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| Citation       | Fantini, Damiano, Shuo Huang, John M. Asara, Srilata Bagchi, and Pradip Raychaudhuri. 2017. "Chromatin association of XRCC5/6 in the absence of DNA damage depends on the XPE gene product DDB2." Molecular Biology of the Cell 28 (1): 192-200. doi:10.1091/mbc.E16-08-0573. http://dx.doi.org/10.1091/mbc.E16-08-0573. |
|----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Published Version | doi:10.1091/mbc.E16-08-0573                                                                                                                                                                        |
| Citable link    | http://nrs.harvard.edu/urn-3:HUL.InstRepos:32072083                                                                                                                                               |
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Chromatin association of XRCC5/6 in the absence of DNA damage depends on the XPE gene product DDB2

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ABSTRACT Damaged DNA-binding protein 2 (DDB2), a nuclear protein, participates in both nucleotide excision repair and mRNA transcription. The transcriptional regulatory function of DDB2 is significant in colon cancer, as it regulates metastasis. To characterize the mechanism by which DDB2 participates in transcription, we investigated the protein partners in colon cancer cells. Here we show that DDB2 abundantly associates with XRCC5/6, not involving CUL4 and DNA-PKcs. A DNA-damaging agent that induces DNA double-stranded breaks (DSBs) does not affect the interaction between DDB2 and XRCC5. In addition, DSB-induced nuclear enrichment or chromatin association of XRCC5 does not involve DDB2, suggesting that the DDB2/XRCC5/6 complex represents a distinct pool of XRCC5/6 that is not directly involved in DNA break repair (NHEJ). In the absence of DNA damage, on the other hand, chromatin association of XRCC5 requires DDB2. We show that DDB2 recruits XRCC5 onto the promoter of SEMA3A, a DDB2-stimulated gene. Moreover, depletion of XRCC5 inhibits SEMA3A expression without affecting expression of VEGFA, a repression target of DDB2. Together our results show that DDB2 is critical for chromatin association of XRCC5/6 in the absence of DNA damage and provide evidence that XRCC5/6 are functional partners of DDB2 in its transcriptional stimulatory activity.

INTRODUCTION DDB2, a product of the xeroderma pigmentosum group E (XPE) gene, plays important roles in the early steps of global genomic repair through the nucleotide excision repair (NER) pathway (Tang and Chu, 2002). It associates with the CUL4-DDB1 E3 ligase (Shiyanov et al., 1999b) to ubiquitinate histones and the NER protein XPC, leading to assembly of the NER repair complex on the damaged chromatin (Wang et al., 2004, 2006; Kapetanaki et al., 2006). In addition, DDB2 has a chromatin-remodeling activity that supports NER (Luijsterburg et al., 2012). It has been suggested DDB2 cooperates with PARP1 to stimulate NER (Pines et al., 2012). DDB2 also possesses transcriptional regulatory activities. Mouse embryonic fibroblasts (MEFs) lacking DDB2 are deficient in undergoing senescence in culture, which is linked to an increase in antioxidant activities. DDB2 represses expression of the antioxidant genes MnSOD and Catalase (Minig et al., 2009; Roy et al., 2010). In DDB2-/- cells or tissues, there is derepression of MnSOD and Catalase, which inhibits accumulation of reactive oxygen species (ROS). In colon cancer cells, depletion of DDB2 leads to epithelial-to-mesenchymal transition (EMT), which is associated with aggressive tumor progression and increased liver metastasis (Roy et al., 2013). The EMT and increased metastasis was related to derepression of Zeb1, Snail, and VEGFA expression. In mesenchymal-type colon cancer cells having reduced expression of DDB2, reexpression of DDB2 causes...
repression of those EMT genes (Roy et al., 2013). Consistent with these observations, a colon cancer tissue microarray indicated a loss of DDB2 expression that coincided with reduced expression of the epithelial cell surface marker E-cadherin and metastatic progression of colon cancer (Roy et al., 2013). Thus the tumor suppression function of DDB2 extends far beyond its role in NER. In colon cancer, its transcriptional regulatory role is clearly important in suppression of aggressive progression and metastasis.

