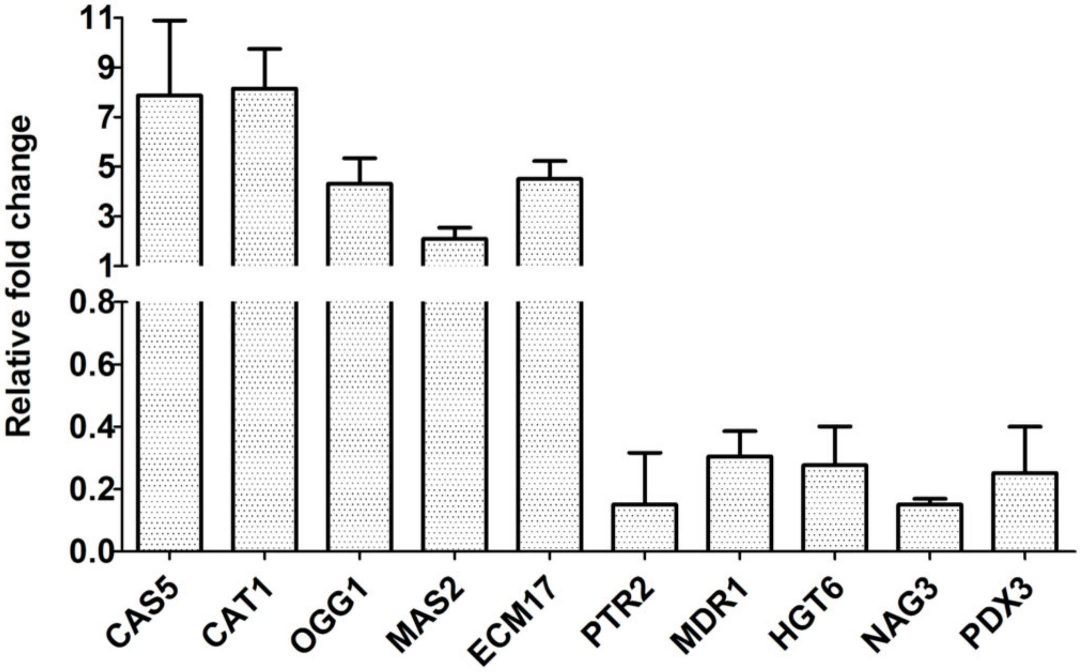

Fig. S1. Real Time RT-PCR analysis of several genes identified as differentially expressed by microarray experiments. 18S rRNA was used to normalize the expression data. Data are shown as mean ± standard deviation from three experiments.

Table S1. List of primers used for Real Time RT-PCR in this study [a]

Primer name	Sequence
CAS5-F	CGCTAGGCCAACTTTGTCA
CAS5-R	TCATCAACAACGGGCCCA
CAT1-F	ACTGTCCTGTCACCGGTG
CAT1-R	TGGAATGGAGTGGCAGCA
OGG1-F	CCTTCGACAAGACCCATGG
OGG1-R	TGCTTCTGGTGTCGGGAA
MAS2-F	GGAGGTCCTGGAAAGGGG
MAS2-R	ACATGAGCAGCTTCAGGGA
ECM17-F	ATCTGGGCCGCATTAGGT
ECM17-R	AACCGCAGAAATGGCACC
PTR2-F	GTCTGCTTTCTCCGCTGC
PTR2-R	CGTGGATTCCTCTGTTGGC
MDR1-F	TGGTGTTGGCCCATTGGT
MDR1-R	CCAAGCGGCTAACCCAAC
HGT6-F	GGTTCCGTTGCCATGTCC
HGT6-R	AGACACCACCAGCCCATG
NAG3-F	TCGCCTTTGCCTGGTCTT
NAG3-R	TGCCCATTCGTCGCCTAA
PDX3-F	ACATTCTTCTGGCCACATGT
PDX3-R	TGGTATTTCGTGGTCCTGCA
18S-F	TCTTTCTTGATTTTGTGGGTGG
18S-R	TCGATAGTCCCTCTAAGAAGTG

[a] Abbreviations: F, forward primer; R, reverse primer

Table S2. Gene expression changes of FLC-resistant *C. albicans* 0304103 in response to combination treatment with 8 μg/ml FLC and 16 μg/ml OST versus mono-treatment with 8 μg/ml FLC. Listed here are all the genes we detected with the mean fold changes ⩾ 2 or ⩽ 0.5, and with a q-value % ⩽ 5 estimated from three biological replicates. (A) Mean fold changes ⩾ 2 indicate up-regulated genes in the combination group cells, and (B) Mean fold changes ⩽ 0.5 indicate down-regulated genes in the combination group cells.

