

Figure S1

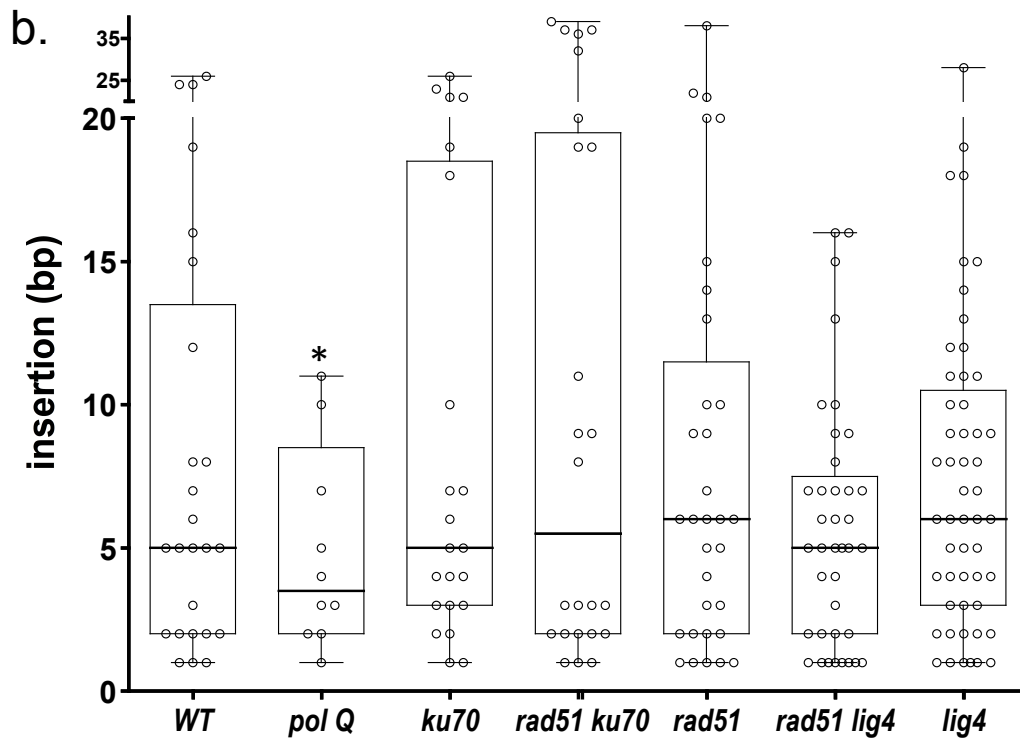
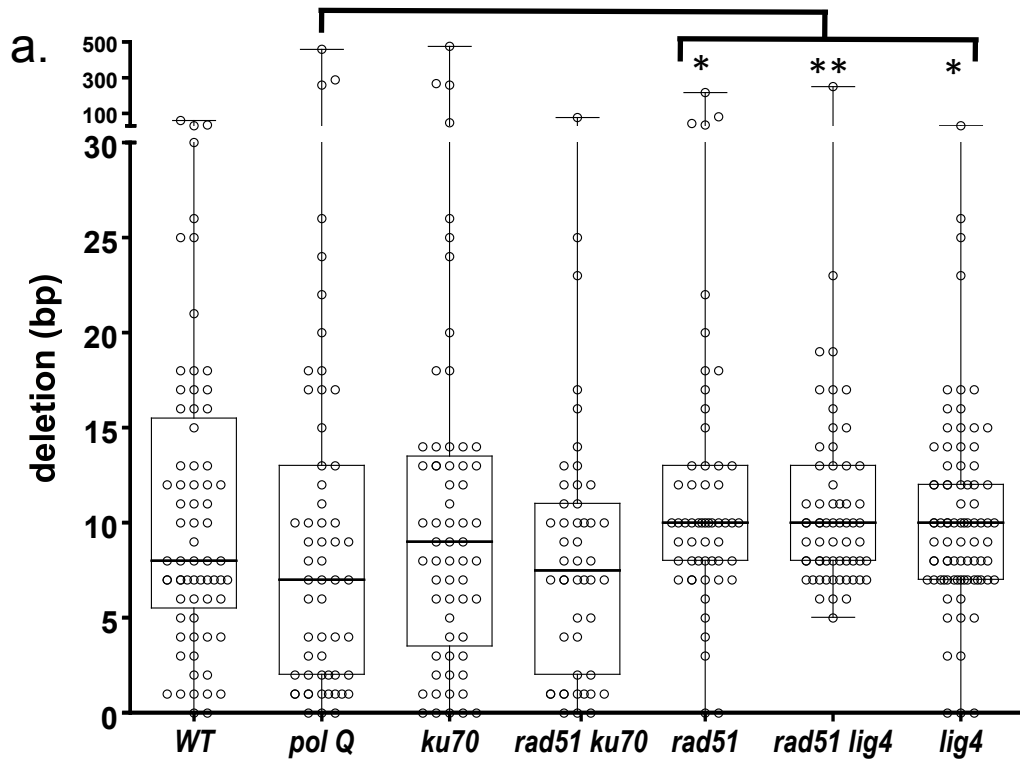


Figure S1. Size of deletions and insertions is not affected by C-NHEJ deficiency.

a. Box and whisker / scatter plots showing distribution of deletion sizes by genotype. Each circle represents one sequence. Bold horizontal lines indicate medians. The median deletion size in WT (8 bp) is not significantly different from the median net deletion in any other genotype assayed. The median deletion size in *polQ* mutants is significantly smaller than that in *rad51* ($p=0.01$), *rad51 lig4* ($p<0.01$), and *lig4* ($p=0.02$) flies (2-tailed Mann-Whitney test). This is consistent with *polQ* mutants less frequently resecting to repeats that could be used for SD-MMEJ. WT $n=70$; *pol Q* $n=57$; *ku70* $n=62$; *rad51 ku70* $n=48$; *rad51* $n=55$; *rad51 lig4* $n=63$; *lig4* $n=83$.

b. Box and whisker / scatter plot of sizes of net insertions at end-joining repair junctions by genotype. Bold horizontal lines indicate medians. Genetic background did not significantly affect median insertion length ($p=0.7$, Kruskal-Wallis test). Variance of insertion lengths is significantly decreased relative to wild-type in *polQ* mutants ($p=0.05$, Levene's Test).

Figure S2

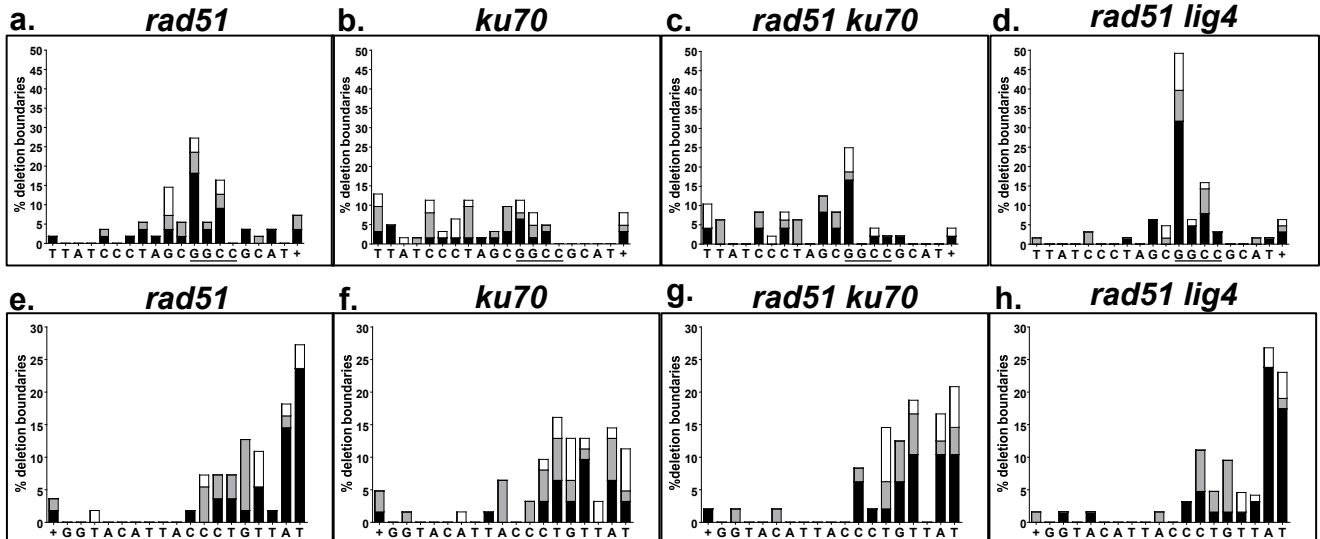


Figure S2. Combined effects of sequence context and genotype on deletion boundary frequency.

Histograms show right (a-d) and left (e-h) deletion boundaries in *rad51*, *ku70*, *rad51 ku70*, and *rad51 lig4* genetic backgrounds. Histograms show frequency, as percentage of total repair products, of deletion boundaries associated with net insertions (black), junctional microhomologies (gray) and apparent blunt joins (white). "Deletion boundary" is defined as the position (including junctional microhomologies, if any) at which an uninterrupted match between the original [lw] sequence and the repair junction resumes. X axis indicates the top strand sequence. Deletions extending beyond the sequence depicted are represented by a plus sign (+).

Figure S3

a.

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TCGGTACATTACCCTGTaccctGCCGCATAGGCCACTAGT
AATTCGGTACATTACCCataGGCCGCATAGGCCACTAGTGG
GTACATTACCCTGTTATaacagGGCCGCATAGGCCACTAGT
GTACATTACCCTGTTATagtGGCCGCATAGGCCACTAGTGG
  
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b.

original	CGGTACAT <u>T</u> accct <u>GT</u> TAT	CCCTAGC <u>G</u> GCCGCATA
repaired	CGGTACAT <u>T</u> accct <u>GT</u> ---	- <u>accct</u> - <u>G</u> GCCGCATA
original	ATTACC <u>C</u> TGTTAT	CCCTAGC <u>GGCC</u> <u>G</u> ata <u>GGCC</u> AC
repaired	ATTACC <u>C</u> -- <u>ata</u> -	----- <u>GGCC</u> <u>G</u> ata <u>GGCC</u> AC
original	CGGTACATTA <u>CC</u> ctggt <u>AT</u>	CCCTAGC <u>GG</u> CCGCATA
repaired	CGGTACATTA <u>CC</u> ctggt <u>AT</u>	- <u>aacag</u> - <u>GG</u> CCGCATA
original	CCCTGTTA <u>T</u>	CCCTAGC <u>GGCC</u> GCATA <u>GGCC</u> act <u>A</u> GT
repaired	CCCTGTTA <u>T</u>	-- <u>agt</u> -- <u>GGCC</u> GCATA <u>GGCC</u> act <u>A</u> GT

Figure S3. Structure of indels formed by repair events includes characteristic patterns of short repeats present in the original sequence. Additional examples illustrating the patterns described in the caption to Figure 4. Sequences are (top to bottom) Supplemental Table S7 sequence 31; Supplemental Table S6 sequence 6; Supplemental Table 7 sequence 65; Supplemental Table S6 sequence 8.

