

SUPPLEMENTAL MATERIAL

TABLE S1 List of primer sequences used for qPCR.

Primer	Sequence
PGK1	Forward: 5'-GGCTTTGGAAAACCCAGAAAGA-3'
	Reverse: 5'-TGAAGGCCATACCACCACCA-3'
HXK2	Forward: 5'-CGGTTACTATTTGGGAGA-3'
	Reverse: 5'-TTGGATGGATAAGAGGC-3'
RAS1	Forward: 5'-CCCAACTATTGAGGATTCTTATCGTAAA-3'
	Reverse: 5'-TCTCATGGCCAGATATTCTTCTTG-3'
ALS3	Forward: 5'-TCTCGTCCTCATTACACCAACCAT -3'
	Reverse: 5'-GGGGATTGTAAAGTGGATTCTGTG-3'
BGL2	Forward: 5'-TGAAGCTGAAAAGGAAGCTTTG -3'
	Reverse: 5'-GCTTCAGAACCAACCAAGAAA-3'
GRP2	Forward: 5'-AGCTGATCCATCAATCCCAGC-3'
	Reverse: 5'-CCCAAGCAGCTTTTTTCAGCAA-3'
TSA1	Forward: 5'-GCCGAAAAGGATGCTCAAGT-3'
	Reverse: 5'-TGCCAATACCACCGTCTTTTCT-3'
ACT1	Forward: 5'-TTGGTGATGAAGCCCAATCC-3'
	Reverse: 5'-CATATCGTCCCAGTTGGAAACA-3'

DATASET S1 Identified peptides in *C. albicans* biofilms and their persisters. It shows the complete list of peptides identified for protein assembling, which are described and presented with the following parameters including peptide sequence, length, number of missed cleavages, mass, charge states, posterior error probability (PEP), Andromeda score and the corresponding UniProt accession number. The intensity values of peptide are presented for the control biofilms (C1-C9) and persisters (P1-P9).

DATASET S2 Identified proteins in *C. albicans* biofilms and their persisters. It shows the complete list of identified proteins/protein groups, which are described and presented with the following parameters including UniProt accession number, protein name, gene name, number of peptides used for protein identification, sequence coverage, molecular weight and posterior error probability (PEP). The intensity values are presented as Log₂ protein intensity of the control biofilms (C1-C9) and persisters (P1-P9) after label-free quantification (LFQ).

DATASET S3 Enriched GO biological processes annotated with significantly changing proteins. **Table S1. List of primer sequences used for qPCR.**