The genetic and biochemical basis of FANCD2 Monoubiquitination

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The Genetic and Biochemical Basis of FANCD2 Monoubiquitination

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of FANCD2 by FANCL in vitro depends on the presence of its binding partner FANCI and DNA (Sato et al., 2012). The roles of other FA subunits are poorly defined, and they largely lack any identifiable domains that could illuminate their function.

Here, we develop a purification strategy for isolating a native FA core complex. The recovered complex is efficient at FANCD2 monoubiquitination in whole-cell extracts and after monoubiquitination in a cell-free system, and our biochemical analysis points to a core subcomplex as being fundamental to this reaction. Finally, genetic ablation studies confirm an essential role for components of this minimal subcomplex in vivo.

RESULTS

Purification of a Native FA Core Complex

We developed a purification strategy to isolate the FA core complex from chicken DT40 cells, a vertebrate model used extensively in the study of the FA pathway (Niedzwiedz et al., 2004; Yamamoto et al., 2003). Our aim was to generate a cell line where the only copy of the FANCB subunit included an affinity purification tag (Figure 1A). First, we deleted the genomic copies of FANCB (Figures 1B and 1C). In wild-type cells, FANCD2 is monoubiquitinated after exposure to DNA damage or replication stress, for example, by the DNA crosslinking agent mitomycin C (MMC) or the DNA synthesis inhibitor hydroxyurea (HU). This can be monitored on western blots by the appearance of a slower migrating monoubiquitinated form of FANCD2 (Figure 1D, lanes 2 and 3). ΔFANCB DT40 cells have a defective FA pathway because they do not exhibit FANCD2 monoubiquitination after MMC treatment (Figure 1D, lanes 5 and 6), which is in agreement with previous work in FA patient cells that lack functional FANCB (Meeitei et al., 2004).

Next, FANCB with a C-terminal protein G-streptavidin binding peptide (GS) tag (Bürckstümmer et al., 2006) was used to complement the ΔFANCB cells (Figure 1A). ΔFANCB/FANCB-GS cells regained the ability to monoubiquitinate FANCD2 after treatment with 1 mM hydroxyurea (HU) or 50 ng/ml mitomycin C (MMC). Western blotting of ΔFANCB monoubiquitination in whole-cell extracts is shown for WT DT40 cells, cells with a deletion of the genomic locus of FANCB gene (ΔF), and ΔB cells stably expressing chicken FANCB with a C-terminal protein G and streptavidin binding peptide tag (ΔB/B-GS).

Figure 1. Generation and Validation of the ΔFANCB/FANCB-GS DT40 Cell Line

(A) Schematic representation of generation of the ΔFANCB/FANCB-GS cell line and the expected effect on FANCD2 monoubiquitination in vivo. G, the IgG binding domain of protein G; SBP, streptavidin binding peptide.

(B) Targeting strategy for the generation of the ΔFANCB cell line. Exons are shown in black (exons 5 and 6) or green (exons 7, 8, and 9) boxes. The location of the Southern blot probe is in red. DrugR, drug resistance cassette.

(C) Southern blot showing gene targeting of FANCB. After BamHI digest, wild-type (WT) alleles are 23 or 18 kb, whereas the knockout allele (KO) is 5.6 kb. A 6.5 kb fragment (#) is present in all cell lines. Lane 1 shows a FANCB+/+ cell line, lane 2 shows FANCB+/−, and lane 3 shows FANCB−/−.

(D) ΔFANCB/FANCB-GS cells regained the ability to monoubiquitinate FANCD2 upon treatment with 1 mM hydroxyurea (HU) or 50 ng/ml mitomycin C (MMC). Western blotting of ΔFANCB monoubiquitination in whole-cell extracts is shown for WT DT40 cells, cells with a deletion of the genomic FANCB gene (ΔF), and ΔB cells stably expressing chicken FANCB with a C-terminal protein G and streptavidin binding peptide tag (ΔB/B-GS).
The FANCM subunit is present in very low abundance, whereas its associated proteins (FAAP10, FAAP16, and FAAP24) and the FANCA-associated protein FAAP20 are not detected in our purification. These subunits are not essential for FANCD2 monoubiquitination or the structural integrity of the FA core complex in vivo but most likely facilitate chromatin localization (Kim et al., 2008; Mosedale et al., 2005; Singh et al., 2009, 2010; Yan et al., 2010). Thus, our purified FA core complex contains all subunits currently known to be required for FANCD2 monoubiquitination, demonstrating that a constitutively assembled core complex exists in asynchronous dividing cells independent of DNA damage (Alpi et al., 2007).