Figure S4

a. **step 1)** CCGTACATTACCCTGTTA ggcata GGCCGCATAGGCC ACTA
step 2) CCGTACATTACCCTGT TAGgc ata GGCCGCATAGGCC ACTA

b. **step 1)** TACAT TACCCT GTTA Aggcta gt GGCCGCATAGGCCACTAGT
step 2) TACATTACCCTGTTA ggg tagt GGCCGCATAGGCCACTAGT

c. **step 1)** TACAT TACCCTGTTA acagggta GGCCGCATAGGCCACTAG
step 2) TACATTACCCTGTTA acaggg ta GGCCGCATAGGCC ACTAG

d.

1)	CGGTACATTA CCCTGT Gtacatta cattacattacattacccggtacattatcca	CTAGC (13bp) ACTAGTGGAT
2)	CGGTACATTA CCCTGT acattacattacattacccggtacattatcca	CTAGC (13bp) ACTAGTGGAT
3)	CGGTACATTA CCCTGT acattacattacattacccggtacattatcca	CTAGC (13bp) ACTAGTGGAT
4)	CGGTACATTA CCCTGT acattacattacattacccggtacattatcca	CTAGC (13bp) ACTAGTGGAT
5)	CGGTACATTACCC TGT acattacattacattacattacc cgggtacattatcca	CTAGC (13bp) ACTAGTGGAT
6)	CGGTACATTA CCCTGT acattacattacattacattacc cgggtacattatcca	CTAGC (13bp) ACTAGTGGAT
7)	CGGTACATTACCC TGT acattacattacattacattacc cgggtacattatcca	CTAGC (13bp) ACTAGTGGAT

e.

1)	CATTACCCTGTTAT Aaat tataaattataattattatagt	GGCCGCATAGGCCACTAG
2)	CATTACCCTGTTAT Aaattataa ttataaattattatagt	GGCCGCATAGGCCACTAG
3)	CATTACCCTGTTAT Aaattataa ttataa ttattatagt	GGCCGCATAGGCCACTAG
4)	CATTACCCTGTTAT Aaattataa tataattat tatagt	GGCCGCATAGGCCACTAG
5)	CATTACCCTGTTAT Aaattataa tataa ttata gt	GGCCGCATAGGCCACTAG
6)	CATTACCCTGTTAT Aaattataa tataa ttata tagt GGCCGCATAGGCCACTAG	

Figure S4. Repair product sequences consistent with multi-step SD-MMEJ.

Repair by multi-step SD-MMEJ produces repair products that can be "dissected" into an uninterrupted series of overlapping direct and/or inverted repeats spanning the insertion and flanking sequence on both sides. Only top strands (3'-5') shown. Notational conventions as described in Figures 5 and 6.

a. SD-MMEJ by two sequential rounds of direct (loop-out) synthesis from the right side of the DSB. *Step 1:* Bottom strand at leftmost GGCC (red, underlined) anneals to the top strand at the right-hand GGCC (white on red). GCATA (white on red) templates synthesis resulting in 3'-CG... (bottom strand, not shown).

Step 2: The 3' CG base-pairs with the leftmost GC in TAGGC (white on red). TAG (white on red) templates synthesis producing 3'-AT... (bottom strand, not shown) which anneals to the top strand TA on the other side of the DSB (red, underlined, capitalized). Sequence shown is sequence 113 in table S8.

b. SD-MMEJ repair via snap-back synthesis on each side of the DSB. *Step 1:* Terminal base A of the 3' end to the left of the DSB (blue, capitalized, underlined) anneals to T four bp to the left (white on blue). Primer extension and dissociation result in a single stranded 3' end with newly synthesized sequence gggta (blue, lowercase, underlined). *Step 2:* The 3' CCGG (complementary to blue underlined GGCC) snaps back and anneals to GGCC (white on blue). ACTA (white on blue) templates synthesis of 5'...TGAT-3' (bottom strand, not shown), which has two bp of microhomology to the 3' end produced in Step 1. Sequence shown is sequence 114 in table S8.

c. SD-MMEJ repair with snap-back synthesis on the left DSB end and loop-out synthesis on the right. Sequence shown is sequence 11 in table S8.

d. Repair product with a long insertion consistent with repair by six iterative rounds of loop-out SD-MMEJ on the right side of the DSB and a single round of snap-back synthesis on the left. Sequence shown is sequences 93 and 94 in table S8.

e. Repair product with a long insertion consistent with repair by five iterative rounds of snap-back SD-MMEJ on the left side of the DSB and one round of snap-back SD-MMEJ on the right. Self-complementarity of the insertion suggests that newly synthesized sequence was subsequently used as a template. Sequence shown is sequence 8 in table S8.

Figure S5

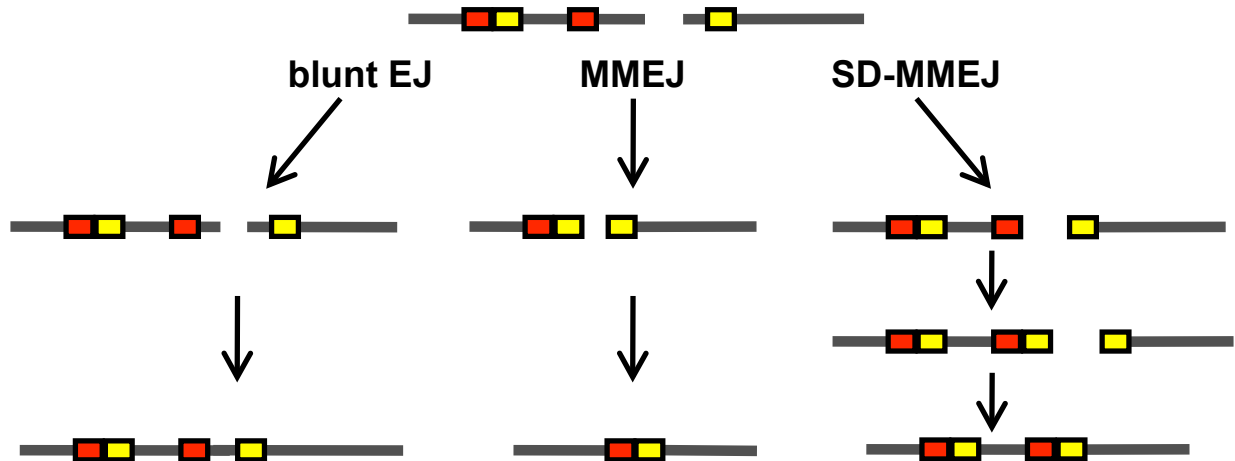


Figure S5. SD-MMEJ events without insertions can be distinguished from true blunt joins by repair product structure.

Deletions associated with true blunt joins (left) do not correlate with any short repeats present in the repair product and do not create longer repeats at the apparent point of ligation. SD-MMEJ events where the template for the newly synthesized microhomology is adjacent to the primer (right) do not produce net insertions, but do create a repeat where one instance of the repeated motif contains the point of ligation. Identically colored boxes represent direct repeats.

Figure S6

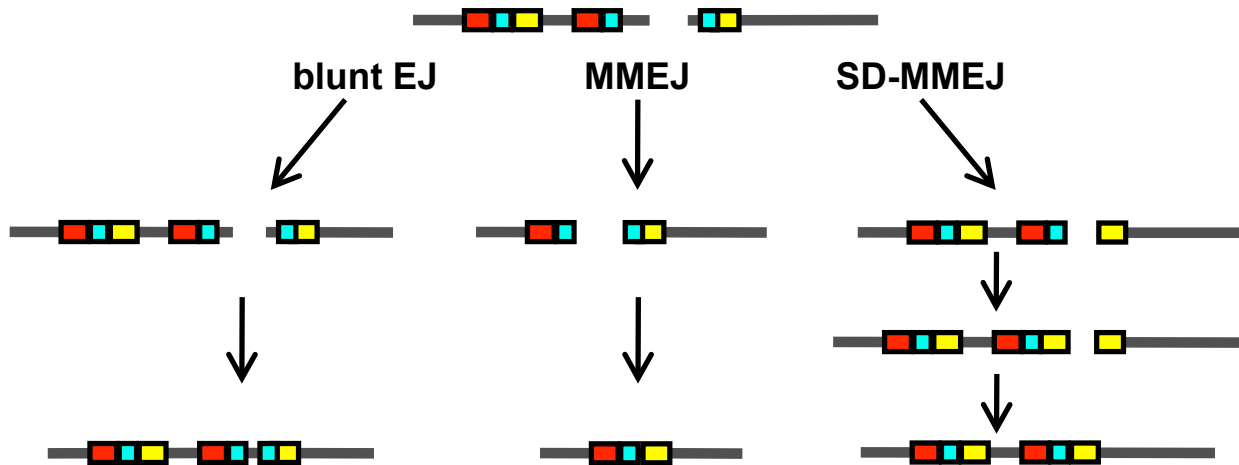


Figure S6. SD-MMEJ events can be distinguished from MMEJ at pre-existing microhomologies by repair product structure.

Deletions associated with true blunt joins (left) do not correlate with any short repeats present in the repair product and do not create longer repeats at the apparent point of ligation. MMEJ at pre-existing direct repeats (center) does not create a longer repeated motif. SD-MMEJ event (right) can create a junction that is locally indistinguishable from MMEJ at pre-existing microhomologies, but unlike MMEJ at pre-existing microhomologies, creates a longer repeated motif. Identically colored boxes represent direct repeats.

Table S1.

	mean (bp)	median (bp)
WT	1.8	2.0
<i>polQ</i>	1.9	2.0
<i>ku70</i>	2.0	2.0
<i>rad51 ku70</i>	1.6	1.0
<i>rad51</i>	1.8	1.0
<i>rad51 lig4</i>	2.1	2.0
<i>lig4</i>	1.9	1.0

Supplemental Table S1. Mean and median junctional microhomology lengths by genotype

Mean and median junctional microhomology length by genotype. Genetic background has no significant effect on either the mean ($p=0.91$, one-way ANOVA) or the median ($p=0.85$, Kruskal-Wallis test) junctional microhomology length.