DDB2 also possesses transcriptional stimulatory activity, which has been implicated in tumor suppression. For example, DDB2 was shown to regulate the invasiveness of breast cancer cells by stimulating expression of the NF-kB inhibitor NFKBIA (Ennen et al., 2013). That study identified a specific sequence element, TCCCTTA, in the NFKBIA promoter that is recognized by DDB2. The same element might also participate in DDB2-mediated repression, as a recent study showed that DDB2 represses NEDD4L, an E3 ligase for Smad2/Smad3, to enhance transforming growth factor β (TGFβ) signaling in ovarian cancer cells by binding to the same DNA element in the NEDD4L promoter (Zhao et al., 2015). This is also related to the tumor suppression function of DDB2 because repression of NEDD4L enhances responsiveness of ovarian cancer cells to growth inhibition by the TGFβ signaling pathway (Zhao et al., 2015).

The transcriptional repressor function of DDB2 involves DDB1 and CUL4. For repression of the MnSOD and Catalase, DDB2 was shown to recruit SUV39h, a histone H3K9 methylase, onto the promoters of those genes to generate chromatin with increased tri-methylation of H3K9 (Roy et al., 2010, 2013). For repression of the NEDD4L promoter, DDB2 was shown to interact with the H3K27 methylase EZH2 (Zhao et al., 2015). It is noteworthy that CUL4 proteins (A and B) have been implicated in histone methylation. Depletion of CUL4 leads to significant loss of trimethylation at both H3K9 and H3K27 (Higa et al., 2006). Therefore it is possible that the CUL4 proteins participate in the recruitment of the histone methylases onto the promoters of the genes repressed by DDB2. The role of CUL4 in the transcription stimulatory function of DDB2 is unclear.

XRCC5/6, also known as Ku86/Ku70, are essential for DNA double-stranded break repair (DSBR) through the nonhomologous end joining (NHEJ) pathway (Weaver, 1996). Moreover, Ku86/Ku70 were also reported to play a role in the transcriptional regulation of selected genes, including ERBB2 (Nolens et al., 2009), alphaMyHC (Sucharov et al., 2004), and osteocalcin (Willis et al., 2002). Of interest, XRCC5/6 interact with DDB2 and negatively regulate its E3 ubiquitin ligase activities around the damaged sites in ultraviolet (UV)-irradiated HeLa cells (Takedachi et al., 2010). Given that DDB2 does not have a direct role in NHEJ, it has been suggested that XRCC5/6-mediated inhibition of the E3 ubiquitin ligase activity is related to prevention of destabilization of DDB2 by excessive autoubiquitination (Takedachi et al., 2010). Here we show that DDB2 plays an essential role in recruiting XRCC5/6 onto chromatin in the absence of DNA DSBs and that DDB2 recruits XRCC5 onto the promoter of a DDB2-stimulated gene, SEMA3A, in colon cancer cells. Our results suggest that XRCC5/6 are important transcriptional activation partners of DDB2.

RESULTS
Identification of protein partners of DDB2
To identify proteins that could regulate the DDB2 transcription regulatory function, we used an unbiased communoprecipitation (colP) strategy. Nuclear extracts from HCT116 stably overexpressing FLAG-HA-DDB2 (FH-DDB2) or control cells (Supplemental Figure 1, A and B) were communoprecipitated using a two-round colP approach using an anti-FLAG antibody and an anti-hemagglutinin (HA) antibody. The colP samples eluted with 1× Laemmli sample buffer from FH-DDB2 cells were highly enriched in FH-DDB2 as well as in known protein partners of DDB2, including DDB1 and CUL4A (Figure 1A). For tandem mass spectrometry (MS/MS) analyses, the proteins after HA IP were released using a buffer containing 0.5 M NaCl and 0.1% SDS. That condition does not elute the antigen. The samples were separated on 10% SDS–PAGE and then silver stained. The strongest bands that were specifically detected in the lane corresponding to the FH-DDB2 colP sample were excised and subjected to MS/MS identification. This analysis led to the identification of some DDB2 binding partners that were not previously described (Figure 1B). Western blotting analyses performed on colP samples from control or FH-DDB2–expressing cells validated the binding of JARID2, CYLD, XRCC5, TBX2, and histone H3 in HCT116 cells (Figure 1C).

