Supplementary Material for:

# Forward genetics in *Candida albicans* that reveals the Arp2/3 complex is required for hyphal formation, but not endocytosis

Elias Epp, Andrea Walther, Guylaine Lépine, Zully Leon, Alaka Mullick, Martine Raymond, Jürgen Wendland, Malcolm Whiteway

Supplementary Text:

## Assessing the efficiency of obtaining diploid homozygous UAU1 insertion mutants

Given that the efficiency of recovering auxotrophs, glycerol sensitive or hyphal deficient mutants was not that high (one in 300, one or two in about 4700, respectively), we assessed the frequency of obtaining homozygous diploid *orf::UAU1/orf::URA3* mutants by arbitrarily selecting 24 mutants from the pool of 4700 and using inverse PCR to identify the site of the transposon insertion. We found that in six of these 24 mutants the transposon had inserted directly in an open reading frame (ORF), in a further six the transposon had inserted in the promoter region (< 1 kb upstream of an ORF), in four transformants the insertion was less than 1 kb downstream of an ORF, while six transposons had inserted in a clear intergenic region (> 1 kb away from any ORF) and two insertions could not be mapped. One of the two unmapped insertions was flanked by an *E. coli* sequence, but how this transposon construct was inserted into the *C. albicans* genome along with *E. coli* coding sequence is unclear. The other unmapped insertion generated an unusually large, very faint band after inverse PCR that gave ambiguous sequence. We used *Mbo*I (restriction digestion site: GATC) to generate the inverse PCR template, so it is possible that this insertion falls in a region with infrequent *Mbo*I sites and thus was difficult to amplify.

Next, we checked the six ORF and the six promoter insertion mutants for aneuploidy. PCR analysis showed that in only one instance was the WT gene clearly missing (Figure S2E, left). Thus, while recombination of a transposon insertion into a gene or potential regulatory region is efficient, insertions that ultimately create a clean homozygous diploid *orf::UAU1/orf::URA3* mutant can be as low as one out of 24 after random selection.

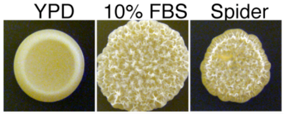
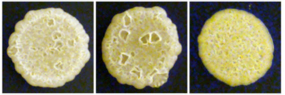
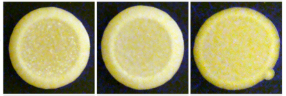
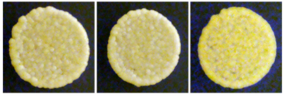
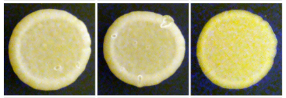
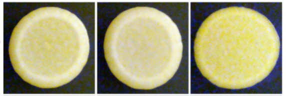
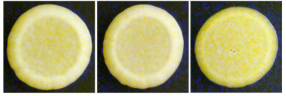
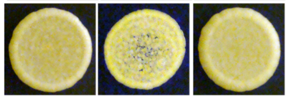
| mutant name | phenotype | systematic name | CGD description | site of insertion relative to start (insertion/ORF length) |
|---|---|---|---|---|
| | YPD 10% FBS Spider | | | |
| BWP17 |  | | WT | |
| *Tn::orf19.5984* |  | *orf19.5984* | uncharacterized | 657/1002 |
| *Tn::orf19.7227* |  | *orf19.7227* | mutation confers hypersensitivity to toxic ergosterol analog | 122/375 |
| *Tn::orf19.6868* |  | *orf19.6868* | uncharacterized | 585/1017 |
| *Tn::orf19.7212* |  | *orf19.7212* | uncharacterized | 1011/2304 |
| *Tn::orf19.2761* |  | *orf19.2761* | uncharacterized | 472/798 |
| *Tn::orf19.1300* |  | *orf19.1300* | uncharacterized | 953/1335 |
| *Tn::orf19.2397.3* |  | *orf19.2397.3* | uncharacterized | 153/1082 |
| *Tn::orf19.6719* |  | *orf19.6719* | uncharacterized | 3677/4796 |
| *Tn::orf19.860* |  | *orf19.860* | uncharacterized | -553/2085 |

**Figure S1. Potential hypo-filamentation phenotypes recovered from the screen**
Hyphal formation was assessed as described in Figure legend 1. The mutants listed here showed reduced wrinkle formation on Spider media, YPD + 10% FBS or on both, but all of these mutants could still form true hyphae under liquid inducing conditions (not shown). For each mutant, a description from CGD (www.candidagenome.org) and the site of insertion relative to the start codon of the coding sequence is given in the last column.

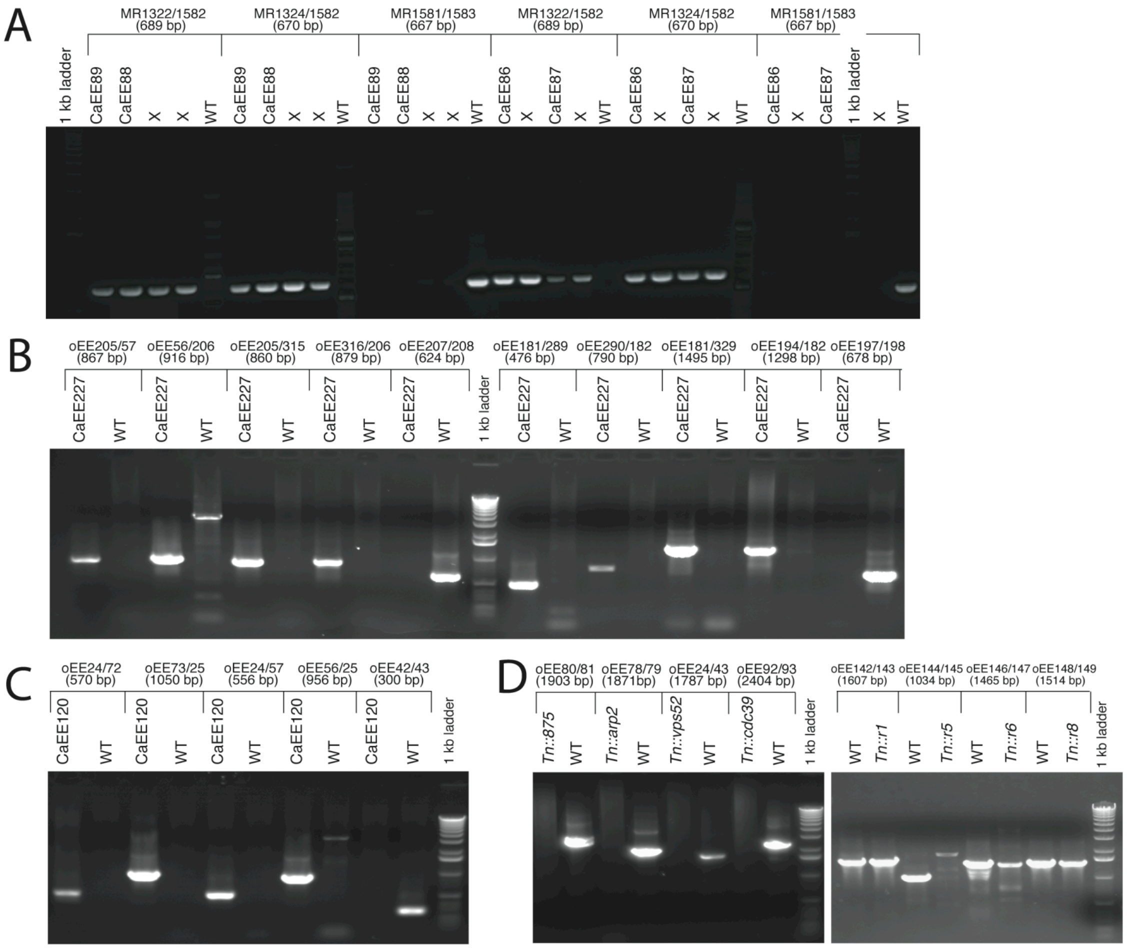


**Figure S2. PCR confirmation of mutant construction**

For each deletion mutant, genomic DNA was used to confirm correct integration of the marker cassettes as well as the absence of the WT gene after the second allele was knocked out. In each case, at least two different homozygous mutants were derived from two independently transformed heterozygotes to ascertain mutant phenotypes. Strain names are given above each picture (SN95 was used as WT, X represent additional mutants not further used), and primers as well as PCR product sizes (in brackets) are indicated. **A.** Deletion mutant construction for *orf19.875Δ/Δ*. **B.** Deletion mutant construction for *arp2Δ/Δ*. **C.** Deletion mutant construction for *arp2Δ/Δarp3Δ/Δ* double knock out. **D.** Deletion mutant construction for *vps52Δ/Δ*. **E.** Examples of PCR confirmation to verify the absence of the WT band in different *orf::UAU1/orf::URA3* insertion mutants. Genomic DNA isolated from a single colony was used in each case. PCR primers were designed so that they flank the site of initial UAU1 insertion by at least 300 bp. Note that this verification strategy could potentially be misleading in cases where the insertion has integrated at non-homologous locations. No WT band was detected in *Tn::875*, *Tn::arp2*, *Tn::vps52*, *Tn::cdc39* and *Tn::r5*, while a WT band was still present in mutants *Tn::r1*, *Tn::r6* and *Tn::r8*. The insertion mutant allele bands, which are roughly three kb larger than the WT band, were not amplified under the PCR conditions used. "*Tn::r*" refers to randomly chosen mutants (see supplementary text).

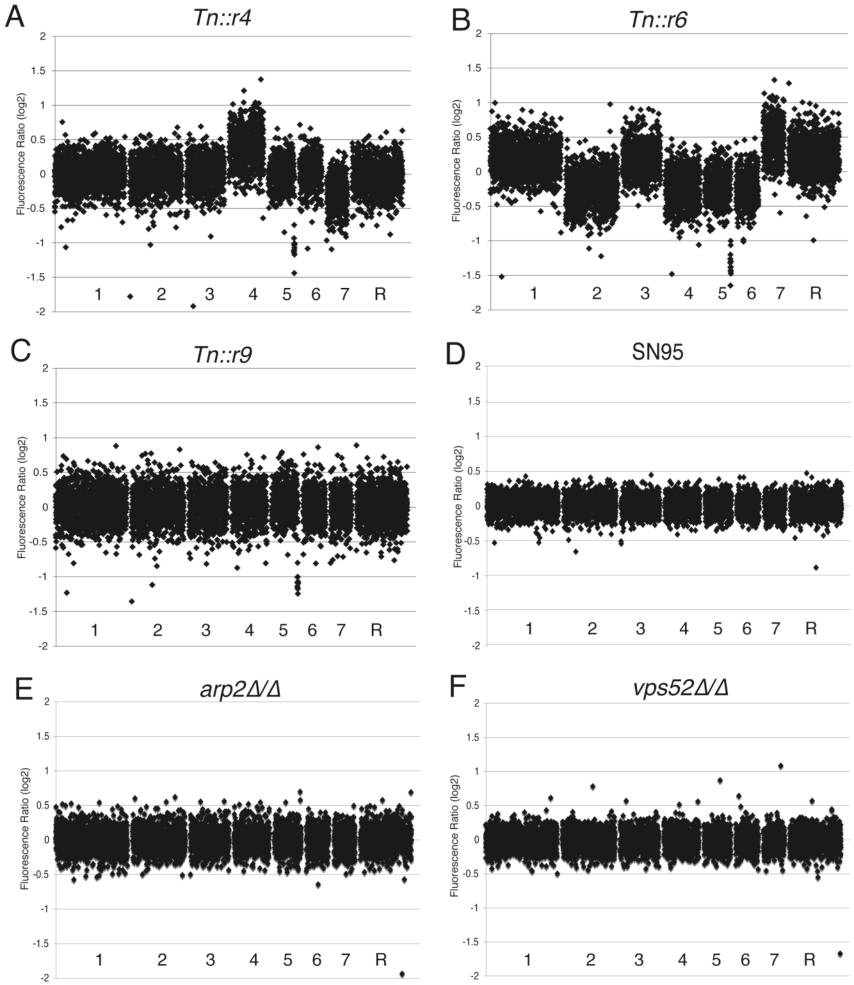


**Figure S3. The UAU1 system can introduce major chromosomal rearrangements**

Cy3 labeled genomic DNA from either three randomly chosen UAU1 mutants (*Tn::r4*, *Tn::r6* and *Tn::r9*) or from strain SN95 was hybridized to DNA microarrays with Cy5 labeled genomic DNA from the reference strain SC5314. Shown are plots of CGH (comparative genome hybridization) analyses, where the y-axis shows the log2 fluorescence ratio of the mutant strains versus SC5314 and the x-axis shows all chromosomes (1 to R). A single black rhombus represents the log2 fluorescence ratio plotted as a function of its position in the *C. albicans'* assembly 21. In this representation, a 1.5-fold increase in fluorescence ratio (i.e. three chromosome copies versus two) equals a log2 ratio of ~0.58. **A.** Mutant *Tn::r4* has at least one more copy of chromosome four and one copy less of chromosome seven compared to SC5314. The UAU1 cassette integrated on chromosome three. **B.** Mutant *Tn::r6* has acquired at least one copy each for chromosomes one, three, seven and R, while chromosomes two, four, five and six have lost at least one copy each. The UAU1 cassette integrated on chromosome R. **C - F.** No aneuploidy was detected in mutant *Tn::r9,* SN95 and the deletion mutants for *arp2Δ/Δ* and *vps52Δ/Δ*.