Table S2.

original [lw] sequence	repair product
CCCT _G TTAT CCCTAGC _G GCCGCATAGGCCACT	ATTACCCT _T . <u>G</u> .GCCGCATAGGCCACT (19) ^A
CGGTACATTACCCT _{TG} TTAT CCCTAGCGGCCGCATA	AATTCGGTACATT _{TA} .CCCT _T AGCGGC (15) ^B
TCGGTACATTACCCT _{TG} TTAT CCCTAGCGG _{CCG}	AATTCGGTACAT _{TAC} .CCGCATAGG (10) ^D
TACATTACCCT _G TTAT CCCTAG _G CGGCCGCATA	ACATTACCCT _T .G.CGGCGGCATAGGC (9) ^E
TACATTACC _{CTG} TTAT CCCTAG _G GCCGCATA	CGGTACATTACC _T CGGCCGCATAGG (7)
T _{CGGT} ACATTACC _{CTG} TTAT CCCTAGCGG _{CCG}	CCGAATT _{CGGT} ACAT _{TA} .CCGCATA (6) ^F
TACA _{TTA} CCCTG _{TTA} TTAT CCCTAGCGGCCGCATA	CGGTACA _T TTA _T TCCCTAGCGGCCGC (6)
TACATTACC _{CTG} TTAT CCCTAGCGGCCGCATA	GTACATTA _{CCC} .T.TAT _{CCCT} AGCGG (4) ^G
TACATTACCCT _G TTAT CCCTAGCGGCCGCATA	GGTACATTACCCT _T CGGCATAGGC (4)
CGGTACATTACCCT _{TG} TTAT CCCTAGCGGCCGCATA	ATTCGGTACATTACCCT _{TG} .T _T ATCCC (3) ^H
CATTACCCTG _T TTAT CCCTAGCGGCCGC _{ATAGG}	CCTGT _{TA} .T _T AGCGGCCGC _{ATAG} GCC (3) ^I
AGCCGAATT _{CGGT} ACATTACCCTG _T TTAT CCCTAG _{CGGC}	AGCAGCCGAATT _T .CGG.CCGCATAGG (3) ^J

Supplemental Table S2. The SD-MMEJ model explains bias in frequency of specific junctional microhomologies.

The most frequently observed junctional microhomology (top row) is consistent with SD-MMEJ repair with a 4 bp direct/inverted repeat as a primer (Compare Figure 3a-c). Junctional microhomologies not consistent with SD-MMEJ are not highlighted. Number of times a sequence was independently recovered is indicated in parentheses. Positions of bottom and top strand nicks in the original sequence indicated by subscripted/superscripted vertical lines. Microhomologies are indicated in the original sequence as white on black with dotted underlines. Blue and red boxed/underlined repeated motifs are SD-MMEJ consistent. Lettered superscripts cross-reference Table S4.

Table S3.

	sequences of apparent blunt joins □ indicates deleted sequence		genotype	deln (bp)
1 ^{A1}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹	WT ¹	7
2 ^{A2}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ²	WT ²	7
3 ^{A3}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ³	WT ³	7
4 ^{A4}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ⁴	WT ⁴	7
5 ^{A5}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ⁵	<i>ku70</i> ¹	7
6 ^{A6}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ⁶	<i>lig4</i> ¹	7
7 ^{A7}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ⁷	<i>rad51 ku70</i> ¹	7
8 ^{A8}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ⁸	<i>rad51 ku70</i> ²	7
9 ^{A9}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ⁹	<i>rad51 lig4</i> ¹	7
10 ^{A10}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁰	<i>rad51 lig4</i> ²	7
11 ^{A11}	GCAGCCGAATTCGGTACATTACCCTGTTAT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹¹	<i>polQ</i> ¹	7
12 ^{B1}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹²	WT ⁵	10
13 ^{B2}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹³	<i>rad51</i> ¹	10
14 ^{B3}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁴	<i>ku70</i> ²	10
15 ^{B4}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁵	<i>lig4</i> ²	10
16 ^{B5}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁶	<i>lig4</i> ³	10
17 ^{B6}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁷	<i>lig4</i> ⁴	10
18 ^{B7}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁸	<i>rad51 lig4</i> ³	10
19 ^{B8}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ¹⁹	<i>rad51 lig4</i> ⁴	10
20 ^{B9}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ²⁰	<i>rad51 lig4</i> ⁵	10
21 ^{B10}	GCAGCAGCCGAATTCGGTACATTACCCTGT□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ²¹	<i>polQ</i> ²	10
22 ^{C1}	AGCAGCCGAATTCGGTACA <u>TTACCC</u> TG <u>TTA</u> □ <u>CCC</u> TAGCGGCCGCATAGGCCACTAGTGGAT	II ¹	WT ⁶	1
23 ^{C2}	AGCAGCCGAATTCGGTACA <u>TTACCC</u> TG <u>TTA</u> □ <u>CCC</u> TAGCGGCCGCATAGGCCACTAGTGGAT	II ²	WT ⁷	1
24 ^{C3}	AGCAGCCGAATTCGGTACA <u>TTACCC</u> TG <u>TTA</u> □ <u>CCC</u> TAGCGGCCGCATAGGCCACTAGTGGAT	II ³	<i>ku70</i> ³	1
25 ^{C4}	AGCAGCCGAATTCGGTACA <u>TTACCC</u> TG <u>TTA</u> □ <u>CCC</u> TAGCGGCCGCATAGGCCACTAGTGGAT	II ⁴	<i>polQ</i> ³	1
26 ^{D1}	AGCAGCCGAATTCGGTACATTACCCTGTTA□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ²²	<i>lig4</i> ⁵	8
27 ^{D2}	AGCAGCCGAATTCGGTACATTACCCTGTTA□GGCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATC	I ²³	<i>rad51 ku70</i> ³	8

28 ^{D3}	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>GGCCGCATAAGGCC</u> ACTAGTGGATCTGGATC	I ²⁴	<i>rad51 lig4</i> ⁶	8
29 ^{E1}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>CCGCATAGGCC</u> ACTAGTGGATCTGGATCCT	-	<i>rad51</i> ²	9
30 ^{E2}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>CCGCATAGGCC</u> ACTAGTGGATCTGGATCCT	-	<i>lig4</i> ⁶	9
31 ^{E3}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>CCGCATAGGCC</u> ACTAGTGGATCTGGATCCT	-	<i>rad51 lig4</i> ⁷	9
32 ^{F1}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>GCGGCCGCATA</u> GGCCACTAGTGGATCTGGA	III ¹	<i>rad51</i> ³	5
33 ^{F2}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>GCGGCCGCATA</u> GGCCACTAGTGGATCTGGA	III ²	<i>lig4</i> ⁷	5
34 ^{G1}	GCGTCGTTTAGAGCAGCAGCCGAATTCGGT- <u>GGCCGCATA</u> GGCCACTAGTGGATCTGGATC	I ²⁵	<i>rad51</i> ⁴	22
35 ^{G2}	GCGTCGTTTAGAGCAGCAGCCGAATTCGGT- <u>GGCCGCATAGGCC</u> ACTAGTGGATCTGGATC	I ²⁶	<i>polQ</i> ⁴	22
36 ^{H1}	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CCGCATAGGCC</u> ACTAGTGGATCTGGATCCT	II ⁵	<i>rad51</i> ⁵	10
37 ^{H2}	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CCGCATAGGCC</u> ACTAGTGGATCTGGATCCT	II ⁶	<i>rad51 ku70</i> ⁴	10
38 ^I	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>TAGCGGCCGCATAGGCC</u> ACTAGTGGATCTG	-	WT ⁸	3
39 ^{I2}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>TAGCGGCCGCATAGGCC</u> ACTAGTGGATCTG	-	<i>ku70</i> ⁴	3
40 ^{J1}	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CGGCCGCATAGGCC</u> ACTAGTGGATCTGGAT	II ⁷	WT ⁹	7
41 ^{J2}	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CGGCCGCATAGGCC</u> ACTAGTGGATCTGGAT	II ⁸	<i>rad51 lig4</i> ⁸	7
42 ^K	CAGCAGCCGAATTCGGTACATTACCCTGAT- <u>CCACTAGTGGAT</u> CTGGATCCTCTAGAGTCG	-	<i>ku70</i> ⁵	20
43 ^L	TCGTTTAGAGCAGCAGCCGAATTCGGTACA- <u>CTAGCGGCCGCATAGGCC</u> ACTAGTGGATCT	-	<i>ku70</i> ⁶	14
44 ^M	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CATAGGCC</u> ACTAGTGGATCTGGATCCTCTA	-	WT ¹⁰	13
45 ^N	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CCACTAGTGGAT</u> CTGGATCCTCTAGAGTCG	II ⁹	<i>rad51 lig4</i> ⁹	19
46 ^O	ACCCTTACGTGGAATAAAAAAAAAAATGAAAT- <u>GCGCCGCATAGGCC</u> ACTAGTGGATCTGGATC	-	<i>polQ</i> ⁵	459
47 ^P	TGCGTCGTTTAGAGCAGCAGCCGAATTCGG- <u>CCCTAGCGGCC</u> GCATAGGCCACTAGTGGAT	-	WT ¹¹	16
48 ^Q	AGCAGCCGAATTCGGTACATTACCCTGTTA- <u>CTAGCGGCCGCATAGGCC</u> ACTAGTGGATCT	II ¹⁰	WT ¹²	3
49 ^S	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>CGGCCGCATAGGCC</u> ACTAGTGGATCTGGAT	-	<i>rad51 lig4</i> ¹⁰	6
50 ^T	GCAGCAGCCGAATTCGGTACATTACCCTGT- <u>ACTAGTGGAT</u> CTGGATCCTCTAGAGTCGAC	-	<i>rad51 ku70</i> ⁵	23
51 ^U	TAGAGCAGCAGCCGAATTCGGTACATTACCCTGTTA- <u>GCGGCCGCATAGGCC</u> ACTAGTGGATCTGGA	IV ¹	<i>rad51</i> ⁶	12
52 ^V	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>GCGGCATA</u> GGCCACTAGTGGATCTGGATCC	-	<i>rad51</i> ⁷	8
53 ^W	GCAGCAGCCGAATTCGGTACATTACCCTGTT- <u>GCGGCCGCATA</u> GGCCACTAGTGGATCTGGA	III ³	<i>rad51</i> ⁸	8
54 ^X	CAGCAGCCGAATTCGGTACATTACCCTGTT- <u>GCGGCCGCATA</u> GGCCACTAGTGGATCTGGA	III ⁴	<i>polQ</i> ⁶	7
55 ^Y	GTTTAGAGCAGCAGCCGAATTCGGTACATT- <u>GCGGCCGCATA</u> GGCCACTAGTGGATCTGGA	-	WT ¹³	15
56 ^Z	AGCAGCAGCCGAATTCGGTACATTACCCTG- <u>CCTAGCGGCCGCATAGGCC</u> ACTAGTGGATC	-	<i>ku70</i> ⁷	5
57 ^{AA}	GCAGCCGAATTCGGTACATTACCCTGTTAT- <u>GCATA</u> GGCCACTAGTGGATCTGGATCCTCT	-	WT ¹⁴	11