Wild-type DDB2, but not XPE mutants, interacts with XRCC5/6 in HCT116 cells
One of the strong DDB2 interactors, as revealed by Western blotting analyses, is the DNA repair protein XRCC5. Of interest, the DDB2–XRCC5 interaction was already described in HeLa cells after UV irradiation (Takedachi et al., 2010). However, we were puzzled by the identification of such an interaction in the nuclei of unirradiated HCT116 cells. XRCC5 interacts with XRCC6 and DNA-PKcs for repair of DSBs by NHEJ. We further assayed the FH-DDB2 colP samples by Western blotting and found that XRCC6, but not DNA-PKcs, communoprecipitated with DDB2 (Figure 2A) in unirradiated HCT116 cells. The specificity of the DDB2–XRCC5/6 interaction was confirmed by performing colP experiments using DDB2 mutants. Point mutation variants of DDB2 isolated from XPE patients (Nichols et al., 1996) were expressed in HCT116 cells and then communoprecipitated using an anti-FLAG antibody (Figure 2B). Of interest, the 2RO and 82TO DDB2 variants were reported to have an
DDB2 knockdown. However, the untreated control cells had a significantly higher amount of detergent- and RNase-resistant XRCC5 than did shDDB2 HCT116 cells (p < 0.001). Phleomycin did not have any significant effect on the total protein and mRNA levels of XRCC5 in the presence or absence of DDB2 (Supplemental Figure S2). Therefore we hypothesized that DDB2 expression could affect XRCC5 recruitment to the chromatin under basal conditions in HCT116 cells but not after DSB.

**DDB2 promotes the accumulation of XRCC5 in a chromatin-enriched fraction of colon cancer cells**

We studied the accumulation of XRCC5 in the chromatin-enriched fraction in control versus shDDB2 HCT116 cells by performing fractionation experiments followed by Western blotting. Control or shDDB2 cells were washed with phosphate-buffered saline (PBS) or with buffers containing detergent alone or detergent supplemented with RNase, similarly to what we described earlier (Figure 3C), and then harvested in 1x Laemmli sample buffer and analyzed by Western blotting (Figure 4A). Whereas control and shDDB2 cells express XRCC5 at similar levels (Figure 4A, lanes 1 and 2), only control cells accumulate XRCC5 in the RNase-resistant fraction (Figure 4A). We further studied the intracellular distribution of XRCC5 in colon cancer cell lines by performing a sequential fractionation experiment. Cell pellets were sequentially extracted with buffers containing detergent (S1 fraction), detergent supplemented with RNase (S2 fraction), and detergent supplemented with nuclease (S3 fraction) as outlined in Figure 4B. As expected, most of the histone H3 protein was released upon nuclease digestion in the S3 fraction, indicating that S3 is a chromatin-enriched fraction (Figure 4B). Interestingly, XRCC5 accumulation in the chromatin under basal conditions in SW620 cells was impaired capacity of importing DDB1 to the nucleus (Shiyanov et al., 1999a). The mutant DDB2 proteins were defective in their ability to bind the XRCC5/6 proteins (Figure 2B). We also performed a coIP using anti XRCC5 antibody and nuclear extracts of control and HCT116 cells stably expressing a short hairpin RNA (shRNA) targeting DDB2 (shDDB2; Figure 2C). DDB2 was detected in coimmunoprecipitates obtained with the XRCC5 antibody. Of note, DDB1 was detected in the XRCC5 coIP samples from both control and shDDB2 cells. On the contrary, CUL4A was never found in the XRCC5 coIP samples. This suggests that the XRCC5/6 proteins may be part of a protein complex that includes DDB2 and DDB1 but not CUL4A and DNA-PKc in HCT116 cells.

