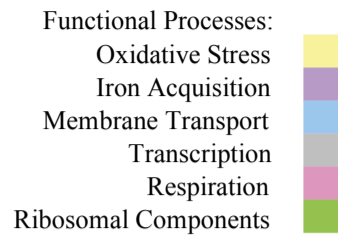
































































Supplemental Table 1. Nitric Oxide Repressed Genes (two-fold or greater in at least one column).



Enhanced repression seen in *yhb1Δ/yhb1Δ* strain at 120 minute time-point  
(see orange vertical bar Figure 1B)

<i>C. albicans</i> ORF19 # <sup>A</sup>	<i>C. albicans</i> Name <sup>B</sup>	<i>S. cerevisiae</i> Homolog <sup>C</sup>	Description/Function <sup>D</sup>		10 min WT <sup>E, F</sup>	120 min WT <sup>E, F</sup>	10 min <i>yhb1Δ/Δ</i> <sup>E</sup>	120 min <i>yhb1Δ/Δ</i> <sup>E</sup>
orf19.637	SDH1	SDH2	Succinate dehydrogenase Fe-S subunit (II)		0.7	1.5	0.7	0.1
orf19.3846		LYS4	Homoaconitase		1.2	2.0	1.0	0.1
orf19.1872			No good BLAST homology		0.5	1.3	0.4	0.1
orf19.1770	CYC1	CYC1	Cytochrome <i>c</i>		0.6	2.1	0.6	0.1
orf19.1549			No good BLAST homology		0.6	1.7	0.5	0.1
orf19.2091			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.9	2.4	0.6	0.2
orf19.5893	RIP1	RIP1	Ubiquinol cytochrome <i>c</i> reductase (III)		0.6	2.2	0.8	0.2
orf19.1467		COX13	Cytochrome <i>c</i> oxidase (IV)		0.5	0.8	0.6	0.2
orf19.2871		SDH1	Flavoprotein succinate dehydrogenase (II)		0.6	1.1	0.8	0.2
orf19.6090		NSR1	rRNA processing protein		0.4	2.8	1.0	0.2
orf19.7590			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.9	2.0	0.7	0.2
orf19.1682			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.9	2.0	0.5	0.2
orf19.1710			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.6	1.4	0.7	0.2
orf19.3175		YOR356W	ETF-ubiquinone oxidoreductase (III)		1.4	1.1	0.8	0.2
orf19.6035			NADH-ubiquinone dehydrogenase (I or III) <sup>K</sup>		0.7	1.2	0.6	0.2
orf19.227		COX7	Cytochrome <i>c</i> oxidase (IV)		0.7	0.9	0.3	0.2
orf19.1480		YMR118C	Succinate dehydrogenase (II)		0.9	1.2	0.7	0.2
orf19.1873			No good BLAST homology		0.5	1.3	0.8	0.2
orf19.440		SDH1	Succinate-ubiquinone dehydrogenase (II)		0.7	1.3	0.7	0.2
orf19.6794			NADH dehydrogenase (I) <sup>I</sup>		0.7	1.7	0.7	0.2
orf19.2954			No good BLAST homology		0.6	1.8	0.6	0.2
orf19.5077			No good BLAST homology		0.6	1.2	0.8	0.2
orf19.7098		YKL070W	Transcriptional regulator <sup>G</sup>		0.8	1.4	1.0	0.2
orf19.1471		COX4	Cytochrome <i>c</i> oxidase (IV)		0.6	0.9	0.4	0.2
orf19.4040		ILV3	Dihydroxyacid dehydratase		1.0	1.2	1.4	0.2
orf19.1625			NADH-ubiquinone oxidoreductase (III) <sup>J</sup>		0.8	1.9	0.7	0.3
orf19.2821			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.8	2.1	0.5	0.3
orf19.3290			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.7	1.4	1.5	0.3
orf19.4016		COR1	Ubiquinol-cytochrome <i>c</i> reductase (III)		0.5	1.5	0.4	0.3
orf19.4759		COX5A	Cytochrome <i>c</i> oxidase (IV)		0.5	1.5	0.4	0.3
orf19.2227			Sulfate transporter <sup>H</sup>		0.6	1.8	1.0	0.3
orf19.429		TRF4	DNA polymerase sigma		0.8	1.2	0.8	0.3
orf19.257			No good BLAST homology		0.8	1.4	0.6	0.3
orf19.236		RPL9B	Protein L9 of large (60S) ribosome		1.0	1.2	0.8	0.3
