Supplemental information

Table S1. Chr3 Primers used for qPCR

Distance (kb)		
-56.59	CCAAAGCGTCATGGACATCT	AGGCCCATCATTCTACTACTGG
-48.148	CACGCCTAGTTTCAGCTTGTTT	CTTCAAGACATAATCAACGACGC
-29.91	TCGTCGTCGCCATCATTTTC	GCCCAAGTTTGAGAGAGGTTGC
-16.712	CGTCTTCTCAGCGAACAACAGC	CGTCTTCTCAGCGAACAACAGC
-9.592	TCAGGGTCTGGTGGAAGGAATG	CAAAGGTGGCAGTTGTTGAACC
-5.358	ATTGCGACAAGGCTTCACCC	CACATCACAGGTTTATTGGTTCCC
-0.186	CATACAGAAACACAGCGG	AGGAAGGAACAGGAATCTGG
0.183	CCTGGTTTTGGTTTTGTAGAGTGG	GAGCAAGACGATGGGGAGTTTC
5.453	GGACTGGTTATAGACGATGAAGTGT	AAGTCGTCCTTCTTCTTGCTCC
9.187	TGGATCATGGACAAGGTCCTAC	GGCGAAAACAATGGCACTCT
18.206	CGGTCCTCGATTTTGTTACCTTC	GCAAGGATATTCCTGCCTTTTTC
26.869	GGAAAGACTGGCTCATCAAAAC	ACATTCTCAGAGAGAACCTCCA
47.693	ACACCCTGAATGGGGAAAC	CTGCATGGGTGCTTGATG
61.721	ATCTCAGCCAGCTGCTGG	CCCTCTATCTGTCCTTCTGC
69.192	AACAACGGTGAACGGTGCTG	GCAGTAGAAACCTGGGATGTGG

Table S2. Chr6 Primers used for qPCR

Distance (kb)		
-62.387	CTGTTACTGACCAAGCTTCCTA	TTCACCAGTGGTAGGCTC
-52.502	GATGAGAAGGTGTACCACACG	GAGCGTCACAACGTCAGA
-42.42	TTGGAATAAAGGTGAAGGTTTCC	CCACGACTCATATCATTACCAAGA
-32.588	TTCTGCATGGAATGGAGGAT	CTTCAGATGCTATCGCAGCTA
-17.512	TCTAGGACATCGTTCATTTCCA	TTGGATACTACTTTACCTGCAGA
-8.302	CGTTCAAGATTACAGCAATGCG	TACCCGGTCGACCATATTGA
-3.849	CATACAGAAACACAGCGG	AGGAAGGAACAGGAATCTGG
-3.515	GCAGCACGGAATATGGGA	TAAGTCTCTTCTTATATAAATGTCATAGA
-2.471	GGTCCCGCTTTCCGATTT	TTGCACCACGTAGAACTCAG
-0.95	GATATAAAATGCTCCAACTGCACA	AGGTGCGACAATGTTCAGTG
-0.172	GCTCAGTGTGCGTTATGCTT	CCTGGTTTTGGTTTTGTAGAGTGG
1.488	ATGTTCGGGGATTCCCAATA	ATTATTCCTTTGCCCTCGGA
5.127	GACTTAATGGTAGCAAACGTAGTG	CACACGCCCGAATTATTGTT
10.086	GCTTCGTTGTTTCTGATTGCAG	AGCGCGAAATAACGTTCTGA
20.097	ATTCAACTTGTTGCGGTTCG	TCTTCTGTCTCAACTGTCTTAGCC
30.085	TCAGAGATTCAACAGAGGGATGT	CAAATCTTCGAGGATCGAACTG
40.079	GGTCAGGTTTTATTGCAGAATG	CCGTCAGAGGTTTAGAACTTGTAGA
55.088	GCAAGTTCTAGTGGAGAATAAGG	GATCATTCTCCGCGTCCTT

The distances listed for Chr 6 are based on a sequence containing the *HMRα*::*LEU2* sequence. The Chr 3 sequence includes the pair of inverted TY's proximal to *MAT*(40). All distances are calculated using the more distal end of the PCR product.

Supplemental Figure legends

Figure S1. Homologous recombination assays used in this study. A) Strain YJK17 is used to study kinetics of inter-chromosoml (or ectopic) gene conversion. A HO induced break at the *MAT* locus on Chr3 is repaired using an ectopic *MAT*a-inc donor present on Chr 5 by gene conversion B) Strain YMV80 repairs an HO break by single strand annealing using a flanking donor 25kb away from the cut site resulting in the deletion of all the intervening sequences C) Strain JRL346 repairs the HO break on Chr 5 by break-induced replication as only one end of the DSB shares homology with its donor sequence on Chr 11. A successful BIR event results in the non-reciprocal translocation of Chr 11 sequences, the loss of the HPH marker on Chr 5 and the restoration of the coding sequence of the *CAN1* gene.

