

Supplementary Information

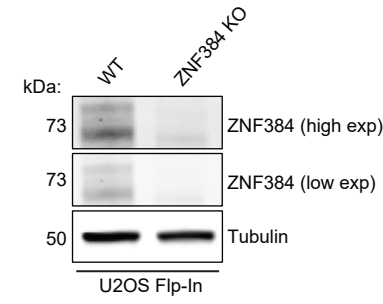
Zinc finger protein ZNF384 is an adaptor of Ku to DNA during classical non-homologous end-joining

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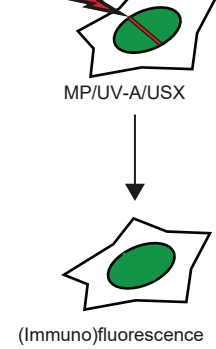
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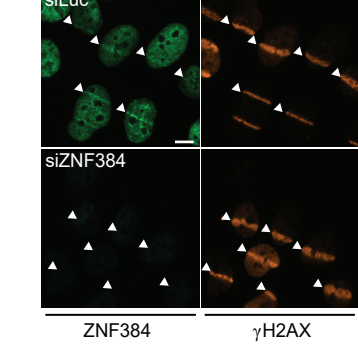
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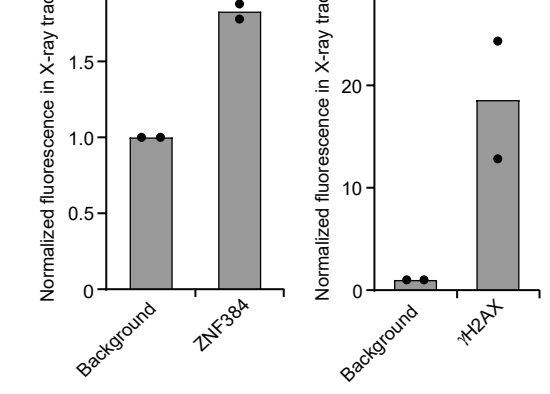
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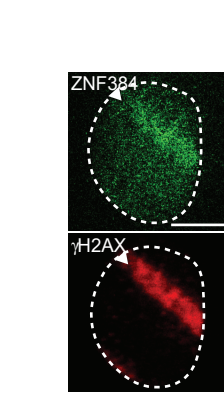
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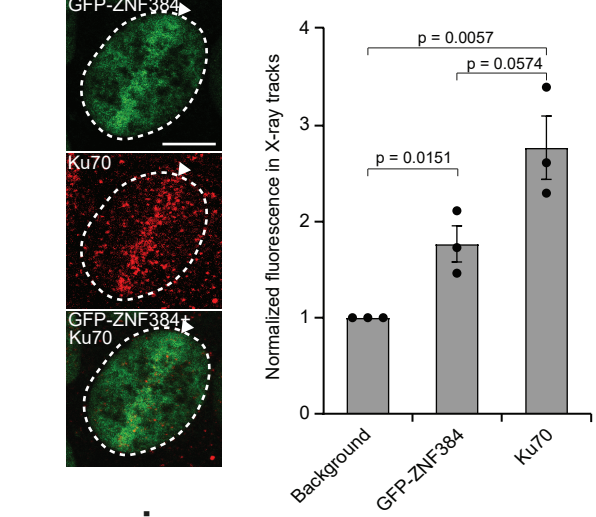
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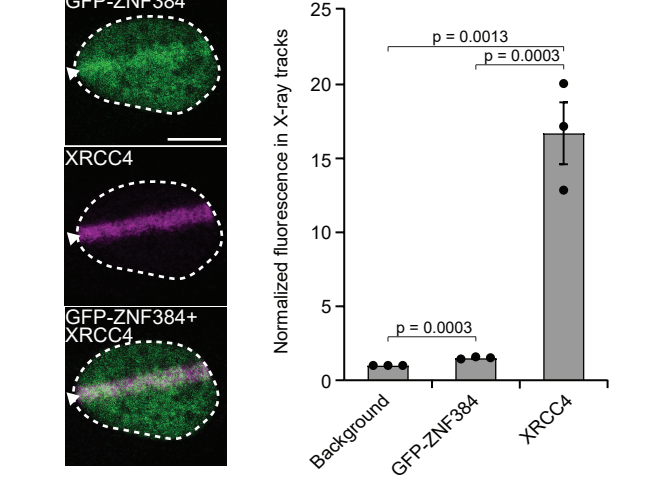
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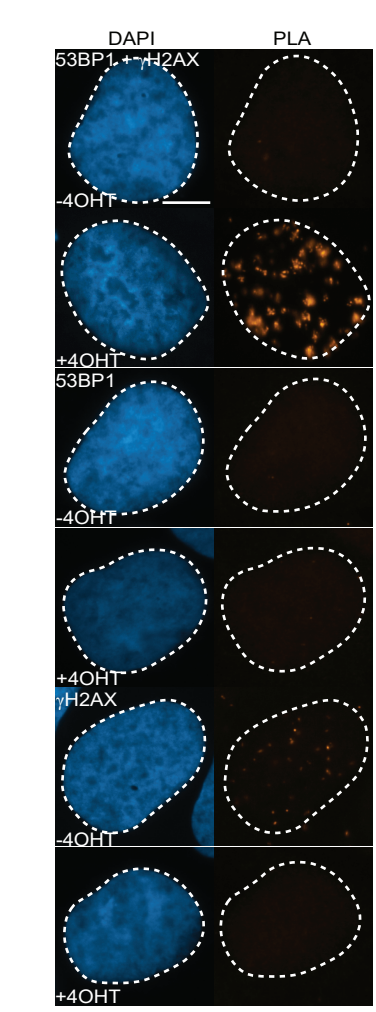
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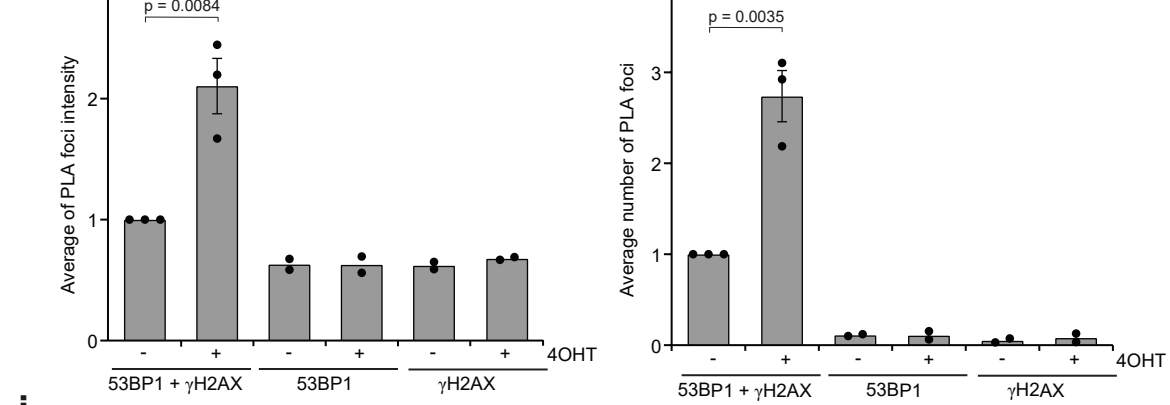
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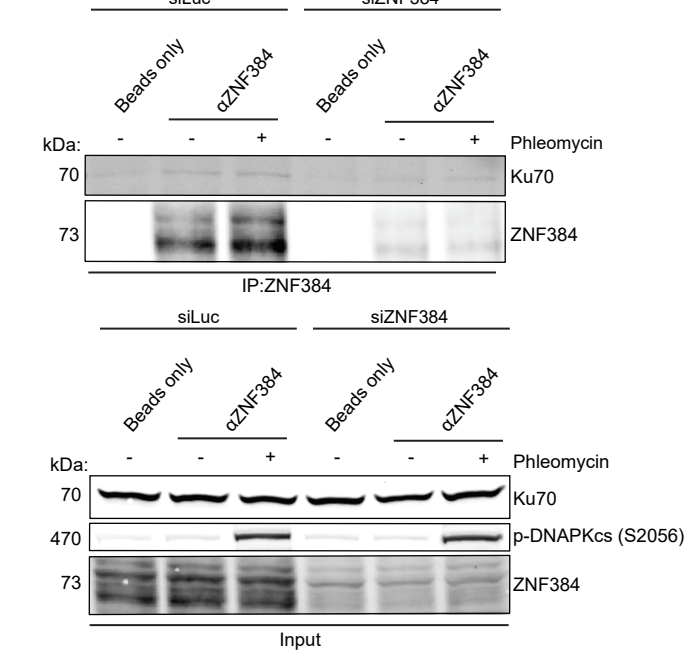
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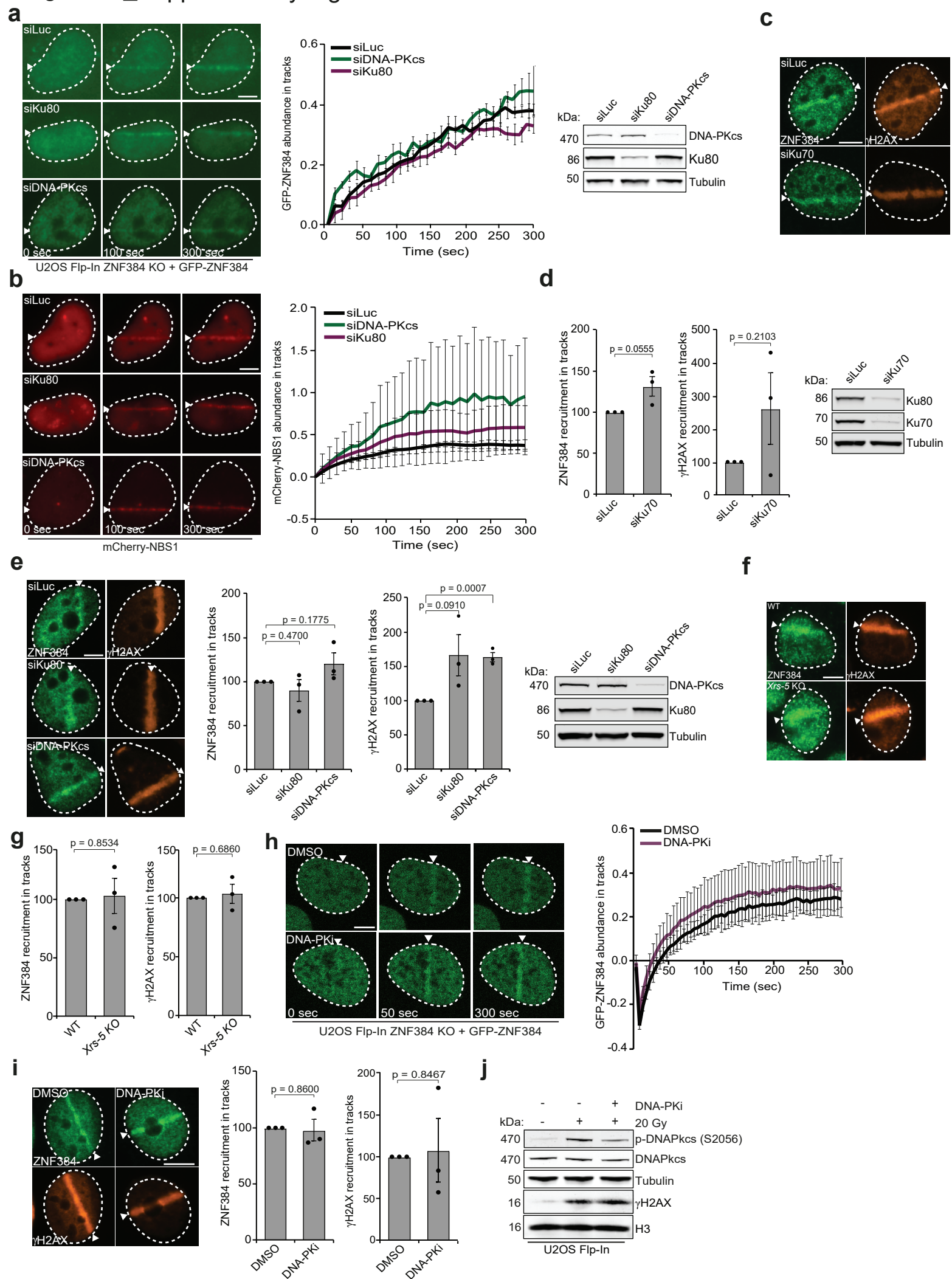


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Supplementary Fig. 1 – related to Fig. 1. ZNF384 is recruited to DNA damage sites (A)

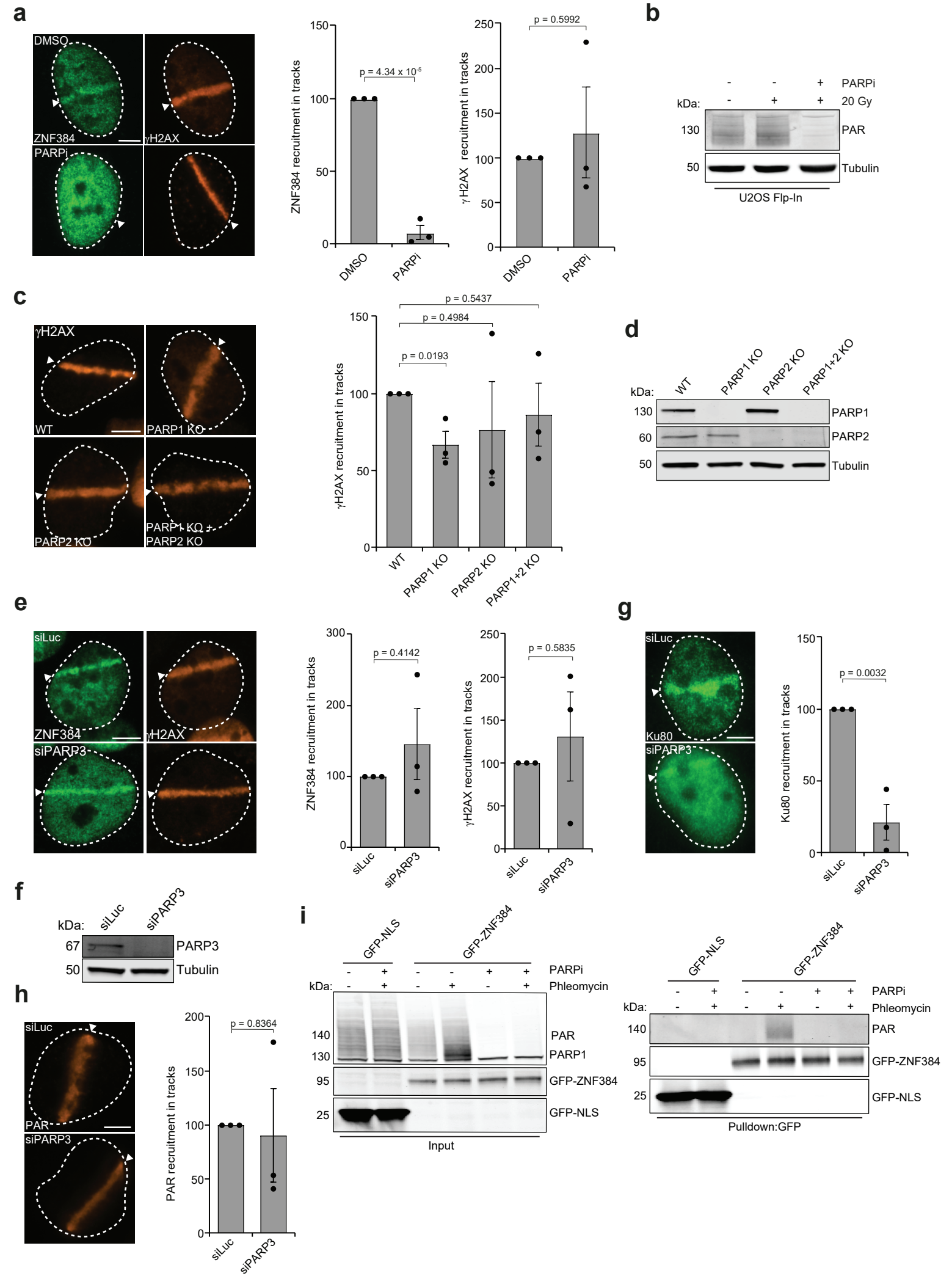
Western blot analysis of ZNF384 expression in cells from Figure 1A. Tubulin is a loading control. Data shown represent 2 independent experiments. (B) Schematic representation of the laser micro-irradiation approach to study protein accumulation at sites of DNA damage. An 800 nm multiphoton (MP) laser, 365 nm UV-A laser or Ultra-soft X-ray (USX) irradiation was used. (C) Representative images of two independent experiments of the accumulation of ZNF384 at γ H2AX-marked 365 nm UV-A tracks in cells transfected with the indicated siRNAs. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. (D) Accumulation of endogenous ZNF384 at γ H2AX-marked DNA damage inflicted by USX irradiation in U2OS Flp-In/T-Rex cells expressing doxycycline (dox)-inducible GFP-ZNF384. Cells were fixed and immunostained 5 minutes after USX irradiation. White triangles indicate irradiated regions. (E) Quantification of ZNF384 and γ H2AX accumulation in cells from D. The mean of at least 40 cells acquired in 2 independent experiments is shown. Data were normalized to the nuclear background outside the irradiated area, which was set to 1. (F) Accumulation of GFP-ZNF384 at sites of Ku70-marked DNA damage inflicted by USX irradiation in U2OS Flp-In/T-Rex cells expressing doxycycline (dox)-inducible GFP-ZNF384. Cells were fixed and immunostained 5 minutes after laser micro-irradiation. White triangles indicate irradiated regions. (left panel). Quantification of ZNF384 and Ku70 is presented as the $\pm$ SEM of >45 cells acquired in 3 independent experiments. Data were normalized to the nuclear background outside the irradiated area, which was set to 1 (right panel). P-values were calculated using the two-tailed unpaired Student's *t* test. (G) As in F, but for GFP-ZNF384 and XRCC4. Quantification of ZNF384 and XRCC4 is presented as the $\pm$ SEM of 60 cells acquired in 3 independent experiments. P-values were calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. (H) PLA of 53BP1 and ZNF384 and γ H2AX in AsiSI-ER-U2OS cells treated with 4-OHT for DSB induction. PLA foci were scored after 5 hours of DSB induction. (I) Quantification of H. PLA foci formation and foci intensity from >200 cells acquired in 2-3 independent experiments are shown. Statistical significance was calculated with the two-tailed Student's *t* test, assuming unequal variances. (J) Immunoprecipitation (IP) of endogenous ZNF384 from 500 μ M Phleomycin treated U2OS cells transfected with the indicated siRNAs. Control IP contained beads only. Blots were probed for ZNF384 and Ku70. Data shown represent 2 independent experiments. Scale bar 5 μ m, except for C in which scale bar is 10 μ m. Source data are provided as Source Data file.



Supplementary Fig. 2 – related to Fig. 1. ZNF384 is recruited to DNA damage sites independent of Ku70/Ku80 and DNA-PKcs

(A) Recruitment of GFP-ZNF384 to 365 nm UV-A tracks in BrdU-sensitized U2OS Flp-In/T-Rex *ZNF384* KO cells. White triangles indicate irradiated regions (left panel). Quantification of the data is plotted on a time scale as relative abundance in tracks. The graph represents the mean $\pm$ SEM of >40 cells acquired in 3 independent experiments (middle panel). Western blot analysis of Ku80 and DNA-Pkcs expression. Tubulin is a loading control. Data shown represent 2 independent experiments (right panel). (B) As in A, except for mCherry-NBS1. (C) Accumulation of endogenous ZNF384 at 365 nm UV-A tracks in BrdU-sensitized U2OS cells following transfection with siLuc and siKu70. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX was used as a DNA damage marker. (D) Quantification of endogenous ZNF384 and γ H2AX levels in laser tracks in cells from D is presented as the mean $\pm$ SEM of >180 cells acquired in 3 independent experiments (left panel). Western blot analysis of Ku70 and K80 expression in cells. Tubulin is a loading control. Data shown represent 2 independent experiments (right panel). (E) Accumulation of endogenous ZNF384 at 365 nm UV-A tracks in BrdU-sensitized U2OS cells following transfection with siLuc, siKu80 and siDNA-PKcs. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX was used as a DNA damage marker (left panel). Quantification of endogenous ZNF384 and γ H2AX levels in laser tracks is presented as the mean $\pm$ SEM of >180 cells acquired in 3 independent experiments (middle panel). Western blot analysis of Ku80 and DNA-Pkcs expression. Tubulin is a loading control. Data shown represent 2 independent experiments (right panel). (F) Accumulation of endogenous ZNF384 at 365 nm UV-A tracks in BrdU-sensitized wildtype (WT) and *xrs-5* KO hamster cells. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX was used as a DNA damage marker. (G) Quantification of F. Endogenous ZNF384 and γ H2AX levels in laser tracks are presented as the mean $\pm$ SEM of >150 cells acquired in 3 independent experiments. (H) Kinetics of GFP-ZNF384 recruitment to 800 nm laser tracks in U2OS Flp-In/T-Rex *ZNF384* KO cells treated for 1 hour with DNA-PKcs inhibitor prior to laser micro-irradiation. White triangles indicate irradiated regions (left panel). Quantification of GFP-ZNF384 in laser tracks is presented as the mean $\pm$ SD from 2 independent experiments (right panel). (I) Accumulation of endogenous ZNF384 at 365 nm UV-A tracks in BrdU-sensitized U2OS cells treated for 1 hour with DNA-PKcs inhibitor prior to laser micro-irradiation. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX was used as a DNA damage marker (left panel). Quantification of endogenous ZNF384 and γ H2AX levels in laser tracks is presented as the mean $\pm$ SEM of >180 cells acquired in 3 independent

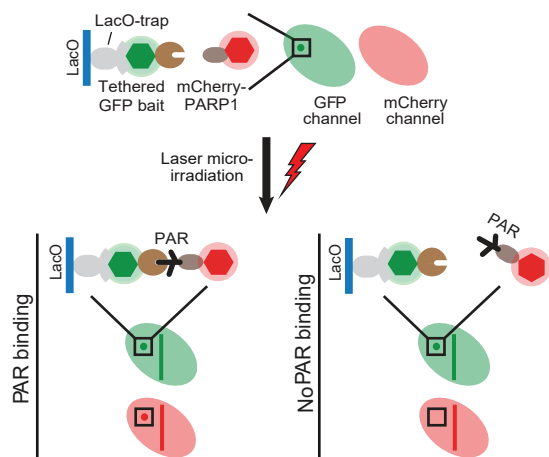
experiments (right panel). Statistical significance was calculated with the two-tailed Student's *t* test, assuming unequal variances. Scale bar 5 μm . (J) Western blot analysis of p-DNA-PKcs (S2056) levels in IR- and DNA-PKcs inhibitor-treated cells used in I. Cells were treated with DNA-PKi 1 hour before IR exposure. Blots were probed for p-DNA-PKcs (S2056), DNA-PKcs, γH2AX . Tubulin and H3 are loading controls. Source data are provided as Source Data file.



