

Supplementary Note S8: Technical details regarding the microarrays used to monitor gene expression in the pathogenic yeast *Candida glabrata*

Microarrays were manufactured with eArray¹ from Agilent Technologies. There are described in the Gene Expression Omnibus (GEO²) database under “Platform GPL27653”. **Table S8.1** presents the number of chromosomal features described in the Candida Genome Database (CGD, January 2020³), for which there is at least one probe on the microarray platform GPL27653. Almost all Open Reading Frames (ORFs) reported as “Uncharacterized” or “Verified” are found (more than 98%), whereas other features (referred to as “centromere”, “long terminal repeat”, “non-coding RNA”, “pseudogene”, “repeat region”, “rRNA” or “tRNA”) are not found. This means they could not be monitored during transcriptomics experiments and are thus not reported in our final results file.

Type of chromosomal feature	Described in CGD	With probes on microarrays	Percentage
centromere	11	0	
long_terminal_repeat	4	0	
ncRNA Uncharacterized	66	0	
ncRNA Verified	2	0	
ORF Merged/Split Uncharacterized	7	0	
ORF Uncharacterized	5044	4955	98.24
ORF Verified	242	239	98.76
pseudogene	18	0	
repeat_region	2	0	
rRNA Uncharacterized	6	0	
tRNA Uncharacterized	230	0	
Sum	5632	5194	

Table S8.1: Number of chromosomal features for which probes are found on the microarrays used in this study. “Uncharacterized” means that ORFs were predicted based on sequence analysis but lack experimental characterization and “Verified” means there is experimental evidence for a functional product.

¹ <https://earray.chem.agilent.com/earray/>

² <https://www.ncbi.nlm.nih.gov/geo/>

³ http://www.candidagenome.org/download/chromosomal_feature_files/C_glabrata_CBS138/