58 ^{AB}	AGCAGCAGCCGAATTCGGTACATTACCCTG GC ATAG GCCA CTAGTGGATCTGGATCCTCT	-	<i>lig4</i> ⁸	15
59 ^{AC}	GCAGCCGAATTCGGTACATTACCCTGTTAT CCACTAGTGGAT CTGGATCCTCTAGAGTCG	-	<i>ku70</i> ⁸	18
60	GCAGCCGAATTCGGTACATTACCCTGTTAT C CTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	WT ¹⁵	1
61	GCAGCCGAATTCGGTACATTACCCTGTTAT C CTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	WT ¹⁶	1
62	GCAGCCGAATTCGGTACATTACCCTGTTAT C CTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	WT ¹⁷	1
63	GCAGCCGAATTCGGTACATTACCCTGTTAT C TAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	WT ¹⁸	2
64	AGCAGCAGCCGAATTCGGTACATTACCCTG CC TAGCGGCCGCATAGGCCACTAGTGGAT	n/a	WT ¹⁹	4
65	AGCAGCAGCCGAATTCGGTACATTACCCTG CC TAGCGGCCGCATAGGCCACTAGTGGAT	n/a	WT ²⁰	4
66	AGCAGCAGCCGAATTCGGTACATTACCCTG CC TAGCGGCCGCATAGGCCACTAGTGGAT	n/a	WT ²¹	4
67	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>ku70</i> ⁹	1
68	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>ku70</i> ¹⁰	1
69	AGCAGCAGCCGAATTCGGTACATTACCCTG ATCC TAGCGGCCGCATAGGCCACTAGTGG	n/a	<i>ku70</i> ¹¹	2
70	GCAGCCGAATTCGGTACATTACCCTGTTAT C TAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	<i>ku70</i> ¹²	2
71	AGCAGCAGCCGAATTCGGTACATTACCCTG CC TAGCGGCCGCATAGGCCACTAGTGGAT	n/a	<i>ku70</i> ¹³	4
72	AGCAGCAGCCGAATTCGGTACATTACCCTG C TAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	<i>ku70</i> ¹⁴	6
73	CAGCAGCCGAATTCGGTACATTACCCTGTT GCCGC CATAGGCCACTAGTGGATCTGGATCC	n/a	<i>ku70</i> ¹⁵	10
74	AGAGCAGCAGCCGAATTCGGTACATTACCC GCCGC CATAGGCCACTAGTGGATCTGGATCC	n/a	<i>ku70</i> ¹⁶	14
75	GCAGCCGAATTCGGTACATTACCCTGTTAT ATAG GCCACTAGTGGATCTGGATCCTCTAG	n/a	<i>lig4</i> ⁹	13
76	TGCGTCGTTTAGAGCAGCAGCCGAATTCGG GGCCGC CATAGGCCACTAGTGGATCTGGATC	n/a	<i>lig4</i> ¹⁰	23
77	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>rad51 ku70</i> ⁶	1
78	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>rad51 ku70</i> ⁷	1
79	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>rad51 ku70</i> ⁸	1
80	GCAGCCGAATTCGGTACATTACCCTGTTAT C CTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	<i>rad51 ku70</i> ⁹	1
81	GCAGCCGAATTCGGTACATTACCCTGTTAT C TAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	<i>rad51 ku70</i> ¹⁰	2
82	CAGCAGCCGAATTCGGTACATTACCCTGTT GCCGC CATAGGCCACTAGTGGATCTGGATCC	n/a	<i>rad51 lig4</i> ¹¹	10
83	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ⁷	1
84	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ⁸	1
85	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ⁹	1
86	GAGCAGCAGCCGAATTCGGTACATTACCCT TTATCC TAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ¹⁰	1
87	CAGCAGCCGAATTCGGTACATTACCCTGTT CCCTAG CGGCCGCATAGGCCACTAGTGGGA	n/a	<i>polQ</i> ¹¹	1

88	GCAGCCGAATTCGGTACATTACCCTGTTAT- - CCTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	<i>polQ</i> ¹²	1
89	GCAGCCGAATTCGGTACATTACCCTGTTAT- - CCTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	<i>polQ</i> ¹³	1
90	GCAGCCGAATTCGGTACATTACCCTGTTAT- - CCTAGCGGCCGCATAGGCCACTAGTGGATC	n/a	<i>polQ</i> ¹⁴	1
91	GCAGCCGAATTCGGTACATTACCCTGTTAT- - CTAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	<i>polQ</i> ¹⁵	2
92	GCAGCCGAATTCGGTACATTACCCTGTTAT- - CTAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	<i>polQ</i> ¹⁶	2
93	GCAGCCGAATTCGGTACATTACCCTGTTAT- - CTAGCGGCCGCATAGGCCACTAGTGGATCT	n/a	<i>polQ</i> ¹⁷	2
94	TAGAGCAGCAGCCGAATTCGGTACATTACC- - TTATCCCTAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ¹⁸	3
95	TAGAGCAGCAGCCGAATTCGGTACATTACC- - TTATCCCTAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ¹⁹	3
96	AGCAGCAGCCGAATTCGGTACATTACCCTG- - CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	<i>polQ</i> ²⁰	4
97	AGCAGCAGCCGAATTCGGTACATTACCCTG- - CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	<i>polQ</i> ²¹	4
98	AGCAGCAGCCGAATTCGGTACATTACCCTG- - CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	<i>polQ</i> ²²	4
99	AGCAGCAGCCGAATTCGGTACATTACCCTG- - CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	<i>polQ</i> ²³	4
100	TTAGAGCAGCAGCCGAATTCGGTACATTAC- - GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	<i>polQ</i> ²⁴	13
101	TGGAGTACGAAATGCGTCGTTTAGAGCAGC- - TTATCCCTAGCGGCCGCATAGGCCACTAGT	n/a	<i>polQ</i> ²⁵	24

Table S3. Sequences of apparent blunt joins. Sequences and genotypes of all repair products with apparent blunt joins (n=101). Deleted bases not shown. Boxed dashes indicate apparent point of ligation (box notation indicates a possible insertion of length zero in SD-MMEJ consistent sequences) . Identical SD-MMEJ consistent sequences are indicated by a lettered superscript on the sequence number; letters cross-reference Table 1. SD-MMEJ consistent repeats are underlined. Predicted SD-MMEJ primer repeats in italics. Primer repeat groups as in Table 1 are indicated by Roman numerals and enumerated in superscripts. 59/101 (58.4%) of sequences are SD-MMEJ consistent (direct or inverted repeat of at least 4 bp within ± 20 bp of the junction). This proportion is significantly greater than would be predicted by random chance ($p < 0.05$ Fisher's Exact Test). Expected proportion of SD-MMEJ consistent blunt joins was estimated by Monte Carlo simulation of random deletion events (See Materials and Methods). Number of sequences of a given genotype enumerated in superscripts. 30 bp on either side of the junction are shown. n/a: not applicable.

Table S4.

	sequence of repair products with junctional microhomology □.nnn□ indicates microhomology		genotype	del (bp)
1 ^{A1}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹	WT ¹	12
2 ^{A2}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ²	WT ²	12
3 ^{A3}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ³	WT ³	12
4 ^{A4}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ⁴	rad51 ¹	12
5 ^{A5}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ⁵	rad51 ²	12
6 ^{A6}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ⁶	rad51 ³	12
7 ^{A7}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ⁷	lig4 ¹	12
8 ^{A8}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ⁸	lig4 ²	12
9 ^{A9}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ⁹	lig4 ³	12
10 ^{A10}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁰	lig4 ⁴	12
11 ^{A11}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹¹	lig4 ⁵	12
12 ^{A12}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹²	lig4 ⁶	12
13 ^{A13}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹³	lig4 ⁷	12
14 ^{A14}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁴	rad51 ku70 ¹	12
15 ^{A15}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁵	rad51 lig4 ¹	12
16 ^{A16}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁶	rad51 lig4 ²	12
17 ^{A17}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁷	rad51 lig4 ³	12
18 ^{A18}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁸	rad51 lig4 ⁴	12
19 ^{A19}	GAGCAGCAGCCGAATTCGGTACATTACCCT□.G□.GCCGCATA <u>GGCCA</u> CTAGTGGATCTGGATCC	I ¹⁹	rad51 lig4 ⁵	12
20 ^{B1}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹	WT ⁴	9
21 ^{B2}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ²	rad51 ⁴	9
22 ^{B3}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ³	ku70 ¹	9
23 ^{B4}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ⁴	ku70 ²	9
24 ^{B5}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ⁵	ku70 ³	9
25 ^{B6}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ⁶	lig4 ⁸	9
26 ^{B7}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ⁷	lig4 ⁹	9
27 ^{B8}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ⁸	lig4 ¹⁰	9
28 ^{B9}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ⁹	rad51 ku70 ²	9
29 ^{B10}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹⁰	rad51 ku70 ³	9
30 ^{B11}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹¹	rad51 lig4 ⁶	9
31 ^{B12}	TTTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> □.CCCT□.AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹²	rad51 lig4 ⁷	9

32 ^{B13}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> . <u>CCCT</u> .AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹³	<i>polQ</i> ¹	9
33 ^{B14}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> . <u>CCCT</u> .AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹⁴	<i>polQ</i> ²	9
34 ^{B15}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TA</u> . <u>CCCT</u> .AGCGGCCGCATAGGCCACTAGTGGATCTGG	IV ¹⁵	<i>polQ</i> ³	9
35 ^{D1}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ¹⁶	WT ⁵	17
36 ^{D2}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ¹⁷	WT ⁶	17
37 ^{D3}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ¹⁸	WT ⁷	17
38 ^{D4}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ¹⁹	<i>lig4</i> ¹¹	17
39 ^{D5}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁰	<i>lig4</i> ¹²	17
40 ^{D6}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²¹	<i>rad51 lig4</i> ⁸	17
41 ^{D7}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²²	<i>rad51 lig4</i> ⁹	17
42 ^{D8}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²³	<i>rad51 lig4</i> ¹⁰	17
43 ^{D9}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁴	<i>polQ</i> ⁴	17
44 ^{D10}	TTAGAGCAGCAGCCGAATTC <u>GGTA</u> CAT <u>TAC</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁵	<i>polQ</i> ⁵	17
45 ^{E1}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ¹	WT ⁸	10
46 ^{E2}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ²	<i>rad51</i> ⁵	10
47 ^{E3}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ³	<i>rad51</i> ⁶	10
48 ^{E4}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ⁴	<i>ku70</i> ⁴	10
49 ^{E5}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ⁵	<i>lig4</i> ¹³	10
50 ^{E6}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ⁶	<i>rad51 ku70</i> ⁴	10
51 ^{E7}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ⁷	<i>rad51 ku70</i> ⁵	10
52 ^{E8}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ⁸	<i>polQ</i> ⁶	10
53 ^{E9}	GAGCAGCAGCCGAATTCGGTACATTACCCT. <u>G</u> . <u>CGGCCGCA</u> TAGGCCACTAGTGGATCTGGAT	III ⁹	<i>polQ</i> ⁷	10
54 ^{Z1}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>rad51</i> ⁷	13
55 ^{Z2}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>rad51</i> ⁸	13
56 ^{Z3}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>ku70</i> ⁵	13
57 ^{Z4}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>ku70</i> ⁶	13
58 ^{Z5}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>ku70</i> ⁷	13
59 ^{Z6}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>rad51 lig4</i> ¹¹	13
60 ^{Z7}	TAGAGCAGCAG <u>GCCG</u> AATTCGGTACATTACC. <u>C</u> . <u>GGCCGC</u> CATAGGCCACTAGTGGATCTGGATC	-	<i>polQ</i> ⁸	13
61 ^{F1}	TTAGAGCAGCAGCCGAATT <u>CGGTA</u> CAT <u>TA</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁶	WT ⁹	18
62 ^{F2}	TTAGAGCAGCAGCCGAATT <u>CGGTA</u> CAT <u>TA</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁷	WT ¹⁰	18
63 ^{F3}	TTAGAGCAGCAGCCGAATT <u>CGGTA</u> CAT <u>TA</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁸	<i>rad51</i> ⁹	18
64 ^{F4}	TTAGAGCAGCAGCCGAATT <u>CGGTA</u> CAT <u>TA</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ²⁹	<i>rad51</i> ¹⁰	18
65 ^{F5}	TTAGAGCAGCAGCCGAATT <u>CGGTA</u> CAT <u>TA</u> . <u>CC</u> .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ³⁰	<i>ku70</i> ⁸	18

