

Supporting Information

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Ca - ATTCCTTTTCGCAGCCAAATTGGGTAACA
 Ca-Δ2 - ATTCCTTTTCGCAGCCAAATTGTTCAACA

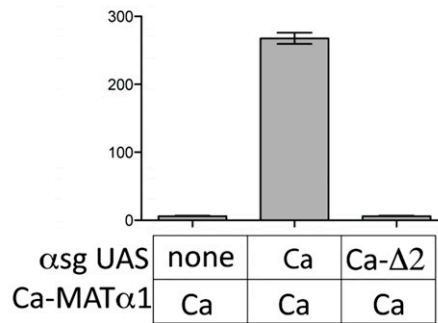


Fig. S1. Mcm1-binding site within *C. albicans* αsg cis-regulatory sequence is necessary for *C. albicans* (Ca)-Matα1-dependent transcriptional activation. In *S. cerevisiae*, Matα1 synergistically binds the αsg cis-regulatory sequence with Mcm1 (1). Disruption of the Mcm1-binding site causes a complete loss of Matα1-dependent transcriptional activation (1). The co-occurrence of Matα1- and Mcm1-binding sites at a fixed distance in *C. albicans* strongly suggests that Matα1 and Mcm1 are also acting synergistically at *C. albicans* αsg cis-regulatory sequences. To test whether, like *S. cerevisiae*, the Mcm1-binding site within *C. albicans* αsg cis-regulatory sequence was essential to Matα1-dependent transcriptional activation, we mutated the Mcm1-binding site within a Ca αsg cis-regulatory sequence promoter (Ca-Δ2). Activity was monitored by β-galactosidase assays. Consistent with a synergistic interaction between Mcm1 and *C. albicans* Matα1, disruption of the Mcm1-binding site eliminated all *C. albicans* Matα1-dependent transcriptional activation.

1. Jarvis EE, Clark KL, Sprague GF Jr. (1989) The yeast transcription activator PRTF, a homolog of the mammalian serum response factor, is encoded by the MCM1 gene. *Genes Dev* 3: 936–945.

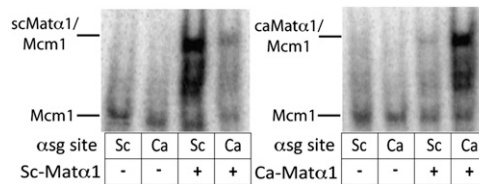


Fig. S2. Species-specific binding to a second set of αsg cis-regulatory sequences. In the reporter construct and gel shift experiments, the αsg cis-regulatory sequences used were derived from the *C. albicans* (Ca) and *S. cerevisiae* (Sc) α-mating pheromone cis-regulatory sequences. Thus, it was a concern that the results were dependent on this specific set of αsg cis-regulatory sequences. To address this directly, electrophoretic mobility gel shift assays were performed on a second set of αsg cis-regulatory sequences taken from the promoter sequences for the *C. albicans* and *S. cerevisiae* a-factor receptor genes (*STE3*). The labeled oligonucleotide used in this experiment was either the *C. albicans* *STE3* αsg cis-regulatory sequence (lanes 2 and 4) or *S. cerevisiae* *STE3* αsg cis-regulatory sequence (lanes 1 and 3) in both images. Extracts were prepared from either the *S. cerevisiae* MATα strain containing a galactose-inducible copy of *C. albicans* (Ca) *MATα1* or the *S. cerevisiae* (Sc) MATα cells containing a galactose-inducible copy of the *S. cerevisiae* *MATα1* (p415GAL). Galactose induction was performed overnight on samples in lanes 3 and 4 (lanes 1 and 2 are grown in glucose) in both images. Each lane contains 5 mg of protein from cell extracts.