(A) Up-regulated genes in the combination group cells

Name	**sequence_id**	**q-value(%)**	**Fold Change**	**Description**
CAS5	orf19.4670	0	14.82768889	Transcription factor; cell wall damage response; required for adherence, response/resistance to caspofungin; repressed in core stress response
CAT1	orf19.6229	0	11.0102	Catalase; role in resistance to oxidative stress, including neutrophils, peroxide; role in systemic virulence in mouse; regulated by iron, ciclopirox olamine, fluconazole, growth, oxidative stress, carbon source, pH, Rim101p, Ssn6p
-	orf19.6741	0	10.20152222	Putative plasma membrane protein; predicted role in cell wall integrity; regulated by Nrg1, Tup1; induced during chlamydospore formation in both *C. albicans* and *C. dubliniensis*
GIN4	orf19.663	0	9.9001	Kinase involved in pseudohyphal-to-hyphal switch; mutant is pseudohyphal; necessary for septin ring within germ tube, but not for septin band at mother cell junction; phosphorylation possibly regulatory
-	orf19.3048	0	9.885344444	Protein of unknown function; repressed by alpha pheromone in SpiderM medium
YHM2	orf19.4197	0	9.828111111	Alkaline upregulated
-	orf19.6770	0	9.587788889	protein with ENTH Epsin domain, N-terminal; Spider biofilm repressed
-	orf19.4657	0	8.626866667	Ortholog(s) have phosphoprotein phosphatase activity and role in negative regulation of phospholipid biosynthetic process, nuclear envelope organization, positive regulation of phosphatidate phosphatase activity, protein dephosphorylation
-	orf19.6920	0	8.468755556	Protein of unknown function; induced during chlamydospore formation in both *C. albicans* and *C. dubliniensis* ; Hap43-induced gene; Spider biofilm induced; F-12/CO2 early biofilm induced
-	orf19.4907	0	8.402577778	Putative protein of unknown function; Hap43p-repressed gene; increased transcription is observed upon fluphenazine treatment; possibly transcriptionally regulated by Tac1p; induced by nitric oxide; fungal-specific (no human/murine homolog
FOX2	orf19.1809	0	8.126333333	Predicted 3-hydroxyacyl-CoA epimerase; upregulated upon phagocytosis; transcription is regulated by Mig1p; expression is regulated upon white-opaque switching
-	orf19.6724	0	7.441277778	Protein described as fumarate hydratase; transcriptionally regulated by iron; expression greater in high iron
PAM18	orf19.4190	0	7.390988889	Predicted component of the presequence translocase-associated import motor (PAM complex) involved in protein import into mitochondrial matrix; rat catheter biofilm induced
-	orf19.6007	0	7.289311111	Predicted fatty acid acyl transferase-related protein domain; repressed by prostaglandins
BEM2	orf19.6573	0	6.8906	Putative Rho1p GTPase activating protein (GAP); serum-induced transcript; Spider biofilm induced; flow model biofilm repressed
HAP41	orf19.740	0	6.461566667	Putative Hap4-like transcription factor; Hap43-repressed; not required for response to low iron; induced by Mnl1 under weak acid stress; Spider biofilm induced
YOX1	orf19.7017	0	5.8783	Putative homeodomain-containing transcription factor; transcriptional repressor; periodic mRNA expression, peak at cell-cycle G1/S phase