**DDB2–XRCC5 may not be linked to the damaged-DNA response functions of XRCC5/6**

We investigated whether the DDB2–XRCC5 interaction could play a role in the damaged-DNA response function of XRCC5 and XRCC6. We treated control and shDDB2 cells with the DSB-inducer phleomycin for 2 h and then replaced medium and incubated the cells for an additional 4 h. The DDB2–XRCC5 interaction remained unperturbed upon and after the phleomycin treatment, as revealed by coIP experiments followed by Western blotting analysis (Figure 3A). Of interest, control and shDDB2 cells responded to the genotoxic stress by accumulating γ-H2AX in a very similar manner (Figure 3B), unlike what we observed after depleting XRCC5 by siRNA transfection (Supplemental Figure S2). The recruitment of XRCC5 to the phleomycin-damaged chromatin was also monitored in control and shDDB2 HCT116 cells by immunofluorescence (Figure 3C). Cells were washed with a buffer containing detergent and RNase immediately before fixation in order to remove the non-chromatin-bound pool of XRCC5, as described previously (Britton et al., 2013). XRCC5 accumulation to the detergent- and RNase-resistant nuclear compartment of phleomycin-challenged cells was not prevented by XRCC5.
We found that HCT116 cells lacking DDB2–XRCC5/6 functional interaction resulted in a significant SEMA3A mRNA down-regulation, whereas mRNA levels of the VEGFA and SEMA3A genes. XRCC5 knockdown by siRNA transfection (Supplemental Figure S4B) and assessed cancer cell lines. Next, we down-regulated XRCC5 in HCT116 cells DDB2 levels can affect the transcriptional levels of SEMA3A in colon (Figure S4A) led to up-regulation of SEMA3A mRNA in both HCT116 and SW620 cells (Figure 5B). Conversely, overexpression of DDB2 (Supplemental Figure S4A) led to up-regulation of SEMA3A mRNA in both HCT116 and SW620 cells (Figure 5C). This suggests that modulation of DDB2 levels can affect the transcriptional levels of SEMA3A in colon cancer cell lines. Next, we down-regulated XRCC5 in HCT116 cells by siRNA transfection (Supplemental Figure S4B) and assessed mRNA levels of the VEGFA and SEMA3A genes. XRCC5 knockdown resulted in a significant SEMA3A mRNA down-regulation, whereas VEGFA mRNA levels were unchanged (Figure 5D). The effect of XRCC5 knockdown on SEMA3A expression was not very strong because, whereas XRCC5-siRNA efficiently knocked down the mRNA level, knockdown at the protein level was less efficient (Supplemental Figure S4B), which is likely related to the long half-life of XRCC5 (Ajmani et al., 1995). Therefore SEMA3A is a transcriptional activation target of both DDB2 and XRCC5.

DDB2–XRCC5 interaction may play a role in transcriptional regulation of selected DDB2 target genes. Our group recently found that DDB2 transcriptionally represses VEGFA, an angiogenic gene (Roy et al., 2013). In the tumor microenvironment, VEGFA effects are antagonized by a set of other antiangiogenic factors that include the protein products of several semaphorin class III genes (Maione et al., 2009, 2012). We assessed the binding of DDB2 to the 6-kb SEMA3A proximal promoter by chromatin immunoprecipitation (ChIP), using a specific anti-DDB2 antibody or normal rabbit immunoglobulin G (IgG). We used 11 sets of primers covering the 6-kb upstream region of the SEMA3A promoter (Supplemental Figure S4C) in PCR assays of ChIP DNAs. Within the 6-kb region, there is one DDB2-cognate element at position 289 base pairs upstream of the transcription start site (Figure 6A), which corresponds to our PCR primer set 1. Consistent with this, primer set 1 showed interaction of DDB2 with the SEMA3A promoter (Figure 6B). Of interest, our ChIP PCR also detected interactions at other sites that apparently do not possess a strong DDB2-cognate element. We suspect that those PCR results are related to interactions of the DDB2 complex with other proteins binding to the SEMA3A promoter. We also carried out ChIP experiments with XRCC5 antibody in cells expressing control or DDB2 shRNA. Clearly, XRCC5 binds to the SEMA3A promoter, and that binding depends on DDB2, as there were significant losses of the fold enrichment in DDB2 shRNA–expressing cells (Figure 6C).