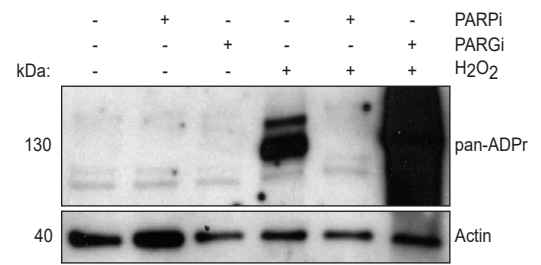
Supplementary Fig. 3 – related to Fig. 1. ZNF384 is recruited to DNA damage sites via

PARP1/PAR (A) Accumulation of endogenous ZNF384 at 365 nm UV-A tracks in BrdU-sensitized U2OS cells treated for 1 hour with PARPi prior to laser micro-irradiation. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX was used as a damage marker (left panel). Quantification of endogenous ZNF384 and γ H2AX levels in laser tracks is presented as the mean $\pm$ SEM of >200 cells acquired in 3 independent experiments (right panel). (B) Western blot analysis of PAR levels in IR treated and PARPi treated cells used in Figure 2A and Figure S3A. Cells were treated with PARPi 1hr before the IR treatment. Tubulin is a loading control. Data shown represent 2 independent experiments. (C) γ H2AX accumulation at 365 nm UV-A tracks 10 minutes after DNA damage induction in BrdU-sensitized wildtype, PARP1 KO, PARP2 KO and PARP1/PARP2 KO U2OS cells. White triangles indicate irradiated regions (left panel). The mean $\pm$ SEM of >180 cells from 3 independent experiments is shown (right panel). (D) Western blot analysis of PARP1 and PARP2 expression in cells from Figure 2B and Figure S3C. Tubulin is a loading control. Data shown represent 2 independent experiments. (E) Accumulation of endogenous ZNF384 at 365 nm UV-A tracks in BrdU-sensitized U2OS cells transfected with the indicated siRNAs. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX was used as a damage marker (left panel). Quantification of endogenous ZNF384 and γ H2AX levels in laser tracks is presented as the mean $\pm$ SEM of > 200 cells acquired in 3 independent experiments (right panel). (F) Western blot analysis of PARP3 expression in cells from Figure S3E. Tubulin is a loading control. Data shown represent 2 independent experiments. (G) Accumulation of endogenous Ku80 at 365 nm UV-A tracks in BrdU-sensitized U2OS cells transfected with the indicated siRNAs. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions (left panel). Quantification of endogenous Ku80 levels in laser tracks is presented as the mean $\pm$ SEM of >120 cells acquired in 3 independent experiments (right panel). (H) As in G, except for PAR. (I) Pull-downs of GFP-ZNF384 and GFP-NLS under denaturing conditions in untreated and phleomycin (Phleo)-treated U2OS Flp-In/T-Rex cells expressing doxycycline (dox)-inducible GFP-ZNF384 or GFP-NLS. Cells were also treated with PARPi (Olaparib) for 1 hour prior to the phleomycin treatment. Blots were probed for PAR, PARP1 and GFP. Data shown represent 2 independent experiments. Statistical significance was calculated with the two-tailed Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.

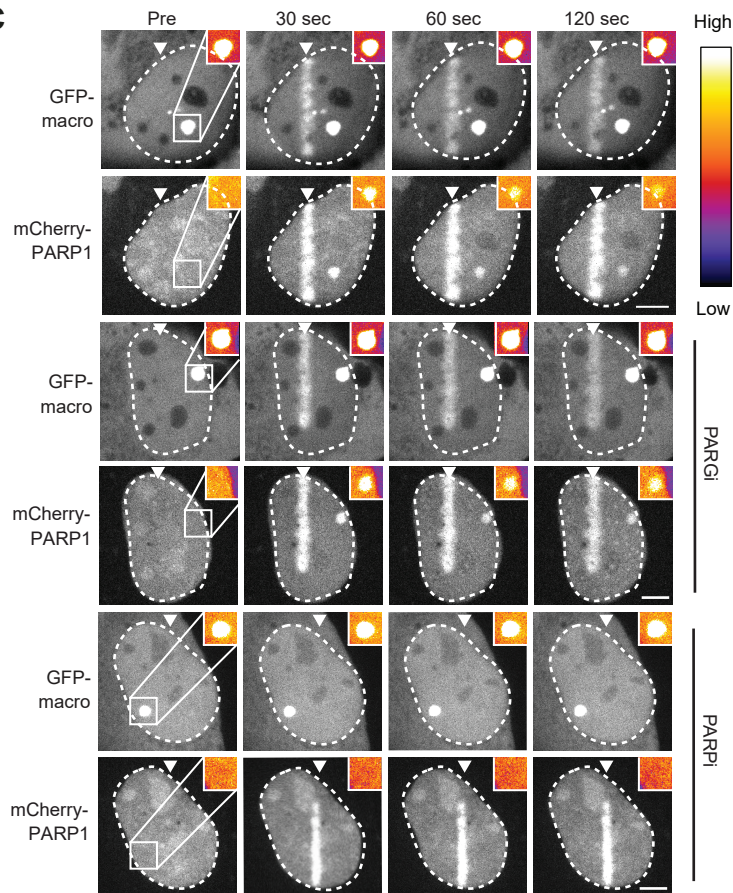
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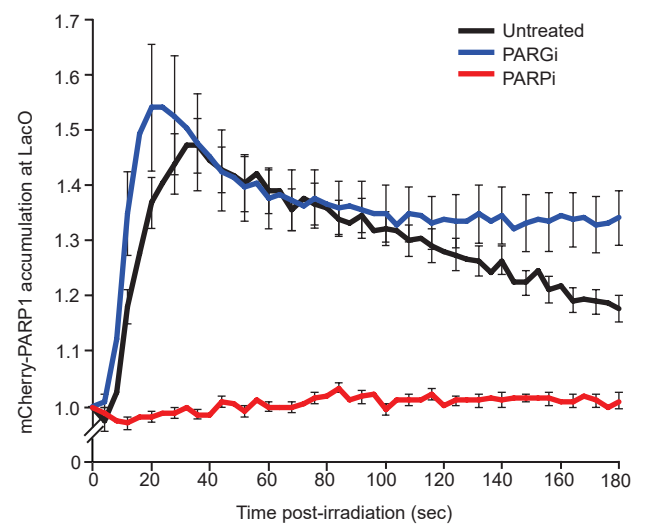
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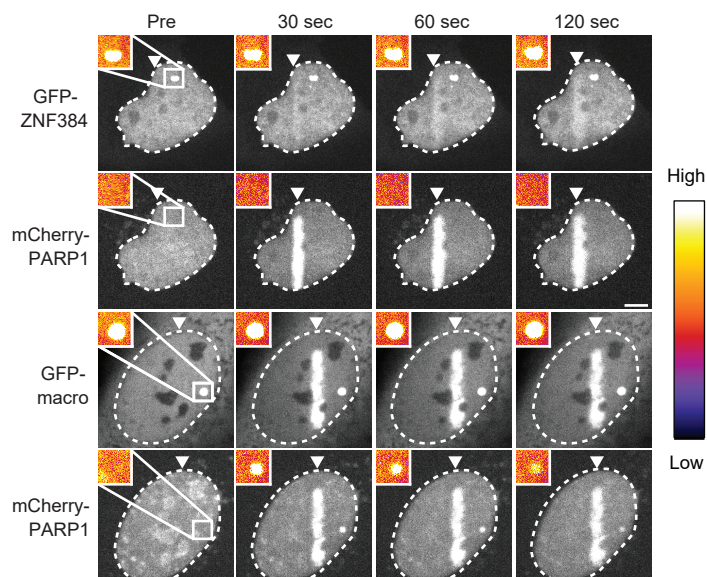
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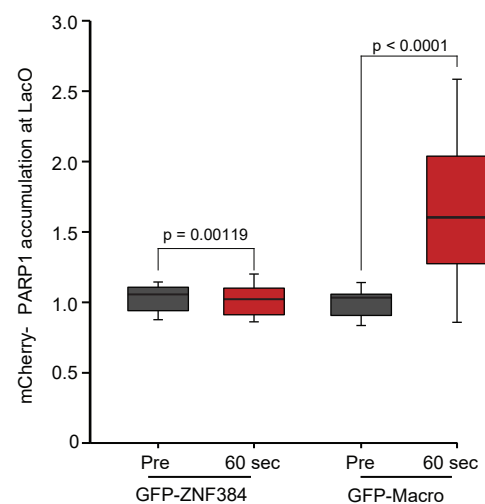
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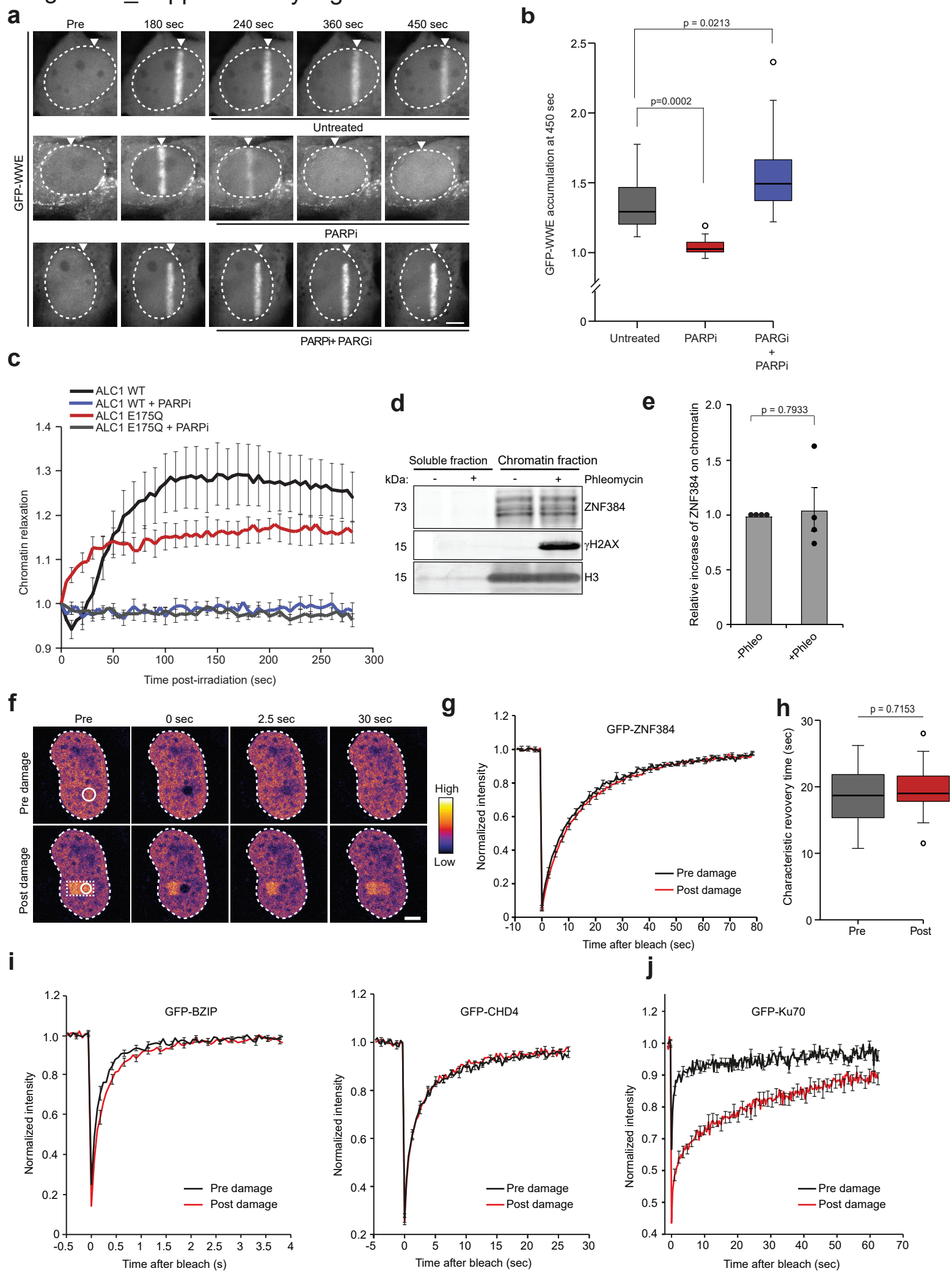


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Supplementary Fig. 4 – related to Fig. 2. ZNF384 is recruited to DNA damage sites via PARP1/PAR dependent chromatin unfolding

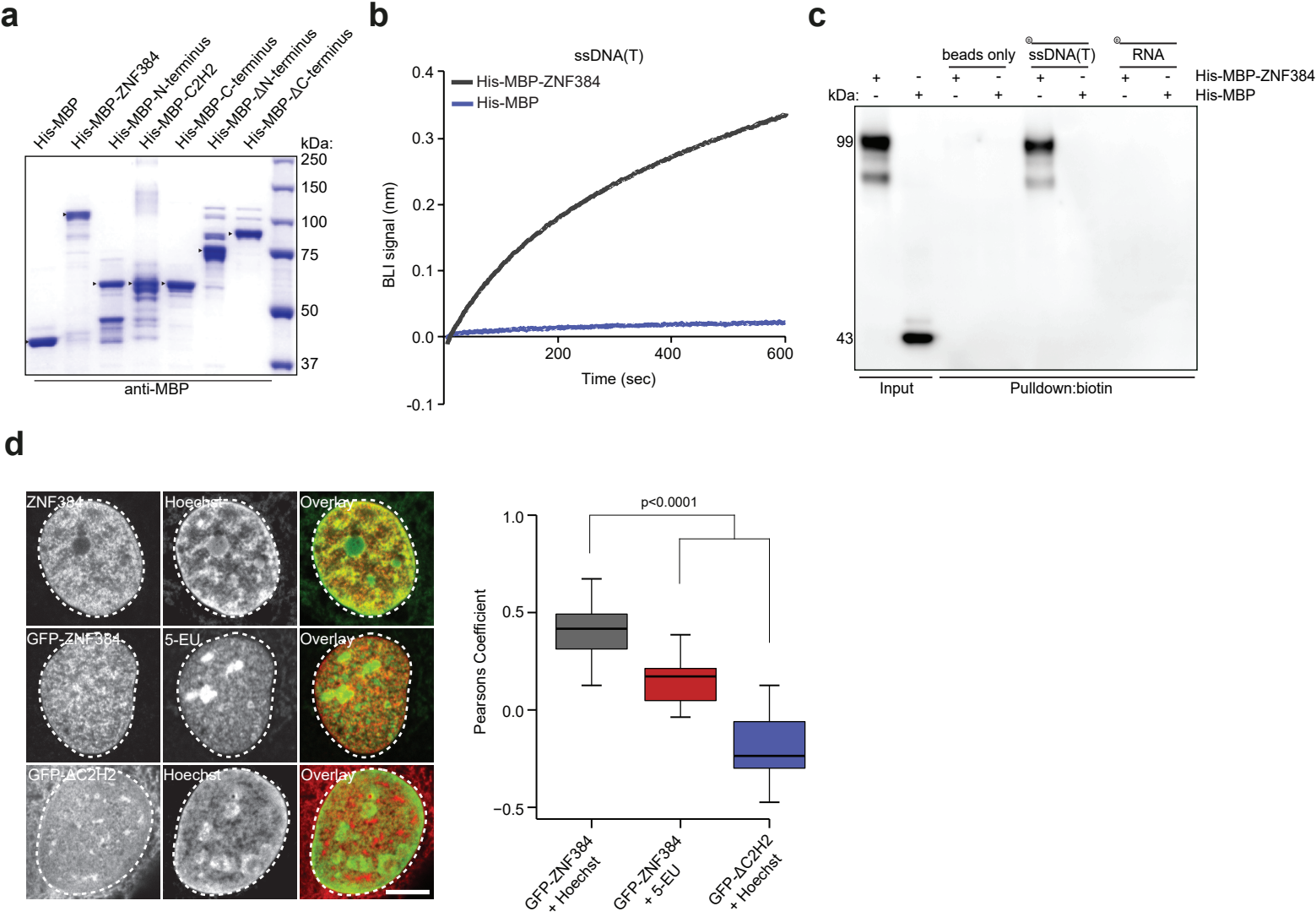
(A) Schematic of the fluorescence three-hybrid assay (F3H). Prior to laser irradiation, a GFP-tagged bait protein which is tethered to a genomically integrated LacO array through a LacI-GFP binding protein (LacO-trap) does not show enrichment of mCherry-PARP1 at the LacO array. After laser micro-irradiation, mCherry-PARP1 diffuses away from the site of damage in a PARylated state. If the tethered GFP-tagged bait protein can interact with PARylated PARP1 (bottom left), mCherry-PARP1 will enrich at the LacO array. If the tethered protein of interest does not interact with the tethered bait protein (bottom right), there is no enrichment of mCherry-PARP1 at the LacO array. (B) Western blot analysis of PAR levels in H₂O₂ and PARPi or PARGi treated cells used in Figure S4D. Cells were treated with 2 mM H₂O₂ for 10 min to induce PARylation. Blot was probed with panADPr. Actin is a loading control. Blots are representative of 3 independent replicates. (C) Fluorescence images of *in situ* PAR binding three-hybrid assays. LacI-GFP-macroH2A1.1 (GFP-macro) was tethered to a LacO array in Hoechst-sensitized cells co-expressing mCherry-PARP1 treated for 1 hour with PARPi or PARGi prior to 405 nm laser micro-irradiation. White triangles indicate irradiated regions. Inset shows the magnified LacO array. Insets are pseudocolored according to the look-up table displayed on the right. Scale bar 5 μ m. (D) The mean intensity of mCherry signal at the LacO array from 19-20 cells was quantified pre damage and 60 seconds post damage. Data shows mean intensity of the mCherry signal at the LacO array $\pm$ SEM. Cells were treated for 1 hour with PARPi or PARGi prior to micro-irradiation. (E) Fluorescence images of *in situ* PAR binding three-hybrid assays. GFP-ZNF384 or GFP-macro was tethered to a LacO array in Hoechst-sensitized cells co-expressing mCherry-PARP1 prior to 405 nm laser micro-irradiation. White triangles indicate irradiated regions. Inset shows the magnified LacO array. Insets are pseudocolored according to the look-up table displayed on the right. (F) The mean intensity of mCherry signal at the LacO array from 12-15 cells was quantified pre damage and 60 seconds post damage. The boxplot limits correspond to the 25th and 75th percentiles and the center line in the box indicates the median value. The whiskers extend 1.5 times the interquartile range. P-values were calculated using the two-tailed Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.