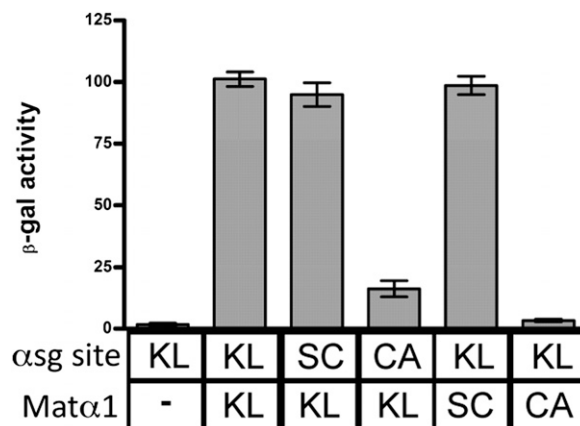


Fig. S3. Functional conservation of Mat α 1 DNA-binding specificity between *S. cerevisiae* (SC) and *K. lactis* (KL). The α sg *cis*-regulatory sequence of the promoter for the α -mating pheromone gene from *K. lactis* was inserted into a basal promoter construct (pLG669z), and the *K. lactis* Mat α 1 was expressed from a 415-translation elongation factor promoter (TEF) plasmid. Plasmids were transformed into an *S. cerevisiae* MAT α Δ mat α 1 strain. Reporter activity was monitored using β -galactosidase assays. CA, *C. albicans*.

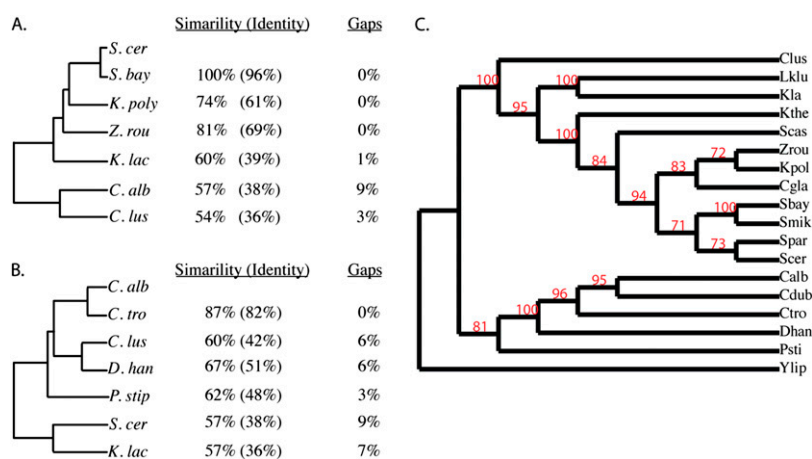


Fig. S4. Evolution of the Mat α 1 HMG DNA-binding domain. A multiple protein sequence alignment for the Mat α 1 HMG DNA-binding domain was computed using ClustalW2. (A) Quantification of Mat α 1 HMG DNA-binding domain divergence relative to the *S. cerevisiae* (*S. cer*) Mat α 1 sequence. Percent protein sequence similarity, identity, and gaps were calculated using BLAST2. (B) Quantification of Mat α 1 HMG DNA-binding domain divergence relative to the *C. albicans* (*C. alb*) Mat α 1 sequence. Note that the *C. lusitanae* (*C. lus*) and *S. cerevisiae* Mat α 1 sequences have comparable similarity scores to *C. albicans* Mat α 1 despite their extensive difference in phylogenetic proximity to *C. albicans*. (C) *C. lusitanae* (Clus) Mat α 1 sequence does not branch with the other CTG-clade species in a tree constructed using the Mat α 1 HMG DNA-binding domain. The tree was generated using the ClustalW2 alignment of the Mat α 1 HMG DNA-binding domain. The bootstrap values in support of this particular branching configuration are shown in red. Notably, in contrast to the ascomycete phylogenetic tree, the *C. lusitanae* Mat α 1 branches outside the CTG-clade. This result is consistent with the divergent DNA-binding specificity of *C. lusitanae* relative to *C. albicans*.

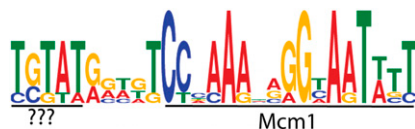


Fig. S5. *Y. lipolytica* α sg *cis*-regulatory PSSM. In Fig. 4, neither the *S. cerevisiae* nor the *C. albicans* PSSMs identified close matches in the promoters of *Y. lipolytica* α sgs. Using MEME, six sequences were located in the promoters of *Y. lipolytica* α sgs. The PSSM built from these six sequences contains a Mcm1-binding site; corroborating the results of Fig. 4, the sequence at the position of the Mat α 1-binding site does not resemble either the *C. albicans* or *S. cerevisiae* Mat α 1 site. Unfortunately, no genomes have been sequenced for species closely related to *Y. lipolytica*, which could provide further support for the possibility of yet another change in Mat α 1 DNA-binding specificity.

