

Supplementary Materials

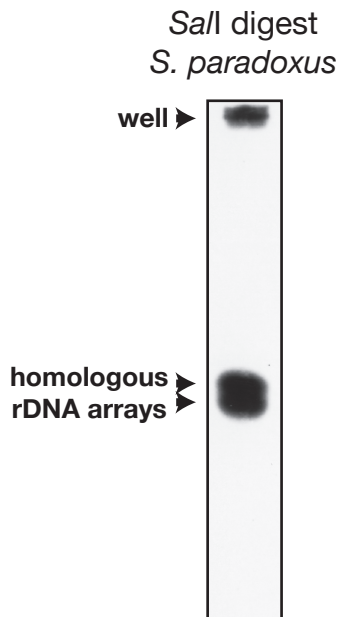
Supplementary Figure 1. The high-frequency polymorphism in the *Saccharomyces paradoxus* IGS is evenly distributed between the two homologous rDNA arrays.

Supplementary Sequence 1. *Aspergillus nidulans* ribosomal DNA repeat unit – complete sequence.

Supplementary Sequence 2. *Saccharomyces cerevisiae* ribosomal DNA repeat unit – complete sequence.

Supplementary Sequence 3. *Saccharomyces cerevisiae* polyubiquitin gene repeat array – complete sequence.

Supplementary Table 1. List of polymorphisms and their respective trace names.



Supplementary Figure 1. The high-frequency polymorphism in the *Saccharomyces paradoxus* IGS is evenly distributed between the two homologous rDNA arrays. The *S. paradoxus* homologous rDNA arrays were separated by CHEF gel electrophoresis after *Bam*HI digestion and blotted as in Fig.3. This blot was then probed with a γ -ATP 32 P end-labelled oligonucleotide (CACATCATAACCACTAAC) specific for the high-frequency polymorphism in the *S. paradoxus* IGS (see Fig. 2). Both homologous rDNA arrays hybridize to the probe with equal intensity, indicating that the mutation is present in approximately equal proportions on both homologues.

***Aspergillus nidulans* ribosomal DNA repeat unit – complete sequence**

length 7465 bp

strain FGSC-A4

tandem repeat_unit 1..7465 ribosomal DNA

rRNA	1..3365 = large subunit ribosomal RNA (25S ribosomal RNA)
spacer	3366..5190 = intergenic spacer (IGS)
rRNA	5191..6989 = small subunit ribosomal RNA (18S ribosomal RNA)
spacer	6990..7142 internal transcribed spacer 1 (ITS1)
rRNA	7143..7300 5.8S ribosomal RNA
spacer	7301..7465 internal transcribed spacer 2 (ITS2)

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***Saccharomyces cerevisiae* ribosomal DNA repeat unit – complete sequence**

length 9081 bp

strain RM11-1a

tandem repeat_unit 1..9081 ribosomal DNA

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spacer	3397..4473 = intergenic spacer 1 (IGS1)
rRNA	4474..4594 = 5S ribosomal RNA
spacer	4595..6530 = intergenic spacer 2 (IGS2)
rRNA	6531..8330 = small subunit ribosomal RNA (18S ribosomal RNA)
spacer	8331..8691 internal transcribed spacer 1 (ITS1)
rRNA	8692..8849 5.8S ribosomal RNA
spacer	8850..9081 internal transcribed spacer 2 (ITS2)

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***Saccharomyces cerevisiae* polyubiquitin gene repeat array – complete sequence**

length 1..1140
mol_type mRNA
strain RM11-1a
CDS 1..1140
codon_start 1
gene UBI4
product polyubiquitin
repeat_region (1..1140)
repeat_type tandem
repeat_family polyubiquitin
 repeatt_unit_range 1..228
 repeat_unit_range 229..456
 repeat_unit_range 457..684
 repeat_unit_range 685..912
 repeat_unit_range 913..1140

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Supplementary table 1. List of polymorphisms and their respective trace names

Position (28S rRNA gene as 1)	Mutation	Read name
<i>Ashbya gossypii</i>		
624	A deletion	NNVS34P627_H4_T3X
638	C to T substitution (l.c.) ^a	NNVS34P694_G3_T3X
3124	C deletion (l.c.)	NNVS34P627_H7_T3X
3876	C to T substitution (l.c.)	NNVS34P627_G8_T3X
5875	G to C substitution	NNVS34P333_B4_T3H
7376	C to T substitution	ngasb21958x
<i>Saccharomyces paradoxus</i>		
1895	A to G substitution	60007RF3
		6715FH4
		6465FB5
		6508RE8
		6535RH8
		6271RA10
		6719RE8
		6455RH4
		6235FE4
		6599RH7
		6481RE11
		6692RC3
		6806RG8
		6506RG10
		6263RC3
		60031RB5
		6524FB3
		6618FF8
2146	C to T substitution	60021FC5
		6365RH7
		6895FG4
		6895FD4
2500-2505	ATAGTT deletion	6573RB1
2670	G insertion	6959FB1
3548	GTGGTGTAT insertion	b
3549-3550	AT to TG substitution (l.c.)	6584RB7
5028	G insertion (l.c.)	6738RF4
5483	T insertion	60006FF12
6155	C to T substitution	6186FE7
		6971FA4
		6587FA9
		6816FF2
		6598FE1
		6630FE12