**DISCUSSION**

Studies in HeLa cells identified strong interactions of DDB2 with the subunits of the Cop9 signalosome (Groisman et al., 2003). Surprisingly, in our experiments with HCT116 cells, we did not detect the Cop9 signalosome as a major DDB2-interacting protein. It is likely that DDB2 possess cell type–specific partners. In colon cancer cells, we detected XRCC5 and histone H3 as strong binding partners of DDB2–XRCC5/6 functional interaction | 195
cells detected an interaction of DDB2 with the PRC2 complex protein EZH2 (Zhao et al., 2015). However, it is noteworthy that immunoprecipitates with the XRCC5 antibody contained DDB2 and DBD1 but not Cul4 (Figure 2). TBX2 is a transcription factor that inhibits expression of the p16ink4a and the p14Arf tumor suppressors to block cellular senescence and promotes EMT (Jacobs et al., 2000; Wang et al., 2012). Our previous studies demonstrated exactly opposite roles of DDB2 with regard to senescence and EMT (Roy et al., 2013). Therefore it is possible that DDB2 regulates TBX2, and that regulation is important in the mechanisms by which DDB2 suppresses tumor development and progression.

XRCC5/6, like DDB2, are multifunctional proteins involved in DSBR (Milne et al., 1996), transcription (Willis et al., 2002; Sucharov et al., 2004; Kim et al., 2008; Nolens et al., 2009; Xiao et al., 2015), and telomere maintenance (Indiviglio and Bertuch, 2009). XRCS5/6 localizes to DSB sites after DNA damage (Britton et al., 2013). We provided evidence that chromatin association of XRCC5 after DSB does not involve DDB2. DDB2 was shown to be involved in the activation of ATM/ATR after UV irradiation (Ray et al., 2013). However, after DSB induced by phleomycin, we did not see evidence for a role of DDB2 in the activation of ATM, as judged by H2AX phosphorylation (Figure 3). Therefore it is likely that the checkpoint activation function of DBB2 is restricted to certain types of DNA damage—for example, UV irradiation. Moreover, our results imply that the DDB2–XRCC5 interaction may have a role in cellular processes other than DNA damage response.

The major finding of this study is that in colon cancer cells, chromatin association of XRCC5/6, in the absence of DNA damage, depends on DDB2. This was observed in colon cancer cells HCT116, SW480, and SW620. However, in HeLa cells, XRCC5/6 accumulation on the chromatin was not affected upon knockdown of DDB2 (Supplemental Figure S3). In addition, in HeLa cells, the DDB2/XRCC5 interaction was detected only after UV irradiation (Takedachi et al., 2010). Therefore it appears that in HeLa cells, other mechanisms are involved in chromatin recruitment of XRCC5/6. Immunoprecipitations with XRCC5 antibody also demonstrated coimmunoprecipitation of DDB2 and DDB1 but not Cul4. Of interest, coprecipitation of DDB1 was detected in the absence of DDB2. Therefore DDB1 plays an important role in the interaction between DDB2 and XRCC5/6. That is also consistent with the observations that naturally occurring mutants of DDB2 that fail to import DDB1 in the nucleus are impaired in binding to XRCC5/6 (Figure 2).

Our results provide evidence for a transcription function of the DDB2–XRCC5 interaction. DDB2 stimulates expression of the SEMA3A gene. We show that depletion of XRCC5 inhibited the
expression of the SEMA3A gene, implying that SEMA3A is stimulated by XRCC5/6. In that experiment, we did not detect any effect of XRCC5 depletion on the repression function of DDB2. For example, depletion of DDB2 increased transcription of VEGFA. Depletion of XRCC5 did not increase the RNA levels of VEGFA. Therefore it is possible that the DDB2–XRCC5/6 interaction is not involved in the transcription repression function of DDB2. That would be consistent with the observation that XRCC5 does not associate with CUL4A, which is involved in the repression of VEGFA and other genes repressed by DDB2 (Roy et al., 2013). We showed that DDB2 recruits XRCC5 onto the promoter of SEMA3A, whose expression in colon cancer cells depends on both DDB2 and XRCC5. Therefore the interaction between DDB2 and XRCC5/6 is related to the transcriptional activation function of DDB2.

