

Additional Data file 3

Because here we studied many codon locations simultaneously and used a less restrictive P-value cut-off, it is very important to further examine the biological signals in other yeast species. Therefore, over-represented locations were examined. Only in frame codon location **UAA+3** showed the same tendency in all other species.

1. Significant P-values are shown in bold (95% confidence level; $p < 0.05$).
2. Under-represented positions are shown as “n.a.”.

		<i>S.cerevisiae</i>	<i>S.bayanus</i>	<i>S.mikatae</i>	<i>S.paradoxus</i>	<i>C. glabrata</i>
		P-value	P-value	P-value	P-value	P-value
UAA+3	Frame+1	9E-07	6E-06	2E-03	1E-04	3E-03
UAG+2	Frame+1	0.053	n.a.	0.3	0.9	0.5
UAA+1	Frame+2	0.005	0.5	0.1	0.013	0.6
UGA+1	Frame+2	0.02	n.a.	0.2	0.3	0.9