**Figure S1, Related to Figure 1. Deletion of Nearest Replication Origin has Little Effect on Recombination Rate.**

(A) Map of replication origins nearest to the assay site on Chr I with the distances of each autonomously replication sequence (ARS) (black ovals) indicated. All other symbols are the same as in Figure 1B.

(B) Recombination rate with the "No Fragile Zone" and "MBR" substrates with or without *ARS104*. These are referred to as "recombination" rate and not "ZBE" rate because the rate calculation does not substract the G418^R colonies that indicated retention of *ars104::KANMX* in order to make the two data sets comparable. Rates were determined by Luria-Delbrück fluctuation analysis and p-values by the Mann-Whitney test.

(C) Recombination rate with the 12x Sγ3 cassetted inververted and transcribed towards the telomere by the *GAL2* promoter. While the rate in this orientation is generatlly higher, loss of *ARS104* has little effect. Rates determined by the method of the median with error bars representing the 95% confidence interval.
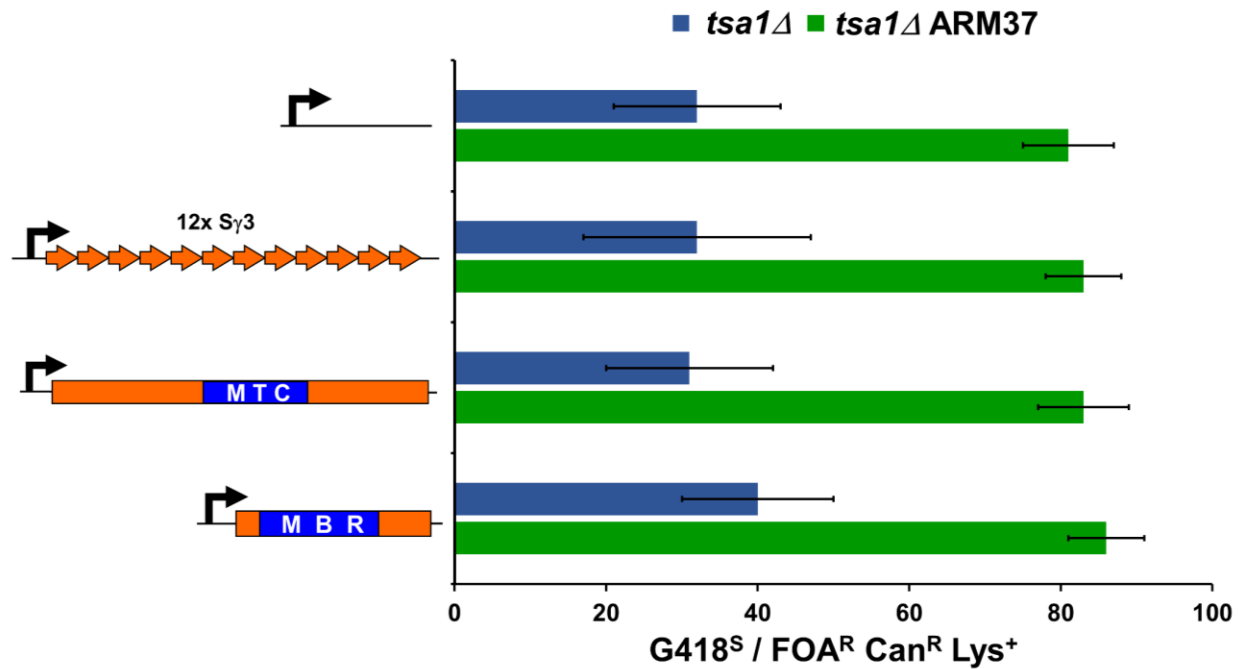
Figure S2, Related to Figure 4. ARM37 expression Results in More Frequent Loss of the *KANMX4* Marker in *tsa1Δ* Mutants. The total number of colonies selected for growth on medium containing 5-FOA and canavanine but lacking lysine were recorded as well as the number of these colonies that were subsequently screened for sensitivity of G418. Therefore, we can compare the percentage of 5-FOA^R Can^R Lys$^+$ colonies that were also G418^S in *tsa1Δ* mutants with or without ARM37 expression. Error bars represent ±2 standard error of the mean.

Table S1, Related to STAR Methods. *S. cerevisiae* strains used in ZBE assays[1,2]

Strain	Genotype
NPX416-1D	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1*
NPX377-4C	*MATa, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*[3]
NPT126[4]	*MATa, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-12xSγ3*
NPX419-3C	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MTC*
NPX417-14C	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR*
NPX372-71B	*MATa, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX374-166B	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX373-144B	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX414-1A	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-RBM*[5]
NPX475-XX[6,7]	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPX474-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3,* pNP171(*AID, hphMX*)
NPX473-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX476-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPX479-XX[6]	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1,* pNP171(*AID, hphMX*)
NPX432-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1*
NPX435-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-12xSγ3*
NPX433-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR*
NPX434-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MTC*
NPX429-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX469-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX431-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX430-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX475-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPX474-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3,* pNP171(*AID, hphMX*)
NPX476-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPX473-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX480-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR,* pNP171(*AID, hphMX*)
NPX381-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX392-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX380-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX389-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX453-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX485-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX454-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX455-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPT148	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPT146	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-*

