**SUPPLEMENTAL FIGURE S1. YJM789 homolog of chromosome III lacks *PAU3* and all genes distal.** (A) Annotations from the *Saccharomyces* Genome Database for chromosome III bases 298,000 through the right telomere. (B) Next generation sequencing data of an isolated YJM789 chromosome III cut out of a CHEF gel. Sequencing read coverage is shown for chromosome III bases 298,000 through the right telomere.

**SUPPLEMENTAL FIGURE S2. Next generation sequencing data of long-tract gene conversion events.** Each LTGC event is shown on a separate page. LTGC 8 and 16 are not included because they are in a figure within the main manuscipt. Part (A) on every page is the initial configuration of the two homologs of chromosome III in our experimental diploid. Only a portion of the right arm of chromosome III is depicted. The gray “S” homolog of chromosome III is related to S288c; the red “Y” homolog of chromosome III is related to YJM789. Origins are represented by white diamonds, delta elements are arrowheads, and Ty elements are arrows. Part (B) on every page is data from whole genome next generation sequencing. Only data from the right arm of chromosome III is shown. Blue graphs show the frequency of the “Y” allele at each SNP. Orange graphs show sequencing coverage across each SNP. Dotted lines indicate junctions between SNPs that are heterozygous for both the “S” and “Y” alleles, and SNPs that are homozygous “Y” alleles. Part (C) on every page is the proposed configuration of the two homologs of chromosome III based on next generation sequencing results and SNP phasing results.

**SUPPLEMENTAL FIGURE S3. Next generation sequencing data of an isolated “S” homolog of chromosome III from LTGC 8 cut out of a CHEF gel.**  Next generation sequencing data of an isolated “S” homolog of chromosome III from LTGC 8 cut out of a CHEF gel. Sequencing read coverage is shown for chromosome III bases 110,000 through 190,000. The deleted region is ~148,600 through ~169,500.

**SUPPLEMENTAL FIGURE S4. Southern analysis of chromosome III using a probe to *PAT1.***(A) DNA was extracted in agarose blocks and chromosomal DNA molecules were separated by clamped homogeneous gel electrophoresis as described in Materials and Methods. The initial sizes of the “S” and “Y” homologs of chromosome III in the “S” and “Y” are indicated. Strains LTGC 1 through LTGC 16 are labeled. (B) The separated chromosome molecules were examined by Southern analysis using a probe to *PAT1*, which is located on the right arm of chromosome III. In strains LTGC 1, 3, and 5, the *PAT1* probe hybridizes to different bands than the *CHA1* probe (Table 2 and Figure 2); in all other LTGC strains the *PAT1* and *CHA1* Southern results are identical.

**SUPPLEMENTAL FIGURE S5. Detailed analysis of “Disjoined Group” strain LTGC 5 is consistent with a mechanism involving both gap repair and half-crossover.** Data from whole next generation sequencing is presented in blue and orange graphs. Blue graphs show the frequency of the “Y” allele at each SNP. Orange graphs show sequencing coverage across each SNP. (A) Whole genome next generation sequencing results from the right arm of chromosome III in strain LTGC 5. Dotted lines flank the LTGC region, which is an expanse of SNPs that are entirely “Y” alleles. (B) Whole genome next generation sequencing results from the left arm of chromosome II. Dotted lines flank a region of 3X sequencing coverage; SNP alleles in this region are 33% “Y” and 66% “S.” (C) Initial configuration of the “S” homolog of chromosome III (shown in gray) and the “S” homolog of chromosome II (shown in blue) in our experimental diploid. Origins are represented by white diamonds, delta elements are arrowheads, and Ty elements are arrows.(D) Proposed configuration of the homolog of chromosome III containing the “S” centromere in LTGC 5. We cut out of the CHEF gel the chromosome III homolog of LTGC 5 that hybridizes to the *CHA1* probe. Next-generation sequencing of this isolated homolog (not shown) reveals that it contains the first ~170 kb of the “S” homolog of chromosome III (including the centromere), and the first ~224 kb of the “S” homolog of chromosome II. If this translocation had resulted from a canonical BIR event in which the broken FS2 on chromosome III invaded chromosome II and copied through the telomere, we would expect 3X coverage of the first ~224 kb of chromosome II in the whole genome sequencing data. This is not what we see; instead, as shown in (B) above, there is only a small region of 3X coverage between delta 7 and *Ty1-1*, and 2X coverage across rest of chromosome II. These data suggest that the broken chromosome III invaded chromosome II at *Ty1-1* and initiated BIR, copying until delta 7, at which point a half-crossover occurred. This would transfer the break to chromosome II, initiating a cascade of BIR events.