

Table S12. Association of LOH events in sectored colonies with various genomic elements on the right arm of chromosome IV

Genome Feature	<i>rnh201</i> Δ			<i>rnh1</i> Δ <i>rnh201</i> Δ		
	expected inside: outside	observed inside: outside	p-value	expected inside: outside	observed inside: outside	p-value
Ty elements	3:165	2:166	0.777	3:109	4:108	0.777
Solo LTRs	5:394	3:396	0.498	7:259	10:256	0.340
Centromeres	0:21	0:21	1.000	0:14	0:14	1.000
Intron-containing genes	7:497	8:496	0.841	8:328	12:324	0.210
ARS elements	8:580	9:579	0.862	10:382	7:385	0.420
tRNA genes	6:477	5:478	0.585	8:314	9:313	0.862
Long genes	10:578	15:573	0.150	11:381	13:379	0.647
Genes with high transcription	10:746	8:748	0.632	13:491	17:487	0.327
Genes with low transcription	6:414	4:416	0.532	7:273	4:276	0.340
ORFs with high GC content	2:166	1:167	0.718	3:109	1:111	0.380
Regions with high G content on the non-transcribed strand	0:21	0:21	1.000	0:14	1:13	1.000
Sites of Rbp3 accumulation in S phase	3:228	3:228	1.000	4:150	3:151	0.806
TER sites	1:62	1:62	1.000	1:41	1:41	1.000
TER sites related to high transcription	1:62	1:62	1.000	1:62	1:62	1:62
Sites of Rrm3 accumulation in S phase	2:124	1:125	0.718	2:82	1:83	0.718
Palindromic sequences	14:1057	17:1054	0.498	18:696	27:687	0.043
Sites of G4 quadruplex formation	6:414	6:414	1.000	7:273	9:271	0.566
Regions of differential transcription in response to NMM	2:145	1:146	0.718	2:96	2:96	1.000
Regions of t ranscription-transcription conflicts resolved by E1c1	4:269	4:269	1.000	5:177	8:174	0.256
Sites of RNA/DNA hybrid accumulation in the <i>rnh1</i> <i>rnh201</i> mutant	3:207	4:206	0.777	4:136	7:133	0.206
Poly A or poly T tracts ≥ 25bp	1:62	1:62	1.000	1:41	2:40	0.610

The associations were examined by the same methods described in Table S11, except analysis was limited to the right arm of chromosome IV. None of the associations was statistically significant after applying the correction for testing multiple samples.