(B) Mre11 interaction of Nbs1 minimal fragments. FLAG-tagged Nbs1 fragments (F2, F3, and F4) were expressed in Nbs1^{+/+} MEFs, and immunoprecipitation with FLAG antibodies was performed followed by western blot for Mre11, Rad50, and Nbs1.

(C) IR-induced ATM signaling in Nbs1^{+/+} MEFs expressing Nbs1 minimal fragments. As an ATM substrate, phosphorylation of KAP1 (S824) was assessed.

(D) IR-induced G2/M cell-cycle checkpoint of Nbs1^{+/+} MEFs expressing Nbs1 minimal fragments. Mitotic cells were detected by measuring mitosis-specific phosphorylation of histone H3 (Ser10).

(E and F) Metaphase spread of Nbs1^{+/+} MEFs expressing Nbs1 minimal fragments. (E) Representative chromosome metaphase images of Nbs1^{+/+} and Nbs1^{-/-} MEFs. (F) The graph indicates the percent ratio of metaphases with aberrations (**p < 0.01 and ***p < 0.001, Fisher's exact test, more than 65 metaphases from two independent experiments).

(G) Immunofluorescence cell staining of Mre11 in Nbs1^{+/+} MEFs expressing Nbs1 minimal fragments. Nuclei are shown by DAPI (4',6-diamidino-2-phenylindole) staining.

(H) Immunofluorescence cell staining of Rad50 and Mre11 in Nbs1^{+/+} MEFs expressing Mre11-NLS. Nbs1^{+/+}-Mre11-NLS cells were achieved by treating Nbs1^{+/+}-creERT2-Mre11-NLS cells with 4-OHT treatment. Cells were stained at day 3 after 4-OHT treatment. Nuclei are shown by DAPI (4',6-diamidino-2-phenylindole) staining.
Biochemical Effects of the Nbs1 Minimal Fragment

These data suggested that Nbs1 influences the stability and assembly of the Mre11 complex in addition to its subcellular localization. To test this interpretation, we examined the effect of human Nbs1 F4 on the biochemical properties of Mre11 in vitro. The human Mre11 core (1–411 amino acids) (Park et al., 2011) was purified and subjected to size exclusion chromatography. Individually, Mre11 and Nbs1 F4 fused to a maltose-binding protein (F4-MBP) primarily appeared as single, monomeric peaks (apparent molecular weight [MW]: 42 kDa for Mre11 and 59 kDa for F4-MBP). When mixed at a 1:1 ratio, we observed a new peak with an apparent molecular weight of 184 kDa, consistent with the co-elution of Mre11 and Nbs1 dimers (i.e., two F4-MBP and two Mre11 cores) (Figures 4A and 4B). The new peak was not observed in F4-mid5-MBP in which the NFKKFKK motif is deleted (Figure S5).

F4-MBP also stimulated DNA binding by the Mre11 core. Mre11 binds DNA as a dimer (Williams et al., 2008). We found that the binding of Mre11 to double-stranded DNA (dsDNA) (Figure 4C) or a hairpin (Figure 4D) substrate was stimulated by Nbs1 F4 in electrophoretic mobility shift assays (EMSAs). Superhifted binding induced by MBP antisera confirmed that the Mre11-DNA complex contains Nbs1 (Figure 4D).

We next examined the effect of F4-MBP on Mre11 nuclease activity. Phosphorylated CtIP has recently been shown to promote Mre11 endonuclease in a manner that depends on Nbs1 (Anand et al., 2016). The Mre11-Rad50 complex was incubated with a 70-bp radiolabeled dsDNA substrate, the ends of which were blocked by streptavidin to prevent exonucleolytic degradation (Figure 4E). In the absence of F4-MBP, or in the presence of the non-interacting F4-mid5-MBP fragment (Figure 4F), CtIP did not promote exonucleolytic cleavage by Mre11 (Figures 4G and 4H). In contrast, wild-type F4-MBP with phosphorylated CtIP promoted the endonuclease of Mre11-Rad50 (Figure 4H).