66 ^{F6}	TTTAGAGCAGCAGCCGAATT CGGTA CAT TAC . CC .GCATAGGCCACTAGTGGATCTGGATCCTCT	IV ³¹	polQ ⁹	18
67 ^{G1}	AGAGCAGCAGCCGAATTCGGTACATT CCC . T .TAT CCCT AGCGGCCGCATAGGCCACTAGTG	-	WT ¹¹	2
68 ^{G2}	AGAGCAGCAGCCGAATTCGGTACATT CCC . T .TAT CCCT AGCGGCCGCATAGGCCACTAGTG	-	ku70 ⁹	2
69 ^{G3}	AGAGCAGCAGCCGAATTCGGTACATT CCC . T .TAT CCCT AGCGGCCGCATAGGCCACTAGTG	-	polQ ¹⁰	2
70 ^{G4}	AGAGCAGCAGCCGAATTCGGTACATT CCC . T .TAT CCCT AGCGGCCGCATAGGCCACTAGTG	-	polQ ¹¹	2
71 ^{H1}	AGCAGCAGCCGAATTCGGT TACA T TACCC TG . T .ATCCCTAGCGGCCGCATAGGCCACTAGTGG	-	rad51 ku70 ⁶	1
72 ^{H2}	AGCAGCAGCCGAATTCGGT TACA T TACCC TG . T .ATCCCTAGCGGCCGCATAGGCCACTAGTGG	-	rad51 ku70 ⁷	1
73 ^{H3}	AGCAGCAGCCGAATTCGGT TACA T TACCC TG . T .ATCCCTAGCGGCCGCATAGGCCACTAGTGG	-	rad51 ku70 ⁸	1
74 ^{I1}	AGCAGCCGAATTCGGTACATTACCCTGTT A . T . AG CGGCCGC ATAG GCCACTAGTGGATCTGG	-	ku70 ¹⁰	4
75 ^{I2}	AGCAGCCGAATTCGGTACATTACCCTGTT A . T . AG CGGCCGC ATAG GCCACTAGTGGATCTGG	-	rad51 ku70 ⁹	4
76 ^{I3}	AGCAGCCGAATTCGGTACATTACCCTGTT A . T . AG CGGCCGC ATAG GCCACTAGTGGATCTGG	-	rad51 ku70 ¹⁰	4
77 ^{J1}	AAATGCGTCGTTTAGAGCAGCAG GCCGAATT . CGG .CCGCATAGGCCACTAGTGGATCTGGATCCT	-	WT ¹²	25
78 ^{J2}	AAATGCGTCGTTTAGAGCAGCAG GCCGAATT . CGG .CCGCATAGGCCACTAGTGGATCTGGATCCT	-	lig4 ¹⁴	25
79 ^{J3}	AAATGCGTCGTTTAGAGCAGCAG GCCGAATT . CGG .CCGCATAGGCCACTAGTGGATCTGGATCCT	-	rad51 ku70 ¹¹	25
80 ^{L1}	TTAGAGCAGCAGCCGAATT CGGTA CAT TAC . C .GGCCGCATAGGCCACTAGTGGATCTGGATC	IV ³²	ku70 ¹¹	14
81 ^{L2}	TTAGAGCAGCAGCCGAATT CGGTA CAT TAC . C .GGCCGCATAGGCCACTAGTGGATCTGGATC	IV ³³	rad51 ku70 ¹²	14
82 ^{M1}	AGCAGCAGCCGAATTCGGT TACA T TACCC TG . T .AGCGGCCGCATAGGCCACTAGTGGATCTGG	-	WT ¹³	7
83 ^{M2}	AGCAGCAGCCGAATTCGGT TACA T TACCC TG . T .AGCGGCCGCATAGGCCACTAGTGGATCTGG	-	polQ ¹²	7
84 ^{N1}	AGAGCAGCAGCCGAATTCGGTACATTACC .TG . GATCTGGATC CTCTAGAGTCGACCTCGAAC	-	WT ¹⁴	31
85 ^{O1}	CGTCGTTTAGAGCAGCAGCCGAATTCGGT A . C . TAG CGGCCGCATAGGCC ACTAG TGGATCTG	-	rad51 ku70 ¹³	16
86 ^{P1}	ATGCGTCGTTTAGAGCAGCAG CCGAATTCG . G .GCCGCATAGGCCACTAGTGGATCTGGATCC	-	ku70 ¹²	24
87 ^{R1}	TTAGAGCAGCAGCCGAATTC GGTA CAT TAC . C .ATAGGCCACTAGTGGATCTGGATCCTCTAG	IV ³⁴	rad51 ¹¹	20
88 ^{S1}	GAGTACGAAATGCGTCGTTTAGAGCAGCAG .CC . CTAGCGCCGCA TAGG CCACTAGTGGATCTG	-	ku70 ¹³	26
89 ^{T1}	TTAGAGCAGCAGCCGAATTCGGTACATT AC . CC . ACTAGTGGAT CTGGATCCTCTAGAGTCGAC	-	WT ¹⁵	26
90 ^{U1}	GGAGTACGAAATGCGTCGTTTAGAG CAGCC . AGC .GGCCGCATAGGCCACTAGTGGATCTGGATC	-	WT ¹⁶	35
91 ^{V1}	TTAGAGCAGCAGCCGAATTCGGTACATT AC . CCT .CTAGAGTCGA CCTC GAAACGTTAACGTTAAC	-	rad51 ¹²	44
92 ^{W1}	GCGTCGTTTAGAGCAGCAGCCGAATTCGGT .C . ACTAGTG GATCTGGATCCTCTAGAGTCGAC	-	WT ¹⁷	60
93 ^{X1}	ATTCGCAGTGG AAGG CTGCACCTGCAA AAG . G .GGCCGCATAGGCCACTAGTGGATCTGGATC	-	polQ ¹³	288
94 ^{Y1}	GAAAATTGTGGGA GCAG AGCCTTGGGT GCA . GCC .GCATAGGCCACTAGTGGATCTGGATCCTCT	-	ku70 ¹⁴	259
95	GAGCAGCAGCCGAATTCGGTACATTACCCT .G .CCGCATAGGCCACTAGTGGATCTGGATCCT	n/a	WT ¹⁸	13
96	GAGCAGCAGCCGAATTCGGTACATTACCCT .G .CATAGGCCACTAGTGGATCTGGATCCTCTA	n/a	WT ¹⁹	16
97	CGTTTAGAGCAGCAGCCGAATTCGGTACAT .TA .GGCCACTAGTGGATCTGGATCCTCTAGAGT	n/a	WT ²⁰	25
98	CAGCAGCCGAATTCGGTACATTACCCTGTT .AT .CTGGATCCTCTAGAGTCGACCTCGAACGTT	n/a	WT ²¹	30
99	GTCGTTTAGAGCAGCAGCCGAATTCGGTAC .AT .CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	WT ²²	11

100	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	WT ²³	6
101	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	WT ²⁴	6
102	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	rad51 ¹³	6
103	GGAGTACGAAATGCGTCGTTTAGAGCAGCA.GCCG.CATAGGCCACTAGTGGATCTGGATCCTCTA	n/a	rad51 ¹⁴	35
104	AGAGCAGCAGCCGAATTCGGTACATTACCCT.TG.CTTCGAGAGAGCGCGCTCGAATGTTTCGCG	n/a	rad51 ¹⁵	216
105	AGCAGCAGCCGAATTCGGTACATTACCCTG.T.T.CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	ku70 ¹⁵	3
106	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	ku70 ¹⁶	6
107	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	ku70 ¹⁷	6
108	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	ku70 ¹⁸	6
109	TCGTTTAGAGCAGCAGCCGAATTCGGTACA.TTA.TCCCTAGCGGCCGCATAGGCCACTAGTGGGA	n/a	ku70 ¹⁹	8
110	TCGTTTAGAGCAGCAGCCGAATTCGGTACA.TTA.TCCCTAGCGGCCGCATAGGCCACTAGTGGGA	n/a	ku70 ²⁰	8
111	TCGTTTAGAGCAGCAGCCGAATTCGGTACA.TTA.TCCCTAGCGGCCGCATAGGCCACTAGTGGGA	n/a	ku70 ²¹	8
112	GAGCAGCAGCCGAATTCGGTACATTACCCT.G.CCGCATAGGCCACTAGTGGATCTGGATCCT	n/a	ku70 ²²	13
113	CGTTTAGAGCAGCAGCCGAATTCGGTACAT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	ku70 ²³	14
114	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GTGGATCTGGATCCTCTAGAGTCGACCTCG	n/a	ku70 ²⁴	25
115	TCGTTTAGAGCAGCAGCCGAATTCGGTACA.TTA.TCCCTAGCGGCCGCATAGGCCACTAGTGGGA	n/a	lig4 ¹⁵	8
116	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	lig4 ¹⁶	6
117	GAGCAGCAGCCGAATTCGGTACATTACCCT.G.CCGCATAGGCCACTAGTGGATCTGGATCCT	n/a	lig4 ¹⁷	13
118	GAGCAGCAGCCGAATTCGGTACATTACCCT.G.CCGCATAGGCCACTAGTGGATCTGGATCCT	n/a	lig4 ¹⁸	13
119	CGTTTAGAGCAGCAGCCGAATTCGGTACAT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	lig4 ¹⁹	14
120	TAGAGCAGCAGCCGAATTCGGTACATTACC.C.CGCATAGGCCACTAGTGGATCTGGATCCTC	n/a	lig4 ²⁰	16
121	CGTCGTTTAGAGCAGCAGCCGAATTCGGTA.CAT.AGGCCACTAGTGGATCTGGATCCTCTAGAG	n/a	lig4 ²¹	26
122	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	rad51 ku70 ¹⁴	6
123	TCGTTTAGAGCAGCAGCCGAATTCGGTACA.TTA.TCCCTAGCGGCCGCATAGGCCACTAGTGGGA	n/a	rad51 lig4 ¹²	8
124	CAGCAGCCGAATTCGGTACATTACCCTGTT.AT.AGGCCACTAGTGGATCTGGATCCTCTAGAG	n/a	rad51 lig4 ¹³	15
125	AAAAATTCGTACTTTGGAGTACGAAATGCG.TCGTT.GCTTCGAGAGAGCGCGCTCGAATGTTTCGC	n/a	rad51 lig4 ¹⁴	250
126	GCAGCCGAATTCGGTACATTACCCTGTAT.TAT.CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	polQ ^{*14}	0
127	GCAGCCGAATTCGGTACATTACCCTGTAT.TAT.CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	polQ ^{*15}	0
128	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	polQ ¹⁶	6
129	GCAGCAGCCGAATTCGGTACATTACCCTGT.TA.GCGGCCGCATAGGCCACTAGTGGATCTGGA	n/a	polQ ¹⁷	6
130	TCGTTTAGAGCAGCAGCCGAATTCGGTACA.TTA.TCCCTAGCGGCCGCATAGGCCACTAGTGGGA	n/a	polQ ¹⁸	8
131	CAGCAGCCGAATTCGGTACATTACCCTGTT.AT.AGGCCACTAGTGGATCTGGATCCTCTAGAG	n/a	polQ ¹⁹	15
132	ACGAAATGCGTCGTTTAGAGCAGCAGCCGA.AT.CCCTAGCGGCCGCATAGGCCACTAGTGGAT	n/a	polQ ²⁰	20
133	CGTCGTTTAGAGCAGCAGCCGAATTCGGTA.CAT.AGGCCACTAGTGGATCTGGATCCTCTAGAG	n/a	polQ ²¹	26

134	GGTCAGACATTTAAAAGGAGGCGACTCAAC G G GGCCGCATAGGCCACTAGTGGATCTGGATC	n/a	<i>polQ</i> ²²	259
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Table S4: Sequences of repair junctions with microhomology. SD-MMEJ consistent repair products with junctional microhomologies. 94/134 (70.1%) of microhomology junctions are SD-MMEJ consistent. This is significantly greater than predicted by random chance ($p=0.05$, Fisher's Exact Test). Junctional microhomologies (bases that cannot be unambiguously assigned to either side of the repair junction) are situated between boxes with dots to represent the uncertainty with regard to the position at which the strands were ligated during repair. The box notation is used to emphasize the possibility of a "zero insertion" SD-MMEJ event. The two sequences containing apparent net insertions (asterisks above genotype) are consistent with mispairing of the 3' DSB ends and are thus classified as junctional microhomologies. Other conventions are as described for Supplemental Table S2.