Previous studies on the transcriptional activation function of XRCC5/6 indicated cooperation with the transcriptional coactivator CBP (Xiao et al., 2015). In that regard, it is interesting that DDB2 also associates with CBP (Datta et al., 2001). It is noteworthy that the XRCC5/6 proteins also have been implicated in elongation steps of mRNA synthesis (Mo and Dynan, 2002). In addition, XRCC5/6 were shown to participate as corepressors in steroid hormone–regulated transcription (Jeyakumar et al., 2007). In those studies, DNA-PKcs was shown to activate histone deacetylases to inhibit transcription. XRCC5/6-associated DNA-PKcs also is involved in the inactivation of human GCN5 histone acetyltransferase by phosphorylation (Barlev et al., 1998). Therefore the observation that DDB2 does not associate with DNA-PKcs further supports the notion that the DDB2–XRCC5/6 interaction is related to transcriptional activation and not repression. However, because chromatin association of XRCC5/6 in colon cancer cells largely depends on DDB2, we cannot rule out other, indirect functions of the DDB2-mediated localization of XRCC5/6 onto chromatin.

FIGURE 5: DDB2 and XRCC5 control SEMA3A expression in colon cancer cells. (A) DDB2, SEMA3A, and VEGFA mRNA expression levels were assessed in control and shDDB2 HCT116 cells by reverse transcription (RT)–qPCR. Averages of three experiments are shown in the bar plots (**p < 0.01, ***p < 0.001, t test). (B) Concentrated conditioned medium from control and shDDB2 HCT116 cells was resolved by SDS–PAGE and then Coomassie stained (left) or probed for SEMA3A by Western blotting (right). (C) SEMA3A mRNA levels were assessed in HCT116 or SW620 cells transfected with an empty vector (pcDNA3) or a construct coding for FLAG-T7-DDB2 by RT-qPCR (**p < 0.01, t test). (D) XRCC5, SEMA3A, and VEGFA mRNA levels were assessed by RT-qPCR in HCT116 cells transfected with a nontargeting siRNA (siCTRL) or a siRNA against XRCC5 (siXRCC5) (**p < 0.05, ***p < 0.001, t test).

MATERIALS AND METHODS

Plasmids

pOZ-FH-N and pOZ-FH-N-DDB2 were a kind gift from Yoshihiro Nakatani (Dana-Farber Cancer Institute, Boston, MA). FLAG-T7-DDB2 WT, 2RO, and 82TO constructs were generated starting from T7-DDB2 expression constructs described previously (Shiyano et al., 1999a). Briefly, the constructs were HindIII and Kpnl double digested and then ligated with a double-stranded DNA fragment obtained by annealing the oligonucleotides 5′-AAG CCT TTG AGC TAC AAG GAC GAC GAT GAC AAC CTG CCT ACC-3′ and 5′-CGA GCT TGT CAT CGT CGT CCT TGT AGT CCA TA-3′.

Cell culture and transfection

HCT116 cells were grown in DMEM containing 10% fetal bovine serum (FBS) and 1% penicillin–streptomycin at 37°C and 5% CO2. SW480 and SW620 were grown in RPMI containing 10% FBS and 1% penicillin–streptomycin at 37°C and 5% CO2. HCT116 cells stably expressing FLAG-HA-tagged DDB2 were established using a retroviral vector (Groisman et al., 2003). HCT116 cells stably expressing siRNA targeting DDB2 were described previously (Roy et al., 2013). Cell transfection experiments were conducted using Lipofectamine2000 (Thermo Fisher Scientific, Waltham, MA), following the manufacturer’s recommendations. Transient knockdown of XRCC5 was carried out by transfecting ON-TARGET Plus XRCC5 siRNA SMARTpool (GE Dharmacon, Lafayette, CO) or nontargeting siRNA SMARTpool (Dharmacon) into HCT116 at a final concentration of 150 nM. Cells were harvested 72 h after siRNA transfection.