Table S1. Sequence sets for *S. cerevisiae*, *K. lactis*, *C. albicans*, *Y. lipolytica*, and the filamentous fungi (sg cis-regulatory sequence PSSMs)***S. cerevisiae* clade sequence set**

6323070_Ylr040cp_[S_cere_+_234
 6325069_Mf(alpha)1p_[S_c_-_368
 22168_YPL187W_[S_paradox_-_313
 6325069_Mf(alpha)1p_[S_c_-_315
 14612_YLR040C_[S_mikatae_+_230
 15773_YLR040C_[S_bayanus_+_246
 21565_YPL187W_[S_mikatae_-_315
 6321349_Mf(alpha)2p_[S_c_+_498
 21565_YPL187W_[S_mikatae_-_366
 13309_YJR004C_[S_bayanus_+_415
 6321349_Mf(alpha)2p_[S_c_-_319
 22168_YPL187W_[S_paradox_-_365
 12315_YJR004C_[S_paradox_+_371
 14144_YKL178C_[S_paradox_+_345
 13094_YKL178C_[S_mikatae_+_330
 12196_YJR004C_[S_mikatae_+_381
 6322463_Sag1p_[S_cerevis_+_357
 14076_YKL178C_[S_bayanus_+_356
 8057_YGL089C_[S_bayanus_-_330
 14679_YLR040C_[S_paradox_+_217
 24677_YPL187W_[S_bayanus_-_384
 7908_YGL089C_[S_mikatae_+_496
 6322671_Ste3p_[S_cerevis_+_339
 8663_YGL089C_[S_paradoxu_+_502
 24677_YPL187W_[S_bayanus_-_333

TTCATTGAACGCCCAAATAGGGAAAA
 TCTATTGAAGGACTAATTAGGAAAGT
 GTCGTTGATGGCCTAATTAGGAAAGT
 GTCGTTGATGGCCTAATTAGGAAAGT
 TTCATTGAAGGCCCAAATAGGGAAAA
 TCTATTGAACGCCCAAATAGGGAAAA
 GTCGTTGATGGCCTAATTAGGAAAGT
 CTCATTGATGTCCTAAAAGGTAATG
 TCAATTGGAGGACTAAATAGGAAAGT
 ATCATTGATAACCTAATTAGGAAAGT
 GGCATTGATGTACCAATGAAGAAATA
 TTTATTGAAGGACTAAATAGGAAAGT
 GTCATTGATGACCAATTAGGAAAGT
 GTCATTGTGACACTAATTAGGAAACT
 GTCATTGTGACACTAATTAGGAAACT
 TTCATTGATGACCAATTAGGAAAGT
 GTCATTGATGACCTAATTAGGAAAGT
 GTCATTGTGACACTAATTAGGAAACT
 GGCATTGATGTACCGATTAGGAAATT
 TTCATTGAACGCCCAAATAGGGAAAA
 TTTATTGAAGGACTGAATAGGAAAGT
 ACCATTGATGTCCAAAATAGGTAATA
 GTCATTGTGACACTAATTAGGAAACT
 CCCATTGATGTCCAGAATAGGTAATG
 GTCGTTGATGGCCTAATTAGGAAAGT

***C. albicans* clade sequence set**

CTRG_04755.3_[C_tropical_-_353
 7.85_[C_dublينيensis]_-_534
 CTRG_04808.3_[C_tropical_-_257
 CTRG_00576.3_[C_tropical_-_335
 orf19.4481_[C_albicans]_-_258
 9.rc.176_[C_dublينيensis]_-_234
 9.rc.176_[C_dublينيensis]_+_308
 orf19.2492_[C_albicans]_+_340
 7.85_[C_dublينيensis]_+_426
 orf19.2492_[C_albicans]_-_248
 7.85_[C_dublينيensis]_-_264
 orf19.4481_[C_albicans]_-_504