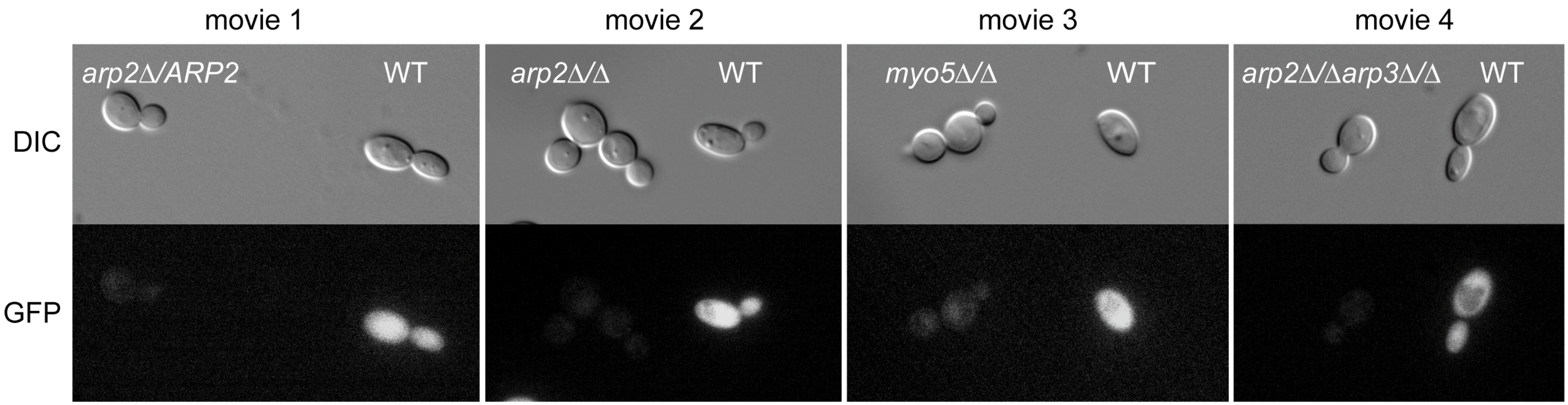


**Figure S4. Coincubation of mutant and WT strains during time-lapse analysis.** A GFP-labeled WT strain was coincubated with different mutant strains to simulate equal conditions for time-lapse analysis. The pictures shown here represent images taken at the beginning of time-lapse movies to distinguish between WT and mutant strains. Movie 1 shows the *arp2Δ/ARP2* heterozygous mutant and WT cells, movie 2 shows the *arp2Δ/Δ* deletion mutant and WT cells, movie 3 shows the *myo5Δ/Δ* deletion mutant and WT cells, and movie 4 shows the *arp2Δ/Δarp3Δ/Δ* double deletion mutant and WT cells. Movies can be found in the supplementary material.

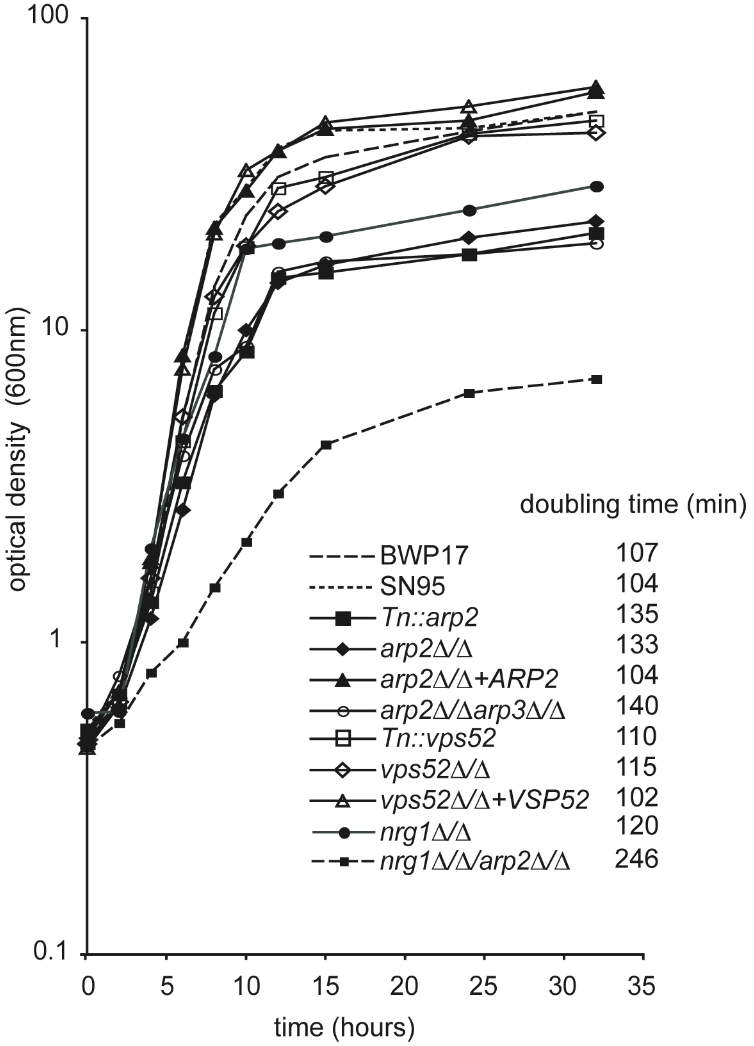


**Figure S5. Growth properties of *VSP52, NRG1* and Arp2/3 complex mutants.** To measure growth, an overnight culture of each strain was diluted to an OD$_{600}$ of 0.5 in YPD media and incubated at 30°C with constant shaking. OD$_{600}$ measurements were taken at indicated times. The doubling time was equal to ln2/[(ln(A/A$_0$)/t] where A is the OD$_{600}$ at time t (12 hours), A$_o$ is the initial OD$_{600}$ (2 hours) and t is the time (10 hours).

**Table S1.**
Pearson correlation of the entire *ARP2* microarray data set and the *MYO5/SLA2* microarray data sets.

| | sla2-H | myo5-H | arp2-H | sla2-Y | myo5-Y | arp2-Y | sla2-HY | myo5-HY | arp2-HY | HY-(Oberholzer) |
|---|---|---|---|---|---|---|---|---|---|---|
| WT-HY (Epp) | 0.126 | 0.067 | -0.112 | 0.213 | 0.152 | 0.246 | 0.578 | 0.308 | 0.273 | 0.631 |
| WT-HY (Oberholzer) | 0.080 | 0.008 | -0.058 | 0.081 | 0.094 | 0.071 | 0.813 | 0.400 | 0.266 | |
| arp2-HY | -0.070 | -0.132 | 0.146 | -0.069 | -0.088 | -0.247 | 0.230 | 0.143 | | |
| myo5-HY | 0.069 | 0.020 | -0.147 | 0.061 | 0.008 | 0.025 | 0.498 | | | |
| sla2-HY | 0.239 | 0.178 | -0.010 | 0.162 | 0.171 | 0.114 | | | | |
| arp2-Y | 0.584 | 0.667 | 0.345 | 0.597 | 0.693 | | | | | |
| myo5- Y | 0.812 | 0.721 | 0.404 | 0.666 | | | | | | |
| sla2-Y | 0.559 | 0.734 | 0.358 | | | | | | | |
| arp2-H | 0.397 | 0.470 | | | | | | | | |
| myo5-H | 0.627 | | | | | | | | | |

The values reported here were used to visualize Figure 5A using TreeView version 1.6 (http://rana.lbl.gov/EisenSoftware.htm).

**Table S2.**
Hyphae specific genes.

Hyphae specific genes are color coded:
Red indicates transcript levels > 4.0; orange indicates transcript levels < 4.0 and > 1.5;
pale green indicates transcript levels < 0.7 and > 0.3; dark green indicates < 0.5

