

Supplemental Figure 1. Sequence analysis of the HCT116 PNKP<sup>-/-</sup> cell clone. 65 nucleotides were deleted and 10 nucleotides were rearranged in Allele 1; 78 nucleotides were inserted and 2 separate nucleotides were mutated in Allele 2. The termination codon in allele 1 is underlined. Targeted sequences in the WT allele corresponding to the guide RNA are also underlined.

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E3-14-1      CTGGGAGTTAACCCCTCAACTACCGGGACCCAGGAGTTGAAGCCGGGGTTGGAGGGCTCT
E3-14-2      CTGGGAGTTAACCCCTCAACTACCGGGACCCAGGAGTTGAAGCCGGGGTTGGAGGGCTCT
PNKP-Exon3   CTGGGAGTTAACCCCTCAACTACCGGGACCCAGGAGTTGAAGCCGGGGTTGGAGGGCTCT
*****
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E3-14-1      CTGGGGGTGGGGGACACACTGTATTTGGTCAATGG-----T
E3-14-2      CTGGGGGTGGGGGACACACTGTATTTGGTCAATGGCCTCCACCCACTGACCCTGCGCTGG
PNKP-Exon3   CTGGGGGTGGGGGACACACTGTATTTGGTCAATGGCCTCCACCCACTGACCCTGCGCTGG
*****
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E3-14-1      GAAGATGCC-----
E3-14-2      GAAGAGACCCGCACACCAGAATCCCAGCCAGATACTCCCGCACACCAGAATCCCAGAAGA
PNKP-Exon3   GAAGAGACCCGCACACCAGAATCCCAGCCAGATACTCC-----
*****
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E3-14-1      -----
E3-14-2      GACCCGCACACCAGAATCCCAGCCAGATACTCCCGCACACCAGAATCCCAGAAGAGACCT
PNKP-Exon3   -----GCCT
*****
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E3-14-1      -----TCTGGTGTCCCAAGATTGAGAAAGAGAGATGCTGAGCTGCCGAAGAAGCATATG
E3-14-2      GGCACCCCTCTGGTGTCCCAAGATGAGAAGAGAGATGCTGAGCTGCCGAAGAAGCATATG
PNKP-Exon3   GGCACCCCTCTGGTGTCCCAAGATGAGAAGAGAGATGCTGAGCTGCCGAAGAAGCATATG
*****
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E3-14-1      CGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGAAGTTGCTAGTGTTCACCGCAGCTGGG
E3-14-2      CGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGAAGTTGCTAGTGTCCACCGCAGCTGGG
PNKP-Exon3   CGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGAAGTTGCTAGTGTTCACCGCAGCTGGG
*****
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E3-14-1      GTGAAACCCCAGGGCAAG
E3-14-2      GTGAAACCCCAGGGCAAG
PNKP-Exon3   GTGAAACCCCAGGGCAAG
*****
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Supplemental Figure 2. Sequence analysis of the HeLa PNKP<sup>-/-</sup> cell clone. Insertions of 1, 171 and 205 nucleotides were found at the target site. Alleles 1 and 3 harbor a termination codon immediately at the beginning of the insertion (underlined). Allele 2 is predicted to encode a 57-aa insertion. Targeted sequence in the WT allele corresponding to the guide RNA is also underlined. The entire region shown for allele 1 was sequenced in all cases; only the segment containing the insertion is shown.