To further examine the hypothesis that Nbs1 mediates proper assembly of Mre11 and Rad50, we carried out scanning force microscopy (SFM). Previous SFM analysis revealed a stoichiometry of two or four Nbs1 proteins per M2R2 complex (van der Linden et al., 2009). However, the addition of two or four Nbs1 proteins to the globular domain of M2R2 obscured possible structural rearrangement. The minimal Nbs1 fragment identified here allowed analysis of Mre11 changes in complex architecture by SFM imaging. The M2R2 complex is characterized by a single globular domain (Mre11 + Rad50 ATPase domains) with two protruding coiled coils (Figure 5A). The coiled coils are usually apart but 32% of the time appear to be linked by the zinc-hook domains at their apexes (de Jager et al., 2004; Moreno-Herrero et al., 2005).

To assess the effect of F4 on Mre11 complex assembly, the full-length human M2R2 complex was incubated at a 1:1 molar ratio with F4-MBP or F4-mid5-MBP (non-binding mutant) before imaging. A striking rearrangement of the Mre11 globular domain was induced in the presence of the F4 peptide, with the globular domain appearing as two distinct but linked globular objects (Figure 5B). The proportion of Mre11 complexes with this conformation increases from 12% to 58% in the presence of the F4 peptide but does not significantly change in the presence of the control F4-mid5 peptide (Figure 5C). This separation into two distinct globular objects is accompanied by an increase in width of the globular domain (Figure 5D), consistent with the coiled coils favoring dimerization of the zinc hooks. Collectively, these data strongly support the view that Nbs1’s influence on the physical disposition of the Mre11 complex constitutes its essential function and that this influence underlies its requirement for nuclear localization, cell viability, and ATM activation.

Nbs1−/− Fetal Liver Cells Reconstitute the Hematopoietic System upon Nbs1 Minimal Fragment Expression

Immortalized cells are likely more tolerant of genotoxic stress than constituents of tissues in vivo. To determine whether the rescue fragments would sustain viability in vivo, we assessed their ability to support the differentiation of lymphocytes. Previous analyses indicated that the Mre11 complex is required for lymphocyte development (Balestrini et al., 2016; Calleñ et al., 2007; Deriano et al., 2009; Reina-San-Martin et al., 2004). Nbs1−/− mice were crossed to vavCre mice, which express cre recombinase in hematopoietic stem cells (HSCs) (Stadtfeld and Graf, 2005). Hematopoietic Nbs1 deficiency resulted in perinatal lethality due to lack of bone marrow development (Figure S6).

Fetal liver cells (FLCs) from embryonic day 13.5 (E13.5) embryos were isolated and transduced with Nbs1 rescue fragment encoding in an IRES-GFP murine stem cell virus (MSCV) retrovirus prior to transplantation into lethally irradiated mice as depicted (Figure 6A). At 10 weeks after transplantation, spleen was isolated and assessed for GFP-positive cells. Although we did not observe complete reconstitution, GFP-positive, B220-positive cells comprised 6% of splenocytes (Figure 6B). The percentages of GFP-positive, B220-positive cells may underestimate the degree of reconstitution by rescue-fragment-containing HSCs due to silencing of the MSCV retrovirus during hematopoietic differentiation as observed previously (Cherry et al., 2000). The Mre11 complex is dispensable for viability of quiescent cells...
Adelman et al., 2009; hence, silencing of F4 expression may be tolerated because splenocytes are largely quiescent.

