

1146 **Supporting Information**

1147 **FIGURE S1**

1148 **Sequence alignment of *C. albicans* members of the Rta family by CLUSTAL OMEGA.**

1149 The black boxes indicate identical residues, whereas grey boxes indicate similar residues that are
 1150 present when three or more sequences are compared. The TMHMM program
 1151 predicts the presence of up to seven TMDs. The red box between TMS6 and TMS7 represents
 1152 the His-Glu-Tyr/Trp motif within a 28 amino acid stretch, considered as the signature motif of
 1153 the Rta1-like family of proteins.

1154

1155 **FIGURE S2**

1156 **Disruption of *RTA3* using the *SAT* flipper strategy.**

1157 (a) Schematic representation of disruption strategy. (b) *RTA3* reconstitution construct used to
 1158 integrate *RTA3* in the *rta3Δ/Δ* cells. (c) Southern hybridization showing genomic configuration
 1159 of *RTA3* in the wild-type (WT) locus and its deletion derivatives. Genomic DNA from strains
 1160 was digested with BglII. Lane 1, wild type (SC5314); lane 2, *RTA3/rta3Δ::SAT1-FLIP*; lane 2,
 1161 *RTA3/rta3Δ::FRT*; lane 3, *rta3Δ::SAT1-FLIP/rta3Δ::FRT*; lane 4, *rta3Δ::FRT/rta3Δ::FRT*; lane
 1162 5, *rta3Δ::FRT/rta3Δ::RTA3-SAT1-FLIP*.

1163

1164 **FIGURE S3**

1165 **NBD-PC is trafficked to the vacuole in *S. cerevisiae* and is concentrated in the**
 1166 **mitochondria in *C. albicans*.**

1167 (a) Wild type strains of *S. cerevisiae* (BY4741) and *C. albicans* (SC5314) were grown to an
 1168 OD₆₀₀ of 1, labelled with 5 μM NBD-PC for 45 min at 30 °C, followed by washing twice with
 1169 SDC. Cells were kept in fresh SDC media at 30 °C and labeled with FM4-64 (40 μM) for 30
 1170 min, washed with ice cold SC-azide three times. Cells were centrifuged, resuspended in ice cold
 1171 SC-azide and visualized by confocal microscopy. (b) *C. albicans* wild type strain (SC5314) was

1172 grown to an OD₆₀₀ of 1, labelled with 5 µM NBD-PC and co-stained with 20 nM MitoTracker™
1173 Red (MTR) for the indicated time points at 30 °C. At the indicated time points, aliquots of cells
1174 were removed and washed with ice cold SC-azide three times and visualized by confocal
1175 microscopy. Values on the right indicate mean fluorescence intensity (MFI) of NBD-PC in all
1176 strains measured by flow cytometry. Data represents the mean ± S.D of three independent
1177 experiments. m denotes mitochondria.

1178

1179 **FIGURE S4**

1180 **NBD-PC labels mitochondria at low temperature in *C. albicans***

1181 Wild type strain grown to an OD₆₀₀ of 1 was stained with 20 nM MitoTracker™ Red (MTR) at
1182 30 °C for 45 min, washed twice with SDC and resuspended in fresh SDC. Cells were then
1183 chilled on ice bath followed by labelling with 5 µM NBD-PC for 45 min at 2 °C and chased for
1184 30 min at 30 °C. At the indicated time points, aliquots were removed and washed with ice cold
1185 SC-azide and visualized by confocal microscopy. Values on the right indicate mean fluorescence
1186 intensity (MFI) of NBD-PC in all strains measured by flow cytometry. Data represents the mean
1187 ± S.D of three independent experiments. m denotes mitochondria.

1188

1189 **FIGURE S5**

1190 **Internalization assays for NBD-PC/PE and apparent flippase activity.**

1191 (a) Cells untreated or treated with 50 µM CCCP were labelled at 2 °C with DMSO solubilized
1192 NBD-PC, washed with cold SC-azide and were subjected to imaging by confocal microscopy.
1193 (b) Wild type and *rta3Δ/Δ* cells were labelled with 5 µM of DMSO solubilized NBD-labelled
1194 PE. Strains were grown till OD₆₀₀ of 1, incubated with NBD-PE for 45 min at 30 °C in SDC
1195 medium and washed with SDC. Samples were then incubated in SDC medium at 30 °C for 30
1196 min, washed with ice cold SC-azide and visualized by confocal microscopy. Values on the right

1197 indicate mean±S.D (n=3) fluorescence measurements by flow cytometry. (c) Flow cytometric
1198 analysis of the apparent flippase activity on the indicated strains by using 2 μM NBD-PE and the
1199 impermeant quencher sodium dithionite. The internalized PE is represented as the percentile
1200 dithionite-resistant NBD-PE fluorescence from total NBD-PE fluorescence.

1201

1202 **FIGURE S6**

1203 **In vitro biofilm formation**

1204 (a) *In vitro* biofilm assays were carried out in Spider medium by growing the biofilm directly on
1205 the bottom on the 96 well polystyrene plates, as described previously (Fox *et al.*, 2015, Lohse *et*
1206 *al.*, 2017). Briefly, strains were grown overnight in YEPD at 30 °C for 12-14 h and diluted to an
1207 optical density at OD₆₀₀ of 0.5 in 200 μl Spider medium. The inoculated plate was covered with
1208 a breathable film and incubated at 37°C for 90 min at 250 rpm agitation on an ELMI incubator
1209 (ELMI, Ltd. Riga, Latvia) for initial adhesion of cells. Post adhesion, the cells were washed with
1210 200 μL 1X PBS, and 200 μl of fresh Spider medium was added. The plate was covered with a
1211 fresh breathable film and incubated at 37 °C for an additional 24 h at 250 rpm agitation to allow
1212 for biofilm formation. Following incubation, the film and medium were removed and the OD₆₀₀
1213 was measured using a standard plate reader to determine the extent of biofilm formation. A well
1214 containing medium alone was included as a contamination control. Statistical significance (*P*
1215 values) was calculated using a Student's one-tailed paired t-test. *P* values are as follows: n.s is
1216 not significant, ** < 0.005 and *** < 0.0005. (b) Visual *in vitro* biofilm assays were carried out
1217 in Spider medium by growing the biofilm on silicone squares in 6-well plates, as described in
1218 Nobile *et al.*, 2012. A silicone square in a well containing medium alone was included as a
1219 contamination control. (c) qPCR based expression analysis of selected genes in the indicated
1220 strains. Fold change is calculated by $2^{-\Delta\Delta CT}$ and normalized to *ACT1* (endogenous control) with

1221 the reference strain as a calibrator. Values are mean \pm S.D and are derived from three
1222 independent experiments.