Table S5.

	sequence		genotype	deln	inst
1 ^{A1}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ¹	WT ¹	10	1
2 ^{A2}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ²	rad51 ¹	10	1
3 ^{A3}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ³	rad51 ²	10	1
4 ^{A4}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ⁴	rad51 ³	10	1
5 ^{A5}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ⁵	lig4 ¹	10	1
6 ^{A6}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ⁶	lig4 ²	10	1
7 ^{A7}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ⁷	lig4 rad51 ¹	10	1
8 ^{A8}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ⁸	lig4 rad51 ²	10	1
9 ^{A9}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ⁹	lig4 rad51 ³	10	1
10 ^{A10}	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CCGCATAGGCCACTAGTGGATCTGGATCCT	II ¹⁰	lig4 rad51 ⁴	10	1
11 ^{B1}	GCAGCCGAATTCGGTACATTACCCTGTT AT a GGCC GC ATAGGCC ACTAGTGGATCTGGATC	I ¹	lig4 ³	7	1
12 ^{B2}	GCAGCCGAATTCGGTACATTACCCTGTT AT a GGCC GC ATAGGCC ACTAGTGGATCTGGATC	I ²	lig4 rad51 ⁵	7	1
13 ^{C1}	GCAGCCGAATTCGG TACAT TACCCTGTT AT a TAG CGGCCGCATAGGCCACTAGTGGATCTG	-	rad51 ⁴	3	1
14 ^{C2}	GCAGCCGAATTCGG TACAT TACCCTGTT AT a TAG CGGCCGCATAGGCCACTAGTGGATCTG	-	lig4 ⁴	3	1
15 ^D	GCAGCAGCCGAATT CGGTACA TTACCCT TGT a CCG CATAGGCCACTAGTGGATCTGGATCCT	-	ku70 ¹	12	1
16 ^E	GCAGCAGCCGAATT GGTACA TTACCCT TGT a CC ACTAGTGGATCTGGATCCTCTAGAGTCG	-	WT ²	21	1
17 ^F	AGCAGCCGAATTCGGTACA TTACCC TG TTA c CGGCCGCATAGGCCACTAGTGGATCTGGAT	II ¹¹	rad51 ku70 ¹	7	1
18 ^G	AGCAGCCGAATTCGGTACATTACCCTGTT a CTAG GCC ACTAG TGGATCTGGATCCTCTAGA	-	rad51 lig4 ⁶	15	1
19 ^H	TTAGAGCAGCAGCCGAATTCGGTACATT a CTAG CGGCCGC CATAG GCCACTAGTGGATCTG	-	polQ ¹	11	1
20 ^I	GCAGCAGCCGAATTCGGTACATTACCCT TGT a GCC GCGCATAG GCCAC TAGTGGATCTGGA	-	rad51 ⁵	8	1
21 ^J	AGCAGCAGCCGAATTCGGTACATTACCCT TGT a CC TAGCGGCCGCATA GGCCA ACTAGTGGAT	-	WT ³	4	1
22 ^K	GCAGCCGAATTCGGTACATTACCCTGTT AT a GCC GC CATAG GCCACTAGTGGATCTGGATCC	-	lig4 ⁵	8	1
23 ^M	AGCAGCAGCCGAATTCGGTACATTACCCT c CGCCCG CATAGGCCACTAGTGGATCTGGAT	-	rad51 lig4 ⁷	10	1
24	AGCAGCCGAATTCGGTACATTACCCTGTT a CGGCC GCATAGGCCACTAGTGGATCTGGAT	n/a	ku70 ²	7	1
25	CAGCAGCCGAATTCGGTACATTACCCTGTT c CGGCC GCATAGGCCACTAGTGGATCTGGAT	n/a	lig4 ⁶	8	1
26	AGCAGCAGCCGAATTCGGTACATTACCCTG a TTATCC CTAGCGGCCGCATAGGCCACTAGT	n/a	rad51 ku70 ²	0	1
27	AGCAGCAGCCGAATTCGGTACATTACCCTG a GGCC GCATAGGCCACTAGTGGATCTGGATC	n/a	rad51ku70 ³	11	1
28	TAGAGCAGCAGCCGAATTCGGTACATTACC c GGCC GCATAGGCCACTAGTGGATCTGGATC	n/a	rad51 lig4 ⁸	14	1

Table S5. Sequences of repair junctions with 1 bp insertions. Sequences and genotypes of all repair products with net insertions of one bp. Inserted sequence is boxed and in lowercase. Notational conventions as for Table S2.

Table S6.

	sequence		genotype	deln	inst
1 ^{A1}	GAGCAGCAGCCGAATTCGGTACATTACCCTatGGCGCCGCATAGGCCACTAGTGGATCTGGA	III ¹	rad51 ¹	10	2
2 ^{A2}	GAGCAGCAGCCGAATTCGGTACATTACCCTatGGCGCCGCATAGGCCACTAGTGGATCTGGA	III ²	ku70 ¹	10	2
3 ^{A3}	GAGCAGCAGCCGAATTCGGTACATTACCCTatGGCGCCGCATAGGCCACTAGTGGATCTGGA	III ³	lig4 ¹	10	2
4 ^{A4}	GAGCAGCAGCCGAATTCGGTACATTACCCTatGGCGCCGCATAGGCCACTAGTGGATCTGGA	III ⁴	rad51 ku70 ¹	10	2
5 ^{B1}	AGCAGCCGAATTCGGTACATTACCCTGTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ¹	WT ¹	8	2
6 ^{B2}	AGCAGCCGAATTCGGTACATTACCCTGTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ²	ku70 ²	8	2
7 ^{B3}	AGCAGCCGAATTCGGTACATTACCCTGTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ³	rad51 lig4 ¹	8	2
8 ^{C1}	AGCAGCCGAATTCGGTACA TTACCC TGTatGGCGCCGCATAGGCCACTAGTGGATCTGGAT	II ¹	rad51 ²	7	2
9 ^{C2}	AGCAGCCGAATTCGGTACA TTACCC TGTatGGCGCCGCATAGGCCACTAGTGGATCTGGAT	II ²	rad51 ku70 ²	7	2
10 ^{C3}	AGCAGCCGAATTCGGTACA TTACCC TGTatGGCGCCGCATAGGCCACTAGTGGATCTGGAT	II ³	polQ ¹	7	2
11 ^{D1}	AGCAGCCGAATTCGGTACATTA CCCT GTTatGGCCGCATAGGCCACTAGTGGATCTGGATC AGCAGCCGAATTCGGTACATTACCCTGTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁴	WT ²	8	2
12 ^{D2}	AGCAGCCGAATTCGGTACATTA CCCT GTTatGGCCGCATAGGCCACTAGTGGATCTGGATC AGCAGCCGAATTCGGTACATTACCCTGTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁵	WT ³	8	2
13 ^{E1}	GCAGCCGAATTCGGTACATTACCCTGTTatGGCCGCATAGGCCACTAGTGGATCTGGATC GCAGCCGAATTCGGTACATTACCCTGTTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁶	WT ⁴	7	2
14 ^{E2}	GCAGCCGAATTCGGTACATTACCCTGTTatGGCCGCATAGGCCACTAGTGGATCTGGATC GCAGCCGAATTCGGTACATTACCCTGTTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁷	lig4 ²	7	2
15 ^F	TTTAGAGCAGCAGCCGAATTCGGTACATTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁷	lig4 ³	16	2
16 ^G	GCAGCAGCCGAATTCGGTACATTACCCTGTatGGCGCCGCATAGGCCACTAGTGGATCTGGA	III ⁵	rad51 ku70 ³	8	2
17 ^H	GCAGCCGAATTCGGTACATTACCCTGTTatGGCGCCGCATAGGCCACTAGTGGATCTGGA	III ⁶	WT ⁵	5	2
18 ^I	GAGCAGCAGCCGAATTCGGTACATTACCCTatGCATAGGCCACTAGTGGATCTGGATCCTCT	-	rad51 ³	16	2
19 ^J	GCAGCCGAATTCGGTACATTACCCTGTTatTAGGCCACTAGTGGATCTGGATCCTCTAGA	-	lig4 ⁴	14	2
20 ^K	GCAGCCGAATTCGGTACATTACCCTGTTatGGCCGCATAGGCCACTAGTGGATCTGGATC GCAGCCGAATTCGGTACATTACCCTGTTatGGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁸	rad51 lig4 ²	7	2
21	GCAGCCGAATTCGGTACATTACCCTGTTatGCCGCATAGGCCACTAGTGGATCTGGATCC	n/a	rad51 ⁴	8	2
22	TAGAGCAGCAGCCGAATTCGGTACATTACCCTTATCCCTAGCGGCCGCATAGGCCACTAGT	n/a	rad51 ku70 ⁴	1	2
23	AGAGCAGCAGCCGAATTCGGTACATTACCCTGGCCGCATAGGCCACTAGTGGATCTGGATC	n/a	rad51 ku70 ⁵	13	2
24	AGCAGCCGAATTCGGTACATTACCCTGTTacGCCGCATAGGCCACTAGTGGATCTGGATCC	n/a	rad51 lig4 ³	9	2
25	CAGCAGCCGAATTCGGTACATTACCCTGTTgtGCCGCATAGGCCACTAGTGGATCTGGATCC	n/a	rad51 lig4 ⁴	10	2
26	CGTTTAGAGCAGCAGCCGAATTCGGTACATccGGCCGCATAGGCCACTAGTGGATCTGGAT	n/a	polQ ²	17	2

Table S6. Sequences of repair junctions with 2 bp insertions. Sequences and genotypes of all repair products with net insertions of 2 bp. Inserted sequence is boxed and in lowercase. For repair products with multiple SD-MMEJ consistent repeats, all repeats are indicated. Notational conventions as for Table S2.