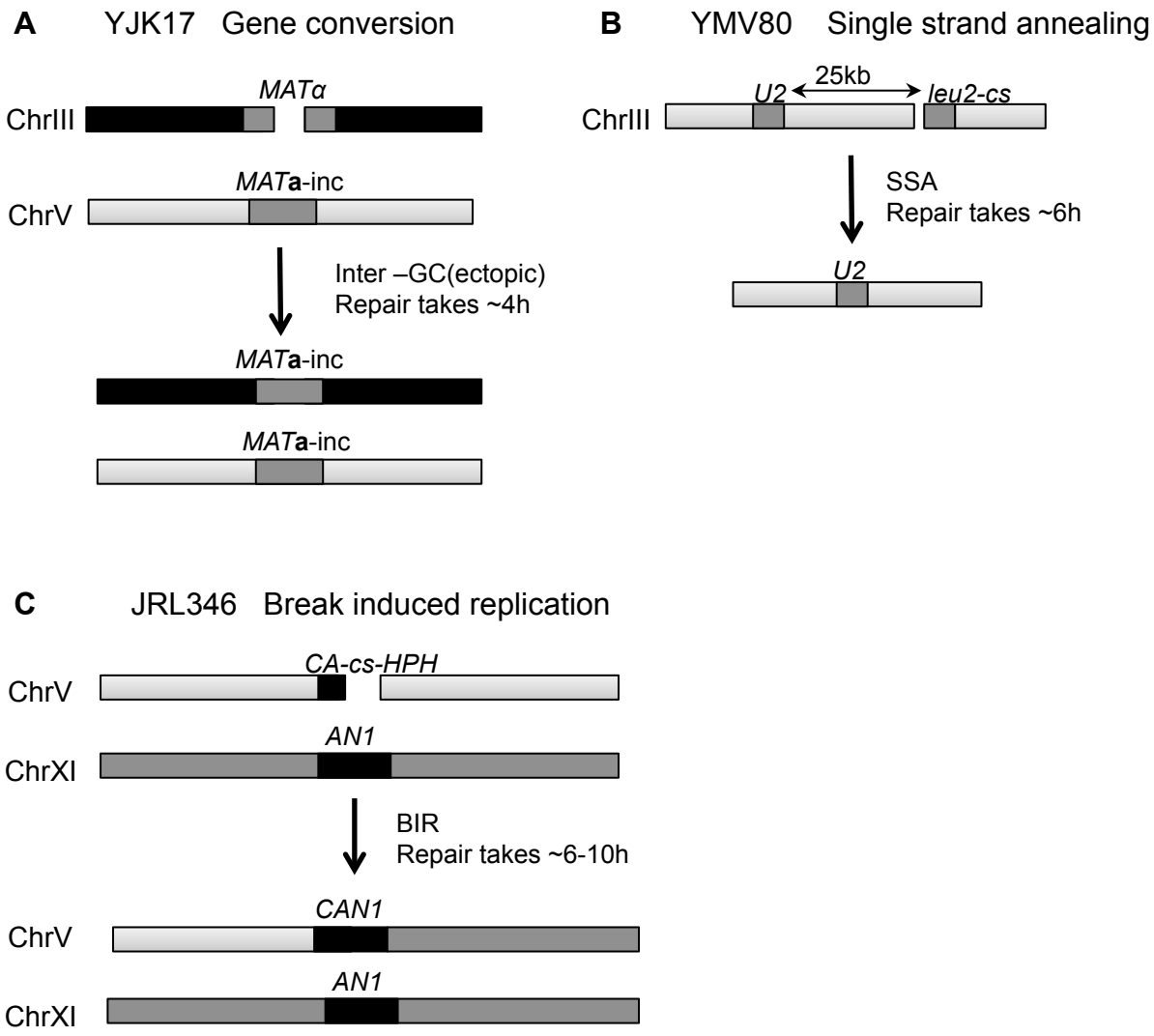
Figure S2. Micrococcal nuclease digestion of nucleosome arrays. In a 200 µl reaction, wild type H2A, H2A S129A or H2A S129E – containing nucleosome array (~180 ng DNA equivalents) assembled on pBlueScript SK(-) was incubated with 2 units of MNase at room temperature. Digestion was stopped by 80 µl of 1% SDS 0.1M EDTA at indicated time points. Asterisks denote lanes with partial or total loss of DNA pellet during sample preparation.