1223

1224 **FIGURE S7**

1225 **Flow cytometric analysis for measuring mitochondrial membrane potential.**

1226 Wild type cells grown to OD₆₀₀ of 1 were treated with 50 μ M CCCP for 30 min and 5 μ g ml⁻¹
1227 miltefosine for 60 min, washed three times with 1X PBS and stained with 2 nM DiOC₆(3). The
1228 stained cells were subjected to flow cytometric analysis. The drug treated wild type cells display
1229 greater percentage of cells with depolarized mitochondria (left quadrant), versus untreated wild
1230 type cells.

1231

1232 **TABLE S1** *C. albicans* strains used in this study

1233 **TABLE S2** Plasmid used in this study

1234 **TABLE S3** Oligonucleotides used in this study

1235 **TABLE S4** Oligonucleotides used for qPCR in this study

1236 **TABLE S5** List of 115 differentially expressed genes whose transcript levels in the *rta3 Δ / Δ*
1237 strain are 1.5-fold up- and down- regulated ($P \leq 0.05$)

1238

1239

Figure S1

scRSB1 1 -----
CaRTA1 1 MDGVSLLNQYLPSWTPSTLPTSTSIISTINPTNTAGLALTLLELQNAIQ---TETNTISLY
CaRTA2 1 ---MSEILNLYLSSWTPSTPTSTTLSSIATSHVSKLSQTVASVISQAT---TETDWNLR
CaRTA3 1 --MNTMDLAVITEWTPSTATSTTLSTIAATYAPALQSKI SGAVHTLTSKGSTIANMDYI
CaRTA4 1 ----MDLASITEWTPTTPTSTTLSTIAATYVPALQSKLSNAIDTLTSKGSTIDIVDYI

scRSB1 1 -----MSNATNN-----TLGSLLP
CaRTA1 58 FLSRAARGVAASYTIISGQQYLATATAT-----QDFPEVTSAMVNA-TL
CaRTA2 55 SLSQAYRGAQASLTIISA EKVLATATDS-----QVQSRATQAI FEA-TL
CaRTA3 59 SASRIIRGAQASLSIISA EHVLETATAT-----DVQAQATQIIWQA-TE
CaRTA4 56 SVSRIIRGAQASLSIISAQQVLATATNINTATATATDVQLQAQIQQAQAIQIIWQA-TE

TMS1 **TMS2**

scRSB1 15 QLEAAANSNSLYGGMVFNLRFNITMIVIWGILLTIHVV-QLLMROYWFSIAFICTGILEV
CaRTA1 101 SLKQLEWKANLYAI-NLSVPFNAFFAAMFGVTLICLLGIGFSTKTKYFTICLACGTILEV
CaRTA2 98 NLKDL SMEQNIYGY-ELNRAANIYLVVYAIIFGYTLLMCIKSKYWWYNVTFVCGYGLEF
CaRTA3 102 NLLDLAWEENVYDIPRLNRTANILFLVLF AITFAIACLMWIKSRYWWFNVAWTCGTALEF
CaRTA4 115 NLLDLAWEMNVYAI PKLNRVANILFLVIFAITFVMTCLMWIKSRYWWFNVS WTTCGTALEF

TMS3

scRSB1 74 LGFIGRTWSHSNVADMDAFLNMICLTIAPVFTMGGIYYQLAKLIEVYGHRFSLLPSPMA
CaRTA1 160 IGYVARTLAHYSWSDPNLFLCQIVSLTVAPAFIMAGVYYLLSQMI I IHGEQYAIL-KPIM
CaRTA2 157 VGFLGRVLSFNDTSNMSHYIMQSVALTIAPAFIMAGVYFLFGQLVVIHGRQYSVL-KPMW
CaRTA3 162 LGYLGRVLSFS DMKKFDYLLQLIALT LSPVFLMAGIYFLFGQLVVIHGRQYSWL-KPLH
CaRTA4 175 LGFLGRVLSFDDMTKFDYLLQLITLTLSPVFLMAGIYFLFGQLVVIHGRQYSML-KPLH

TMS4 **TMS5**

scRSB1 134 YSFI FICS DIVSLV VQAVGGGLCGVAVTDGTS TTTGNHVF IAGLAIQVASMAIFLMLWFH
CaRTA1 219 VSIIFIFCDVVS L FVQASGGAAA VSLRSFKDTELGTYIMVGGIGFQVVSMTLFLYFLFD
CaRTA2 216 YSYFFITADVVSLLIQAGGGIASVASSNHKDS SVGTNIMIAGIAAQVVAMTIFLVWFE
CaRTA3 221 YSYIFITCDVVS LVIQAVGGGMTAIAAQEYDDVDPGTYTMIAGIAFQVFSMSVFLCWL V
CaRTA4 234 YSYIFITCDVVS L VVQAVGGGMTSIAAQRYENVDSGTYTMIAGIAFQVFSMSVFLTFWFV

scRSB1 194 FLFR IYISVRWEHIN-SRP--IS-----ISL-----LKISQTEVDYLYREKFHF LRL
CaRTA1 279 FVYRSFFTANSN-----IKYSFSTYCSLLENTKKGRLL-RQDLEPFYDVG YKHIRQ
CaRTA2 276 FLNRIYFKNSRSDLIVDCP-YGRRSISNYFKLLLN VKSVRGHRHTHLEKY YNEKFASIRQ
CaRTA3 281 FCWNIYFRDISVNESKPS P-YQKKS FMTFIKLLLN GDDANMYKLKVL D KYN S SYKDLRR
CaRTA4 294 FCWNIYFRDISVNESKPS SYQKKS LITFIKLLLN GDDANKYKLQVLDKHYNLGYQDLRG

