**Table S3:** Strains used in this study.

|  |  |  |  |
| --- | --- | --- | --- |
| **Strain Name** | **Alias** | **Genotype** | **Source** |
| CauLC5083 | *C. auris* Ci6684 | Clinical isolate | (1) |
| CauLC5280 | *C. auris* Ci6684 *cdr1Δ*  | CauLC5083 + *cdr1Δ::NatMX* | (2) |
| CauLC6554 | *C. auris* B12037 | Clinical isolate Clade III | Gift from Philippe Dufresne |
| CauLC6750 | *C. auris* B12037 *cdr1Δ* | CauLC6654 + *cdr1Δ::NatMX* | (3) |
| CauLC7351 | *C. auris* Ci6684 *B9J08\_003323Δ* | CauLC5083+ *B9J08\_003323Δ::NatMX* | This study |
| CaLC239 | *C. albicans* SN95 | *arg/arg4 his1/his1 URA3/ura3::imm434 IRO1/iro1::imm434* | (4) |
| CaLC2924 | *C. albicans* SN95 *yor1Δ/Δ* | As CaLC239, *yor1::FRT/yor1::FRT* | (5) |
| CaLC5860 | *C. albicans* SN95 *msu1Δ/Δ* | As CaLC239, *msu1::FRT/msu1::FRT* | This study |
| CaLC5862 | *C. albicans* SN95 *shy1Δ/Δ* | As CaLC239, *shy1::FRT/shy1::FRT* | This study |
| CaLC6106 | *C. albicans* GRACE parent strain (CaSS1) | *ura3::imm434/ura3::imm434 his3::hisG/his3::hisG leu2::tetR-GAL4AD-URA/LEU2* | (6) |
| CaLC6239 | *C. albicans* SN95 *cdr1Δ/Δ* | As CaLC239, *cdr1::FRT/cdr1::FRT* | This study |
| CaLC7185 | *C. albicans* SN95 *yor1Δ/Δ msu1Δ/Δ* | As CaLC239, *yor1::FRT/yor1::FRT msu1::FRT/msu1::FRT* | This study |
| CaLC7187 | *C. albicans* SN95 *yor1Δ/Δ shy1Δ/Δ* | As CaLC239, *yor1::FRT/yor1::FRT shy1::FRT/shy1::FRT* | This study |
| CaLC7189 | *C. albicans* SN95 *cdr1Δ/Δ msu1Δ/Δ* | As CaLC239, *cdr1::FRT/cdr1::FRT msu1::FRT/msu1::FRT* | This study |
| CaLC7191 | *C. albicans* SN95 *yor1Δ/Δ shy1Δ/Δ* | As CaLC239, *cdr1::FRT/cdr1::FRT shy1::FRT/shy1::FRT* | This study |
| GELC1561 | *C. albicans tetO-YOR1/yor1Δ* | As GRACE parent, *SAT1::tetO-YOR1/ yor1::HIS3* | This study |
| HELC1561 | *C. albicans YOR1/yor1Δ* | As GRACE parent, *YOR1/yor1::HIS3* | This study |

**Table S4:** Plasmids used in this study.

|  |  |  |
| --- | --- | --- |
| Plasmid | Description | Source |
| pLC49 | p863 (for gene disruption with *FLP-NAT*) | (7) |
| pLC763 | *Ca-FLP-NAT-tetO* | (8) |
| pLC963 | pV1393-1 (CaCas9/sgRNA entry expression vector, contains NatR gene, targeting *NEUT5L*) | (9) |
| pLC1049 | *C. auris* *NATMX* marker | (2) |
| pLC1081 | *C. albicans CAS9* vector pV1093 | (10, 11) |
| pLC1083 | *C. albicans CDR1-SAT1* flipper | (11) |
| pLC1251 | *Ca-HIS3* (for gene disruption) | (8) |