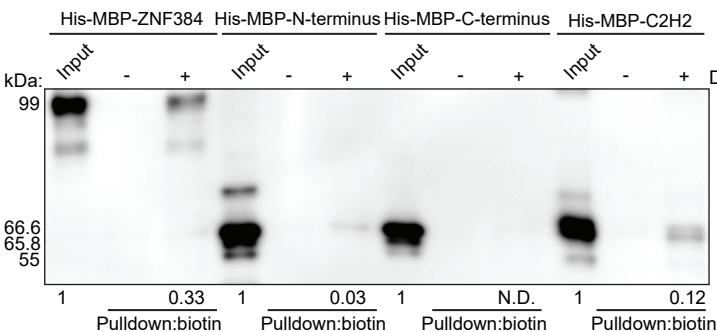
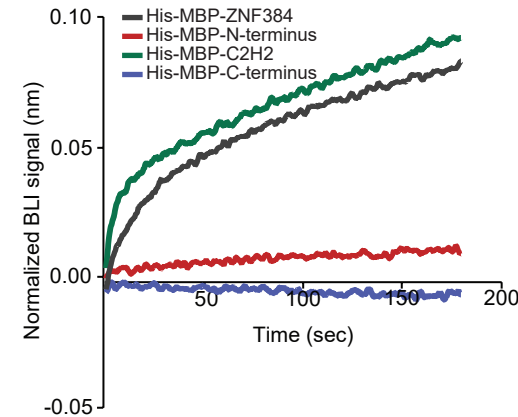
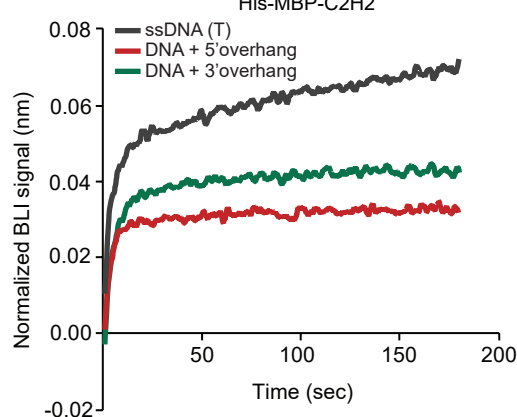
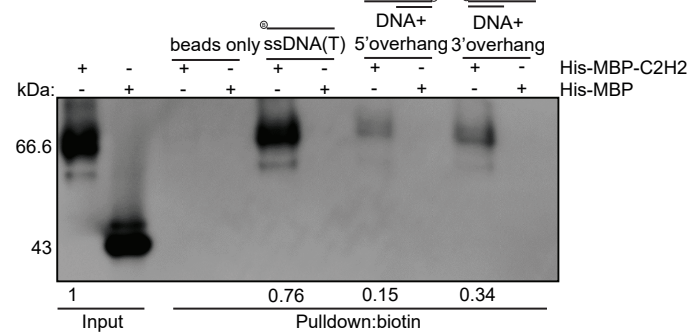
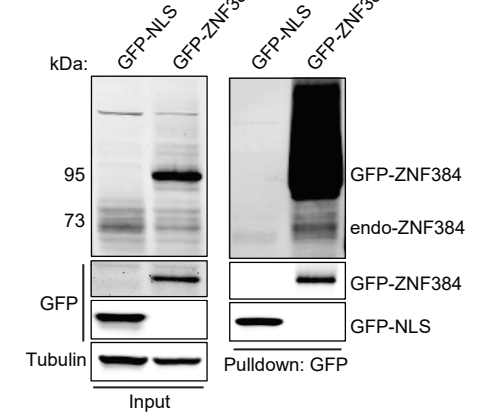
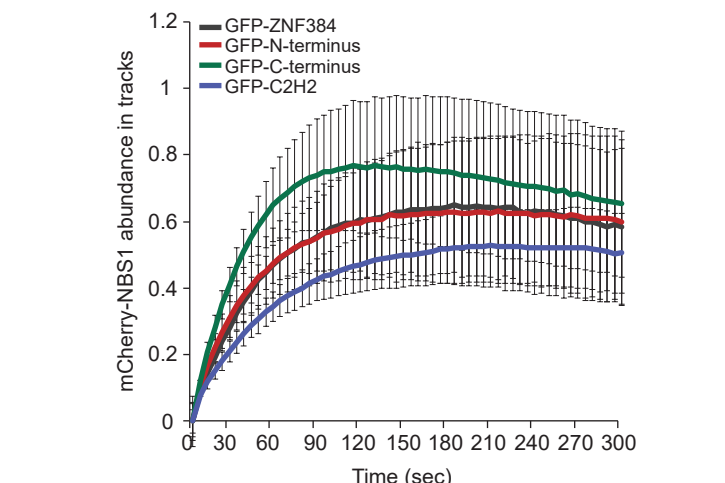
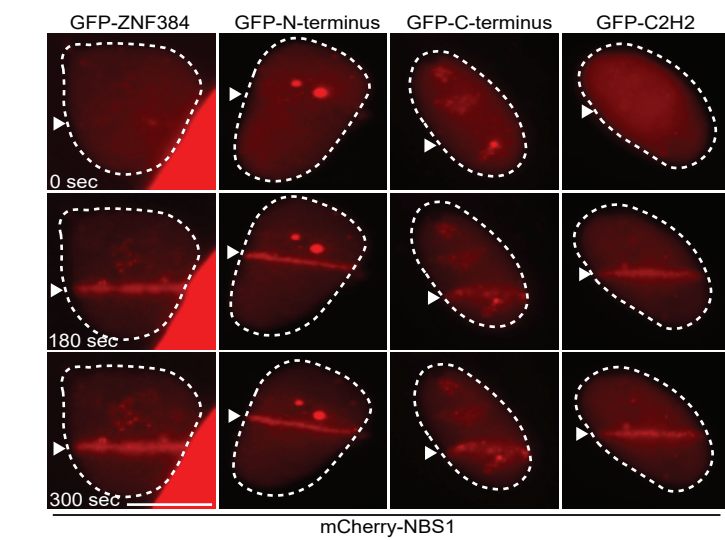
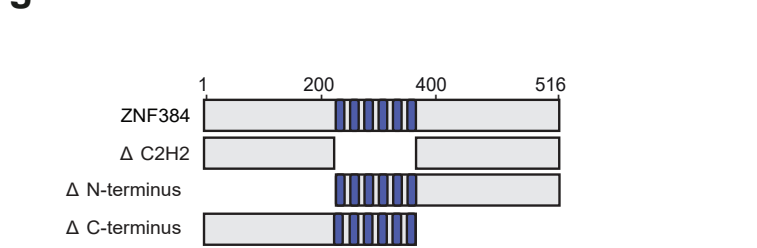
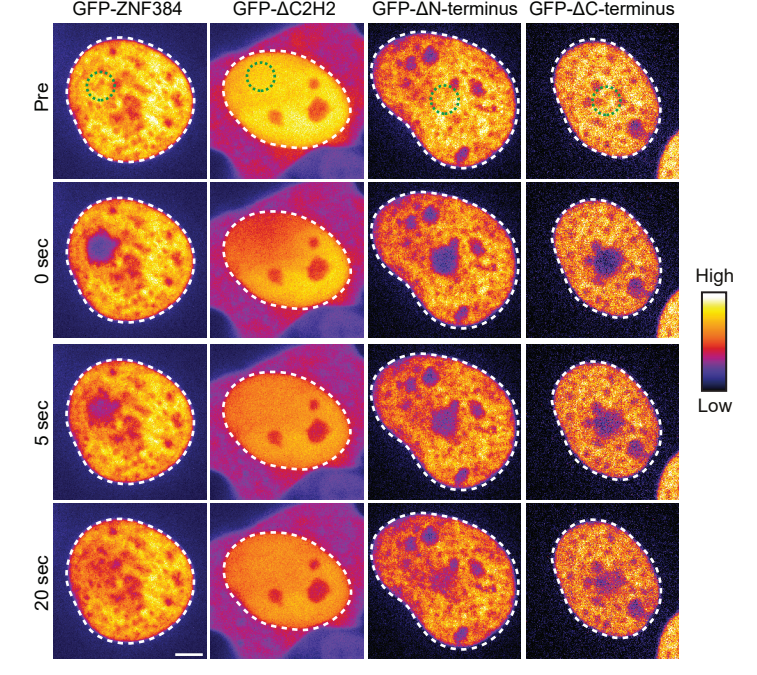
Supplementary Fig. 5 – related to Fig. 2. ZNF384 is recruited to DNA damage sites via PARP1/PAR dependent chromatin unfolding.

(A) Confocal images showing accumulation of GFP-WWE at sites of 405 nm laser micro-irradiation in Hoechst-sensitized U2OS cells. Cells were left untreated or treated with PARPi or PARPi and PARGi 240 seconds after DNA damage induction. White triangles indicate irradiated regions. Scale bar 5 μ m. (B) Boxplot showing the accumulation of GFP-WWE at 450 seconds post irradiation from cells in A. Boxplots show the first, median and third quartiles from a representative of 3 independent replicates. The whiskers extend 1.5 times the interquartile range. P-values were calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. (C) Chromatin relaxation was measured for each of the overexpression conditions from Figure 2G. The mean $\pm$ SEM from 13-16 cells from a representative of 3 independent experiments is shown. (D) Western blot analysis of the indicated proteins in soluble and chromatin fractions from untreated and phleomycin treated U2OS cells. H3 is the loading control. γ H2AX is a DNA damage marker. A representative experiment is shown. (E) Quantification of ZNF384 levels on chromatin in cells from D. H3 is a loading control, which was used for normalization of ZNF384 levels on chromatin. The mean $\pm$ SEM from 4 independent experiments is shown. P-values were calculated using the Student's *t* test, assuming unequal variances. (F) Representative images of Hoechst-sensitized U2OS Flp-In/T-Rex *ZNF384* KO cells in which FRAP measurements were performed to assess the local turnover of GFP-ZNF384 at DNA damage sites. DNA damage was induced in the region indicated with a dashed line using 405 laser micro-irradiation. Subsequent FRAP was induced in a subarea within the damaged region, as indicated with an unbroken line. Images are pseudocolored according to the look-up table displayed on the right. Scale bar 4 μ m. (G) Normalized FRAP curves from F. Data show mean $\pm$ SEM from 14 cells per condition from a representative of 3 independent replicates (H) Boxplot showing the characteristic recovery times estimated from the FRAP curves shown in F. The boxplot limits correspond to the 25th and 75th percentiles and the center line in the box indicates the median value. The whiskers extend 1.5 times the interquartile range. P-values were calculated using the two-tailed paired Student's *t* test. (I) Normalized FRAP curves of the GFP-tagged DNA binding domain BZIP from the transcription factor C-EBPa and DNA damage induction in U2OS cells (left panel). Normalized FRAP curves of GFP-tagged CHD4 and DNA damage induction in U2OS cells (right panel). (J) Normalized FRAP curves of GFP-Ku70 and DNA damage induction in RPE1-hTERT cells. The mean $\pm$ SD is shown from 14 cells per condition from a representative of 2 independent replicates. Source data are provided as Source Data file.

Singh et al_Supplementary Fig. 6



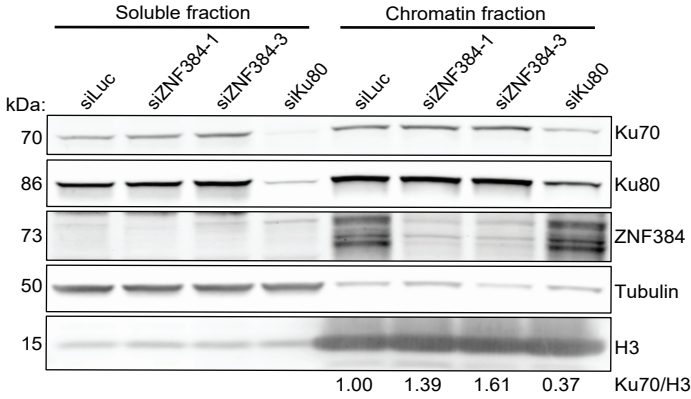
Supplementary Fig. 6 – related to Fig. 3. ZNF384 is recruited to sites of DNA damage in manner dependent on its ability to bind DNA (A) SDS-PAGE analysis of the indicated purified His-MBP-tagged proteins. Data shown represent 2 independent experiments. (B) DNA binding by His-MBP-ZNF384 and His-MBP to biotinylated T-rich ssDNA (ssDNA(T)) by BLI. (C) Pulldowns of the indicated biotinylated DNA or RNA substrates in the presence of His-MBP-ZNF384 or His-MBP. Blots were probed for MBP. Data shown represent 2 independent experiments. (D) Representative images of U2OS Flp-In/T-Rex *ZNF384* KO cells expressing either GFP-tagged full-length ZNF384 or Δ C2H2. Cells were co-stained with Hoechst or 5-Ethynyl Uridine (5-EU) to assess their colocalization with DNA or RNA (left panel). The levels of colocalization between ZNF384 or Δ C2H2 and DNA or RNA were assessed using the Pearson coefficient (right panel). The mean $\pm$ SD is shown from >23 cells per condition. The boxplot limits correspond to the 25th and 75th percentiles and the center line in the box indicates the median value. The whiskers extend 1.5 times the interquartile range. For GFP-ZNF384 + Hoechst vs GFP-ZNF384 + 5-EU, $p = 7.1156 \times 10^{-7}$. For GFP-ZNF384 + Hoechst vs GFP- Δ C2H2 + Hoechst, $p = 4.027 \times 10^{-12}$. P-values were calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. Source data are provided as Source Data file.

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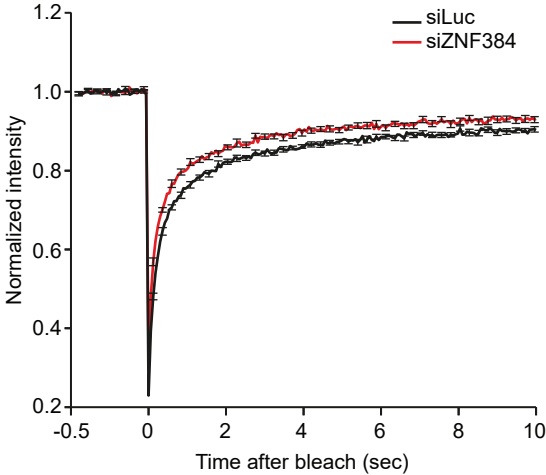
Supplementary Fig. 7 – related to Fig. 3. ZNF384 is recruited to sites of DNA damage via its C2H2 domain

(A) DNA pulldowns of biotinylated DNA with a 3'overhang in the presence of the indicated ZNF384 proteins. Blots were probed for MBP. For each protein, input signals were used for normalization of the pulldown signals. The mean of 2 independent experiments is indicated below the blot. A representative experiment is shown. N.D. = not detectable. (B) DNA binding by the indicated ZNF384 proteins to DNA with a 3'overhang as measured by BLI. Quantification of the data is plotted on a time scale and normalized to His-MBP alone. (C) DNA pulldowns of biotinylated T-rich ssDNA (ssDNA(T)), biotinylated DNA with a 5'overhang or biotinylated DNA with a 3'overhang in the presence of His-MBP-C2H2 or His-MBP (control). Blots were probed for MBP. His-MBP-C2H2 pulldown signals were normalized to that in the input, which was set to 1. The mean from 3 independent experiments is indicated below the blot. His-MBP was not detectable in pulldowns. A representative experiment is shown. (D) DNA binding of His-MBP-C2H2 to biotinylated T-rich ssDNA (ssDNA(T)), biotinylated DNA with a 5'overhang or biotinylated DNA with a 3'overhang as measured by BLI. Quantification of the data is plotted on a time scale and normalized to His-MBP (control). (E) Pulldowns of the indicated GFP-fusion proteins in U2OS Flp-In/T-Rex cells. Blots were probed for GFP, ZNF384 and Tubulin. Data shown represent 2 independent experiments. (F) Live cell imaging of mCherry-NBS1 to 365 nm UV-A tracks in BrdU-sensitized *ZNF384* KO U2OS Flp-In/T-Rex cells. mCherry-NBS1, which was co-expressed with GFP-ZNF384 proteins, served as a DNA damage marker for Figure 3D. Representative images are shown. White triangles indicate irradiated regions. Scale bars 10 μ m (upper panel). Quantification of the data is shown as mean $\pm$ SEM from 30-40 cells (lower panel). (G) Schematic representation of full-length ZNF384 and three deletion mutants (Δ C2H2, Δ N-terminus and Δ C-terminus). (H) Representative images of cells from Figure 3E in which the FRAP measurements are performed to assess the local dynamics of the indicated GFP-ZNF384 constructs. FRAP area is indicated with a dashed line. Images are pseudocolored according to the look-up table displayed on the bottom. Scale bar: 4 μ m. Source data are provided as Source Data file.

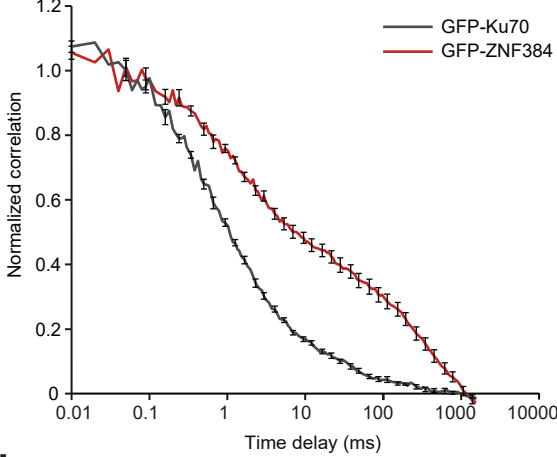
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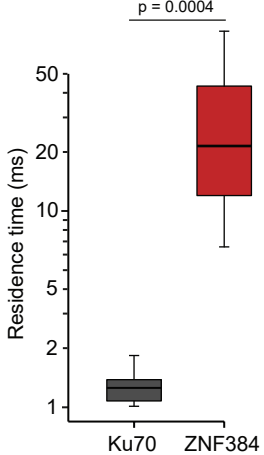
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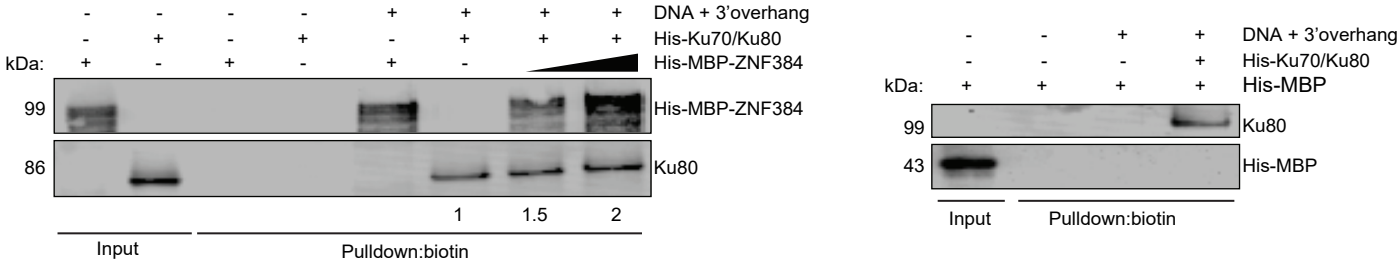
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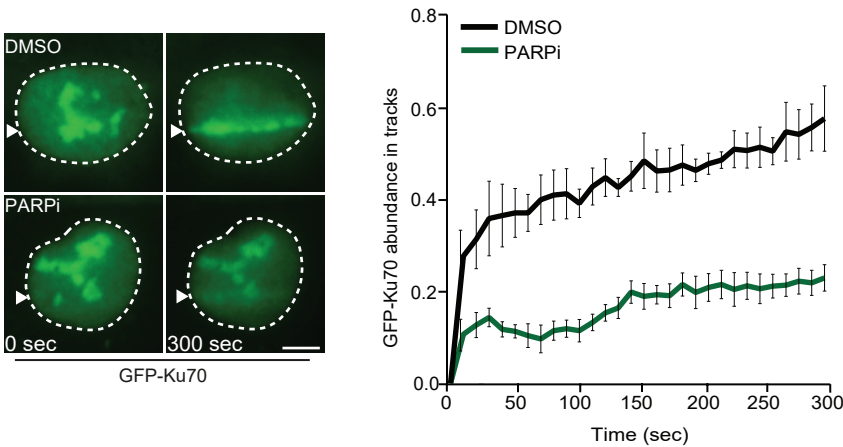
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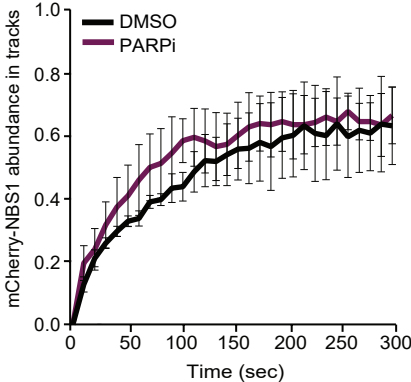
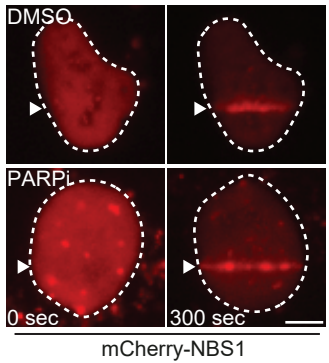
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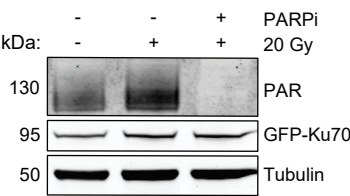
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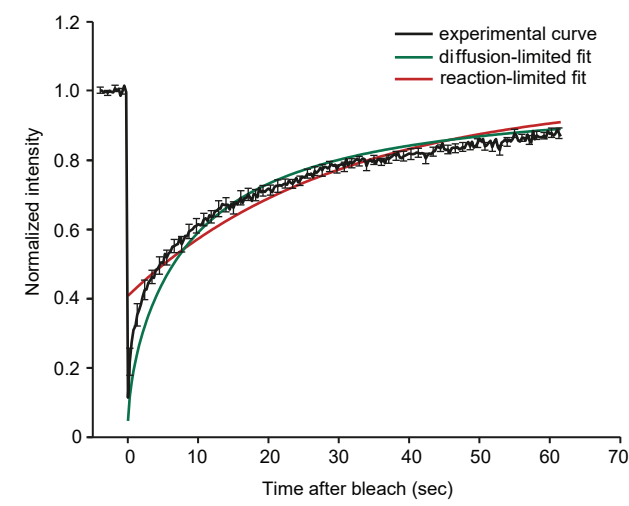
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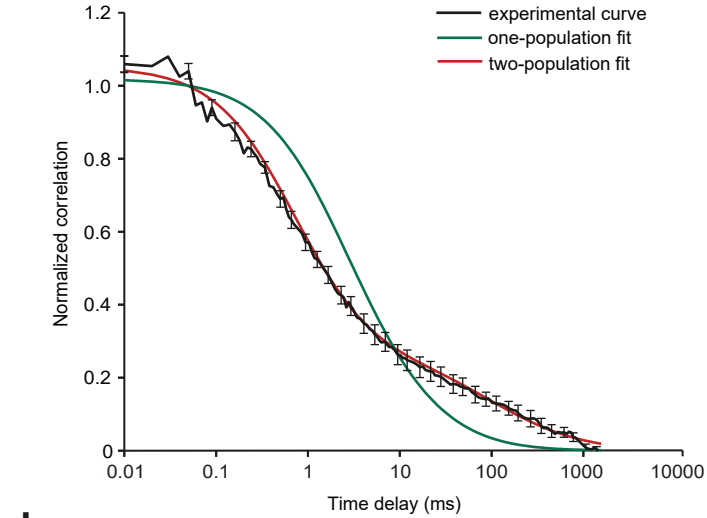
Supplementary Fig. 8 – related to Fig. 4. ZNF384 modulates the loading of Ku70/Ku80 at DNA damage sites

(A) Western blot analysis of the indicated proteins in soluble and chromatin fractions from U2OS cells. Blots were probed for the indicated proteins. H3 and Tubulin are loading controls. A representative experiment is shown. Ku70 levels in chromatin were first normalized to H3 levels. Ku70/H3 ratios were then normalized to that for siLuc, which was set to 1. Quantifications are shown as the mean from 2 independent experiments. (B) Normalized FRAP curves of GFP-Ku70 in RPE-hTERT cells transfected with the indicated siRNAs in the absence of DNA damage. The mean $\pm$ SD is shown from 20-21 cells per condition. (C) Normalized FCS autocorrelation curves of GFP-Ku70 in RPE1-hTERT cells and GFP-ZNF384 in U2OS cells in the absence of DNA damage. The mean $\pm$ SEM is shown from 10-16 cells analyzed per condition. (D) Boxplot showing the residence times of GFP-Ku70 and GFP-ZNF384 in RPE1-hTERT and U2OS cells, respectively, as measured by FCS. 10-15 cells were analyzed per condition. The boxplot limits correspond to the 25th and 75th percentiles and the center line in the box indicates the median value. The whiskers extend 1.5 times the interquartile range. P-values were calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. (E) DNA pulldowns of biotinylated DNA with a 3' overhang in the presence of His-Ku70/Ku80, His-MBP-ZNF384 or His-MBP (control) alone or His-Ku70/Ku80 in combination with His-MBP-ZNF384 or His-MBP (control). Blots were probed for MBP and Ku80. Ku80 pulldown signals were normalized to that in the pulldown lacking His-MBP-ZNF384, which was set to 1. The mean from 4 independent experiments is indicated below the blot. His-MBP was not detectable in pulldowns. (F) GFP-Ku70 recruitment to 365 nm UV-A tracks in cells treated with PARPi for 1 hour before laser micro-irradiation. White triangles indicate irradiated regions (left panel). Quantification of the data is presented as the mean $\pm$ SEM of >100 cells acquired in 3 independent experiments (right panel). (G) As in F, except for mCherry-NBS1. (H) Western blot analysis of PAR levels, which likely reflect PARP1 autoPARylation, in phleomycin- and PARPi-treated cells from F and G. Cells were treated with PARPi for 1 hour before IR treatment. Blots were probed for PAR, GFP and Tubulin. Tubulin is a loading control. Data shown represent 2 independent experiments. Statistical significance was calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.

