

Table S5: List of *C. neoformans* differentially expressed genes assigned to oxidation-reduction functional category that exhibited persistent induction or repression for a minimum of three time points during H₂O₂ induced oxidative stress.

| GENE ID | ANNOTATION | NAME | Time after H ₂ O ₂ addition (min) | | | | | |
|------------|---|---------------|---|-------|-------|-------|-------|--------|
| | | | 5 | 10 | 15 | 30 | 45 | |
| CNAG-01846 | Pyridine nucleotide-disulphide oxidoreductase | | Red | Red | Green | Green | Green | |
| CNAG-00462 | Flavoprotein-ubiquinone oxidoreductase | <i>CIR2</i> | Red | Red | Green | Green | Green | Yellow |
| CNAG-02266 | NADH ubiquinone oxidoreductase | | Red | Red | Green | Green | Green | |
| CNAG-04325 | Aromatic ring-opening dioxygenase | | Red | Green | Green | Green | Green | |
| CNAG-02580 | No Information | | Red | Green | Green | White | Green | |
| CNAG-02722 | Aldo/keto reductase family | | | | Green | Green | Green | |
| CNAG-04351 | Aldehyde dehydrogenase family | <i>ALD52</i> | | Green | Green | Green | White | Yellow |
| CNAG-00984 | short chain dehydrogenase | <i>FOX22</i> | | | Green | Green | Green | |
| CNAG-03674 | Dehydrogenase E1 component | <i>KGD1</i> | | | Green | Green | Green | Yellow |
| CNAG-03589 | 2Fe-2S iron-sulfur cluster binding domain | <i>YAH1</i> | | | Green | Green | Green | Yellow |
| CNAG-06169 | Alcohol dehydrogenase GroES-like domain | <i>BDH1</i> | | Green | Green | Green | Green | |
| CNAG-02933 | Zinc-binding dehydrogenase | <i>ZTA1</i> | | Green | Green | Green | Green | |
| CNAG-05842 | Cytochrome P450 | <i>ERG110</i> | | Green | Green | Green | Green | |
| CNAG-00575 | Catalase (CAT3) no in Bahns data | <i>CTA12</i> | | White | Green | Green | Green | Yellow |
| CNAG-02868 | Indoleamine 2,3-dioxygenase | <i>BNA2</i> | | Green | Green | Green | Green | |
| CNAG-01542 | No Information | <i>0</i> | | White | Green | Green | Green | |
| CNAG-06638 | Malic enzyme, NAD binding domain | <i>MAE1</i> | | Green | Green | Green | Green | Yellow |
| CNAG-06383 | Cytochrome b5-like Heme/Steroid binding | <i>CYB25</i> | | Green | Green | Green | Green | Yellow |
| CNAG-04553 | short chain dehydrogenase | | Green | Green | Green | White | White | |
| CNAG-03517 | Pyridine nucleotide-disulphide oxidoreductase | <i>NDE2</i> | Green | Green | Green | Green | Green | Yellow |
| CNAG-03874 | Pyridine nucleotide-disulphide oxidoreductase | <i>AIF12</i> | Green | Green | Green | White | White | |
| CNAG-02577 | Fatty acid hydroxylase | <i>SCS7</i> | Green | Green | Green | Green | Green | |
| CNAG-02815 | FAD dependent oxidoreductase | <i>GUT2</i> | Green | Green | Green | White | White | Yellow |
| CNAG-03834 | Sterol desaturase | <i>SUR2</i> | Green | Green | Green | Green | Green | |
| CNAG-04687 | Fatty acid desaturase | <i>OLE1</i> | Green | Green | Green | Green | Green | |
| CNAG-00654 | No Information | <i>SRX1</i> | Green | Green | Green | Green | Green | |
| CNAG-05090 | Zinc-binding dehydrogenase | <i>ZTA13</i> | Red | Red | Red | White | Green | |
| CNAG-03238 | No Information | <i>0</i> | Red | Red | Red | Red | White | |
| CNAG-03389 | Taurine catabolism dioxygenase TauD | <i>JLP1</i> | Red | White | Red | Red | Red | |
| CNAG-00993 | Ubiquinone biosynthesis protein COQ7 | <i>CAT5</i> | Red | Red | Red | Red | Red | Yellow |
| CNAG-05440 | Pyridoxamine 5'-phosphate oxidase | <i>PDX3</i> | Red | Red | Red | White | White | |
| CNAG-03266 | lactate/malate dehydrogenase | <i>MDH1</i> | White | White | Red | Red | Red | Yellow |
| CNAG-01914 | No Information mitochondrial protein | <i>YLR290</i> | White | White | Red | Red | Red | Yellow |
| CNAG-02830 | Ergosterol biosynthesis | <i>ERG4</i> | White | Red | Red | Red | Red | |
| CNAG-06917 | AhpC/TSA family | <i>TSA3</i> | White | Red | Red | Red | White | |
| CNAG-00879 | Glut/Leu/Phe/Val dehydrogenase | <i>GDH2</i> | White | Green | Red | Red | Red | Yellow |
| CNAG-04488 | short chain dehydrogenase | <i>IFA38</i> | White | Red | Red | Red | White | Yellow |
| CNAG-07749 | short chain dehydrogenase 2.3xe-16 | <i>TSC10</i> | White | Red | Red | Red | White | Yellow |
| CNAG-01120 | 2-oxoacid dehydrogenases acyltransferase | <i>LAT1</i> | White | Red | Red | Red | White | Yellow |
| CNAG-04969 | UDP-glucose/GDP-mannose dehydrogenase | <i>UDG1</i> | White | Red | Red | Red | Red | |
| CNAG-06012 | Oxidoreductase FAD-binding domain | <i>CBR1</i> | White | Red | Red | Red | Red | Yellow |
| CNAG-06764 | short chain dehydrogenase | <i>FOX21</i> | White | Red | Red | Red | White | Yellow |
| CNAG-05059 | Transketolase, pyridine binding domain | <i>PDB1</i> | White | Red | Red | Red | Red | Yellow |
| CNAG-00012 | Oxidoreductase family, NAD-binding | | White | Red | Red | Red | White | |
| CNAG-07660 | Dehydrogenase E1 component | <i>PDA1</i> | White | Red | Red | Red | White | Yellow |
| CNAG-03322 | NAD dependent epimerase/dehydratase family | <i>GAL1</i> | White | Red | Red | Red | Red | |

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|------------|--|--------------|--|---|---|---|---|---|---|
| CNAG-04605 | 3-beta hydroxysteroid dehydrogenase/family | <i>ERG26</i> | | | ■ | ■ | ■ | ■ | ■ |
| CNAG-02590 | NAD bind 6-phosphogluconate dehydrogenase | <i>0</i> | | | ■ | ■ | ■ | ■ | ■ |
| CNAG-04652 | Zinc-binding dehydrogenase | | | | ■ | ■ | ■ | ■ | ■ |
| CNAG-02099 | Acyl transferase domain | <i>FAS1</i> | | ■ | ■ | ■ | ■ | ■ | ■ |
| CNAG-02208 | Ribonucleotide reductase, barrel domain | <i>RNR1</i> | | | ■ | ■ | ■ | ■ | ■ |

- down-regulation
- up-regulation
- Potential homologs in *S. cerevisiae* predicted to be located to mitochondria.

Each gene has been named after identification of its potential ortholog in *S. cerevisiae* genome. Mitochondrial location of *S. cerevisiae* gene has been obtained from individual gene annotation page at *S. cerevisiae* genome database.