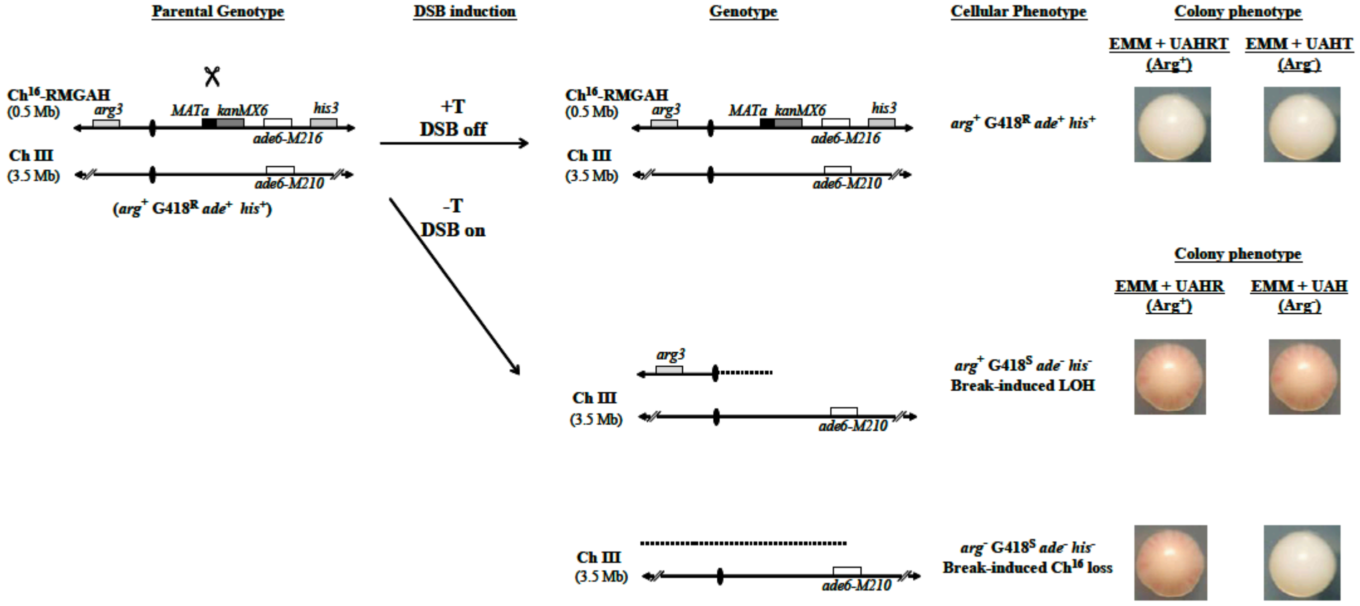
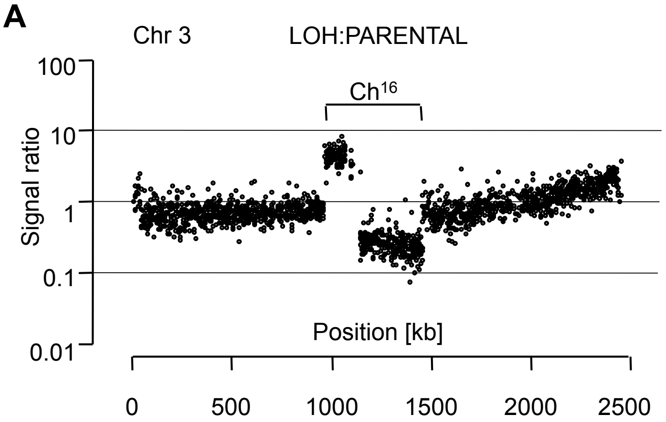
Blaikley et al Supplementary Figure 1

