

## Supplemental Figure Legends

**Supplemental Figure S1.** Analysis of 2  $\mu$ m hyperamplification. (A) DNA from *siz1 $\Delta$  siz2 $\Delta$*  cells was prepared either embedded in agarose (Schwartz and Cantor, 1984) (left panel) or in solution (Holm *et al.*, 1986) (right panel). Agarose-embedded DNA was either melted and loaded directly (lane 1) or treated with  $\beta$ -agarase (lane 2). DNA in solution was loaded directly (lane 4) or brought to 0.6% low melting agarose before loading (lane 3). (B) Uncut DNA from the indicated strains was analyzed by Southern blotting as in Figure 3. Lanes were normalized to contain equal amounts of 2  $\mu$ m DNA, although the *xrs2 $\Delta$*  sample was underloaded. Designations as in Figure 3. (C) Indicated strains containing plasmids expressing thymidine kinase (TK) and a nucleoside transporter (hENT) (Vernis *et al.*, 2003) were grown to log phase or arrested with nocodazole (noc) for three hours prior to labeling for 1 hour with bromo-deoxyuridine (BrdU) as described (Vernis *et al.*, 2003). DNA was left uncut or digested with the indicated restriction enzyme, as indicated, and analyzed by agarose gel electrophoresis, followed by immunoblotting with an Ab against BrdU. Note the absence of a 6.3 kb 2  $\mu$ m band in the noc-arrested samples digested with *Pst*I, which cuts 2  $\mu$ m once.

**Supplemental Figure S2.** Diagram of locus-specific QAOS (Booth *et al.*, 2001). A “tagging primer” with 8 b of homology with a particular locus is incubated with target DNA sample, Taq polymerase and dNTPS at low temperature. If ssDNA is present at this locus, the primer will anneal and be extended. The primer will not anneal to dsDNA because the DNA has not been denatured. Next qPCR is performed using one primer specific for the tag sequence in the tagging primer (in red) and one primer to a sequence flanking the target locus. This reaction will only generate a product if the tagging primer was extended during the first reaction because the tagging primer cannot anneal at the temperatures used during PCR. Thus, it cannot initiate amplification of DNA that was originally double-stranded, but which is denatured during the PCR reaction. Unlike in Booth *et al.*, our tagging primers contained only 8 b of homology with the

target sequence. Longer sequences gave high background signals, presumably because the tagging primer could prime to some degree during the PCR portion of the protocol.