**Table S5:** Oligonucleotides used in this study.

|  |  |  |
| --- | --- | --- |
| Name | Description | Sequence (5' -> 3') |
| oLC274 | pJK863down-F | CTGTCAAGGAGGGTATTCTGG |
| oLC275 | pJK863up-R | AAAGTCAAAGTTCCAAGGGG |
| oLC1815 | Ca-MPA-flipper-R | GATGCTTAGAATGATTCTGG |
| oLC2285 | Ca\_*ACT1*AB+855-F | GACCTTGAGATACCCAATTG |
| oLC2286 | Ca\_*ACT1*AB+1076-R | CAGCTTGAATGGAAACGTAG |
| oLC2535 | TetOp-F | GTTTGGTTCAGCACCTTGTCG |
| oLC4158 | Ca\_*SHY1*-KO-pLC49M13R F | TAATGCAATGTATTACTTCAAATTAGAATACAACCCATTCCATCAAAAGACATTGAAAAAACTCAACCATGGGAAACAGCTATGACCATG |
| oLC4159 | Ca\_*SHY1*-KO-pLC49M13F R | CATAGGTATGTGGATTGAGCTATATACATCTTAAGTATTTTACATAATAGTTAAATAAAAACAAAAAAAATTCAGTAAAACGACGGCCAG |
| oLC4160 | CaSHY1-519F | GCTGCTGCTTGATATAGTTG |
| oLC4161 | CaSHY1+1352R | GGGGTTATTTCATGCAGCCA |
| oLC5978 | pLC963-SNR52-F | GACTGTCAAGGAGGGTATTC |
| oLC5979 | pLC963-SNR52-N-F | CCGCAAGTGATTAGACTTAG |
| oLC5980 | pLC963-sgRNA-R | GAATACCACTTGTTTACCGG |
| oLC5981 | pLC963-sgRNA-N-R | GGTGGCGGCAAAACTAATTC |
| oLC6296 | pLC605 NAT F | ACTGGATGGCGGCGTTAGTA |
| oLC6304 | pLC605 NAT R | ATCAAGCTTGCCTCGTCC |
| oLC6308 | pLC605NAT\_26 | TGGTCGCTATACTGCTGTCG |
| oLC6701 | Ca\_*HIS3*prom\_UPtag\_R10 | CCACCATCTAAATTAAGGGC |
| oLC6853 | SAT1\_R | CGCAGAAAGTAATATCATGC |
| oLC6924 | CaCas9/for | ATCTCATTAGATTTGGAACTTGTGGGTT |
| oLC6925 | CaCas9/rev | TTCGAGCGTCCCAAAACCTTCT |
| oLC6927 | sgRNA/R | ACAAATATTTAAACTCGGGACCTGG |
| oLC6928 | SNR52/N | GCGGCCGCAAGTGATTAGACT |
| oLC6929 | sgRNA/N | GCAGCTCAGTGATTAAGAGTAAAGATGG |
| oLC6966 | SNR52/R\_*CDR1* | ATACAAGTGAAAACATTCAGCAAATTAAAAATAGTTTACGCAAGTC |
| oLC6967 | sgRNA/F\_*CDR1* | CTGAATGTTTTCACTTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAA |
| oLC6968 | sCdr1 NQ sense | ATTCTAAGATGTCGTCGCAAGATG |
| oLC6968 | sCdr1 NQ sense | ATTCTAAGATGTCGTCGCAAGATG |
| oLC6969 | sCdr1 NQ anti | AGTTCTGGCTAAATTCTGAATGTTTTC |
| oLC7493 | *MSU1*-KO-pLC49-F | ATTTTGATAAATTATTCAATAGTGATATACAAGACCTACTCCCCCACCTCCATATTTAGTGACCGATTCAGGAAACAGCTATGACCATG |
| oLC7494 | *MSU1*-KO-pLC49-R | ATTGAACACTTTCTATTTACATGAACTTTTAAAAGTCTTATAATGACTCTTTCTCTCTCTCTATTTCTCTGTAAAACGACGGCCAG |
| oLC7495 | *MSU1*\_sgRNA\_F | GCATCAGGTATACCAATAGGGTTTTAGAGCTAGAAATAGCAAGTTAAA |