**In Vitro FANCD2 Monoubiquitination by Purified FA Core Complex**

The E3 ligase in the FA core complex is the RING-finger-containing FANCL subunit (Alpi et al., 2008; Cole et al., 2010; Meetei et al., 2003a). The roles of other subunits are unclear. In vivo mutation of any one of the core complex components is thought to abolish FANCD2 monoubiquitination and lead to defective DNA repair and disease (Garcia-Higuera et al., 2001). To investigate the biochemical activity of the FA core complex, we reconstituted its monoubiquitination activity in vitro. We incubated purified FA core complex with recombinant E1 ubiquitin-activating enzyme, UBE2T, HA-tagged ubiquitin, and the His-tagged substrates FANCD2 and FANCI (Figures 3A and S1A–S1C). To eliminate species incompatibilities, we used the chicken homologs of UBE2T, FANCD2, and FANCI. We monitored monoubiquitination of His-FANCD2 and His-FANCI by western blotting. In this assay, our purified FA core complex catalyzes the transfer of ubiquitin onto FANCD2, as shown by the appearance of a discrete slower migrating band above FANCD2 on both anti-His and anti-HA western blots in Figures 3B and S1D (lanes 3 and 6).

The reaction goes to near completion at late time points, where unmodified FANCD2 is barely visible (Figure S1D, lane 6). Thus, our purified complex is active.

FANCD2 forms a complex in vivo with FANCI, and both are monoubiquitinated and recruited to sites of DNA damage in chromatin (Smogorzewska et al., 2007; Matsushita et al., 2005; Montes de Oca et al., 2005). We found that the in vitro activity of purified FA core complex is dependent on the presence of FANCI and is greatly stimulated by 5'-flapped DNA (Figure 3B), reflecting the in vivo context of its activity.

**The Intact FA Core Complex Is More Active and More Specific than Isolated FANCL**

As mentioned above, all previous in vitro studies of FANCD2 monoubiquitination had been performed with isolated FANCL (Alpi et al., 2008; Sato et al., 2012). We sought to compare this with the activity of our purified complex (Figures S1E and S1F).

Strikingly, the FA core complex is much more active than recombinant chicken FANCL (Figure 4). First, approximately five times more isolated FANCL is required to monoubiquitinate FANCD2 to the same level as FA core complex (Figure 4A, compare lanes 5 and 9; Figures S2A and S2B). Under these conditions, the FA core complex is also more specific, given that only isolated FANCL shows significant ubiquitin conjugation onto itself and UBE2T (Figure 4A, HA blot lanes 8 and 9). Second, when equimolar amounts of FA core complex and isolated FANCL are used in a time course of FANCD2 monoubiquitination, the rate of FANCD2 monoubiquitination is dramatically higher with FA core complex (Figures 4B, 4C, and S2C). Finally, FA core complex ubiquitinates FANCD2 on only the physiologically relevant lysine 563 (Figure 4D), whereas FANCL exhibits weak, but reproducible nonspecific, monoubiquitination of FANCD2K563R (see Figure S3A, lanes 23 and 35) (Sato et al., 2012). Cumulatively, these data show that the FA core complex is much more active and more specific than isolated FANCL.

Purified FA core complex catalyzes only the physiologically relevant formation of monoubiquitin linkages because a single discrete ubiquitinated FANCD2 species is observed (Figure 3).
In contrast, reactions containing isolated FANCL demonstrate weak poly- or multiple monoubiquitination activity, seen as higher-molecular-weight smears on the gel (Figure S2A, HA blot lanes 8 and 9). Also unlike the FA core complex (Figure 3B, lanes 2 and 5), recombinant FANCL has FANCD2 monoubiquitination activity even in the absence of FANCI (see Figure S3A, HA blot lane 3) (Alpi et al., 2008; Sato et al., 2012). Altogether, these data suggest that other FA core complex subunits most likely contribute to activity, substrate recognition, and specificity required to retain exclusive monoubiquitination activity on FANCD2 in the context of FANCI.

