Table S10. Number of genomic elements represented on the microarrays

Element	# elements per genome	# elements on whole-genome array[1]	# elements in *rnh201Δ*[2]	# elements in *rnh201Δ pol2-M644L*[2]	# elements in *rnh1Δ rnh201Δ*[2]	# elements on chromosome IV array[3]
Ty elements	50	48	48	48	35	8
Solo LTRs	291	280	280	276	246	19
Centromeres	16	16	16	16	16	1
Intron-containing genes	345	331	331	323	287	24
ARS elements	352	317	317	308	275	28
tRNA genes	275	274	274	270	236	23
Long genes	306	306	306	295	259	28
Regions of high transcription	330	329	329	318	270	36
Regions of low transcription	328	312	312	303	272	20
ORFs with high GC content	115	115	115	114	96	8
High G content on the non-transcribed strand	41	41	41	40	34	1
Sites of Rbp3 accumulation in S phase	93	93	93	93	70	11
TER sites	71	71	71	69	69	3
TER sites related to high transcription	58	58	58	56	56	3
Sites of Rrm3 accumulation	115	112	112	112	103	6
Palindromic sequences	611	589	589	573	517	51
Sites of G4 quadruplex formation (predicted by sequence context *in silico*)	636	543	543	536	480	20
Sites of differential transcription in response to NMM	114	107	107	105	96	7
Regions of transcription-transcription conflicts resolved by Elc1.	144	144	144	137	125	13

Tracts of poly A or poly T ≥ 25 bp	43	41	41	40	36	3
Sites of RNA/DNA hybrid accumulation in *rnh1 rnh201*	163	129	129	127	112	10

[1]In our analysis, we examined twenty-one types of genomic elements. The references for the locations of these elements are described in Table S9 and in File S1. The total size of the yeast genome, as presented in SGD, is about 12.1 Mb. Since this calculated size counts only two of the approximately 150 ribosomal rRNA genes, there are about 12.1 Mb of single-copy yeast sequences. Our whole-genome microarrays omit most repetitive sub-telomeric repeats. 11.6 Mb of the genome are represented on our whole-genome arrays (details in Dataset S1 of Song *et al*., 2014). The coordinates and sequences of all oligonucleotides on the whole-genome arrays are in Table S5 of St. Charles *et al.* (2012).

[2]In several of the mutant strains, LOH events existed in the starting strains. These regions were omitted from the analysis. The summary of these omissions is: 1) *rnh201*Δ (no pre-existing LOH events, therefore, no omissions necessary), 2) *rnh201*Δ *pol2-M644L* (sequences distal to SGD coordinate 592645 on chromosome XIII were homozygous and deleted from the analysis; 11.3 Mb were in the remaining analysis), and 3) *rnh1 rnh201* (most of these strains had terminal LOH events beginning at SGD coordinate 1263027 on chromosome IV, and coordinate 447834 on chromosome XII; the remaining portion of the genome was about 11.0 Mb). The numbers of elements in each strain were corrected for these deletions.

[3]The chromosome IV-specific microarrays monitor SNPs from *CEN4* to near the right telomere of chromosome IV (coordinate 1511708), a region of about 1.1 Mb). The locations of SNPs on the chromosome IV-specific arrays are in Table S9 of St. Charles and Petes (2013).