Supplement to Healey et al., "*Candida glabrata* mutants demonstrating paradoxical caspofungin reduced susceptibility but micafungin increased susceptibility"

TABLE S1. DNA primers used in this study

Primer[a]	Application	Sequence (5′-3′)
CgFKS1c1-ScURA3F	*fks1Δ*	TCTTTCATTTCTAGAGTTTTATCTTTTTTTTTTGCTCTTGTTTGATATACATTC GCTATGTCGAAAGCTACATATAAGGA[b]
CgFKS1c620-ScURA3dR	*fks1Δ*	AGTGGTAGACAAAATTCTGATTGGATCTCTTAGAGATAGAATCAAGAAGTAGTA TGATTCGGTATTTCACACCGCATAGG[b]
CgFKS2c1-ScURA3F	*fks2Δ*	CAAGTCTCTATCAGCCAATAAAGGAATAAGAACAAGACAGAAAAAGAAAATTCC AACCATGTCGAAAGCTACATATAAGG[b]
CgFKS2c1897-ScURA3R	*fks2Δ*	ATTCCTAATTAGAAAAATTCTTGAAAATCATACTCAATTAGGGGATTATCTATT GCCTCTTTAGTTTTGCTGGCCGCATC[b]
CgFKS3c584-ScURA3uF	*fks3Δ*	TCATTGCAAAATATGTTGAATCTTACTTTTTTTTAACGTTGAGTGCACCATACC ACAGCT[b]
CgFKS3c1324F-ScURA3dR	*fks3Δ*	GCAATAAAGAATACAATAAATATGGAAAATACAAAAATTGGGTATTTCACACCG CATAGG[b]
CgFKS1u225F	amplify	AGGGTCTTTTCGAATCTTGCT
CgFKS1c622R	amplify	GATTCAGCGTACTTAGCAGC
CgFKS1u115F	sequence	ATAACAAATTCACATTCGCTTAG
CgFKS1c207F	sequence	CAAGAAATGGTACTTCGCCG
CgFKS1c558F	amplify	GTTGCAGTCGCTACATTGCTA
CgFKS1c1242R	amplify	AATTGTACCAAAACCTAAATCTC
CgFKS1c594F	sequence	CCTCCTTTGCACCTTTGCAT
CgFKS1c828F	sequence	TTTACCGTTTTGACTCCTCAC
CgFKS1c999F	sequence	CCACATGAACTGGAAAACGC
CgFKS1c1214F	amplify,sequence	GAATGCCCTATTACGTGGTG
CgFKS1d118R	amplify	TGTAGTATGGAGGTAAATGATG
CgFKS1c1446F	sequence	GTTGCTTTTCGGTACCGTTG
CgFKS1c1649F	sequence	GGGTTCTTGAAGGTTTCAACT
CgFKS2u114F	amplify	CGCTTAAGTTAAAGAACAAGGT
CgFKS2c1000R	amplify	TCTCTCTCAAGACCTTCAGC
CgFKS2u61F	sequence	TCCCAAGTCTCTATCAGCCA
CgFKS2c218F	sequence	AAGCGTTGCTATCTGTCCAC
CgFKS2c473F	sequence	GGATTATGCACGTTTCCGTC
CgFKS2c730F	sequence	TTCCATCTTAACTCCTTGGAG
CgFKS2c965F	amplify	CCCAAACCTTGTACCGTACT
CgFKS2d187R	amplify	AGACTGTTATTGTTACCATCGC
CgFKS2c974F	sequence	TCATGAACTACGCTAGAGCG
CgFKS2c1225F	sequence	GAAGTGGTCTATCCAAGGCT
CgFKS2c1471F	sequence	GGCCAGATCTATGCTGATGT
CgFKS2c1719F	sequence	ATGACCATGCTAACACGGCT
CgFKS3u136F	amplify	TCTGCGATAAGTGGAGTTTC
CgFKS3c828R	amplify	CCATTCTTCGGGATGAAGGT
CgFKS3u97F	sequence	ACTCTAATAACCTTGGAACTAG
CgFKS3c231F	sequence	TGAAAGACCTAACCCCAAAAC
CgFKS3c495F	sequence	CAATGTTCACTCGAAATCTGC
CgFKS3c769F	amplify	CACTGTCGACCCCATTATTG
CgFKS3d30R	amplify	TTCAACTTTAAACGGATCCATC
CgFKS3c776F	sequence	TCCTGTCCCTGTTGAATGCA
CgFKS3c1044F	sequence	CAATCCAATTTTAGGGGATGG
CgFKS3c1316F	sequence	ACTCCGGCACTGCACTGG
CgFKS3c1580F	sequence	GGTAATATTATTCGGGCAAGG

[a] Numbers represent location in nucleotides or codons: u, upstream (nucleotides); c, codons; d, downstream (nucleotides).
[b] Sequences corresponding to *S. cerevisiae URA3* flanking sequences in pRS416 are underlined.

TABLE S2. CSP and MCF susceptibilities of *C. glabrata* WT strains and their CRS-MIS mutants determined by broth microdilution in RPMI medium

Strain	Source[a]	WT CSP/MCF MIC (μg/ml)[c]	Selection[b,c]	Mutant CSP/MCF MIC (μg/ml) – CRS-MIS differential C1	C2	C3
66032u	15	0.5/0.016	YPD/0.2	1/0.002 – 16	2/0.004 – 16	1/0.004 – 8
			RPMI/0.25	4/0.004 – 32	4/0.008 – 16	-
380	14	0.5/0.016	YPD/0.25	1/0.016 – 2	1/0.008 – 4	-
			RPMI/0.25	2/0.004 – 16	-	-
945	14	1/0.016	YPD/0.2	4/0.004 – 16	2/0.002 – 16	2/0.004 – 8
2807990	16	1/0.016	YPD/0.25, 0.3	2/0.002 – 16	2/0.001 – 32	-
2806145	16	0.5/0.03	YPD/0.3	0.5/0.008 – 4	0.5/0.008 – 4	-
34-023-157	9	0.5/0.016	YPD/0.25	-	0.5/0.008 – 2	0.5/0.008 – 2
34-507-038.02	9	0.5/0.016	YPD/0.25	0.5/0.004 – 4	-	-
33-94R-0024-119	9	1/0.016	YPD/0.25	2/0.004 – 8	-	-
38326	ATCC	0.5/0.016	YPD/0.25	1/0.008 – 4	2/0.008 – 8	-
2001	ATCC	1/0.016	YPD/0.2	-	1/0.008 – 2	-

[a] Strain source: numbers indicate relevant reference; ATCC, American Type Culture Collection, Masnassas, VA.

[b] Mutants were selected on YPD or RPMI agar with the indicated concentration (μg/ml) of CSP. Following selection, 3 to 22 (median = 6) colonies were tested for each strain, yielding 1 to 6 (median = 3) CRS-MIS mutants.

[c] In our hands, CSP MICs determined by broth microdilution in RPMI were 2 to 4 fold higher than CSP MICs determined on RPMI agar (not shown); this explains why CRS-MIS mutants could be selected on RPMI agar with CSP concentration 2-fold lower than the broth microdilution MIC.