**UBE2T, but Not UBE2W, Functions as a Specific E2 for FANCD2 Monoubiquitination In Vivo and In Vitro**

Although UBE2T is established as an E2 for FANCD2 monoubiquitination in vivo (Alpi et al., 2007, 2008; Machida et al., 2006), UBE2W also binds FANCL (Alpi et al., 2008; Zhang et al., 2011). We found that, in assays with FANCL, UBE2W weakly monoubiquitinates FANCD2 and FANCI, but this was not dependent on the presence of the FANCI-FANCD2 complex (Figure S3A, lanes 4, 6, 10, and 12), stimulated by DNA (Figure S3A, lanes 6 and 12), and not site specific (Figure S3A, lanes 26 and 38). Similar observations were made in assays with the FA core complex (Figure S4B). These data indicate that UBE2W mediates nonspecific monoubiquitination of the FANCI-FANCD2 complex in vitro. To investigate its in vivo role, we deleted *UBE2W* in DT40 cells and examined FA pathway activity (Figures S3C and S3D). ΔUBE2W cells did not display significant cellular sensitivity to MMC (Figure S3E) and had normal levels of basal and MMC-induced FANCD2 monoubiquitination, unlike ΔUBE2T or ΔFANCB cells (Figure S3F). Along with previous work (Alpi et al., 2007; Machida et al., 2006), our results emphatically show that UBE2W does not play a major role in site-specific monoubiquitination of FANCD2 and that UBE2T is the major E2 in the FA pathway.

We only observed weak FANCI monoubiquitination in our assay that was not affected by the presence of FANCD2 or DNA and did not significantly increase over time, suggesting that it may not be physiologically relevant (HA blots in Figures 3B, S1D, and S3). Therefore, the factors enhancing FANCI monoubiquitination remain elusive but could include an alternate chromatin and/or DNA context or interplay with ATR-dependent FANCI phosphorylation (Ishiai et al., 2008, Tomida et al., 2013).

**Purified FA Core Complex Lacking FANCC and FANCE Retains In Vitro Activity**

FA can result from the loss of a single FA core complex subunit, which is thought to interfere with the integrity of the entire complex. To further investigate the stability and in vitro activity of the FA core complex, we deleted the FANCC gene (Niedzwiedz et al., 2004) in ΔFANCB/FANCB-GS cells. Cellular fractionation before and after FANCC deletion revealed that although FANCD2 monoubiquitination was significantly impaired, a residual amount was detectable in the chromatin-bound fraction after MMC treatment (Figure 5A, lane 8). This suggested that even with the loss of FANCC, the FA complex remains partially competent for FANCD2 monoubiquitination in vivo. To verify this, we purified the FA core complex from the ΔFANCC/ΔFANCB/FANCB-GS cell line. This yielded a preparation specifically lacking the deleted FANCC gene product and its known binding partner FANCE (Figure 5B) (Pace et al., 2002; Taniguchi and D'Andrea, 2002). FANC, thought to bridge the FANCC-FANCE and FANCA-FANCG subunits (Leveille et al., 2004), was also depleted. Thus, although FANCC deletion partially destabilized the complex through loss of FANCE and FANC, the remaining subunits (FANCA, FANCB, FANCG, FANCL, and FAAP100) were stably associated and the yield of purified complex was similar to wild-type cells.
Surprisingly, when we assayed the FA core complex lacking FANCC and FANCE, FANCD2 monoubiquitination activity was comparable to the wild-type complex (Figure 5C). There was no discernable difference in the rate of monoubiquitination, the effect of DNA, or the lack of FANCI monoubiquitination. These data demonstrate that the FANCC-FANCE subcomplex is dispensable for the overall stability and catalytic activity of the FA core complex.

Residual In Vivo FANCD2 Monoubiquitination Activity after Deletion of FANCA, FANCC, FANCF, or FANCG but Not FANCB, FANCL, or FAAP100

We were surprised that purified FA core complex lacking FANCC and FANCE (and with substantially reduced FANCF) had normal activity in vitro. To understand the roles of other core complex subunits, we took further advantage of the genetic tractability of the DT40 system. Specifically, we examined FANCD2 ubiquitination in vivo in a panel of DT40 cell lines in which each individual FA core complex subunit, with the exception of FANCE, had been deleted. Although very weak in comparison to wild-type or DFANCM cells, residual chromatin-associated FANCD2 monoubiquitination is still present in cells lacking FANCA, FANCC, FANCF, or FANCG (Figure 5D, bottom two panels). This is an unexpected result, given that work on human FA patient-derived lymphocytes shows an absence of FANCD2 monoubiquitination in all of the FA core complex complementation groups except FANCM (Garcia-Higuera et al., 2001; Singh et al., 2009).