AATCCTTCGAGCCAAATCAGGAAA
 GTTCCTTAGCGATACTAAAGAGGAAA
 ATTCCTTTGATATCCAACTGGGTTG
 GATCCTTAGCTTTCGAAAAGAGTTG
 ATTCCTTCGAGCCAAATGGGTAA
 ATTCCTTTGCAATCCAAATCGGGAT
 GTTCCTTTGCAACTAAAGGGGAAA
 GTTCCTTTGCAACTAAAGAGGAAA
 CTTCCCTACCCCCCAAAAAAAAAA
 ATTCCTTTGCAATCCCAATCGGGAT
 ATTCCTTTGAGCCAAATGGGTAA
 GTTCCTTACCGATACTAAAGAGGAAA

***K. lactis* clade sequence set**

00082.8_+_32434-33745_[K_+_424
 00034.rc.7_-_67410-67020_-_276
 50306787_[K_lactis]_-_241
 50309605_[K_lactis]_-_465
 00082.8_+_32434-33745_[K_+_336
 00215.4_+_23082-25671_[K_-_183
 50302709_[K_lactis]_+_416
 50311651_[K_lactis]_+_134
 00201.23_+_24401-24854_[+_465
 00648.rc.5_-_9278-8468_[+_133
 00834.2_+_1798-2458_[K_w_+_123
 00201.23_+_24401-24854_[_-_302
 00008.rc.4_-_23286-21879_+_252
 00008.rc.4_-_23286-21879_+_368

TCCATTTAAA CCCTAATCAG GAAGTT
 TGCTTTGTTT GACAGATTAG GAAAGT
 ATCATTGAA CCCAGATTAG GGAAAG
 AGCTTTACAT GACAGTTAG GAAAGA
 ACCATTGAAG GACCAAATAG GAAAGT
 TGCATTTAAA CACTAAATAG GAAAAC
 TGCATAAAG GCTTAATCCG GAAATC
 ATCATATATT GCCGAAAAAG GAAACC
 TCCTTTAATA CCCGAAAGAG GAAAGT
 TGCATTGCGT GCCTAAAACG GAAAGG
 ATTATTAGTC GCTCGAAAAG GAAACC
 TACCTTGATC GACAGATTAG GAAACT
 AACATTGATG TTCGAAAGGG GAAACA
 CTCATTAAT CCTCGAACAG GAAATT

Filamentous fungi sequence set

CIMG_06159.2_[C_immitis]_+_580
 SS1G_04155.1_[S_sclerotii]_+_272
 CIMG_06159.2_[C_immitis]_+_446
 FG07270.1_[F_graminearum]_+_273
 UREG_04230.1_[U_reesii]_+_463
 UREG_04230.1_[U_reesii]_+_596
 AN7743.3_[A_nidulans]_+_517
 FG07270.1_[F_graminearum]_-_529

CCTTATTGAT ACCCAAATCG GGTTAG
 ATCTATTGAG ACCCTCAATA GGAAAA
 CGTTATTGAG GCCCTGTATA GGAAGC
 CCTTATTGAC AGGCTGAACT GGCCTA
 CGTTATTGAG GCCCTGTATA GGAATC
 CCTTATTGAT ACCCAAATCG GGTTAG
 ATCTATTGAC ACCCAAATCA GGCAAT
 GTCTATTGAC AACCCGATCG GGTAAG

Table S1. Cont.

MGG_06452.5_[M_grisea]_–_600	CTCTATTCAG ACCCGAATAG GGAATT
<i>Y. lipolytica</i> sequence set	
49649895_[Y_lipolytica]_–_464	TCGATACTGT CCCAAATAGG TAATTT
49651178_[Y_lipolytica]_+_179	TGTATGGTGT CCAAAGGGGG CAATTC
49650459_[Y_lipolytica]_–_105	TGGAAGGGCT CCCATGGTGT TTATAT
49649895_[Y_lipolytica]_–_191	CGTATGGATT CTGCAAAGGG TAATTT
49651178_[Y_lipolytica]_+_230	TGTATAGTAT CCTAAAAACAG TAATAT
49650459_[Y_lipolytica]_+_600	TGTTTGAATG CCCAAATAGG AAATAT