| Systematic name | Description | Common name | WT-HY (Epp) | WT-HY (Oberholzer) | arp2-HY | myo5-HY | sla2-HY | arp2-Y | myo5-Y | sla2-Y | arp2-H | myo5-H | sla2-H |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| orf19.1816 | agglutinin-like protein | ALS3-1 | 31.1 | | 1.8 | | | 1.0 | | | 0.0 | | |
| orf19.3374 | secreted cell elongation protein | ECE1 | 30.4 | 81.2 | 6.2 | 3.3 | 18.9 | 1.0 | 1.1 | 1.0 | 0.2 | 0.2 | 0.7 |
| orf19.4082 | flocculent specific protein;contains NNDDNSYG motif | DDR48 | 26.7 | 4.4 | 0.9 | 0.7 | 1.6 | 29.5 | 6.1 | 6.1 | 1.1 | 3.7 | 3.0 |
| orf19.5760 | Induced in Hyphal Development;membrane protein | IHD1 | 24.4 | 10.6 | 2.5 | 5.6 | 5.0 | 0.9 | 0.3 | 0.7 | 0.1 | 0.5 | 0.6 |
| orf19.4975 | hyphally regulated protein | HYR1 | 20.2 | 1.3 | 1.6 | 1.0 | 1.1 | 1.0 | 1.2 | 1.0 | 0.1 | 0.9 | 1.0 |
| orf19.5636 | repressed by TUP1 protein 5 | RBT5 | 19.9 | | 0.6 | | | 3.9 | | | 0.5 | | |
| orf19.1327 | repressed by Tup1, related to HWP1 | RBT1* | 17.2 | | 7.4 | | | 1.3 | | | 0.6 | | |
| orf19.5585 | secreted aspartyl proteinase 5 | SAP5 | 17.2 | 19.1 | 1.2 | 1.5 | 3.1 | 1.0 | 1.3 | 1.1 | 0.1 | 0.7 | 1.5 |
| orf19.1321 | hyphal wall protein | HWP1* | 16.4 | 25.6 | 3.5 | 9.5 | 9.1 | 1.5 | 0.9 | 0.8 | 0.5 | 0.6 | 1.5 |
| orf19.4215 | multicopper ferro-O2-oxidoreductase involved in high-affinity iron uptake | FET35* | 13.7 | | 4.0 | | | 2.5 | | | 0.3 | | |
| orf19.5674 | glycosyl-phosphatidylinositol protein;similar to RBT5 | RBT8* | 12.0 | 13.8 | 1.2 | 2.5 | 9.2 | 0.8 | 0.8 | 1.0 | 0.1 | 1.4 | 0.8 |
| orf19.251 | conserved hypothetical protein | - | 11.7 | 4.8 | 3.0 | 1.1 | 2.2 | 5.7 | 2.7 | 2.4 | 1.6 | 1.7 | 3.3 |
| orf19.2355 | | | 9.4 | | 1.3 | | | 1.2 | | | 0.1 | | |
| orf19.4943 | mannose-1-phosphate guanyltransferase | PSA2* | 9.0 | 2.0 | 3.0 | 1.9 | 1.2 | 1.8 | 1.0 | 1.0 | 0.3 | 1.0 | 1.3 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| orf19.3829 | pH regulated GPI-anchored membrane protein that is required for morphogenesis | PHR1 | 8.9 | 5.0 | 0.9 | 3.8 | 2.6 | 3.1 | 2.0 | 5.5 | 0.6 | 1.1 | 2.4 |
| orf19.2210 | hypothetical protein | - | 8.6 | 1.4 | 1.0 | 1.2 | 1.1 | 1.3 | 1.1 | 1.3 | 0.3 | 1.0 | 1.1 |
| orf19.4980 | heat shock protein 70 | HSP70* | 8.5 | 1.5 | 1.4 | 1.2 | 1.5 | 2.6 | 1.2 | 0.9 | 0.3 | 1.2 | 1.1 |
| orf19.5542 | candidapepsin 6 precursor | SAP6 | 8.0 | 3.7 | 1.5 | 1.5 | 1.5 | 0.7 | 1.3 | 1.4 | 0.2 | 0.7 | 1.2 |
| orf19.4527 | hexose transporter | HGT1 | 8.0 | 4.6 | 2.2 | 2.1 | 3.3 | 1.2 | 1.2 | 1.1 | 0.4 | 0.9 | 1.0 |
| orf19.1691 | conserved hypothetical protein | - | 7.2 | 3.9 | 3.9 | 1.2 | 1.3 | 0.8 | 0.7 | 1.0 | 0.1 | 0.5 | 0.6 |
| orf19.5265 | kinesin heavy chain homolog | KIP4* | 6.7 | 1.3 | 1.8 | 1.2 | 1.2 | 1.4 | 1.0 | 1.0 | 0.3 | 1.0 | 1.0 |
| orf19.7610 | protein tyrosine phosphatase | PTP3* | 6.6 | 1.7 | 1.7 | 2.1 | 1.5 | 2.3 | 1.0 | 1.2 | 0.6 | 1.1 | 1.0 |
| orf19.716 | similar to pore-forming bacterial Septicolysin | - | 5.8 | 1.1 | 1.7 | 1.1 | 1.0 | 1.2 | 1.0 | 1.1 | 0.6 | 0.9 | 1.0 |
| orf19.2241 | 1,4-benzoquinone reductase;brefeldin A resistance protein;Protoplast-SecreTed protein | PST1* | 5.8 | 1.2 | 1.6 | 1.0 | 1.0 | 1.3 | 1.6 | 1.7 | 0.5 | 1.0 | 1.0 |
| orf19.113 | closely related to cadmium-induced protein CIP1 | CIP1* | 5.8 | 1.2 | 1.2 | 0.9 | 1.0 | 1.0 | 1.1 | 1.1 | 0.4 | 0.8 | 1.1 |
| orf19.3384 | | | 5.7 | 3.0 | 1.1 | 1.5 | 1.5 | 1.2 | 1.4 | 1.1 | 0.6 | 0.6 | 1.1 |
| orf19.6202 | pathogenesis related protein, repressed by TUP1 protein 4 | PRY4* | 5.3 | 5.6 | 0.4 | 1.4 | 2.0 | 14.5 | 6.3 | 1.2 | 1.3 | 1.4 | 4.3 |
| orf19.85 | glutathione peroxidase | GPX1* | 4.9 | 3.6 | 1.7 | 1.1 | 1.8 | 0.3 | 0.9 | 0.6 | 0.1 | 0.3 | 0.7 |
| orf19.815 | DOCK180 protein | - | 4.6 | 2.1 | 2.6 | 1.4 | 1.7 | 1.3 | 1.0 | 1.0 | 0.3 | 0.9 | 1.0 |
| orf19.1996 | catabolic serine/threonine dehydratase | CHA2* | 4.5 | 3.1 | 1.3 | 1.4 | 2.0 | 2.5 | 2.9 | 2.4 | 1.6 | 1.8 | 2.7 |
| orf19.2952 | exo-1,3-beta-glucanase | EXG1* | 4.4 | 1.3 | 2.3 | 1.3 | 1.4 | 1.4 | 1.2 | 1.5 | 0.8 | 1.1 | 1.5 |
| orf19.5645 | O-acetylhomoserine sulfhydrylase | MET15 | 4.4 | | 0.4 | | | 1.1 | | | 0.2 | | |
| orf19.2125 | hypothetical protein | - | 4.3 | 2.9 | 0.9 | 0.8 | 1.4 | 19.9 | 17.9 | 6.4 | 3.9 | 5.1 | 6.7 |
| orf19.4477 | aryl-alcohol dehydrogenase | IFD4* | 4.1 | | 1.5 | | | 8.0 | | | 4.2 | | |
| orf19.7531 | conserved hypothetical protein | - | 4.1 | 1.9 | 1.3 | 1.9 | 2.0 | 1.8 | 1.9 | 1.7 | 1.0 | 1.7 | 1.8 |
| orf19.4590 | similar to DNA-binding protein but may be missing DNA-binding domain | RFX1* | 4.0 | 1.2 | 1.3 | 1.0 | 1.0 | 1.4 | 1.0 | 1.0 | 0.4 | 0.9 | 1.0 |
| orf19.6608 | transposase | - | 4.0 | 2.4 | 1.4 | 2.4 | 1.8 | 2.0 | 0.9 | 1.3 | 0.7 | 0.9 | 0.7 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| orf19.4530.1 | hypothetical protein | - | 4.0 | 1.0 | 1.6 | 1.0 | 1.1 | 1.2 | 1.3 | 1.2 | 0.4 | 1.0 | 1.1 |
| orf19.2959.1 | conserved hypothetical protein | - | 3.9 | | 1.1 | | | 4.1 | | | 6.0 | | |
| orf19.7323 | corticosteroid- binding protein | CBP1 | 3.9 | | 3.6 | | | 0.6 | | | 0.4 | | |
| orf19.675 | hypothetical protein | - | 3.9 | 4.8 | 0.2 | 1.1 | 2.4 | 23.9 | 7.1 | 1.7 | 2.8 | 3.9 | 7.1 |
| orf19.7053 | regulatory subunit for phosphoprotein phosphatase type 1 (PP-1) | GAC1* | 3.9 | | 1 .1 | | | 1.4 | | | 0.4 | | |
| orf19.4749 | hypothetical membrane protein | - | 3.8 | 1.7 | 2.2 | 1.1 | 1.1 | 0.8 | 1.3 | 1.3 | 0.6 | 1.0 | 0.9 |
| orf19.6420 | hypothetical membrane protein with repeated hydrophobic/hydrophilic domains | - | 3.8 | 4.2 | 0.4 | 3.2 | 2.5 | 7.5 | 1.8 | 1.3 | 1.3 | 1.6 | 6.5 |
| orf19.6287 | aspartate aminotransferase | AAT2* | 3.8 | 1.2 | 1.5 | 1.0 | 1.3 | 1.0 | 1.1 | 1.1 | 0.5 | 1.5 | 1.4 |
| orf19.1799 | general amino acid permease | GAP6* | 3.7 | 1.0 | 1.3 | 1.0 | 1.1 | 0.9 | 1.1 | 1.1 | 0.5 | 0.9 | 1.0 |
| orf19.1655 | fatty-acyl coenzyme A oxidase | POX3* | 3.7 | 1.0 | 0.7 | 1.0 | 1.0 | 1.5 | 1.2 | 0.9 | 0.5 | 0.9 | 1.0 |
| orf19.5614 | ribonuclease H | RNH2* | 3.6 | 2.0 | 1.3 | 1.2 | 2.4 | 6.5 | 4.0 | 1.5 | 1.5 | 2.7 | 2.8 |
| orf19.3746 | oligopeptide transporter protein | OPT2 | 3.5 | 1.2 | 0.9 | 1.0 | 1.0 | 1.1 | 0.9 | 1.0 | 0.4 | 1.0 | 0.9 |
| orf19.6705 | conserved hypothetical protein | - | 3.5 | 1.8 | 1.3 | 1.4 | 1.6 | 1.2 | 0.8 | 1.0 | 0.4 | 0.8 | 0.8 |
| orf19.7362 | glucan synthase subunit involved in cell wall assembly | SKN1 | 3.4 | 2.3 | 2.2 | 1.7 | 2.5 | 1.0 | 1.6 | 2.0 | 1.2 | 1.3 | 2.2 |
| orf19.2372 | | | 3.3 | 1.3 | 1.8 | 1.6 | 1.3 | 0.9 | 0.8 | 1.1 | 0.3 | 1.0 | 0.5 |
| orf19.5373 | | | 3.3 | 1.8 | 2.1 | 1.6 | 1.4 | 0.9 | 0.6 | 0.8 | 0.3 | 0.7 | 0.5 |
| orf19.7304 | hypothetical protein | - | 3.3 | 2.9 | 2.4 | 1.7 | 2.5 | 0.8 | 1.0 | 0.9 | 0.9 | 1.2 | 1.2 |
| orf19.6021 | Induced in Hyphal Development | IHD2 | 3.3 | 1.3 | 1.2 | 1.1 | 1.1 | 1.3 | 1.6 | 1.1 | 0.8 | 1.1 | 1.1 |
| orf19.7504 | conserved hypothetical protein | - | 3.2 | 2.1 | 0.8 | 1.1 | 1.4 | 3.9 | 3.0 | 1.7 | 1.3 | 1.4 | 2.4 |
| orf19.715 | hypothetical protein | - | 3.2 | 1.2 | 1.9 | 0.9 | 1.0 | 1.5 | 0.9 | 1.0 | 2.1 | 0.7 | 1.1 |
| orf19.5025 | ATP sulfurylase, Amino acid metabolism | MET3* | 3.2 | 1.3 | 1.2 | 0.9 | 1.0 | 0.5 | 1.0 | 1.0 | 0.2 | 0.9 | 0.8 |