PCR genotyping confirmed that recipient mice contain differentiated cells derived from Nbs1 fragment containing Nbs1/C0/FLCs and that the fragment-encoding construct is present; the Nbs1F allele was not detected (Figure 6C). This confirms that this rescue is not by remaining undeleted Nbs1F allele in donor FLCs. No reconstitution was observed in control mice transduced with FLCs lacking the rescue fragments (data not shown). These data indicate that as with transformed cells, the 108 amino acids spanning the Mre11 interaction interface of Nbs1 (F4; Figure 3A) are sufficient to promote viability in vivo and, moreover, that minimal Nbs1 fragment was sufficiently functional to support differentiation of HSCs into splenic B cells.

**DISCUSSION**

To examine the role of Nbs1 in Mre11 complex functions, we undertook mutagenesis of Nbs1 in an attempt to weaken the interaction with Mre11 and thereby examine the functionality of the
core Mre11-Rad50 complex disassociated from Nbs1. Mutations that disrupted Mre11 interaction caused inviability. Hence, the presence of a non-interacting but otherwise intact Nbs1 protomer was not sufficient for viability, establishing that Nbs1 interaction per se is essential. Conversely, we found that 108 amino acids of Nbs1 spanning the Mre11 interaction domain were sufficient to promote cell viability. Although ATM activation was reduced in that setting, it was not abolished. Collectively, the data strongly argue that ATM activation is not directly dependent on Nbs1. Instead, we propose that essential functions of Nbs1 are to ensure proper assembly and subcellular localization of the Mre11 complex, which in turn promotes viability and influences ATM activation by Mre11 and Rad50.

The Role of Nbs1 in the Mre11 Complex: Essential Functions

Nbs1 clearly mediates essential as well as non-essential functions. With respect to the former, the data presented here indicate that the Mre11-Nbs1 interaction is specifically required for cellular and organismal viability. The levels of Mre11 and Rad50 protein were not changed in Nbs1mid mutant cells. Hence, it is the loss of interaction, rather than global destabilization of Mre11 complex components that accounts for the loss of viability in non-interacting Nbs1mid mutants. Further, this emphasizes the fact that Mid2 (the conserved NFKKxFxK motif, which was the target of the TALEN-based mutagenesis) is the major determinant of Nbs1’s association with the Mre11 complex. These data are consistent with the finding that the human Nbs1tr645 allele in which the C-terminal 100 amino acids of Nbs1 were deleted was unable to support viability of mouse embryos (Difilippantonio et al., 2005).

What are the essential functions of Nbs1 in the Mre11 complex? First, it is clear that the nuclear localization of Mre11 is influenced by Nbs1, but this does not solely depend on the Mre11 interaction domain. Mre11 complex mislocalization is observed in human NBS and A-TLD cells, as well as in Nbs1DB/DB and Mre1ATLD1/ATLD1 mouse models of those human mutations, neither of which harbor alterations in their respective interaction domains (Carney et al., 1998; Difilippantonio et al., 2005; Reina-San-Martin et al., 2005; Stewart et al., 1999; Williams et al., 2002). Nbs1 and Mre11 levels are reduced in those settings, raising the possibility that the stoichiometry of complex components may also influence nuclear localization. Alternatively, those mutations may disrupt as-yet-undescribed interactions required for nuclear localization.

Nevertheless, promoting nuclear localization of Mre11 and Rad50 is likely not the only function of Nbs1 required for viability. Enforced nuclear localization by Mre11-NLS could not restore nuclear localization of Rad50 in human NBS cells (Lakdawala et al., 2008), nor did it compensate for Nbs1 deficiency in MEFs (Figure 3H). The data presented here are most consistent with the interpretation that Nbs1 influences the assembly and disposition of the complex. Supporting that view, we showed that dimerization and DNA binding by the N-terminal 411-amino-acid core of Mre11 was enhanced by the F4 fragment (Figures 4A–4D), although it is likely that dimeric assemblies of full-length Mre11 may exhibit greater stability. Further support comes from the fact that only in the presence of Nbs1 or the minimal fragment is...
mains, which are disrupted in the canonical forkhead-associated (FHA) and BRCA1 C-terminal (BRCT) domains. Nbs1 contains N-terminal physical data resonate with genetic data indicating that mutations in Rad50 exert effects on regions distal to the altered residues (Alt et al., 2005; Chapman and Jackson, 2008; Kobayashi et al., 2001; Larsen et al., 2014; Lloyd et al., 2009; Maser et al., 2001; Falck et al., 2005; You et al., 2005), and recent genetic and biochemical analyses have shown that Rad50 influences the activation of ATM or its budding yeast ortholog, Tel1 (Alt et al., 2005; Chapman and Jackson, 2008; Kobayashi et al., 2001; Larsen et al., 2014; Lloyd et al., 2009; Maser et al., 2001; Falck et al., 2005; You et al., 2005), had no effect on ATM activation or cell viability but is required for ATM-dependent apoptosis (Stracker et al., 2007).

