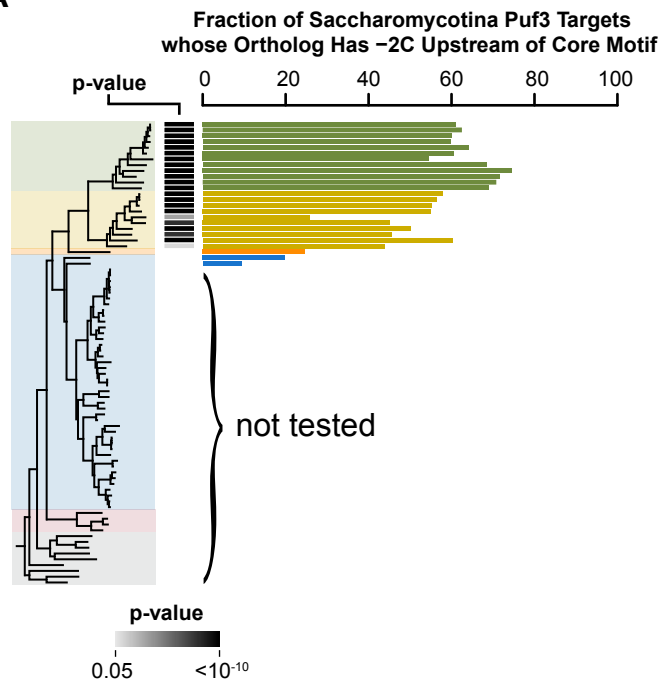


A

- Saccharomycetaceae
- CTG clade
- *Y. lipolytica*
- Pezizomycotina
- Schizosaccharomycetes
- Other Fungi

B

Species	Target Group	Non-target Group	-2C enrichment Odds-ratio	p-value*	Residues Aligned to <i>S. cerevisiae</i> -2C Contacts#
<i>S. cerevisiae</i>	141/231 (61%)	135/801 (17%)	7.7	8e-36	K, LAS
<i>S. cerevisiae</i> RM11.1a	140/224 (62%)	129/730 (18%)	7.7	1.8e-34	?
<i>S. paradoxus</i>	128/213 (60%)	121/723 (17%)	7.5	9.5e-32	K, LAS
<i>S. mikatae</i>	116/194 (60%)	96/612 (16%)	8	8.1e-30	K, LAS
<i>S. kudriavzevii</i>	109/170 (64%)	101/511 (20%)	7.2	2.4e-24	?
<i>S. bayanus</i>	129/213 (61%)	110/741 (15%)	8.8	2.1e-36	K, LAS
<i>C. glabrata</i>	121/222 (55%)	80/477 (17%)	5.9	3e-22	R, LAS
<i>S. castellii</i>	132/193 (68%)	78/476 (16%)	11	1.4e-36	R, LAS
<i>K. waltii</i>	135/181 (75%)	69/285 (24%)	9.1	7.4e-26	R, LAS
<i>S. kluyveri</i>	161/225 (72%)	103/489 (21%)	9.4	1.1e-36	R, LAS
<i>K. lactis</i>	160/226 (71%)	108/559 (19%)	10	9.1e-41	R, LAS
<i>E. gossypii</i>	113/164 (69%)	64/339 (19%)	9.5	2.1e-26	R, LAS
<i>C. albicans</i> WO1	130/225 (58%)	60/461 (13%)	9.1	3.7e-32	K, LAS
<i>C. albicans</i> SC5314	129/229 (56%)	64/486 (13%)	8.5	7.3e-31	K, LAS
<i>C. dubliniensis</i>	127/230 (55%)	61/467 (13%)	8.2	1.9e-29	K, LAS
<i>C. tropicalis</i>	126/229 (55%)	64/455 (14%)	7.4	5.1e-27	K, LAS
<i>L. elongisporus</i>	51/198 (26%)	54/483 (11%)	2.8	1e-04	K, LAS
<i>C. parapsilosis</i>	88/195 (45%)	52/288 (18%)	3.7	6.4e-09	G, --S or G, KKS
<i>D. hansenii</i>	105/230 (46%)	106/480 (22%)	3	7.7e-09	K, LAS
<i>P. stipitis</i>	122/243 (50%)	68/447 (15%)	5.6	1.2e-20	K, LAS
<i>C. guilliermondii</i>	68/155 (44%)	39/156 (25%)	2.3	0.013	K, LAS
<i>C. lusitanae</i>	118/196 (60%)	41/179 (23%)	5.1	6.5e-12	K, LAS
<i>Y. lipolytica</i>	46/186 (25%)	91/522 (17%)	1.6	0.99	K, LAS
<i>A. oligospora</i>	29/146 (20%)	48/312 (15%)	1.4	1	K, LNA
<i>T. melanosporum</i>	4/43 (9.3%)	31/137 (23%)	0.35	1	R, INA

* - Bonferroni corrected

- *S. cerevisiae* -2C contacting residues are 819, 864-866