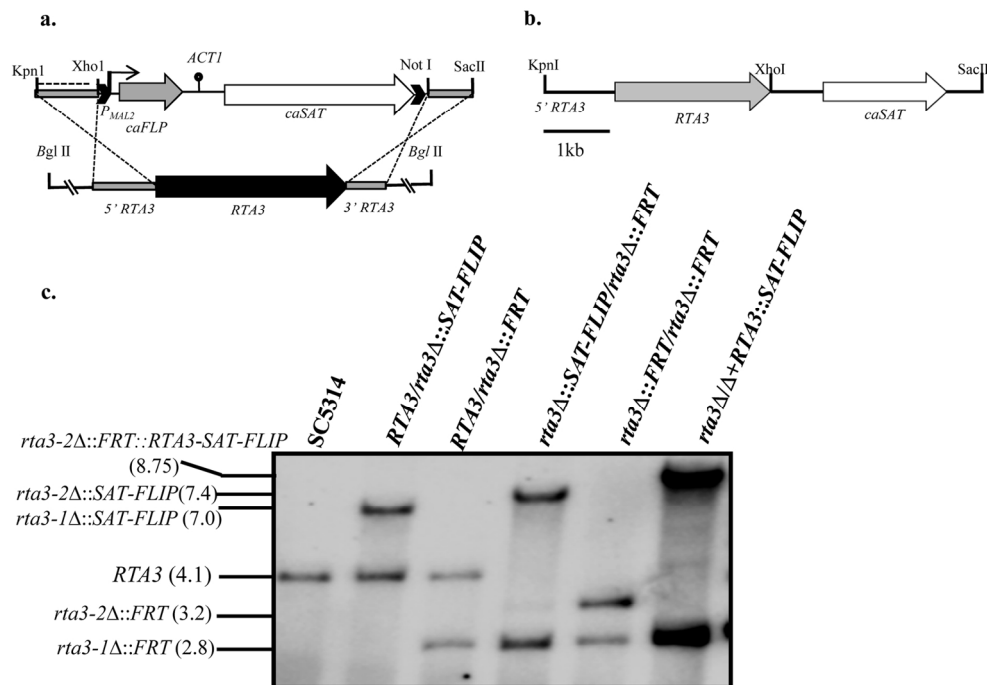
TMS6 **TMS7**

scRSB1 238 EPKRWFH YFNLAITVA VLTIFTRCCYRLAELVVGWDGYLITHEWYFIILDALMMAIATV
CaRTA1 329 ---RSLFN YMPLVIIISVGF IYIRCIYRVIELSEGWRGYLITHEEYIFALDALMVLLTCI
CaRTA2 335 ---IPLFDY MVLA MTI AVIVVYIRCVYRVAELAE GWGGYLF THEP YLMILDAAMIAIAGL
CaRTA3 340 ---RPLYNYAIAITLAVIAVYIRCIYRVVELAQGFSGYLITHEVYIMTLDAAMIGICCI
CaRTA4 354 ---RPLYNYAIAITSAVIAVYIRCVYRVVELAQGFRGYLITHEAYIMTLDAAMIAICCI

scRSB1 298 TLTIFHPGF AFKGRSTSIPI T-PGHVDPETLPHTDDVEDI----LDTS DSKQF-DIEKEE
CaRTA1 386 TYVFFHPGLVFGKQMTAQISVSA-NKSESAADHESHCGNSRMYNYSKNHSNSPQSSHDEK
CaRTA2 392 IFIPFHPVWVFGKNNIVKLATIKNLDENEKNQDVE-----Y--NDDVES--QERSS
CaRTA3 397 IFILFHPQVVMGSSNVVGLRSIAKNKDQETGDKSYE-----EKTNNDIVS--DNEES
CaRTA4 411 IFMLFHPQFVMG SINVI GFRSIAKNQDQEMGDTSTE-----VKTNEMKSL--V*---

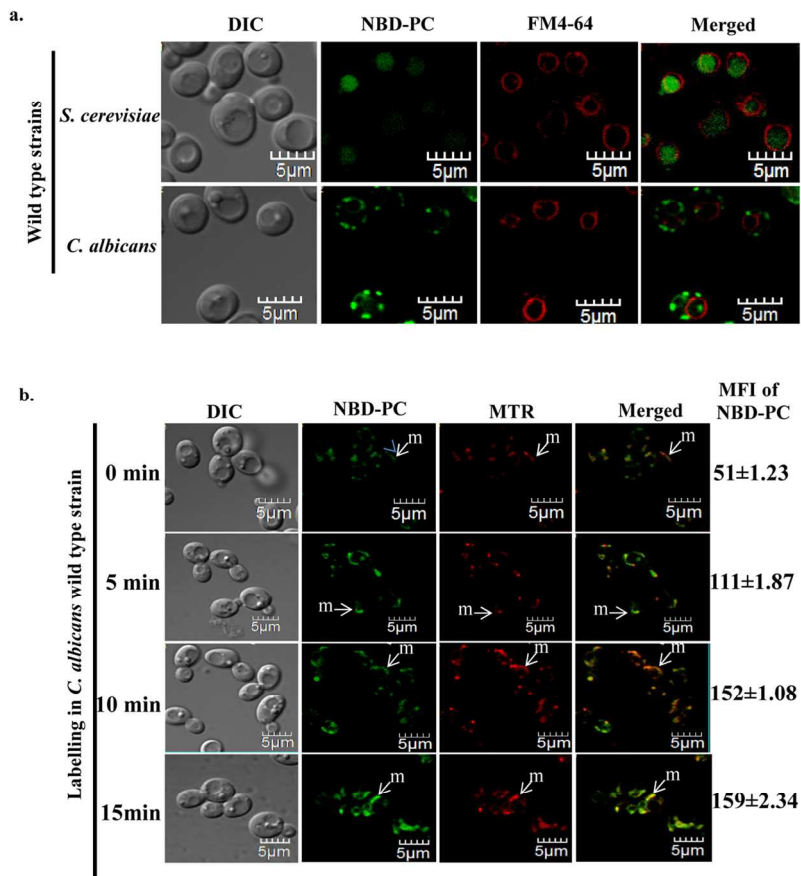
scRSB1 352 FQ--ASMK--YPI---STFKQFMSKIAN-----LFSSKKKAKL*-----
CaRTA1 445 FIMDQRQKY YNPYFLPTKFSQYN SHSCPSSETYTYSSYN SKLET KSESSWQNS*
CaRTA2 440 SVVANDIH-----CLNSKL*-----
CaRTA3 447 TLQGQNIVRGDP IQENKE*-----
CaRTA4 -----

Figure S2



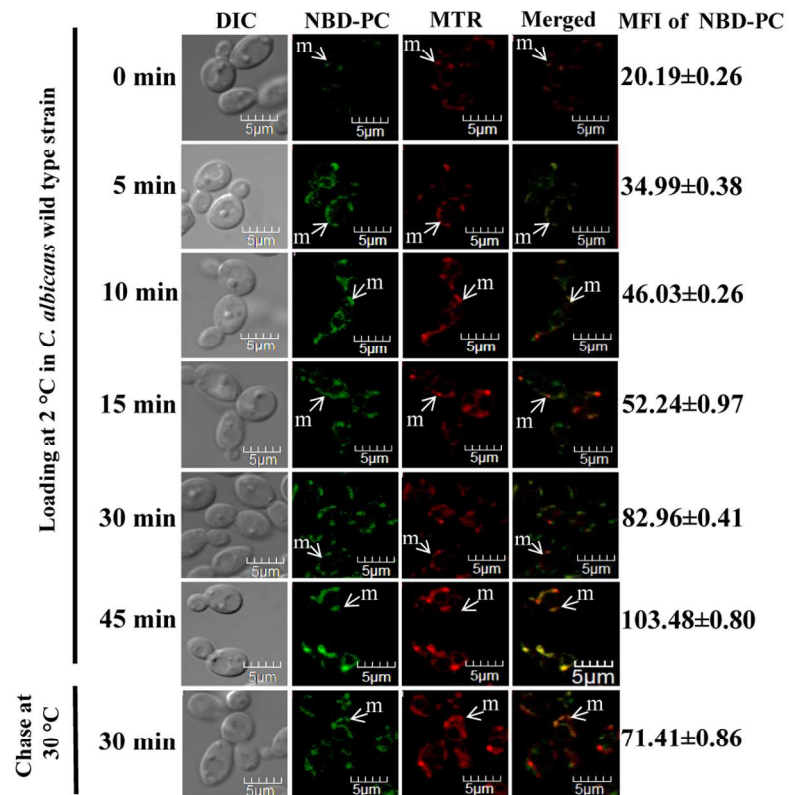
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Figure S3



