METHODS

Strain/plasmid construction. The parental strains for SC5314-derived mutants were based on auxotrophic strains described previously¹⁰. Gene deletions were constructed using the fusion PCR or SAT1 flipper methods described previously^{27,28}. All strains are listed in Supplementary Table 1. The *bar1* mutant strains CAY320/321 were generated as described previously¹⁰ except an ARG4 marker was used in place of the HIS1 marker. To delete STE2, oligonucleotides 1/2 were used to amplify the 5' flank and oligonucleotides 3/4 to amplify the 3' flank of the gene from SC5314. Oligonucleotides 1/4 were then used to generate a disruption cassette containing either the LEU2 or HIS1 selectable marker²⁷. The cassette was transformed into RBY1118 and integration checked using oligonucleotides 5 or 6 together with primers internal to the marker, and loss of the ORF was confirmed by PCR using oligonucleotides 7/8, resulting in strains RBY1107 and RBY1108. A similar method was used to delete STE3 and MFa genes. For STE3, oligonucleotides $9/10$ and $11/12$ were used to amplify the 5' and 3' flanks, respectively, whereas for MFa, oligonucleotides 17/18 and 19/20 were used to amplify the flanking regions. Disruption cassettes were then generated using oligonucleotides 9/12 and 17/20 to amplify the selective marker together with flanking gene sequences. Correct integration of the cassette at STE3 was confirmed using flanking primers 13/14 and loss of the ORF using 15/16, resulting in strains RBY1113 and RBY1114. For MFa, integration was checked using oligonucleotides 21/22 and deletion of the ORF was confirmed using oligonucleotides 23/24 resulting in strains RBY1081 and RBY1082. To generate the plasmid pDS1 for deletion of BAR1, oligonucleotides 25/26 were used to generate a 5' flank that was digested with ApaI and XhoI and ligated into pSFS2a. Subsequently, oligonucleotides 27/28 were used to generate a 3' flank that was digested with SacI and SacII and ligated into the vector to generate plasmid pDS1. ApaI/SacI-digested pDS1 was then used to transform strains RBY1107, RBY1113 and RBY1081, to generate bar1 mutant strains DSY760/761, DSY792/793 and DSY762/768, respectively. Integration was checked using oligonucleotides 29/30 paired with oligonucleotides internal to pSFS2a, and loss of the ORF was confirmed using oligonucleotides 31/32. To generate plasmids for integration of GFP under the control of a test promoter, GFP was amplified from plasmid pNIM1³¹ using oligonucleotides 33/34, cut with ApaI and SalI and ligated into an ApaI/XhoIdigested pSFS2a, generating pRS2. The promoters of FUS1 and FIG1 were then amplified using oligonucleotides 35/36 and 37/38, respectively. The PCR products were digested with KpnI/ApaI and ligated into pRS2 to generate pDS2 and pDS3 respectively. The plasmid pDS2 was linearized with AflII and transformed into RBY1117 and RBY1197 and integration checked using oligonucleotides 39/40 to generate DSY702 and DSY690, respectively. The plasmid pDS3 was linearized with AflII and transformed into RBY1117 and RBY1220, and integration checked using oligonucleotides 40/41 to generate DSY700 and DSY696, respectively. To generate the mating tester strains DSY170/171, RBY1118 was transformed with a fragment containing SAT1 from the plasmid pNIM1. This fragment targets an intergenic region of chromosome 5 near MTL and was created using oligonucleotides 42/43. To generate the strain CAY371, a WOR1–YFP fusion construct (white–opaque regulator 1–yellow fluorescent protein) was transformed into CAY320 (ref. 32). To generate fluorescently labelled nuclei, strains RBY1197 and DSY168 were transformed with HTB– RFP and $HTB-YFP$ constructs as described previously^{21,33} to generate strains DSY906 and DSY908, respectively. Select clinical isolates were also obtained from D. MacCallum of the Aberdeen Fungal group and grown on sorbose media to generate homozygous **a** and α derivatives, as described previously³⁴.

Clinical mating crosses. All clinical isolates were crossed with the SC5314 $\Delta bar1$ a strain, CAY371. Clinical a isolates correspond as follows: 1, AM2003/0165; 2, L1086 derivative (DSY159); 3, YSU751 derivative (DSY161); 4, Hun92 derivative (DSY165); 5, IHEM16614 derivative (DSY183); 6, 19F; 7, 78048; 8, J981315 derivative (DSY167); CAY371 with WO-1 is not shown . Clinical a isolates correspond as follows: 9, L1086 derivative (DSY164); 10, P37005; 11, 12C; 12, L26; 13, AM2003/0191 derivative (DSY162); 14, IHEM16614 derivative (DSY168); 15, T101; 16, J981315 derivative (DSY194); 17, RIH09; 18, AM2005/0377.

- 31. Park, Y. N. & Morschhauser, J. Tetracycline-inducible gene expression and gene deletion in Candida albicans. Eukaryot. Cell 4, 1328–1342 (2005).
- 32. Alby, K. & Bennett, R. J. Stress-induced phenotypic switching in Candida albicans. Mol. Biol. Cell 20, 3178–3191 (2009).
- 33. Sherwood, R. K. & Bennett, R. J. Microtubule motor protein Kar3 is required for normal mitotic division and morphogenesis in Candida albicans. Eukaryot. Cell 7, 1460–1474 (2008).
- 34. Janbon, G., Sherman, F. & Rustchenko, E. Monosomy of a specific chromosome determines L-sorbose utilization: a novel regulatory mechanism in Candida albicans. Proc. Natl Acad. Sci. USA 95, 5150–5155 (1998).