## REFERENCES

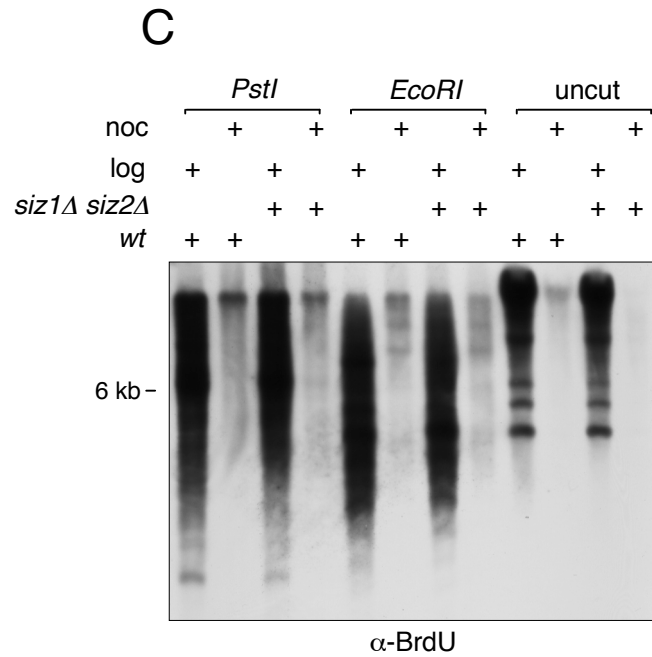
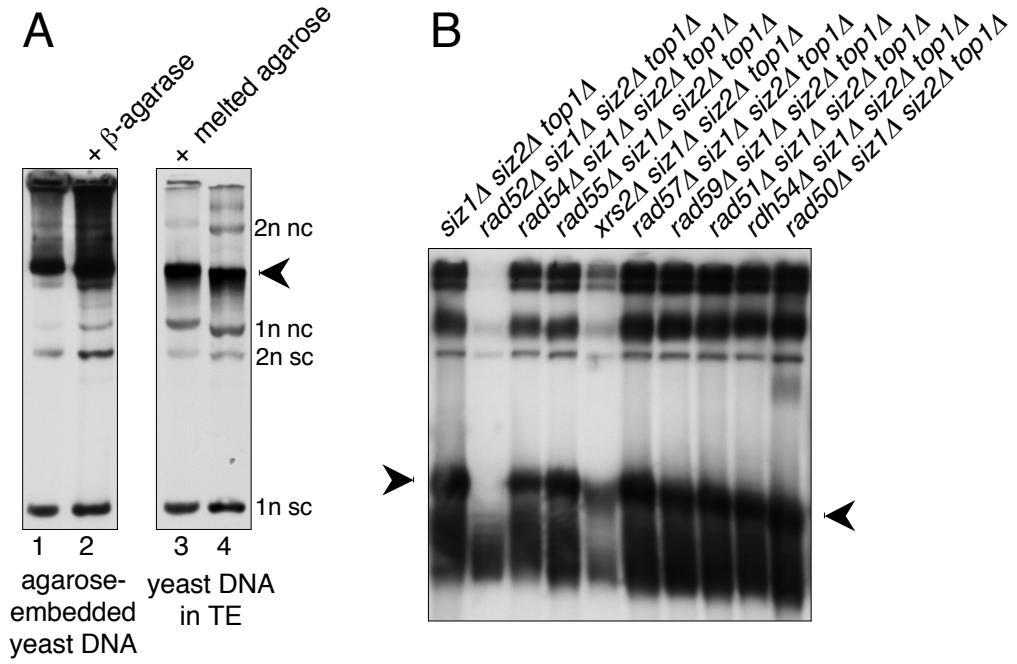
Booth, C., Griffith, E., Brady, G., and Lydall, D. (2001). Quantitative amplification of single-stranded DNA (QAOS) demonstrates that *cdc13-1* mutants generate ssDNA in a telomere to centromere direction. *Nucleic Acids Res* 29, 4414-4422.

Holm, C., Meeks-Wagner, D.W., Fangman, W.L., and Botstein, D. (1986). A rapid, efficient method for isolating DNA from yeast. *Gene* 42, 169-173.

Schwartz, D.C., and Cantor, C.R. (1984). Separation of yeast chromosome-sized DNAs by pulsed field gradient gel electrophoresis. *Cell* 37, 67-75.

Vernis, L., Piskur, J., and Diffley, J.F. (2003). Reconstitution of an efficient thymidine salvage pathway in *Saccharomyces cerevisiae*. *Nucleic Acids Res* 31, e120.

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**QAOS method**  
(technique modified from C. Booth et al. 2001, NAR)