	GAL1p-12xSγ3, pNP171(*AID, hphMX*)
NPT147	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPT149	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX388-26B	*MATa, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX394-8B	*MATa, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX386-5C	*MATa, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX387-5A	*MATα, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX475-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPX474-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3,* pNP171(*AID, hphMX*)
NPX473-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX476-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPX441-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX470-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX452-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX442-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX525-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX526-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX524-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX523-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPT137	*MATa, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPT141	*MATa, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3,* pNP171(*AID, hphMX*)
NPT139	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPT138	*MATα, can1::LEU2, ura3::TRP1, lys2-Δ4443, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX529-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*
NPX530-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3*
NPX528-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX527-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPT144	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPT145	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3,* pNP171(*AID, hphMX*)
NPT143	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPT142	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ung1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX421-12A	*MATa, can1::LEU2, ura3::TRP1, lys2::ARM37,ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1*
NPX423-13C	*MATα, can1::LEU2, ura3::TRP1, lys2::ARM37,ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MTC*
NPX422-8D	*MATa, can1::LEU2, ura3::TRP1, lys2::ARM37,ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR*
NPX439-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-12xSγ3*
NPX438-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MTC*
NPX426-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1*
NPX428-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MTC*
NPX427-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR*
NPX438-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, top1::LEU2, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MTC*
NPX403-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p*

NPX402-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX404-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX461-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC*
NPX462-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, top1::LEU2, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR*
NPX480-XX	*MAT, can1::LEU2, ura3::TRP1, lys2-Δ4443, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR,* pNP171(*AID, hphMX*)
NPX480-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX478-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p,* pNP171(*AID, hphMX*)
NPX474-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-12xSγ3,* pNP171(*AID, hphMX*)
NPX476-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MTC,* pNP171(*AID, hphMX*)
NPX473-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-GAL1p-MBR,* pNP171(*AID, hphMX*)
NPX480-XX	*MAT, can1::LEU2, ura3::TRP1, lys2::ARM37, tsa1::HIS3, ars104::KANMX, bdh1::LYS2, bdh2::URA3-CAN1-MBR,* pNP171(*AID, hphMX*)
NPX220-18B	*MATa, can1::LEU2, ura3::TRP1, bdh2::URA3-CAN1-GAL1p, ARS104*
NPX205-12A	*MATa, can1::LEU2, ura3::TRP1, bdh2::URA3-CAN1-GAL1p, ARS104*
NPX246-3D	*MATα, can1::LEU2, ura3::TRP1, bdh2::URA3-CAN1-12xSγ3-GAL2p[8], ARS104*
NPX326-5B	*MATa, can1::LEU2, ura3::TRP1, bdh2::URA3-CAN1-12xSγ3-GAL2p, ars104::KANMX*

[1]Strains are isogenic to W303-1A (*MATa, ade2-1, can1-100, his3-11, 15, leu2-3, 112, trp1-1, ura3-1*) with a WT *RAD5* allele. Deviations from this genotype are indicated in the table.

[2] Strains are listed in order of appearance in the manuscript.

[3] *GAL1p = GAL1* promoter.

[4] NPT strains are the result of a transformation while NPX strains are the result of a cross.

[5] RBM = MBR in reverse orientation.

[6] "XX" indicates that freshly dissect segregants were used each time from a frozen diploid stock. This is due to the strain containing a mutator allele or construct.

[7] Some haploids were derived from the same parent diploid.

[8] The *12xSγ3-GAL2p* substrate is inverted to transcribe towards the telomere and driven by the *GAL2* promoter.

Table S2, Related to Figures 1-5. ZBE Rates ($\times 10^{-10}$)[1]

