

**Table S11. Association of LOH events in sub-cultured strains with various genomic elements.**

Genome Feature	<i>rnh201Δ</i>			<i>rnh201Δ pol2-M644L</i>			<i>rnh1Δ rnh201Δ</i>		
	Exp inside: outside	Obs inside: outside	p-value	Exp inside: outside	Obs inside: outside	p-value	Exp inside: outside	Obs inside: outside	p-value
Ty elements	8:904	7:905	0.863	5:811	6:810	0.823	9:761	5:765	0.240
Solo LTRs	33:5287	24:5296	0.138	22:4670	12:4680	0.042	51:5779	66:5764	0.041
Centromeres	2:302	0:304	0.286	1:271	3:269	0.133	3:349	3:349	1.000
Intron- containing genes	39:6250	30:6259	0.173	26:5465	22:5469	0.493	60:6738	59:6739	1.000
ARS elements	37:5986	31:5992	0.362	25:5211	19:5217	0.269	57:6367	54:6370	0.729
tRNA genes	32:5174	22:5184	0.092	22:4568	16:4574	0.238	50:5626	48:5628	0.823
Long genes	46:5768	45:5769	0.920	31:4984	35:4980	0.527	72:6220	67:6225	0.597
Genes with high transcription	39:6212	35:6216	0.578	25:5381	25:5381	1.000	58:6564	63:6559	0.554
Genes with low transcription	37:5891	37:5891	1.000	24:5127	27:5124	0.610	57:6367	51:6373	0.467
ORFs with high GC content	14:2171	9:2176	0.227	9:1929	15:1923	0.066	20:2246	14:2252	0.218
High G content on the non-transcribed strand	5:774	4:775	0.823	3:677	1:679	0.387	7:763	9:761	0.572
Sites of Rbp3 accumulation in S phase	11:1756	11:1756	1.000	7:1574	6:1575	0.842	16:1766	20:1762	0.377
TER sites	8:1341	5:1344	0.377	6:1167	8:1165	0.538	18:1500	15:1503	0.554
TER sites related to high transcription	9:1093	5:1097	0.242	6:946	5:947	0.842	14:1218	11:1221	0.498
Sites of Rrm3 accumulation in S phase	13:2115	17:2111	0.330	9:1895	12:1892	0.406	21:2311	12:2320	0.063
Palindromic sequences	70:11121	80:11111	0.254	46:9695	42:9699	0.603	110:12320	85:12345	0.008
Sites of G4 quadruplex formation (predicted <i>in silico</i> )	64:10253	45:10272	0.020	43:9069	47:9065	0.597	99:11121	73:11147	0.010
Regions of differential transcription in response to NMM	13:2020	12:2021	0.888	8:1777	5:1780	0.377	20:2246	15:2251	0.313
Regions of transcription-transcription conflicts resolved by Elc1	17:2719	18:2718	0.920	11:2318	18:2311	0.050	27:2987	25:2989	0.777
Regions of RNA/DNA hybrid accumulation in the <i>rnh1 rnh201</i> mutant	15:2436	14:2437	0.888	10:2149	13:2146	0.427	24:2660	28:2656	0.475
Poly A or poly T tracts $\geq$ 25 bp	5:774	8:771	0.262	3:677	2:678	0.777	8:850	6:852	0.597

The details of the association analysis are described in File S1. In brief, we summed the amount of sequences inside the LOH association windows and the amount of sequences located outside of those windows for all isolates of the individual mutant strains. Based on the total number of elements examined by the array (Table S10), we calculated the number of elements expected within and outside of those windows; this information is summarized in the column labeled “Exp inside:outside.” We then counted the elements within and outside of the association windows (Column “Obs inside:outside”). The observed and expected values were compared using Chi-square “Goodness of Fit” test. Because of the multiple comparisons, we then applied the Benjamini-Hochberg correction to the data (Benjamini and Hochberg, 1995). Following this correction, none of the LOH events in any of the strains were significantly associated with any of the tested genomic elements.