Antibodies

We used the following commercial antibodies: JARID2 (NB100-2214; Novus Biologicals, Littleton, CO), CYLD (sc-28211; Santa Cruz Biotechnology, Santa Cruz, CA), XRCC5 (sc-9034; Santa Cruz Biotechnology), XRCC6 (ALS14031; Abgent, San Diego, CA), TBX2 (H00006909-M01; Novus Biologicals), H3 (4499; Cell Signaling, Danvers, MA), DDB2 (Western blotting: 5416; Cell Signaling; ChIP: 2214; Novus Biologicals, Littleton, CO), CYLD (sc-28211; Santa Cruz Biotechnology), DNA-PKcs (NB2P-22128; Novus Biologicals), SEMA3A (AF1250; Novus Biologicals), actin (A4700; Sigma-Aldrich, St. Louis, MO), and y-H2AX (9718; Cell Signaling). DDB1 and CUL4A antibodies were described previously (Nag et al., 2004). Horseradish peroxidase–conjugated secondary antibodies were purchased from Bio-Rad.

Nuclei extraction and communoprecipitation

Nuclear extracts for coIP were prepared starting from 100 million cells that were harvested by scraping. Cell pellets were resuspended in hypotonic buffer containing 10 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES), pH 7.4, 10 mM KCl, 1.5 mM MgCl2, and 0.5 mM ethylene glycol tetraacetic acid (EGTA) supplemented with 1 mM phenylmethylsulfonfluoride (PMSF) and 1× protease inhibitor cocktail (Roche, Basel, Switzerland) and then lysed using a 7-mL Glass Tenbroek homogenizer (Wheaton, Millville, NJ). Cell lysates were spun through a sucrose cushion (15 mM Tris-HCl, pH 7.5, 15 mM NaCl, 60 mM KCl, 5 mM MgCl2, 0.1 mM EGTA, and
nuclear extracts. CoIP was performed immediately by rotating 5-mg nuclear extracts and 100 μL of anti-FLAG M2 agarose bead slurry (Sigma-Aldrich) for 12 h, followed by four washes in IP buffer (50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 0.5 mM EGTA, and 0.05% Triton X-100 supplemented with 1 mM PMSF). Beads were eluted for 30 min with 250 μl of 0.15 mg/ml 3× FLAG peptide (Sigma-Aldrich) in IP buffer. For dual-round coIPs, supernatants were further rotated for 5 h at 4°C with 15 μg of anti-HA monoclonal antibody (Roche). Protein G–Sepharose beads were added, and samples were further rocked for 1 h. After three washes with IP buffer, beads were eluted with 1× Laemmli sample buffer (Western blotting) or in 50 mM Tris-HCl, 500 mM NaCl, 0.1% SDS, and 1 mM PMSF (MS/MS identification). Coimmunoprecipitates were separated on a 10% SDS–PAGE, and then gels were silver stained, and selected bands were excised from the gel for MS/MS identification.

**Conditioned medium preparation**

Cells were grown for 48 h at 37°C in DMEM, high glucose, HEPES, and no Phenol Red (Thermo Fisher Scientific). Cell supernatant was filtered through a Millex-GP Syringe Filter Unit with a 0.22-μm cutoff (EMD Millipore), spun down at 8000 × g to remove insoluble material, and then 10-fold concentrated using an Amicon Ultra-4 10-kDa filter unit (EMD Millipore, Billerica, MA). Concentrated conditioned medium was diluted in 1 volume of 4× Laemmli sample buffer (120 mM Tris-HCl, pH 6.8, 40% glycerol, 8% SDS, 60 mM dithiothreitol) and stored at −20°C.