The Nbs1DBc allele is a composite of the Nbs1DB and Nbs1DC. The outcomes of Nbs1DB and Nbs1DC are simply additive in Nbs1DBcDBc mice rather than synergistic; the phenotypic outcomes attributable to Nbs1DB and Nbs1DC are unchanged in the composite Nbs1DBc (Shull et al., 2009; Stracker et al., 2007). Therefore, we propose that Nbs1 serves as a platform for Mre11 complex assembly and the recruitment of ATM substrates to enhance access of the activated kinase to substrates that govern ATM- and Nbs1-dependent functions. In this context, we draw a distinction between ATM activation and ATM activities: in the former circumstance, a properly assembled and localized complex is required for ATM activation, whereas in the latter, Nbs1 potentiates ATM activity by promoting access of the active kinase to its downstream effectors.

Although viability and ATM activation are lost upon genetic ablation of Nbs1, the protein does not appear to influence those outcomes directly. Rather, its association with Mre11 (and so Rad50) via its conserved interaction interface appears to influence both the subcellular localization and the proper assembly of the Mre11 complex, which in turn accounts for its influence on viability as well as ATM activation (Figure 7). Indeed, most of the Nbs1 protein, save for the Mre11 interaction interface, is dispensable for viability as well as ATM activation. Therefore, the mechanism(s) underlying ATM activation would appear to be mediated by Mre11 and Rad50. Notably, ATM appears to interact with Rad50 in vitro (Lee and Paull, 2005), and recent genetic and biochemical analyses have shown that Rad50 influences the activation of ATM or its budding yeast ortholog, Tel1 (Alt-Ahmadie et al., 2014; Deshpande et al., 2014; Hohl et al., 2014). These data underlie the speculation that Rad50 is likely to be the proximal effector of ATM activation.

The Role of Nbs1 in the Mre11 Complex: Non-essential Functions

The non-essential functions of Nbs1 have been illuminated by genetic analyses in human cells and mice. Nbs1 contains N-terminal forkhead-associated (FHA) and BRCA1 C-terminal (BRCT) domains, which are disrupted in the canonical Nbs1DBcDB allele inherited by NBS patients and the corresponding Nbs1DBc allele in mice. Those mutants exhibit defects in DSB end resection, DNA repair, and cell-cycle checkpoint activation, presumably due to the loss of protein interactions mediated by those domains (Alt et al., 2005; Chapman and Jackson, 2008; Kobayashi et al., 2002; Larsen et al., 2014; Lloyd et al., 2009; Maser et al., 2001; Melander et al., 2008; Morishima et al., 2007; Spycher et al., 2008; Williams et al., 2009; Wu et al., 2008, 2012). However, human and mouse cells lacking those domains are viable and retain the ability to activate ATM (Difilippantonio et al., 2005; Williams et al., 2002). Deletion of the Nbs1C terminus (the Nbs1DC allele), which has been reported to bind ATM (Falck et al., 2005; You et al., 2005), had no effect on ATM activation or cell viability but is required for ATM-dependent apoptosis (Stracker et al., 2007).

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were previously described (Williams et al., 2002), and Nbs1 mid1 mice. 