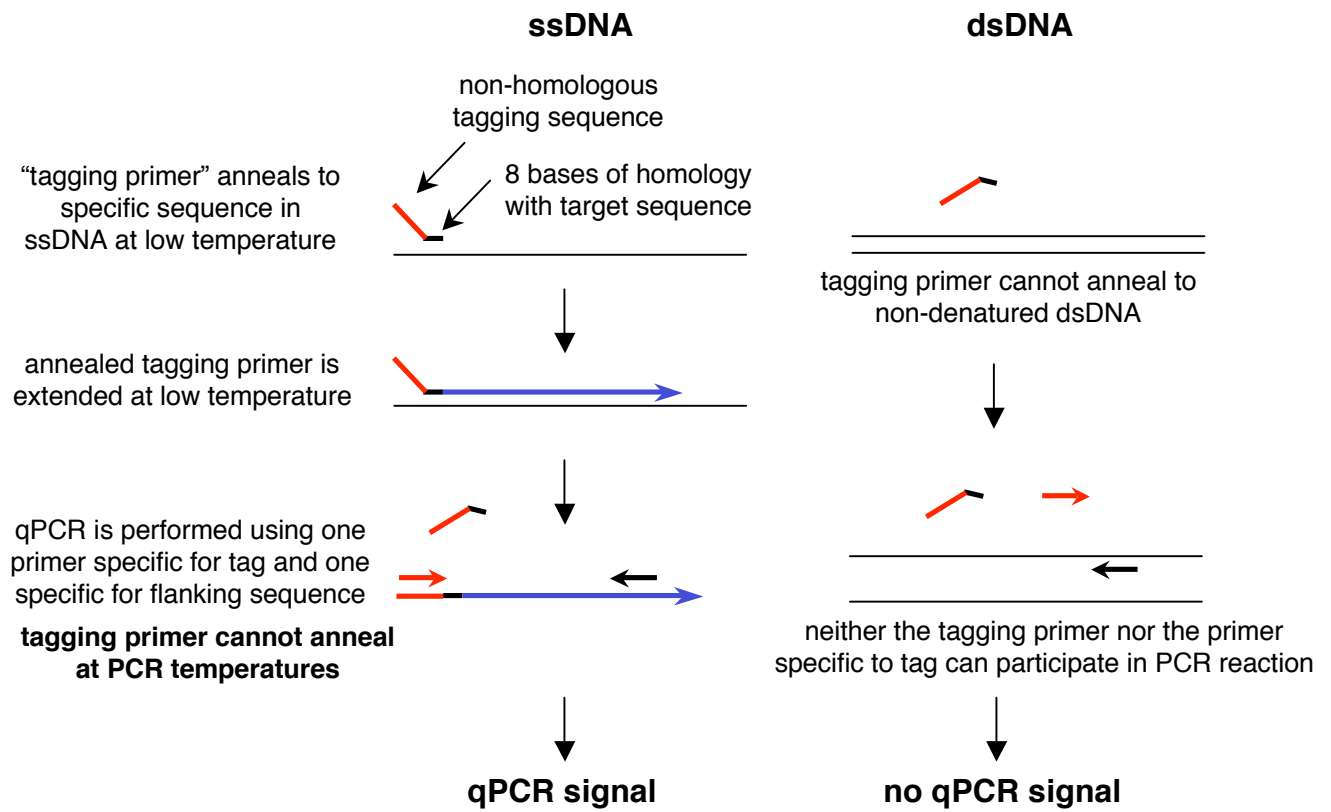


Table S1. *S. cerevisiae* strains

| Name              | Relevant genotype  | Source                |
|-------------------|--|-----------------------|
| JD52 <sup>a</sup> | <i>MATa trp1-Δ1 ura3-52 his3-Δ200 leu2-3,112 lys2-801</i> [cir <sup>+</sup> ]            | J. Dohmen             |
| EJY326            | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1</i> [cir <sup>+</sup> ]                                  | Johnson and Gupta (20 |
| EJY341            | <i>MATa</i> [cir <sup>o</sup> ]  | Chen et al (2005)     |
| EJY346            | <i>MATa</i> [cir <sup>+</sup> <i>FLP1-HA-His8::HIS3</i> ]                                | Chen et al (2005)     |
| EJY349            | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1</i> [cir <sup>+</sup> <i>FLP1-HA-His8::HIS3</i> ]        | Chen et al (2005)     |
| EJY356            | <i>MATa</i> [cir <sup>+</sup> <i>FLP1(K375R)-HA-His8::HIS3</i> ]                         | Chen et al (2005)     |
| EJY359            | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1</i> [cir <sup>+</sup> <i>FLP1(K375R)-HA-His8::HIS3</i> ] | Chen et al (2005)     |
| EJY416            | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3</i> [cir <sup>o</sup> ]                      | Chen et al (2007)     |
| EJY420            | <i>MATa rad52Δ::kanMX siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3</i> [cir <sup>o</sup> ]        | Chen et al (2007)     |
| EJY509            | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3</i> [cir <sup>+</sup> ]                      | this study            |
| EJY510            | <i>MATa rad52Δ::kanMX siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3</i> [cir <sup>+</sup> ]        | this study            |
| EJY511            | <i>MATa rad52Δ::kanMX</i> [cir <sup>+</sup> ]  | this study            |
| EJY512            | <i>MATa rad52Δ::kanMX siz1Δ::LEU2 siz2Δ::TRP1</i> [cir <sup>+</sup> ]                    | this study            |
| EJY513            | <i>MATa hex3Δ::kanMX</i> [cir <sup>+</sup> ]   | this study            |
| EJY514            | <i>MATa hex3Δ::kanMX rad52Δ::kanMX</i> [cir <sup>+</sup> ]                               | this study            |
| EJY515            | <i>MATa slx8Δ::kanMX</i> [cir <sup>+</sup> ]   | this study            |
| EJY516            | <i>MATa slx8Δ::kanMX rad52Δ::kanMX</i> [cir <sup>+</sup> ]                               | this study            |
| EJY517            | <i>MATa RAD52-GFP::URA3</i> [cir <sup>o</sup> ]  | this study            |
| EJY518            | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 RAD52-GFP::URA3</i> [cir <sup>o</sup> ]                  | this study            |