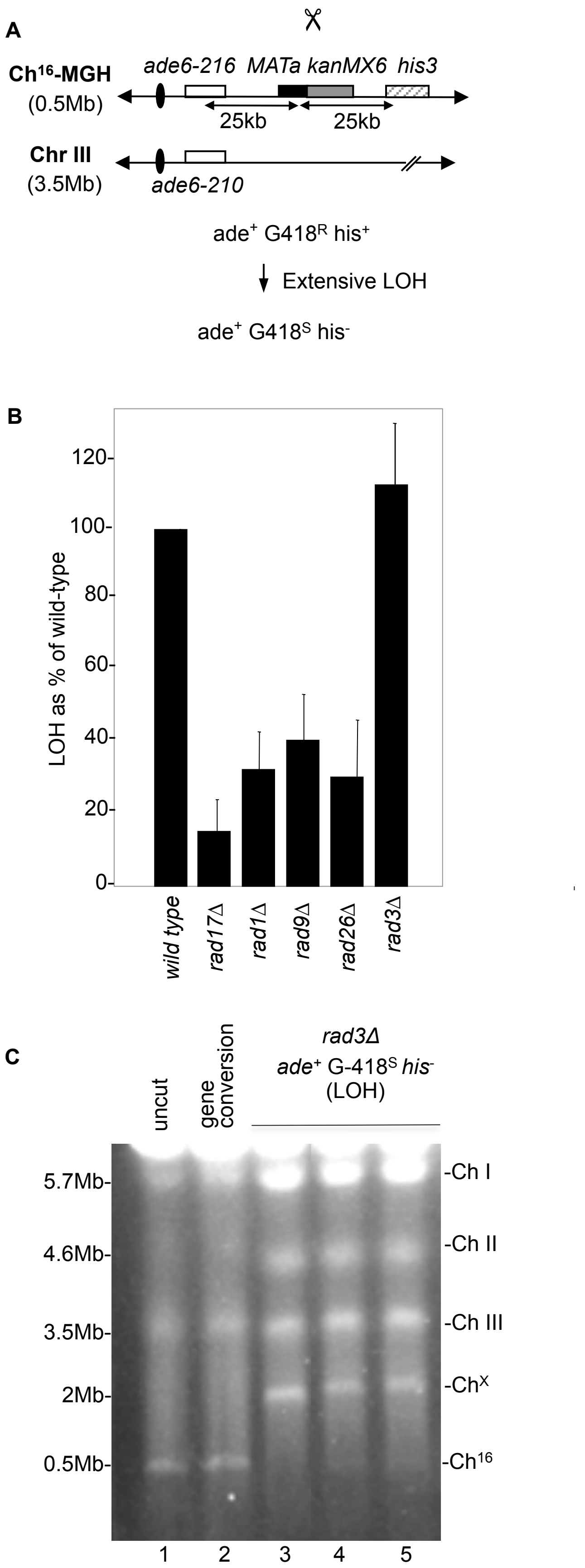


Blaikley et al Supplementary Figure 2

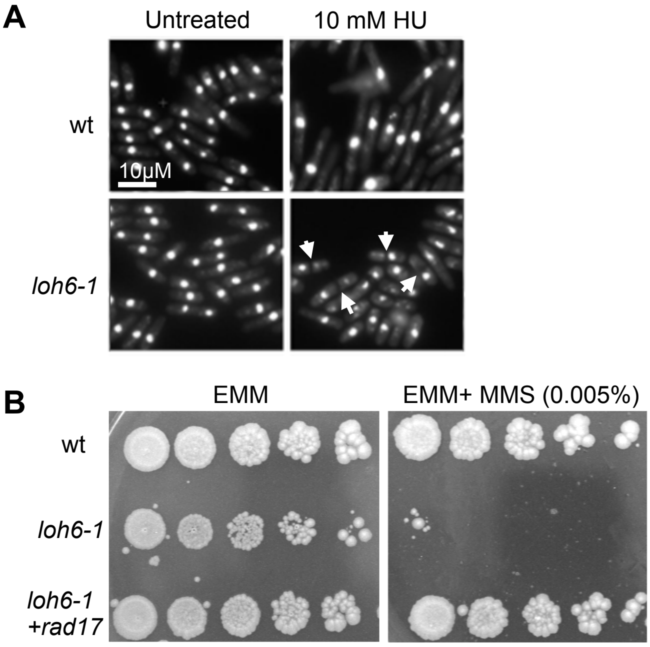
A



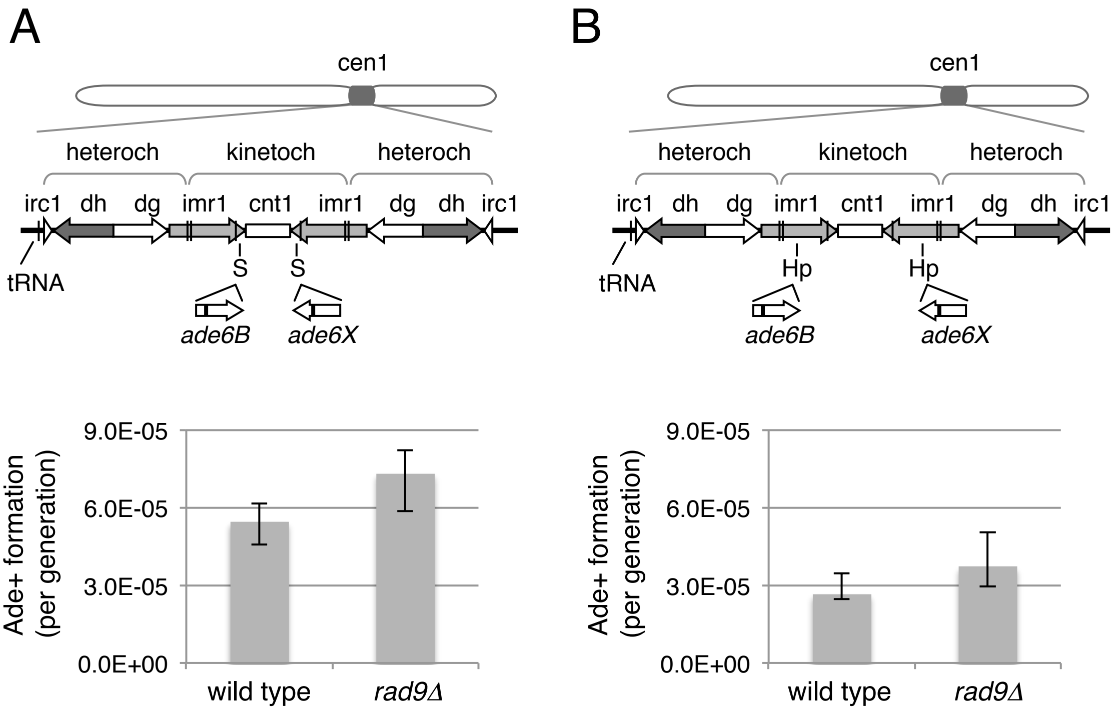
Blaikley et al Supplementary Figure 3



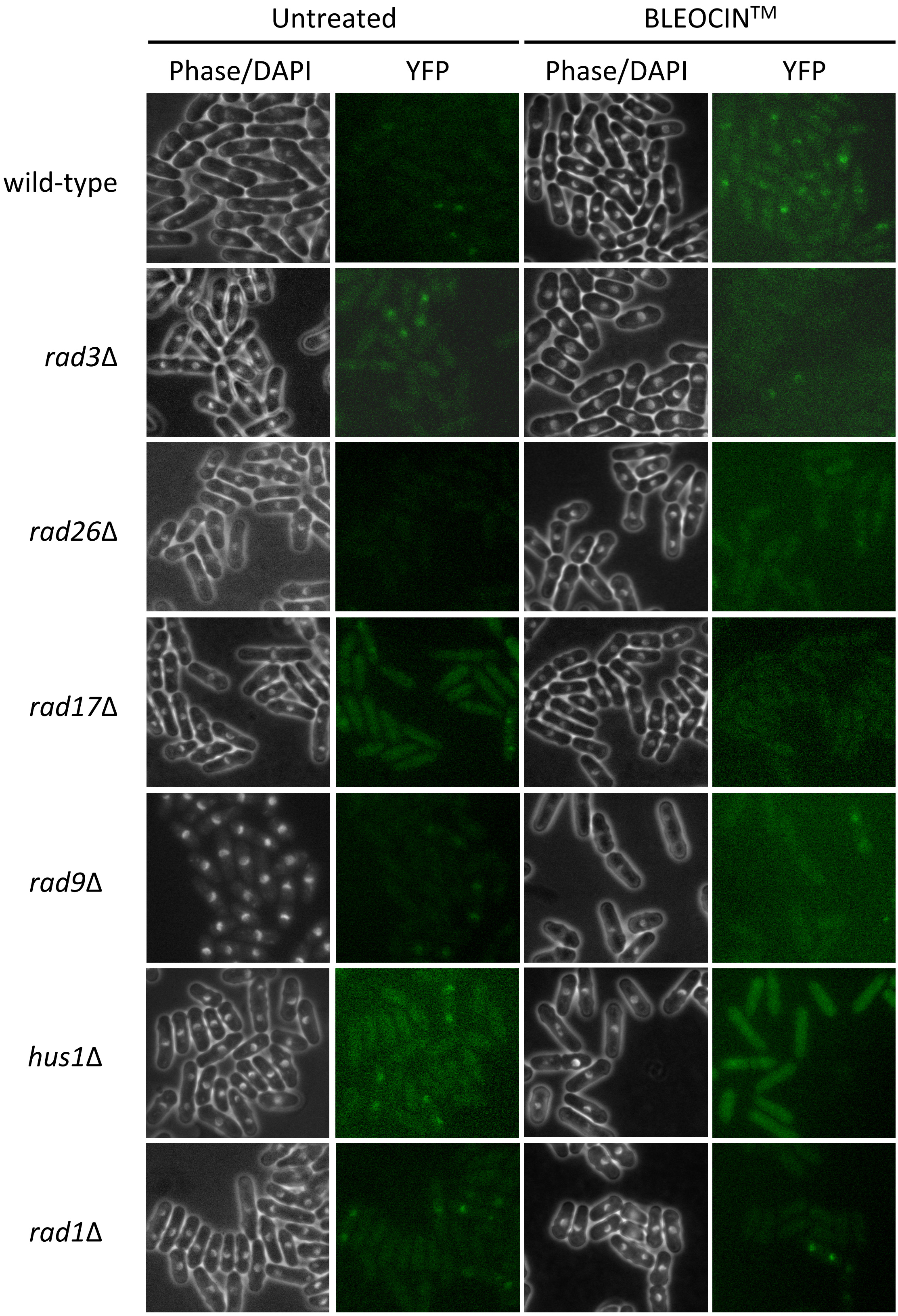
Blaikley et al Supplementary Figure 4



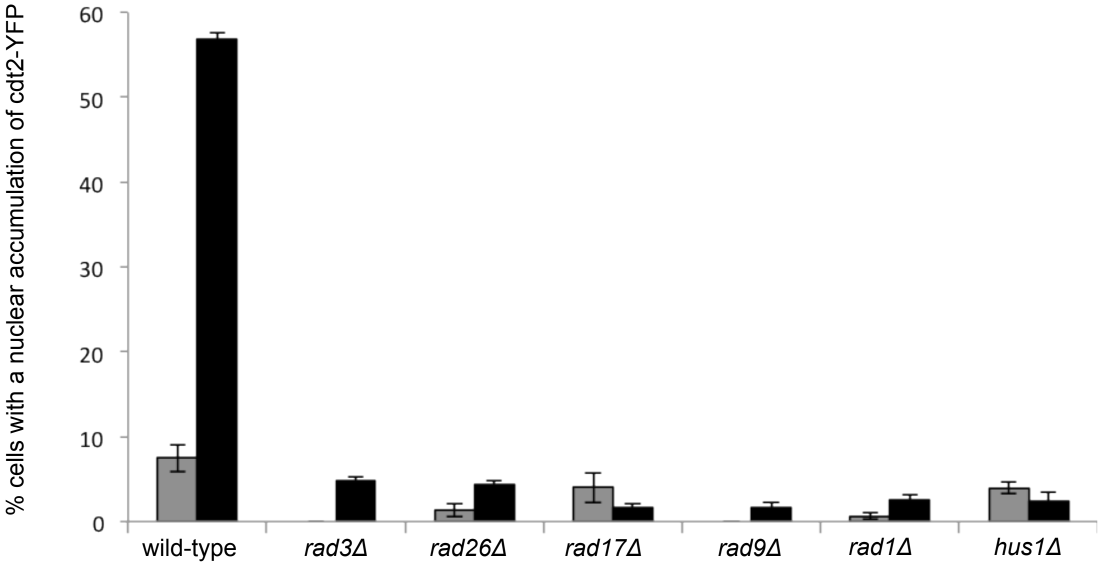
Blaikley et al Supplementary Figure 5



Blaikley et al Supplementary Figure 6A



Blaikley et al Supplementary Figure 6B



Blaikley et al Supplementary data

Supplementary Figure 1

Colony-sectoring assay for identifying suppressors of break-induced LOH. Schematic of Ch^{16}-RMGAH. Ch^{16}-RMGAH, ChIII, centromeric regions (ovals), complementary heteroalleles (*ade6-M216* and *ade6-M210*; white), and the *his3* marker (vertical stripes; inserted ~50 Kb centromere-distal from *ade6-M216*) are shown as previously described (Cullen *et al.*, 2007). The *MATa* site (black) with an adjacent *kanMX6* resistance marker (grey) is inserted into *spcc23B6.06,* ~30 Kb centromere-proximal from *ade6-M216,* and in Ch^{16}-RMHAH, *kanMX6* is replaced by *hph*. The *arg3* marker is inserted into *spcc1795.09* on the left arm of the minichromosome. The intact minichromosome (arg^+ $G418^R$ ade^+ his^+) remains when there is repression of