| orf19.7214 | glucan 1,3-beta-glucosidase | - | 3.1 | 1.9 | 1.3 | 0.9 | 1.6 | 2.9 | 2.8 | 2.7 | 1.8 | 2.3 | 3.9 |
| orf19.682 | | | 3.1 | 1.0 | 0.6 | 1.0 | 1.1 | 2.3 | 1.0 | 1.0 | 0.6 | 1.2 | 1.0 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| orf19.6079 | hypothetical protein | - | 3.0 | | 1.1 | | | 1.0 | 1.0 | 1.0 | 0.8 | 1.2 | |
| orf19.6601.1 | non-native actin binding complex polypeptide | YKE2* | 3.0 | 0.9 | 2.0 | 1.0 | 1.2 | 1.3 | 1.2 | 1.0 | 1.6 | 1.0 | 1.1 |
| orf19.2685 | hypothetical protein | - | 2.9 | 1.7 | 0.6 | 1.1 | 1.5 | 3.8 | 1.9 | 1.6 | 0.7 | 1.5 | 1.8 |
| orf19.7350 | highly charged conserved protein of unknown function | - | 2.9 | 2.0 | 1.1 | 1.1 | 0.9 | 1.9 | 6.7 | 1.7 | 0.6 | 2.5 | 1.9 |
| orf19.7219 | plasma membrane iron permease | FTR1 | 2.9 | 2.3 | 2.4 | 1.2 | 3.8 | 1.9 | 2.3 | 1.2 | 0.7 | 1.8 | 1.2 |
| orf19.4056 | GATA-family DNA binding proteins | - | 2.9 | 2.5 | 0.8 | 2.1 | 1.2 | 4.4 | 1.0 | 1.0 | 0.5 | 1.0 | 0.8 |
| orf19.5615 | 1-acyl dihydroxyacetone phosphate reductase | AYR1* | 2.8 | 1.6 | 1.7 | 1.0 | 1.2 | 0.8 | 1.1 | 1.0 | 0.6 | 1.0 | 1.0 |
| orf19.5619 | hypothetical protein | - | 2.8 | 1.6 | 0.6 | 1.5 | 1.3 | 1.9 | 1.5 | 1.0 | 0.6 | 1.2 | 1.2 |
| orf19.1690 | conserved hypothetical protein | TOS1* | 2.8 | 1.4 | 0.6 | 1.2 | 1.1 | 2.8 | 1.4 | 1.1 | 0.6 | 1.2 | 1.3 |
| orf19.2947 | stationary phase protein | SNZ1* | 2.8 | 2.7 | 1.6 | 1.9 | 1.2 | 0.7 | 0.6 | 1.3 | 0.4 | 0.8 | 1.4 |
| orf19.6741 | conseved hypothetical protein | - | 2.8 | 1.3 | 1.8 | 1.3 | 1.1 | 0.9 | 1.5 | 1.4 | 0.7 | 1.3 | 1.2 |
| orf19.13 | | | 2.7 | 3.9 | 2.1 | 0.9 | 1.4 | 0.6 | 1.4 | 1.1 | 0.2 | 0.9 | 0.8 |
| orf19.413 | hypothetical protein | - | 2.7 | 2.1 | 1.6 | 2.3 | 1.7 | 1.0 | 1.4 | 1.0 | 0.6 | 1.1 | 1.0 |
| orf19.7324 | pyrimidine precursor biosynthesis enzyme | THI13* | 2.6 | 1.1 | 1.4 | 1.1 | 1.0 | 1.0 | 1.1 | 1.5 | 0.7 | 1.3 | 1.1 |
| orf19.2292 | | | 2.6 | | 1.2 | | | 0.8 | | | 0.2 | | |
| orf19.2886 | MAP kinase involved in pheromone signal transduction | CEK1 | 2.6 | 1.3 | 1.1 | 1.0 | 1.0 | 3.7 | 1.4 | 2.4 | 1.8 | 1.8 | 1.4 |
| orf19.2903 | conserved hypothetical protein | - | 2.5 | 1.7 | 1.0 | 0.9 | 1.3 | 1.8 | 1.5 | 1.2 | 0.6 | 1.2 | 1.0 |
| orf19.3219 | phosphohydrolase | - | 2.5 | 1.0 | 1.7 | 1.1 | 0.9 | 1.1 | 0.6 | 1.0 | 0.8 | 0.8 | 0.9 |
| orf19.3483 | possible glycerophosphoryl phosphodiesterase | - | 2.5 | 1.3 | 2.0 | 1.2 | 1.4 | 2.1 | 1.2 | 1.0 | 2.0 | 1.1 | 1.3 |
| orf19.1964 | conserved hypothetical protein | - | 2.5 | 1.8 | 0.8 | 1.5 | 1.7 | 0.7 | 0.4 | 0.9 | 0.2 | 0.8 | 0.8 |
| orf19.1408 | | | 2.5 | 3.9 | 2.2 | 0.9 | 1.4 | 0.6 | 1.4 | 1.1 | 0.2 | 0.8 | 0.8 |
| orf19.1654 | hypothetical protein | - | 2.5 | 1.5 | 1.5 | 1.1 | 1.2 | 1.0 | 1.0 | 1.1 | 0.4 | 0.9 | 1.3 |
| orf19.6028 | G1 cyclin | HGC1 | 2.4 | 1.3 | 0.9 | 1.1 | 1.1 | 1.1 | 1.0 | 1.1 | 0.4 | 0.9 | 1.0 |
| orf19.7308 | alpha-1 tubulin | TUB1 | 2.4 | 1.6 | 0.5 | 1.2 | 1.1 | 1.3 | 1.0 | 1.4 | 0.3 | 1.3 | 1.1 |
| orf19.2777 | | | 2.4 | | 0.5 | | | 2.1 | | | 0.3 | | |
| orf19.1652 | fatty-acyl coenzyme A oxidase | POX1* | 2.3 | 1.0 | 0.8 | 0.7 | 1.0 | 2.1 | 1.1 | 1.2 | 0.5 | 1.1 | 1.1 |
| orf19.4607 | conserved hypothetical | - | 2.3 | 0.9 | 1.5 | 0.9 | 1.0 | 1.6 | 1.2 | 1.1 | 0.9 | 1.0 | 1.0 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | protein | | | | | | | | | | | | |
| orf19.7583 | potential fungal Zn(2)-Cys(6) binuclear cluster domain | - | 2.3 | 1.0 | 1.6 | 1.0 | 1.0 | 1.9 | 1.5 | 1.2 | 0.8 | 1.1 | 1.0 |
| orf19.6116 | aldohexose specific glucokinase | GLK4* | 2.3 | 2.0 | 2.4 | 0.9 | 1.2 | 0.6 | 1.2 | 1.1 | 0.2 | 0.7 | 0.9 |
| orf19.2762 | alkyl hydroperoxide reductase | AHP1* | 2.3 | 1.5 | 1.5 | 1.1 | 1.2 | 1.0 | 1.1 | 1.2 | 0.6 | 0.8 | 1.1 |
| orf19.7021 | glycogen phosphorylase | GPH1* | 2.3 | 4.6 | 2.0 | 1.5 | 1.9 | 1.6 | 1.6 | 1.1 | 0.6 | 1.0 | 1.2 |
| orf19.4033 | RNA-dependent ATPase | PRP22* | 2.3 | 1.0 | 0.7 | 1.1 | 1.0 | 1.0 | 0.8 | 1.0 | 0.3 | 0.9 | 1.0 |
| orf19.1153 | glutamate decarboxylase | GAD1* | 2.3 | 1.7 | 1.1 | 1.3 | 1.2 | 1.9 | 1.2 | 1.3 | 0.6 | 1.2 | 1.2 |
| orf19.467 | hypothetical protein | - | 2.3 | 1.5 | 1.0 | 1.4 | 0.9 | 1.1 | 0.9 | 0.9 | 0.6 | 0.9 | 0.8 |
| orf19.4263 | hypothetical protein | - | 2.2 | | 1.4 | | | 1.3 | | | 0.8 | | |
| orf19.1847 | pyruvate decarboxylase | ARO10* | 2.2 | 3.5 | 2.3 | 1.2 | 2.0 | 0.6 | 1.6 | 1.5 | 1.1 | 1.2 | 1.2 |
| orf19.7657 | RNase P and RNase MRP subunit | POP3* | 2.2 | 0.9 | 1.1 | 1.0 | 0.9 | 1.0 | 0.9 | 0.9 | 0.7 | 0.8 | 0.9 |
| orf19.3150 | similar to plant dihydroflavonol 4-reductase | GRP4* | 2.2 | 2.0 | 1.3 | 0.8 | 1.2 | 1.3 | 1.8 | 1.1 | 0.9 | 1.0 | 1.8 |
| orf19.5799 | conserved hypotheticalprotein | - | 2.2 | 1.6 | 0.5 | 1.1 | 1.8 | 3.4 | 2.9 | 2.5 | 1.2 | 1.8 | 5.1 |
| orf19.4349.6 | | | 2.2 | | 1.1 | | | 1.4 | | | 1.3 | | |
| orf19.6402 | cystathionine gamma-lyase | CYS3* | 2.2 | 1.1 | 0.9 | 0.9 | 1.3 | 1.1 | 1.0 | 0.9 | 0.3 | 1.1 | 1.2 |
| orf19.1592 | conserved hypothetical protein | - | 2.2 | | 1.1 | | | 1.0 | | | 0.5 | | |
| orf19.5620 | conserved hypothetical protein | - | 2.1 | 2.0 | 2.2 | 0.9 | 1.0 | 0.5 | 1.0 | 1.1 | 0.7 | 0.9 | 1.0 |
| orf19.1995 | alpha-1,2-mannosyltransferase | MNN5* | 2.1 | 1.2 | 1.4 | 1.0 | 1.1 | 1.2 | 1.1 | 1.0 | 1.3 | 1.2 | 1.2 |
| orf19.7635 | ATP dependent RNA helicase | DRS1* | 2.1 | 1.0 | 1.2 | 1.1 | 1.0 | 1.4 | 0.9 | 1.0 | 0.9 | 1.0 | 1.0 |
| orf19.5451 | hypothetical protein | - | 2.1 | | 1.4 | | | 1.3 | | | 0.9 | | |
| orf19.3013 | septin | CDC12 | 2.1 | 1.1 | 1.3 | 1.0 | 1.2 | 1.9 | 1.3 | 1.1 | 1.0 | 1.2 | 1.1 |
| orf19.2721 | highly conserved hypothetical protein | CDC123* | 2.1 | 1.0 | 1.5 | 1.0 | 1.0 | 0.7 | 1.0 | 1.0 | 1.0 | 1.1 | 1.0 |
| orf19.4433 | transcription factor modulated by MAP kinase cascade and involved in filamantous growth;homolog of budding yeast Ste12p | CPH1 | 2.1 | 0.8 | 0.8 | 1.2 | 0.8 | 1.3 | 0.8 | 0.9 | 0.6 | 0.8 | 0.8 |
| orf19.4649 | zinc finger transcription | - | 2.1 | 0.9 | 1.3 | 1.0 | 1.0 | 1.1 | 1.0 | 1.0 | 0.8 | 1.0 | 1.0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | factor | | | | | | | | | | | | |
| orf19.6073 | heme binding protein | HMX1* | 2.1 | 1.1 | 1.3 | 0.8 | 1.1 | 1.2 | 1.2 | 1.1 | 1.1 | 1.1 | 1.2 |
| orf19.4666 | hypothetical protein | - | 2.1 | 1.7 | 1.1 | 1.5 | 1.7 | 1.9 | 2.3 | 1.4 | 1.4 | 2.0 | 1.7 |
| orf19.3941 | CTP synthase | URA7* | 2.0 | 0.9 | 1.4 | 1.3 | 1.5 | 1.1 | 0.8 | 1.0 | 0.5 | 1.1 | 1.0 |
| orf19.156 | hypothetical protein | - | 2.0 | | 2.2 | | | 1.2 | | | 1.2 | | |
| orf19.2346 | highly conserved hypothetical protein | - | 2.0 | 1.0 | 1.3 | 1.0 | 1.0 | 1.4 | 0.9 | 1.0 | 1.0 | 1.0 | 1.1 |
| orf19.3984 | conserved hypothetical protein | - | 2.0 | | 0.9 | | | 1.8 | | | 1.4 | | |
| orf19.6864 | conserved hypothetical protein | - | 2.0 | 1.2 | 1.2 | 0.9 | 1.0 | 1.7 | 1.8 | 1.1 | 1.4 | 1.0 | 1.3 |
| orf19.6724 | mitochondrial fumarate hydratase, 5-prime end | FUM2* | 0.5 | | 2.0 | | | 0.6 | | | 0.6 | | |
| orf19.4318 | transcriptional regulator | MIG1 | 0.5 | 1.0 | 0.9 | 1.1 | 1.1 | 1.1 | 1.0 | 0.9 | 0.9 | 0.8 | 0.9 |
