Table S4. Summary statistics for all *Saccharomyces* and each species using *COX2*.

Species	#Seq	s	k	π	#hap	Hd	Fs	Tajima's D	Fu and Li's D
*Saccharomyces**	566	106	20.90505	0.03574±0.00112	110	0.9629	-12.371	0.28795	**-2.33439**
S. cerevisiae	418	51	12.274	0.02099±0.00015	57	0.941	-4.065	0.82531	**-5.54661**
S. paradoxus	23	32	13.581	0.02322±0.00093	16	0.964	-1.287	1.50954	0.87179
S. mikatae	2	11	11.000	0.01904±0.00940	2	1	ND	ND	
S. kudriavzevii	9	25	6.500	0.01111±0.00524	5	0.833	1.854	-1.45966	-1.48111
S. arboricola	1	ND	ND	ND	1	ND	ND	ND	
S. eubayanus	31	22	2.84301	0.00514±0.00148	12	0.856	-3.362	-1.69139	**-2.71438**
S. uvarum	34	21	3.35651	0.00607±0.00170	8	0.731	0.729	-1.29327	-1.94720

#Seq: number of sequences; s: number of segregating sites; k: average number of differences between sequences; π: nucleotide diversity; #hap: number of haplotypes; Hd: haplotype diversity; Fs: Fu's Fs; Tajima's D and Fu and Li's D. Significant values are highlighted in bold (p-value < 0.05). Asterisk indicate that hybrid sequences were included to calculate statistics.