pREP81-HO and a DSB is not induced (+T DSB off). An intact minichromosome would give white colonies (colony phenotype) on both EMM+UAHRT (Arg^+; EMM plus arginine, uracil, histidine, low adenine and thiamine) and EMM+UAHT (Arg^-; EMM plus uracil, histidine, low adenine and thiamine). Derepression of pREP81X-HO (not shown) generates a DSB (-T DSB on) at the *MATa* target site (scissors). Break-induced LOH (arg^+ $G418^S$ ade^- his^-) would result in loss of the *ade6-M216* heteroallele, which would accumulate a pink by-product on both EMM+UAHR (Arg^+; EMM plus arginine uracil, histidine, and low adenine) and EMM+UAH (Arg^-; EMM plus uracil, histidine and low adenine). Break-induced minichromosome loss (Ch^{16} loss *;* arg^- $G418^S$ ade^- his^-)

would result in loss of the *arg3* marker and the *ade6-M216* heteroallele, which would accumulate a pink by-product on low adenine plates containing arginine (EMM+UAHR). However, on low adenine plates without the addition of arginine (EMM+UAH) cells lacking the minichromosome would not grow, therefore only the cells containing the intact minichromosome would survive, resulting in white colonies.

Supplementary Figure 2. CGH data of an isochromosome taken from (1) for comparison with Figure 2B. Note the increased signal ratio is across the left arm of the minichromosome (Ch16) is consistent with duplication and isochromosome formation. This is not observed in the truncated bands described in Figure 2.

Supplementary Figure 3. DNA damage checkpoint does not suppress break-induced LOH associated with DSB repair. (A) Schematic of the Ch^{16}-MGH strain. Ch^{16}-MGH, ChIII, centromeric regions (ovals), complementary heteroalleles (*ade6-M216* and *ade6-M210*; white) *ade5*$^{+}$ (vertical stripes), *MATa* site (black) with an adjacent *kanMX6* resistance marker (grey) and *his3*$^{+}$ marker (dark grey) are shown as previously described (2). Derepression of pREP81X-HO (not shown) generates a DSB at the *MATa* target site (scissors). Schematic for break-induced extensive LOH in this context is shown. (B) Percentage DSB-induced LOH in rad17Δ (TH1365), *rad1Δ*(TH1401), *rad9Δ*(TH1373), *rad26Δ*(TH1362), *and rad3*Δ (TH1369), as a percentage of wild type LOH are shown. (C) High resolution PFGE analysis from *rad3*Δ Ch^{16}-MGH uncut parental strain (TH1369; lane 1), *rad3*Δ Ch^{16}-MGH ade^{+}G418^{S} his^{+} gene conversion colony (lane 2), and individual *rad3*Δ ade^{+}G418^{S} his^{-} (LOH) colonies. Band and chromosome sizes are shown.