| orf19.868 | putative adenosine deaminase;transcriptional regulation | - | 0.5 | 1.2 | 0.7 | 0.9 | 0.8 | 1.3 | 1.3 | | 1.4 | 1.2 | 1.3 |
| orf19.1067 | phosphoglycerate mutase | GPM2* | 0.5 | 1.0 | 2.2 | 1.0 | 0.9 | 0.6 | 1.0 | 1.0 | 1.1 | 0.7 | 0.9 |
| orf19.4167 | hypothetical protein | - | 0.5 | | 1.2 | | | 0.4 | | | 1.1 | | |
| orf19.1776 | pantotheine-phosphate adenylyltransferase | - | 0.5 | 0.9 | 1.1 | 0.9 | 1.0 | 0.5 | 0.8 | 0.9 | 1.4 | 1.0 | 0.9 |
| orf19.4577.3 | involved in import of mitochondrial protein | TIM10* | 0.5 | 1.1 | 0.9 | 0.8 | 1.0 | 0.7 | 1.0 | 1.1 | 1.9 | 0.8 | 1.1 |
| orf19.2116 | N-acetyltransferase for N-terminal methionine | NAT2* | 0.5 | 1.0 | 0.5 | 1.1 | 1.3 | 1.0 | 1.2 | 1.0 | 0.6 | 1.5 | 1.2 |
| orf19.7498 | 3-isopropylmalate dehydratase | LEU1* | 0.5 | 1.0 | 0.4 | 0.8 | 0.6 | 0.9 | 0.7 | 0.9 | 0.6 | 0.8 | 0.7 |
| orf19.6645 | high mobility group-like protein | HMO1* | 0.5 | 0.6 | 0.6 | 0.7 | 0.7 | 1.0 | 1.1 | 1.0 | 1.0 | 1.1 | 0.7 |
| orf19.4676 | conserved hypothetical protein | - | 0.5 | 0.7 | 1.1 | 0.9 | 0.8 | 0.5 | 0.8 | 1.0 | 1.3 | 0.9 | 0.9 |
| orf19.5911 | Ca2+/calmodulin-dependent protein kinase | CMK1* | 0.5 | 0.9 | 0.8 | 1.0 | 0.8 | 1.0 | 1.1 | 0.9 | 0.5 | 0.7 | 0.6 |
| orf19.1857 | histone acetyltransferase and transcription regulatory protein | SPT11* | 0.5 | 0.9 | 1.2 | 0.6 | 0.7 | 0.6 | 1.2 | 1.3 | 1.4 | 0.9 | 1.2 |
| orf19.3893 | Soluble Cell Wall protein | SCW11* | 0.5 | | 1.4 | | | 0.9 | | | 1.7 | | |
| orf19.3526 | myo-inositol transporter | ITR2* | 0.5 | 0.7 | 0.6 | 0.7 | 0.9 | 1.2 | 0.8 | 0.9 | 1.0 | 1.0 | 1.0 |
| orf19.4444 | 4-nitrophenyl phosphatase | PHO15* | 0.5 | 1.5 | 1.2 | 1.1 | 0.9 | 0.7 | 1.0 | 1.0 | 0.9 | 0.9 | 1.0 |
| orf19.2655 | cell cycle arrest protein | BUB3* | 0.5 | 1.3 | 2.1 | 1.0 | 1.1 | 0.5 | 0.6 | 1.0 | 0.7 | 1.0 | 0.9 |
| orf19.1485 | mitochondrial ribosomal | MRPL31* | 0.5 | 0.7 | 1.4 | 0.8 | 0.6 | 0.4 | 0.8 | 0.9 | 2.2 | 0.9 | 0.7 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | protein | | | | | | | | | | | |
| orf19.4952.1 | FK506-binding protein 2 precursor | FKB2* | 0.5 | 1.0 | 1.1 | 0.7 | 0.8 | 0.5 | 1.2 | 1.0 | 1.8 | 0.9 | 1.2 |
| orf19.2896 | peroxisomal 2,4- dienoyl-CoA reductase, and sorbitol utilization protein | SOU1* | 0.4 | 0.9 | 0.6 | 0.5 | 0.7 | 1.4 | 2.7 | 0.9 | 3.2 | 1.1 | 1.8 |
| orf19.5228 | 3,4-dihydroxy-2-butanone 4- phosphate synthase, riboflavin biosynthesis | RIB3* | 0.4 | 1.2 | 1.3 | 0.9 | 0.7 | 0.6 | 0.8 | 0.9 | 0.7 | 0.7 | 0.8 |
| orf19.1340 | aldose reductase | - | 0.4 | 0.9 | 1.0 | 0.9 | 1.0 | 0.7 | 0.9 | 1.0 | 1.9 | 1.0 | 1.1 |
| orf19.6660 | unknown protein | - | 0.4 | 1.3 | 0.9 | 1.9 | 1.1 | 1.2 | 1.2 | 1.1 | 1.4 | 1.0 | 1.5 |
| orf19.4602 | mitochondrial malate dehydrogenase | MDH1* | 0.4 | 0.8 | 0.4 | 1.1 | 0.9 | 1.1 | 1.1 | 1.5 | 1.1 | 1.9 | 1.3 |
| orf19.254 | hypothetical protein | - | 0.4 | 0.9 | 0.6 | 0.8 | 0.9 | 1.1 | 0.9 | 0.8 | 0.7 | 0.9 | 0.9 |
| orf19.2977 | conserved hypothetical protein | - | 0.4 | 0.6 | 0.9 | 0.9 | 0.5 | 0.6 | 1.0 | 0.9 | 1.2 | 0.9 | 0.9 |
| orf19.3803 | Golgi alpha-1,2-mannosyltransferase | MNN22* | 0.4 | 0.8 | 1.0 | 1.1 | 1.1 | 0.7 | 0.8 | | 0.9 | 1.3 | 1.1 |
| orf19.4393 | nuclear citrate synthase | CIT1* | 0.4 | 0.7 | 0.2 | 0.9 | 1.1 | 1.4 | 1.3 | 1.1 | 1.1 | 1.1 | 1.6 |
| orf19.2398 | hypothetical protein | - | 0.4 | 1.2 | 0.4 | 1.7 | 0.9 | 1.3 | 0.8 | 1.0 | 0.8 | 1.0 | 1.0 |
| orf19.6874 | myb-like transcription factor | - | 0.4 | 0.9 | 0.3 | 1.0 | 1.0 | 1.7 | 1.2 | 0.9 | 1.2 | 1.1 | 0.9 |
| orf19.7218 | homology to plant PR-1 class of proteins | PRY2* | 0.4 | 1.0 | 1.0 | 1.1 | 1.1 | 0.7 | 0.9 | 0.6 | 1.1 | 0.9 | 0.6 |
| orf19.2846 | hypothetical protein | - | 0.4 | 1.0 | 1.2 | 1.1 | 1.1 | 2.2 | 1.3 | 1.0 | 5.5 | 1.1 | 1.2 |
| orf19.2397.3 | conserved hypothetical protein | - | 0.4 | 1.1 | 1.3 | 1.1 | 1.0 | 0.6 | 0.8 | 1.0 | 1.1 | 1.0 | 1.2 |
| orf19.780 | urea amidolyase | DUR1* | 0.4 | 1.2 | 0.8 | 1.0 | 1.0 | 0.7 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| orf19.5118 | spindle-pole body protein | SDS24 | 0.4 | 1.0 | 0.3 | 1.4 | 1.1 | 1.2 | 1.1 | 1.0 | 0.9 | 1.0 | 1.0 |
| orf19.633 | putative methyltransferase | - | 0.4 | 1.1 | 1.3 | 0.7 | 0.9 | 0.4 | 0.9 | 1.0 | 1.0 | 0.7 | 0.9 |
| orf19.3869 | hypothetical protein | - | 0.4 | 0.7 | 0.5 | 0.8 | 0.9 | 1.4 | 1.1 | 0.7 | 0.8 | 1.3 | 0.8 |
| orf19.5626 | conserved hypothetical protein | - | 0.3 | 3.1 | 1.3 | 3.4 | 1.2 | 1.0 | 0.8 | 0.9 | 1.3 | 0.8 | 0.7 |
| orf19.4195.1 | cytosine deaminase | FCY1* | 0.3 | 0.8 | 1.5 | 0.8 | 0.7 | 0.3 | 0.9 | 0.8 | 1.9 | 0.7 | 0.9 |
| orf19.5917 | zinc finger protein involved in pre-tRNA splicing | STP3* | 0.3 | 0.5 | 0.9 | 0.7 | 0.9 | 0.6 | 0.6 | 0.8 | 1.0 | 1.0 | 0.9 |
| orf19.6514 | copper homeostasis, peptide import regulation | CUP9* | 0.3 | 0.9 | 0.7 | 0.8 | 1.0 | 1.1 | 0.8 | 1.0 | 0.9 | 1.1 | 1.2 |
| orf19.1614 | low affinity high capacity ammonium permease | MEP1 | 0.3 | 0.9 | 1.1 | 0.9 | 0.7 | 0.2 | 0.4 | 1.0 | 0.8 | 1.0 | 0.9 |
| orf19.2876 | centromere-binding kinetochore protein | CBF1 | 0.3 | 0.5 | 0.8 | 1.0 | 0.5 | 0.5 | 0.6 | 1.1 | 0.8 | 0.8 | 0.4 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| orf19.2173 | nuclear-cytoplasmic transport;negative effector of Pol III synthesis | MAF1* | 0.3 | 1.2 | 1.6 | 1.1 | 1.1 | 0.4 | 0.8 | 0.9 | 0.9 | 0.8 | 0.9 |
| orf19.6937 | peptide transporter | PTR2* | 0.3 | 0.6 | 0.4 | 1.3 | 0.7 | 0.7 | 0.8 | 0.6 | 0.9 | 1.0 | 0.5 |
| orf19.449 | predicted phosphatidyl synthase | - | 0.2 | 1.1 | 1.4 | 1.3 | 1.0 | 0.6 | 0.7 | 0.9 | 1.1 | 1.0 | 1.0 |
| orf19.3895 | chitinase 2 precursor | CHT2 | 0.2 | 0.9 | 0.3 | 0.6 | 1.0 | 0.3 | 0.3 | 0.9 | 0.4 | 0.2 | 0.6 |
| orf19.4716 | NADP-glutamate dehydrogenase | GDH3* | 0.2 | 0.6 | 0.3 | 0.4 | 0.8 | 0.2 | 0.4 | 0.9 | 0.3 | 0.7 | 0.5 |
| orf19.5282 | hypothetical protein | - | 0.2 | 1.2 | 1.0 | 0.9 | 0.9 | 0.4 | 0.7 | 1.1 | 0.9 | 0.9 | 1.0 |
| orf19.5267 | hypothetical protein | - | 0.2 | 0.7 | 1.2 | 0.9 | 1.1 | 0.4 | 0.4 | 0.9 | 1.4 | 0.9 | 0.8 |
| orf19.7150 | transcriptional repressor | NRG1 | 0.2 | 1.2 | 0.3 | 2.0 | 1.1 | 1.1 | 0.6 | 0.7 | 1.9 | 1.1 | 0.8 |
| orf19.5288 | Zn-containing alcohol dehydrogenase | YAL60* | 0.2 | 1.4 | 1.9 | 1.1 | 1.0 | 0.1 | 0.4 | 0.9 | 0.3 | 0.7 | 0.8 |
| orf19.6570 | purine nucleoside permease | NUP3 | 0.2 | 0.9 | 0.9 | 1.2 | 0.8 | 0.3 | 0.9 | 1.0 | 0.9 | 1.0 | 0.8 |
| orf19.4737 | membrane transporter of the MFS-MDR family | DHA12* | 0.1 | 1.0 | 0.6 | 1.1 | 1.1 | 0.4 | 0.4 | 0.5 | 0.9 | 0.7 | 1.0 |
| orf19.5305 | conserved protein reressed in hyphal development | RHD3 | 0.1 | 0.7 | 0.7 | 0.9 | 0.6 | 0.3 | 0.3 | 1.2 | 0.9 | 0.6 | 0.7 |
| orf19.4211 | multicopper ferro-O2-oxidoreductase involved in high-affinity iron uptake | FET3* | 0.1 | 0.4 | 0.3 | 0.7 | 0.7 | 1.2 | 1.9 | 1.4 | 1.8 | 2.4 | 2.1 |
| orf19.54 | Repressed in Hyphal Development;family of conserved protein of unknown function | RHD1 | 0.1 | 0.3 | 0.5 | 0.4 | 0.5 | 0.5 | 1.2 | 1.1 | 2.7 | 1.5 | 1.5 |
| orf19.3618 | putative cell wall protein | YWP1 | 0.0 | 0.7 | 0.1 | 0.8 | 0.5 | 0.6 | 0.9 | 0.9 | 2.0 | 0.7 | 0.7 |