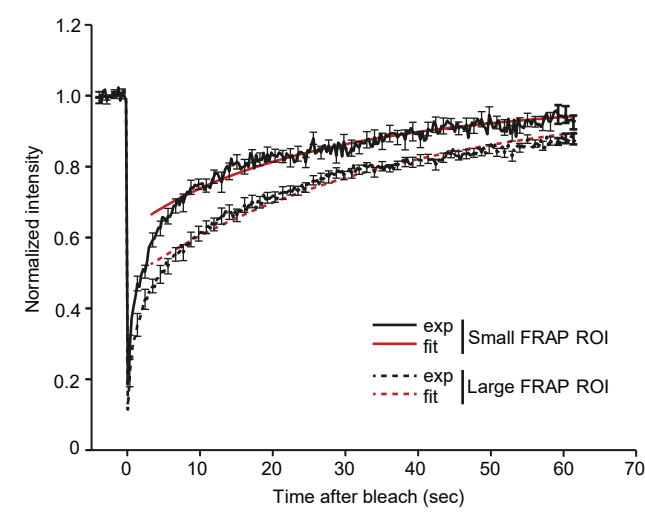
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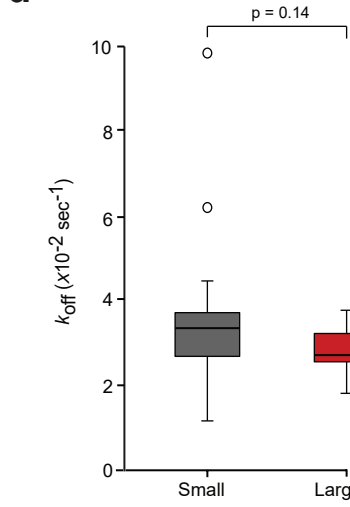
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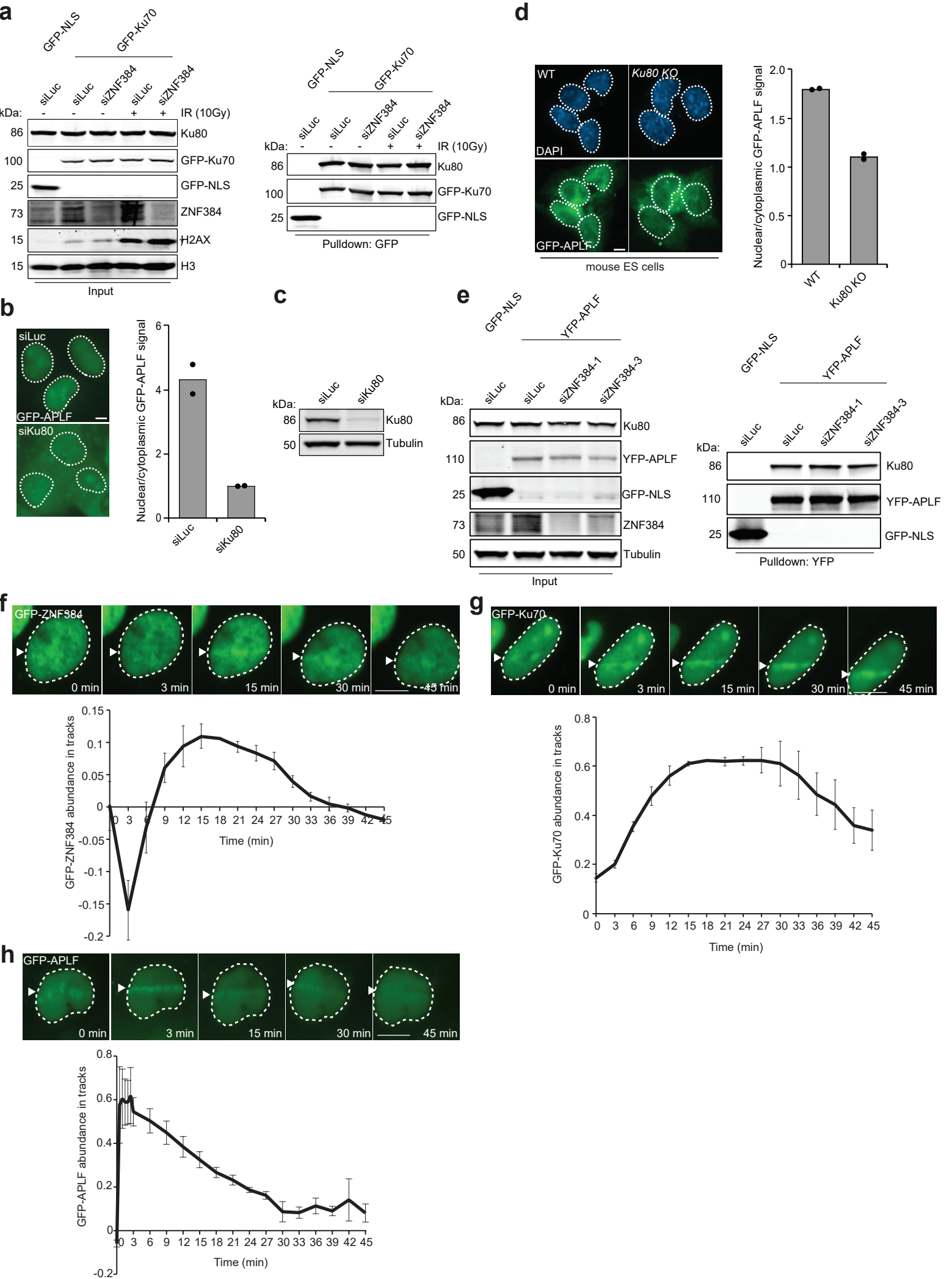
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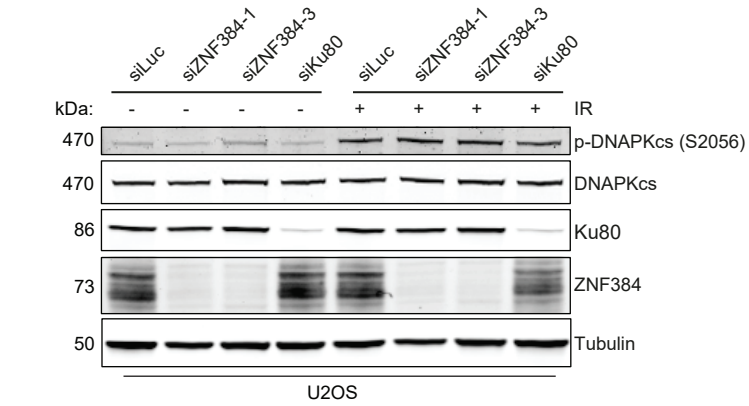
Supplementary Fig. 9 – related to Fig. 4. ZNF384 facilitates the recruitment rather than the retention of Ku70/Ku80 at sites of DNA damage (A) FRAP curves of GFP-Ku70 at the DNA lesions fitted with two alternative models: i) a diffusion-limited model which assumes that Ku interacts only very transiently with DNA at the sites of damage, and ii) a reaction-limited model which is valid if the fluorescence recovery is limited by the long lifetime of the interaction between Ku and the DNA lesions [1]. The mean $\pm$ SEM is shown from 15 cells from a representative of 3 independent experiments is shown. (B) FCS curves of GFP-Ku70 at the DNA lesions fitted with models assuming either one or two population dynamics. Based on the 2-population fit, the fast population displays a characteristic diffusion time of 590 ± 70 μ seconds within the confocal volume. Given that the molecular weight of the GFP-tagged Ku70/Ku80 complex (180 kDa) is ~ 6 times larger than GFP only, and that GFP shows a diffusion time of approximately 300 μ seconds when diffusing through the nucleus [2], the Stokes-Einstein equation predicts that the diffusion time on an unbound Ku70/Ku80 complex should be equal to $300 \times 6^{1/3} = 550$ μ seconds. Therefore, it seems reasonable to assume that the fast population of Ku seen by FCS corresponds to freely diffusing Ku complexes. The mean $\pm$ SEM is shown from 10 cells from a representative of 3 independent experiments. (C) FRAP curves of GFP-Ku70 at the DNA lesions obtained for two different bleaching area and fitted with a reaction-limited model for the timepoints at more than 3 seconds post photobleaching. The mean $\pm$ SEM is shown from 15 cells from a representative of 3 independent experiments is shown. (D) k_{off} parameters estimated from the reaction-limited model for the two different sizes of bleached area from C. The mean $\pm$ SEM is shown from 15 cells from a representative of 3 independent experiments is shown. The boxplot limits correspond to the 25th and 75th percentiles and the center line in the box indicates the median value. The whiskers extend 1.5 times the interquartile range. P-values were calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. Source data are provided as Source Data file.



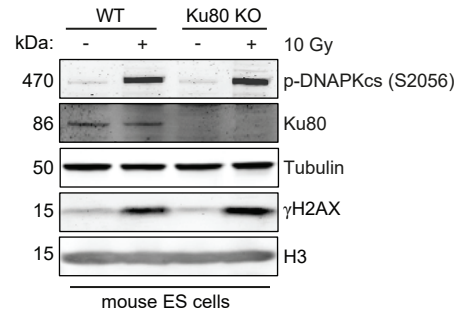
Supplementary Fig. 10 – related to Fig. 5 and 6. ZNF384 is dispensable for cNHEJ complex stability

(A) Pull-downs of the indicated GFP fusion proteins in IR treated RPE-hTERT cells transfected with indicated siRNAs. Blots were probed for GFP, Ku80, ZNF384, γ H2AX and H3. Data shown represent 2 independent experiments. (B) Nuclear localization of GFP-APLF in U2OS Flp-In/T-Rex cells expressing doxycycline (dox)-inducible GFP-APLF transfected with the indicated siRNAs (left panel). Quantification of the data is presented as the mean of >200 cells acquired in 2 independent experiments (right panel). (C) Western blot analysis of Ku80 in cells from B. Tubulin is a loading control. Data shown represent 2 independent experiments. (D) Nuclear localization of GFP-APLF in wildtype and *Ku80*^{-/-} mouse embryonic stem (ES) cells (left panel). Quantification of the data is presented as the mean of >60 cells acquired in 2 independent experiments (right panel). (E) Pull-downs of the indicated GFP fusion proteins transfected with indicated siRNAs in U2OS cells. Blots were probed for GFP, Ku80, ZNF384 and tubulin. Data shown represent 2 independent experiments. (F) Kinetics of GFP-ZNF384 recruitment to 365 nm UV-A tracks in BrdU-sensitized U2OS Flp-In/T-Rex *ZNF384* KO cells. White triangles indicate irradiated regions (left panel). Quantification of GFP-ZNF384 is presented as the mean $\pm$ SD from >120 cells acquired in 2 independent experiments (right panel). (G) Kinetics of GFP-Ku70 recruitment to 365 nm UV-A tracks in BrdU-sensitized RPE1-hTERT cells. White triangles indicate irradiated regions. (left panel). Quantification of GFP-Ku70 is presented as the mean $\pm$ SD from >120 cells acquired in 2 independent experiments (right panel). (H) Kinetics of GFP-APLF recruitment to 365 nm UV-A tracks in BrdU-sensitized U2OS Flp-In/T-Rex GFP-APLF cells. White triangles indicate irradiated regions (left panel). Quantification of GFP-APLF is presented as the mean $\pm$ SD from <120 cells acquired in 2 independent experiments (right panel). Statistical significance was calculated with the two-tailed unpaired Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.

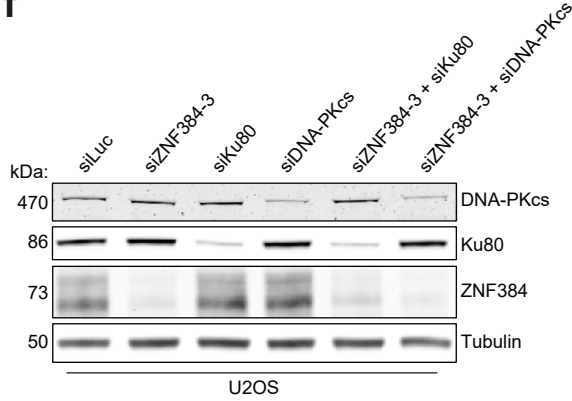
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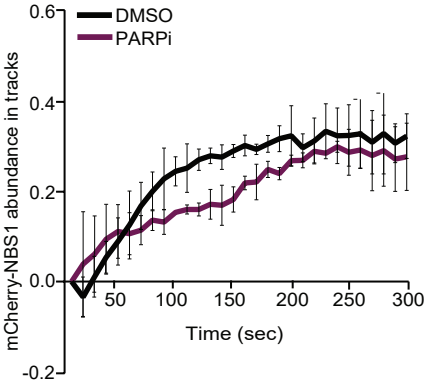
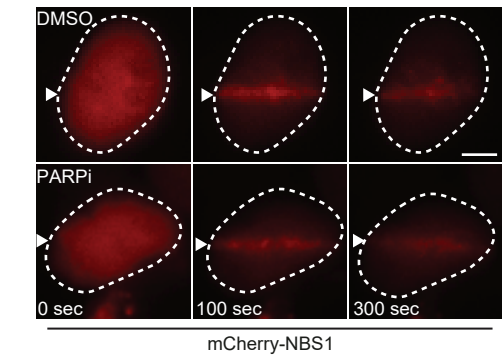
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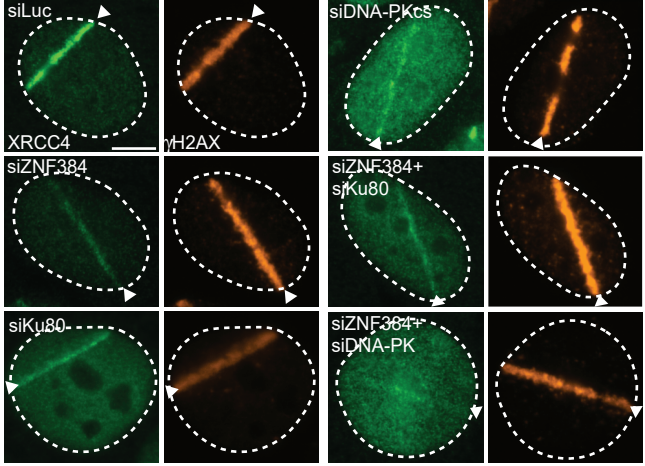
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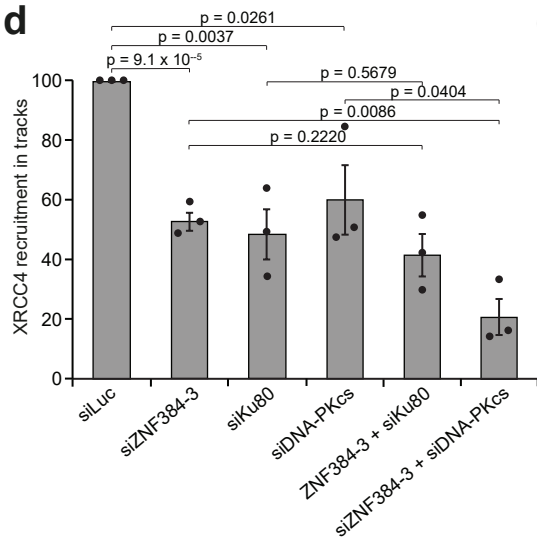
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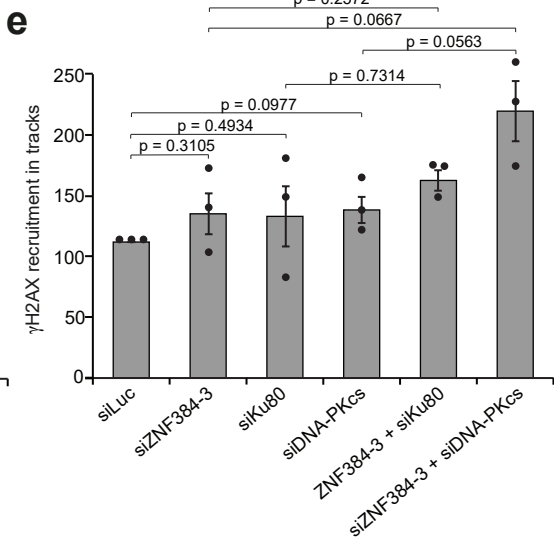
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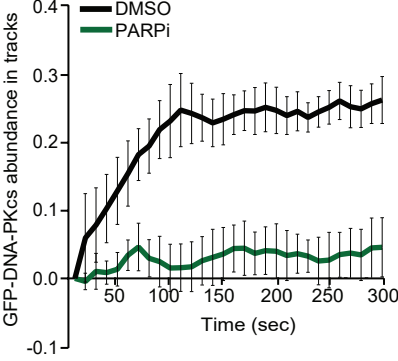
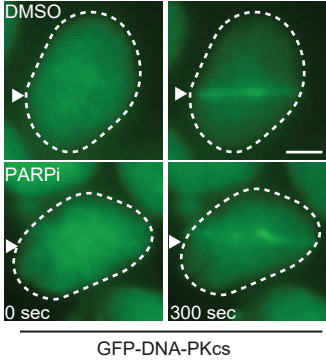
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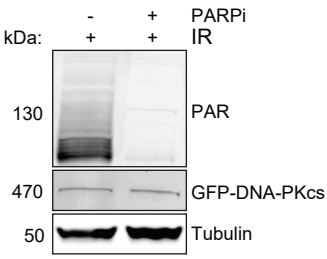
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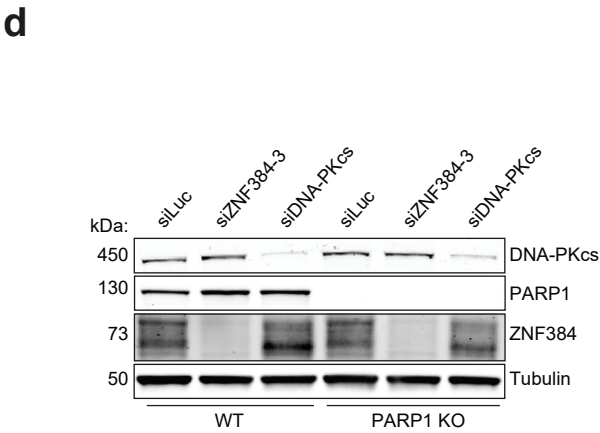
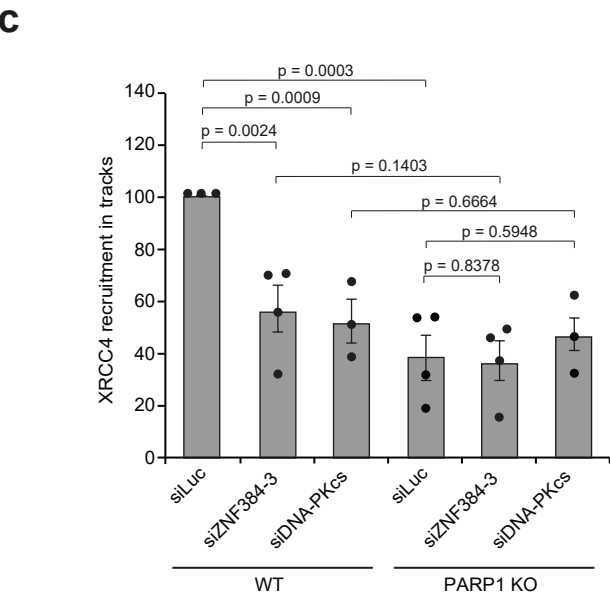
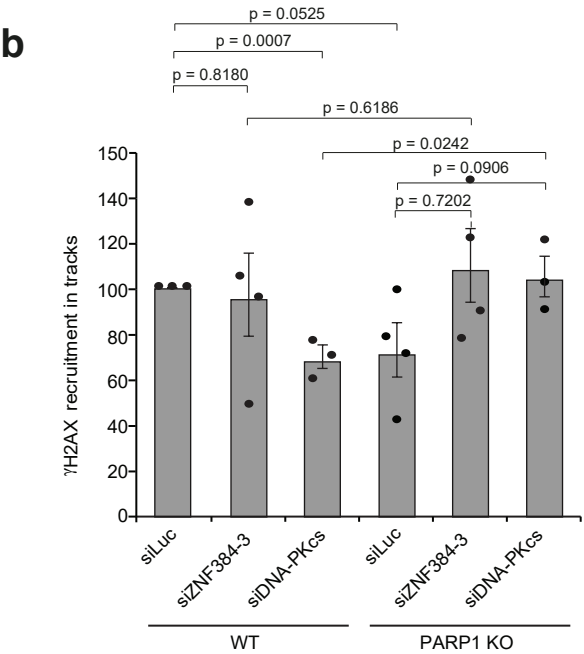
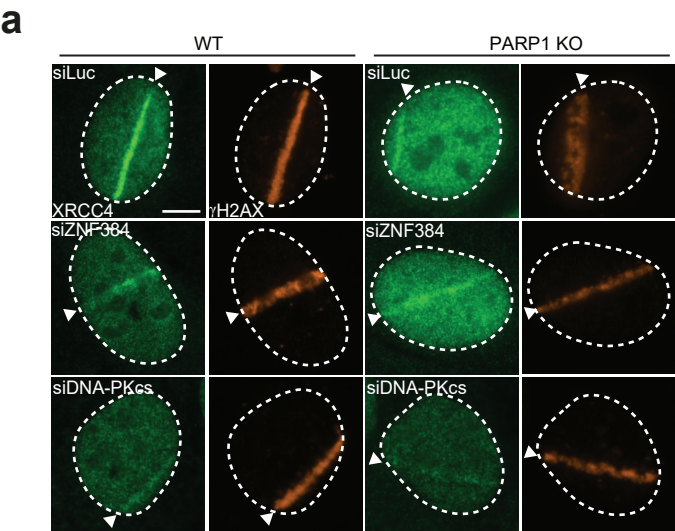
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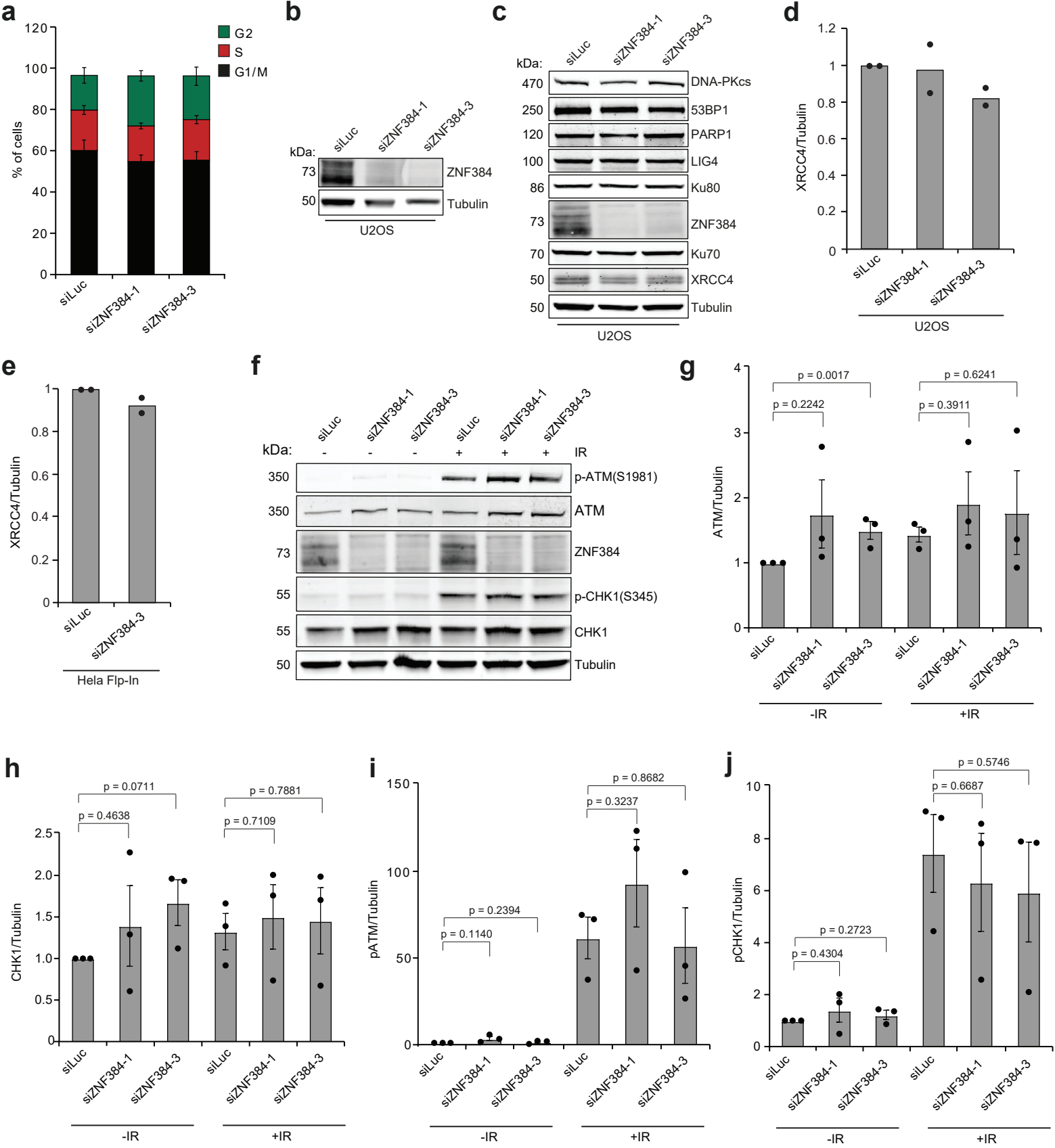
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Supplementary Fig. 11 – related to Fig. 6. ZNF384 promotes recruitment of cNHEJ proteins independently of DNA-PKcs. (A) Western blot analysis of DNA-PK activation 1 hour after 10 Gy of irradiation radiation (IR) in U2OS cells transfected with the indicated siRNAs. Blots were probed for p-DNA-PKcs (S2056), DNA-PKcs, Ku80 and ZNF384. Tubulin is a loading control. Data shown represent 3 independent experiments. (B) Western blot analysis of DNA-PK activation 1 hour after 10 Gy of irradiation radiation (IR) in wildtype and *Ku80*^{-/-} mouse embryonic stem cells. Blots were probed for p-DNA-PKcs (S2056), Ku80 and γ H2AX. H3 and tubulin are loading controls. Data shown represent 2 independent experiments. (C) Endogenous XRCC4 recruitment to 365 nm UV-A tracks 10 minutes after damage induction in U2OS cells transfected with the indicated siRNAs. γ H2AX is a damage marker. White triangles indicate irradiated regions. (D) XRCC4 quantification of C. Data shows the mean $\pm$ SEM of >150 cells acquired in 3 independent experiments (E) γ H2AX quantification of C. The mean $\pm$ SEM from 3 independent experiments is shown. Data were normalized to siLuc, which was set to 100%. (F) Western blot analysis of DNA-PKcs, Ku80, ZNF384, γ H2AX and Tubulin in cells from C. Tubulin is a loading control. Data shown represent 2 independent experiments. (G) GFP-DNA-PKcs recruitment to 365 nm UV-A tracks in BrdU-sensitized HCT116 cells treated with PARPi for 1 hour before laser micro-irradiation. White triangles indicate irradiated regions (left panel). Quantification of the data is presented as the mean $\pm$ SEM of >100 cells acquired in 3 independent experiments (right panel). (H) As in G, except for mCherry-NBS1. (I) Western blot analysis of PAR levels in IR- and PARPi -treated cells from G. Cells were treated with PARPi for 1 hour before IR treatment. Blots were probed for PAR, GFP and Tubulin. Tubulin is a loading control. Data shown represent 2 independent experiments. Statistical significance was calculated with the two-tailed unpaired Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.