Allele 1:

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PNKP3 (WT)          CACTACCGGGACCCAGGAGTTGAAGCCGGGGTTGGAGGGCTCTCTGGGGGTGGGGGACAC
PNKP3-1-1c         CACTACCGGGACCCAGGAGTTGAAGCCGGGGTTGGAGGGCTCTCTGGGGGTGGGGGACAC
*****

PNKP3              ACTGTATTTGGTCAATGGCCTCCACCCACTGACCCTGCGCTGGGAAGAGACCCGCACACC
PNKP3-1-1c         ACTGTATTTGGTCAATGGCCTCCACCCACTGACCCTGCGCTGGGAAGAGACCCGCACACC
*****

PNKP3              AGAATCCCAGCCAGATACTCCGCCTGGCACCCCTCTGGTGTCCAAGATGAGAAGAGAGA
PNKP3-1-1c         AGAATCCCAGCCAGATACTCCGCCTGGCACCCCTCTGGTGTCCAAGATGAGAAGAGAGA
*****

PNKP3              TGCTGAGCTGCCGAAG-AAGCGTATGCGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGA
PNKP3-1-1c         TGCTGAGCTGCCGAAGTAAGCGTATGCGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGA
*****

PNKP3              AGTTGCTAGTGTTACCCGCAGCTGGGGTGAAACCCAGGGCAAGGTGAGGGCCACGCCGA
PNKP3-1-1c         AGTTGCTAGTGTTACCCGCAGCTGGGGTGAAACCCAGGGCAAGGTGAGGGCCACGCCGA
*****

PNKP3              GGGCTGAGGGAGCCGCCACAGACTGGGACCCAATCCCACGTTTGTTCGCTGCTCTCA
PNKP3-1-1c         GGGCTGAGGGAGCCGCCACAGACTGGGACCCAATCCCACGTTTGTTCGCTGCTCTCA
*****

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1 nucleotide was inserted.

Allele 2:

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PNKP3 (WT)          GCTGAGCTGCCGAAGA-----
PNKP3-1-1a         GCTGAGCTGCCGAAGACCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGC
*****

PNKP3              -----
PNKP3-1-1a         GTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTG

PNKP3              -----
PNKP3-1-1a         ATCGCCAGCTGCCGGCGAGAAGAAGAATGGCCTGTTTCGGAACCTGATTGCCCTGAGC

PNKP3              -----AGCGTATGCGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGAAGTTGCTAGTG
PNKP3-1-1a         CTGGGCAAGCGTATGCGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGAAGTTGCTAGTG
*****

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171 nucleotides were inserted. (continued)

Allele 3:

PNKP-E3 (WT) GGCACCCCTCTGGTGTCCCAAGATGAGAAGAGAGATGCTGAGCTGCCGAAG-----  
PNKP3-1-1jR GGCACCCCTCTGGTGTCCCAAGATGAGAAGAGAGATGCTGAGCTGCCGAAGTAAGCGCGG  
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PNKP-E3 -----  
PNKP3-1-1jR CGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCTTAGCGCCCGCTC

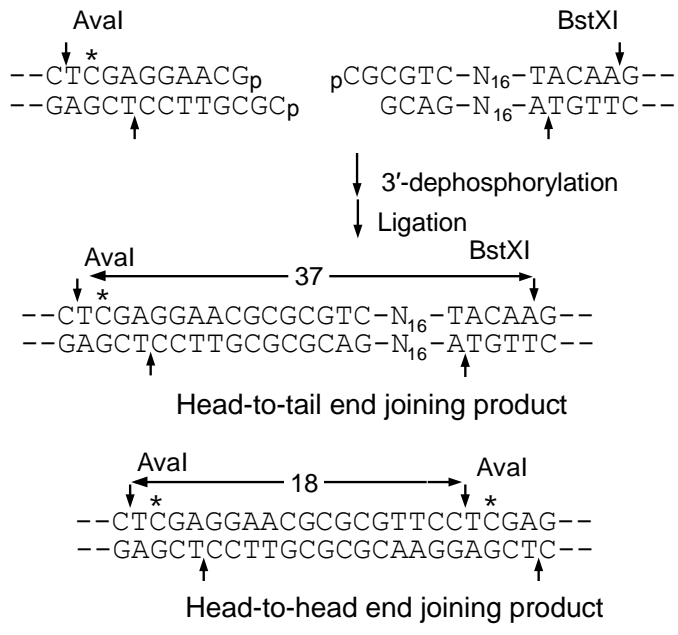
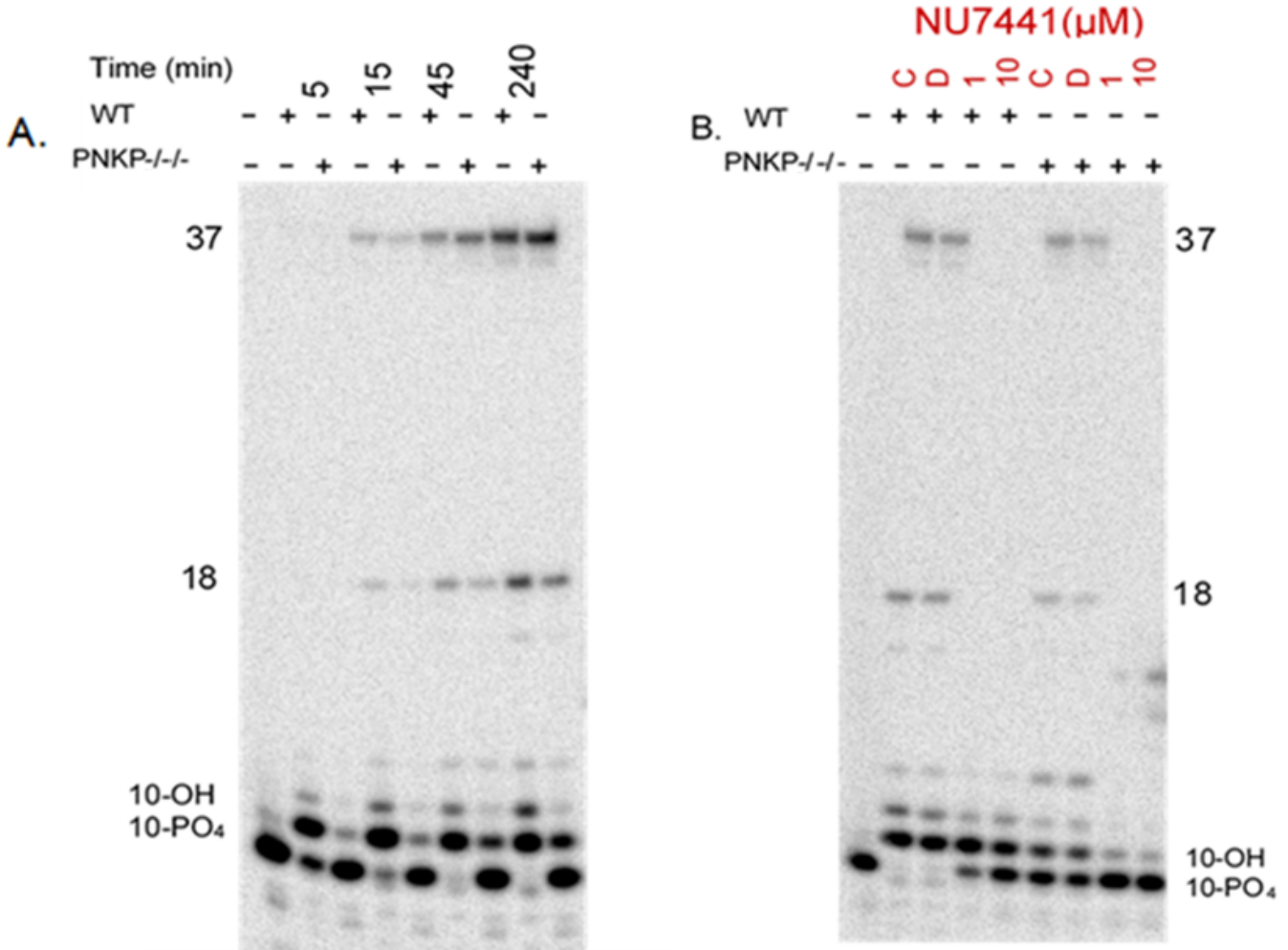
PNKP-E3 -----  
PNKP3-1-1jR CTTTCGCTTTCTTCCCTTCCCTTCTCGCCACGTTGCGCCGGCTTTCCCGTCAAGCTCTAA

