Supplementary Information

Table S1. *Saccharomyces cerevisiae* strains used in this study.

Strain	Relevant genotype	Source or Reference
W303	*MAT*a *ade2-1 can1-100 his3-11,15 leu2-3,112 trp1-1 ura3-1 rad5-535*	
YLL2479	W303 *dnl4Δ::KANMX*	This study
YLL2920	W303 *TBF1::LEU2*	This study
YLL3089	W303 *tbf1-1::LEU2*	This study
YLL3098	W303 *tbf1-2::LEU2*	This study
YLL3099	W303 *tbf1-3::LEU2*	This study
YLL3158	W303 *rsc2Δ::NATMX*	This study
YLL3163	W303 *env11Δ::NATMX*	This study
YLL3167	W303 *arp8Δ::NATMX*	This study
YLL3204	W303 *swr1Δ::KANMX*	This study
YLL3206	W303 *vid22Δ::TRP1 rsc2Δ::KANMX*	This study
DMP4499	W303 *rpd3Δ::HIS3*	This study
DMP5267	W303 *vid22Δ::TRP1*	This study
DMP5321/2D	W303 *tbf1-1::LEU2 rad51Δ::HIS3*	This study
DMP5321/4C	W303 *rad51Δ::HIS3*	This study
DMP5322/10D	W303 *tbf1-1::LEU2 rad52Δ::TRP1*	This study
DMP5322/7C	W303 *rad52Δ::TRP1*	This study
DMP5323	W303 *vid22Δ::TRP1 rad51Δ::HIS3*	This study
DMP5324	W303 *vid22Δ::TRP1 rad52Δ::TRP1*	This study
DMP5431	W303 *tbf1-1::LEU2 rsc2Δ::NATMX*	This study
DMP5433	W303 *vid22Δ::TRP1 arp8Δ::NATMX*	This study
DMP5434	W303 *tbf1-1::LEU2 arp8Δ::NATMX*	This study
DMP5492	W303 *tbf1-1::LEU2 swr1Δ::KANMX*	This study
DMP5493	W303 *vid22Δ::TRP1 swr1Δ::KANMX*	This study
esa1-1851	W303 *esa1-1851::URA3*	Bird *et al,* 2002
DMP5518	W303 *tbf1-1::LEU2 esa1-1851 ::URA3*	This study
DMP5519	W303 *tbf1-1::LEU2 rpd3Δ::HIS3*	This study
DMP5587	W303 *tbf1-1::LEU2 dnl4Δ::KANMX*	This study
DMP5588	W303 *vid22Δ::TRP1 dnl4Δ::KANMX*	This study
DMP5589	W303 *rad52Δ::TRP1 dnl4Δ::KANMX*	This study
DMP5591	W303 *tbf1-3::LEU2 rad51Δ::HIS3*	This study
DMP5592	W303 *tbf1-3::LEU2 rad52Δ::TRP1*	This study
DMP5604	W303 *tbf1-1::LEU2 rad52Δ::TRP1 dnl4Δ::KANMX*	This study
DMP5605	W303 *vid22Δ::TRP1 rad52Δ::TRP1 dnl4Δ::KANMX*	This study
YMV45	*ho hml::ADE1 mata::hisG hmr::ADE1 leu2::leu2(Asp718-SalI)-URA3-*pBR332-*MATa ade3::GAL::HO ade1 lys5 ura3-52 trp1::hisG*	Vaze *et al,* 2002