In contrast, cells lacking FANCB, FANCL, or FAAP100 completely lost the ability to ubiquitinate FANCD2 (Figure 5D). This is consistent with FANCL’s role as the E3 ligase and the direct interaction of these three subunits (Ling et al., 2007). This surprising result demonstrates that, at least in DT40 cells, FANCB, FANCL, and FAAP100 are the only subunits whose deletion results in complete loss of FANCD2 monoubiquitination. To further
Figure 5. Deletion of FANCC Does Not Impact the In Vitro Ubiquitin Ligase Activity of the FA Core Complex, and the FANCB-FANCL-FAAP100 Subcomplex Is Essential for Monoubiquitination In Vivo

(A) Western blots of ΔFANCB/FANCB-GS (ΔB/B-GS) and ΔFANCB/FANCB-GS/ΔFANCC (ΔB/B-GS/ΔC) cells (with and without MMC treatment) after subcellular fractionation into cytonucleoplasmic (S) and chromatin (P) fractions with anti-FANCD2. Low and high exposures are shown.

(B) SDS-PAGE and silver stain analysis of the FA core complex purified from ΔB/B-GS and ΔB/B-GS/ΔC cell lines in parallel. The inset shows loss of FANCC and FANCE proteins and reduction of FANCF.

(C) In vitro ubiquitination assays of the FA core complexes (~80 nM) shown in (B) monitored by western blotting against FANCD2 and FANCI (anti-His) and ubiquitin (anti-HA).

(D) DT40 cell lines with FA core complex subunit deletions were treated with MMC, fractionated into cytonucleoplasmic (S) and chromatin (P) fractions and subjected to western blotting with anti-FANCD2. An additional high exposure is shown for the bottom panel.

(E and F) Cellular sensitivity of WT, ΔFANCA, ΔFANCG, ΔFANCB, ΔFANCC, and ΔFANCF DT40 cells after exposure to indicated doses of MMC. The mean percentage of survival ± SEM of three independent colony-formation assays are plotted relative to untreated cells. ΔFANCB cl. 31 is the unloxed parental line to ΔFANCB cl. 5.

See also Figure S4.
establish that this striking finding is broadly applicable to the mammalian FA pathway, we examined FANCD2 monoubiquitination in mammalian cell lines (human, mouse, and hamster) with targeted disruption of a FA subunit and compared this to isogenic wild-type cell lines. Chromatin-bound FANCD2 from cells with targeted disruption of FANCG, but not FANCB, retains residual FANCD2 ubiquitination (Figure S4). Furthermore, residual FANCD2 monoubiquitination has recently been demonstrated in a panel of human cell lines with targeted disruption of FA core complex subunits with the exception of DFANCB, DFANCL, or DFAAP100, which have no monoubiquitination activity (Huang et al., 2014).

Ubiquitinated FANCD2 is thought to act as an adaptor for DNA repair enzymes, allowing incision at sites of DNA crosslinks and promoting repair by homologous recombination (Crossan and Patel, 2012). Therefore, residual FANCD2 ubiquitination in certain FA core complex subunit knockout cells (Figure 5D) would be expected to show attenuated cellular sensitivity to DNA damage in comparison to knockout cells with no FANCD2 ubiquitination. To test this, we exposed DT40 cells to MMC and determined their survival. As shown in Figures 5E and 5F, DFANCB cells are more sensitive to MMC than DFANCA, DFANCG, DFANCC, and DFANCF cells. Thus, the amount of FANCD2 monoubiquitination correlates with MMC sensitivity in cells.

**Recombinant B-L-100 Monoubiquitates FANCD2**

FANCC and FANCE are biochemically dispensable for FANCD2 ubiquitination by a purified FA core complex (Figure 5C), and only FANCB, FAANL, and FAAP100 are genetically essential in vivo for monoubiquitination (Figure 5D). Therefore, we reasoned that FANCB, FAANL, and FAAP100 could constitute the catalytic core of the FA core complex. We expressed and purified a complex of B-L-100 (Figure 6 A). In vitro reconstitution assays show that B-L-100 is more active than FANCL alone (Figures 6B and 6C). In the presence of DNA, the B-L-100 subcomplex is 5- to 6-fold more active at ubiquitinating FANCD2 than isolated FANCL and thus comparable with the intact core complex. However, unlike the intact core complex, weak FANCD2 ubiquitination in the absence of FANCI (Figure S5A) and very weak multiple ubiquitination could be observed (Figure S5B).