PNKP-E3 -----  
PNKP3-1-1jR ATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAAC

PNKP-E3 -----AAGCGTATGCGGAAGTCAAACCCCGGCTGGGAGAACTTGGAGAA  
PNKP3-1-1jR TTGATTTGGGCGATGGAAGCGTATGCGGAAGTCAAACCCCGGCTGGGAGA  
ACTTGGAGAA  
\*\*\*\*\*

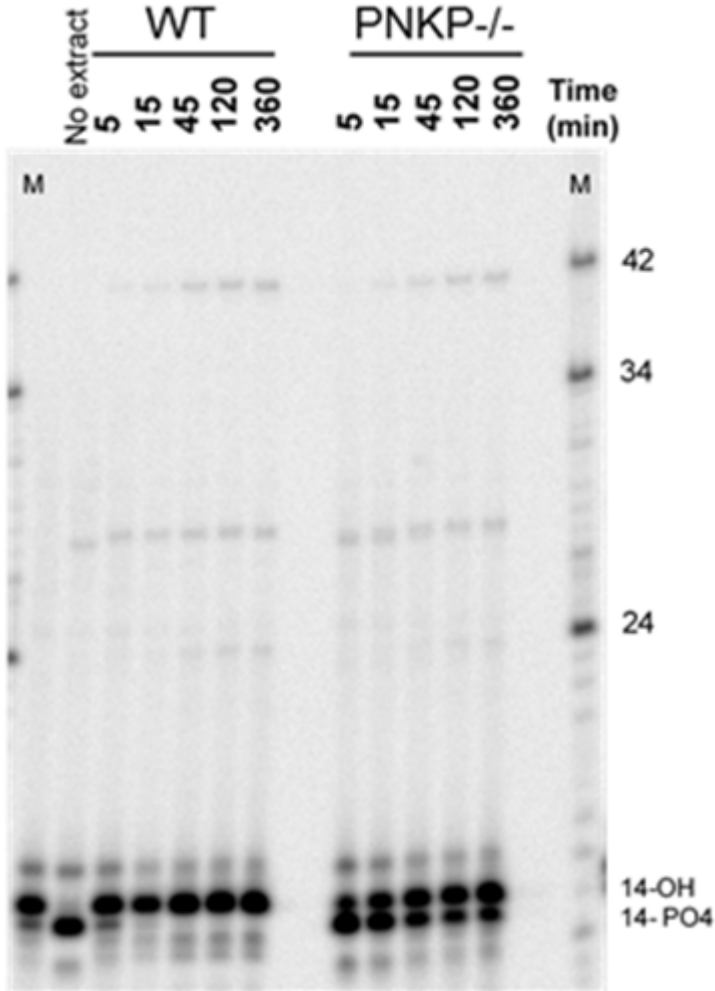
205 nucleotides were inserted.

Supplemental Figure 3. Dephosphorylation and end joining of a recessed 3'-phosphate DSB in HeLa and PNKP<sup>-/-</sup> whole-cell extracts and the effect of DNA-PKi. The substrate shown below was incubated in extracts for the indicated times (A), cut with *Ava*I and *Bst*XI, and labeled products analyzed on a sequencing gel. In (B), NU7441 (DNA-PKi) was added 10 min before addition of substrate, followed by incubation for 6 hr. "C" = incubation with no DMSO; "D" = incubation in 1% DMSO (solvent for NU7441). The unprocessed substrate (10-mer) and the head-to-tail end joining product (37-mer) are one base longer than in Fig. 3 because of cleavage by *Ava*I instead of *Taq*I. See Fig. 3B for quantitation of these results.

