APPENDIX. Table of polymorphisms of European strains at six loci. Position numbers with reference to published sequence for *S. paradoxus* (CBS432T) in Genbank, numbers starting at first coding nucleotide; for noncoding regions, numbers start at beginning of noncoding region, and negative numbers indicate upstream regions. Coding regions denoted by C and shading; nonsynonymous substitutions by N and bold. R indicates the repeat region in MFalpha1 and RN gives the number of repeats. Consensus nucleotides are shown for European, Far Eastern and Canadian/Brazilian strains and for S. cerevisiae Type strain. Only one heterozygous site was found, in the SAG1 fragment of strain T18.2. Identical genotypes within geographic regions have been merged using MacClade's option of considering taxa redundant even if states are not identical, as along as a resolution of missing data could make them identical.

This table incorporates data from Johnson *et al.* (2004).

Position Coding (C)/Noncoding Nonsynonymous (N)/Synonymous Location Strain ID Russia Leningrad YPS3 Moscow YPS4 YPS8 ATCC96975 ATCC96983 ATCC96986 Latvia Sigulda SIG1+SIG8 SIG3		SAG1	AGA2	STE2	STE3	MFA1	MFalpha1
Russia Leningrad Moscow YPS3 YPS4 YPS8 ATCC96975 ATCC96983 ATCC96986 Latvia Sigulda SIG1+SIG8 SIG1+SIG8		1 8 9 9 9 4 2 2 7 7 8 5 0 6 7 5 C C C C C N N N	8 3 7 7 2 3 8 9 C N	1 1 8 1 2 3 0 3 8 9 7 6 3 7 2 C C C	1 1 1 1 1 2 2 1 1 1 9 0 5 7 1 9 6 6 0 9 2 3 3 0 2 5 8 7 8 7 5 0 9 3 1 1 C C C C C C C N N N N	8 9 1 3 4 4	1 1 3 3 3 3 3 4 1 3 0 1 2 3 3 5 5 1 0 8 8 4 1 3 4 5 7 C C C C C C N N N
Moscow YPS4 YPS8 ATCC96975 ATCC96983 ATCC96986 Latvia Sigulda SIG1+SIG8	Clone ID						
		A C A A G	A A T T	C C C A C T . A	T G G C C C	C A G G T T T T A T	C C T AT - A - 2
SIG6			G -	T . A		T	
Riga RIG3 RIG10 RIG11				T		T T T	G 3 G 3
Sweden Stockholm STOC3 Unknown CBS432T Denmark CBS5829					G A T G C T A G A T		A
Spain J. Santa Maria CECT10176 CECT10308+0	CFCT10329		G -	T	T A		A 3
U.K. Silwood Park & T62.1 Windsor Great Park T76.6+Q31.4 Q4.1 Q32.3 Q59.1 Q70.8+T68.2 Y1+(3Ys) Y2+Y10 Y2.2+(3Ys) Y4+(4Ys+6Zs) Y4.5 Y5+Y7.1 Y6 Y6.5+(1Y+2Zs) Y7 Y8.1 Y8.6+(3Ys) Z1+(19Zs)+Q	m o h +6Ts) a t p s s s) n v u	G A		T	T . C A T A C C T	T - T - T - T - T - T - T - T - T - T -	T

W7			G -																			. A		3	3
S36.7			G -		ΤТ		С.											- 1				. G	;	3	3
T18.2	A/0	3	G -																			. G	;	3	3
T26.3	Α																	- 1							
Q6.1	Α													Т								. A		3	3
Q14.4+Q69.8			G -		ΤТ													- 1				. A		1	1
Q15.1+Q16.1	Α				ΤТ																	A A			
Q43.5+Q74.4			G -															- 1				. A		3	3
Q62.5					ΤТ																	. G	;	3	3
Q89.8	Α		G -		ΤT		С.															. G	;	3	3
																		- 1							
	A C A A G	Α	AG-	C C C	A C	ТА	T 6	G (C C	G	ΤТ	A G	АТ-	С	Α (G G	Т	. C (С	Т	Α 7	ГО	A -	. 3	3
	A C A A G	Α	AG-	T C C	A C	ТА	TG	G (C C					Т	- (G G	Т	. C (С	Т	G T	ГО	A -	. 2	2
																		7	Т	Т				3	3
	A C A A G	Α	AG-	T C C	A C		TG	G (СТ					С	- (G G	i	- 1			G T	ГО	A	3	3
																		- 1						4	4
	ACAAG	Α	AG-	TCT	A C	- A	TC	GG	CCC	G	СС	ΑТ	A A A	Т	Α (GG	Т	. C (С	Т			A (3	3

Consensus Europe Far East Asia Canada & Brazil S. cerevisiae