| oLC7496 | *MSU1*\_sgRNA\_R | CCTATTGGTATACCTGATGCCAAATTAAAAATAGTTTACGCAAGTC |
| oLC7497 | *MSU1*\_UPcheck\_F | CCAATTGGATATCACGGTACG |
| oLC7498 | *MSU1*\_DNcheck\_R | GAGGTCGTGTGGAAATGGAT |
| oLC7499 | *MSU1*\_sense\_check | TGATGAGTCGGCATATTTGG |
| oLC7500 | *MSU1*\_antisense\_check | TTAGGGGTTTCATTGGCAAG |
| oLC7501 | *SHY1*\_sgRNA\_F | TACACGATCACATAGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAA |
| oLC7502 | *SHY1*\_sgRNA\_R | CCAGTCTATGTGATCGTGTACAAATTAAAAATAGTTTACGCAAGTC |
| oLC7503 | *SHY1*\_sense\_check | CACCAAACTTGGATCCATCA |
| oLC7504 | *SHY1*\_antisense\_check | GCAATTGGCACACCTTCATT |
| oLC8016 | Ca\_*HIS3*+561-F | CATCATCGAGCTGAAAGTGC |
| oLC9059 | Ca\_*YOR1* +2485-F | GATGAAGAAGGACGTCATCG |
| oLC9060 | Ca\_*YOR1* +2645-R | ACAGGAACAACAATCCAAGG |
| oLC9274 | Cau\_*YOR1* -954 F | TATTCTGGACCCCTGACTCG |
| oLC9275 | NAT\_Cau\_*YOR1* -79 R | CTATACTGCTGTCGATTCGATACTAACGCCGCCATCCAGTGCAACCTACGGAGAAAAAGC |
| oLC9276 | NAT\_Cau\_*YOR1*+18 F | CGCTGGCCGGGTGACCCGGCGGGGACGAGGCAAGCTTGATCCATACTATGGCATCGTTGC |
| oLC9277 | Cau\_*YOR1* +924 R | ACTTCAATGAGGATGAGAAG |
| oLC9278 | Cau\_*YOR1* -384 F | CCGTTTTGAGCGCTATTCTC |
| oLC9279 | Cau\_*YOR1* +861 R | AATGTGGGTGCAACACTTCA |
| oLC9280 | Cau\_*YOR1* -979 F | AGCTACGTGAACAAACCTGG |
| oLC9281 | Cau\_*YOR1* +979 R | AGTATGTTACAGAAGACTCC |
| oLC9282 | Cau\_*YOR1* orf1728 F | TCCTTATTGAATGCCCTTGC |
| oLC9283 | Cau\_*YOR1* orf2611 R | ATCCGACCAAAATGTCAACC |
| Grace strain construction |
| oLC1561.1 | *YOR1* Primer1 | TTTTCACTCTTCTCAAACCACAGAAGCTTATTCTTCTTAATTTTTTTTTTTTTGCTAAATTGTTCACATTACTGGATGGCGGCGTTAGTATC |
| oLC1561.2 | *YOR1* Primer2 | TTAATAATCGTTTCTGTCGTTGAAGTAACTCTTGATTTTCAAGAGCATCTGAATTAGGTGGGGGTGCCATCGACTATTTATATTTGTATG |
| oLC1561.3 | *YOR1* Primer3 | AGACAGCAAAATCGATAACTGC |
| oLC1561.4 | *YOR1* Primer4 | ACAAATCATCGGGTTGCAAAGT |
| oLC1561.5 | *YOR1* Primer5 | TTCTTCTTAATTTTTTTTTTTTTGCTAAATTGTTCACATTATGGATGTCCACGAGGTCTCTGCTGCCTGTGTTATGCTTAACGTACGCTGCAGGTCGAC |
| oLC1561.6 | *YOR1* Primer6 | TACAATACAATAACAACAATTGTCACCACTTAACCAATCTTAACGGTGTCGGTCTCGTAGACGACGTCACCAAGCGTCGTATCGATGAATTCGAGCTCG |
| oLC1561.7 | *YOR1* Primer7 | CCTAATTCGAGAGCTCCACCTG |