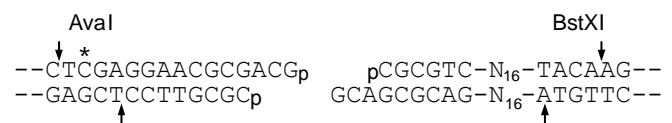
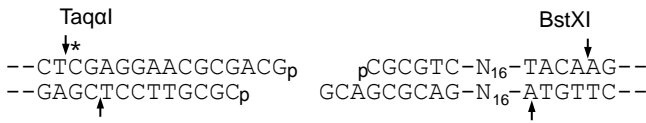
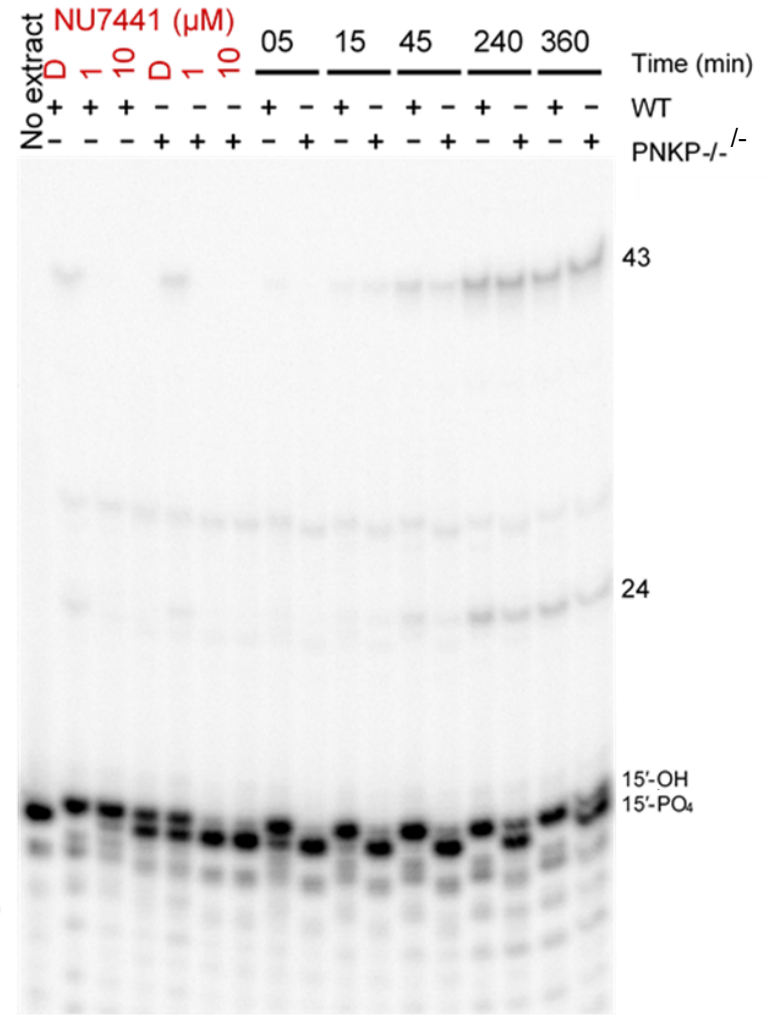


Supplemental Figure 4. Dephosphorylation and end joining of the 3'-overhang 3'-phosphate DSB substrate in whole cell extracts of HCT116 (A) or HeLa cells (B) and their PNKP-deficient derivatives, and the effect of DNA-PKi. The substrate shown below was incubated in extracts for the indicated times, cut with BstXI and either TaqI (A) or Aval (B), and labeled products analyzed on a sequencing gel. In (B), NU7441 (DNA-PKi) was added 10 min before addition of substrate, followed by incubation for 6 hr. "D" = incubation in 1% DMSO (solvent for NU7441). The unprocessed substrate and the head-to-tail end joining product are one base longer in (B) than in (A) because of cleavage by Aval instead of TaqI. See Fig. 4 and Fig. 7E-F for quantitation of these results.