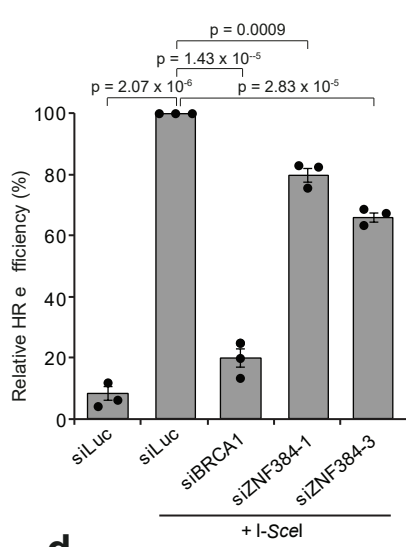
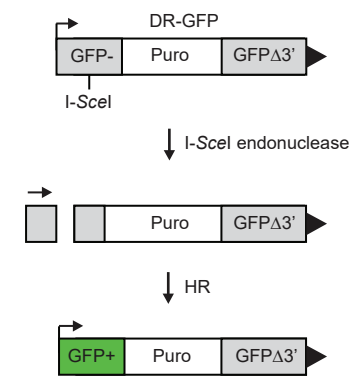
Supplementary Fig. 12 – related to Fig. 6. ZNF384 and PARP1, as well as DNA-Pkcs and PARP1, function epistatically in cNHEJ (A) Endogenous XRCC4 recruitment to 365 nm UV-A tracks in BrdU-sensitized U2OS cells transfected with the indicated siRNAs. Cells were fixed and immunostained 10 minutes after laser micro-irradiation. White triangles indicate irradiated regions. γ H2AX is a damage marker. (B) γ H2AX quantification of A. Data shows the mean $\pm$ SEM of >240 cells acquired in 4 independent experiments (C) XRCC4 quantification of A. The mean $\pm$ SEM from 3 independent experiments is shown. Data were normalized to siLuc, which was set to 100%. (D) Western blot analysis of ZNF384, DNA-PKcs and PARP1 in cells from A. Tubulin is a loading control. Data shown represent 2 independent experiments. Statistical significance was calculated with the two-tailed unpaired Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.



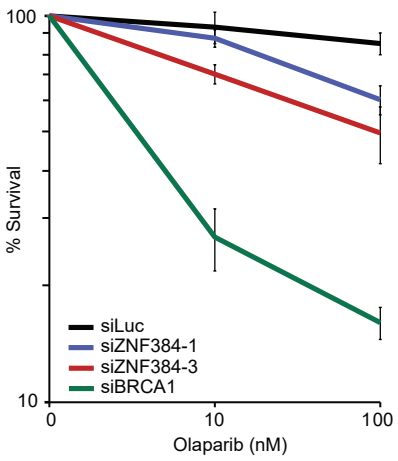
Supplementary Fig. 13 – related to Fig. 7. ZNF384 promotes efficient NHEJ independently of transcription

(A) Cell cycle profile of the indicated siRNA-transfected U2OS cells. The fraction of G1-, S- and G2-phase cells was determined by propidium iodide staining and FACS analysis. >30000 cells per condition were analyzed. Data show mean $\pm$ SEM from 3-4 independent experiments. (B) Western blot analysis of ZNF384 expression in U2OS cells from A. Tubulin is a loading control. Data shown represent 2 independent experiments. (C) Western blot analysis of the expression of NHEJ factors in siRNA transfected ZNF384 knockdown U2OS cells. Blots were probed for ZNF384, 53BP1, DNA-PKcs, Ku80, Ku70, PARP1, XRCC4 and LIG4. Tubulin is a loading control. (D) Quantification of XRCC4 expression in cells from C. Tubulin is a loading control, which was used for normalization of XRCC4 expression. The mean $\pm$ SD from 2 independent experiments is shown. Data were normalized to WT + siLuc, which was set to 1. (E) Quantification of XRCC4 expression in cells from Figure 7E. Tubulin is a loading control, which was used for normalization of XRCC4 expression. The mean $\pm$ SD from 2 independent experiments is shown. Data were normalized to WT + siLuc, which was set to 1. (F) Western blot analysis of IR-induced ATM phosphorylation (p-ATM) at Ser1981 and CHK1 phosphorylation (p-CHK1) at Ser345. Cells were collected 1 hour after exposure to 10 Gy of IR. Blots were also probed for ATM, ZNF384, CHK1 and Tubulin. Tubulin is a loading control. A representative blot from 3 independent experiments is shown. (G) Quantification of ATM expression in cells from F. Tubulin was used for normalization of ATM expression. The mean $\pm$ SEM from 3 independent experiments is shown. Data were normalized to siLuc - IR, which was set to 1. (H) As in G, except for CHK1. (I) As in G, except for pATM. (J) As in G, except for pCHK1. Statistical significance was calculated with the two-tailed unpaired Student's *t* test, assuming unequal variances. Source data are provided as Source Data file.

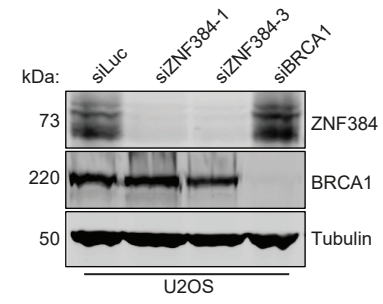
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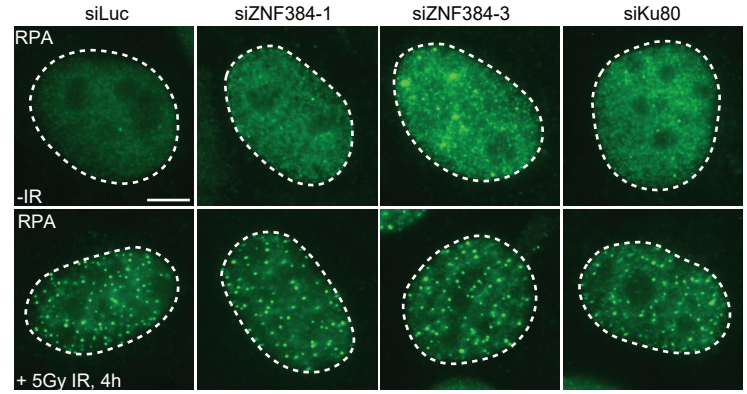
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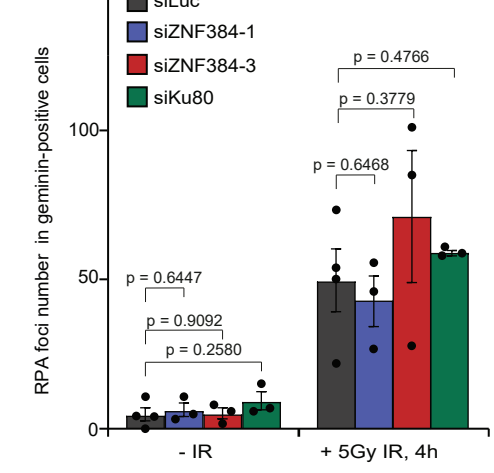
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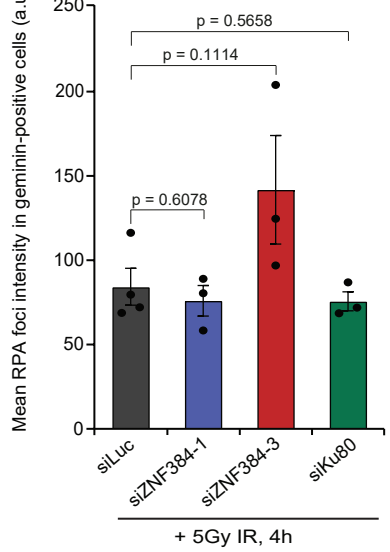
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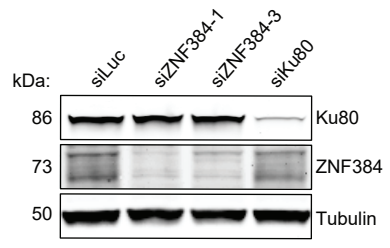
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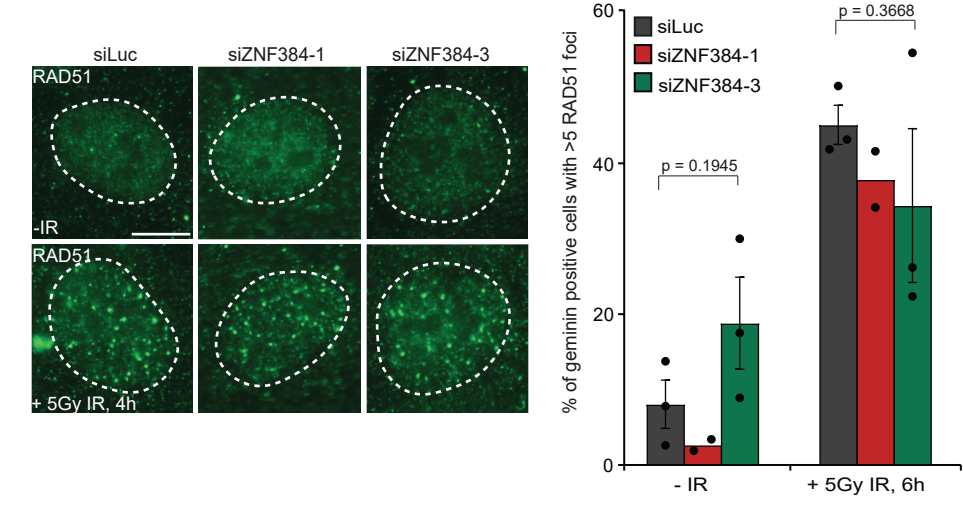
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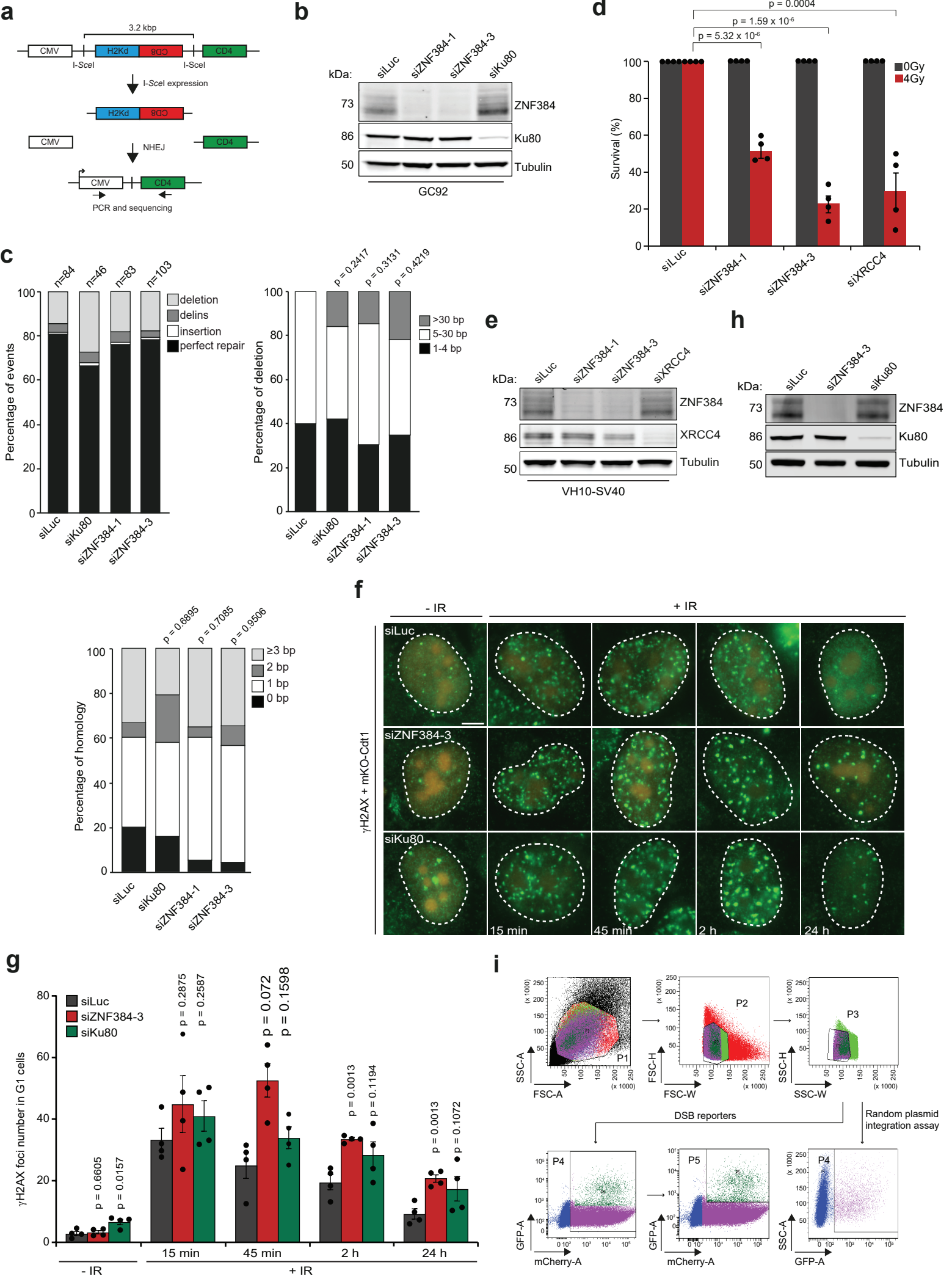
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Supplementary Fig. 14 – related to Fig. 7. ZNF384 is dispensable for HR (A) Schematic of the DR-GFP reporter for HR (left panel). Quantification of HR efficiencies in 3 independent DR-GFP- U2OS transfected cells with the indicated siRNAs. I-SceI transfection was corrected by co-transfection with mCherry expression vector. The mean $\pm$ SEM from 3 independent experiments is shown (right panel). (B) Clonogenic survival of U2OS cells transfected with the indicated siRNAs following treatment with the PARPi. The mean $\pm$ SEM from 3 independent experiments is shown. (C) Western blot analysis of ZNF384 and BRCA1 expression in U2OS cells. Tubulin is a loading control. Data shown represent 2 independent experiments. (D) RPA foci formation in U2OS cells transfected with the indicated siRNAs. Cells were exposed to 5 Gy of IR and foci were scored after 4 hours. (E) Quantification of RPA foci formation in cells from D. Foci were quantified in immuno-stained, geminin-positive S/G2 phase cells. The mean $\pm$ SEM from >200 cells from 3-4 independent experiments is shown. (F) As in E, except that RPA foci intensity was measured. (G) Western blot analysis of ZNF384 and Ku80 expression in cells from D. Tubulin is a loading control. (H) RAD51 foci formation in U2OS cells transfected with the indicated siRNAs. Cells were exposed to 5 Gy of IR and foci were quantified after 6 hours (left panel) The mean $\pm$ SEM from >300 cells from 2-3 independent experiments is shown. Foci were quantified in immuno-stained, geminin-positive S/G2 phase cells (right panel). Statistical significance was calculated with the two-tailed unpaired Student's *t* test, assuming unequal variances. Scale bar 5 μ m. Source data are provided as Source Data file.



Supplementary Fig. 15 – related to Fig. 7. ZNF384 promotes DSB repair via cNHEJ (A)

Schematic of the GC92 reporter for NHEJ. (B) Western blot analysis of ZNF384 and Ku80 expression in GC92 fibroblasts. Tubulin is a loading control. Data shown represent 2 independent experiments. (C) Mutational signatures (top left panel, deletion sized (top right panel) and microhomology usage (in case of deletion formation) (bottom panel) at repair junctions in GC92 reporter for NHEJ. GC92 cells were transfected with the indicated siRNAs and I-SceI expression vector. Repair junctions were amplified by PCR and Sanger-sequenced. (D) Clonogenic survival of VH10-SV40 cells transfected with the indicated siRNAs and exposed to 4 Gy of IR. The mean $\pm$ SEM from 4 independent experiments is shown. P-values were calculated using the two-tailed unpaired Student's *t* test, assuming unequal variances. (E) Western blot analysis of ZNF384 and XRCC4 expression in cells used in D. Tubulin is a loading control. Data shown represent 2 independent experiments. (F) γ H2AX foci formation (green) in stable Monomeric Kusabira-Orange (mKO)-Cdt1 expressing U2OS cells transfected with the indicated siRNAs. Cells were exposed to 2 Gy of IR and foci were scored after 15 minutes, 45 minutes, 2 hours and 24 hours. (G) Quantification of γ H2AX foci formation in Cdt1-positive G1 phase cells from F. The mean $\pm$ SEM from 2-4 independent experiments. Statistical significance was calculated with the two-tailed unpaired Student's *t*-test, assuming unequal variances. (H) Western blot analysis of ZNF384 and Ku80 expression in cells from F. Tubulin is a loading control. Data shown represent 2 independent experiments. (I) Gating strategy for flow cytometric analysis of cells for DR-GFP and EJ5- GFP reporter assays, as well as random plasmid integration assays. Scale bar 10 μ m. Source data are provided as a Source Data file.