Table S7.

	sequence		genotype	deln	inst
1 ^{A1}	TAGAGCAGCAGCCGAATTCGGTACATTACCt aat GGCGCCGCATAGGCCACTAGTGGATCTGGA	III ¹	WT ¹	12	3
2 ^{A2}	TAGAGCAGCAGCCGAATTCGGTACATTACCt aat GGCGCCGCATAGGCCACTAGTGGATCTGGA	III ²	rad51 ku70 ¹	12	3
3 ^{A3}	TAGAGCAGCAGCCGAATTCGGTACATTACCt aat GGCGCCGCATAGGCCACTAGTGGATCTGGA	III ³	rad51 ku70 ²	12	3
4 ^{B1}	GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC	I ¹	ku70 ¹	10	3
5 ^{B2}	GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC	I ²	rad51 ku70 ³	10	3
6 ^C	AGAGCAGCAGCCGAATTCGGTACATTACC ata GGCCGCATAGGCCACTAGTGGATCTGGATC	I ³	ku70 ²	13	3
7 ^D	GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁴	lig4 ¹	10	3
8 ^E	GCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁵	rad51 lig4 ¹	7	3
9 ^F	AGCAGCCGAATTCGGTACATTACCCTGT aca GGCCGCATAGGCCACTAGTGGATCTGGATC AGCAGCCGAATTCGGTACATTACCCTGT aca GGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁶	lig4 ²	8	3
10 ^G	TTTAGAGCAGCAGCCGAATTCGGTACATTACC aac GGCCGCATAGGCCACTAGTGGATCTGGATCCT	-	polQ ¹	18	3
11 ^H	GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCCGCATAGGCCACTAGTGGATCTGGATC	-	ku70 ³	11	3
12 ^I	GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCGCCGCATAGGCCACTAGTGGATCTGGA GCAGCAGCCGAATTCGGTACATTACCCTGT aat GGCGCCGCATAGGCCACTAGTGGATCTGGA	III ⁴	lig4 ³	8	3
13 ^J	GCAGCCGAATTCGGTACATTACCCTGT att GGCCGCATAGGCCACTAGTGGATCTGGATC GCAGCCGAATTCGGTACATTACCCTGT att GGCCGCATAGGCCACTAGTGGATCTGGATC	I ⁷	rad51 ku70 ⁴	7	3
14	GCAGCCGAATTCGGTACATTACCCTGT ggt GGCCGCATAGGCCACTAGTGGATCTGGATC	n/a	rad51 ¹	7	3
15	AGCTTGAGGGAAAAAATTCGTACTTTGGAG gat ATCTGGATCCTCTAGAGTCGACCTCGAACG	n/a	rad51 ²	81	3
16	CAGCAGCCGAATTCGGTACATTACCCTGT ggt GGCCGCATAGGCCACTAGTGGATCTGGATC	n/a	polQ ²	9	3

Supplemental Table S7. Sequences and genotypes of all repair products with net insertions of 3 bp. Inserted sequence is boxed and in lowercase. For repair products with multiple SD-MMEJ consistent repeats, all repeats are indicated. Notational conventions as for Table S2.

Table S8.

	sequence of junctions with ≥4 bp insertions	genotype	del	ins
1	AGCAGCCGAATTCGGTACATTACCCCTGTTA catta TCCTAGCGGCCGCATAGGCCACTAGTGGA	WT	0	5
2	GCAGCCGAATTCGGTACATTACCCCTGTTA ttacattacattaccccta CCCTAGCGGCCGCATAGGCCACTAGTGGA	WT	0	19
3	GCAGCCGAATTCGGTACATTACCCCTGTTA gggtaatggtat GCGGCCGCATAGGCCACTAGTGGA	WT	5	12
4	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA taataa TAGCGGCCGCATAGGCCACTAGTGGA	WT	6	5
5	GCAGCCGAATTCGGTACATTACCCCTGTTA aggg CGGCCGCATAGGCCACTAGTGGA	WT	6	5
6	GCAGCCGAATTCGGTACATTACCCCTGTTA gctatgt GGCCGCATAGGCCACTAGTGGA	WT	7	7
7	GCAGCCGAATTCGGTACATTACCCCTGTTA tcacgtgccgaagtgt GGCCGCATAGGCCACTAGTGGA	WT	7	16
8	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA aattataattataattattatagt GGCCGCATAGGCCACTAGTGGA	WT	7	24
9	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA aacaggttatgcgataaccactat GGCCGCATAGGCCACTAGTGGA	WT	7	26
10	AGCAGCAGCCGAATTCGGTACATTACCCCTGTTA cggtta AGCGGCCGCATAGGCCACTAGTGGA	WT	8	5
11	AGCAGCCGAATTCGGTACATTACCCCTGTTA acagggta GGCCGCATAGGCCACTAGTGGA	WT	8	8
12	AGCAGCAGCCGAATTCGGTACATTACCCCTGTTA ctatgt GGCCGCATAGGCCACTAGTGGA	WT	11	6
13	AGAGCAGCAGCCGAATTCGGTACATTACCCCTGTTA ggttc CGGCCGCATAGGCCACTAGTGGA	WT	12	5
14	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA ggcctttt GCATAGGCCACTAGTGGA	WT	13	8
15	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA aatgtaatgtaacgtatagccat ATAGGCCACTAGTGGA	WT	16	24
16	TAGAGCAGCAGCCGAATTCGGTACATTACCCCTGTTA gaatagggtaatgtg GCATAGGCCACTAGTGGA	WT	18	15
17	AGCAGCAGCCGAATTCGGTACATTACCCCTGTTA cattaccctacattaccattc TTATCCCTAGCGGCCGCATAGGCCACTAGT	rad51	0	21
18	GCAGCCGAATTCGGTACATTACCCCTGTTA ttat CCCTAGCGGCCGCATAGGCCACTAGTGGA	rad51	0	4
19	AGCAGCCGAATTCGGTACATTACCCCTGTTA ccctgt TAGCGGCCGCATAGGCCACTAGTGGA	rad51	4	6
20	GCAGCCGAATTCGGTACATTACCCCTGTTA ccctgggtatgtagggatagggatgtatccctgt GCCGCATAGGCCACTAGTGGA	rad51	8	38
21	GCAGCCGAATTCGGTACATTACCCCTGTTA gttagt GGCCGCATAGGCCACTAGTGGA	rad51	7	6
22	GCAGCCGAATTCGGTACATTACCCCTGTTA atatatagt GGCCGCATAGGCCACTAGTGGA	rad51	7	9
23	GCAGCCGAATTCGGTACATTACCCCTGTTA gtacattagt GGCCGCATAGGCCACTAGTGGA	rad51	7	10
24	GCAGCCGAATTCGGTACATTACCCCTGTTA acaggtattaccct GGCCGCATAGGCCACTAGTGGA	rad51	7	14
25	AGCAGCCGAATTCGGTACATTACCCCTGTTA ccctgt GGCCGCATAGGCCACTAGTGGA	rad51	8	6
26	AGCAGCCGAATTCGGTACATTACCCCTGTTA ccctgt GGCCGCATAGGCCACTAGTGGA	rad51	8	6
27	CAGCAGCCGAATTCGGTACATTACCCCTGTTA gtgtagt GGCCGCATAGGCCACTAGTGGA	rad51	9	7
28	GCAGCCGAATTCGGTACATTACCCCTGTTA aggccgatatac CCGCATAGGCCACTAGTGGA	rad51	9	13
29	TTAGAGCAGCAGCCGAATTCGGTACATTACCCCTGTTA ataggcataggtaatgtag CTAGCGGCCGCATAGGCCACTAGTGGA	rad51	10	20
30	AGAGCAGCAGCCGAATTCGGTACATTACCCCTGTTA gaattacattaccggccggc AGCGGCCGCATAGGCCACTAGTGGA	rad51	10	20
31	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA accct GGCCGCATAGGCCACTAGTGGA	rad51	10	5
32	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA attaccgggtacagt GGCCGCATAGGCCACTAGTGGA	rad51	10	15
33	AGCAGCCGAATTCGGTACATTACCCCTGTTA ctagatcgtggatcgtgttac CCGCATAGGCCACTAGTGGA	rad51	10	22
34	GCAGCCGAATTCGGTACATTACCCCTGTTA aggg ATAGGCCACTAGTGGA	rad51	13	5
35	GCAGCCGAATTCGGTACATTACCCCTGTTA taggt ATAGGCCACTAGTGGA	rad51	13	6
36	GCAGCCGAATTCGGTACATTACCCCTGTTA agggtaatca AGGCCACTAGTGGA	rad51	15	10
37	AGAGCAGCAGCCGAATTCGGTACATTACCCCTGTTA cgttaccct GCATAGGCCACTAGTGGA	rad51	17	9
38	AGCAGCAGCCGAATTCGGTACATTACCCCTGTTA gatccattatccagatcca TTATCCCTAGCGGCCGCATAGGCCACTAGT	ku70	0	21
39	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA tattat TATCCCTAGCGGCCGCATAGGCCACTAGTG	ku70	0	5
40	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA ggtaataaccctgttacattgt TATCCCTAGCGGCCGCATAGGCCACTAGTG	ku70	0	21
41	GCAGCAGCCGAATTCGGTACATTACCCCTGTTA accctgtacattaccctgtacat TATCCCTAGCGGCCGCATAGGCCACTAGTG	ku70	0	23
42	AGCAGCCGAATTCGGTACATTACCCCTGTTA tatccctattattaccacattattat CCTAGCGGCCGCATAGGCCACTAGTGGA	ku70	0	26
43	GAGCAGCAGCCGAATTCGGTACATTACCCCTGTTA ttaca TTATCCCTAGCGGCCGCATAGGCCACTAGT	ku70	1	5