**A. HCT116.**

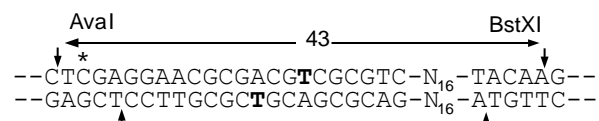
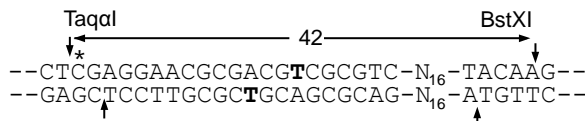


**B. HeLa**



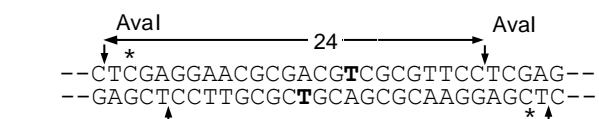
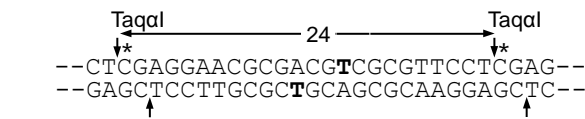
3'-dephosphorylation  
 Alignment  
 Gap filling (T)  
 Ligation

3'-dephosphorylation  
 Alignment  
 Gap filling (T)  
 Ligation



Head-to-tail end joining product

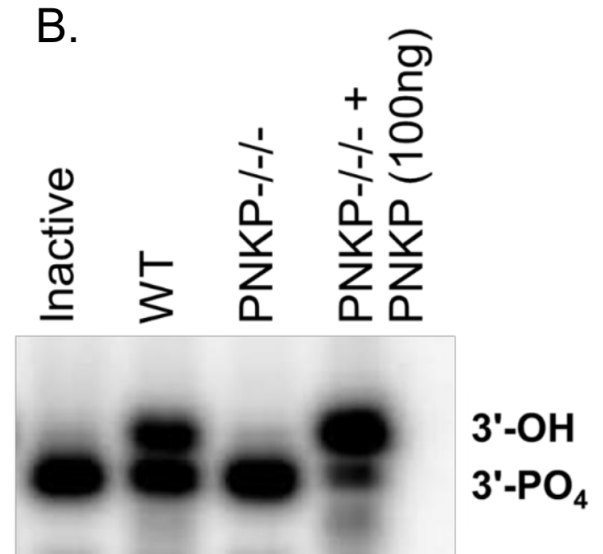
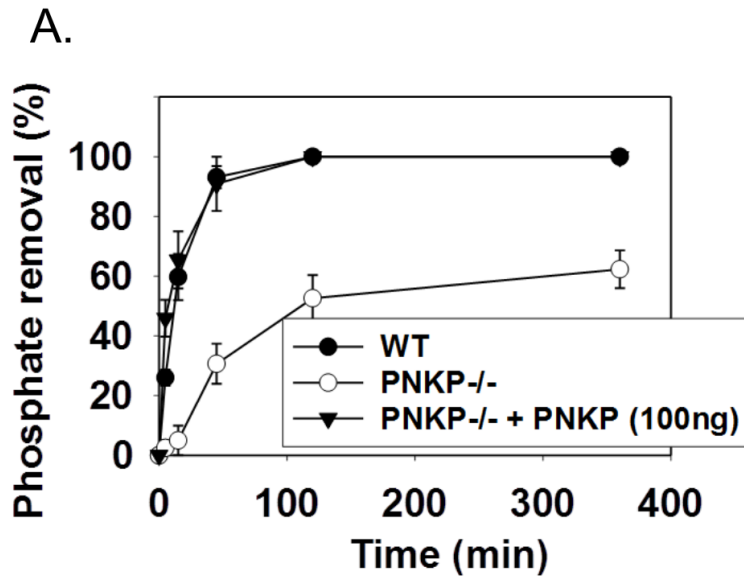
Head-to-tail end joining product