Supplementary Figure 4. *loh6-1* encodes an allele of rad17**.** (A) *loh6-1* exhibits a cut phenotype in HU. DAPI stained wild-type Ch^{16}-RMGAH (TH2130) or *loh6-1* (TH5735) strains either untreated or following exposure to 5mM HU for 6 h. 10μM size bar indicated. (B) Serial dilutions of wild type Ch^{16}-RMGAH (TH2130) and *loh6-1* (TH5735) with pREP41X empty vector or pREP41X-rad17 on EMM plates with 0.005% MMS, as indicated.

Supplementary Figure 5. Loss of Rad9 does not increase spontaneous recombination levels within the centromere. Spontaneous levels of recombination within the centromere were determined by a fluctuation test using wild-type and *rad9Δ* strains. 10 ml of EMM+Ade was inoculated with independent colonies formed on YE+Ade plates and incubated overnight at 33°C. The cells were plated onto EMM+Ade and EMM+Guanine to determine the number of colony-forming units and that of Ade+ recombinants, respectively. The Ade+ prototroph formation rate per generation was determined using the method of medians (3,4). (A) Recombination between *ade6B* and *ade6X* heteroalleles integrated at the SnaBI sites in imr1. (B) Recombination between the *ade6* heteroalleles integrated at the HpaI sites in imr1. The median and 95% confidential intervals(5) are shown. *n* ≥12.