Supplementary Table 1. Statistical analysis comparing LFQ intensities of proteins identified by LC-MS/MS in GFP-pulldowns from U2OS Flp-In/T-Rex cells expressing either GFP-ZNF384 or GFP-NLS. -Log p-value and average fold-enrichment (log2) are indicated. Additional information from the analysis of identified proteins is also included.

GENE			GFP-ZNF384 vs GFP		Peptide: Razor		Unique p Sequence		Unique p Sequence		Miscellaneous		MS/MS		Protein I Majority		Values							
Fasta headers	Protein names	Gene name	Significant	-test p-value	Difference	Unique	Unique	Unique	Unique	Mol. weight	Q-value	Score	Intensity	MS/MS	Protein I Majority	GFP-1	GFP-2	GFP-3/NF384	NF384-384-3					
sp P168-2J2K Zinc finger protein RNF384			+	5.13	13.01	22	22	19	46.9	46.9	39	56.105	0	323.3	3E+11	442	Q81F68	Q81F68	23.73	24.28	22.87	36.54	36.46	36.91
sp P13010 XRO X-ray repair cross- XROC5			+	3.46	7.90	28	28	28	54.8	54.8	54.8	82.704	0	323.3	1.3E+10	116	P13010	P13010	23.92	24.36	25.68	32.40	32.19	32.12
sp P12956 XRO X-ray repair cross- XROC6			+	5.33	7.85	32	32	32	51.4	51.4	51.4	69.842	0	320.9	1.5E+10	179	P12956	P12956	23.28	24.49	26.99	32.36	32.31	32.69
sp Q8NUA2 ZBT1 Zinc finger and BT ZBTB40			+	1.85	6.21	34	34	34	34.7	34.7	34.7	136.12	0	323.3	7.5E+09	158	Q8NUA2	Q8NUA2	27.93	24.02	23.31	32.29	30.33	30.68
sp P34932 HSP Heat shock 70 kDa HSPA4			+	2.93	5.41	23	23	21	30.7	30.7	27.9	70.153	0	216.2	3.0E+09	92	P34932	P34932	25.10	23.39	26.12	30.70	30.33	30.33
sp P11021 BIP 78 kDa glucose-rs HSPA5			+	5.49	4.23	42	42	41	56.6	56.6	56.6	72.332	0	323.3	5.5E+10	331	P11021	P11021	30.11	29.91	30.07	34.31	34.01	34.40
sp P11142 HSP Heat shock cognat HSPA8			+	5.01	3.94	39	38	21	61.3	61.3	35.6	70.897	0	323.3	1.7E+11	418	P11142	P11142	31.97	31.91	31.94	35.88	35.64	36.12
sp Q08209-2 PSP Serine/threonine-p PPR3CA			+	2.84	3.74	13	13	7	26.4	26.4	14.7	57.658	0	37.58	2E+09	50	Q08209	Q08209	25.02	25.99	26.08	30.10	29.97	29.25
tr A0A0G2J1W1 Heat shock 70 kDa HSPA1B;H			+	5.25	3.73	28	24	11	51.1	46.6	22.4	70.108	0	323.3	2.5E+10	172	A0A0G2	A0A0G2	29.42	29.29	29.50	33.16	32.95	33.29
sp P09874 PARI Poly [ADP-ribose] PARP1			+	4.54	3.68	47	47	47	48.6	48.6	48.6	113.08	0	323.3	2.8E+10	281	P09874	P09874	29.80	29.72	29.27	33.37	33.25	33.19
sp P38646 SRF Stress-70 protein, HSPA9			+	4.85	3.63	40	40	40	55.8	55.8	55.8	73.682	0	323.3	5E+10	345	P38646	P38646	30.50	30.41	30.48	34.07	33.86	34.36
sp Q02598-2 HSP Heat shock protein HSPH1			+	4.81	3.50	22	21	20	31.8	30.8	29.1	92.115	0	280	7.2E+09	99	Q02598	Q02598	28.00	27.68	27.77	31.44	31.12	31.40
sp O15294 OGT UDP-N-acetylglucosyl OGT			+	3.64	3.38	4	4	4	6.3	6.3	6.3	116.62	0	17.23	3E+08	12	O15294	O15294	23.04	23.75	23.58	26.73	26.62	27.16
sp P14618 PKYI Pyruvate kinase PI PKM			+	4.89	3.26	35	35	35	56.9	56.9	56.9	57.936	0	323.3	7E+10	312	P14618	P14618	31.18	31.29	31.35	34.43	34.42	34.77
sp Q93009 UBP Ubiquitin kinase USP7			+	1.82	3.20	6	6	6	6.7	6.7	6.7	128.3	0	18.33	2.7E+08	18	Q93009	Q93009	20.17	21.87	23.99	26.05	26.65	26.93
sp P16298 PP2F Serine/threonine-p PPR3CB			+	2.92	2.96	9	3	3	19.7	8.2	8.2	59.024	0	10.24	2.2E+08	4	P16298	P16298	23.36	23.92	22.97	26.05	26.26	26.82
sp P35251-2 RFR Replication factor 1 RFC1			+	3.64	2.92	12	12	12	11.8	11.8	11.8	128.18	0	37.24	1E+09	35	P35251	P35251	25.61	25.38	25.44	28.24	28.17	28.87
tr E7EWP2 E7E Triple functional d1 TRIO			+	3.16	2.89	4	4	4	2.2	2.2	2.2	262.68	0	4.157	2.3E+08	5	E7EWP2	E7EWP2	23.82	22.89	23.68	26.31	26.19	26.54
sp O43143 DXX Pre-mRNA-splicing DHX15			+	1.01	2.89	6	6	6	9.1	9.1	9.1	90.932	0	9.827	4.6E+08	8	O43143	O43143	23.15	22.53	26.87	26.28	27.51	27.23
sp Q9Y3F4 STR Serine-threonine k STRAP			+	1.86	2.56	4	4	4	17.7	17.7	17.7	98.438	0	16.15	2.3E+08	5	Q9Y3F4	Q9Y3F4	22.67	24.12	24.67	26.32	26.28	26.35
sp P28482 MKO Mitogen-activated MAPK1			+	3.73	2.38	4	4	4	15.6	15.6	15.6	41.389	0	20.78	3.4E+08	12	P28482	P28482	24.61	24.31	24.63	26.82	26.58	27.04
sp Q08J23-3 INS IRNA (cytosine)34 SUN2			+	1.22	2.34	3	3	3	8.3	8.3	8.3	59.383	0	9.354	1.2E+08	4	Q08J23	Q08J23	23.02	24.52	24.12	25.31	25.20	25.48
tr H0Y4R1 H0Y4 Inosine-5-monophos IMPDH2			+	3.21	2.27	10	10	10	23.2	23.2	23.2	50.957	0	112.5	3.6E+09	74	H0Y4R1	H0Y4R1	27.99	27.68	28.09	30.06	29.93	30.57
sp Q8NH2-2 C0 E3 ubiquitin-protein RFWHD2			+	2.17	2.09	2	2	2	4.7	4.7	4.7	77.69	0	10.22	9.6E+07	5	Q8NH2Y	Q8NH2Y	23.45	22.25	23.41	25.24	24.95	24.58
sp O14744-2 AN Protein arginine N- PRMT5			+	1.72	2.05	4	4	4	9.4	9.4	9.4	71.319	0	13.39	2E+08	6	O14744	O14744	23.19	24.46	24.13	26.50	25.23	26.22
tr A0A2C9F2P4 Palmityl-2 protein t PPT1			+	0.97	1.99	2	2	2	10.8	10.8	10.8	34.136	0	8.25	2.8E+08	5	A0A2C9	A0A2C9	23.28	25.61	22.42	25.66	25.70	25.91
sp P35249 RFC Replication factor 1 RFC4			+	1.77	1.94	6	6	6	26.4	26.4	26.4	39.681	0	12.12	5E+08	15	P35249	P35249	25.62	25.73	24.41	27.01	26.87	27.70
tr B4DX26 B4DX Fragile X mental k STRAP			+	1.93	1.73	6	6	6	19.9	19.9	19.9	68.326	0	73.33	1.2E+09	31	B4DX26	B4DX26	26.59	26.80	26.52	28.37	28.25	28.37
sp P06903 S10A Protein S100-A10 S100A10			+	1.73	1.90	2	2	2	35.1	35.1	35.1	11.203	0	55.54	4.4E+09	33	P06903	P06903	28.96	28.61	27.60	29.74	30.44	30.69
sp P35250-2 RFR Replication factor 1 RFC2			+	1.59	1.88	3	3	3	11.9	11.9	11.9	35.243	0	8.589	2.7E+08	4	P35250	P35250	24.16	25.29	23.84	26.09	25.91	26.23
sp Q95816 BAG BAG family molec BAG2			+	3.98	1.72	6	6	6	29.9	29.9	29.9	23.772	0	47.15	9.6E+08	31	Q95816	Q95816	26.28	26.47	26.62	28.24	28.07	28.91
sp Q9Y303 RTC1 IRNA-splicing ligat RTCB			+	2.72	1.57	10	10	10	26.1	26.1	26.1	55.21	0	32.71	1.3E+09	30	Q9Y303	Q9Y303	27.14	26.92	26.79	28.38	28.28	28.89
sp Q9HB71 CYC Calycin-binding j CACYBP			+	2.12	1.56	2	2	2	16.2	16.2	16.2	26.21	0	14.21	1.6E+08	4	Q9HB71	Q9HB71	23.80	23.36	24.26	25.56	25.02	25.51
sp Q9Y224 RTR UPF568 protein (C14orf168			+	2.52	1.49	5	5	5	25.8	25.8	25.8	28.068	0	30.36	7.9E+08	31	Q9Y224	Q9Y224	26.61	26.45	26.01	27.82	27.60	28.11
sp Q43684-2 BUB Mitotic checkpoint BUB3			+	0.82	1.48	3	3	3	9.5	9.5	9.5	36.954	0	1.72	1.5E+08	6	Q43684	Q43684	25.09	22.23	23.78	25.19	24.93	25.51
sp P62259 I433 14-3-3 protein esp YNHAIE			+	2.69	1.47	5	5	5	18.8	9.9	9.9	29.174	0	5.388	2.5E+08	5	P62259	P62259	23.23	24.09	26.15	25.42	25.07	25.97
tr A0A0A0M0S1 Pyrolysine-5-cabox PYCRL			+	2.16	1.46	2	2	2	7.7	7.7	7.7	29.892	0	4.908	9E+07	5	A0A0A0	A0A0A0	23.68	23.61	22.97	25.22	24.65	24.77
tr F1T0B3 F1T01 ATP-dependent R1 DDK1			+	2.41	1.43	7	7	7	14.7	14.7	14.7	73.915	0	54.44	8.5E+08	39	F1T0B3	F1T0B3	26.53	26.42	26.67	27.72	27.70	28.32
tr J3QLD9 J3QL Fliotilin-2 FLOT2			+	0.45	1.43	6	6	6	15.7	15.7	15.7	47.142	0	30.52	1.5E+08	9	J3QLD9	J3QLD9	23.34	22.78	23.33	23.37	23.07	27.30
sp P46063 REO ATP-dependent D1 REQLQ			+	0.73	1.42	4	4	4	7.9	7.9	7.9	73.457	0	13.97	3.6E+08	5	P46063	P46063	26.02	25.81	23.27	26.54	26.37	26.44
sp P40937-2 RFR Replication factor 1 RFC5			+	1.66	1.36	4	4	4	17.9	17.9	17.9	36.104	0	70.34	3.5E+08	13	P40937	P40937	25.51	25.10	25.00	26.08	26.41	27.22
tr C9K025 C9K0 60S ribosomal pr RPL35A			+	1.17	1.26	2	2	2	20.2	20.2	20.2	10.645	0	4.883	6.1E+07	5	C9K025	C9K025	23.54	23.29	23.70	23.86	24.90	25.55
sp O75555 FLO Fliotilin-1 FLOT1			+	0.41	1.26	4	4	4	12.4	12.4	12.4	47.355	0	70.13	1.9E+08	5	O75555	O75555	23.68	23.99	23.71	23.71	23.80	27.64
tr F8VPD4 F8V CAD protein, Gluta CAD			+	1.24	1.44	14	14	14	8.3	8.3	8.3	236.02	0	5.14	8.9E+08	41	F8VPD4	F8VPD4	26.83	26.50	26.76	28.07	27.65	28.08
sp P53396-3 AC ATP-citrate synthet ACYL			+	0.66	1.17	2	2	2	2.8	2.8	2.8	91.099	0	3.886	9E+07	3	P53396	P53396	25.93	21.76	24.19	24.91	24.28	24.22
tr A0A180GUA1 Alpha-aminoacid ALDH71			+	2.57	1.07	5	5	5	16.9	16.9	16.9	56.465	0	26.72	4.3E+08	13	A0A180	A0A180	25.73	25.95	25.80	26.06	26.69	26.72
sp P07195 LDH L-lactate dehydrog LDHA			+	0.44	1.06	9	9	9	32.9	32.9	32.9	36.638	0	65.2	2E+09	37	P07195	P07195	27.20	27.14	28.85	30.23	28.67	27.26
tr P11166 GTR Solute carrier fam SLG2A1			+	0.64	1.06	2	2	2	3.7	3.7	3.7	54.083	0	4.252	1.5E+08	10	P11166	P11166	24.80	24.80	22.58	25.18	24.96	25.20
tr A0A0A0MR02 Voltage-dependent VDAC2			+	1.66	1.00	7	7	7	33.7	33.7	33.7	30.348	0	82.09	1.5E+09	41	A0A0A0	A0A0A0	27.53	27.52	27.62	28.72	28.24	29.03
sp P46881 NES Nestin NES			+	0.27	0.98	11	11	11	8.3	8.3	8.3	177.44	0	6.82	3.8E+08	18	P46881	P46881	24.81	24.18	24.48	23.71	23.09	25.15
tr A0A3B3S3 CK NADH dehydrog NDUF9A			+	0.97	0.97	4	4	4	7.8	7.8	7.8	64.217	0	7.62	2.1E+08	5	A0A3B3	A0A3B3	24.97	24.66	24.75	26.08	25.93	26.80
sp Q9UJ59 CKM Calcium-binding n SLG2A13			+	1.70	0.97	5</																		

sp Q9UMS4 PRI Pre-mRNA-proces PRPF19	+	1.55	0.33	3	3	3	6	6	55.18	0	7.133	2.8E+08	8	Q9UMS-Q9UMS4	25.51	25.74	25.63	26.04	25.81	26.02	
sp P60488 SC8 Protein transport p SEC61B		0.40	0.33	3	3	3	37.5	37.5	37.5	9.9743	0	12.38	3.9E+08	17	P60488-P60488	26.60	25.81	26.09	26.89	25.99	26.62
sp Q00289 CLIC Chloride intracellular CLIC1		0.10	0.33	3	3	3	16.2	16.2	16.2	26.922	0	5.435	1.9E+08	5	Q00289-Q00289	24.30	24.44	24.74	26.62	25.38	22.47
sp P02545 LMN Prelamin-A/C-Lamin LMNA		0.67	0.33	16	14	14	25.9	24	24.5	74.139	0	95.93	1.5E+09	79	P02545-P02545	27.95	27.96	28.49	28.78	28.70	28.25
sp P50990 TCPI T-complex protein CCT8		0.86	0.32	19	19	19	39.8	39.8	39.8	59.62	0	70.58	2.9E+09	92	P50990-P50990	29.09	28.91	29.20	29.66	29.13	29.37
sp Q9NV17-3 AT ATPase family AA ATAD3A		0.97	0.32	5	5	2	11.6	11.6	6.3	57.947	0	11.48	2.4E+08	12	Q9NV17-Q9NV17	25.71	25.25	25.47	25.87	25.64	25.88
sp Q99832-4 TC T-complex protein CCT7		0.45	0.32	5	5	5	11.6	11.6	11.6	50.352	0	12.31	2.3E+08	11	Q99832-Q99832	25.34	25.20	25.55	26.26	25.39	25.99
sp P12236 ADT ADP/ATP transloc SLC25A6		0.51	0.31	11	5	4	34.6	16.4	12.8	32.866	0	33.25	1.5E+09	25	P12236-P12236	28.29	28.13	27.74	28.56	27.94	28.80
sp P31689 DNJ1 DnaJ homolog sub DNAJ1	+	1.49	0.31	3	3	3	10.3	10.3	10.3	44.866	0	6.626	2.6E+08	17	P31689-P31689	25.58	25.66	25.46	26.02	25.76	25.87
tr Q5JF53 Q5JF Tubulin beta chain TUBB		1.24	0.30	19	19	4	54.2	54.2	16.7	47.766	0	32.33	8.1E+10	354	Q5JF53-Q5JF53	33.85	33.67	33.68	34.03	33.87	34.22
tr Q5TE02 Q5TE Histone H3,Histone H3T2,H3P52,H3F3C		0.29	0.30	5	1	1	32.4	8.1	15.43	15.43	0.001	0.289	1.7E+09	16	Q5TE02-Q5TE02	28.29	27.93	28.24	27.80	29.22	28.34
sp A0180V UGU Glutamine-RNA I QARS		0.47	0.30	4	4	4	6.5	6.5	6.5	83.782	0	9.649	4.1E+08	15	A0180V-A0180V	25.45	25.83	26.27	26.67	26.72	26.07
tr H0Y5H9 H0Y5 Serpin B4 SERPINB4		0.20	0.30	8	2	2	20.8	6.2	6.2	42.388	0	21.53	1.7E+08	13	H0Y5H9-H0Y5H9	24.77	23.86	25.83	25.09	25.36	24.90
sp P07737 PRO Profilin-1 PFN1		0.15	0.30	6	6	6	52.9	52.9	52.9	15.054	0	19.16	9.1E+08	24	P07737-P07737	26.84	26.70	27.17	28.51	27.55	26.54
sp P30101 PDIA Protein disulfide-is PDIA3		0.27	0.30	5	5	5	13.3	13.3	13.3	56.782	0	12.85	5E+08	17	P30101-P30101	26.25	26.24	26.76	27.50	26.55	26.81
sp Q99714 HCD 3-hydroxyacyl-CoA HSD17B10		0.67	0.29	5	5	5	30.7	30.7	30.7	26.923	0	51.73	4.7E+08	28	Q99714-Q99714	26.71	26.06	26.41	26.65	26.59	26.19
tr B4DR61 B4DR Protein transport p SEC61A1,SEC61A2		0.67	0.29	2	2	2	4.1	4.1	4.1	52.949	0	3.799	3.1E+08	9	B4DR61-B4DR61	25.99	25.49	25.91	26.30	25.88	26.09
sp P63261 ACT1 Actin, cytoplasmic ACT1,ACTB		0.84	0.29	17	17	6	49.9	49.9	24.8	41.792	0	32.33	3.9E+10	297	P63261-P63261	32.99	32.58	32.73	33.25	32.83	32.77
sp P14866 HNR Heterogeneous nu HNRNP1		0.90	0.29	9	9	9	25.5	25.5	25.5	64.132	0	160.3	2.3E+09	49	P14866-P14866	28.79	28.50	28.70	28.87	28.80	29.18
tr G3V2K7 G3V Transmembrane e TMED10		0.47	0.28	2	2	2	15	15	15	16.904	0	3.301	1.9E+08	2	G3V2K7-G3V2K7	25.18	24.97	25.09	25.83	24.99	25.26
tr A0A2U3T3H3 Elongation factor 1 EEF1A2		0.36	0.27	10	2	2	26.8	7.3	7.3	54.34	0	17.45	4.9E+08	18	A0A2U3-A0A2U3	25.55	26.31	26.70	27.37	26.37	26.64
tr H0Y198 H0Y19 Dynactin subunit 2 DCTN2		1.02	0.26	2	2	2	10.4	10.4	10.4	29.326	0	4.24	1.6E+08	8	H0Y198-H0Y198	25.04	24.72	24.73	25.01	25.21	25.07
tr X6RJUP X6RJ Transgelin-2 TAGLN2		0.24	0.25	5	5	5	29.9	29.9	29.9	21.086	0	15.38	6.2E+08	22	X6RJUP-X6RJUP	26.63	26.71	27.04	27.78	26.91	26.45
sp P30044-2 PR Peroxidoxin-5, m PROX5		0.40	0.25	3	3	3	20.4	20.4	20.4	17.031	0	5.005	2.2E+08	5	P30044-P30044	25.42	25.25	25.46	26.15	25.38	25.35
sp Q14697 GAN Neutral alpha-gluc GANAB		0.42	0.25	6	6	6	10.1	10.1	10.1	106.87	0	51.65	5.1E+08	17	Q14697-Q14697	26.65	26.49	26.55	27.08	26.32	27.04
tr A0A1C7C7Y3 Dihydropyrimidine DPYSL2		0.51	0.25	3	3	3	5.5	5.5	5.5	73.502	0	11.2	2.3E+08	15	A0A1C7-A0A1C7	25.50	25.48	25.27	26.01	25.31	25.66
sp Q14204 DYH Cytoplasmic dyne DYNC1H1		0.80	0.25	13	13	3	32.8	3.3	3.3	33.229	0	27.32	4.2E+08	11	Q14204-Q14204	26.98	26.70	26.75	27.02	26.92	27.34
sp Q13268 DH9 Dehydrogenase dHRS2		0.53	0.24	6	6	6	27.9	27.9	27.9	29.926	0	12.62	4.8E+09	34	Q13268-Q13268	29.09	29.58	29.51	29.85	30.14	29.91
sp P63104 1433 14-3-3 protein Lc1 YWHAZ		0.33	0.24	9	6	6	40	29.8	29.8	27.745	0	136.5	1.8E+09	39	P63104-P63104	28.37	28.17	28.56	29.17	28.22	28.43
tr A0A494C1L1 Lamin-B receptor LBR		0.49	0.24	4	4	4	13.6	13.6	13.6	46.925	0	24.73	4E+08	21	A0A494-A0A494	26.15	26.20	26.36	26.86	26.16	26.41
sp Q00325-2 MF Phosphate carrier SLC25A3		0.62	0.24	8	8	8	21.3	21.3	21.3	39.958	0	19.38	2.1E+09	53	Q00325-Q00325	28.72	28.65	28.53	29.17	28.60	28.85
sp P42704 LPPF Leucine-rich PPR LRPPRC		0.37	0.24	4	4	4	2.7	2.7	2.7	157.9	0	5.152	1.6E+08	7	P42704-P42704	25.14	24.62	24.79	25.52	24.76	24.98
sp P16989-2 YB Y-box-binding prot YBX3		0.50	0.24	4	2	2	8.6	14.9	14.9	31.947	0	47.77	3.8E+08	8	P16989-P16989	26.37	26.18	25.89	26.43	26.21	26.32
sp Q13347 EIF3 Eukaryotic transl EIF3		0.28	0.24	2	2	2	25.4	25.4	8.8	92.468	0	10.15	2.5E+08	9	Q13347-Q13347	24.96	24.84	23.61	24.47	24.75	24.74
sp P22695 QCR Cytochrome b-c1 UQCRC2		0.57	0.21	6	6	6	22.2	22.2	22.2	48.442	0	22.79	8.5E+08	26	P22695-P22695	26.69	27.51	27.52	27.69	27.51	27.55
tr A0A289YFA2 D-3-phosphoglyc PHGDH		0.57	0.23	5	5	5	14.6	14.6	14.6	47.603	0	25.45	1.1E+09	31	A0A289-A0A289	27.50	27.73	27.77	27.97	27.99	28.14
sp P05141 ADT ADP/ATP transloc SLC25A5		0.68	0.23	11	11	4	38.3	38.3	14.4	32.852	0	71.77	2.2E+10	124	P05141-P05141	32.12	31.88	31.93	32.24	31.96	32.42
sp Q06830 PRD Peroxidoxin-1 PRDX1		0.86	0.23	16	16	12	55.8	55.8	40.7	22.11	0	74.1	5E+10	168	Q06830-Q06830	33.24	33.13	33.12	33.30	33.25	33.63
sp Q15149-4 PL Plectin PLEC		0.19	0.23	119	119	119	29.6	29.6	29.6	516.19	0	323.3	1.4E+10	426	Q15149-Q15149	31.16	30.88	31.46	30.76	32.18	31.24
sp Q6Y1H2 HAC Very-long-chain (3 HACD2		0.29	0.22	2	2	2	7.9	7.9	7.9	28.368	0	2.972	7E+07	4	Q6Y1H2-Q6Y1H2	23.89	24.27	23.97	24.62	23.92	24.05
sp P00167-2 CY Cytochrome b5 CYB5A		0.31	0.22	2	2	2	22.4	22.4	22.4	11.268	0	3.491	1.2E+08	5	P00167-P00167	24.19	24.75	24.98	25.09	24.53	24.95
sp P14825 ENP Endoplasmic r RPB2		0.19	0.22	7	5	5	8.6	6.8	6.8	92.468	0	10.15	2.5E+08	9	P14825-P14825	25.45	25.50	25.46	25.65	25.21	25.30
sp P51019 RAB Ras-related protein RAB2A,RA52B		0.67	0.21	6	6	6	36.3	36.3	36.3	54.545	0	22.78	8.5E+08	18	P51019-P51019	27.40	27.14	27.36	27.74	27.25	27.55
tr A0A0U1R0F0 Fatty acid synth FASN		0.62	0.21	37	37	37	22	22	22	273.2	0	249.4	6.4E+09	142	A0A0U1-A0A0U1	30.23	30.04	30.49	30.57	30.30	30.52
sp P68363 TBA Tubulin alpha-1b TUBA1B,TUBA1C,TUBA		0.88	0.21	19	19	1	51.9	51.9	3.1	50.151	0	323.3	8E+10	290	P68363-P68363	33.89	33.79	33.91	34.12	33.87	34.03
sp Q75821 EIF3 Eukaryotic transl EIF3G		0.48	0.21	3	3	3	11.9	11.9	11.9	35.611	0	7.405	3E+08	12	Q75821-Q75821	25.75	25.95	25.49	26.16	25.67	26.20
sp P84077 ARF ADP-ribosylation f ARF1,ARF3,ARF5		0.64	0.20	7	7	4	54.7	54.7	26	20.697	0	38.78	2.2E+09	43	P84077-P84077	28.73	28.52	28.91	29.10	28.80	28.88
sp P31946-2 14: 14-3-3 protein bet YWHAZ		0.19	0.20	8	5	4	36.1	25.8	22.1	27.85	0	51.74	5.7E+08	16	P31946-P31946	26.63	26.49	27.15	27.67	26.54	26.65
sp P51149 RAB Ras-related protein RAB7A		0.48	0.20	6	6	6	29.5	29.5	29.5	23.489	0	63.89	1.3E+09	33	P51149-P51149	27.93	27.81	28.16	28.40	27.89	28.20
tr J3KXP7 J3KP Prohibitin-2 TUBM		0.26	0.20	14	14	14	53	53	53	33.239	0	146.2	7.1E+09	111	J3KXP7-J3KXP7	30.29	30.17	30.71	31.03	30.13	30.63
sp P26647 IEF1 Elongation factor 1 EEF1G		0.26	0.20	11	11	11	26.3	26.3	26.3	50.118	0	51.46	1.6E+09	65	P26647-P26647	28.14	28.04	28.65	28.93	28.37	28.13
sp Q13148 TAD TAR DNA-binding TARDBP,TDP43		0.46	0.20	5	5	5	17.1	17.1	17.1	44.739	0	48.95	9.2E+08	31	Q13148-Q13148	27.54	27.53	27.22	27.60	27.38	27.89
sp P04406 G3P Glyceraldehyde-3- GAPDH		0.12	0.19	17	17	17	65.1	65.1	65.1	36.053	0	323.3	1.4E+10	140	P04406-P04406	30.85	31.33	31.46	32.44	31.32	30.46
sp P31942-2 HN Heterogeneous nu HNRNP3		0.37	0.19	3	3	3	10.6	10.6	10.6	35.238	0	8.458	4.3E+08	13	P31942-P31942	26.40	26.39	26.07	26.81	26.16	26.47
sp P62424 RL7 60S ribosomal pro RPL7A		0.08	0.19	4	4	4	15	15	15	25.995	0	44.99	4.9E+08	11	P62424-P62424	26.23	25.99	25.99	25.03	27.94	25.82
sp P35232 PHB Prohibitin PHB		0.22	0.19	13	13	13	66.9	66.9	66.9	29.804	0	273.9	7.6E+09	110	P35232-P35232	30.45	30.40	30.67	31.26	30.34	30.69
tr H0Y1H2 HAC Very-long-chain (3 HACD2		0.61	0.19	6	6	6	36.9	3													