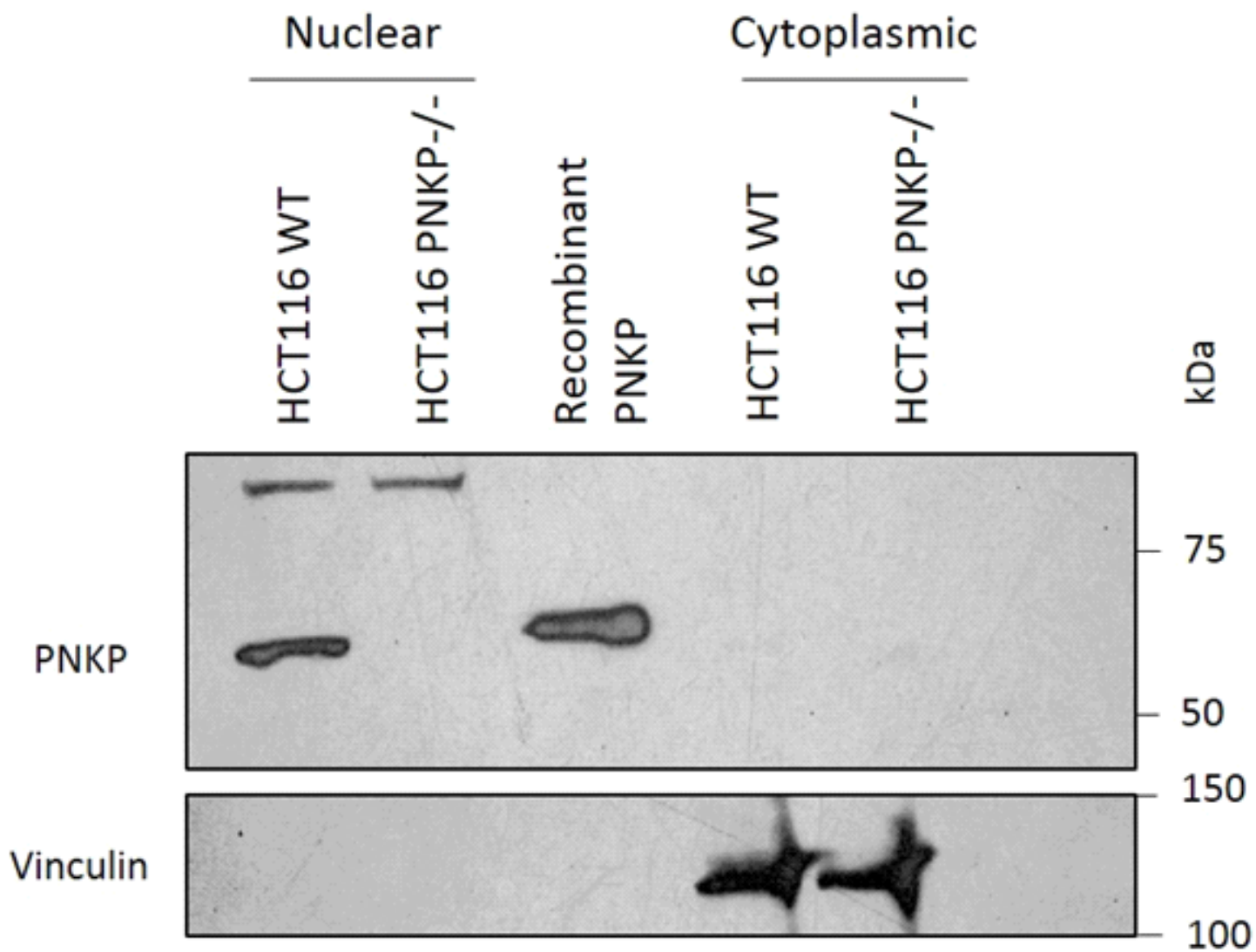
Head-to-head end joining product

Head-to-head end joining product

Supplemental Figure 5. Restoration of 3'-dephosphorylation activity in whole-cell extracts by addition of recombinant PNKP. **A.** A substrate bearing a 3'-phosphate on a 1-base 3' overhang was incubated for the indicated times in WT and PNKP<sup>-/-</sup> HCT116 extracts, as well as PNKP<sup>-/-</sup> extracts supplemented with 100 ng PNKP. Dephosphorylation was assessed as in Fig. 4. Error bars indicate mean ± SEM for 3 experiments. **B.** A substrate with a 3'-phosphate on a 3-base 3' overhang was incubated for 1.5 min in HeLa extract, PNKP<sup>-/-</sup> extract, or PNKP<sup>-/-</sup> extract supplemented with 100 ng PNKP, and dephosphorylation was similarly determined.

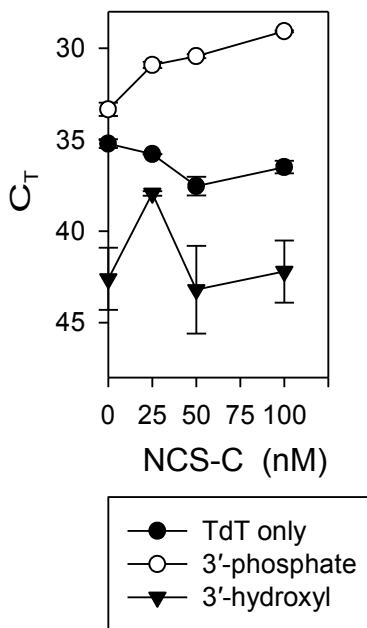


Supplemental Figure 6. Nuclear HCT116 and PNKP<sup>-/-</sup> extracts lack the cytoplasmic marker vinculin. Nuclear and cytoplasmic extracts were prepared using a BioVision fractionation kit, and 50 µg of each were analyzed by PAGE and western blot.



Supplemental Figure 7. Formation of 3'-hydroxyl and 3'-phosphate DSB termini following treatment of isolated human DNA with NCS-C. HCT116 DNA at 40  $\mu\text{g/ml}$  was treated with the indicated concentrations