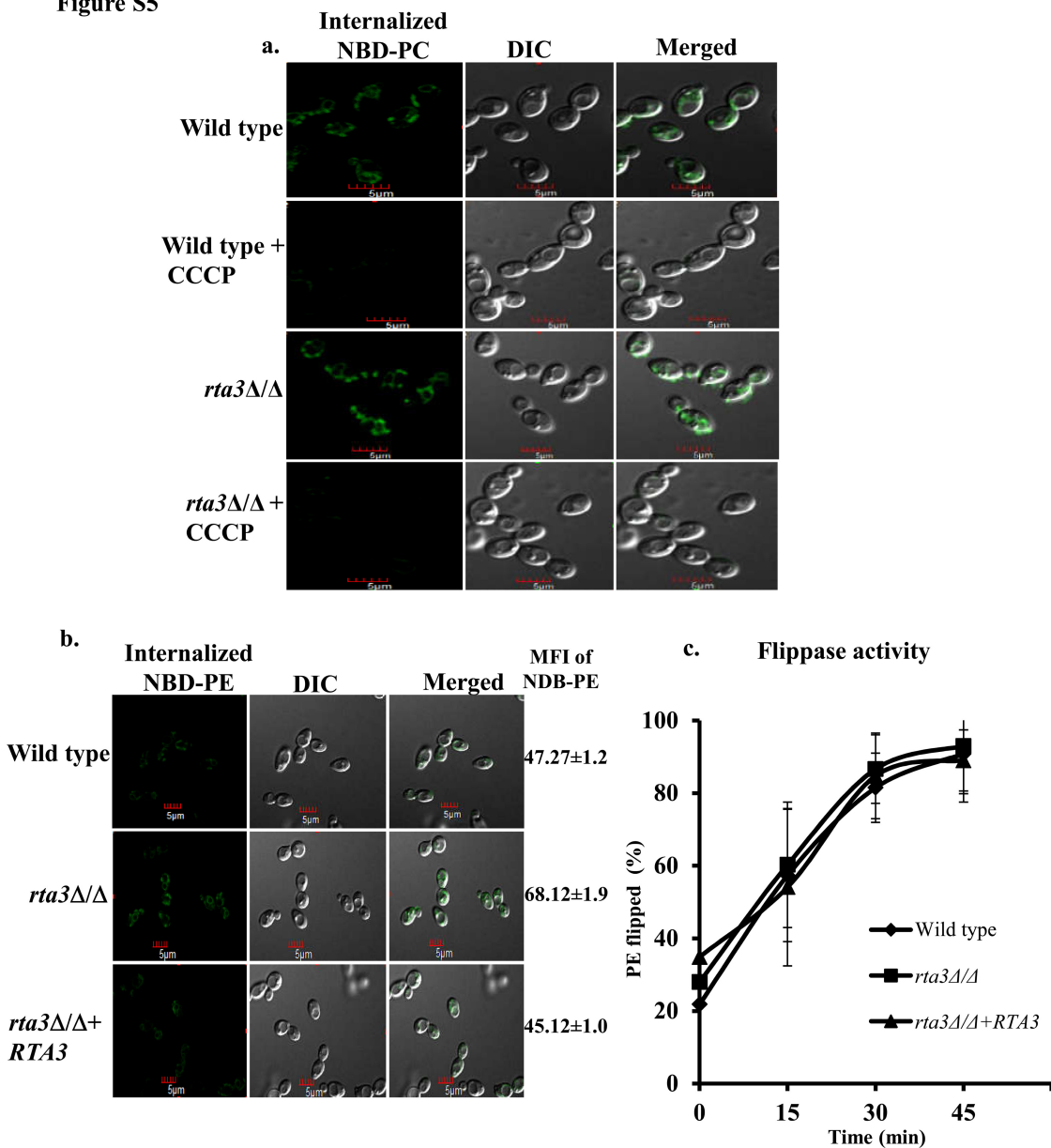
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Figure S4

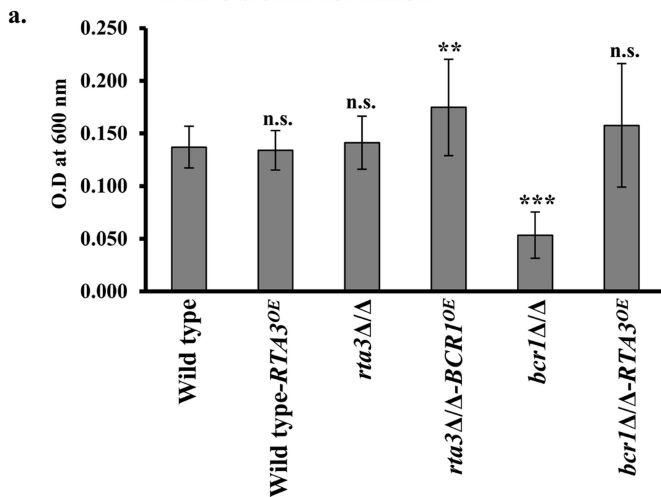


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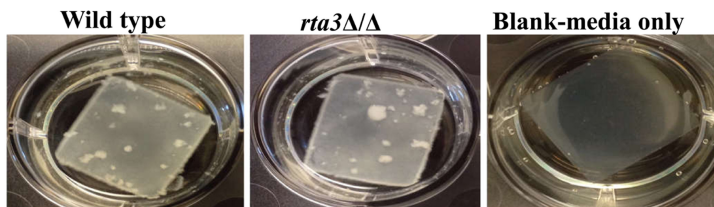
Figure S5



In vitro biofilm formation



b.



c.