44	AGCAGCCGAATTCGGTACATTACCCTGTTA gcta CTAGCGCCGCATAGGCCACTAGTGGATCT	ku70	3	4
45	GCAGCCGAATTCGGTACATTACCCTGTTAT aaca GGCCGCATAGGCCACTAGTGGATCTGGATC	ku70	7	4
46	GAGCAGCAGCCGAATTCGGTACATTACCCT aacatta TAGCGCCGCATAGGCCACTAGTGGATCTG	ku70	8	7
47	AGAGCAGCAGCCGAATTCGGTACATTACC ggta CCGCCGCATAGGCCACTAGTGGATCTGGAT	ku70	12	4
48	AGCAGCAGCCGAATTCGGTACATTACCCTG catagggcataacataggc CCGCATAGGCCACTAGTGGATCTGGATCCT	ku70	13	19
49	GTTTAGAGCAGCAGCCGAATTCGGTACATT cggtac AGCGCCGCATAGGCCACTAGTGGATCTGG	ku70	14	6
50	GCCGAATTCGGTACATTACCCTGTTAGTTA ccctgttacc GCAGCTCGAACGTTAACGTTAACGTTAACGTT	ku70	47	10
51	GAGCAGCAGCCGAATTCGGTACATTACCCT agagtaatgtacctacc AAATAGAGGCGCTTCGTCGACGGAGCGTCA	ku70	267	18
52	CAATTTTTTTTTGAAACATTACCCTTAC agggtta CCTAGCGCCGCATAGGCCACTAGTGGATC	ku70	476	7
53	AGCAGCCGAATTCGGTACATTACCCTGTTA atgtaccctatgtacatta FCCCTAGCGCCGCATAGGCCACTAGTGGGA	lig4	0	19
54	GCAGCCGAATTCGGTACATTACCCTGTTAT tattatoccta CCCTAGCGCCGCATAGGCCACTAGTGGAT	lig4	0	12
55	GCAGCCGAATTCGGTACATTACCCTGTTAT cctgttat CCCTAGCGCCGCATAGGCCACTAGTGGAT	lig4	0	8
56	GCAGCCGAATTCGGTACATTACCCTGTTAT gtactatg TAGCGCCGCATAGGCCACTAGTGGATCTG	lig4	3	8
57	GCAGCCGAATTCGGTACATTACCCTGTTAT gcgccctat GCGCCGCATAGGCCACTAGTGGATCTGGA	lig4	5	9
58	GCAGCCGAATTCGGTACATTACCCTGTTAT aagtggccacattat GCGCCGCATAGGCCACTAGTGGATCTGGA	lig4	5	15
59	GCAGCCGAATTCGGTACATTACCCTGTTAT tatc CCGCCGCATAGGCCACTAGTGGATCTGGAT	lig4	6	4
60	GCAGCAGCCGAATTCGGTACATTACCCTGT aattac AGCGCCGCATAGGCCACTAGTGGATCTGG	lig4	7	6
61	GCAGCAGCCGAATTCGGTACATTACCCTGT caagcctgtca AGCGCCGCATAGGCCACTAGTGGATCTGG	lig4	7	11
62	AGCAGCCGAATTCGGTACATTACCCTGTTA atgtatgtac CCGCCGCATAGGCCACTAGTGGATCTGGAT	lig4	7	10
63	GCAGCCGAATTCGGTACATTACCCTGTTAT aagt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	4
64	GCAGCCGAATTCGGTACATTACCCTGTTAT taca GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	4
65	GCAGCCGAATTCGGTACATTACCCTGTTAT aacag GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	5
66	GCAGCCGAATTCGGTACATTACCCTGTTAT aacagt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	6
67	GCAGCCGAATTCGGTACATTACCCTGTTAT aacaggt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	8
68	GCAGCCGAATTCGGTACATTACCCTGTTAT aacaggtat GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	10
69	GCAGCCGAATTCGGTACATTACCCTGTTAT aacatagtgtagt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	13
70	GCAGCCGAATTCGGTACATTACCCTGTTAT aacaggtattaccct GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	15
71	GCAGCCGAATTCGGTACATTACCCTGTTAT aatgtaccctatgtaatgtatggccct GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	7	28
72	AGCAGCAGCCGAATTCGGTACATTACCCTG cgcccta AGCGCCGCATAGGCCACTAGTGGATCTGG	lig4	8	7
73	AGCAGCCGAATTCGGTACATTACCCTGTTA atgt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	8	4
74	AGCAGCCGAATTCGGTACATTACCCTGTTA ccctgt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	8	6
75	AGCAGCCGAATTCGGTACATTACCCTGTTA ccctgt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	8	6
76	TAGAGCAGCAGCCGAATTCGGTACATTACC gacattaca CTAGCGCCGCATAGGCCACTAGTGGATCT	lig4	9	9
77	GCAGCAGCCGAATTCGGTACATTACCCTGT acat GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	10	4
78	GCAGCAGCCGAATTCGGTACATTACCCTGT gggtaata GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	10	8
79	GCAGCAGCCGAATTCGGTACATTACCCTGT ggccggtacatagtg GCCGCATAGGCCACTAGTGGATCTGGATCC	lig4	10	14
80	AGCAGCCGAATTCGGTACATTACCCTGTTA catac CCGCATAGGCCACTAGTGGATCTGGATCCT	lig4	10	5
81	GAGCAGCAGCCGAATTCGGTACATTACCCT acctacattac CCGCCGCATAGGCCACTAGTGGATCTGGAT	lig4	11	11
82	GCAGCAGCCGAATTCGGTACATTACCCTGT aatacctat GCCGCATAGGCCACTAGTGGATCTGGATCC	lig4	11	9
83	GCAGCAGCCGAATTCGGTACATTACCCTGT acattac CCGCATAGGCCACTAGTGGATCTGGATCCT	lig4	12	7
84	TAGAGCAGCAGCCGAATTCGGTACATTACC tcattacctat GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	14	11
85	GCAGCAGCCGAATTCGGTACATTACCCTGT aggcct GCATAGGCCACTAGTGGATCTGGATCCTCT	lig4	14	6
86	TTAGAGCAGCAGCCGAATTCGGTACATTAC tggatcacagggtaaatgt GGCCGCATAGGCCACTAGTGGATCTGGATC	lig4	15	18
87	AGAGCAGCAGCCGAATTCGGTACATTACC atgta CCGCATAGGCCACTAGTGGATCTGGATCCT	lig4	15	5

88	AGCAGCAGCCGAATTCGGTACATTACCTGccactagtgGCATAGGCCACTAGTGGATCTGGATCCTCT	lig4	15	9
89	GCAGCAGCCGAATTCGGTACATTACCTGTaccgagggcctcgTAGGCCACTAGTGGATCTGGATCCTCTAGA	lig4	17	12
90	TACGAAATGCGTCGTTTAGAGCAGCAGCCGggttaaggccgggctaagtGCCGCATAGGCCACTAGTGGATCTGGATCC	lig4	31	18
91	GCAGCCGAATTCGGTACATTACCTGTTATcctattatCCCTAGCGCCGCATAGGCCACTAGTGGAT	rad51 ku70	0	8
92	GCAGCCGAATTCGGTACATTACCTGTTATccattatccattatccattatcctaccattatCCCTAGCGCCGCATAGGCCACTAGTGGAT	rad51 ku70	0	32
93	GCAGCAGCCGAATTCGGTACATTACCTGTacattacattacattacattaccgggtacattatccaCTAGCGCCGCATAGGCCACTAGTGGATCT	rad51 ku70	5	37
94	GCAGCAGCCGAATTCGGTACATTACCTGTacattacattacattacattaccgggtacattatccaCTAGCGCCGCATAGGCCACTAGTGGATCT	rad51 ku70	5	37
95	GCAGCCGAATTCGGTACATTACCTGTTATcattacattatGGCCGCATAGGCCACTAGTGGATCTGGATC	rad51 ku70	7	11
96	GCAGCCGAATTCGGTACATTACCTGTTATagggatatataatcggtatGGCCGCATAGGCCACTAGTGGATCTGGATC	rad51 ku70	7	20
97	AGCAGCCGAATTCGGTACATTACCTGTTAacgggtaacgggtaacagtGGCCGCATAGGCCACTAGTGGATCTGGATC	rad51 ku70	8	19
98	GCAGCAGCCGAATTCGGTACATTACCTGTaatgtaccacagggtaacatcgccacagggcctatgtGGCCGCATAGGCCACTAGTGGATCTGGATC	rad51 ku70	10	36
99	AGCAGCCGAATTCGGTACATTACCTGTTAacataacatagttaacattacatagttaatggcctatgCGCATAGGCCACTAGTGGATCTGGATCCTC	rad51 ku70	11	39
100	AGCAGCAGCCGAATTCGGTACATTACCTGggttaattacCGCATAGGCCACTAGTGGATCTGGATCCT	rad51 ku70	13	9
101	AGCAGCCGAATTCGGTACATTACCTGTTAggcccgatgGGCCACTAGTGGATCTGGATCCTCTAGAGTC	rad51 ku70	17	9
102	TAATGAAAATAAGAGCTTGAGGGAAAAATcctatggccacctaataaggGCATAGGCCACTAGTGGATCTGGATCCTCT	rad51 ku70	77	19
103	GCAGCCGAATTCGGTACATTACCTGTTAacgggccaacagggCGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	5	13
104	AGCAGCCGAATTCGGTACATTACCTGTTAatgctatGGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	6	7
105	GCAGCCGAATTCGGTACATTACCTGTTAacagccggcCGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	6	10
106	GCAGCCGAATTCGGTACATTACCTGTTActgttacctGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	7	9
107	GCAGCCGAATTCGGTACATTACCTGTTAagataGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	7	5
108	GCAGCCGAATTCGGTACATTACCTGTTAaacagGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	7	5
109	GCAGCCGAATTCGGTACATTACCTGTTAacattaccctGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	7	10
110	GAGCAGCAGCCGAATTCGGTACATTACCTAatgtacaTAGCGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	8
111	AGCAGCCGAATTCGGTACATTACCTGTTAatgtatGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	6
112	AGCAGCCGAATTCGGTACATTACCTGTTAccctggGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	6
113	AGCAGCCGAATTCGGTACATTACCTGTTAagcataGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	6
114	AGCAGCCGAATTCGGTACATTACCTGTTAaggtagtGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	7
115	AGCAGCCGAATTCGGTACATTACCTGTTAaggtaatggccacatGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	15
116	AGCAGCCGAATTCGGTACATTACCTGTTAattaccgggtatagtgGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	16
117	GCAGCCGAATTCGGTACATTACCTGTTAgtatGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	8	4
118	GCAGCCGAATTCGGTACATTACCTGTTAaacatacCGGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	9	7
119	AGCAGCCGAATTCGGTACATTACCTGTTAacaggggCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	11	7
120	CAGCAGCCGAATTCGGTACATTACCTGTTAgggtCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	12	4
121	AGAGCAGCAGCCGAATTCGGTACATTACCTgaataGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	13	5
122	AGAGCAGCAGCCGAATTCGGTACATTACCTgcatagtGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	13	7
123	AGAGCAGCAGCCGAATTCGGTACATTACCTgaattcgggtacatagtgGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	13	16
124	TAGAGCAGCAGCCGAATTCGGTACATTACCTatagtGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	14	5
125	GCAGCAGCCGAATTCGGTACATTACCTGTaatgtATAGGCCACTAGTGGATCTGGATCCTCTAG	rad51 lig4	16	5
126	CGTCGTTTAGAGCAGCAGCCGAATTCGGTAttccactatGGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	19	9
127	TGCGTCGTTTAGAGCAGCAGCCGAATTCGGctagtGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	rad51 lig4	23	5
128	AGCAGCCGAATTCGGTACATTACCTGTTAcattaTCCCTAGCGCCGCATAGGCCACTAGTGGATCCTGGA	polQ	0	5
129	GCAGCCGAATTCGGTACATTACCTGTTAagcggtaCTAGCGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	polQ	2	7
130	AGCAGCCGAATTCGGTACATTACCTGTTAccctGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	polQ	8	4
131	GCAGCAGCCGAATTCGGTACATTACCTGTaatgtactagtGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	polQ	10	11
132	AGAGCAGCAGCCGAATTCGGTACATTACCTgaataataaccCGGCCGCATAGGCCACTAGTGGATCTGGATCCTGGA	polQ	12	10

Supplemental Table S8. Sequences and genotypes of all repair products with net insertions of ≥ 4 bp. Inserted sequence is boxed and in lowercase. Notational conventions as for Table S2.