

Table S2: Parameters influencing the results of the *in silico* TGA detection method.

Species	L _{CDS} X 3 threshold = 10		L _{CDS} X 3 threshold = 15		L _{CDS} X 2 threshold = 10		L _{CDS} X 2 threshold = 15	
	Number of TGAs	Number of tagged CDSs ^a	Number of TGAs	Number of tagged CDSs	Number of TGAs	Number of tagged CDSs	Number of TGAs	Number of tagged CDSs
<i>S. cerevisiae</i>	35	35	35	16	34	21	33	6
<i>C. glabrata</i>	43	14	41	4	36	16	32	10
<i>Z. rouxii</i>	35	30	31	13	32	21	28	9
<i>K. thermotolerans</i>	27	27	25	12	28	18	24	8
<i>S. kluyveri</i>	40	42	36	13	36	38	32	13
<i>K. lactis</i>	28	22	24	7	25	20	21	7
<i>A. gossypii</i>	29	28	26	7	28	26	24	6
<i>D. hansenii</i>	95	57	88	32	89	49	83	28
<i>Y. lipolytica</i>	24	52	21	16	20	42	16	17
All nine species ^b	356	307	327 (-8.1 %)	120 (-61 %)	328 (-7.9 %)	251 (-18 %)	293 (-18 %)	104 (-66 %)

^aNumber of CDSs with a relic tag.

^bThe percentage in brackets indicates the proportion of lost TGAs or tagged CDSs according to the sum obtained with the reference parameters L_{CDS} X 3 and threshold = 10.