sp P0DP25 CALM3_HUMAN Calm: CALM2;CALM3;CALM1	0.04	-0.03	5	5	5	41.6	41.6	41.6	16.837	0	46.35	1.6E+09	34	P0DP25	P0DP25	28.21	28.52	28.15	28.52	27.80	28.47	
sp Q00839 HNR Heterogeneous nu HNRNP1	0.05	-0.03	18	18	1	27	27	2.4	90.583	0	313.9	7.5E+09	142	Q00839	Q00839	30.90	30.55	30.19	30.69	30.40	30.45	
tr F8W1 F8W1 Myosin light polyp MYL6	-0.04	-0.04	6	6	6	46.9	46.9	46.9	16.29	0	14.62	5.5E+08	28	F8W1R2	F8W1R2	26.88	26.69	27.16	27.14	26.57	26.91	
sp P05676 ATP ATP synthase subc ATP5B	0.04	-0.04	15	15	15	46.9	46.9	46.9	56.559	0	187.1	7E+09	107	P05676	P05676	30.36	30.28	30.86	30.96	30.05	30.38	
sp P51571 SSR1 Translocase-associ: SSR4	0.10	-0.04	2	2	2	18.5	18.5	18.5	18.998	0	14.82	4.9E+08	16	P51571	P51571	26.89	26.55	26.48	26.76	26.56	26.47	
sp Q00059 2JTF Transcription factc: TFAM	0.06	-0.04	2	2	2	12.1	12.1	12.1	25.465	0	6.077	2.3E+08	6	Q00059	Q00059	25.92	25.42	25.17	25.26	25.29	25.73	
sp Q07065 CKA Cytoskeleton-asso CKAP4	0.04	-0.04	10	10	10	22.1	22.1	22.1	66.022	0	47.19	8.3E+08	32	Q07065	Q07065	27.36	26.99	27.93	27.97	27.11	27.08	
sp O60664 JPL Penlin-3 PLIN3	0.11	-0.05	3	3	3	11.4	11.4	11.4	45.803	0	28.65	3.4E+08	14	O60664	O60664	26.09	26.10	26.21	26.39	25.82	26.04	
sp P07384 CAN Calpain-1 catalytic CAPN1	0.12	-0.05	3	3	3	4.8	4.8	4.8	81.889	0	16.3	2.5E+08	12	P07384	P07384	25.76	25.51	25.93	25.75	25.81	25.49	
sp P04844 2JRF Dolichyl-diphosph: RPN2	0.08	-0.05	8	8	8	21.1	21.1	21.1	67.723	0	15.52	2.3E+09	47	P04844	P04844	28.74	28.76	29.13	29.20	28.72	28.55	
sp Q08598 LAN Lan-liko protein 2: LANCL2	0.07	-0.06	3	3	3	10	10	10	50.854	0	28.09	9E+08	23	Q08598	Q08598	27.92	27.27	27.31	27.34	27.22	27.78	
sp P25731 QEPF Nuclear pore com: NUP155	0.12	-0.06	5	5	5	4.1	4.1	4.1	148.09	0	18.85	3.2E+08	10	E99F10	E99F10	26.33	25.96	25.76	25.94	26.08	25.88	
sp P17987 TCP1 T-complex protein TCP1	0.15	-0.06	8	8	8	18.7	18.7	18.7	60.343	0	27.57	9.7E+08	22	P17987	P17987	27.78	27.61	27.57	27.78	27.70	27.68	
sp Q9UDW1 QYC Cytochrome b-c1: UQCRC10	0.10	-0.07	2	2	2	38.1	38.1	38.1	7.3084	0	11.76	3.7E+08	18	Q9UDW	Q9UDW	26.51	25.88	26.51	26.43	26.08	26.19	
sp Q15758 AAA Neutral amino acid: SLC1A5	0.21	-0.07	2	2	2	5.7	5.7	5.7	56.598	0	7.576	1.5E+08	6	Q15758	Q15758	25.08	24.83	24.87	25.04	24.86	24.68	
sp Q03252 LMN Lamin-B2 LMNB2	0.12	-0.07	9	9	9	12.7	12.7	12.7	10	69.948	0	16.56	3E+08	22	Q03252	Q03252	26.01	25.64	26.29	26.10	25.88	25.74
sp Q13185 CBX Chromobox protein CBX3	0.08	-0.08	3	3	3	23.5	23.5	23.5	20.811	0	30.51	3.9E+08	16	Q13185	Q13185	26.64	26.02	26.23	25.73	26.67	26.27	
sp Q9P258 RCC Protein RCC2 RCC2	0.14	-0.08	12	12	12	32.6	32.6	32.6	56.084	0	123.9	3.3E+09	70	Q9P258	Q9P258	29.69	29.32	29.24	29.19	29.17	29.65	
sp P05389 RLA1 60S acidic riboso: RPLP0;RPLP6	0.04	-0.09	4	4	4	21.1	21.1	21.1	34.273	0	38.39	7E+08	15	P05389	P05389	27.42	26.68	26.47	25.99	28.03	26.29	
sp P25705 ATP ATP synthase sub: ATP5A1	0.09	-0.09	23	23	23	45	45	45	59.75	0	283.4	1E+10	158	P25705	P25705	30.86	30.76	31.50	31.43	30.67	30.75	
tr U3KQE2 U3K1 Calpain small sub: CAPNS1;CAPNS2	0.14	-0.09	2	2	2	13.7	13.7	13.7	18.445	0	6.553	2.3E+08	12	U3KQE2	U3KQE2	25.53	25.05	25.97	25.76	25.22	25.75	
sp Q96F06 S10 Protein S100-A16: S100A16	0.61	-0.10	3	3	3	33	33	33	11.801	0	13.04	3.1E+08	18	Q96F06	Q96F06	26.04	25.86	26.05	25.93	25.91	25.82	
sp Q09666 AHN Neuroblast differ: AHNAK	0.44	-0.10	50	50	50	20.5	20.5	20.5	629.09	0	213.1	9E+09	204	Q09666	Q09666	30.87	30.75	31.03	30.85	30.69	30.82	
tr Q5W0J0 Q5W Ras-related protein RAB18	0.21	-0.10	2	2	2	16.1	16.1	16.1	18.023	0	3.501	1.8E+08	9	Q5W0JX	Q5W0JX	25.17	25.23	25.39	25.15	24.89	25.45	
sp Q13185 CBX Chromobox protein CBX3	0.07	-0.11	4	4	4	32.2	32.2	32.2	14.369	0	9.152	4.9E+08	20	Q13185	Q13185	26.79	26.31	26.60	25.57	27.47	26.33	
tr A0A087X21P 26S protease regu: PSMC6	0.21	-0.11	2	2	2	6.7	6.7	6.7	45.796	0	15.44	2.4E+08	14	A0A087X21P	A0A087X21P	25.43	25.71	25.88	25.66	25.25	25.78	
sp Q17389 SEC2 Vesicle-trafficking: SEC22B	0.18	-0.11	2	2	2	6.1	6.1	6.1	37.428	0	6.11	4.5E+08	15	Q17389	Q17389	27.51	27.36	27.65	27.33	26.97	27.41	
tr A0A180GWA AKlydyl-diphosph: AGPS	0.24	-0.11	3	3	3	8.5	8.5	8.5	80.807	0	9.853	2.2E+08	8	A0A180	A0A180	25.48	25.68	25.39	25.73	25.23	25.22	
sp P62913 RL1 60S ribosomal pro: RPL11	0.20	-0.12	4	4	4	23.6	23.6	23.6	20.252	0	28.97	1.3E+09	37	P62913	P62913	28.28	28.41	28.04	27.61	28.21	27.97	
sp P05023 3AT Sodium/potassium: ATP1A1;ATP1A3;ATP13	0.13	-0.12	9	9	9	11.5	11.5	11.5	109.55	0	46.13	1.2E+09	25	P05023	P05023	27.78	27.93	28.08	28.40	27.30	27.93	
sp P17844 DDX Probable ATP-dep: DDX5	0.25	-0.13	24	24	19	34.4	34.4	25.9	69.147	0	140.5	1.2E+10	159	P17844	P17844	31.61	31.21	31.06	30.95	31.19	31.36	
sp P06766 2KH KH domain-contai: KHDRBS1;KHDRBS2	0.23	-0.13	4	4	4	10.3	10.3	10.3	45.86	0	19.11	5.5E+08	20	Q07666	Q07666	27.13	26.75	26.75	27.08	26.48	26.69	
sp Q9Y490 TLN1 Talin-1 TLN1	0.07	-0.13	3	3	3	1.6	1.6	1.6	269.76	0	9.762	1.5E+08	9	Q9Y490	Q9Y490	24.96	24.80	24.77	25.65	23.45	25.04	
sp Q15161 PYR Inorganic pyropho: PPA1	0.17	-0.13	4	4	4	24.9	24.9	24.9	42.66	0	74.72	3.9E+08	10	Q15161	Q15161	26.54	26.38	26.03	26.70	25.88	26.96	
sp P62269 RS2 40S ribosomal pro: RPS23	0.13	-0.3	3	3	3	5.3	5.3	5.3	103.84	0	9.528	1.8E+08	13	P62269	P62269	26.29	26.77	26.82	26.97	26.94	26.19	
tr A0A383R12A CTP synthase 1: CTPS1	0.37	-0.14	10	10	10	28	28	28	63.723	0	70.18	1.8E+09	50	A0A383	A0A383	28.79	28.54	28.46	28.52	28.21	28.64	
sp P25205 MCM DNA replication ic: MCM3	0.63	-0.15	10	10	10	17.1	17.1	17.1	90.98	0	48.34	1.3E+09	47	P25205	P25205	28.12	28.07	28.22	27.97	27.84	28.17	
sp P39023 RL3 60S ribosomal pro: RPL3	0.05	-0.15	7	7	7	20.8	20.8	20.8	46.108	0	29.06	9.7E+08	17	P39023	P39023	25.18	25.58	26.61	25.70	26.80	26.65	
sp P46940 IQG Ras GTPase-activ: IQGAP1	0.22	-0.15	5	5	4	4.2	4.2	4.2	3.6	189.25	0	18.56	1.7E+08	9	P46940	P46940	28.28	24.94	25.20	25.45	24.90	24.63
sp P35221 CTN Catenin alpha-1: C: CTNNA1;CTNNA3	0.51	-0.15	2	2	2	2.9	2.9	2.9	100.07	0.0013	2.292	5.7E+09	6	P35221	P35221	30.36	29.92	30.22	30.03	29.97	30.05	
sp Q16777 H2A Histone H2A type: HIST1H2AC;HIST1H2AU	0.15	-0.16	7	7	1	63.6	63.6	22.5	13.988	0	50.65	3.3E+10	63	Q16777	Q16777	32.90	32.34	32.68	31.94	33.13	32.34	
sp P51572 BAP B-cell receptor-as: BAP31	0.1	-0.16	4	4	4	16.7	16.7	16.7	27.991	0	13.4	3E+08	17	P51572	P51572	25.67	25.59	26.78	26.54	25.34	25.70	
sp P55265 SDS Double-stranded F: ADAR4	0.14	-0.16	4	4	4	5.3	5.3	5.3	103.84	0	9.528	1.8E+08	13	P55265	P55265	25.47	25.05	25.17	25.15	24.94	25.13	
tr H0YFD6 H0Y1 Trifunctional enzy: HADHA	0.49	-0.16	9	9	9	13.6	13.6	13.6	86.371	0	18.59	1E+09	29	H0YFD6	H0YFD6	27.70	27.84	27.65	27.84	27.37	27.69	
sp P67809 YBO Nuclease-sensitive YBK1	0.38	-0.17	7	7	5	41	41	31.2	35.924	0	98.44	8.8E+08	37	P67809	P67809	27.81	27.65	27.21	27.34	27.46	27.98	
sp P55884 EIF3 Eukaryotic transl: EIF3B	0.22	-0.17	2	2	2	2.8	2.8	2.8	92.48	0	9.189	1.9E+08	18	P55884	P55884	25.31	25.52	25.30	25.80	24.47	24.96	
sp Q86X51 EZH1 Uncharacterized p: CXorf67	0.31	-0.18	3	3	3	6.2	6.2	6.2	51.893	0	15.52	1.3E+08	9	Q86X51	Q86X51	24.85	24.66	24.73	24.82	24.12	24.77	
tr F8VZJ2 F8VZ Nascent polypept: NACA	0.46	-0.18	4	4	4	40.4	40.4	40.4	15.016	0	45.07	7.2E+08	27	F8VZJ2	F8VZJ2	27.45	27.44	26.95	27.13	27.00	27.15	
sp P62937 PP1A Peptidyl-prolyl-ase: PP1A	0.34	-0.19	8	8	8	35.8	35.8	35.8	18.012	0	75.69	5.9E+09	80	P62937	P62937	30.29	30.20	30.50	30.55	29.84	30.03	
sp P22629 ROA Heterogeneous nu: HNRNPA2B1	0.19	-0.19	16	16	15	42.2	42.2	42.2	46.799	0	147.1	4.3E+09	110	P22629	P22629	29.99	29.68	29.69	29.86	29.60	29.97	
tr A0A0C4D0A Dolichyl-diphosph: DDC3A2	0.30	-0.20	5	5	5	16.2	16.2	16.2	48.759	0	94.24	1E+09	17	A0A0C4	A0A0C4	28.47	28.21	28.31	27.89	27.97	27.68	
sp P51991 ROA Heterogeneous nu: HNRNPA3	0.39	-0.20	7	7	7	31.2	31.2	31.2	39.594	0	103.4	1.2E+09	40	P51991	P51991	28.45	27.91	27.75	27.96	27.71	27.63	
sp P61026 RAB Ras-related protein RAB10	0.23	-0.20	4	3	3	20.5	15	15	22.541	0	13.53	4.8E+08	4	P61026	P61026	26.54	26.37	27.17	26.97	26.18	26.33	
sp P55060 4XP Exportin-2 CSE1L	0.44	-0.21	14	14	14	18.6	18.6	18.6	103.88	0	199.4	1.3E+10	62	P55060	P55060	31.38	31.34	31.24	31.49	31.10	31.08	
tr A0A2R8Y811 40S ribosomal pro: RPS14	0.31	-0.21	4	4	4	36.7	36.7	36.7	16.159	0	18.52	7.9E+08	15	A0A2R8	A0A2R8	27.53	27.18	27.34	26.21	27.52	27.14	
tr U3KQKQ U3K1 Histone H2B;Histo: HIST1H2B;HIST1H2BI	0.16	-0.21	9	9	2	44	44	6	18.804	0	164.2	5.5E+10	79	U3KQKQ	U3KQKQ	33.66	33.16	32.96	32.33	33.88	32.94	
sp Q86UF2 2KJ Kinetin KTN1																						

