

**Table S2. Barcodes and Primers used in barcode sequencing.**

Barcode ID	Sequence (5' -> 3')
A03	CGGTGTCGGTCTCGTAGTACAATAAAGGGCAGGTGCAACCATAGAGACCTCGTGGACATC
A10	CGGTGTCGGTCTCGTAGTGACCAAGCCTGAATAGCGTCATAAAGAGACCTCGTGGACATC
A12	CGGTGTCGGTCTCGTAGACGAAGCGTGAAACGTATCGAACGCAGAGACCTCGTGGACATC
B04	CGGTGTCGGTCTCGTAGTAGCGTTAGCGGCCACGGAACATCAAGAGACCTCGTGGACATC
B05	CGGTGTCGGTCTCGTAGTTAATTGCGGGCAGCCACCGTGAATAGAGACCTCGTGGACATC
B07	CGGTGTCGGTCTCGTAGTCTCTCGGGAGGCCAATAGAAACGAGAGACCTCGTGGACATC
C12	CGGTGTCGGTCTCGTAGTTTAAGCATACTCCCATCCGTGCGCAGAGACCTCGTGGACATC
D02	CGGTGTCGGTCTCGTAGTAGTTAGGGCGGCCGAAGTTATCCAAGAGACCTCGTGGACATC
A08	CGGTGTCGGTCTCGTAGCACAGACGACGTAACTTTTATAGGCAGAGACCTCGTGGACATC
A11	CGGTGTCGGTCTCGTAGCGTGTATTAGAGTAATCGCATCTAGAGAGACCTCGTGGACATC
B08	CGGTGTCGGTCTCGTAGTACGCTTGACCCGTGTAGCTGTCAGAGAGACCTCGTGGACATC
B11	CGGTGTCGGTCTCGTAGTGGTTAACACGGAACCTGAGATCCCAGAGACCTCGTGGACATC
C10	CGGTGTCGGTCTCGTAGTAGCACACCTAGCGTGAACCGAGCCAGAGACCTCGTGGACATC
C11	CGGTGTCGGTCTCGTAGTCTAATAACCCCGGATAGGCATGCCAGAGACCTCGTGGACATC
D01	CGGTGTCGGTCTCGTAGTATCTGAGTGTTTGCGGGCTATGCAAGAGACCTCTTGGACATC
Barcode amplification primers	Sequence (5' -> 3')
seqBC_F	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGCTCTTCCGATCTCCTAGG
seqBC_R	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGATAGCCGCGCTGCTAGC

**Table S2: Barcodes and Primers used in barcode sequencing.** The isogenic set of barcoded wild type *C. albicans* strains was generated in the parental strain *C. albicans* CAI4 using Clp10-PTET-GTW plasmids containing the barcodes described here. These plasmids, which are from the *C. albicans* ORFeome project [1,2], were generously provided by Professor Carol Munro.

## References

1. Cabral V, Znaidi S, Walker LA, Martin-Yken H, Dague E, Legrand M, et al. Targeted changes of the cell wall proteome influence *Candida albicans* ability to form single- and multi-strain biofilms. *PLoS Pathog.* 2014;10: e1004542.
2. Chauvel M, Bachellier-Bassi S, Guérout AM, Lee KK, Maufrais C, Permal E, et al. High-throughput functional profiling of the human fungal pathogen *Candida albicans* genome. *Res Microbiol.* 2023; 174: 104025.