Supplementary Figure 6. (A) role for the DNA damage checkpoint pathway in RNR regulation. A. Methanol-fixed samples of asynchronous Cdt2-YFP wild-type, *rad3*Δ, *rad26*Δ, *rad17*Δ, *rad9*Δ, *rad1*Δ, or *hus1*Δ cells imaged following their growth in the presence or absence of 1μg/ml Bleocin for 1 hour. **(B)** Quantitation of Cdt2-YFP nuclear accumulation from experiments described above. A Minimum of 100 cells were counted and scored for nuclear accumulation of Cdt2-YFP. Mean +/- standard errors are shown for three independent experiments.

Supplementary Materials and Methods

Fluorescence microscopy Asynchronous cultures were treated with 1μg/ml Bleocin for 1hr at 26°C or left untreated before being fixed in 100% methanol and stored in 100% acetone at -20°C. Samples were rehydrated and stained with 6′-diamidino-2-phenylindole (DAPI) and mounted (ProLong® Gold antifade reagent with DAPI; Invitrogen) before examination using Zeiss Axioplan 2ie microscope, Hamamatsu Orca ER camera and micromanager software.

Supplementary References

1. Tinline-Purvis, H., Savory, A.P., Cullen, J.K., Dave, A., Moss, J., Bridge, W.L., Marguerat, S., Bahler, J., Ragoussis, J., Mott, R. *et al.* (2009) Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. *Embo J*, **28**, 3400-3412.
2. Cullen, J.K., Hussey, S.P., Walker, C., Prudden, J., Wee, B.Y., Dave, A., Findlay, J.S., Savory, A.P. and Humphrey, T.C. (2007) Break-induced loss of heterozygosity in fission yeast: dual roles for homologous recombination in promoting translocations and preventing de novo telomere addition. *Mol Cell Biol*, **27**, 7745-7757.
3. Lea, D.E. and Coulson, C.A. (1949) The distribution of the numbers of mutants in bacterial populations. *J. Genet.*, **49**, 264-285.

4. Lin, M., Chang, C.J. and Green, N.S. (1996) A new method for estimating high mutation rates in cultured cells. *Mutat Res*, **351**, 105-116.
5. Dixon, W.J. and Massey, F.J., Jr. (1969) *Introduction to Statistical Analysis*. McGraw-Hill Book Company, New York.
6. Moss, J., Tinline-Purvis, H., Walker, C.A., Folkes, L.K., Stratford, M.R., Hayles, J., Hoe, K.L., Kim, D.U., Park, H.O., Kearsey, S.E. *et al.* (2010) Break-induced ATR and Ddb1-Cul4(Cdt)(2) ubiquitin ligase-dependent nucleotide synthesis promotes homologous recombination repair in fission yeast. *Genes Dev*, **24**, 2705-2716.
7. Watson, A.T., Werler, P. and Carr, A.M. (2011) Regulation of gene expression at the fission yeast Schizosaccharomyces pombe urg1 locus. *Gene*, **484**, 75-85.

Supplementary Table 1. ***S. pombe*** **strains used in this study.**

Strain	Genotype	Source
TH2125/6	*leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} /h^{-}	J. Cullen, 2007 (2)
TH2130, 2131, 2132	*leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} pREP81X-HO	J. Cullen, 2007 (2)
TH2357	*leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} pREP81X	J. Cullen, 2007 (2)
TH2654/3165	*leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMHAH h^{+} /h^{-}	J. Cullen, 2007 (2)
TH3317, 3316, 3318	*leu1-32 ade6-M210 ura4-D18 his3-D1* Ch^{16}-YAMGH h^{+} pREP81X-HO	This study
TH3319	*leu1-32 ade6-M210 ura4-D18 his3-D1* Ch^{16}-YAMGH h^{+} pREP81X	This study
TH3382, 3378, 3380	*exo1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} pREP81X-HO	This study
TH3392	*exo1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} pREP81X	This study
TH4089	$rad3^{W1700X}$ *leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{-} pREP81X-HO	This study
TH4090	$rad3^{W1700X}$ *leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{-} pREP81X-HO	This study
TH2941, 2939, 3940	*rad3::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{-} pREP81X-HO	This study
TH2938	*rad3::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{-} pREP81X	This study
TH3410, 3408, 3409	*rad26::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} pREP81X-HO	This study
TH3267	*rad26::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{+} pREP81X	This study
TH3153, 3156, 3157	*chk1::ura4 leu1-32 ade6-M210 ura4-D18 his3-D1* Ch^{16}-YAMGH h^{-} pREP81X-HO	This study
TH3159	*chk1::ura4 leu1-32 ade6-M210 ura4-D18 his3-D1* Ch^{16}-YAMGH h^{+} pREP81X	This study
TH3383, 3384, 3385	*crb2::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^{-} pREP81X-HO	This study