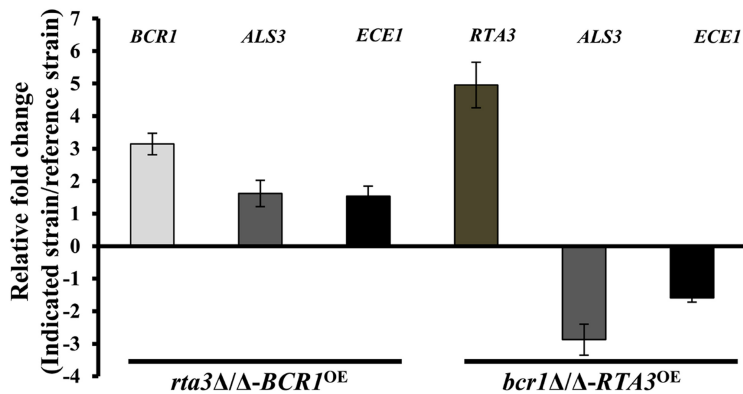


Figure S7

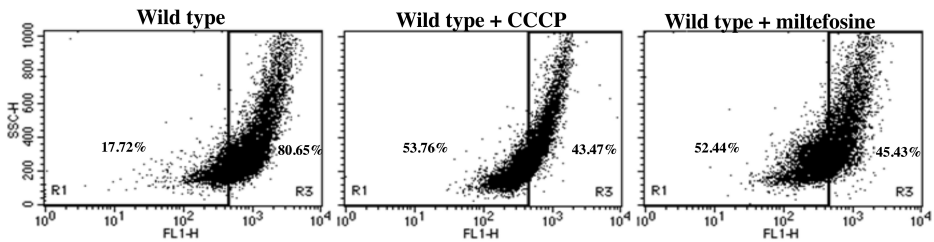


Table S1: Strains used in this study

Strain	Parent	Genotype	Source of reference
SC5314		Wild type	<i>Gillum AM, et al.</i> (1984)
AS10	SC5314	<i>RTA3/rta3Δ::SAT1-FLIP</i>	This study
AS11	AS10	<i>RTA3/rta3Δ::FRT</i>	This study
AS12	AS11	<i>rta3Δ::SAT1-FLIP/rta3Δ::FRT</i>	This study
AS13	AS12	<i>rta3Δ::FRT/rta3Δ::FRT</i>	This study
AS14	AS13	<i>rta3Δ::FRT/rta3Δ::RTA3-SAT-FLIP</i>	This study
AS15	SC5314	<i>RTA3-Myc-FRT-SAT1-FRT</i>	This study
AS16	SC5314	<i>RTA3-Myc-FRT</i>	This study
DSY2906	CAF4-2	<i>tac1Δ::hisG/tac1Δ::hisG</i>	<i>Coste et al.</i> (2004)
DSY2926	DSY2906	<i>tac1Δ::hisG/tac1Δ::hisG LEU2::TAC1-2/URA3</i>	<i>Coste et al.</i> (2004)
<i>bcr1Δ/Δ</i>	BWP17	<i>bcr1Δ::ARG4/bcr1Δ::URA3</i>	Nobile <i>et al.</i> (2006)
AS17	<i>bcr1Δ/Δ</i>	<i>bcr1Δ/Δ -TDH3-RTA3::NAT1</i>	This study
AS18	SC5314	<i>SC5314-TDH3-RTA3::NAT1</i>	This study
AS19	AS13	<i>rta3Δ/Δ-TDH3-BCR1::NAT1</i>	This study
AS20	SC5314	<i>SC5314-TDH3-BCR1::NAT1</i>	This study

TABLE S2 Plasmids used in this study

Plasmid	Description	Source or reference
pSFS2B	<i>SAT1</i> flipper carrying nourseothricin resistance gene	<i>Reuss O et al.</i> 2004.
pAS1	pSFS2B flanked 5' and 3' <i>RTA3</i> ^{NCR} for disruption of first allele of <i>RTA3</i>	This study
pAS2	pSFS2B flanked 5' and 3' <i>RTA3</i> ^{NCR} for disruption of second allele of <i>RTA3</i>	This study
pAS3	<i>RTA3</i> reconstitution construct	This study
pADH34	C-terminal Myc tagging plasmid	<i>Nobile et al.</i> (2009)
pCJN542	<i>NAT1-TDH3</i> promoter plasmid	<i>Nobile et al.</i> (2008)

Table S3. Oligonucleotides used in this study

Oligonucleotide	Description	Sequence (5'→3')
RTA3P1	Forward primer for amplifying 5' <i>RTA3</i> NCR bearing Kpn1 site	5' -GGGGTACCTGAAATGACTTCATAATGCTCAT- 3'
RTA3P2	Reverse primer for amplifying 5' <i>RTA3</i> NCR bearing Xho1 site	5' -CCGCTCGAGGAGCCTGTCTTTTTTTCAATATT- 3'
RTA3P3	Forward primer for amplifying 3' <i>RTA3</i> ^{NCR} bearing Not1 site	5' -ATTTGCGGCCGCATTTGAATGTAACTAAGG- 3'
RTA3P4	Reverse primer for amplifying 3' <i>RTA3</i> ^{NCR} bearing SacII site	5' -TCCCCGCGGGAAGGGTGGGAATGAACTG- 3'
RTA3P5	Forward primer for amplifying 3' <i>RTA3</i> ^{ORF} bearing Not1 site	5' -ATTTGCGGCCGCAGTGTTTTCCATGTCGGTG- 3'
RTA3P6	Reverse primer for amplifying 3' <i>RTA3</i> ^{ORF} bearing SacII site	5' -TCCCCGCGGTTTCTTCATAACTTTTGTC- 3'
RTA3P7	Reverse primer for amplifying 5' <i>RTA3</i> ^{NCR} + <i>RTA3</i> ^{ORF} bearing Xho1 site	5'-CTCGAGTCATTCCTTAT TCTCTTG-3'
RTA3 mycF nostop	To amplify 65 bp <i>RTA3</i> ORF myc tag region	5'-GAATCGACGTTGCAAGGTCAAATATTGTTAGGGGTG ATCCTATTCAAGAGAATAAGGAACGGATCCCCGGGTTA ATTAACGG-3'
RTA3 mycR UTR	To amplify 65 bp <i>RTA3</i> UTR myc tag region	5'-ATAGCCACCTTTTTCACTTGCATTTAAGTTGCTAGGA ATCATACCACCCTTAGTTAACATTCAAATGGCGGCCG CTCTAGAAGTAGTGGATC-3'
DET RTA3F	To detect <i>RTA3</i> myc construct integration	5'-TGTTTTTATTATGTTGGCTTGTC-3'
DET RTA3 R	To detect <i>RTA3</i> myc construct integration	5'-CGAAGATCTCTACAATAAGCC-3'
AHO300	To detect <i>RTA3</i> myc construct integration	5'-CCGTTAATTAACCCGGGGATC-3'
AHO301	To detect <i>RTA3</i> myc construct integration	5'-GGAACTTCAGATCCACTAGTTCTAGAGC-3'
AHO302	To detect <i>RTA3</i> myc construct integration	5'-TCACTAGTGAATTCGCGCTCGAG-3'
AHO283	To detect <i>RTA3</i> myc	5'- GGCGGCCGCTCTAGAAGTAGTGGATC-3'