**Table S3.**
Relative induction of upregulated hyphae specific genes in *myo5Δ/Δ* and *arp2Δ/Δ* mutants.

Green indicates hyphae specific genes are less upregulated in *arp2Δ/Δ* mutants compared to *myo5Δ/Δ* mutants.
Red indicates hyphae specific genes are more upregulated in *arp2Δ/Δ* mutants compared to *myo5Δ/Δ* mutants.

| | column B | column C | column D | column E | column F | column G | |
|---|---|---|---|---|---|---|---|
| Systematic name | WT-HY (Epp) | arp2-HY | WT-HY (Oberholzer) | myo5-HY | ratio of columns C over B | ratio of columns E over D | ratio of columns G over F |
| orf19.1816 | 31.09 | 1.80 | | | 0.06 | | |
| orf19.3374 | 30.38 | 6.15 | 81.22 | 3.33 | 0.20 | 0.04 | 4.9 |
| orf19.4082 | 26.66 | 0.91 | 4.36 | 0.70 | 0.03 | 0.16 | 0.2 |
| orf19.5760 | 24.42 | 2.51 | 10.56 | 5.58 | 0.10 | 0.53 | 0.2 |
| orf19.4975 | 20.21 | 1.60 | 1.25 | 1.03 | 0.08 | 0.82 | 0.1 |
| orf19.5636 | 19.92 | 0.57 | | | 0.03 | | |
| orf19.1327 | 17.25 | 7.42 | | | 0.43 | | |
| orf19.5585 | 17.16 | 1.16 | 19.10 | 1.53 | 0.07 | 0.08 | 0.8 |
| orf19.1321 | 16.43 | 3.50 | 25.56 | 9.55 | 0.21 | 0.37 | 0.6 |
| orf19.4215 | 13.68 | 3.98 | | | 0.29 | | |
| orf19.5674 | 11.96 | 1.18 | 13.82 | 2.45 | 0.10 | 0.18 | 0.6 |
| orf19.251 | 11.74 | 3.02 | 4.85 | 1.08 | 0.26 | 0.22 | 1.2 |
| orf19.2355 | 9.40 | 1.33 | | | 0.14 | | |
| orf19.4943 | 9.00 | 2.96 | 1.99 | 1.86 | 0.33 | 0.93 | 0.4 |
| orf19.3829 | 8.89 | 0.87 | 5.04 | 3.85 | 0.10 | 0.76 | 0.1 |
| orf19.2210 | 8.55 | 1.02 | 1.41 | 1.17 | 0.12 | 0.83 | 0.1 |
| orf19.4980 | 8.53 | 1.41 | 1.48 | 1.18 | 0.17 | 0.79 | 0.2 |
| orf19.5542 | 8.05 | 1.50 | 3.74 | 1.51 | 0.19 | 0.40 | 0.5 |
| orf19.4527 | 7.96 | 2.17 | 4.63 | 2.07 | 0.27 | 0.45 | 0.6 |
| orf19.1691 | 7.18 | 3.89 | 3.91 | 1.23 | 0.54 | 0.31 | 1.7 |
| orf19.5265 | 6.73 | 1.77 | 1.33 | 1.22 | 0.26 | 0.92 | 0.3 |
| orf19.7610 | 6.62 | 1.66 | 1.66 | 2.09 | 0.25 | 1.26 | 0.2 |
| orf19.716 | 5.84 | 1.69 | 1.09 | 1.07 | 0.29 | 0.98 | 0.3 |
| orf19.2241 | 5.82 | 1.57 | 1.17 | 1.00 | 0.27 | 0.86 | 0.3 |
| orf19.113 | 5.79 | 1.24 | 1.21 | 0.86 | 0.21 | 0.71 | 0.3 |
| orf19.3384 | 5.68 | 1.14 | 3.00 | 1.51 | 0.20 | 0.50 | 0.4 |
| orf19.6202 | 5.31 | 0.39 | 5.58 | 1.44 | 0.07 | 0.26 | 0.3 |
| orf19.85 | 4.94 | 1.74 | 3.58 | 1.11 | 0.35 | 0.31 | 1.1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| orf19.815 | 4.56 | 2.58 | 2.08 | 1.35 | 0.56 | 0.65 | 0.9 |
| orf19.1996 | 4.51 | 1.28 | 3.09 | 1.40 | 0.28 | 0.45 | 0.6 |
| orf19.2952 | 4.41 | 2.28 | 1.35 | 1.27 | 0.52 | 0.94 | 0.6 |
| orf19.5645 | 4.37 | 0.35 | | | 0.08 | | |
| orf19.2125 | 4.35 | 0.89 | 2.95 | 0.82 | 0.20 | 0.28 | 0.7 |
| orf19.4477 | 4.09 | 1.48 | | | 0.36 | | |
| orf19.7531 | 4.09 | 1.26 | 1.86 | 1.89 | 0.31 | 1.02 | 0.3 |
| orf19.4590 | 4.05 | 1.26 | 1.22 | 1.01 | 0.31 | 0.83 | 0.4 |
| orf19.6608 | 3.99 | 1.35 | 2.40 | 2.38 | 0.34 | 0.99 | 0.3 |
| orf19.4530.1 | 3.96 | 1.64 | 1.01 | 0.98 | 0.42 | 0.97 | 0.4 |
| orf19.2959.1 | 3.93 | 1.07 | | | 0.27 | | |
| orf19.7323 | 3.91 | 3.55 | | | 0.91 | | |
| orf19.675 | 3.90 | 0.21 | 4.83 | 1.11 | 0.05 | 0.23 | 0.2 |
| orf19.7053 | 3.85 | 1.09 | | | 0.28 | | |
| orf19.4749 | 3.77 | 2.24 | 1.72 | 1.09 | 0.59 | 0.63 | 0.9 |
| orf19.6420 | 3.76 | 0.42 | 4.18 | 3.17 | 0.11 | 0.76 | 0.1 |
| orf19.6287 | 3.75 | 1.54 | 1.18 | 0.96 | 0.41 | 0.81 | 0.5 |
| orf19.1799 | 3.70 | 1.27 | 1.04 | 0.99 | 0.34 | 0.95 | 0.4 |
| orf19.1655 | 3.67 | 0.71 | 1.04 | 0.98 | 0.19 | 0.95 | 0.2 |
| orf19.5614 | 3.59 | 1.31 | 1.96 | 1.23 | 0.36 | 0.63 | 0.6 |
| orf19.3746 | 3.50 | 0.94 | 1.18 | 1.05 | 0.27 | 0.89 | 0.3 |
| orf19.6705 | 3.49 | 1.28 | 1.84 | 1.39 | 0.37 | 0.76 | 0.5 |
| orf19.7362 | 3.40 | 2.25 | 2.32 | 1.68 | 0.66 | 0.73 | 0.9 |
| orf19.2372 | 3.34 | 1.83 | 1.28 | 1.63 | 0.55 | 1.27 | 0.4 |
| orf19.5373 | 3.29 | 2.11 | 1.84 | 1.56 | 0.64 | 0.85 | 0.8 |
| orf19.7304 | 3.28 | 2.45 | 2.91 | 1.67 | 0.75 | 0.57 | 1.3 |
| orf19.6021 | 3.27 | 1.20 | 1.26 | 1.13 | 0.37 | 0.90 | 0.4 |
| orf19.7504 | 3.23 | 0.83 | 2.14 | 1.14 | 0.26 | 0.53 | 0.5 |
| orf19.715 | 3.22 | 1.93 | 1.17 | 0.91 | 0.60 | 0.78 | 0.8 |
| orf19.5025 | 3.21 | 1.21 | 1.35 | 0.89 | 0.38 | 0.66 | 0.6 |
| orf19.7214 | 3.14 | 1.33 | 1.93 | 0.87 | 0.42 | 0.45 | 0.9 |
| orf19.682 | 3.10 | 0.62 | 1.02 | 1.01 | 0.20 | 0.99 | 0.2 |
| orf19.6079 | 2.98 | 1.13 | | | 0.38 | | |
| orf19.6601.1 | 2.96 | 1.97 | 0.92 | 0.97 | 0.67 | 1.06 | 0.6 |
| orf19.2685 | 2.94 | 0.58 | 1.65 | 1.10 | 0.20 | 0.66 | 0.3 |
| orf19.7350 | 2.91 | 1.06 | 2.01 | 1.08 | 0.36 | 0.54 | 0.7 |
| orf19.7219 | 2.90 | 2.42 | 2.34 | 1.23 | 0.84 | 0.53 | 1.6 |
| orf19.4056 | 2.88 | 0.76 | 2.49 | 2.10 | 0.26 | 0.84 | 0.3 |
| orf19.5615 | 2.81 | 1.75 | 1.59 | 1.00 | 0.62 | 0.63 | 1.0 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| orf19.5619 | 2.81 | 0.60 | 1.64 | 1.53 | 0.21 | 0.93 | 0.2 |
| orf19.1690 | 2.78 | 0.57 | 1.36 | 1.25 | 0.20 | 0.91 | 0.2 |
| orf19.2947 | 2.78 | 1.56 | 2.69 | 1.89 | 0.56 | 0.70 | 0.8 |
| orf19.6741 | 2.76 | 1.78 | 1.32 | 1.34 | 0.64 | 1.01 | 0.6 |
| orf19.13 | 2.71 | 2.11 | 3.89 | 0.92 | 0.78 | 0.24 | 3.3 |
| orf19.413 | 2.67 | 1.59 | 2.06 | 2.33 | 0.60 | 1.13 | 0.5 |
| orf19.7324 | 2.62 | 1.44 | 1.15 | 1.12 | 0.55 | 0.98 | 0.6 |
| orf19.2292 | 2.56 | 1.24 | | | 0.48 | | |
| orf19.2886 | 2.56 | 1.05 | 1.31 | 0.95 | 0.41 | 0.73 | 0.6 |
| orf19.2903 | 2.53 | 1.00 | 1.75 | 0.89 | 0.39 | 0.51 | 0.8 |
| orf19.3219 | 2.52 | 1.66 | 1.02 | 1.08 | 0.66 | 1.06 | 0.6 |
| orf19.3483 | 2.51 | 1.96 | 1.30 | 1.19 | 0.78 | 0.91 | 0.9 |
| orf19.1964 | 2.50 | 0.78 | 1.83 | 1.47 | 0.31 | 0.81 | 0.4 |
| orf19.1408 | 2.48 | 2.20 | 3.90 | 0.90 | 0.89 | 0.23 | 3.9 |
| orf19.1654 | 2.46 | 1.52 | 1.46 | 1.10 | 0.62 | 0.76 | 0.8 |
| orf19.6028 | 2.42 | 0.87 | 1.27 | 1.06 | 0.36 | 0.84 | 0.4 |
| orf19.7308 | 2.38 | 0.53 | 1.59 | 1.18 | 0.22 | 0.74 | 0.3 |
| orf19.2777 | 2.36 | 0.54 | | | 0.23 | | |
| orf19.1652 | 2.33 | 0.83 | 1.02 | 0.71 | 0.36 | 0.69 | 0.5 |
| orf19.4607 | 2.32 | 1.55 | 0.93 | 0.93 | 0.67 | 1.00 | 0.7 |
| orf19.7583 | 2.32 | 1.65 | 1.01 | 1.01 | 0.71 | 1.00 | 0.7 |
| orf19.6116 | 2.32 | 2.45 | 1.95 | 0.91 | 1.06 | 0.47 | 2.3 |
| orf19.2762 | 2.31 | 1.49 | 1.48 | 1.07 | 0.64 | 0.72 | 0.9 |
| orf19.7021 | 2.30 | 1.97 | 4.56 | 1.47 | 0.85 | 0.32 | 2.6 |
| orf19.4033 | 2.30 | 0.66 | 1.04 | 1.09 | 0.29 | 1.05 | 0.3 |
| orf19.1153 | 2.26 | 1.06 | 1.71 | 1.26 | 0.47 | 0.73 | 0.6 |
| orf19.467 | 2.25 | 1.01 | 1.51 | 1.43 | 0.45 | 0.94 | 0.5 |
| orf19.4263 | 2.24 | 1.44 | | | 0.64 | | |
| orf19.1847 | 2.23 | 2.31 | 3.52 | 1.18 | 1.04 | 0.34 | 3.1 |
| orf19.7657 | 2.23 | 1.10 | 0.94 | 0.96 | 0.49 | 1.02 | 0.5 |
| orf19.3150 | 2.19 | 1.33 | 2.03 | 0.82 | 0.61 | 0.40 | 1.5 |
| orf19.5799 | 2.17 | 0.51 | 1.65 | 1.08 | 0.24 | 0.66 | 0.4 |
| orf19.4349.6 | 2.17 | 1.08 | | | 0.50 | | |
| orf19.6402 | 2.16 | 0.95 | 1.07 | 0.94 | 0.44 | 0.88 | 0.5 |
| orf19.1592 | 2.16 | 1.10 | | | 0.51 | | |
| orf19.5620 | 2.13 | 2.22 | 1.97 | 0.87 | 1.04 | 0.44 | 2.3 |
| orf19.1995 | 2.13 | 1.37 | 1.16 | 1.04 | 0.64 | 0.90 | 0.7 |
| orf19.7635 | 2.13 | 1.21 | 0.96 | 1.06 | 0.57 | 1.10 | 0.5 |
| orf19.5451 | 2.12 | 1.44 | | | 0.68 | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| orf19.3013 | 2.11 | 1.31 | 1.05 | 1.01 | 0.62 | 0.96 | 0.6 |
| orf19.2721 | 2.08 | 1.47 | 1.04 | 1.04 | 0.71 | 1.00 | 0.7 |
| orf19.4433 | 2.07 | 0.80 | 0.82 | 1.17 | 0.38 | 1.43 | 0.3 |
| orf19.4649 | 2.07 | 1.30 | 0.88 | 1.02 | 0.63 | 1.16 | 0.5 |
| orf19.6073 | 2.06 | 1.31 | 1.11 | 0.79 | 0.64 | 0.71 | 0.9 |
| orf19.4666 | 2.05 | 1.12 | 1.66 | 1.45 | 0.54 | 0.87 | 0.6 |
| orf19.3941 | 2.05 | 1.35 | 0.85 | 1.33 | 0.66 | 1.56 | 0.4 |
| orf19.156 | 2.05 | 2.24 | | | 1.09 | | |
| orf19.2346 | 2.02 | 1.30 | 1.02 | 1.01 | 0.64 | 0.99 | 0.6 |
| orf19.3984 | 2.02 | 0.95 | | | 0.47 | | |
| orf19.6864 | 2.01 | 1.20 | 1.25 | 0.93 | 0.60 | 0.74 | 0.8 |
| | | | | | | | |

**Table S4.**
*NRG1* dependent hyphae specific genes.

This gene list shows the 28 *NRG1*-dependent hyphae specific genes as described in Kadosh et al. (2005).

Note that 'nrg1/arp2-H' represents the microarray data for the comparison of the *nrg1Δ/Δ/arp2Δ/Δ* mutant grown under hyphal conditions to WT cells grown under hyphal conditions.

