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Corrigendum

Mechanism of efficient double-strand break repair by a long non-coding RNA

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The Authors wish to correct an error in Figure 6. In Figure 6B the panel label should read ‘Ku + DNA-PKcs + LINP1, 6 kbp bridge’ instead of ‘Ku + DNA-PKcs + PAXX, 6 kbp bridge’.

The published article has been updated. This error does not affect the conclusions of the article.

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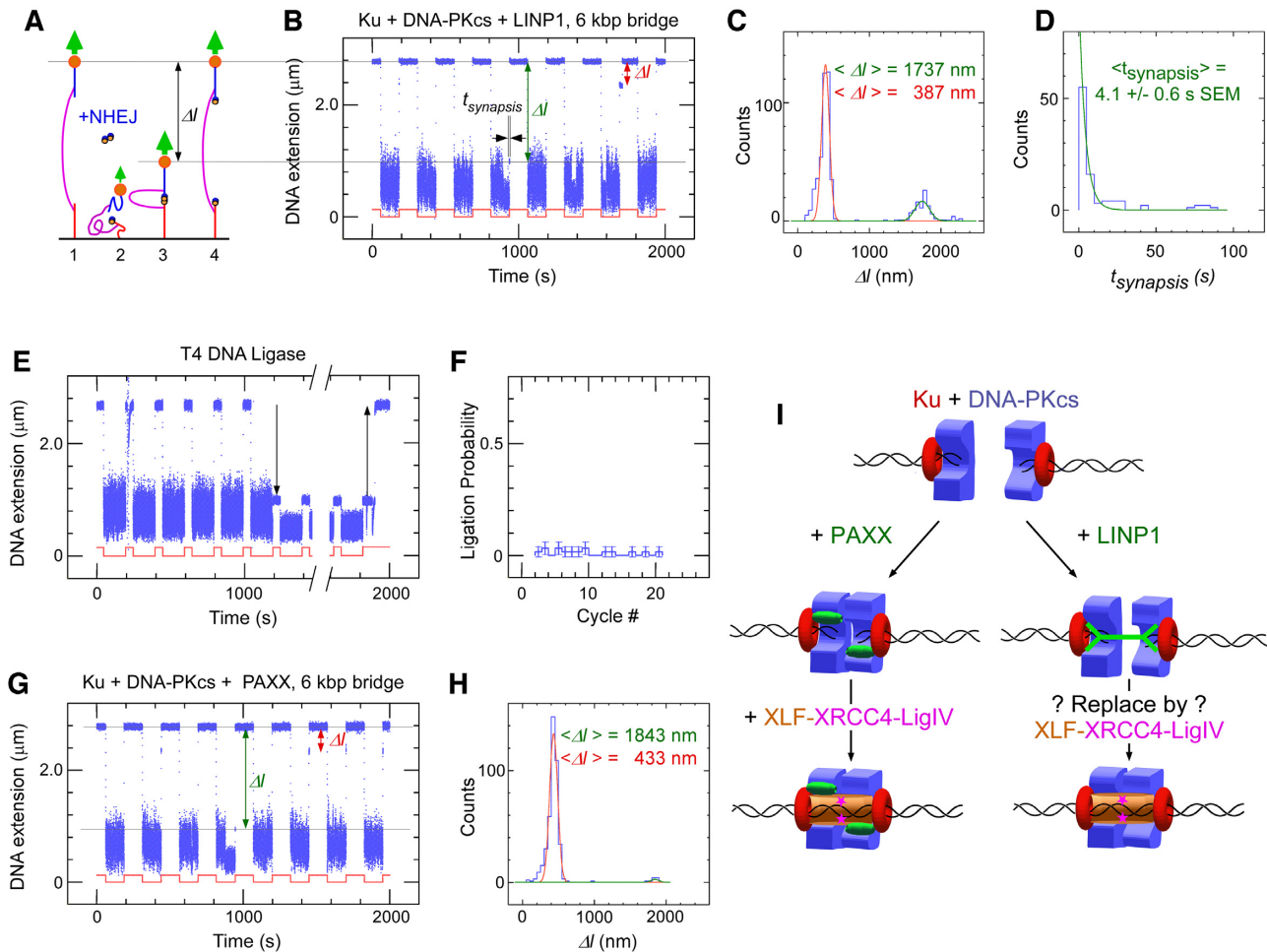


Figure 6. LINP1 is able to promote DNA-PK-dependent synthesis on DNA constructs with a 6 kbp bridge. (A) Sketch of the molecular DNA forceps with 6 kbp bridge extended in a magnetic trap. Two ends of the construct are attached to the slide surface and magnetic bead, respectively. The bead is initially held by a 1.4 pN force (1) before the force is lowered to 0.001 pN (2) allowing the two DNA ends to meet in the presence of NHEJ components. The force is then raised again, but any synthesis prevents the bead from recovering its original position (3) until synthesis is broken (4). (B) Representative time-trace for Ku + DNA-PKcs + full-length LINP1 obtained upon application of the force-modulation pattern (red). DNA is prepared with blunt ends by SmaI digest. The fourth pulling cycle shows an end-interaction rupture event which can be characterized by both the change in DNA extension upon rupture, Δl , and the duration of the synaptic event prior to rupture, t_{synapsis} . (C) Histogram of DNA extension change, Δl , upon synthesis rupture in the presence of Ku + DNA-PKcs + full-length LINP1. Green line and red line are from a fit to a double Gaussian distribution, with a peak (green) at 1737 nm and displaying 101 nm standard deviation ($n = 95$ events), and a peak (red) at 387 nm and displaying 54 nm standard deviation ($n = 395$ events). The entire histogram contains $n = 526$ events. (D) Lifetime distribution of the specific synaptic state for Ku + DNA-PKcs + full-length LINP1 is fit to a single-exponential distribution (green line), giving a lifetime of 4.1 ± 0.6 s (SEM, $n = 95$). (E) Representative time-trace obtained by force-cycling in the presence of T4 DNA ligase a forceps DNA prepared with sticky ends by XmaI digest. A stable, ~ 1.7 μm reduction in extension is observed (down arrow), and is reversed upon introduction of Sma I (up arrow). (F) Histogram of ligation events per cycle in the presence of T4 DNA ligase. (G) Representative time-trace obtained as in (B) but in the presence of Ku + DNA-PKcs + PAXX. (H) Histogram of DNA extension change, Δl , upon synthesis rupture in the presence of Ku + DNA-PKcs + PAXX. Green line and red line are from a fit to a double Gaussian distribution, with a peak (green) at 1843 nm displaying a 57 nm standard deviation ($n = 10$ events), and a peak (red) at 433 nm displaying a 56 nm standard deviation ($n = 392$ events). (I) Schematic model for the role of LINP1 from single-molecule studies.