	construct integration/amplicon sequencing	
rta3myc(150bp upstream of stop codon)	To detect <i>RTA3</i> myc construct integration/amplicon sequencing	5'-TCCACAAGTTGTAATGGGATCA-3'
BCR1-F-OE-Ag-NAT-Ag-TEF1p	Forward primer for <i>BCR1</i> ^{OE}	5'- AGGGTCATACTTGAATTATATTATATTAACCAAAC ACACACACAGTAATAAGTTTTCTCCAGTGACAACTTTT CACTTTACTCCCTCCTTTAATTTATCAAGCTTGCCTCG TCCCC-3'
BCR1-R-OE-Ag-NAT-Ag-TDH3p	Reverse primer for <i>BCR1</i> ^{OE}	5'-GTGGTGGTGGATACATCATTGGTTGTCTTTGATTATA AGCCATAGATGCGTGCTGTGATTGATGGGAATCGTTTT GAAGTACTTGTGATGTCCTGACATATTTGAATTCAATT GTGATG-3'
RTA3-F-OE-Ag-NAT-Ag-TEF1p	Forward primer for <i>RTA3</i> ^{OE}	5'-ATAAGTTATTCCTAATCTGCTAAAAAA AAGAAACAT GGTTACTCTTAGAATAGTTATAGATCCACACGGAAGTC GGAAATTATGCACTGAATGTAAATCAAGCTTGCCTCGT CCCC-3'
RTA3-R-OE-Ag-NAT-Ag-TDH3p	Reverse primer for <i>RTA3</i> ^{OE}	5'-AAGCTGGGGCATAAGTTGCAGCAATGGTGGATAGAG TTGTTGAAGTTGCAGTTGAGGTAGGAGTCCTTCTGTAA TTACCGCAAGATCCATAGTATTCATATTTGAATTCAATT G TGATG-3'
Nat-OE-R-det2-CJN	Detection primer for OE	5'- GAAACAACAACGAAACCAGC -3'
BCR1-OE-F-det	Detection primer for OE	5'- CAGTAATAAGTTTTCTCCAGTGAC -3'
RTA3-OE-F-det	Detection primer for OE	5'-CATGGTTACTCTTAGAATAGTTAT -3'

Table S4. Oligonucleotides used for qPCR in this study

qACT1-F	5'-GAAGCCCAATCCAAAAGA-3'
qACT1-R	5'-CTTCTGGAGCAACTCTCAATTC-3'
qRTA3-F	5'-TACAGAATGGACTCCTACCT-3'
qRTA3-R	5'-CCCGTACCATTTAATCGA-3'
qALS1-F	5'-GCAGTCGTCTGCAAAGTAAACCT-5'
qALS1-R	5'-CCGTTAGATCCGGCATCACT-3'
qALS3-F	5'-CCCCAACTTGGAATGCTGTT-3'
qALS3-R	5'-TGTATCTCCCGGACTTGCACTA-3'
qBCR1-F	5'-CGCCGACATTAACCAATGCT-3'
qBCR1-R	5'-CCGACGATTCAGCTGATGAA-3'
qECE1-F	5'-CATGACTTCTGTTGCTTCTACCAAGA-3'
qECE1-R	5'-CAATCTGACGACGGCATTAGC-3'
qHWP1-F	5'-TGGTTCAGAACCATCCATGC-3'
qHWP1-R	5'-GGAATAGATGGTTGTGAACCAGC-3'
qSOD5-F	5'-TCACGCCAACAATGGTACCA -3'
qSOD5-R	5'-AAGGCAGCAATGACACCAAC -3'
qUME6-F	5'-TGGCTCCACTTACAAATCATAGTG-3'
qUME6-R	5'-CAATCCTAGTCCCAACTCCAGATC-3'