|        |   |            |
|--------|---|------------|
| EJY519 | <i>MATa hex3Δ::kanMX RAD52-GFP::URA3 [cir<sup>o</sup>]</i>  | this study |
| EJY520 | <i>MATa nup60Δ::kanMX RAD52-GFP::URA3 [cir<sup>o</sup>]</i>                                       | this study |
| EJY521 | <i>MATa RAD52-GFP::URA3 [cir<sup>+</sup>]</i>   | this study |
| EJY522 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 RAD52-GFP::URA3 [cir<sup>+</sup>]</i>                             | this study |
| EJY523 | <i>MATa hex3Δ::kanMX RAD52-GFP::URA3 [cir<sup>+</sup>]</i>  | this study |
| EJY524 | <i>MATa nup60Δ::kanMX RAD52-GFP::URA3 [cir<sup>+</sup>]</i>                                       | this study |
| EJY525 | <i>MATa hex3Δ::kanMX [cir<sup>+</sup> FLP1(K375R)-HA-His<sub>8</sub>::HIS3]</i>                   | this study |
| EJY526 | <i>MATa slx8Δ::kanMX [cir<sup>+</sup> FLP1(K375R)-HA-His<sub>8</sub>::HIS3]</i>                   | this study |
| EJY527 | <i>MATa [cir<sup>+</sup> FLP1(Y343F)-HA-His<sub>8</sub>::HIS3]</i>                                | this study |
| EJY528 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 [cir<sup>+</sup> FLP1(Y343F)-HA-His<sub>8</sub>::HIS3]</i>        | this study |
| EJY529 | <i>MATa hex3Δ::kanMX [cir<sup>+</sup> FLP1(Y343F)-HA-His<sub>8</sub>::HIS3]</i>                   | this study |
| EJY530 | <i>MATa slx8Δ::kanMX [cir<sup>+</sup> FLP1(Y343F)-HA-His<sub>8</sub>::HIS3]</i>                   | this study |
| EJY531 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 pol32Δ::kanMX [cir<sup>+</sup>]</i>                               | this study |
| EJY532 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3 rad51Δ::kanMX [cir<sup>+</sup>]</i>                   | this study |
| EJY533 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3 rad59Δ::kanMX [cir<sup>+</sup>]</i>                   | this study |
| EJY534 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3 rad51Δ::kanMX<br/>rad59Δ::kanMX [cir<sup>+</sup>]</i> | this study |
| EJY535 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3 rad54Δ::kanMX [cir<sup>+</sup>]</i>                   | this study |
| EJY536 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3 rdh54Δ::kanMX [cir<sup>+</sup>]</i>                   | this study |
| EJY537 | <i>MATa siz1Δ::LEU2 siz2Δ::TRP1 top1Δ::HIS3 rad54Δ::kanMX<br/>rdh54Δ::kanMX [cir<sup>+</sup>]</i> | this study |

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<sup>a</sup> Strains are in the JD52 background.