Strain	**Genotype**	**Source**
TH3390	*crb2::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{-}$ pREP81X	This study
TH3395, 3394	*cdc25::ura4 adh-cdc25 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X-HO	This study
TH3396	*cdc25::ura4 adh-cdc25 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X	This study
TH3258, 3257, 3256	*cds1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{-}$ pREP81X-HO	This study
TH3269	*cds1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{-}$ pREP81X	This study
TH3231, 3253, 3254	*mrc1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X-HO	This study
TH3261	*mrc1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{-}$ pREP81X	This study
TH3623, 3475, 3476	*rad3::ura4 chk1::ura4 leu1-32 ade6-M210 ura4-D18 his3-D1* Ch^{16}-YAMGH *h*$^{-}$ pREP81X-HO	This study
TH3477	*rad3::ura4 chk1::ura4 leu1-32 ade6-M210 ura4-D18 his3-D1* Ch^{16}-YAMGH *h*$^{-}$ pREP81X	This study
TH3382, 3381	*rad3::ura4 exo1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X-HO	This study
TH3389	*rad3::ura4 exo1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X	This study
TH3247, 3245, 3246	*rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{-}$ pREP81X-HO	This study
TH3264	*rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{-}$ pREP81X	This study
TH3241	*rad1::kanMX6 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMHAH *h*$^{+}$ pREP81X-HO	This study
TH3376	*rad1::kanMX6 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMHAH *h*$^{+}$ pREP81X	This study
TH3250, 3248, 3249	*rad9::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X-HO	This study
TH3263	*rad9::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH *h*$^{+}$ pREP81X	This study
TH3244	*hus1::kanMX6 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMHAH *h*$^{+}$ pREP81X-HO	This study
TH3697	*hus1::kanMX6 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMHAH *h*$^{+}$ pREP81X	This study

Strain	**Genotype**	**Source**
TH3701, 3621, 3622	*exo1::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^+ pREP81X-HO	This study
TH3658	*exo1::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^+ pREP81X	This study
TH3618, 3455, 3456	*rad3::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^+ pREP81X-HO	This study
TH3446	*rad3::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^+ pREP81X	This study
TH3529, 3527, 3528	*crb2::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^- pREP81X-HO	This study
TH3540	*crb2::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^- pREP81X	This study
TH3454, 3453, 3703	*rad9::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^- pREP81X-HO	This study
TH3452	*rad9::ura4 rad17::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^- pREP81X	This study
TH4093	$rad3^{W1700X}$ *leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMGAH h^- pREP41X-*rad3*	This study
TH2093	*arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^+	Lab stock
TH2094	*arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^-	Lab stock
TH4355	*spd1::hph leu1-32 arg3-D4 ade6- ura4-D18 his3-D1* h^-	Lab stock
TH7329	*rad3::kanMX, arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^-	This study
TH8295	*rad3::kanMX, spd1::hph arg3-D4, ade6-, ura4-D18, leu1-32, his3-D1*	This study
TH7330	*rad26::kanMX, arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^-	This study
TH8194	*rad26::kanMX, spd1::hph arg3-D4, ade6-, ura4-D18, leu1-32, his3-D1*	This study
TH7331	*rad17::kanMX, arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^-	This study
TH7794	*rad17::kanMX, spd1::hph arg3-D4, ade6-, ura4-D18, leu1-32, his3-D1*	This study
TH7414	*rad9::kanMX, arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^+	This study
TH7146	*rad9::kanMX, spd1::hph arg3-D4, ade6-, ura4-D18, leu1-32, his3-D1*	This study

