|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | log2(fold change) EV vs WCL | | | |  |  |  |
| Name | Function | DAY Y | A9 | A1 | DAY B | TM | SP | VDM |
| **Cytoplasm** | | | | | | | | |
| ARO3 | Phospho-2-dehydro-3-deoxyheptonate aldolaseb | -1.28 | -2.55 | -1.51 | -1.46 |  |  |  |
| ARO8 | Aromatic transaminase of the Ehrlich fusel oil pathwaya | -2.37 | -1.81 | ex | -2.36 |  |  |  |
| GDB1 | Putative glycogen debranching enzyme | ex | ex | ex | -1.99 |  |  |  |
| HOM2 | Aspartate-semialdehyde dehydrogenaseb | ex | -3.41 | ex | ex |  |  |  |
| orf19.1889 | Putative phosphoglycerate mutase family proteinb | ex | -1.60 | ex | ex |  |  |  |
| orf19.5943.1 | *S. cerevisiae* ortholog is Stm1, regulates translationa | ex | -3.98 | -4.57 | ex |  |  |  |
| orf19.6596 | Putative esterasea | ex | ex | ex | -2.90 |  |  |  |
| orf19.7263 | Putative X-Pro aminopeptidasea | ex | ex | ex | ex |  |  |  |
| SBP1 | *S. cerevisiae* ortholog is Sbp1, eIF4G binding proteina | ex | -4.30 | -3.80 | -2.15 |  |  |  |
| STI1 | HSP90 co-chaperonea | ex | -2.20 | ex | ex |  |  |  |
| URA4 | Predicted succinate semialdehyde dehydrogenasea | ex | ex | ex | ex |  |  |  |
| XKS1 | Putative xylulokinaseb | ex | ex | ex | ex |  |  |  |
| YNK1 | Nucleoside disphosphate kinase | -3.07 | -2.57 | -2.17 | -1.40 |  |  |  |
| **Cytosol and mitochondria** | | | | | | | | |
| ACH1 | Acetyl-CoA hydrolaseb | -3.24 | -5.09 | -2.79 | -4.03 |  |  |  |
| GLR1 | Glutathione reductaseb | ex | ex | ex | -3.28 |  |  |  |
| HSP60 | Heat shock protein 60b | -4.66 | -1.59 | -4.22 | -4.06 |  |  |  |
| **Mitochondria** | | | | | | | | |
| AAT1 | Aspartate aminotransferasea | ex | -2.11 | -1.48 | -5.70 |  |  |  |
| BAT22 | Putative branched chain amino acid aminotransferaseb | ex | -3.57 | -1.44 | -3.12 |  |  |  |
| ETR1 | Putative 2-enoyl thioester reductasea | ex | ex | ex | ex |  |  |  |
| GCV2 | Glycine decarboxylase P subunita | ex | ex | ex | ex |  |  |  |
| IDH1 | Isocitrate dehydrogenase subunita | -2.67 | -2.48 | -1.85 | -2.22 |  |  |  |
| IDH2 | Isocitrate dehydrogenasea | -3.21 | -2.88 | -3.54 | -3.37 |  |  |  |
| IDP1 | Putative isocitrate dehydrogenasea | ex | ex | ex | ex |  |  |  |
| ILV5 | Ketol-acid reductoisomeraseb | -3.68 | -2.62 | -2.27 | -5.48 |  |  |  |
| KGD2 | Putative dihydrolipoamide S-succinyltransferasea | ex | -2.20 | -2.04 | ex |  |  |  |
| LPD1 | Dihydrolipoamide dehydrogenase | ex | -7.49 | -4.08 | -7.91 |  |  |  |
| NIF3 | *S. cerevisiae* ortholog is Nif3, mitochondrial proteina | ex | ex | ex | ex |  |  |  |
| orf19.2966 | Predicted dienelactone hydrolase domaina | ex | ex | ex | ex |  |  |  |
| orf19.449 | Putative phosphatidyl synthaseb | ex | ex | ex | ex |  |  |  |
| orf19.7215.3 | *S. cerevisiae* ortholog is Hsp10, mitochondrial co-chaperonina | ex | ex | ex | ex |  |  |  |
| PDX3 | Pyridoxamine-phosphate oxidasea | ex | -1.85 | ex | ex |  |  |  |
| SOD2 | Superoxide dismutase | ex | ex | ex | ex |  |  |  |
| **Nucleus** | | | | | | | | |
| DOT5 | Thioredoxin peroxidasea | ex | ex | ex | ex |  |  |  |
