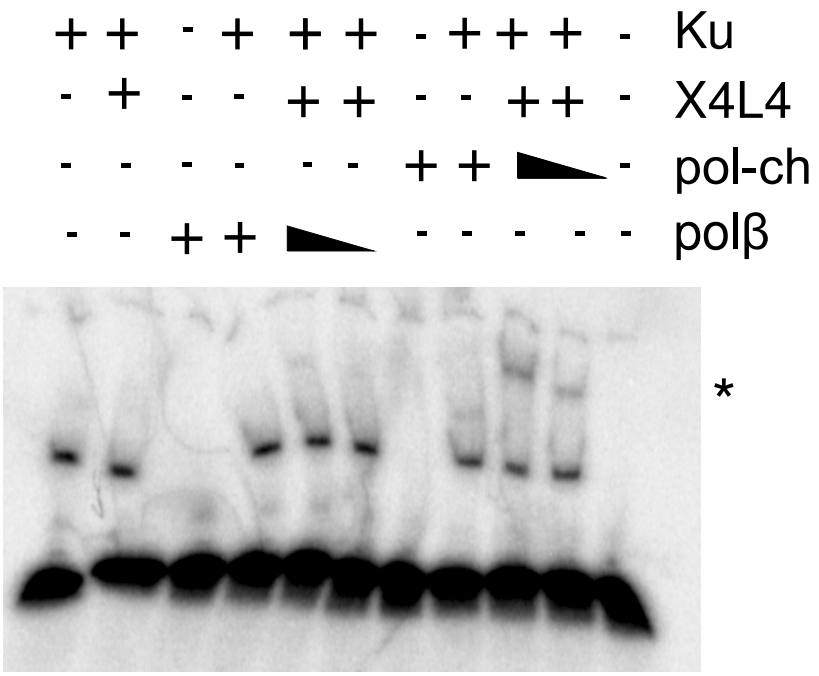
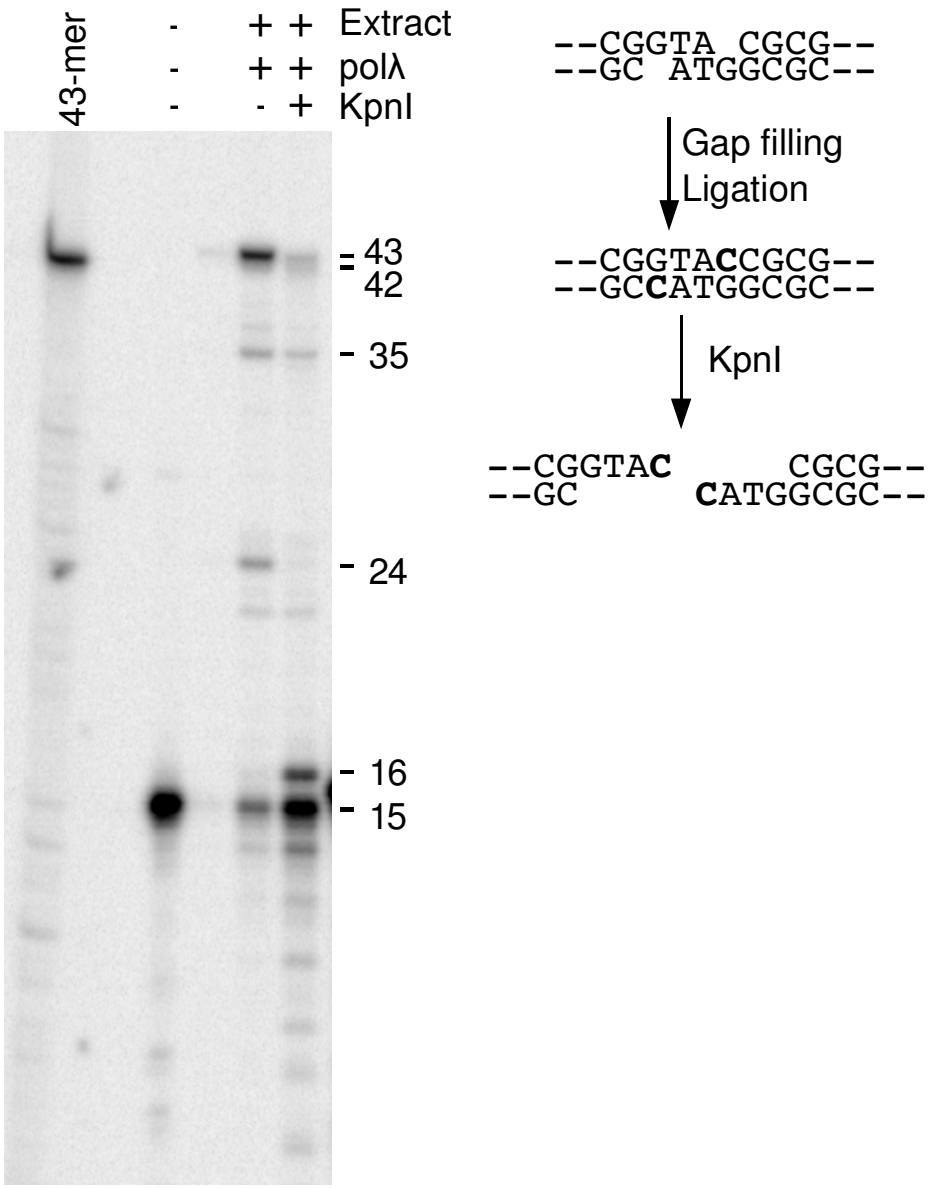


Supplementary Figure 1. Interaction of the chimeric polymerase (pol-ch) and polβ with core end joining proteins. A labeled 60-base duplex was incubated with 5 nM Ku, 25 nM X4L4, and 25 or 100 nM polymerase ("+" = 100 nM), and complexes were resolved on a neondenaturing gel. An apparent ternary complex (*) is formed tenfold more efficiently by the chimera than by polβ (2.5% vs 0.24% of total labeled duplex at 100 nM), confirming the importance of the BRCT domain in polymerase binding to the end joining complex.



Supplementary Figure 2. Verification of the joint sequence of the major product formed from -GTA 3' overhangs. The substrate shown, bearing a partially self-complementary -GTA overhang at each end, was incubated in nuclear extracts supplemented with X4L4 and polλ, then cut with AvaI and BstXI, as described in Fig. 6. One sample was also cut with KpnI, which cleaves the expected repair joint (GGTAC↓C) in the 43-base product. KpnI cleavage reduced the abundance of 43-mer from 41% to 2.6%, yielding the expected labeled 16-mer, thus confirming accurate repair by alignment-based gap filling and ligation. Note that the putative 24-base accurate head-to-head end joining product is also eliminated by KpnI cleavage as expected.