Strain	Genotype	Source
TH7333	*rad1::kanMX, arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^-	This study
TH8249	*rad1::kanMX, spd1::hph arg3-D4, ade6-, ura4-D18, leu1-32, his3-D1*	This study
TH8296	*hus1::kanMX, arg3-D4, ade6-D1, ura4-D18, leu1-32, his3-D1* h^-	This study
TH8195	*hus1::kanMX, spd1::hph arg3-D4, ade6-, ura4-D18, leu1-32, his3-D1*	This study
TH4125	*leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^- pREP81X	Moss et al (6)
TH4121 TH4122 TH4104*	*leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	Moss et al (6)
TH4076	*spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^- pREP81X	Moss et al (6)
TH4077 TH4078 TH4079*	*spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	Moss et al (6)
TH7423	*rad26::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^+ pREP81X	This study
TH7424 TH7425 TH7426*	*rad26::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7584	*rad26::kanMX spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^+ pREP81X	This study
TH7585 TH7586 TH7587*	*rad26::kanMX spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7427	*rad17::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^+ pREP81X	This study
TH7429 TH7430*	*rad17::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7565	*rad17::kanMX spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^- pREP81X	This study
TH7566 TH7567 TH7568*	*rad17::kanMX spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7588	*rad9::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^+ pREP81X	This study
TH7589 TH7590 TH7591*	*rad9::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7463	*rad9::kanMX spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH h^- pREP81X	This study
TH7464 TH7465 TH7466*	*rad9::kanMX spd1::ura4 leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study

Strain	Genotype	Source
TH7493	*rad1::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH *h* pREP81X	This study
TH7494 TH7495 TH7496*	*rad1::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7431	*hus1::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH *h* pREP81X	This study
TH7432 TH7433 TH7434*	*hus1::kanMX leu1-32 arg3-D4 ade6-M210 ura4-D18 his3-D1* Ch^{16}-RMYAH pREP81X-HO	This study
TH7165	*cdt2-YFP-hph leu1-32 ade6-M216 ura4-D18 h*$^{+}$	This study
TH7197	*cdt2-YFP-hph leu1-32 ade6-M216 ura4-D18 h*$^{-}$	This study
TH7169	*rad3::kanMX cdt2-YFP-hph leu1-32 ade6- ura4-D18 h*$^{-}$	This study
TH7170	*rad26::kanMX cdt2-YFP-hph leu1-32 ade6- ura4-D18 h*$^{-}$	This study
TH7171	*rad17::kanMX cdt2-YFP-hph leu1-32 ade6-M210 ura4-D18 his3-D1 h*$^{+}$	This study
TH7172	*rad9::kanMX cdt2-YFP-hph leu1-32 ade6-M210 ura4-D18 h*$^{+}$	This study
TH7174	*rad1::kanMX cdt2-YFP-hph leu1-32 ade6-M210 ura4-D18 h*$^{-}$	This study
TH7175	*hus1::kanMX cdt2-YFP-hph leu1-32 ade6-M210 ura4-D18 his3-D1 h*$^{-}$	This study
TH7184	*urg1::urg1* $P_{urg1lox}$*-HO LE_L-HOcs-his3+-EU_R his3-D1 leu1-32*	*A. Watson et al* 2011 (7)
TH8091	*rad3::ura4 urg1::urg1* $P_{urg1lox}$*-HO LE_L-HOcs-his3+-EU_R his3-D1 leu1-32 ura4-D18*	This study
TH8040	*rad17::ura4 urg1::urg1* $P_{urg1lox}$*-HO LE_L-HOcs-his3+-EU_R his3-D1 leu1-32 ura4-D18*	This study
TH8050	*rad9::ura4 urg1::urg1* $P_{urg1lox}$*-HO LE_L-HOcs-his3+-EU_R his3-D1 leu1-32 ura4-D18*	This study

Ch^{16}-RMGAH (Ch^{16} *yps1::arg3 ert1::MATa-kanMX6 ade6-M216 cid2::his3*). Ch^{16}-YAMGH (Ch^{16} *chk1::Hph ade6-M216 rad21::MATa-kanMX6 cid2::his3*) Mating type for the first strain only. Ch^{16}-RMHAH (Ch^{16} *yps1::arg3 ert1::MATa-Hph ade6-M216 cid2::his3*). *independent isolates (*h*$^{+}$ or *h*$^{-}$).