Figure S3. Deletion of *HTZ1* does not suppress *fun30*Δ's adaptation defect. The indicated strains were micro-manipulated onto YEP-GAL plates, as described in materials and methods and Fig 8A and monitored for adaptation at 24 hr. Error bars reflect the range from 2 independent experiments.

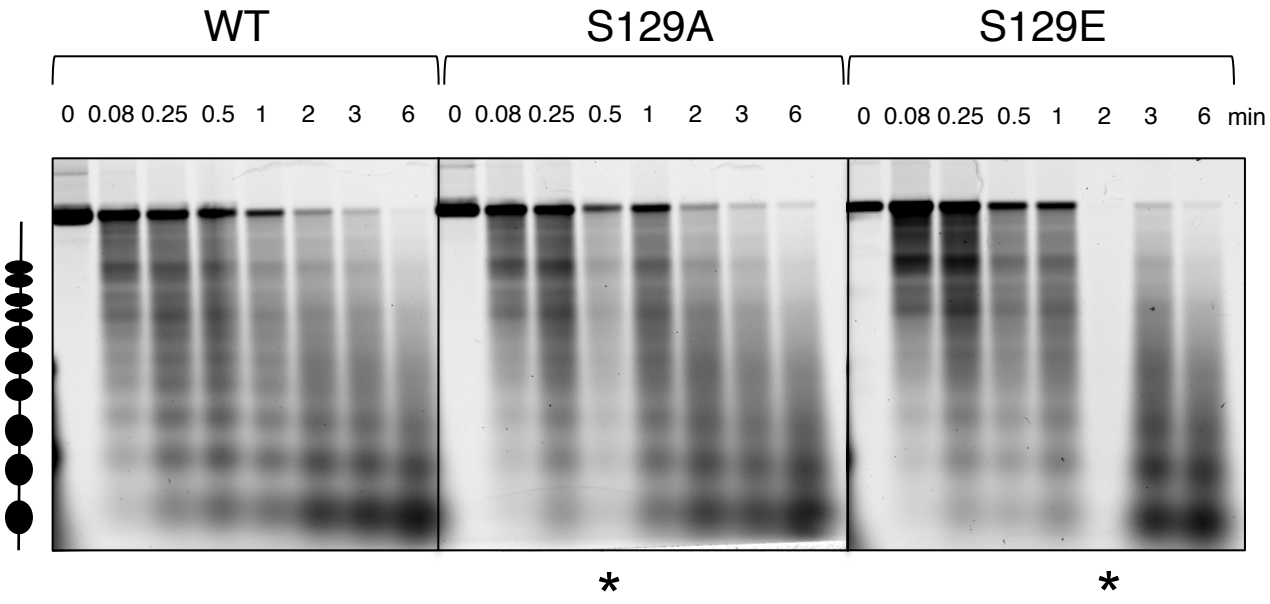
Figure S4. Over-expression of ExoI causes faster and more extensive resection. A. *GAL::EXOI* carried on a plasmid was over-expressed at the same time that *GAL::HO* creates a DSB in a donorless strain, with or without *fun30*Δ. PCR products were amplified using primers located at different distances from the DSB. Template DNA was isolated from galactose-induced cells at the times shown. All values were normalized as described in Fig 3.

Figure S5. *fun30*Δ exacerbates camptothecin sensitivity of *sgs1*Δ and *exo1*Δ. Ten-fold serial dilutions of the indicated strains were plated on YEPD plates with and without 3mM camptothecin.