YLL2760	YMV45 *bar1Δ::HPHMX*	This study
YLL2958	YMV45 *rad52Δ::NATMX bar1Δ::HPHMX*	This study
YLL3090	YMV45 *tbf1-1::LEU2 bar1Δ::HPHMX*	This study
YLL3134	YMV45 *exo1Δ::NATMX bar1Δ::HPHMX*	This study
YLL3135	YMV45 *tbf1-3::LEU2 exo1Δ::NATMX bar1Δ::HPHMX*	This study
YLL3168	YMV45 *tbf1-1::LEU2 rad52Δ::NATMX bar1Δ::HPHMX*	This study
YLL3169	YMV45 *tbf1-3::LEU2 rad52Δ::NATMX bar1Δ::HPHMX*	This study
YLL3170	YMV45 *vid22Δ::TRP1 bar1Δ::HPHMX*	This study
YLL3227	YMV45 *MRE11-18MYC::TRP1 bar1Δ::HPHMX*	This study
YLL3228	YMV45 *tbf1-1::LEU2 MRE11-18MYC::TRP1 bar1Δ::HPHMX*	This study
YLL3237	YMV45 *TBF1-18MYC::TRP1 bar1Δ::HPHMX*	This study
YLL3238	YMV45 *VID22-18MYC::TRP1 bar1Δ::HPHMX*	This study
YLL3241	YMV45 *vid22Δ::TRP1 rad52Δ::KANMX bar1Δ::HPHMX*	This study
YLL3253	YMV45 *tbf1-3::LEU2 bar1Δ::HPHMX*	This study
YLL3272	YMV45 *DNL4-18MYC::TRP1 bar1Δ::HPHMX*	This study
YLL3273	YMV45 *tbf1-1::LEU2 DNL4-18MYC::TRP1 bar1Δ::HPHMX*	This study
YLL3274	YMV45 *vid22Δ::KANMX DNL4-18MYC::TRP1 bar1Δ::HPHMX*	This study
JKM139	*MATa hmlΔ hmrΔ ade1 lys5 leu2-3,112 trp1::hisG ura3-52 ho ade3::GAL-HO site*	Lee *et al,* 1998
YLL2285	JKM139 *dnl4Δ::KANMX*	This study
YLL3152	JKM139 *vid22Δ::TRP1*	This study
YLL3153	JKM139 *tbf1-1::LEU2*	This study
YLL3195	JKM139 *VID22-18MYC::URA3*	This study
YLL3196	JKM139 *tbf1-1::LEU2 VID22-18MYC::URA3*	This study
YLL3254	JKM139 *mre11Δ::KANMX TBF1-18MYC::HIS3*	This study
YLL3255	JKM139 *mre11Δ::KANMX VID22-18MYC::URA3*	This study
YLL3262	JKM139 *tbf1-3::LEU2*	This study
DMP5466	JKM139 *TBF1-18MYC::HIS3*	This study
DMP5497	JKM139 *vid22Δ::TRP1 TBF1-18MYC::HIS3*	This study
DMP5499	JKM139 *hta2Δ::NATMX hta1-S129A::URA3 TBF1-18MYC::HIS3*	This study
tGI354	*ho hmlΔ::ADE1 MATa-inc hmrΔ::ADE1 ade1 leu2-3;112 lys5 trp1::hisG ura3-52 ade3::GAL::HO arg5,6::MATa::HPHMX*	Saponaro *et al*, 2010
YLL3088	tGI354 *tbf1-1::LEU2*	This study
YLL3092	tGI354 *vid22Δ::TRP1*	This study

References

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Lee SE, Moore JK, Holmes A, Umezu K, Kolodner RD, Haber JE (1998) *Saccharomyces* Ku70, mre11/rad50 and RPA proteins regulate adaptation to G2/M arrest after DNA damage. *Cell* **94:** 399-409.

Saponaro M, Callahan D, Zheng X, Krejci L, Haber JE, Klein HL, Liberi G (2010) Cdk1 targets Srs2 to complete synthesis-dependent strand annealing and to promote recombinational repair. *PLoS Genet* **6:** e1000858.