		6759FD4
		6516FH8
		6894FD6
		6719RC9
6633	A insertion (l.c.)	6570FD5
7284	G to A substitution	60018RA9
		6593FE9
		6405FD12
		6716RB4
		6718RB1
		6611RE12
		6800RB10
8089	C to T substitution	6056FG2
		6557FB2
		6254RD5
		6088RD4
		6792FA11
		6425FB8
		6306RB9
8141	C to T substitution	6463RC1
		6539RA3
8445	G to A substitution	60036RH6
		6805RE11
		6199RH9
		60032RC5
		6442RE8
8831	C to T substitution	6499RE3
		6726FA9
		6708RF12
9034	C deletion	6343RD4
		6484RF12
		6423RG3
<i>Saccharomyces cerevisiae</i>		
695	C to T substitution	5104RC2
		5114RD2
		5147RA3
		6169RA4
		6322RB8
		6366FH6
		6392FB7
		6451FD8
		6468FH6
		6491FH5
		6499RF10
		6503FA8
		6564FG8
		6609FE2
		8104RC7
		8133RF2
		853FH9
2244	A to T substitution (l.c.)	6522FE8

2572	C to G substitution (l.c.)	6655FG9
		6655FF11
3283	T to C substitution (l.c.)	6110RC1
4413	G to T substitution	c
4467	G to A substitution	6554RG12
6223	A to C substitution (l.c.)	867FG10
6488	G to A substitution	5171FH11
8264	T insertion (l.c.)	5144FA9
8961	G to A substitution	d
<i>Aspergillus nidulans</i>		
87	G insertion (l.c.)	5524RH7
155	C insertion (l.c.)	5633RH8
161-163	GAT deletion	60063RE7
387	GA insertion	61955FA1
529	G insertion (l.c.)	60736RD12
576	C to G substitution (l.c.)	5232FG4
832	G insertion	8337RF10
3069	T deletion	60304FE1
3164	G to A substitution	61627RB2
3340	T insertion	62552FD10
3397	G to T substitution (l.c.)	62430RE10
3470	G to A substitution	5520FB11
3770	G insertion (l.c.)	5504RB12
4346	C to G substitution (l.c.)	61989RE5
4694	C insertion	8283RB11
5119	C to T substitution (l.c.)	5532FH11
5532	A deletion	61950FC7
6069	G to A substitution	8288RC5
6940	T insertion (l.c.)	8443RA12
7190	G insertion	5655RG7
<i>Cryptococcus neoformans</i>		
235	A deletion (l.c.)	718228C06.x1
793-806	TCTGTGATGGATTT to CCTGTTTTAATCTTTTTTTTACTGATTC replacement	1026451B12.x1
1038	G to A substitution	968019F08.x1
1098	T deletion	926352C10.x1
1488-1501	AGTGAGAACCTTGA to TGTGCAGGTGACC replacement (l.c.)	967254F09.x2
1560-1561	TA deletion	735110H12.y1
1787	A deletion	718267H07.x1
1918-1936	AGATAAGGGAAGTCGGCAA to CAGCTTGATCCAATAGGCAG replacement	968024B11.x1
1976-1979	GTTG to TTT substitution	1026268A08.x1
2131	A deletion	735077F12.y1
2183	G deletion	967267A11.x1
2244	A deletion	967179G07.x1
2346-2347	TG deletion	967216F03.x1
2498-2501	ATAC to CT substitution	968273B04.x1

2508	ACTACC duplication	1026136B06.x1
2868	T deletion	967258E04.x1
2935	C to T substitution	1026492G07.x1
3057-3068	ATAATTGGTATT to AATATGCTTATCGGCGATC replacement	967270D07.x1
3147	CT insertion	967419E09.x1
3855	A deletion	968230B09.x1
4003	G deletion	1026389G05.x1
4676	A deletion	968234D06.x1
4879	G deletion	1028057G08.x1
4987-4988	AT deletion	967493F01.x1
5110-5119	TGCAAGAAAA to GGCAATAATC replacement	718096F05.x1
5896	C insertion (l.c.)	967422C10.x1
5913	G to C substitution	968377H05.x1
		1026378E11.x1
		967217G04.x1
		1026459E04.x1
		1028061F11.x1
		1026405F04.x1
		968276B05.x1
		967328B05.x1
		926190A12.x1
		968049G10.x1
5974	C insertion (l.c.)	1028031E10.x1
6032-6042	TAAAAAACCAA to ATTAAAAACAGG replacement	718149D06.x1
6046	G to C substitution	968600D07.x1
		967110C02.x1
		1026058F02.x1
		968371C05.x1
		967282A04.x1
		1026107F03.x1
6307-6308	CT deletion	735054F08.x1
6317	C deletion	968171G08.x1
6355	G to A substitution	967283A06.x1
6931	A deletion	1026345G08.x1
6980	C deletion	735011H05.x1
7387	C deletion	967449C11.x1
7404	T deletion (l.c.)	967382F11.x1
7571-7572	AA deletion	1026323D12.x1
7683	T deletion	967354H12.x1
7720	T deletion	968093F01.x1
7769-7771	CTT deletion	926188C10.x1
7970	G insertion (l.c.)	1026394B08.x1
8006-8007	GA deletion	967241E12.x1

a: l.c. = low confidence polymorphism.

b: Polymorphism is present in 62 reads covering this position; read names are not shown.

c: Polymorphism is present in 159 reads covering this position; read names are not shown.

d: Polymorphism is present in 207 reads covering this position; read names are not shown.