**Immunofluorescence**

Immunofluorescence experiments were performed on cells grown on 12-mm coverslips for 48 h after seeding. Cells were treated with 200 μg/ml phleomycin (Sigma-Aldrich) for 2 h, medium was replaced, and cells were further incubated at 37°C for the indicated times. Cells were washed with PBS or CSK buffer (10 mM 1,4-piperazinediethanesulfonic acid, pH 6.8, 100 mM NaCl, 3 mM MgCl₂, 300 mM glycerol) supplemented with 0.7% (GEPAL CA630 and 0.1 mg/ml RNase A (Thermo Fisher Scientific) for 3 min at room temperature (Britton et al., 2013). After two washes with ice-cold PBS, cells were cross-linked for 15 min with 4% paraformaldehyde at room temperature. Coverslips were blocked for 1 h at room temperature in blocking buffer (5% BSA in PBS). Cells were fixed with 4% paraformaldehyde in PBS, cells were cross-linked for 15 min with 4% paraformaldehyde at room temperature (Britton et al., 2013). After two washes with ice-cold PBS, cells were cross-linked for 15 min with 4% paraformaldehyde at room temperature. Coverslips were blocked for 1 h at room temperature in blocking buffer (5% BSA in PBS). XRCC5 antibody was diluted 1:500 in blocking buffer and incubated for 2 h at room temperature. Anti-rabbit secondary antibody Alexa Fluor 488 (Thermo Fisher Scientific) was then added for 1 h at room temperature. Coverslips were counterstained with Hoechst 33342 (Thermo Fisher Scientific) and then mounted onto glass slides using ProLong Gold Antifade reagent (Thermo Fisher Scientific). Images were acquired using a Zeiss LSM 510 microscope.

**Protein extraction experiments and Western blotting**

For preextraction experiments, cells were seeded in six-well multiwell plates at a density of 400,000 cells/well. At 48 h later, cells were washed twice with PBS and then incubated for 5 min at room temperature with PBS, CSK-T (CSK buffer supplemented with 0.7% Triton X-100 and 0.5 mM PMSF), or CSK-T RNase (CSK-T supplemented with 0.1 mg/ml RNase A). Wells were further washed with 1 ml of ice-cold PBS, and 1× Laemmli sample buffer was then added; samples were boiled at 95°C for 5 min and loaded on gels. For sequential fractionation experiments, 2.0 M cells were seeded in a 10-cm plate. At 48 h later, cells were washed with PBS and harvested by scraping. Samples were spun at 800 × g for 5 min at 4°C. Pellets were resuspended in 500 μl of CSK-T buffer and incubated on ice for 5 min. Samples were centrifuged at 3000 × g for 6 min at 4°C,
supernatants were saved as S1 fractions, and pellets were washed twice with ice-cold PBS and then resuspended in 500 μl of CSK-T RNase buffer. Samples were incubated at room temperature for 5 min and then centrifuged at 6000 × g for 6 min at 4°C. Supernatants were collected as S2 fractions, and pellets were washed twice with PBS and then resuspended in 500 μl of nuclease-containing CSK buffer (CSK-T supplemented with Benzonase [EMD Millipore] and 0.1% SDS). Samples were rocked at room temperature for 10 min and then centrifuged at 16,000 × g for 10 min at 4°C. Supernatants were collected as S3 fractions, and pellets were washed once with PBS, boiled for 5 min at 95°C in 1× Laemmli sample buffer, and saved as P3 fractions. Whole-cell lysates were prepared by boiling cell pellets in 1× Laemmli sample buffer for 5 min at 95°C. Samples were separated on 12% SDS–PAGE (unless otherwise stated), and Western blotting was performed using standard procedures and the antibodies described diluted in 5% nonfat dry milk in Tris-buffered saline supplemented with 0.1% Tween 20 (Sigma-Aldrich).

RNA extraction and quantitative PCR
Total RNA was extracted using TRizol (Thermo Fisher Scientific) and following manufacturer’s instructions. cDNA was synthesized using iScript cDNA Synthesis Kit (Bio-Rad), and quantitative PCR (qPCR) was performed using iTaq Universal SYBR Green Supermix (Bio-Rad) and a CFX96 system (Bio-Rad). Oligonucleotides used as primers are described in Supplemental Table S1.

Chromatin immunoprecipitation
Chromatin immunoprecipitation experiments were performed as previously described (Roy et al., 2013). De-cross-linked chromatin was analyzed by qPCR, using the primers described in Supplemental Table S2.

ACKNOWLEDGMENTS
We thank Vania Vidmar for insightful discussions and editorial assistance in the writing of the manuscript. The work was supported by National Institutes of Health/National Cancer Institute Grants CA156164 and CA77637 to P.R. and S.B. P.R. is also supported by National Institutes of Health/National Cancer Institute Grants CA156164 and CA77637 to P.R. The work was supported in part by VA Merit Grant BX000131.

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