Table S2. Oligonucleotides and codon-changed *C. albicans* Mat α 1 sequence

<i>C. albicans</i> α -pheromone cis-regulatory sequence	tcgacAAAATTCCTTTTCGAGCCAAATGGGTAACAAATAATg
<i>C. albicans</i> α -pheromone cis-regulatory sequence (RC)	tcgacATTATTTGTTACCCAATTTGGCTGCGAAAGGAATTTTg
<i>C. albicans</i> Mat α 1 codon-changed	ATGGGAAATGAGAAAAAGACAAGAAAAACTGTTCCAAAAGAGTTT ATTCATTGTTTAGAGTACATTCAGGGAGAGATGCTCCTAGACG TGATACTAGGGAAGTTCAAAGAGTAAGAAGCACGGCTTCCGTTTT ACTAGTTTGCTGATTTGCCAGTCGCCAGTAATGCTTTACAAGAGTTATTGTT AGAGTATGGATTACTGAACGATATCAAATGGGATTCCAAAGGG CTTAAAGGGTTCCAAAAACAAAAAGACAAAGTTGAAGCCAATCAA CTCTTTCATAGCATTAGATCCTTCTATTCAAGAACTATTTCTAA CCCAGAACATCAGAGAGAATTGTCATCTAAGCTAGCCGATGTAT GGACACAAGAATCAAATCAGGAAGTGTGGAACAATACACACAA TCTTACAATAACTACTCTTTTACCTGATGCTAACTAACTTCG TTGACTGGCTGTGTGAAGCATTGGACTACACTATTGACAACAC TACACCACAATAGAGGACATCTCACTAACCTTACAACCAACT CTTCTGGTACCATCGAAGATGTCTACATTATGAAGTAA GGGTTTGGATCCTTACTTCATAATGTAGACATCTTCGATGGTACCAG AGAGAGTCTAGAATGGGAAATGAGAAAAAGACAAGAAAAACTGTTCC tcgacAAAATTAATTCGAGCCAAATGGGTAACAAATAATg tcgacATTATTTGTTACCCAATTTGGCTGCGAAATTTAATTTTg tcgacATGTTCTATTGAAAGACTAATTAGGAAAGTTAATTTg TCGACAATTAACCTTCTAATTAGTCTTCAATAGAACATG ACGCTATATACACGCTGCGGATCTGATGTTCTTTTCGAGACTAATTAGGAAAGTT AATTCCTAAAAATTTTTCTTTCTGCTTT AAAGCAGGAAAGGAAAAAATTTTTAGGAATTAACCTTCTAATTAGTCTGCGAAAGGAA CATCAGATCCGCCAGGCGTGTATATAGCGT AAAGCAGGAAAGGAAAAAATTTTTAGGATAATTCTATTGAAAGCCAAATTGAAAGTT AATTCAGATCCGCCAGGCGTGTATATAGCGT ACGCTATATACACGCTGCGGATCTGAATTAACCTTCCAATTTGGCTTCAATAGAAATTAT CCTAAAAATTTTTCTTTCTGCTTT AGAGAGTCTAGAATGTTTACTTCGAAGCCTGCTTTC AGAGAGTCTAGAGGGTTTGGATCCCTATAAGGCCAAATGTACAAACACATC ACGCTATATACACGCTGCGGATCTGgtctaaccgattgggtatcaataaggagCCTAAAAA TTTTTCTTTCTGCTTT AAAGCAGGAAAGGAAAAAATTTTTAGGctcttattgataccaaatcggttagacCAGATCCG CCAGGCGTGTATATAGCGT tcgacAAAATTCCTTTTCGAGCCAAATGTTCAACAAATAATg tcgacATTATTTGTTTGGCAATTTGGCTGCGAAAGGAATTTTg TATTGTTCTATTGTTCTTTGCGACTAAAGAGGAAATCAATTTTACTTAGTTGCAA TTTGCAACTAAGTAAAAATTTGATTTCTTTAGTCTGCAAAGGAAACAATAGAACAA ACATTGATAGTCGAGAAGTTTCTAATTAGTGTCAATGACAGAGAAAAATTGTACCAGC GCTGGTACAATTTTCTGTCTATTGTGACTAATTAGGAAACTTCTCGACTATCAATGT tcgagAAAATTCCTTTGAGAGCCTAACTAGGAACTAGAGTCAAc tcgagTTGACTCTAGTTCTAGTTAGGCTCTCAAAGGAAATTTc tcgacAATTAACCTTCTAATTAGTCTTAAATGAGAACATg tcgacATGTTCTCATTAAAGGACTAATTAGGAAAGTTAATTTg AGAGAGTCTAGAATGCAAAAGCCTGAAGTTGGGATTTTg GGGTTTGGATCCTTAGTCAACAAAGACATCTCCACATTTT CCC TTT GTC GAC TCA GAC TGA GTT CAT CAA GGA ATA GC AGA GAG GGA TCC ATG AAA TCG AAT GCT CCA ACC TTT AAA GTG
<i>C. albicans</i> Mat α 1 BamH1 3'	
<i>C. albicans</i> Mat α 1 Xba1 5'	
<i>C. albicans</i> α -pheromone Δ Mat α 1 site	
<i>C. albicans</i> α -pheromone cis-regulatory sequence (RC)	
<i>S. cerevisiae</i> α -pheromone Δ Mat α 1 site	
<i>S. cerevisiae</i> α -pheromone Δ Mat α 1 site (RC)	
Sc/Ca	
Sc/Ca (RC)	
Ca/Sc	
Ca/Sc	
<i>S. cerevisiae</i> Mat α 1 Xba1 5'	
<i>S. cerevisiae</i> Mat α 1 BamH1 3'	
<i>U. reesii</i> Ste3 cis-regulatory sequence	
<i>U. reesii</i> Ste3 cis-regulatory sequence (RC)	
<i>C. albicans</i> α -pheromone Δ Mcm1 site	
<i>C. albicans</i> α -pheromone Δ Mcm1 site (RC)	
<i>C. albicans</i> ste3 cis-regulatory sequence	
<i>C. albicans</i> ste3 cis-regulatory sequence (RC)	
<i>S. cerevisiae</i> ste3 cis-regulatory sequence (RC)	
<i>S. cerevisiae</i> ste3 cis-regulatory sequence	
<i>C. lusitaniae</i> α -pheromone cis-regulatory site	
<i>C. lusitaniae</i> α -pheromone cis-regulatory site (RC)	
<i>K. lactis</i> α -pheromone cis-regulatory site	
<i>K. lactis</i> α -pheromone cis-regulatory site (RC)	
<i>C. lusitaniae</i> Mat α 1 Xba1 5'	
<i>C. lusitaniae</i> Mat α 1 Bamh1 3'	
<i>K. lactis</i> Mat α 1 Sal1 5'	
<i>K. lactis</i> Mat α 1 Bamh1 3'	

