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Supplementary Materials: Differential Regulation of Echinocandin Targets Fks1 and Fks2 in *Candida glabrata* by the Post-Transcriptional Regulator Ssd1

Table S1. Primers used in this study.

Primer[†]	Application	Sequence (5′-3′)[‡]
CgFKS1c1757F	hotspot 1 PCR	ACGTCGCTTCTCAAACCTTC
CgFKS1c2225R	hotspot 1 PCR/sequence	GCGTTCCAGACTTGGGAAAT
CgFKS1c1674F	screen/sequence	GTTGCAGTCGCTACATTGCTA
CgFKS1c3918F	hotspot 2 PCR	CGCTCTTGCACACGAATCTA
CgFKS1c4225R	hotspot 2 PCR/sequence	CACCACCAACAGTCAAATCG
CgFKS2c1790F	hotspot 1 PCR	CGATTATGCCATTAGGTGGTC
CgFKS2c2165R	hotspot 1 PCR/sequence	CCAACAGAGAAGACAGTGTTGA
CgFKS2c1419F	screen/sequence	GGATTATGCACGTTTCCGTC
CgFKS2c3930F	hotspot 2 PCR	GCATCCTGGTTTCCATTTGA
CgFKS2c4312R	hotspot 2 PCR/sequence	GATTGGATCAGACGTTATACATTG
CgSSD1-TRP1F	ssd1Δ	CCTTTTCCCCAGAACAAAGGACAGAAGTGTAAGCGCCGAG GGTCACTATTCTAACTGAAAACCCCAAATGTCTGTTATTAAT TTCACAGG
CgSSD1-TRP1R	ssd1Δ	TATTATAATTACTCAAAAAAGCAACAACGTAAAACTTACAA GGTTCATAGTAATTTAAGGAATGAGCCTATTTCTTAGCATTT TTGACGA
CgSSDu280F	screen/sequence	GTCCCTTGTTGTACAGGTG
ScTRP1c417R	screen	CGAATGAGGTTTCTGTGAAGC
CgSSD1c583R	screen	AGTGCGTTCTGGACCTGTTG
CgSSD1u143F	screen	TTCAGCGTCTTCCCTATCGC
CgSSD1u172F	PCR/screen	CTTTGCGCCATTCGTTCTCC
CgSSD1d301R	PCR	AACAAGCAGTGAAATGAATGTC
pCN-PDC1-SSD 1F	gap-repair	CAAAAAACATTAACATCTAGAACTAGTGGATCCCCCGGGCT GCAGGAATTCATGTCGAAGTTTCATCGCCA
pCN-PDC1-SSD 1R	gap-repair	TGGTGGTAGCTGTGGGTTGTGTTCTCGAGGTCGACGGTATCG ATAAGCTTTTAGTGTTTTGGTTCCACTTTC
pCN-PDC1F	PCR/screen	GAGACCAGACTAATACAACTG
pCN-reverse	PCR/sequence	GTTGCCTGCTACGTAAAGTG
CgSSD1c894R	sequence	GTTTGAGTTGCTTCTGCGATG
CgSSD1c1739R	sequence	GGACGTTGTTTCAATGAGCC
CgSSD1c2476R	sequence	CACCTGACGATCTCTTTCTG
CgSSD1c3280R	sequence	CATCTGAATAAGGAACATCG
CgFKS1expF	qRT-PCR	CAATTGGCAGAACACCGATCCCAA
CgFKS1expR	qRT-PCR	AGTTGGGTTGTCCGTACTCATCGT
CgFKS2expF	qRT-PCR	TACCAACCAGAAGACCAACAGAATGG
CgFKS2expR	qRT-PCR	TCACCACCGCTGATGTTTGGGT
CgRDN5.8F	qRT-PCR	CTTGGTTCTCGCATCGATGA
CgRDN5.8R	qRT-PCR	GGCGCAATGTGCGTTCA

[†]Numbers in primer names correspond to nucleotide location upstream (u) or within the coding region (c) relative to the start codon, or downstream (d) relative to the stop codon. [‡]Underlined regions of deletion primers correspond to *S. cerevisiae TRP1* coding sequences; underlined regions of gap-repair cloning primers correspond to *C. glabrata SSD1* upstream or downstream sequences, and non-underlined regions correspond to sequences on pCN-PDC1 surrounding EcoRV restriction site.