orf19.917			No good BLAST homology		0.6	1.5	0.5	0.3
orf19.6002		RPL8B	Protein L4 of large (60S) ribosome		0.8	1.2	0.6	0.3
orf19.4026	HIS1	HIS1	ATP phosphoribosyl transferase		1.2	1.3	0.7	0.3
orf19.5928	RPP2B	RPP2B	Protein P2-B of large (60S) ribosome		0.6	1.2	1.0	0.3
orf19.7018		RPS18B	Protein of small (40S) ribosome		0.8	1.4	0.6	0.3
orf19.4632		RPL2B	Protein of large (60S) ribosome		0.8	1.3	0.5	0.3
orf19.1448		APT1	Adenine phosphoribosyltransferase		1.3	1.2	1.1	0.3
orf19.2644		QCR2	Ubiquinol cytochrome <i>c</i> reductase 2 (III)		0.6	1.7	0.8	0.3
orf19.1700		RPS7A	Protein of small (40S) ribosome		0.6	1.4	0.6	0.3
orf19.3790		RPL24A	Protein L30 of large (60S) ribosome		0.8	1.3	0.7	0.3
orf19.6367	SSB1	SSB2	Putative heat shock protein		0.8	1.1	0.8	0.3
orf19.3611			NADH-ubiquinone oxidoreductase (III)		1.0	1.7	0.6	0.4
orf19.840		RPL21A	Protein of the large (60S) ribosome		0.6	1.1	0.6	0.4
orf19.6265		RPS22A	Protein S22 of small (40S) ribosome		0.8	1.2	0.7	0.4
orf19.6887			No good BLAST homology		0.6	2.0	0.8	0.4
orf19.2489		KAP123	Karyopherin-beta		0.4	1.4	0.4	0.4
orf19.3870		ADE13	Adenylosuccinate lyase		1.0	1.5	0.6	0.4
orf19.287			NADH-ubiquinone oxidoreductase (III) <sup>K</sup>		0.6	1.1	1.0	0.4
orf19.6948		CCC1	Transmembrane Ca <sup>2+</sup> transporter		0.8	2.9	0.8	0.4
orf19.5982		RPL18A	Protein of large (60S) ribosome		0.7	1.3	0.8	0.4
orf19.6136		MRPL4	Mitochondrial protein of (60S) ribosome		0.9	1.5	1.4	0.4
orf19.6785		RPS12	Protein S12 of small (40S) ribosome		0.7	1.9	0.5	0.5
orf19.6983		REG1 (2e <sup>-09</sup> )	Negative regulator		0.8	1.0	0.9	0.5
orf19.4506		LYS21	Homocitrate synthase		0.8	2.6	0.8	0.5
orf19.1843		ALG6	Glucosyltransferase		1.0	1.1	0.9	0.5
orf19.5254			No good BLAST homology		0.7	0.8	0.7	0.5
orf19.772		LYS21	Homocitrate synthase isoenzyme		0.9	1.6	0.9	0.5
orf19.2831		RPC31	RNA polymerase III subunit C31		0.6	1.4	1.2	0.5
orf19.3475			No good BLAST homology		0.6	1.4	1.1	0.5
orf19.3335			No good BLAST homology		0.4	2.2	0.5	1.2
orf19.1224		ADY2	Transmembrane transporter		0.4	2.0	0.6	1.4

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

<sup>B</sup> Gene names taken from CGD for named *C. albicans* genes

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

<sup>D</sup> 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

<sup>E</sup> If more than one microarray spot corresponded to an ORF, the average of the fold changes is represented

<sup>F</sup> Average fluorescence signal of CAF2-1, RM1, RM1000

<sup>G</sup> BLAST to *Mesorhizobium loti* (1e-31)

<sup>H</sup> BLAST to *Kluyveromyces lactis* (4e-11)

<sup>I</sup> BLAST to *Homo sapiens* (2e-73)

<sup>J</sup> Bovine

<sup>K</sup> *Neurospora crassa*

Complex I: NADH dehydrogenase (prosthetic groups: FMN, Fe-S)

Complex II: Succinate dehydrogenase (prosthetic groups: FAD, Fe-S)

Complex III: Ubiquinone-cytochrome *c* oxidoreductase (prosthetic groups: Heme, Fe-S)

Complex IV: Cytochrome oxidase (prosthetic groups: Heme, CuA, CuB)