**Supplemental References:**

1. Chatterjee, S., Alampalli, S. V., Nageshan, R. K., Chettiar, S. T., Joshi, S., and Tatu, U. S. (2015) Draft genome of a commonly misdiagnosed multidrug resistant pathogen *Candida auris*. *BMC Genomics*. **16**, 686

2. Kim, S. H., Iyer, K. R., Pardeshi, L., Muñoz, J. F., Robbins, N., Cuomo, C. A., Wong, K. H., and Cowen, L. E. (2019) Genetic analysis of *Candida auris* implicates Hsp90 in morphogenesis and azole tolerance and Cdr1 in azole resistance. *mBio*. **10**, e02529-18

3. Iyer, K. R., Camara, K., Daniel-Ivad, M., Trilles, R., Pimentel-Elardo, S. M., Fossen, J. L., Marchillo, K., Liu, Z., Singh, S., Muñoz, J. F., Kim, S. H., Porco, J. A., Cuomo, C. A., Williams, N. S., Ibrahim, A. S., Edwards, J. E., Andes, D. R., Nodwell, J. R., Brown, L. E., Whitesell, L., Robbins, N., and Cowen, L. E. (2020) An oxindole efflux inhibitor potentiates azoles and impairs virulence in the fungal pathogen *Candida auris*. *Nat. Commun.* **11**, 6429

4. Noble, S. M., and Johnson, A. D. (2005) Strains and strategies for large-scale gene deletion studies of the diploid human fungal pathogen *Candida albicans*. *Eukaryotic Cell*. **4**, 298–309

5. Shekhar-Guturja, T., Tebung, W. A., Mount, H., Liu, N., Köhler, J. R., Whiteway, M., and Cowen, L. E. (2016) Beauvericin potentiates azole activity via inhibition of multidrug efflux, blocks *Candida albicans* morphogenesis, and is effluxed via Yor1 and circuitry controlled by Zcf29. *Antimicrob. Agents Chemother.* **60**, 7468–7480

6. Roemer, T., Jiang, B., Davison, J., Ketela, T., Veillette, K., Breton, A., Tandia, F., Linteau, A., Sillaots, S., Marta, C., Martel, N., Veronneau, S., Lemieux, S., Kauffman, S., Becker, J., Storms, R., Boone, C., and Bussey, H. (2003) Large-scale essential gene identification in *Candida albicans* and applications to antifungal drug discovery. *Mol. Microbiol.* **50**, 167–181

7. Shen, J., Guo, W., and Köhler, J. R. (2005) *CaNAT1*, a heterologous dominant selectable marker for transformation of *Candida albicans* and other pathogenic *Candida* species. *Infect. Immun.* **73**, 1239–1242

8. Hossain, S., Veri, A. O., and Cowen, L. E. (2020) The proteasome governs fungal morphogenesis via functional connections with Hsp90 and cAMP-protein kinase A signaling. *mBio*. **11**, e00290-20

9. Veri, A. O., Miao, Z., Shapiro, R. S., Tebbji, F., O’Meara, T. R., Kim, S. H., Colazo, J., Tan, K., Vyas, V. K., Whiteway, M., Robbins, N., Wong, K. H., and Cowen, L. E. (2018) Tuning Hsf1 levels drives distinct fungal morphogenetic programs with depletion impairing Hsp90 function and overexpression expanding the target space. *PLoS Genet.* **14**, e1007270

10. Min, K., Ichikawa, Y., Woolford, C. A., and Mitchell, A. P. (2016) *Candida albicans* gene deletion with a transient CRISPR-Cas9 system. *mSphere*. **1**, e00130-16

11. Liu, Z., and Myers, L. C. (2017) Mediator tail module is required for Tac1-activated *CDR1* expression and azole resistance in *Candida albicans*. *Antimicrob. Agents Chemother.* **61**, e01342-17