|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | log2(fold change) EV vs WCL | | | |  |  |  |
| Name | Function | DAY Y | A9 | A1 | DAY B | TM | SP | VDM |
| **Plasma membrane** | | | | | | | | |
| ARF3 | Arf family GTPasea | ex | 1.69 | ex | 3.45 |  |  |  |
| CDC42 | Rho family GTPase | ex | ex | ex | ex |  |  |  |
| CDR1;CDR2 | Multidrug transporter of ABC superfamily | ex | ex | ex | 11.19 | 12;12 |  |  |
| CHS3 | Major chitin synthase of yeast and hyphae | ex | 4.12 | ex | ex | 5 |  |  |
| ENA21 | Predicted P-type ATPase sodium pumpa | ex | ex | ex | ex | 9 |  |  |
| FAA4 | Long-chain fatty acid-CoA ligasea | 2.89 | 2.24 | 2.28 | 1.45 |  |  |  |
| FET34 | Multicopper feroxidase | ex | ex | ex | 6.18 | 1 | Y |  |
| GAP4 | High-affinity S-adenosylmethionine permease | ex | ex | ex | 4.28 | 12 |  |  |
| GSC1 | 1,3-beta-glucan synthase | 2.57 | 3.45 | 5.97 | 8.01 | 15 |  |  |
| HGT1 | High-affinity MFS glucose transporter | ex | ex | ex | ex | 12 |  |  |
| HGT6 | Putative high-affinity MFS glucose transporter | 4.04 | 4.78 | 6.53 | 5.68 | 11 |  |  |
| HGT7 | Putative MFS glucose transporter | ex | 5.95 | ex | ex | 11 |  |  |
| MTS1 | Sphingolipid C9-methyltransferase | 2.20 | 1.86 | 1.41 | 2.13 | 2 |  |  |
| NCE102 | Non-classical protein export protein | 3.34 | 2.20 | ex | 5.32 | 4 |  |  |
| EVP1d | *S. cerevisiae* ortholog is Pun1, plasma membrane proteina | ex | ex | ex | ex | 3 |  | Y |
| PHM7 | Putative ion transporter | ex | ex | ex | ex | 11 |  |  |
| PMA1 | Plasma membrane ATPase | 5.65 | 4.38 | 5.60 | 6.46 | 8 |  |  |
| RAC1 | G-protein of RAC subfamily | ex | ex | ex | 3.92 |  |  |  |
| RHO1 | Rho family GTPase | 2.81 | 3.68 | 3.74 | 4.03 |  |  |  |
| RHO3 | Rho family GTPase | ex | ex | ex | ex |  |  |  |
| SSO2 | Plasma membrane t-SNAREa | ex | 1.88 | 3.57 | ex | 1 |  |  |
| SUR7 | Protein required for normal cell wall, plasma membranec | ex | ex | ex | 7.04 | 4 |  |  |
| YCK2 | *S. cerevisiae* ortholog is Yck2, casein kinase | ex | 4.42 | ex | ex |  |  |  |
| **Cell wall, cell surface** | | | | | | | | |
| BGL2 | 1,3-beta-glucanosyltransferase | 7.26 | 9.44 | 11.08 | ex |  | Y | Y |
| CRH11 | GPI-anchored cell wall transglycosylase | ex | ex | ex | ex |  | Y | Y |
| ECM33 | GPI-anchored cell wall protein | 4.39 | 5.28 | 8.31 | 7.03 |  | Y | Y |
| GPD2 | Glycerol-3-phosphate dehydrogenase | ex | 3.48 | 2.39 | 1.30 |  |  |  |
| MP65 | Cell surface mannoprotein | ex | ex | ex | ex |  | Y | Y |
| MSB2 | Mucin family adhesin-like protein | ex | ex | ex | ex | 1 | Y | Y |
| PGA4 | 1,3-beta-glucanosyltransferase | ex | ex | ex | ex |  | Y | Y |
| PGA52 | GPI-anchored cell surface protein of unknown function | ex | ex | ex | ex |  | Y | Y |
| PHR1 | Cell surface glycosidase | ex | ex | ex | 5.65 |  | Y |  |
| PHR2 | Glycosidase | ex | 3.51 | 6.44 | ex |  | Y | Y |
| PLB4.5 | Phospholipase B | ex | ex | ex | ex |  | Y | Y |
| SAP9 | Secreted aspartyl protease | ex | ex | ex | ex | 1 | Y | Y |
| YWP1 | Secreted yeast cell wall protein | 2.37 | 3.51 | 6.17 | ex |  | Y | Y |
| **Endoplasmic reticulum** | | | | | | | | |
| ERO1 | ER oxidoreductin | ex | ex | 2.32 | 1.68 |  | Y | Y |
| orf19.1054 | *S. cerevisiae* ortholog is Pom33, transmembrane nucleoporinb | 5.66 | ex | ex | 2.51 | 4 |  |  |
| orf19.2168.3 | *S. cerevisiae* ortholog is Yop1, reticulon-interacting proteina | 4.77 | 1.98 | 2.29 | 1.81 | 4 |  |  |
| orf19.3799 | *S. cerevisiae* ortholog is Rtn1, reticulon proteinb | 2.24 | 1.40 | 3.00 | 1.29 | 2 |  |  |
| SEC61 | ER protein-translocation complex subunit | 2.53 | 2.16 | 2.10 | 1.46 | 8 |  |  |
| **Endosome, Golgi, transport vesicle** | | | | | | | | |
| SEC4 | Rab family GTPasea | 1.88 | 1.20 | 1.86 | 2.90 |  |  |  |
| YKT6 | Palmitoyltransferase, putative vacuolar SNARE complex proteina | ex | 4.01 | 5.46 | 3.20 |  |  |  |
| YPT31 | Rab family GTPasea | ex | 1.57 | 1.33 | 3.33 |  |  |  |
| **Vacuole** | | | | | | | | |
| VAC8 | Protein involved in vacuolar inheritancea | 2.79 | ex | ex | 3.83 |  |  |  |
| **Mitochondrion** | | | | | | | | |
| MIR1 | Putative mitochondrial phosphate transportera | 3.68 | 4.38 | 4.24 | 1.60 |  |  |  |
| POR1 | Mitochondrial outer membrane porina | 3.44 | 2.51 | 3.69 | 1.38 |  |  |  |

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 Presence of transmembrane domains and absence of a signal peptide was predicted using TOPCONS2 [59].

d The name Evp1 for the protein encoded by orf19.6741 was proposed in the present study.