Ca, *C. albicans*; RC, reverse complement; Sc, *S. cerevisiae*.

Table S3. *S. cerevisiae* strains constructed

Fig. 2

a Lane 1	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS
a Lane 2	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS-Ca
a Lane 3	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS-Ca Δ
a Lane 4	W303 MAT α p415TEF-codon-changed-caMat α 1 pLG669z-Cyc1- Δ UAS-Ca
a Lane 5	W303 MAT α p415TEF-codon-changed-CaMat α 1 pLG669z-Cyc1- Δ UAS-Ca Δ
b Lane 1	W303 MAT α p415GAL-codon-changed-caMat α 1
b Lane 2	W303 MAT α p415GAL-codon-changed-caMat α 1
b Lane 3	W303 MAT α p415GAL-codon-changed-caMat α 1
b Lane 4	W303 MAT α p415GAL-codon-changed-caMat α 1

Fig. 3

a Lane 1	EG123 MAT α Δ Mat α 1 p415TEF pLG669z-Cyc1- Δ UAS-Sc
a Lane 2	EG123 MAT α Δ Mat α 1 p415TEF-scMat α 1 pLG669z-Cyc1- Δ UAS-Sc
a Lane 3	EG123 MAT α Δ Mat α 1 p415TEF-codon-changed caMat α 1 pLG669z-Cyc1- Δ UAS-Sc
a Lane 4	EG123 MAT α Δ Mat α 1 p415TEF pLG669z-Cyc1- Δ UAS-Ca
a Lane 5	EG123 MAT α Δ Mat α 1 p415TEF-scMat α 1 pLG669z-Cyc1- Δ UAS-Ca
a Lane 6	EG123 MAT α Δ Mat α 1 p415TEF-codon-changed caMat α 1 pLG669z-Cyc1- Δ UAS-Ca
b Lane 1	W303 MAT α p415GAL-scMat α 1
b Lane 2	W303 MAT α p415GAL-scMat α 1
b Lane 3	W303 MAT α p415GAL-codon-changed-caMat α 1
b Lane 4	W303 MAT α p415GAL-codon-changed-caMat α 1
b Lane 5	W303 MAT α p415GAL-scMat α 1
b Lane 6	W303 MAT α p415GAL-codon-changed-caMat α 1
c Lane 1	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS-Sc/Ca
c Lane 2	W303 MAT α p415TEF-codon-changed caMat α 1 pLG669z-Cyc1- Δ UAS-Sc/Ca
c Lane 3	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS-Ca/Sc
c Lane 4	W303 MAT α p415TEF-codon-changed caMat α 1 pLG669z-Cyc1- Δ UAS-Ca/Sc