Note that 'nrg1/arp2-H vs arp2-H' represents the microarray data for the comparison of the *nrg1Δ/Δ/arp2Δ/Δ* mutant grown under hyphal conditions to the *arp2Δ/Δ* mutant grown under hyphal conditions.

| | | nrg1/arp2-H | nrg1/arp2-H vs arp2-H | |
|---|---|---|---|---|
| Systematic name | Common name | Normalized log2 ratio | Normalized log2 ratio | Description |
| orf19.4975 | HYR1 | 0.9 | 10.9 | Nonessential, GPI anchored, predicted cell wall protein; macrophage-induced protein; induced in hyphae; induction associated with azole resistance; regulated by Rfg1p, Efg1p, Nrg1p, Tup1p, Cyr1p |
| orf19.5585 | SAP5 | 0.2 | 5.9 | Secreted aspartyl proteinase; sap4 sap5 sap6 triple mutant has defects in virulence and utilization of protein as nitrogen source; expressed in mucosal & systemic infections, oral carriage; absent from less virulent species, C. dubliniensis |
| orf19.5716 | SAP4 | 0.3 | 5.5 | Secreted aspartyl proteinase; sap4 sap5 sap6 triple mutant has defects in systemic virulence (mouse, guinea pig), survival in macrophage, and protein utilization for nitrogen; expressed during mucosal and systemic infections, oral carriage |
| orf19.5265 | KIP4 | 0.9 | 3.3 | Transposon mutation affects filamentous growth; filament induced; shows Mob2p-dependent hyphal regulation; regulated by Nrg1p, Tup1p |
| orf19.6079 | | 2.2 | 2.6 | Predicted ORF in retrotransposon Tca8 with similarity to the Gag region encoding nucleocapsid-like protein; transcription is downregulated in response to treatment with ciclopirox olamine; filament induced; regulated by Rfg1p, Tup1p |
| orf19.1816 | ALS3 | 0.2 | 2.4 | Adhesin; ALS family; role in epithelial adhesion, endothelial invasiveness; allelic variation in adhesiveness; immunoprotective in mice; predicted GPI-anchor cell wall protein; macrophage, hyphal induced, pH, Nrg1p, Rfg1p, Tup1p regulated |
| orf19.1822 | UME6 | 1.8 | 2.2 | Transcription factor; required for wild-type hyphal extension, virulence; zinc cluster DNA-binding motif; similar to S. cerevisiae Ume6p, which is a meiotic regulator; alkaline upregulated; filament induced; regulated by Nrg1p, Tup1p, RFG1p |
| orf19.5760 | IHD1 | 1.0 | 1.9 | Putative GPI-anchored protein of unknown function; alkaline upregulated; greater transcription in hyphal form than yeast form; regulated by Nrg1p, Rfg1p, Tup1p; regulated by Tsa1p, Tsa1Bp in minimal media at 37; not essential for viability |

| | | | | |
|---|---|---|---|---|
| orf19.7323 | CBP1 | 0.8 | 1.7 | Corticosteroid binding protein; transcription induced at late log-phase or upon adherence to polystyrene; not induced by corticosterone; contains a possible NAD/FAD binding region; regulated by Nrg1p, Tup1p |
| orf19.6705 | | 0.9 | 1.6 | Putative guanyl nucleotide exchange factor with Sec7 domain; transcriptionally regulated upon yeast-hyphal switch; filament induced; regulated by Nrg1p, Tup1p; shows Mob2p-dependent hyphal regulation |
| orf19.2355 | ALS10 | 0.5 | 1.5 | ALS family protein; ALS family includes cell-surface glycoproteins, some with adhesin function; putative GPI-anchor; filament induced; regulated by Nrg1p, Rfg1p, Tup1p; merged with orf19.1816 in Assembly 20 |
| orf19.3374 | ECE1 | 0.4 | 1.4 | Protein comprising eight 34-residue repeats; hyphal-specific expression increases with extent of elongation of the cell; regulated by Rfg1p, Nrg1p, Tup1p, Cph1p, Efg1p, Hog1p, farnesol, phagocytosis; may contribute to biofilm formation |
| orf19.1691 | | 0.1 | 1.4 | Predicted ORF in Assemblies 19, 20 and 21; fluconazole-induced; filament induced; Hog1p-induced; regulated by Nrg1p, Tup1p; increased expression in response to prostaglandins |
| orf19.207 | PGA55 | 1.3 | 1.3 | Putative GPI-anchored protein of unknown function; filament induced; regulated by Nrg1p, Tup1p; possibly transcriptionally regulated upon hyphal formation |
| orf19.2060 | SOD5 | 1.0 | 1.2 | Copper- and zinc-containing superoxide dismutase; protective role against oxidative stress; induced by neutrophil contact, hyphal growth, caspofungin, osmotic or oxidative stress; member of a gene family including SOD1, SOD4, SOD5, and SOD6 |
| orf19.6582 | PRE10 | 1.1 | 1.1 | Alpha7 (C8) subunit of the 20S proteasome; multiple phosphorylated residues; transcription is induced upon filamentous growth |
| orf19.5076 | PFY1 | 1.0 | 1.1 | Profilin, functional homolog of S. cerevisiae Pfy1p; hyphal-induced; macrophage/pseudohyphal-induced; regulated by Nrg1p, Tup1p; gene lacks intron (unlike S. cerevisiae PFY1); complements growth of S. cerevisiae srv2 mutant; nonessential |
| orf19.7561 | DEF1 | 1.0 | 1.1 | Protein required for filamentous growth and for escape from epithelial cells and dissemination in an RHE model; transcription induced in oral candidiasis clinical isolates; induced by fluconazole, high cell density; hyphally regulated |
| orf19.1120 | FAV2 | 1.1 | 1.1 | Induced by mating factor in MTLa/MTLa opaque cells; greater mRNA abundance observed in a cyr1 homozygous null mutant than in wild type; filament induced; regulated by Nrg1p, Rfg1p, Tup1p; possibly spurious ORF (AWG prediction) |
| orf19.5968 | RDI1 | 1.1 | 1.1 | Protein similar to S. cerevisiae Rdi1p, an inhibitor of Rho-GDP dissociation; transposon mutation affects filamentous growth; farnesol-, filament-induced; regulated by Nrg1p, Tup1p |
| orf19.3829 | PHR1 | 1.1 | 1.1 | Glycosidase of cell surface; may act on cell-wall beta-1,3-glucan prior to beta-1,6-glucan linkage; E169 and E270 at active site; role in systemic but not vaginal virulence (neutral, not low pH); high pH or filamentation induced |
| orf19.4255 | ECM331 | 1.9 | 1.0 | GPI-anchored protein; mainly at plasma membrane, also at cell wall; caspofungin induced; Plc1p-regulated; repressed by Rim101p, Hog1p; colony morphology-related gene regulation by Ssn6p; induced in cyr1 homozygous null mutant yeast-form cel |

| | | | | |
|---|---|---|---|---|
| orf19.1321 | HWP1 | 1.0 | 1.0 | Hyphal cell wall protein; covalently crosslinked to epithelial cells by host transglutaminase; opaque- and a-specific, alpha-factor induced; at MTLa side of conjugation tube; assessment of virulence role complicated by URA3 effects |
| orf19.3380 | HWP2 | 1.0 | 1.0 | Putative GPI-anchored protein; cell wall localization predicted; hyphal-specific expression; regulated by Efg1p, Tup1p; has similarity to Hwp1p, Ece2p, Rbt1p domains; predicted signal sequence and O-glycosylation |
| orf19.1860 | LSC2 | 1.4 | 1.0 | Protein described as beta subunit of succinate-CoA ligase; transcription regulated by Mig1p and Tup1p; transcriptionally regulated by iron; expression greater in high iron; filament induced |
| orf19.1825 | | 1.1 | 0.9 | Protein not essential for viability; filament induced; regulated by Nrg1p, Rfg1p, Tup1p |
| orf19.3698 | | 1.2 | 0.9 | Predicted ORF in Assemblies 19, 20 and 21; filament induced |
| orf19.5567 | POP4 | 1.0 | 0.7 | Protein likely to be essential for growth, based on an insertional mutagenesis strategy; similar to S. cerevisiae Pop4p, which is a subunit of both RNase MRP and nuclear RNase P; filament induced; regulated by Nrg1p, Tup1p |

**Table S5.**

Ergosterol genes that are downregulated (< 2 fold change) in either "arp2-H" or "arp2-Y".

| | | WT-HY vs arp2-HY | | WT-Y vs arp2-Y | | |
|---|---|---|---|---|---|---|
| systematic name | common name | Normalized log2 ratio | t-test P-value | Normalized log2 ratio | t-test P-value | Description |
| orf19.922 | ERG11 | 0.49 | 2.7E-01 | 0.48 | 5.4E-04 | cytochrome P450 lanosterol 14a-demethylase |
| orf19.406 | ERG1 | 0.19 | 1.7E-02 | 0.37 | 2.6E-02 | squalene epoxidase(monooxygenase), erosterol biosynthesis |
| orf19.5178 | ERG5 | 0.44 | 2.5E-02 | 0.71 | 1.4E-01 | cytochrome P450 |
| orf19.3240 | ERG27 | 0.47 | 1.8E-02 | 0.96 | 6.2E-01 | 3-keto sterol reductase |
| orf19.1591 | ERG10 | 0.24 | 4.0E-02 | 1.47 | 1.8E-01 | acetyl-CoA acetyltransferase;acetoacetyl CoA thiolase |
| orf19.1631 | ERG6 | 0.75 | 4.7E-01 | 0.48 | 1.2E-01 | S-adenosyl-methionine delta-24- sterol-c-methyltransferase |
| orf19.4631 | ERG252 | 0.29 | 1.0E-01 | 0.60 | 4.3E-02 | C-4 sterol methyl oxidase;membrane-bound non-heme di-iron oxygenase involved in lipid metabolism |

**Table S6.**

Strains used in this study.

| name | description | parent strain | relavent genotype | reference |
|---|---|---|---|---|
| SC5314 | WT strain | clinical isolate | prototroph | Gillum et al. (1984) |
| BWP17 | WT strain | RM1000 | arg4/arg4 his1/his1 ura3/ura3 | Wilson et al. (1999) |
| SN95 | WT strain | SN76 | arg4/arg4 his1/his1 | Noble et al. (2005) |
| SN148 | WT strain | SN76 | arg4/arg4 his1/his1 ura3/ura3 leu2/leu2 | Noble et al. (2005) |
| nrg1 | nrg1 deletion strain | CAI4 | nrg1::HisG/nrg1::HisG | Murad et al. (2001) |
| Tn:trp1 | transposon mutant | BWP17 | trp1::UAU1/trp1::URA3 | This study |
| Tn::cdc39 | transposon mutant | BWP17 | cdc39::UAU1/cdc39::URA3 | This study |
| Tn::arp2 | transposon mutant | BWP17 | arp2::UAU1/arp2::URA3 | This study |
| Tn::vps52 | transposon mutant | BWP17 | vps52::UAU1/vps52::URA3 | This study |
| Tn::875 | transposon mutant | BWP17 | orf19.875:UAU1/orf19.875::URA3 | This study |
| arp2 heterozygote 1 |  | SN95 | arp2::HIS1/ARP2 | This study |
| arp2 heterozygote 2 |  | SN95 | arp2::HIS1/ARP2 | This study |
| CaEE86 | arp2 deletion mutant | arp2 heterozygote 1 | arp2::ARG4/arp2::HIS1 | This study |
| CaEE87 | arp2 deletion mutant | arp2 heterozygote 1 | arp2::ARG4/arp2::HIS1 | This study |
| CaEE88 | arp2 deletion mutant | arp2 heterozygote 2 | arp2::ARG4/arp2::HIS1 | This study |
| CaEE89 | arp2 deletion mutant | arp2 heterozygote 2 | arp2::ARG4/arp2::HIS1 | This study |
| CaEE193 | arp2 revertant 1 | CaEE86 | ARP2::SAT1-FLIP/arp2::HIS1 | This study |
| CaEE195 | arp2 revertant 2 | CaEE86 | arp2::ARG4/ARP2::SAT1-FLIP | This study |
| CaEE196 | arp2 revertant | CaEE193 | ARP2::FRT/arp2::HIS1 | This study |
| CaEE198 | arp2 revertant | CaEE195 | arp2::ARG4/ARP2::FRT | This study |
| CaEE63 | vps52 heterozygote 1 | SN95 | vps52::HIS1/VPS52 | This study |
| CaEE64 | vps52 heterozygote 2 | SN95 | vps52::HIS1/VPS52 | This study |
| CaEE105 | vps52 deletion mutant | CaEE63 | vps52::HIS/vps52::ARG4 | This study |
| CaEE120 | vps52 deletion mutant | CaEE64 | vps52::HIS/vps52::ARG4 | This study |
| CaEE191 | vps52 revertant | CaEE120 | vps52::HIS1/VPS52::SAT1-FLIP | This study |
| CaEE192 | vps52 revertant | CaEE191 | vps52::HIS1/VPS52::FRT | This study |
| orf19.875 heterozygote 1 |  | SN95 | orf19.875::HIS1/ORF19.875 | This study |

| | | | | |
|---|---|---|---|---|
| orf19.875 heterozygote 2 | | SN95 | orf19.875::HIS1/ORF19.875 | This study |
| CaEE90 | orf19.875 deletion mutant | orf19.875 heterozygote 1 | orf19.875::HIS1/orf19.875::ARG4 | This study |
| CaEE91 | orf19.875 deletion mutant | orf19.875 heterozygote 1 | orf19.875::HIS1/orf19.875::ARG4 | This study |
| CaEE92 | orf19.875 deletion mutant | orf19.875 heterozygote 2 | orf19.875::HIS1/orf19.875::ARG4 | This study |
| CaEE93 | orf19.875 deletion mutant | orf19.875 heterozygote 2 | orf19.875::HIS1/orf19.875::ARG4 | This study |
| CaEE175 | orf19.875 revertant 1 | CaEE90 | orf19.875::HIS1/ORF19.875::SAT1-FLIP | This study |
| CaEE176 | orf19.875 revertant 2 | CaEE90 | ORF19.875::SAT1-FLIP/orf19.875::ARG4 | This study |
| CaEE182 | orf19.875 revertant | CaEE175 | orf19.875::HIS1/ORF19.875::FRT | This study |
| CaEE183 | orf19.875 revertant | CaEE176 | ORF19.875::FRT/orf19.875::ARG4 | This study |
| CaEE218 | arp2 heterozygote | SN148 | arp2::LEU2/ARP2 | This study |
| CaEE221 | arp3 heterozygote | CaEE218 | arp2::LEU2/ARP2 arp3::URA3/ARP3 | This study |
| CaEE224 | arp3 deletion mutant | CaEE221 | arp2::LEU2/ARP2 arp3::URA3/arp3::ARG4 | This study |
| CaEE227 | arp2/arp3 double KO | CaEE224 | arp2::LEU2/arp2::HIS1 arp3::URA3/arp3::ARG4 | This study |
| TEF1-GFP | TEF1 tagged with GFP | BWP17 | BWP17, tef1::TEF1p-GFP-HIS1/TEF1, ura3, arg4 | This study |
| CaEE329 | arp2 heterozygote | nrg1 deletion strain | arp2/ARP2 nrg1/nrg1 | This study |
| CaEE335 | nrg1/arp2 deletion mutant | arp2 deletion in nrg1 mutant | arp2/arp2::SAT1-FLIP nrg1/nrg1 | This study |