ProbeName	p Value	FC (absolu	Regulation	Alias	Gene Name	Gene Symbol
GT_Calbica	0.03	1.61	up	orf19.9791	Adenine deaminase; purine	AAH1
GT_Calbica	0.04	1.54	up	IPF3082.1	Protein similar to a region o	ACB1
GT_Calbica	0.03	2.00	down	orf19.1322	NAD-aldehyde dehydrogena	ALD5
GT_Calbica	0.01	2.43	down	orf19.8361	Putative aldehyde dehydrog	ALD6
GT_Calbica	0.02	7.27	down	orf19.9379	Cell wall adhesin; epithelial	ALS3
GT_Calbica	0.03	1.68	up	orf19.1036	Aquaporin water channel; o	AQY1
GT_Calbica	0.02	8.44	down	AFF2 CaO	Putative fungal-specific tran	ATO1
GT_Calbica	0.00	2.90	down	orf19.1113	Copper transporter; transcri	CTR1
GT_Calbica	0.01	1.64	up	orf19.1290	Putative allantoinase; trans	DAL1
GT_Calbica	0.01	22.23	down	orf19.1088	Hypha-specific protein; regu	ECE1
GT_Calbica	0.04	1.78	down	orf19.1169	Multicopper ferroxidase; ind	FET34
GT_Calbica	0.01	1.71	down	orf19.8477	Protein with a monooxygen	FMO2
GT_Calbica	0.01	1.80	down	orf19.8991	Major cell-surface ferric red	FRE10
GT_Calbica	0.03	2.89	down	orf19.1355	Copper-regulated cupric red	FRE7
GT_Calbica	0.01	2.17	down	IPF868.1 C	High-affinity iron permease;	FTR1
GT_Calbica	0.03	2.08	down	orf6.7739	General amino acid permea	GAP2
GT_Calbica	0.00	1.84	up	orf19.9325	Glycerol-3-phosphate dehyd	GPD1
GT_Calbica	0.01	1.68	up	orf19.8310	Surface protein similar to gl	GPD2
GT_Calbica	0.04	1.72	up	orf19.7992	Ortholog(s) have glutathion	GTT12
GT_Calbica	0.03	9.45	down	orf19.1301	3-hydroxypropionate dehyd	HPD1
GT_Calbica	0.02	19.98	down	orf19.8901	Hyphal cell wall protein; hos	HWP1
GT_Calbica	0.03	1.64	down	orf19.1244	GPI-anchored hyphal cell wa	HYR1
GT_Calbica	0.02	1.93	up	orf19.1322	Putative hydantoin utilizatio	HYU1
GT_Calbica	0.02	2.53	up	orf19.1253	Putative protein kinase; role	IRE1
GT_Calbica	0.03	1.55	down	IPF492.1 C	Copper fist transcription fac	MAC1
GT_Calbica	0.03	1.90	down	orf19.1146	Putative high-affinity maltos	MAL31
GT_Calbica	0.04	1.53	down	IPF2363.1	Transcription factor; regulat	MCM1
GT_Calbica	0.04	1.85	up	IPF2441.1	Putative protein constituent	NSA2
GT_Calbica	0.02	1.50	up	orf6.8731	Neutral trehalase; hyphal in	NTH1
GT_Calbica	0.00	1.78	down	CaO19.260	Oligopeptide transporter; tr	OPT1
GT_Calbica	0.01	2.21	down	orf19.1311	Putative oligopeptide transp	OPT7
GT_Calbica	0.04	1.67	down	orf19.1011	Probable pseudogene simila	OPT9
GT_Calbica	0.01	1.53	down	orf19.1064	NAD(P)H oxidoreductase far	OYE32
GT_Calbica	0.00	4.35	down	orf19.1377	GPI-anchored cell wall prote	PGA13
GT_Calbica	0.01	1.69	down	orf19.1122	Putative GPI-anchored prote	PGA23
GT_Calbica	0.04	1.63	down	orf19.1264	Thioredoxin peroxidase; tra	PRX1
GT_Calbica	0.02	1.56	down	CaO19.140	Putative peptidyl-prolyl cis/	RRD1
GT_Calbica	0.04	1.84	up	orf19.7691	Putative serine/threonine-p	RTS1
GT_Calbica	0.04	2.16	down	orf19.1303	Secreted aspartyl proteinase	SAP5
GT_Calbica	0.00	2.10	down	orf19.8319	Protein with similarity to pe	SEO1
GT_Calbica	0.00	1.62	down	orf19.1141	Putative succinate-fumarate	SFC1
GT_Calbica	0.01	6.58	down	orf19.9607	Cu and Zn-containing super	SOD5
GT_Calbica	0.04	2.25	up	orf19.1107	DNA endonuclease; require	SPO11
GT_Calbica	0.04	1.55	down	orf19.8421	Putative GABA transaminase	UGA1
GT_Calbica	0.03	4.06	down	orf19.9381	Zn(II)2Cys6 transcription fac	UME6
GT_Calbica	0.01	1.50	down	CaO19.132	Predicted amino acid transmembrane transporter	

GT_Calbica	0.04	1.52	down	IPF18710.1	Dubious open reading frame
GT_Calbica	0.03	1.52	down	0	Ortholog of <i>Candida tropicalis</i> MYA-3404 : CTRG_
GT_Calbica	0.01	1.52	down	orf19.1263	Ortholog(s) have cytosol, nucleus localization
GT_Calbica	0.01	1.53	down	orf19.9363	D-arabinose 5-phosphate isomerase; has GutQ do
GT_Calbica	0.02	1.54	down	IPF13883.1	Ortholog of <i>C. dubliniensis</i> CD36 : Cd36_73420, D
GT_Calbica	0.05	1.56	up	IPF27310.1	Ortholog of <i>Candida albicans</i> WO-1 : CAWG_0287
GT_Calbica	0.01	1.57	down	orf19.8714	Protein similar to <i>Candida boidinii</i> formate dehyd
GT_Calbica	0.02	1.57	up	orf19.1024	Putative plasma membrane protein; Plc1-regulate
GT_Calbica	0.03	1.59	down	orf19.8751	Protein similar to <i>A. nidulans</i> CysA serine O-trans-
GT_Calbica	0.02	1.61	up	CaO19.108	Ortholog of <i>C. parapsilosis</i> CDC317 : CPAR2_6011
GT_Calbica	0.03	1.61	down	CaO19.126	Ortholog of <i>Candida albicans</i> WO-1 : CAWG_0564
GT_Calbica	0.04	1.61	down	orf19.1388	Similar to bacterial DnaJ; transcript upregulated in
GT_Calbica	0.02	1.61	down	orf19.1056	Ortholog(s) have protein kinase activity, role in ac
GT_Calbica	0.01	1.62	down	orf19.9176	Ortholog(s) have cytosol, nucleus localization
GT_Calbica	0.01	1.63	down	TCD2 CaO	<i>S. pombe</i> ortholog SPBC460.04c is a predicted sul
GT_Calbica	0.05	1.64	down	IPF2232.1	Putative oxidoreductase; mutation confers hypers
GT_Calbica	0.04	1.65	down	IPF1286.1	Has domain(s) with predicted nucleic acid binding
GT_Calbica	0.01	1.65	down	orf19.8043	Protein of unknown function; induced by Sfu1; Sp
GT_Calbica	0.01	1.65	up	orf19.1357	Ortholog of <i>C. dubliniensis</i> CD36 : Cd36_06640, C
GT_Calbica	0.02	1.71	down	orf19.8351	Possible dehydrogenase; flow model biofilm induc
GT_Calbica	0.00	1.71	up	LPF44 CaO	Protein of unknown function; Hap43-repressed ge
GT_Calbica	0.03	1.73	up	CaO19.856	Protein of unknown function; transcript repressed
GT_Calbica	0.05	1.74	down	orf19.1398	Protein of unknown function; expression decrease
GT_Calbica	0.04	1.75	down	0	Predicted ORF in retrotransposon Tca16 with simi
GT_Calbica	0.02	1.76	up	CaO19.191	Protein of unknown function; Spider biofilm repre
GT_Calbica	0.02	1.78	down	orf19.8762	Putative DnaJ-like molecular chaperone; Spider bi
GT_Calbica	0.00	1.80	up	orf19.1088	Putative protein of unknown function; transcript v
GT_Calbica	0.04	1.82	up	IPF27469.1	Dubious open reading frame
GT_Calbica	0.05	1.84	up	IPF21763.1	Ortholog of <i>Candida albicans</i> WO-1 : CAWG_0235
GT_Calbica	0.04	1.91	down	orf19.1193	Predicted heme-binding stress-related protein; Tr
GT_Calbica	0.04	1.93	up	IPF2138.1	Ortholog(s) have TRC complex, nucleus localizatio
GT_Calbica	0.03	1.94	down	orf19.1096	Protein of unknown function; oxidative stress-ind
GT_Calbica	0.01	1.96	down	orf19.1116	Putative oxidoreductase; Spider biofilm induced
GT_Calbica	0.04	2.03	down	0	Protein of unknown function; Spider biofilm induc
GT_Calbica	0.00	2.05	up	orf19.1381	Ortholog of <i>C. dubliniensis</i> CD36 : Cd36_72300, C
GT_Calbica	0.02	2.09	down	orf6.8476	Putative ferric reductase; induced by Mac1 under
GT_Calbica	0.03	2.10	up	IPF29232.1	Dubious open reading frame
GT_Calbica	0.03	2.11	down	orf19.1365	Has domain(s) with predicted phosphatidylinosito
GT_Calbica	0.03	2.11	down	orf19.9714	Putative sterol deacetylase; flow model biofilm in
GT_Calbica	0.01	2.12	up	IPF28792.1	Ortholog of <i>Candida albicans</i> WO-1 : CAWG_0346
GT_Calbica	0.05	2.13	up	orf19.9113	Protein of unknown function; F-12/CO2 early biof
GT_Calbica	0.00	2.13	up	IPF5225.1	Ortholog of <i>Candida albicans</i> WO-1 : CAWG_0000
GT_Calbica	0.04	2.15	up	orf19.9338	Ortholog(s) have G-protein beta/gamma-subunit
GT_Calbica	0.04	2.19	down	IPF26615.1	Protein of unknown function; hypoxia, Hap43-rep
GT_Calbica	0.03	2.20	down	IPF26615.1	Protein of unknown function; hypoxia, Hap43-rep
GT_Calbica	0.01	2.21	up	orf19.1328	Ortholog of <i>C. dubliniensis</i> CD36 : Cd36_84160, C
GT_Calbica	0.05	2.21	up	orf19.8216	Has domain(s) with predicted heme binding, pero

