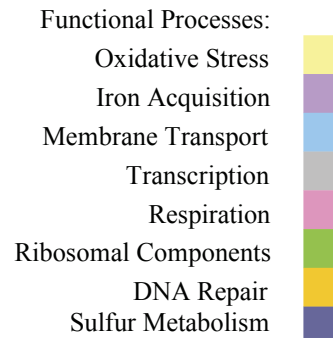


Supplemental Table 2. Nitric Oxide Induced Genes (two-fold or greater in at least one column).



Transcripts induced late in time-course and only in *yhb1Δ/yhb1Δ* strain
(see grey vertical bar Figure 1A)

<i>C. albicans</i> ORF19 # ^A	<i>C. albicans</i> Name ^B	<i>S. cerevisiae</i> Homolog ^C	Description/Function ^D		10 min WT ^{E,F}	120 min WT ^{E,F}	10 min <i>yhb1Δ/Δ</i> ^E	120 min <i>yhb1Δ/Δ</i> ^E
orf19.4082	DDR48	DDR48	DNA repair ATPase/GTPase		1.9	1.5	1.5	57.1
orf19.5952			No good BLAST homology		1.3	0.9	2.5	55.0
orf19.6844	ICL1	ICL1	Isocitrate lyase		1.0	1.1	2.5	22.4
orf19.1263	CFL1	FRE2	Ferric reductase		1.0	2.0	1.0	17.1
orf19.4647		HAP3	Heme-activated transcription factor		1.1	1.2	1.7	15.3
orf19.3018		SPP1	Transcriptional silencing/methylates H3 of Lys4		1.5	1.1	1.5	14.7
orf19.2240			No good BLAST homology		1.2	0.8	1.2	13.6
orf19.7114	CSA1	MUC1	Surface antigen		1.6	1.6	1.2	12.8
orf19.7554		SGE1	Xenobiotic ATPase transporter		1.1	0.9	2.3	9.0
orf19.4690		SMF1	Manganese transporter		0.9	1.5	0.9	7.9
orf19.6482			No good BLAST homology		0.8	1.1	1.0	7.6
orf19.1631	ERG6	ERG6	Sterol 24-C-methyltransferase		0.6	1.0	0.9	7.3
orf19.2345 ^G			No good BLAST homology		1.5	0.8	1.6	6.4
orf19.3932			p53 antigen homolog ^H		1.6	1.4	1.6	5.4
orf19.7209		RDI1	Rho GDP dissociation inhibitor		1.6	1.0	1.6	4.3
orf19.4505		ADH3	Zinc-containing alcohol dehydrogenase		1.0	0.8	1.0	4.1
orf19.5063			No good BLAST homology		1.5	1.1	1.2	3.9
orf19.2297		ARL3	ADP-ribosylation GTPase		0.8	1.1	1.5	3.7
orf19.2761		GPI11	GPI anchor biosynthesis transferase		1.0	0.9	1.0	3.7
orf6.3291 ^G		FIG2 (4e ⁻⁰⁴)	No good BLAST homology		1.4	1.3	1.3	3.5
orf19.4690		SMF1	Manganese transporter		1.2	1.0	1.0	3.5
orf19.839		BDH1	Zinc-containing alcohol dehydrogenase		1.7	1.4	1.3	3.4
orf19.133			No good BLAST homology		0.9	0.9	0.8	3.4
orf19.1724			No good BLAST homology		1.2	0.9	2.6	3.4
orf19.3108		MGT1	DNA repair methyltransferase		1.3	1.5	2.2	3.2
orf19.7324	THI13	THI13	Hydroxymethylpyrimidine synthase		1.1	0.8	1.2	3.1
orf19.2850		MDN1	AAA ATPase		1.5	1.4	2.2	3.1
orf19.3901			Oxidoreductase ^I		1.1	1.2	1.3	3.1
orf19.1077		ATM1	ABC transporter		1.3	1.1	1.1	3.0
orf19.5345		DSK2	Involved in duplication of spindle pole body		1.4	1.4	1.2	2.9
orf19.26		PNG1	Peptide-N4-asparagine amidase		1.8	0.9	1.6	2.9
orf19.4114		FAA2	Long-chain fatty acid CoA ligase		1.0	1.3	1.2	2.8
orf19.4371		TAL1	Transaldolase		1.6	1.2	1.8	2.8
orf19.7244		YNL168C	Involved in degradation of aromatic compounds		1.4	1.0	1.3	2.7

^A Unless noted, all ORF19 # designations were taken from the *Candida* Genome Database (CGD) (<http://www.candidagenome.org/>)

^B Gene names taken from CGD for named *C. albicans* genes

^C Gene names taken from the *Saccharomyces* Genome Database (SGD) for named *S. cerevisiae* homologs (<http://www.yeastgenome.org/>)

^D Unless noted, all gene descriptions and functions taken from published sources, or:

1. CGD for named *C. albicans* genes

2. SGD when no CGD description present and closest homolog is a *S. cerevisiae* gene

^E If more than one microarray spot corresponded to an ORF, the average of the fold changes is represented

^F Average fluorescence signal of CAF2-1, RM1, RM1000

^G NO ORF 19 # of ORF 19 # not in CGD

^H Description name taken from *Schizosaccharomyces pombe*

^I Similarity to *C. albicans* protein