

Table S8 Characteristics of tandemly duplicated gene arrays

species	Nbr. of TGA		total nbr. of CDSs	Nbr. of CDSs in TGA	proportion of CDSs in TGA (%)	Nbr. of TGA in direct orientation	Nbr. of TGA in convergent orientation	Nbr. of TGA in divergent orientation	Nbr. of TGA in mixte orientation
	total	with relic							
<i>Saccharomyces cerevisiae</i>	52	3	5859	111	1.895	42 (80.8)	5 (9.6)	4 (7.7)	1 (1.9)
<i>Candida glabrata</i>	44	1	5200	114	2.192	31 (70.5)	6 (13.6)	3 (6.8)	4 (9.1)
<i>Zygosaccharomyces rouxii</i>	47	8	4991	97	1.943	41 (87.2)	3(6.4)	2 (4.3)	1 (2.1)
<i>Kluyveromyces thermotolerans</i>	37	6	5092	77	1.512	30 (81.1)	4 (10.8)	2 (5.4)	1 (2.7)
<i>Kluyveromyces lactis</i>	36	2	5075	72	1.419	27 (75.0)	4 (11.1)	4 (11.1)	1 (2.8)
<i>Debaryomyces hansenii</i>	128	19	6264	273	4.358	110 (85.9)	8 (6.3)	9 (7.0)	1 (0.8)
<i>Pichia sorbitophila</i> hybrid	75	2	11252	153	1.359	51 (68.0)	4 (5.3)	18 (24.0)	2 (2.7)
<i>eq. haploid*</i>	38	1	5736	77	1.359	25	2	9	1
<i>Yarrowia lipolytica</i>	43	7	6426	80	1.245	31 (72.1)	4 (9.3)	8 (18.6)	0 (0.0)

*The number of TGA and genes identified in *P. sorbitophila* genome (hybrid) are converted into an equivalent haplotype for a best comparison with the other haploid hemiascomycetous yeasts described.

Numbers in brackets indicate the percentage of each orientation