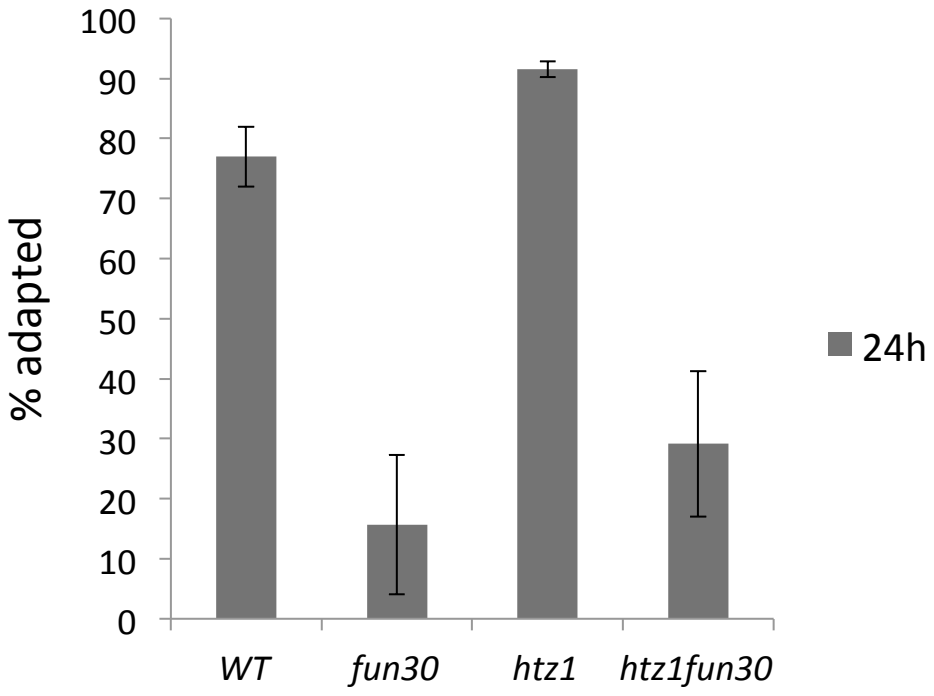
Figure S6. *fun30*Δ increases the rate of non-homologous end joining. JKM179 and *fun30*Δ derivatives were diluted such that roughly 100 cells were plated on YEPD and 100 fold more plated on YEP-Galactose plates; for yku70Δ derivatives approximately 10,000-fold more cells were plated. The percentage viability was calculated by dividing the number of colonies of galactose plates to those on YEPD plates, corrected for dilutions. Error bars reflect the standard deviation of 3 independent experiments.