Fig. 4

c Lane 1	EG123 MAT α Δ Mat α 1 p415TEF pLG669z-Cyc1- Δ UAS-KI
c Lane 2	EG123 MAT α Δ Mat α 1 p415TEF-klMat α 1 pLG669z-Cyc1- Δ UAS-KI
c Lane 3	EG123 MAT α Δ Mat α 1 p415TEF-klMat α 1 pLG669z-Cyc1- Δ UAS-Sc
c Lane 4	EG123 MAT α Δ Mat α 1 p415TEF-klMat α 1 pLG669z-Cyc1- Δ UAS-Ca
c Lane 5	EG123 MAT α Δ Mat α 1 p415TEF-scMat α 1 pLG669z-Cyc1- Δ UAS-KI
c Lane 6	EG123 MAT α Δ Mat α 1 p415TEF-codon-changed-caMat α 1 pLG669z-Cyc1- Δ UAS-KI
e Lane 1	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS-FF
e Lane 2	W303 MAT α p415TEF pLG669z-Cyc1- Δ UAS-FF Δ
e Lane 3	W303 MAT α p415TEF-codon-changed caMat α 1 pLG669z-Cyc1- Δ UAS-FF
e Lane 4	W303 MAT α p415TEF-codon-changed caMat α 1 pLG669z-Cyc1- Δ UAS-FF Δ

Fig. 5

b Lane 1	EG123 MAT α Δ Mat α 1 p415TEF pLG669z-Cyc1- Δ UAS-CI
b Lane 2	EG123 MAT α Δ Mat α 1 p415TEF-CIMat α 1 pLG669z-Cyc1- Δ UAS-CI
b Lane 3	EG123 MAT α Δ Mat α 1 p415TEF-CIMat α 1 pLG669z-Cyc1- Δ UAS-Ca
b Lane 4	EG123 MAT α Δ Mat α 1 p415TEF-klMat α 1 pLG669z-Cyc1- Δ UAS-Sc
b Lane 5	EG123 MAT α Δ Mat α 1 p415TEF-codon-changed-caMat α 1 pLG669z-Cyc1- Δ UAS-CI
b Lane 6	EG123 MAT α Δ Mat α 1 p415TEF-scMat α 1 pLG669z-Cyc1- Δ UAS-CI

Fig. S1

Lane 1	W303 MAT α p415TEF-codon-changed-caMat α 1 pLG669z-Cyc1- Δ UAS
Lane 2	W303 MAT α p415TEF-codon-changed-caMat α 1 pLG669z-Cyc1- Δ UAS-Ca
Lane 3	W303 MAT α p415TEF-codon-changed-caMat α 1 pLG669z-Cyc1- Δ UAS-Ca Δ 2 (Mcm1 site mutant)

Fig. S2

Lane 1	W303 MAT α p415GAL-scMat α 1
Lane 2	W303 MAT α p415GAL-codon-changed-caMat α 1
Lane 3	W303 MAT α p415GAL-scMat α 1
Lane 4	W303 MAT α p415GAL-codon-changed-caMat α 1
Lane 5	W303 MAT α p415GAL-scMat α 1
Lane 6	W303 MAT α p415GAL-codon-changed-caMat α 1
Lane 7	W303 MAT α p415GAL-scMat α 1
Lane 8	W303 MAT α p415GAL-codon-changed-caMat α 1

Ca, *C. albicans*; Ca Δ 2; Sc, *S. cerevisiae*.