GT_Calbica	0.05	2.25	down	IPF27249.1	Ortholog of Candida albicans WO-1 : CAWG_0224
GT_Calbica	0.01	2.31	up	orf19.1353	Protein of unknown function; transcript detected
GT_Calbica	0.04	2.31	down	IPF26615.1	Protein of unknown function; hypoxia, Hap43-rep
GT_Calbica	0.01	2.41	up	orf19.1292	Protein of unknown function; induced by Mnl1 un
GT_Calbica	0.02	2.41	down	orf19.1221	Protein of unknown function; hyphal-induced exp
GT_Calbica	0.05	2.42	up	orf19.1149	Similar to <i>S. pombe</i> mug180, a predicted esterase
GT_Calbica	0.01	2.46	up	IPF23870.1	Putative mitochondrial phosphatidylglycerophosp
GT_Calbica	0.02	2.49	up	IPF5217.1	Protein of unknown function; Spider biofilm repre
GT_Calbica	0.01	2.52	up	orf19.1073	Putative rRNA processing protein; Spider biofilm i
GT_Calbica	0.00	2.73	up	orf19.1242	Ortholog(s) have spermine synthase activity, role
GT_Calbica	0.04	2.74	up	IPF29760.1	Dubious open reading frame
GT_Calbica	0.01	2.79	up	orf19.1153	Protein similar to <i>S. cerevisiae</i> Ybr075wp; transpo
GT_Calbica	0.04	2.79	up	CaO19.184	Predicted lipid-binding ER protein; involved in ER-
GT_Calbica	0.00	2.88	up	orf19.1351	Cardiolipin synthase; ortholog of <i>S. cerevisiae</i> Crd
GT_Calbica	0.01	2.94	down	orf19.8411	Ortholog(s) have protein serine/threonine kinase
GT_Calbica	0.04	2.98	down	0	Protein of unknown function; Spider biofilm induc
GT_Calbica	0.02	2.98	up	orf19.1353	Protein of unknown function; transcript detected
GT_Calbica	0.01	3.18	up	IPF5228.1	Putative zinc-finger domain protein with a predict
GT_Calbica	0.01	3.67	up	0	ORF added to Assembly 21 based on comparative
GT_Calbica	0.00	4.48	down	orf19.1408	Protein of unknown function; Sef1, Sfu1, and Hap
GT_Calbica	0.00	4.98	up	IPF5661.2	Protein of unknown function; Spider biofilm repre
GT_Calbica	0.01	5.21	up	IPF26207.1	Protein of unknown function

Gene Type	ORF_ID						
ORF Verified	orf19.2251						
ORF Uncharacterized	orf19.7043.1						
ORF Uncharacterized	orf19.5806						
ORF Uncharacterized	orf19.742						
ORF Verified	orf19.1816						
ORF Verified	orf19.2849						
ORF Uncharacterized	orf19.6169						
ORF Verified	orf19.3646						
ORF Uncharacterized	orf19.5454						
ORF Verified	orf19.3374						
ORF Verified	orf19.4215						
ORF Uncharacterized	orf19.857						
ORF Verified	orf19.1415						
ORF Verified	orf19.6139						
ORF Verified	orf19.7219						
ORF Verified	orf19.6993						
ORF Verified	orf19.1756						
ORF Verified	orf19.691						
ORF Uncharacterized	orf19.359						
ORF Verified	orf19.5565						
ORF Verified	orf19.1321						
ORF Verified	orf19.4975						
ORF Uncharacterized	orf19.5804						
ORF Verified	orf19.5068						
ORF Verified	orf19.7068						
ORF Uncharacterized	orf19.3981						
ORF Verified	orf19.7025						
ORF Uncharacterized	orf19.7424						
ORF Verified	orf19.7479						
ORF Verified	orf19.2602						
ORF Verified	orf19.5673						
pseudogene	orf19.2584						
ORF Verified	orf19.3131						
ORF Verified	orf19.6420						
ORF Verified	orf19.3740						
ORF Verified	orf19.5180						
ORF Uncharacterized	orf19.6792						
ORF Uncharacterized	orf19.20						
ORF Verified	orf19.5585						
ORF Uncharacterized	orf19.700						
ORF Verified	orf19.3931						
ORF Verified	orf19.2060						
ORF Verified	orf19.3589						
ORF Uncharacterized	orf19.802						
ORF Verified	orf19.1822						
ORF Uncharacterized	orf19.5826						

ORF Dubious	orf19.4196						
ORF Uncharacterized	orf19.2018.2						
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ORF Dubious	orf19.7348						
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ORF Uncharacterized	orf19.6530						
ORF Uncharacterized	orf19.3049						
ORF Uncharacterized	orf19.1608						
ORF Uncharacterized	orf19.6398						
ORF Verified	orf19.6899						
ORF Uncharacterized	orf19.7380						
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ORF Uncharacterized	orf19.951						
ORF Uncharacterized	orf19.6688						
ORF Uncharacterized tra	orf19.1490.1						
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ORF Verified	orf19.4459						
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ORF Dubious	orf19.7555						
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ORF Uncharacterized	orf19.1105.3						