ACO2	orf19.6632	0	5.747811111	Protein described as aconitate hydratase 2; regulated by Gcn4p; repressed in response to amino acid starvation (3-aminotriazole treatment); transcriptionally regulated by iron; expression greater in high iron
-	orf19.7288	0	5.683822222	Protein with predicted oxidoreductase and dehydrogenase domains; Hap43-repressed; Spider biofilm induced
PPR1	orf19.3986	0	5.446533333	Transcription factor with zinc cluster DNA-binding motif involved in regulation of purine catabolism; has similarity to S. cerevisiae Ppr1p, which is a transcription factor involved in the regulation of uracil biosynthesis genes
ESC4	orf19.1445	0	5.435588889	Protein similar to S. cerevisiae Esc4p, which represses transposition; transposon mutation affects filamentous growth
ALT1	orf19.346	0	4.975355556	Putative alanine transaminase; mutation confers hypersensitivity to 5-fluorocytosine (5-FC); rat catheter and flow model biofilm induced
CHO2	orf19.169	0	4.922477778	Putative phosphatidyl-ethanolamine N-methyltransferase; fungal-specific (no human or murine homolog); amphotericin B repressed
-	orf19.7194	0	4.797577778	Protein not essential for viability; decreased transcription is observed upon fluphenazine treatment; induced upon adherence to polystyrene
TES1	orf19.5217	0	4.694266667	Putative acyl-CoA thioesterase
IFD3	orf19.3311	0	4.636433333	Putative aldo/keto reductase; Mig1-regulated
DUR1,2	orf19.780	0	4.594311111	Urea amidolyase; hydrolyzes urea to CO2; use of urea as N source and for hyphal switch in macrophage; regulated by Nrg1/Hap43; required for virulence; promotes mouse kidney and brain colonization; rat catheter and flow model biofilm induced
-	orf19.3089	0	4.594066667	Predicted mitochondrial intermembrane space protein; predicted role in phospholipid metabolism; rat catheter and Spider biofilm induced
-	orf19.7033	0	4.5663	Putative dual specificity protein phosphatase, similar to S. cerevisiae Pps1p
CSH1	orf19.4477	0	4.511011111	Member of aldo-keto reductase family, similar to aryl alcohol dehydrogenases; role in adhesion to fibronectin, cell surface hydrophobicity; regulated by Ca-upg_4erature, growth phase, benomyl, macrophage interaction; azole resistance associated
HPD1	orf19.5565	0	4.351844444	Putative 3-hydroxyisobutyrate dehydrogenase
ILV5	orf19.88	0	4.309033333	Protein described as ketol-acid reductoisomerase; antigenic during murine systemic infection; regulated by Gcn4p; induced in response to amino acid starvation (3-aminotriazole treatment); fungal-specific (no human or murine homolog)
GAL1	orf19.3670	0	4.280822222	Galactokinase; transcription regulated by galactose; transcription regulated by Mig1p and Tup1p; not required for systemic mouse virulence; farnesol-downregulated in biofilm; fluconazole-induced
FOX3	orf19.1704	0	4.256244444	Putative peroxisomal 3-oxoacyl CoA thiolase; expression is regulated upon white-opaque switching
NTH1	orf19.7479	0	4.189144444	Neutral trehalase; hyphal induction in homozygous null mutant is delayed but not reduced overall; not required for virulence in mouse systemic infection; homodimeric enzyme; possible regulatory cAMP-dependent phosphorylation at S10 and S213
STP4	orf19.909	0	4.1479	C2H2 transcription factor; induced in core caspofungin response; colony morphology-related gene regulation by Ssn6; induced by 17-beta-estradiol, ethynyl estradiol; rat catheter and Spider biofilm induced
CPA2	orf19.3221	0	4.081377778	Putative arginine-specific carbamoylphosphate synthetase; protein enriched in stationary phase yeast cultures; rat catheter biofilm induced; Spider biofilm induced
-	orf19.3684	0	4.076911111	Putative oxidoreductase; Spider biofilm induced
-	orf19.3470	0	3.980211111	Putative flavodoxin; similar to S. cerevisiae Tyw1, an iron-sulfur protein required for synthesis of wybutosine modified tRNA; predicted Kex2p substrate; Spider biofilm induced