Interestingly, the B-L-100 subcomplex retained significant activity in the absence of DNA (compare Figures 4C and 6C). To gain insight into the mechanism of DNA stimulation, we tested a panel of DNAs with different structures for their abilities to stimulate B-L-100 monoubiquitination (Figures 6D-F). In the absence of DNA, the B-L-100 subcomplex is more active than FANCL alone (Figures 6B and 6C), and DNA stimulation is observed with polyT DNA substrates (Figure 6D).
stimulate FANCD2 monoubiquitination. A variety of different DNA substrates stimulated the reaction (Figures 6D–6F and S5C). Intriguingly, unstructured polyT DNA did not stimulate the activity of B-L-100 or the intact core complex to the same extent as other DNAs (Figures 6E and 6F). In comparison to B-L-100, the intact core complex has lower basal FANCD2 monoubiquitination activity in the absence of DNA. This suggests DNA may be required to activate the FA core complex.

USP1 Deletion Permits Accumulation of FANCD2 Monoubiquitination in Cells with Residual Activity

The deubiquitinase enzyme USP1, in complex with UAF1, has been shown to deubiquitinate FANCD2 (Nijman et al., 2005). USP1 disruption leads to constitutive, chromatin-targeted monoubiquitinated FANCD2 (Kim et al., 2009; Oestergaard et al., 2007). To understand the functional importance of weak residual FANCD2 ubiquitination found in a FA-core-complex-defective cell line, we targeted both USP1 and FANCC in DT40 cells (Figure S6A). Strikingly, FANCD2 monoubiquitination was restored in the double mutant, supporting the observation of a partially active core complex in ΔFANCC cells (Figures 7A, S6B, S6D, and S6E). However, ubiquitination was not induced upon DNA damage, and monoubiquitinated FANCD2 was largely chromatin bound, though it was not as heavily enriched on chromatin as in ΔUSP1 cells (Oestergaard et al., 2007). Another target of USP1 activity, PCNA, was not affected in the double mutant (Figures S6B and S6C). As previously reported (Oestergaard et al., 2007), a ΔUSP1/ΔFANCL mutant showed no rescue of FANCD2 ubiquitination, given that the catalytic activity of the core complex was fully compromised (Figure 7A).

Although monoubiquitinated FANCD2 was present in ΔUSP1/ΔFANCC cells, the double mutant was more sensitive to MMC (Figure 7B). In comparison, we have previously shown that ΔUSP1/ΔFANCL cells are not more sensitive to DNA damage than the FANCL mutant alone (Oestergaard et al., 2007). Altogether, these results support the notion of epistasis between the gene products essential for monoubiquitination (FANCB, FANCL, and FAAP100) and deubiquitination (USP1) events in crosslink repair. Even though the residual FANCD2 ubiquitination in ΔFANCC cells is sufficient to partially attenuate MMC sensitivity in comparison to ΔFANCB cells that entirely lack ubiquitination (Figure 5F), simply restoring the
ubiquitinated FANCD2 (by deleting ΔUSP1) in this context is not sufficient to restore a functional FA DNA repair response.

**DISCUSSION**

In this study, we have combined a stringent biochemical purification strategy with genetic analyses in DT40 cells to establish a system for mechanistic interrogation of the FA pathway. We report the purification of a native FA core complex and the constitution of its FANCD2 monoubiquitination activity in vitro. The intact complex is more active and specific than the FA core complex lacking FANCC with all subunits present. We verified the catalytic competence of FA core complex lacking FANCC with all subunits are required for monoubiquitination. We reported that destabilization and inactivation of the FA core complex in patients, not determined by data showing intrinsic DNA binding of FANCA (Yuan et al., 2012) and the association of FANCA with FAAP20, a ubiquitin-binding-zinc-finger-containing protein that binds ubiquitin chains assembled by RNF8 and promotes chromatin targeting of the core complex and FANCD2 in vivo (Ali et al., 2012; Leung et al., 2012; Yan et al., 2012).

Our finding that combined USP1 and FAANCC deletion restores monoubiquitinated FANCD2 but cannot rescue MMC sensitivity challenges the broadly held view of a linear FA pathway in which substrate ubiquitination by the FA core complex alone leads to DNA repair. The ubiquitinated FANCD2 in ΔUSP1/ΔFAANCC cells, although near wild-type levels, is substantially chromatin bound and not induced by DNA damage. Clearly, the ubiquitination and deubiquitination of FANCD2 must be a tightly regulated response in a functional FA pathway. That ΔUSP1/ΔFAANCC cells are more sensitive than either single mutant suggest that the FA core complex may serve other functions in DNA repair in addition to ubiquitination. Elucidating these functions may ultimately explain why the FA core complex has such a highly conserved yet poorly understood macromolecular composition.