| NHP6A | Non-histone chromosomal protein 6a | ex | ex | ex | ex |  |  |  |
| **Vacuole** | | | | | | | | |
| AMS1 | Putative alpha-mannosidasea | ex | ex | ex | -2.23 |  |  |  |
| APR1 | Vacuolar aspartic proteinase | -1.83 | ex | ex | -1.07 |  | Y |  |
| CPY1 | Carboxypeptidase Y | ex | ex | ex | -1.59 |  | Y |  |
| LAP41 | Putative aminopeptidase yscI precursor | ex | -3.96 | -1.80 | -2.64 |  |  |  |
| **Cell wall, cell surface, fungal biofilm matrix** | | | | | | | | |
| CPR3 | Putative peptidyl-prolyl cis-trans isomerase | ex | -2.59 | ex | ex |  |  |  |
| GCY1 | Glycerol 2-dehydrogenase | ex | ex | ex | ex |  |  |  |
| GLX3 | Glutathione-independent glyoxalase | ex | -6.21 | ex | -1.49 |  |  |  |
| GPM1 | Phosphoglycerate mutase | -6.84 | -4.93 | -3.80 | -2.78 |  |  |  |
| GRP2 | NAD(H)-linked methylglyoxal oxidoreductase | ex | -7.45 | -2.46 | -1.42 |  |  |  |
| HSP21 | Small heat shock protein | ex | -4.97 | ex | -2.24 |  |  |  |
| MET15 | O-acetylhomoserine O-acetylserine sulfhydrylase | ex | -2.91 | -2.00 | -2.72 |  |  |  |
| orf19.3053 | Protein of unknown function | ex | -4.71 | -2.35 | -3.02 |  |  |  |
| orf19.590 | Putative thiamine biosynthesis enzyme | ex | ex | ex | ex |  |  |  |
| PGI1 | Glucose-6-phosphate isomerase | -6.91 | -5.44 | -4.14 | -1.68 |  |  |  |
| PST2 | Flavodoxin-like protein | ex | ex | ex | -2.07 |  |  |  |
| RIB3 | 3,4-Dihydroxy-2-butanone 4-phosphate synthase | ex | -1.06 | -1.23 | -2.11 |  |  |  |
| **Proteasome** | | | | | | | | |
| orf19.2755 | *S. cerevisiae* ortholog is Pre7, Beta 6 subunit of 20S proteasomea | ex | -2.34 | ex | ex |  |  |  |
| orf19.4230 | 20S proteasome subunit (beta7)a | ex | ex | ex | ex |  |  |  |
| PUP2 | Alpha5 subunit of the 20S proteasome | ex | -4.13 | -2.53 | ex |  |  |  |
| SCL1 | Proteasome subunit YC7alphaa | ex | ex | ex | ex |  |  |  |
| **Cytoplasmic stress granule** | | | | | | | | |
| TIF11 | Translation initiation factor eIF1aa | ex | ex | ex | ex |  |  |  |
| TMA19 | *S. cerevisiae* ortholog is Tma19, ribosome associated proteina | ex | -3.05 | -2.74 | ex |  |  |  |
| **Peroxisome** | | | | | | | | |
| orf19.1433 | *S. cerevisiae* ortholog is Lpx1, peroxisomal lipasea | ex | ex | ex | ex |  |  |  |
| **Actin cortical patch** | | | | | | | | |
| ABP1 | Actin-binding protein | ex | -1.47 | ex | ex |  |  |  |
| **Unknown** | | | | | | | | |
| orf19.2125 | Protein of unknown functionc | ex | ex | ex | ex | 1 |  |  |
| orf19.2737 | Carbohydrate kinase domain-containing proteinc | ex | ex | ex | -1.48 |  |  |  |
| orf19.5620 | Stationary phase enriched proteinc | ex | ex | ex | -3.43 |  |  |  |
| OYE32 | NADPH oxidoreductase family proteinc | ex | ex | ex | -2.90 |  |  |  |

a Protein localisation was inferred from sequence similarity with S. cerevisiae homolog as annotated in the Candida Genome Database [48, 49].

b Protein localisation was obtained from the GO Cellular Component annotation in the C. albicans UniProt reference proteome UP000000559 [58].

c Protein and has no Cellular Component annotation in the Candida Genome Database or UniProt reference proteome.