

FIGURE S1. Restriction map and Southern blot analysis of the *FS2* region of chromosome III. (A) Restriction digest map of *S. cerevisiae* strain BY4741. Regions of the genome that were confirmed by PCR and sequence analysis are shaded in grey. The map is drawn to scale and restriction enzyme cut sites are indicated for *Eco*RI (*E*) and *Xba*I (*X*). The positions of the Southern blot hybridization probes, *FS2-2* and *FEN2*, and the expected fragment sizes are depicted above and below the map, respectively. (B) Restriction digest and Southern blot analysis using genomic DNA isolated from BY4741 yielded fragment sizes that correspond to the restriction digest map and confirm the presence of an inverted pair of *Ty1* retrotransposons at the *FS2* position of chromosome III.



FIGURE S2. Comparison of Ddc2 foci and a-like faker genome instability screens. (A) Comparison of genes screened in our study with those screened by Li *et. al.* using ts-alleles. (B) Comparison of Ddc2 foci positives in our study and in Li *et. al.* with the set of genes screened in both studies. (C) Comparison of genes screened in our study with those screened by Stirling et al. using a combination of ts-alleles and DAmP alleles. (D) Comparison of a-like faker positives in our study and in Stirling *et. al.* with the set of genes screened in both studies.

Tables S1-S8 Supporting Tables

Tables S1-S8 are available for download at

http://www.genetics.org/content/suppl/2012/06/05/genetics.112.141051.DC1.

Table S1. Quantification of Ddc2 foci in Tet allele strains

Table S2. GO function and GO process annotations of genes whose depletion results in elevated levels of Ddc2 foci

Table S3. a-like faker scores from patch mating test with Tet allele strains

Table S4. Comparison of Tet alleles and ts-alleles with elevated levels of Ddc2 foci

Table S5. Comparison of Tet alleles and ts-alleles with a-like faker phenotype

Table S6. Strain Genotypes

Table S7. Primers used to generate probes in Southern blot analysis

Table S8. Primers used for PCR amplification and sequencing of FS1 and FS2