**Table S7.**

Plasmids used in this study.

| name | description |
|---|---|
| pEE18 | *VPS52* cloned in pSFS2A |
| pEE20 | downstream VPS52 sequence cloned in pEE18 |
| pEE22 | *ARP2* cloned in pSFS2A |
| pEE23 | *ORF19.875* cloned in pSFS2A |
| pEE30 | downstream *ORF19.875* sequence cloned in pEE23 |
| pEE33 | downstream *ARP2* sequence cloned in pEE22 |
| pEE59 | upstream *ARP2* sequence cloned into KpnI/NotI digested pEE33 |

**Table S8.**
Primers (oligonucleotids) used in this study.

| name | sequence[1] | description |
|---|---|---|
| MR1538/9 | GTTTCCACTCACCGAGAAAACCAGCAAGAGAAAATAGAAAAGTGAAAGCTGGGTTGGACACTAGTATCTTTT TTTGCTGTGTTGACACATTCATAGTAAAGCAATTAATATATCTATATCgaagcttcgtacgctgcaggtc | ARP2 upstream flanking primer |
| MR1540/1 | GTGATAGATATGATGCTTTGGTTGACTCTGTAATGAAACAAATACAAAACTTAAACTACAGCTAGTGTA TAAAATATTTATATCTATGTTAATGAAAATACAAAATCATATATGTAAACCctcgaattcatcgatgatatcaga | ARP2 downstream flanking primer |
| MR1546/7 | TTTGTTGTATATGTTCAAAATCGTAGATTGTATAGTATATTTTGCTTCAACTAGATATGAGTGAGTGGGAA TGTTTCCATTTTTGTAAATCATCGACTTTTTTTTTTGGCCAACCCTTTAgaagcttcgtacgctgcaggtc | ORF19.875 upstream flanking primer |
| MR1548/9 | GGCGAAACAGACCTAATAATAAATAGTTTATGTATACTTTGTATATTCTGCTTATTTACAAGTCAACTATTAA AGTAGTTTACGGATATATGTATACCTACAATAAGGAAAAAAAAAAACgaagcttcgtacgctgcaggtc | ORF19.875 downstream flanking primer |
| MR1322 | GGAGTTCCATTTAGAGAAACTCATC | pRS-ARG F |
| MR1588 | ACGAGGATCAAGAGTCTCCTCTCAC | ORF19.875 external R |
| MR1324 | GAAGTTGTGTGGGAAAAATCTTCAC | pGEM-HIS F |
| MR1587 | TTTACGAAAACGATTAGACCCTGTG | ORF19.875 external F |
| MR1589 | TTTCTTAATGGGATCAACGCCACTTC | ORF19.875 internal R |
| MR1582 | TACACCGTGACCCAAACGATAGATG | ARP2 external R |
| MR1581 | AGTCACACTTCATACTTGACGTTTGC | ARP2 external F |
| MR1583 | GGGTTCATAGGTGGTTCTGTTAACAAG | ARP2 internal R |
| oEE58 | ACGAGGAAAAAAAAAATAAAAGTTAGATCAACTCAATATATATTTTTATACAGATTGGTAACAAACCACCACGT TGACTTAAACTTTTGTGATAATCATGgaagcttcgtacgctgcaggtc | VPS52 upstream flanking primer |
| oEE59 | TGGATGTGATCAAAGAAATTGGGTTTGCCCATATGCGGGTGTTGGAGGGTGTTGCTACATATTTACAATT GTGTGGTTTGTACGCAAAGATATGTGACCTTCTGgaagcttcgtacgctgcaggtc | VPS52 downstream flanking |

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|---|---|---|
| | | primer |
| oEE42 | GTACAAAAGTCACAGGCTAAATTGC | VPS52 internal F |
| oEE43 | TCTCATCAAATAGCTCTCGTACTCG | VPS52 internal R |
| oEE199 | GCTAAGACCAATAAGGTGGAACC | ORF19.875 internal F |
| oEE200 | GTATCAAATCATCAGCCCAACC | ORF19.875 internal R |
| oEE166 | CGGGGTACCCCGCAAAATGGACGCAAGACAGG | ARP2 Kpn1 |
| oEE167 | TCCCCGCGGGGATAATGCTGTACCTGACCACACC | ARP2 SacII |
| oEE169 | ATAAGAATGCGGCCGCTAAACTATCATAGATATAAATATTTTATACACTAGC | ARP2 Not1 |
| oEE170 | CGGGGTACCCCGAGGTGCTACTGGAACATCTGTCG | ORF19.875 Kpn1 |
| oEE174 | CGGGGTACCCCGACCTTCTCTAACCTCCAGTAATGC | ORF19.7660 Kpn1 |
| oEE228 | CCGCTCGAGCGGGTGCCTGTTAGTGCTATCG | Arp2 Xho1 |
| oEE229 | CCGCTCGAGCGGCGTCTTGTTCCAAGCTATGC | ORF19.875 Xho1 |
| oEE230 | AAGGAAAAAAGCGGCCGCAAAAGGAAAAGATACAGAAATCCACAAAAGACG | ORF19.875 Not1 |
| oEE231 | TCCCCGCGGGGATGTGTCGAGTGACATTACCG | ORF19.875 SacII |
| oEE232 | CCGCTCGAGCGGGACACTGACATTCAAAGTGGC | VPS52 Xho1 |
| oEE233 | AAGGAAAAAAGCGGCCGCAAAAGGAAAATTCCAAACGTTGACAGATGC | VPS52 Not1 |
| oEE234 | TCCCCGCGGGGACTTTGCAGTCACGTTGTGCG | VPS52 SacII |
| oEE5 | TGTTGAAAGTTGCTGTAGTG | inverse PCR F |
| oEE6 | CCAACCAGATAAGTGAAATC | inverse PCR R |
| oEE9 | TATTAGCTTACGACGCTACAC | sequencing F after inverse PCR |
| oEE23 | CTAATTCTGTATTAGTCATTCC | sequencing R after inverse PCR |
| oEE3 | GTTACGAATCAATGGCACTAC | check for Tn presence F |

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|---|---|---|
| oEE4 | GTGGAAATGGAGTTTTTAAGG | check for Tn presence R |
| oEE282 | AAAATGGACGCAAGACAGG | GSP1 ARP2 |
| oEE283 | cacggcgcgcctagcagcggGGAAGGCGAAGTTGAGAAATCAACA | GSP2 ARP2 |
| oEE284 | gtcagcggccgcatccctgcCATAGATATAAATATTTTATACACTAGC | GSP3 ARP2 |
| oEE285 | TAATGCTGTACCTGACCACACC | GSP4 ARP2 |
| oEE181 | GTTGAAGTGGCGGCTAAACG | ARP2 F |
| oEE182 | GAAATTGGATGCTCCGTTGG | ARP2 R |
| oEE197 | GTGATGGTGTGACTCATATTGTGC | ARP2 internal F |
| oEE198 | ACACTCTTGGTCCTTGTTCTTCC | ARP2 internal R |
| oEE201 | TCTCGGTAAGGGAACTAATGATATG | GSP1 ARP3 |
| oEE202 | cacggcgcgcctagcagcggAACTGATTGTGATTGCTGATTTCTC | GSP2 ARP3 |
| oEE203 | gtcagcggccgcatccctgcAAAATTGCTTAGATTGGAGTTGTCG | GSP3 ARP3 |
| oEE204 | GCTAACTTACCCAAAGTACGAATAGC | GSP4 ARP3 |
| oEE205 | CGAAGGTATCAGAGCATTACACG | ARP3 F |
| oEE206 | GGCTGCATGTCTTCTATTCTCG | ARP3 R |
| oEE207 | GCCATTAAGAATATCCCACTCG | ARP3 internal F |
| oEE208 | ATCATAGTCGCTCTTCGTGTAGC | ARP3 internal R |
| oEE24 | ATAACTACATCACCTGTATCACCTC | VPS52 external F |
| oEE72 | ACACATGTTGTGATAGATTTTAC | pFA-HIS1 F |
| oEE73 | AAGAGGACTGGGTTGCCATCTCATC | pFA-HIS1 R |
| oEE25 | ACATTACCATCAAGCTACTATGGAG | VPS52 external R |
| oEE57 | GAATTATGTCGGTCAATATGTC | pFA-ARG4 R |
| oEE56 | AGAGATGCTATTGGTGGTACTGC | pFA-ARG4 F |
| oEE315 | GTGTTACGAATCAATGGCACT | pFA-URA3 R |
| oEE316 | GTGAAGGGGGAGATTTTCACT | pFA-URA3 F |
| oEE289 | ATTGAACCCGGCTGCGGAACCC | pFA-CmLeu R |
| oEE290 | CGAATATTATTAATACAAAATGAACACCG | pFA-CmLeu F |
| oEE329 | CATCTTCGTCGTCACTGTGTTTATCC | CdHIS1 R |

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|---|---|---|
| oEE194 | GATACGTTGGTGGTTCAGTTGAGG | pSN52 F |
| oEE80 | GGTTCTAATGCTAGTCAAGCTAATGC | ORF19.875 F |
| oEE81 | ATATTCGTCTTGTTCCAAGCTATGC | ORF19.875 R |
| oEE78 | TGACGTTTGCTTGTAAGATTCC | ORF19.7292 F |
| oEE79 | CCGCATATAAAGATTTCCTTCC | ORF19.7292 R |
| oEE92 | GCCACTGAACATGAATTACG | ORF19.1084 F |
| oEE93 | TAGCAACTTCTGCATCTTGG | ORF19.1084 R |
| oEE142 | TCAATGCTGCCAATAGAACG | Tn r1 F |
| oEE143 | TCAACTCCAGTGACTTGTTCG | Tn r1 R |
| oEE144 | GATTATCCACCACCCAATTACC | Tn r5 F |
| oEE145 | GCAAAGTTGGACCTAAGAATCG | Tn r5 R |
| oEE146 | ACGGTTCTATCACCCAAGTGC | Tn r6 F |
| oEE147 | CAGGTCGTTCTGAGTTCTACCC | Tn r6 R |
| oEE148 | CTCCTCGATGTCGTATTTTCG | Tn r8 F |
| oEE149 | TCATCTTCCTCCGAAGTTAAGC | Tn r8 R |
| oEE382 | CCGCTCGAGCGGGATATAGATATATTAATTGCTTTAC | ARP2 NotI 2nd |

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[1] Lower-case letters (in blue) indicate annealing sequences for auxotrophic marker amplification or, as in the case for *G*ene *S*pecific *P*rimers (GSP), annealing sequences for fusion PCR (Noble et al. Strains and Strategies for Large-Scale Gene Deletion Studies of the Diploid Human Fungal Pathogen *Candida albicans*. Eukaryotic Cell (2005). Underlined sequences indicate restriction recognition sites. PCR verification of mutant constructs was done as previously described (Schaub et al. New pFA-cassettes for PCR-based gene manipulation in *Candida albicans*. J Basic Microbiol (2006).