Genotype	No Fragile Zone -trans	No Fragile Zone +trans	12x Sγ3 -trans	12x Sγ3 +trans	MTC -trans	MTC +trans	MBR -trans	MBR +trans
Wild-type	<0.48 n=20	1.8 n=20	<0.4 n=20	15.6 (4.7-26) n=20	<0.57 n=20	2.6 n=20	<0.55 n=20	1.2 n=40
tsa1Δ	3.5 n=19	20.3 (0-25) n=40	2.7 n=20	49 (18.9-116) n=20	2.5 n=20	13.3 (5.4-30) n=40	1.3 n=20	22.8 (9.8-36) n=60
ARM37	<0.42 n=20	2.9 n=40	ND[2]	31.4 (15-160) n=20	<0.48 n=20	2.3 n=20	<0.46 n=19	3.8 n=79
tsa1Δ ARM37	ND	281 (225-357) n=60	4.2 n=20	443 (391-531) n=59	8.5 n=19	410 (310-580) n=58	ND	462 (395-558) n=60
top1Δ	<0.5 n=17	1.7 n=20	ND	80.3 (26-200) n=19	<0.45 n=20	2.6 n=20	<0.41 n=20	0.74 n=19
top1Δ *tsa1Δ*	ND	50.2 (29-91) n=39	ND	283 (239-403) n=40	6.0 n=19	56.1 (42-81) n=40	ND	80.2 (54-120) n=39
top1Δ AID	ND	59.4 (25-210) n=20	ND	690 (452-939) n=20	ND	286 (196-352) n=20	ND	170 (64-312) n=20
top1Δ ARM37	ND	23.2 (12-35) n=20	ND	ND	ND	5.4 (0-9.7) n=20	ND	11.2 (4.7-21) n=20
top1Δ *tsa1Δ* ARM37	ND	ND	ND	ND	ND	423 (319-612) n=20	ND	373 (265-450) n=20
AID	<0.46 n=20	61.5 (39-91) n=73	ND	143 (93-170) n=72	ND	97.7 (72-150) n=60	<0.46 n=20	85.1 (64-100) n=74
AID *tsa1Δ*	ND	3863 (3075-5725) n=45	ND	6070 (4031-9429) n=40	ND	7089 (4595-11320) n=60	3.8 (0-21) n=20	4147 (3000-6895) n=72
AID ARM37	ND	92.0 (69-110) n=79	ND	175 (140-240) n=74	ND	103 (75-157) n=60	1.0 n=20	120 (83-180) n=96
AID ARM37 *tsa1Δ*	ND	6645 (4500-9800) n=20	ND	4304 (3047-6112) n=20	ND	4087 (3100-10000) n=20	4.9 n=20	3601 (2641-6643) n=17
ung1Δ	ND	0.28 n=39	ND	5.6 (2.6-10) n=20	ND	0.26 n=20	ND	0.67 n=20
ung1Δ AID	ND	1.9 n=40	ND	8.6 (0-57) n=19	ND	5.8 (0-58) n=19	ND	21.6 (12-34) n=40
ung1Δ ARM37	ND	2.1 n=19	ND	2.4 (0-14.9) n=20	ND	0.92 n=20	ND	0.65 n=20
ung1Δ AID ARM37	ND	8.0 (0-24) n=17	ND	74.3 (47-236) n=18	ND	12.6 (0-53) n=20	ND	30.2 (9.4-47) n=40

[1]ZBE rates for each of the indicate substrates with or without transcription ("trans"). Rates determined by the method of the median have a 95% confidence interval in parentheses. All other rates were determined by Luria-Delbrück fluctuation analysis. The number of cultures included for each rate calculation is indicated ("n").

[2]ND = Not Determined

Table S3, Related to STAR Methods. Oligonucleotides

Oligo	Sequence (5'→3')
NP386	GATGTACCTGTACATTGTGCAGAAGGTGAGTTTAAGCTAGGCTGTA AATGATTGTACGCG
NP387	ACTGCTTATCGATAAGATAAGTAATATCTCATTGGCTCCCTCTCCGCA GATGGCATCG
NP397	TTGCTGACCGCTTCTAGAGGCATCGCACAGTTTTAGCGAGGAAAACT CTTCAATAGTTTTGCCAGCGGAACGTCGTCATCCTTGTAATCC
NP398	GAGTTTTTAAGTGACATCACCCGAAAAGAAGCTAAGTCTTTCTCCTAA TTCATATTTAATTATTCTACATAGTCAGTGAGCGAGGAAGC
NP413	CTATTGAAGAGTTTTCCTGCG
NP414	TGGCTATGTGATCCATGACG
NP415	GTACAATAATTAAATATGAATTAGG
NP416	AAACATGAGTGGCAAGTGGC
NP428	TTTTACAATTCCAAACCATGTGATGCTTGTCAGAGGGGCAGTGAAAA TCTATGTACCCACCAGCGGAATTCCACTTGC
NP429	TTACTTCATTTCACCGTGATTGTTAGGCGTCAATAGAATCTTAACGTT GGATTCCTTGTGGGACATATCATACGTAATGC
NP459	ATGGTCGCTCAAGTTCAAAAGCAAGCTCCAACTTTTAAGAAAACTGC CGTCGTCGACGGTCATGTACGTGAGCGTATTTCC
NP460	TTATTTGTTGGCAGCTTCGAAGTATTCCTTGGAGTCTTCAACGGTTG GCTTGATGGTAGCTGTTATTTCTGGCACTTCTTGG
NP474	GATACACCATCAAATGGCTGTTTAGCTTGCCTTGTCC
NP475	GATACACCAATAGGTGGGATGGCGGCGTTAGTATCG
NP493	CCCCCATAAGAGGAATACTAAACTCTTACCGTCGGCCTCTCTGTCCT GGATCAACAACTGCCTGTTCCCTAGCATGTACG
NP494	GGTGCATGAGAAGATTGCCAACAAATTCAGTTATGACGGTGGCTCGA AAGAGAAAGCAAATCCATCTACCACCAGAACGG