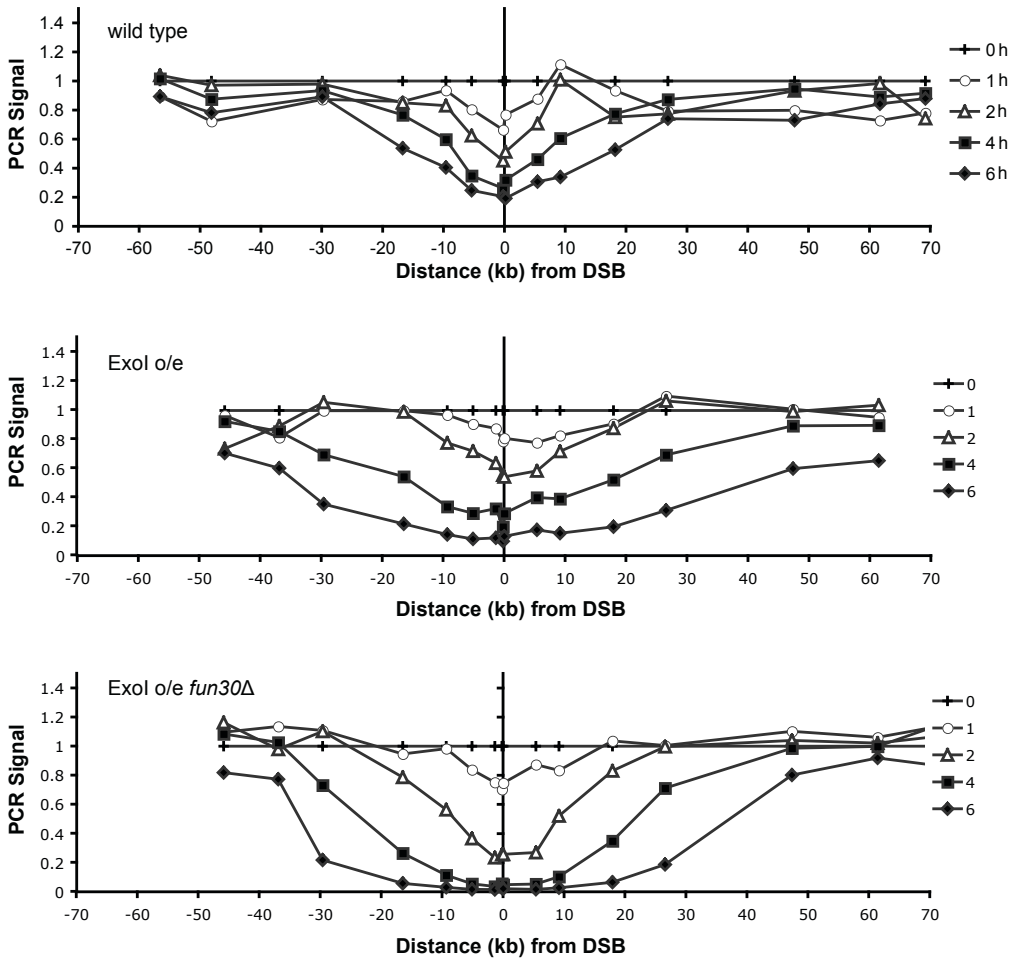
Supplemental Figure 1



Supplemental Figure 2



Supplemental Figure 3



Supplemental Figure 4

WT

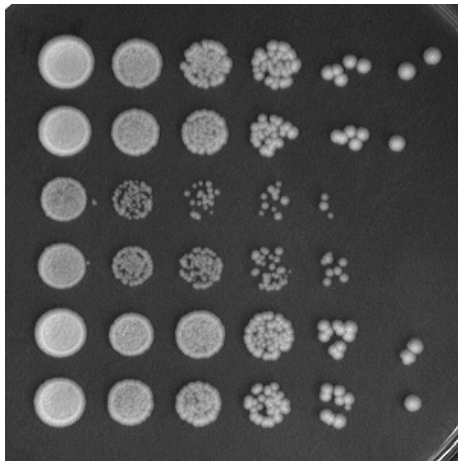
fun30Δ

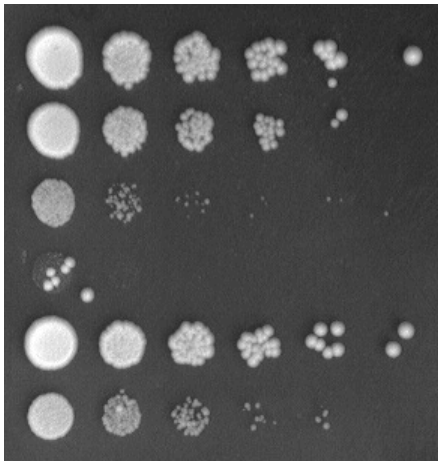
sgs1Δ

sgs1Δ fun30Δ

exo1Δ

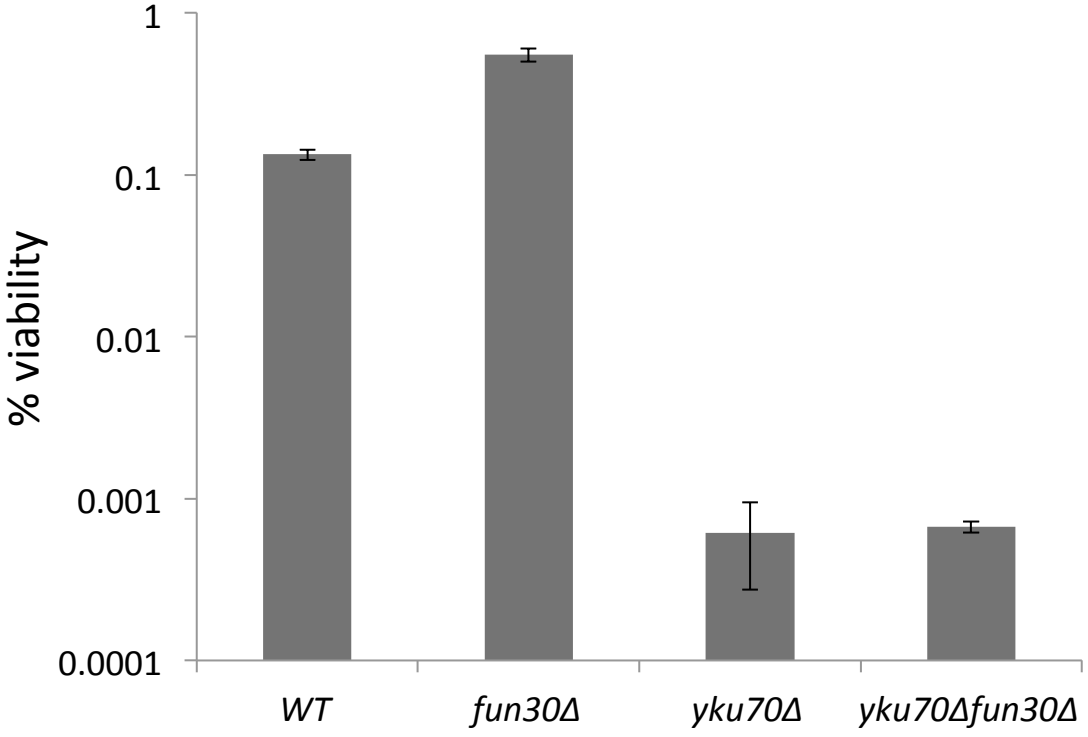
exo1Δ fun30Δ





YEPD CPT 30 uM

Supplemental Figure 5



Supplemental Figure 6