**EXPERIMENTAL PROCEDURES**

Detailed purification protocols and generation of cell lines are described in the Supplemental Information. The tandem affinity purification scheme is modified from Bürckstümmer et al. (2006) and was performed at 4°C. In brief, to purify a
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Purification and Activity of FA Core Complex

FA core complex, ΔB/B-GS, or ΔB/B-GS/ΔC DT40 cells were lysed in GS buffer (50 mM HEPES [pH 8.0], 150 mM NaCl, 5% glycerol, 0.1% Igepal CA-630, 1.5 mM MgCl₂, 25 mM NaF, 2 mM Na₃VO₄, 40 mM β-glycerophosphate, 1 mM phenylmethylsulfonyl flouride, 10 mM β-mercaptoethanol [BME], and PhosSTOP inhibitor cocktail [Roche] and protease inhibitor cocktail) by passing through 19 G and 25 G needles multiple times. After clarification, the lysate was incubated with IgG-agarose beads (Sigma-Aldrich) for 2 hr with gentle rotation. The beads were washed with wash buffer (50 mM HEPES [pH 8.0], 150 mM NaCl, 10% glycerol, and phosphatase/protease inhibitors) and then wash buffer supplemented with 5 mM BME. To elute, the beads were incubated with TEV protease at 16°C for 2 hr with gentle agitation. For the second affinity step, the supernatant was incubated with Ultralink Streptavidin Plus Resin (Pierce) with gentle rotation for 1 hr, washed with 100 bed volumes of wash buffer supplemented with 5 mM BME, and eluted with wash buffer supplemented with 3 mM BME and 6 mM D-biotin (Sigma-Aldrich). The complex was resolved by SDS-PAGE and analyzed by Coomassie, silver (Sigma-Aldrich), or SYPRO-Ruby (Lonza) staining. Bands were excised, digested, and identified by tandem mass spectrometry (data not shown) with multiple independent purifications. The major species identified in each band is indicated in Figure 2B. Purified complex was used fresh, immediately after purification, for downstream biochemical analyses. A titration against known concentrations of recombinant FANCL was used to approximate the concentration of prepared FA core complex (normalized to its FANCL band) on SDS-PAGE. We estimate that, from a ~3 g DT40 cell pellet (2–4 L cell culture), we purified ~5 μg FA core complex.

Western blotting was performed after SDS-PAGE on 4%–12% Bis-Tris gels or 3%–8% Tris-Acetate gels (Life Technologies) and transfer to polyvinylidene fluoride membranes (Millipore). The antibodies used were HRP-conjugated anti-α-HA (F-7, Santa Cruz Biotechnology), HRP-conjugated anti-α-His (H-38 SCBT), anti-β-actin (AC-15, Sigma-Aldrich), anti-chicken FANCG (Alpi et al., 2007), anti-chicken FANCM (Mosedale et al., 2005), or anti-chicken FANCD2 (gift of Michael Hodskinson, Medical Research Council Laboratory of Molecular Biology).

For ubiquitination assays, reactions in 10–20 μl volumes were performed in a buffer comprising 50 mM HEPES (pH 7.5), 64 mM NaCl, 4% glycerol, 5 mM MgCl₂, 2 mM ATP, and 0.5 mM dithiothreitol. In all assays, 75 mM E1 (Boston Biochem) and 1 μM E2 (UBE2T or UBE2W) enzymes, 1 μM substrate (FANCI, FANCD2, FANCD2Δα, and FANCD2Δαβγδε) were added. Each reaction was incubated at 30°C for 90 min (or for indicated times as part of a time course) and quenched by the addition of LDS sample buffer (Life Technologies). Samples were analyzed by western blotting. Additional details of experimental procedures are contained in the Supplemental Information.

SUPPLEMENTAL INFORMATION

Supplemental Information contains Supplemental Experimental Procedures, seven figures, and one table and can be found with this article online at http://dx.doi.org/10.1016/j.molcel.2014.05.001.

AUTHOR CONTRIBUTIONS

E.R., K.J.P., and L.A.P. designed the study, interpreted data, and wrote the paper. E.R. planned and executed the majority of experiments. E.R., V.H.O., F.L., and M.W. generated cell lines. F.L. performed clonogenic assays. G.L.D. generated baculoviruses. L.A.P. and K.J.P. supervised the project. V.H.O. and F.L. contributed equally to this work.

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