Supporting Information

Kim and Haber 10.1073/pnas.0812578106

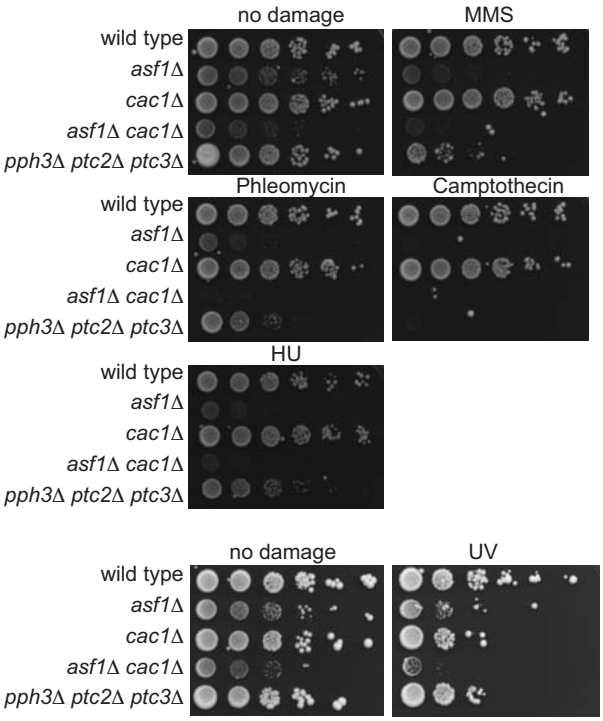

Fig. S1. DNA damage sensitivities of *asf1*Δ, *cac1* Δ, and *asf1* Δ *cac1* Δ cells. Wild-type, *asf1*Δ, *cac1* Δ, *asf1* Δ *cac1* Δ, and *pph3*Δ *ptc2* Δ *ptc3* Δ cells were grown in YEP/Dextrose medium to the exponential phase. The cells were serially diluted in 1:10-fold and then spotted onto YEP/Dextrose plus 0.005% methyl methane sulfonate (MMS), 0.1 μg/mL of phleomycin, 1 μg/mL of camptothecin, or 50 mM hydroxyurea (HU). To induce UV damage, serially diluted cells were spotted onto YEP/Dextrose plate and then irradiated with 3J/m^2 of UV. The pictures were taken 3 days after spotting; *pph3*Δ *ptc2* Δ *ptc3* Δ cells were used as a control showing DNA damage sensitivity.

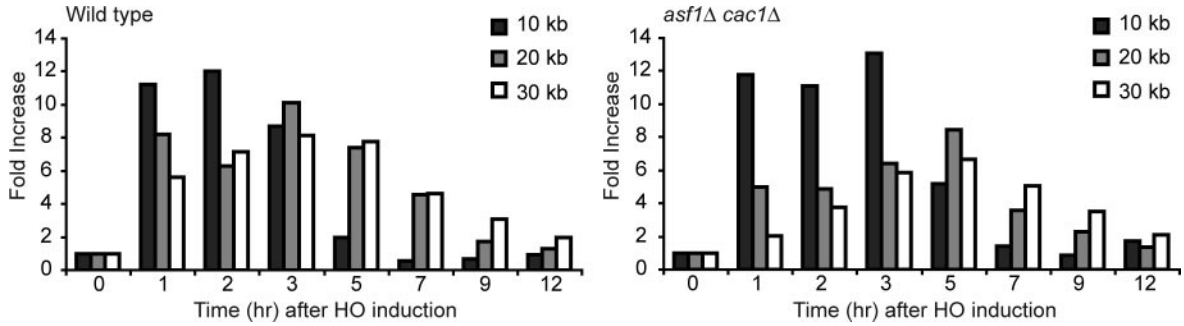

Fig. S2. Appearance and disappearance of γ-H2AX is not effected by the absence of both Asf1 and Cac1. γ-H2AX ChIP values at 10 kb (black bars), 20 kb (gray bars), or 30 kb (white bars) to the right of the DSB at *MAT* in wild-type cells were measured several time points (1, 2, 3, 5, 7, 9, and 12 hrs) after HO induction and normalized with the value prior to HO induction (0 hr).

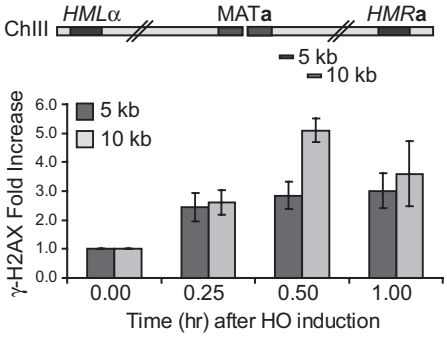

Fig. S3. γ-H2AX occurs around MAT locus during normal mating type switching. γ-H2AX ChIP values at 5 kb (black bars) and 10 kb (gray bars) to the right of the DSB at *MAT* in wild-type cells containing both *HML* and *HMR*, where an HO-induced DSB is repaired by intrachromosomal recombination, were measured different time points (15, 30, and 60 mins) after HO induction and normalized with the value prior to HO induction (0 min).

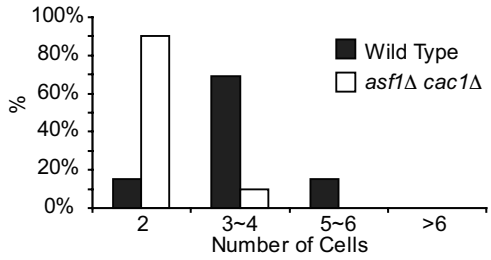

Fig. S4. The *asf1*Δ *cac1*Δ cells grow twice as slow as wild-type cells. Cells containing the mutated HO cut site (inc) were synchronized to G1 by growth to saturation and unbudded cells were spread onto galactose plates. The number of buds or cells was counted at 12 h after spreading (HO induction).

Table S1. PCR primers to analyze recombination and histone H2A phosphorylation

Sense primer	Sequence	Antisense primer	Sequence	Usage
MAT7	CCTGGTTTTGGTTTTGTAGAGTGG	MATD p1	CCGCATGGGCAGTTTACCT	Probe for the Southern analysis in Fig. 1
YCR043C p1	CCAAGGAACTAATGATCTAAGCACA	YCR043C p2	GGCGAAAACAATGGCACTCT	ChIP in Fig. S4; 5 kb away
IMG1 p1	TGGATCATGGACAAGGTCCTAC	IMG1 p2	GGCGAAAACAATGGCACTCT	ChIP in Fig. 3 and Figs. S3 and S4; 10 kb away
PWP2 p1	GACACACTTTACTTTGGCTTGGTT	PWP2 p2	GACTTCCAAAGACTTAAGCGCA	ChIP in Fig. 3 and Fig. S4; 20 kb away
RAD18 p1	TGTCATCGTTGGGACTGTCA	RAD18 p2	GAAACATAACCATCCATCCTTTCC	ChIP in Fig. 3 and Fig. S4; 30 kb away
CEN8 p1	TGACAAAACTCTCCCTTAGTGC	CEN8 p2	CTCCAACAATTACACATCCACA	ChIP in Fig. 3 and Figs. S2–S4; reference for ChIP normalization