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Figure S1

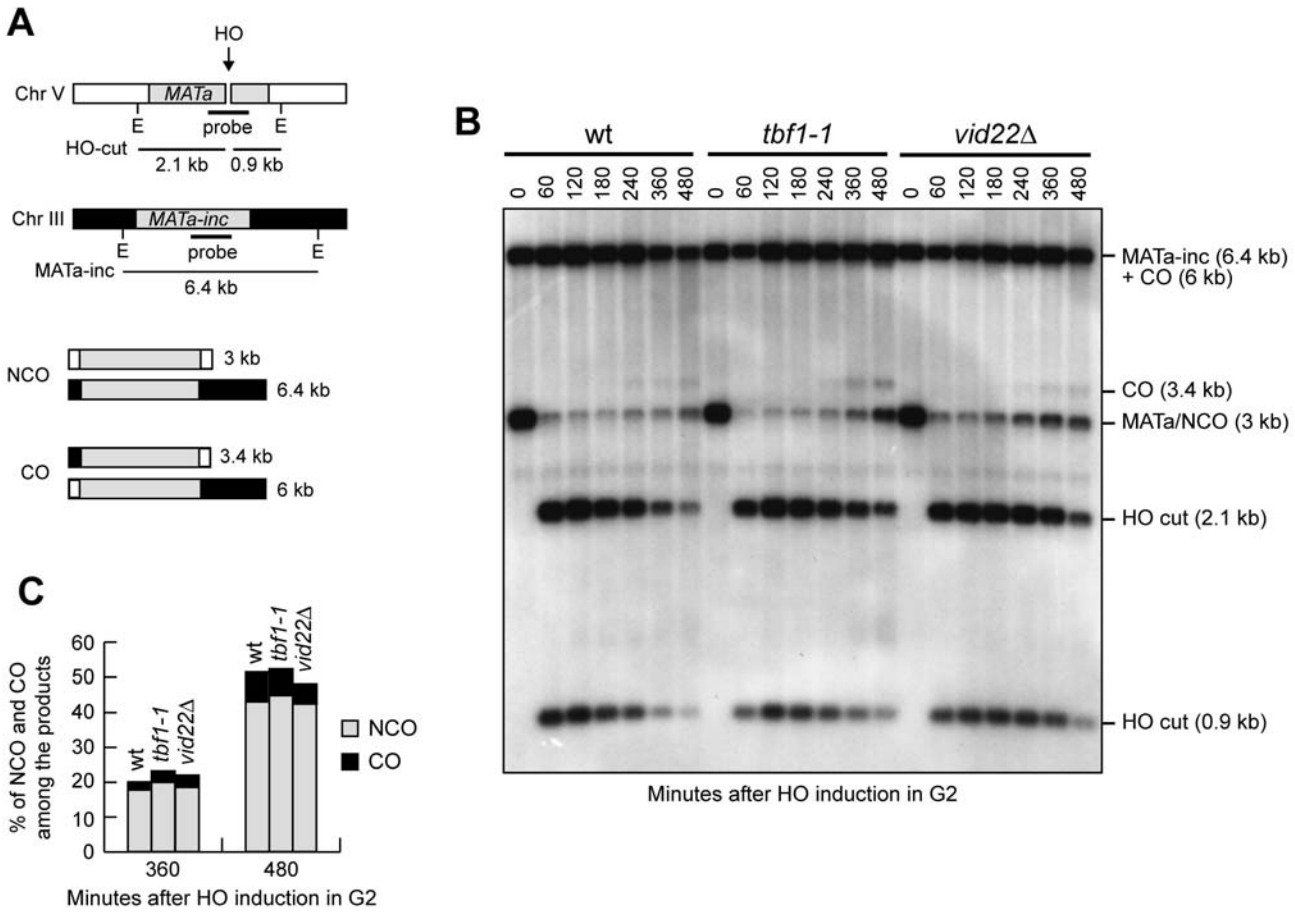

Figure S1 Analysis of crossover and non-crossover frequency during ectopic recombination in *tbf1* and *vid22Δ* mutants. (**A**) Schematic representation of the ectopic recombination assay. Galactose-induced HO generates a DSB at a *MATa* DNA sequence inserted on chromosome V, while the homologous *MATa-inc* region on chromosome III cannot be cut by HO and is used as a donor for HR-mediated repair, which can generate both noncrossover (NCO) and crossover (CO) products. The sizes of EcoRI (E) fragments detected by the depicted probe are indicated. (**B-C**) Exponentially growing YEPR (exp) cell cultures were arrested in G2 with nocodazole (time zero) and transferred to YEPRG in the presence of nocodazole. (**B**) Southern blot analysis of EcoRI-digested genomic DNA with the MATa probe depicted in (**A**). (**C**) Densitometric analysis of CO versus NCO repair bands at the indicated time points from break induction. To determine the amount of non-crossover and crossover products, the normalized intensity of the corresponding bands at different time points after DSB formation was divided by the normalized intensity of the uncut *MATa* band at time zero before HO induction (100%). The repair efficiency (NCO+CO) was normalized with respect to the efficiency of DSB formation by subtracting the value calculated 2 hours after HO induction (maximum efficiency of DSB formation) from the values calculated at the subsequent time points after galactose addition.