tr F6S8N6 F6S8 Protein-L-isoscapr PCMT1	+	1,42	-0,67	4	4	4	31,2	31,2	31,2	26,626	0	67,41	8,8E+08	18	F6S8N6; F6S8N6	28,02	27,78	27,36	27,14	27,17	26,83
sp P29508 SPB Serpin B3 SERPINB3		0,57	-0,89	9	9	3	24,9	24,9	11	44,584	0	26,3	7,6E+08	27	P29508; P29508	27,29	26,99	28,49	26,49	27,45	26,76
sp Q96H79 ZCC Zinc finger CCHC ZC3HAV1L	+	1,59	-0,69	4	4	4	16,7	16,7	16,7	32,962	0	15,37	3,9E+08	19	Q96H79; Q96H79	26,90	26,55	26,24	25,99	25,82	25,90
sp Q9HA64 KT3 Kotosamine-3-kin FNAKRP	+	1,85	-0,71	6	6	6	23,9	23,9	23,9	34,412	0	32,44	2,8E+09	43	Q9HA64; Q9HA64	29,59	29,40	29,40	28,54	28,67	29,07
tr J3QR09 J3QR Ribosomal protein RPL19		0,32	-0,72	4	4	4	22,8	22,8	22,8	23,134	0	29,32	4,5E+08	15	J3QR09; J3QR09	26,76	26,35	26,33	24,18	27,33	25,77
sp Q16527 CSR Cysteine and glyci CSR2	+	2,04	-0,73	5	5	5	35,8	35,8	35,8	20,954	0	33,58	2,8E+09	49	Q16527; Q16527	29,70	29,29	29,32	28,60	28,65	28,87
sp P10599 THIC Thiodioxin TXN	+	2,17	-0,74	5	5	5	42,9	42,9	42,9	11,737	0	28,86	3E+09	47	P10599; P10599	29,46	29,73	29,60	28,64	29,05	28,88
sp P62906 RLL1 60S ribosomal pro RPL10A		0,41	-0,75	3	3	3	13,4	13,4	13,4	24,831	0	5,087	2,2E+08	6	P62906; P62906	25,46	25,54	25,79	23,50	25,16	24,86
sp P84103-2 SR Serine/arginine-rich SRSF3	+	1,37	-0,77	4	4	3	30,6	30,6	30,6	14,203	0	21,2	1,6E+09	31	P84103-2; P84103-2	29,08	28,57	28,21	27,72	27,87	27,97
sp P50454 SER Serpin H1 SERPINH1		0,36	-0,78	3	3	3	11,7	11,7	11,7	46,44	0	16,11	2E+08	11	P50454; P50454	25,68	25,50	25,12	25,41	25,67	22,88
sp P04899 GNA Guanine nucleotid GNAI2;GNA5;GNAO1;C		0,54	-0,79	2	2	2	7,3	7,3	7,3	40,45	0	2,967	2,3E+08	10	P04899; P04899	25,51	25,88	25,58	25,41	25,60	23,59
tr E9PPU1 E9PP 40S ribosomal pro RPS3		0,57	-0,80	9	9	9	63,3	63,3	63,3	17,407	0	21,97	1,3E+09	40	E9PPU1; E9PPU1	28,35	28,13	28,14	26,40	28,54	27,29
tr A0A590 U0K4 Serine/arginine-rich SRSF6	+	1,56	-0,80	5	5	3	20,8	20,8	11,5	26,306	0	8,505	5,6E+08	19	A0A590; A0A590	27,44	27,17	26,95	26,76	26,21	26,19
tr E7EX73 E7EX Eukaryotic translat EIF4G1		0,64	-0,82	2	2	2	1,7	1,7	1,7	158,64	0	8,418	8,2E+07	4	E7EX73; E7EX73	24,24	24,39	24,42	24,12	22,38	24,09
sp P46781 RS9 40S ribosomal pro RPS9		0,61	-0,83	10	10	10	43,8	43,8	43,8	22,591	0	16,33	1,2E+09	36	P46781; P46781	28,28	27,90	28,11	26,42	28,43	26,96
sp P05109 S10A Protein S100-A8;F S100A8		0,56	-0,83	3	3	3	26,9	26,9	26,9	10,834	0	9,963	9,9E+08	20	P05109; P05109	27,61	27,34	28,86	26,40	27,98	26,95
tr A0A494 C0U7 Protein-glutamine TGM3		1,07	-0,85	6	6	6	8,6	8,6	8,6	78,856	0	11,45	4,8E+08	15	A0A494; A0A494	26,36	26,98	27,47	25,77	26,42	26,08
sp P62277 RS13 40S ribosomal pro RPS13		1,04	-0,85	6	6	6	35,8	35,8	35,8	17,222	0	25,31	1,2E+09	38	P62277; P62277	28,47	28,22	27,96	26,92	28,06	27,12
sp P26373 RLL13 60S ribosomal pro RPL13		0,26	-0,85	7	7	7	29,9	29,9	29,9	24,261	0	48,13	8,4E+08	25	P26373; P26373	27,61	28,80	27,34	24,17	28,51	26,53
sp P04040 CAT Catalase CAT		0,93	-0,86	6	6	6	18	18	18	59,755	0	42,37	6,3E+08	18	P04040; P04040	26,82	27,91	27,13	26,05	26,99	26,24
tr J3KT73 J3KT 60S ribosomal pro RPL38		1,03	-0,87	3	3	3	39,1	39,1	39,1	7,5649	0	39,6	1,1E+09	23	J3KT73; J3KT73	28,57	28,22	27,91	26,71	27,47	27,90
sp P53007 TXXT Tricarboxylate tran SLC25A1		0,66	-0,88	2	2	2	7,7	7,7	7,7	34,012	0	11,6	1,3E+08	6	P53007; P53007	25,43	25,41	23,72	23,53	24,16	24,22
sp P42357-2 HJ Histidine ammonia HAL		0,84	-0,89	2	2	2	3,4	3,4	3,4	64,887	0	2,736	1E+08	8	P42357-2; P42357-2	24,42	24,57	25,50	23,26	24,48	24,06
sp Q9HCY8 S10 Protein S100-A14 S100A14		0,81	-0,91	2	2	2	25	25	25	11,662	0	12,49	1,1E+08	9	Q9HCY8; Q9HCY8	24,83	24,64	24,96	24,37	24,46	22,89
sp Q9UBV8 PEP Peflin PEF1	+	2,04	-0,92	4	4	4	12	12	12	30,381	0	8,4	2,5E+08	13	Q9UBV8; Q9UBV8	26,26	25,91	26,20	25,22	24,92	24,85
sp Q52688-2 JAN Acidic leucine-rich ANP3ZB		0,68	-0,93	5	4	4	28,7	22,1	22,1	22,276	0	10,01	6,8E+08	16	Q52688-2; Q52688-2	27,85	27,96	26,13	26,74	26,20	26,25
sp P61313 RLL15 60S ribosomal pro RPL15		0,32	-0,93	6	6	6	32,8	32,8	32,8	24,146	0	30,22	4,7E+08	16	P61313; P61313	26,80	26,17	26,62	23,39	27,48	25,93
tr H7C469 H7CA Cathespin D;Cath CTSD		1,08	-0,93	4	4	4	12,2	12,2	12,2	35,785	0	21,92	3,9E+08	13	H7C469; H7C469	26,18	26,83	27,08	25,68	26,33	25,29
tr Q5JR95 Q5JR 40S ribosomal pro RPS8		0,56	-0,95	4	4	4	27,7	27,7	27,7	21,879	0	54,49	1,2E+09	27	Q5JR95; Q5JR95	28,11	28,19	28,15	25,90	28,52	27,17
sp P35998 PRS 26S protease regu PSMC2		0,39	-0,96	3	3	3	7,6	7,6	7,6	48,633	0	4,264	2,6E+08	5	P35998; P35998	26,11	25,78	25,99	26,16	25,88	22,97
sp P17096 HMG High mobility grou HMGAI1	+	1,32	-0,96	2	2	1	22,4	22,4	15	11,676	0	16,07	2E+08	8	P17096; P17096	26,28	25,54	25,17	24,81	24,52	27,47
tr H0YEN5 H0Y1 40S ribosomal pro RPS2		0,69	-0,99	4	4	4	22,6	22,6	22,6	21,154	0	29,08	1,1E+09	23	H0YEN5; H0YEN5	28,21	28,15	27,82	26,10	28,29	26,81
sp Q96P63 SPB Serpin B12 SERPINB1	+	1,85	-1,03	6	6	6	17,8	17,8	17,8	46,276	0	35,11	9,8E+08	29	Q96P63; Q96P63	27,87	28,33	27,99	26,63	27,26	27,21
tr J3KR62 J3KR Gasterdemin-1a GSDMA		0,71	-1,04	2	2	2	13,9	13,9	13,9	17,791	0	4,491	7,1E+07	3	J3KR62; J3KR62	23,77	23,79	25,43	22,53	23,72	23,61
tr H0R210 MR2 40S ribosomal pro RPS16		0,90	-1,04	5	5	5	40,3	40,3	40,3	14,419	0	16,88	9,6E+08	33	MR210; MR210	28,28	27,53	27,95	26,09	27,80	26,74
tr H0YMT0 H0Y1 Proteasome activa PSME2		0,41	-1,06	5	5	5	23,2	23,2	23,2	26,011	0	25,41	7,5E+08	8	H0YMT0; H0YMT0	27,56	26,97	27,41	27,30	24,09	27,36
sp Q6YN16-2 HJ Hydroxyteroid del HSDL2		0,57	-1,07	2	2	2	10,1	10,1	10,1	37,32	0	18,41	2,3E+08	13	Q6YN16; Q6YN16	26,40	25,36	25,21	25,40	25,25	23,10
sp Q58FF8 H90 Putative heat shoc HSP90AB2P		0,41	-1,08	6	1	1	16,3	3,9	3,9	44,348	0	3,401	4,9E+08	13	Q58FF8; Q58FF8	27,05	26,36	26,55	26,68	26,68	23,37
sp P46109 CRK1 Crk-like protein CRKL	+	2,03	-1,14	7	7	7	33	33	33	33,777	0	60,5	1,3E+09	31	P46109; P46109	28,69	28,64	28,46	27,09	27,40	27,88
tr X6R700 X6R7 Chromatin target c CHTOP		1,11	-1,17	2	2	2	11,7	11,7	11,7	23,661	0	18,42	1,5E+08	12	X6R700; X6R700	25,47	24,58	24,65	23,36	23,29	24,54
sp J3KTL2 J3KT Serine/arginine-rich SRSF1	+	2,06	-1,19	7	7	7	26,1	26,1	26,1	28,329	0	20,69	8,9E+08	32	J3KTL2; J3KTL2	28,36	27,87	27,52	26,65	26,70	26,83
sp P47929 LEG1 Glectin-7 LGALS7		1,28	-1,23	4	4	4	35,3	35,3	35,3	15,075	0	12,66	6,8E+08	17	P47929; P47929	26,78	27,71	28,26	26,21	26,61	26,22
sp Q01650 LAT1 Large neutral amin SLC7A5		1,10	-1,27	2	2	2	6,3	6,3	6,3	55,01	0	18,79	2,4E+08	17	Q01650; Q01650	26,07	25,98	26,28	25,39	23,76	25,37
tr Q2L6G8 Q2L6 Cornedoesmosin CDSN		0,89	-1,28	3	3	3	9,6	9,6	9,6	51,539	0	45,11	8,9E+08	16	Q2L6G8; Q2L6G8	27,80	28,81	26,77	26,06	27,12	26,35
tr H3BV85 H3BV BOLA-like protein 2 BOLA2B;BOLA2		0,89	-1,29	2	2	2	46,3	46,3	46,3	6,3612	0	15,71	1,4E+08	5	H3BV85; H3BV85	25,07	25,61	24,99	22,63	24,49	24,68
sp P53999 TCP: Activated RNA pol SUB1	+	1,64	-1,29	7	7	7	46,5	46,5	46,5	14,395	0	28,62	3,7E+09	34	P53999; P53999	30,31	30,36	29,34	28,88	28,43	28,82
sp P14923 PLA1 Junction plakogel JUP	+	1,58	-1,31	23	23	23	33,8	33,8	33,8	81,744	0	22,74	1,3E+10	179	P14923; P14923	31,58	32,39	31,25	30,13	30,72	30,44
sp Q08554-2 D5 Desmocollin-1 DSC1		1,23	-1,31	10	10	10	16,2	16,2	16,2	93,834	0	136,1	4,1E+09	69	Q08554-2; Q08554-2	30,05	30,85	29,28	28,43	29,16	28,65
sp P05089 ARG Arginase-1 ARG1	+	1,66	-1,32	13	13	13	57,1	57,1	57,1	34,735	0	105,6	2,5E+09	53	P05089; P05089	28,97	29,84	29,52	27,66	28,54	28,19
sp O75340-2 PD Programmed cell c PDCD6	+	1,38	-1,35	2	2	2	10,1	10,1	10,1	21,664	0	4,348	9,5E+07	6	O75340-2; O75340-2	25,05	24,79	24,77	23,44	22,78	24,33
tr H3BV11 H3BV Nuclear pore comp NUP93		0,62	-1,37	3	3	3	33,8	33,8	33,8	15,23	0	6,954	1,7E+08	4	H3BV11; H3BV11	25,28	24,99	25,07	25,72	22,79	22,69
tr H0YN26 H0Y1 Acidic leucine-rich ANP32A		0,83	-1,39	6	6	5	24,9	24,9	24,9	19,997	0	25,62	1,1E+09	17	H0YN26; H0YN26	28,83	28,87	26,61	27,10	26,35	26,68
sp P15924 DES1 Desmoplakin DSP	+	1,46	-1,42	102	102	102	32,6	32,6	32,6	331,77	0	323,3	3,1E+10	553	P15924; P15924	32,97	33,74	32,27	31,26	31,78	31,67
sp P26006 ITA3 Integrin alpha-3;Ita ITGA3	+	1,90	-1,42	2	2	2	1,9	1,9	1,9	116,61	0	4,294	1,3E+08	5	P26006; P26006	25,07	24,99	25,30	23,18	24,27	23,65
tr F8W6P5 F8W Hemoglobin subur HBB;HBD	+	2,28	-1,45	4	4	4	64,4	64,4	64,4	9,67	0	11,53	3,6E+08	16	F8W6P5; F8W6P5	26,98	26,89	26,22	25,04	25,40	25,31
sp Q02413 D5C Desmoglein-1 DSG1	+	1,33	-1,45	18	18	18	24,9	24,9	24,9	113,75	0	313,4	1E+10	124	Q02413; Q02413	31,20	32,15	30,66	29,37	30,26	

Supplementary Table 2. List of siRNAs

Target	Sequence (5'-3')
BRCA1	AGAUAGUUCUACCAGUAAA
ZNF384-1	GCACAUCCGUAUACACUCA
ZNF384-3	GGCAACACAACAAAGAUAA
DNA-PKcs	CUUUAUGGUGGCCAUGGAG
Ku80	CAAGGAUGAGAUUGCUUUAGU
Luciferase	CGUACGCGGAUACUUCGA
PARP1	CCAUCGAUGUCAACUAUGA
XRCC4	AUAUGUUGGUGAACUGAGA
PARP3	SMARTpool: ON-TARGETplus (Dharmacon)
Ku70	SMARTpool: siGENOME (Dharmacon)

Supplementary Table 3. List of primers

Name	Sequence (5'-3')
HindIII FW	TAAAAAGCTTATATGGAAGAATCTCACTTCAATTCTAAC
KpnI RV	TAATAATGGTACCCTAAGAGCTGGCCAGGTGC
ZNF384-3_siRNAres_HindII Rv	ACTTGAAGGGCTTGTCTTATTATGCTGTCGTCT
ZNF384-3_siRNAres_KpnI FW	AGACGACAGCATAATAAGGACAAGCCCTTCAAGT
CMV1 FW	TGGCCCGCCTGGCATTATGCC
CD4int RV	GCTGCCCCAGAATCTTCCTCT
M13 FW	GTAAACGACGGCCAGT
M13 RV	CAGGAAACAGCTATGAC
ZNF384 ΔN-terminus(1-209) Fw	CGAGCTCAAGCTTATATGGACCATCAGAAAGAC
ZNF384 ΔN-terminus(1-209) Rv	GCCGTCTTTCTGATGGTCCATATAAGCTTGAGC
ZNF384 ΔC2H2(205-410) Fw	ATGCTGGAATCAGGGCTGGCAGTGGCCCAG
ZNF384 ΔC2H2(205-410) Rv	GGCCTGGGCCACTGCCAGCCCTGATTCGTC
ZNF384 ΔC-terminus(401-516) Fw	CCGCCTGATCTTCAGCCGTTTAAACCCGCT
ZNF384 ΔC-terminus(401-516) Rv	AGCGGGTTTAAACGGCTGAAGATCAGGCGG
ZNF384 N-terminus Fw	ATTAAAAAGCTTCTATGGAAGAATCTCACTTCAATTCTAACC C
ZNF384 N-terminus Rv	TAATAATGAATTCTTAGAATTCTTAATCATCATCCTCAGGGG AGAGGAC
ZNF384 C-terminus Fw	ATTAAAAAGCTTCTCAACAGGTGCAGGCAGCAG
ZNF384 C-terminus Rv	TAATAATGAATTCCTAAGAGCTGGCCAGGTGC
ZNF384 C2H2 Fw	ATTAAAAAGCTTCTCCCGAGATGAATGACCCTTATGTCC
ZNF384 C2H2 Rv	TAATAATGAATTCCTATGCCGCTGCTGCTGCTG
pET-His6-MBP-ZNF384 Fw	TACTTCCAATCCAATGCAATGGAAGAATCTCACTTCAATTCT AAC
pET-His6-MBP-ZNF384 Rv	TTATCCACTTCCAATGTTATTACTAAGAGCTGGCCAGGTG
pET-His6-MBP-N-term Fw	ATTAAAAATATTATGGAAGAATCTCACTTCAATTCTAACCC
pET-His6-MBP-N-term Rv	TAATAATGGATVTTAATCATCATCCTCAGGGGAGAGGAC
pET-His6-MBP-C-term Fw	ATTAAAAATATTCAACAGGTGCAGGCAGCAG
pET-His6-MBP-C-term Rv	TAATAATGGATCCCTAAGAGCTGGCCAGGTGC
pET-His6-MBP-C2H2 Fw	ATTAAAAATATTCCCGAGATGAATGACCCTTATGTCC
pET-His6-MBP-C2H2 Rv	TAATAATGGATCCTTATGCCGCTGCTGCTGCTG
ssDNA T-strand / 3'overhang FW / dsDNA ^{3'-T} FW	/5Biosg/CGCTATCGTCTACGTCATGATCGCAGAAAAAGAAAA AAAAAGAA
ssDNA A-strand / dsDNA ^{5'T} FW	TTCTTTTTTTTTCTTTTTCTGCGATCATGACGTAGACGATAGC G
forward 5'overhang / dsDNA ^{5'T} RV	CGCTATCGTCTACGTCATGATCGC
5'overhang RV	/5Biosg/CGCTATCGTCTACGTCATGATCGC
3'overhang RV	/5Biosg/GCGATCATGACGTAGACGATAGCGTTCTTTTTTTTTCT TT TTTCT
dsDNA ^{3'-T} RV	AGAAAAAGAAAAAAAAAAGAACGCTATCGTCTACGTCATGATC GC
RNA U-strand	/5Biosg/GCGAUGACGUAGACGAUAGCGUUCUUUUUUU UUCUUUUUUCU

Supplementary Table 4. List of primary antibodies

Protein	Host	Company	IF	WB
BRCA1	Mouse	Santa Cruz (sc-6954)		1:500
DNA-PKcs	Mouse	Abcam (clone 18-2)		1:750
p-DNA-PKcs (S2056)	Rabbit	Abcam (ab18192)		1:750
GFP	Mouse	Roche (11814460001)		1:2500
Ku80	Rabbit	Santa Cruz (H-300, sc-9034)	1:500	1:1000
PAR	Rabbit	Enzo Lifesciences	1:1000	1:2000
Ku70	Mouse	Santa Cruz (sc-17789)		1:1000
RAD51	Mouse	GeneTex (clone 14B4)	1:200	
α -Tubulin	Mouse	Sigma (cloneDM1A, T6199)		1:5000
XRCC4	Rabbit	Gift from D. van Gent	1:500	
XRCC4	Mouse	SAB (40455)		1:1000
ZNF384	Rabbit	Abcam (ab176689)		1:1000
γ H2AX	Mouse	Millipore (clone JBW301, 05-636)	1:2000	1:1000
PARP1	Rabbit	Cell signaling (9542S)		1:1000
GFP	Mouse	Sigma (11814460001)		1:1000
H3	Rabbit	Abcam (ab1791)		1:10000
LIG4	Rabbit	Abcam (ab193353)		1:1000
53BP1	Rabbit	Novus Biologicals (NB100-304)		1:2000
γ H2AX	Mouse	Upstate (clone JBW301, #05-636)	1:100	
ZNF384	Rabbit	ATLAS antibodies	1:1000	
PARP3	Rabbit	Gift from F. Dentzer		1:10000
Geminin	Rabbit	Proteintech (10802-1AP)	1:400	
ATM	Rabbit	Cell signaling (clone D2E2)		1:2000
pATM (S1981)	Mouse	Cell signaling (4526)		1:2000
CHK1	Mouse	Santa Cruz (clone G-4, sc8408)		1 :1000
pCHK1 (S345)	Rabbit	Cell signaling (clone 133D3)		1 :1000
RPA32	Mouse	Abcam (ab1275)	1 :1000	
PARP2	Mouse	ENZO lifesciences		1 :1000
Pan-ADPr	Rabbit	Sigma (MABE1016)		1 :1500
Actin	Rabbit	Sigma (A5060)		1 :1000
MBP	Mouse	NEB (E8032S)		1 :10000

Supplementary Table 5. List of biotin-labeled DNA substrates

Name	Sequence
ssDNA T-strand	/5Biosg/- GCGATCATGACGTAGACGATAGCGTTCTTTTTTTTTCTTTTTCT
ssDNA A-strand	TTCTTTTTTTTTCTTTTTCTGCGATCATGACGTAGACGATAGCG- /5Biosg
5'overhang	TTCTTTTTTTTTCTTTTTCTGCGATCATGACGTAGACGATAGCG CGCTAGTACTGCATCTGCTATCGC- /5Biosg/
3'overhang	/5Biosg/- GCGATCATGACGTAGACGATAGCGTTCTTTTTTTTTCTTTTTCT CGCTAGTACTGCATCTGCTATCGC
dsDNA ^{3'-T}	/5Biosg/- GCGATCATGACGTAGACGATAGCGTTCTTTTTTTTTCTTTTTCT CGCTAGTACTGCATCTGCTATCGCAAGAAAAAAAAAGAAAAAGA
dsDNA ^{5'T}	TTCTTTTTTTTTCTTTTTCTGCGATCATGACGTAGACGATAGCG AAGAAAAAAAAAGAAAAAGACGCTAGTACTGCATCTGCTATCGC- /5Biosg/

Supplementary References

1. Sprague, B.L., et al., *Analysis of binding reactions by fluorescence recovery after photobleaching*. Biophys J, 2004. **86**(6): p. 3473-95.
2. Smith, R., et al., *Poly(ADP-ribose)-dependent chromatin unfolding facilitates the association of DNA-binding proteins with DNA at sites of damage*. Nucleic Acids Res, 2019. **47**(21): p. 11250-11267.