File S1

Associations of LOH breakpoints with various elements of chromosome structure

In chromosomes with LOH events, the regions of transition likely contain the sites of the recombinogenic DNA lesion. Consequently, for each recombination event listed in Tables S2 and S4, we assigned "windows" likely to contain the initiating lesion; the method that we used is described in detail in Yin and Petes (2013). In brief, the window was defined from the leftmost coordinate of the first transition to the rightmost coordinate of the last transition. For example, in sector 1R/W, for the hybrid conversion tract on chromosome VII, the window is from SGD coordinates 663893 to 686220.

The *exo1* data for UV-induced recombination events (Table S2) was analyzed separately from the spontaneous events (Table S4). For each of the two datasets, we summed the sizes of all of the recombination windows. For the UV-induced samples, we restricted the analysis to unselected recombination events (those that did not occur on the left arm of chromosome V). This sum was 817,055 bp for these events. We examined 16 sectored colonies induced by UV, and the amount of genomic DNA (other than the left arm of chromosome V) that is represented on the SNP microarray is about 11.4 Mb. Thus, for the UV-induced events, the fraction of genomic DNA represented in the windows is 817 kb/11.4 x 16 Mb) or 4.48×10^{-3}. Based on the number and location of elements in the relevant region of the genome, we can then calculate the expected numbers of elements if they are randomly distributed with respect to the recombination windows. For example, from an examination of the location of palindromic sequences greater than 16 bp in length (Lisnic *et al*., 2005), we calculate that there are 563 palindromes in the genomic region that does not include the right arm of V. Examining sixteen genomes, therefore, we expect, therefore, that there will be 40 palindromes located in the windows and 8968 located outside the windows (Table S5). We observed almost exactly these numbers (38 in the windows and 8970 outside of the windows). By chi-square analysis, there is no significant difference between the expectation and the observations. The comparable calculations were done using 13 other genetic elements (Table S5).

We performed a similar calculation with the spontaneous recombination events. The sum of the recombination windows for the spontaneous events selection on chromosome IV was 1,259,222 bp. The amount of DNA represented on the right arm of chromosome IV that is on the SNP microarray is 1,074,795 bp, and we examined a total of 109,629,090 bp (1,074,795 bp x 102 sectored colonies). The windows, therefore, represent about 1.14×10^{-2} of the total DNA examined. We compared the observed

and expected chromosome elements within the windows, and outside of the windows as described above for UV-induced events. Since we performed multiple comparisons, we corrected p values using the method of Hochberg and Benjamini (1990). After this correction was applied, only one comparison was significant. Tandemly-arrayed repeats were significantly under-represented in the spontaneous crossovers.

The references for the number and location of various genomic elements are: ncRNAs, snoRNAs, snRNAs, retrotransposons, tRNA genes, centromeres, ARS elements, solo LTRs (SGD Website: http://www.yeastgenome.org/cgi-bin/seqTools); G4 quadruplex DNA (Capra *et al*., 2010); strongly- and weakly-transcribed genes (Nagalakshmi *et al*., 2008); Rrm3p pause sites (Azvolinsky *et al.*, 2008); gamma-H2AX peaks (Szilard *et al.*, 2010); TER sequences (Fachinetti *et al*., 2010). The strongly- and weakly-transcribed genes were based on examining the transcription of genes within the analyzed area, and picking the top 5% and bottom 5% levels of transcription, respectively.

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