of NCS-C in the presence of 5 mM glutathione at 22°C for 1 hr. DSB termini were then analyzed by LMPCR as in Fig. 9. Results are from a single experiment and error bars represent mean  $\pm$  SD for 2 PCR reactions. NCS-C concentrations were chosen to give approximately the same level of 3'-phosphate termini as treatment of cells with 5  $\mu\text{M}$  NCS-C. Only 3'-phosphate ends and not 3'-hydroxyl ends show a concentration-dependent increase upon NCS-C treatment, and in contrast to DNA in treated cells, which contain roughly equal numbers of 3'-phosphate and 3'-hydroxyl ends, the treated isolated DNA contains at the highest NCS-C concentration 8,000 times as many 3'-phosphate as 3'-hydroxyl DSB termini (difference of 13 PCR cycles in  $C_T$ ). Thus NCS-C does not directly induce any 3'-hydroxyl-terminated DSBs and any such termini must have been formed by 3'-dephosphorylation in cells.

### NCS-C-treated DNA





Supplemental Fig. 8. Formation of 3'-hydroxyl and 3'-phosphate DSB termini following treatment of HeLa WT and PNKP<sup>-/-</sup> cells with NCS-C. Cells were incubated in suspension at 22°C for the indicated times and DSB ends were analyzed by LMPCR as in Fig. 9. Results are from a single experiment and error bars represent mean ± SD for 2 PCR reactions.