For detailed protocols of cell lines, cellular assay, fetal liver cell transplantation, EXPERIMENTAL PROCEDURES

ATM interacting motif, respectively. Nbs1 protein is dispensable for Mre11 complex functions. Mid1, Mid2, and essential role for Nbs1 is via its interaction with Mre11 and that most of the Mre11 DNA binding and nuclease activity. These data indicate an interface is sufficient to sustain the viability of cells and stabilize Mre11 dimer function. An Nbs1 minimal fragment spanning just the Mre11-Nbs1 interaction lethality and increased tumorigenesis due to a defect in Mre11 complex function. An Nbs1 minimal fragment spanning just the Mre11-Nbs1 interaction interface is sufficient to sustain the viability of cells and stabilize Mre11 dimer and Mre11 DNA binding and nuclease activity. These data indicate an essential role for Nbs1 is via its interaction with Mre11 and that most of the Nbs1 protein is dispensable for Mre11 complex functions. Mid1, Mid2, and AMI denote Mre11-interacting domain 1, Mre11-interacting domain 2, and ATM interacting motif, respectively.

Manipulation of the DDR for therapeutic benefit offers significant potential (O’Connor, 2015). Accordingly, understanding of ATM activation is an important issue. This study thus provides important mechanistic insight toward that goal by defining the role of Nbs1 in promoting Mre11 complex functions in the DDR.

EXPERIMENTAL PROCEDURES

For detailed protocols of cell lines, cellular assay, fetal liver cell transplantation, immunofluorescence staining, and histopathology, see Supplemental Experimental Procedures.

Mice

Nbs1flox mice were generated by help of the Memorial Sloan Kettering Mouse Genetics core. Detailed protocol will be provided upon request. Nbs1flox mice were previously described (Williams et al., 2002), and Nbs1flox and vavCre mice were kindly provided by Zhao-Qi Wang (Fritz Lipmann Institute, Germany) and Hans-Guido Wendel (Memorial Sloan Kettering Cancer Center, USA), respectively. The Institutional Animal Care and Use Committee of Memorial Sloan Kettering Cancer Center approved all protocols for animal use.

Protein Purification and Analysis

Bacterial expression vector for N-terminal his-tagged human Mre11 (2–411 amino acids) was gifted from Dr. John Tainer (Lawrence Berkeley National Laboratory, USA). With C-terminal his tag, human Nbs1 (F4; 622–729 amino acids) was constructed in pMAL vector (New England Biolabs) for N-terminal his tag, human Nbs1 (F4; 622–729 amino acids) was constructed in pMAL vector (New England Biolabs) for N-terminal his tag.

Nbs1 minimal fragment (108 aa)

Figure 7. The Mre11 Interaction Domain of Nbs1 Is Necessary and Sufficient for Mre11 Complex Functions

Disruption of the Mre11-Nbs1 interaction results in cellular and organismal lethality and increased tumorigenesis due to a defect in Mre11 complex function. An Nbs1 minimal fragment spanning just the Mre11-Nbs1 interaction interface is sufficient to sustain the viability of cells and stabilize Mre11 dimer and Mre11 DNA binding and nuclease activity. These data indicate an essential role for Nbs1 is via its interaction with Mre11 and that most of the Nbs1 protein is dispensable for Mre11 complex functions. Mid1, Mid2, and AMI denote Mre11-interacting domain 1, Mre11-interacting domain 2, and ATM interacting motif, respectively.

Statistical Analysis

Statistical significance was analyzed by unpaired t test, Fisher’s exact test, or Wilcoxon rank sum test and expressed as a p value as indicated in the figure legends.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, six figures, and one table and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2016.12.035.

AUTHOR CONTRIBUTIONS

J.H.K., M.G., and R.A. performed the experiments and analyzed the data. J.H.K., C.W., P.C., and J.H.J.P. designed the experiments. J.H.K. and J.H.J.P. wrote the paper.

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