SSD1	orf19.3959	0	3.959044444	Functional homolog of S. cerevisiae Ssd1p, which suppresses various mutant phenotypes; constitutively expressed and not cell-cycle regulated; suppresses S. cerevisiae swi4 ssd1-d and pph21 pph3 pph22-12 ts mutations
ECM17	orf19.4099	0	3.892711111	Predicted enzyme of sulfur amino acid biosynthesis; putative role in regulation of biogenesis of the cell wall; upregulated in biofilm; possibly adherence-induced; regulated by Tsa1p, Tsa1Bp under H2O2 stress conditions; Gcn4p-regulated
-	orf19.4365	0	3.888188889	Has domain(s) with predicted RNA methyltransferase activity and role in RNA processing
-	orf19.6840	0	3.8492	Protein of unknown function; transcript detected in high-resolution tiling arrays; transcription induced by alpha pheromone in SpiderM medium; Spider and early-stage flow model biofilm induced
OGG1	orf19.7190	0	3.845	Mitochondrial glycosylase/lyase; repairs oxidative damage to mitochondrial DNA, contributes to UVA resistance, role in base-excision repair; Spider biofilm induced
YHB5	orf19.3710	0.010562201	3.806533333	Protein related to flavohemoglobins; not required for wild-type nitric oxide resistance; has predicted globin, FAD-binding, and NAD(P)-binding domains but lacks some conserved residues of flavohemoglobins; mRNA detected; filament induced
-	orf19.2747	0	3.795333333	Predicted zinc-finger protein of unknown function; has similarity to S. cerevisiae Rgt1p, which is a transcription factor involved in the regulation of glucose transporter genes
ADR1	orf19.2752	0	3.7947	Protein similar to S. cerevisiae Adr1p, which is a transcription factor involved in peroxisome function; transposon mutation affects filamentous growth
-	orf19.3559	0	3.760844444	S. cerevisiae ortholog Mrps35p is a structural constituent of ribosome and localizes to mitochondrial small ribosomal subunit; the snoRNA CD39 is encoded within the MRPS35 intron
-	orf19.5698	0	3.737577778	Putative mitochondrial ribosomal protein of the large subunit; transcript is upregulated in clinical isolates from HIV+ patients with oral candidiasis; Spider biofilm repressed
MIT1	orf19.4077	0	3.728455556	Protein involved in sphingolipid biosynthesis; required for mannosylation of inositol phosphoceramide (IPC) to form mannosylated sphingolipids MIPC and M(IP)2C; fluconazole-induced; putative ortholog of S. cerevisiae Sur1p
-	orf19.6565	0	3.708233333	Conserved mitochondrial inner membrane insertase; mediates insertion of mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane; Spider biofilm repressed
CDR1	orf19.6000	0	3.629722222	Multidrug transporter of ATP-binding cassette (ABC) superfamily; transports phospholipids in an in-to-out direction; transcription induced by beta-estradiol, progesterone, corticosteroid, or cholesterol
MDM34	orf19.1826	0	3.5759	Putative zinc finger transcription factor; macrophage-downregulated; flow model biofilm induced; flow model and Spider biofilm induced
-	orf19.2639	0	3.571688889	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization
CHO1	orf19.677	0	3.5472	Putative phosphatidylserine synthase; similar to S. cerevisiae Cho1p, which is involved in phosphatidylserine biosynthesis; transposon mutation affects filamentous growth; regulated by Nrg1p, Tup1p; no human or murine homolog
-	orf19.6311	0	3.522466667	Protein of unknown function; Hap43-induced; rat catheter and Spider biofilm induced
-	orf19.5235	0	3.516966667	Putative mitochondrial ribosomal protein of the large subunit; Hap43-induced; mutants are viable; protein level decreases in stationary phase
-	orf19.932	1.259043568	3.488466667	Putative aminophospholipid translocase (flippase); merged with orf19.2226 in Assembly 21; possibly an essential gene, disruptants not obtained by UAU1 method
-	orf19.2515	0	3.440955556	ZZ-type zinc finger protein; rat catheter and Spider biofilm induced

PXP2	orf19.1655	0	3.431922222	Putative acyl-CoA oxidase; enzyme of fatty acid beta-oxidation; induced during macrophage infection; expression is opaque specific; has putative peroxisome targeting signal
PDR16	orf19.1027	0	3.365733333	Phosphatidylinositol transfer protein; increased transcription correlates with CDR1 and CDR2 overexpression and azole resistance; transcription induced by fluphenazine; farnesol-downregulated in biofilm; induced by nitric oxide
-	orf19.749	0	3.326044444	Protein likely to be essential for growth, based on an insertional mutagenesis strategy
YML6	orf19.7019	0	3.281822222	Protein described as a mitochondrial ribosomal protein; induced upon adherence to polystyrene
HXT5	orf19.4386	0	3.270066667	Protein described as a sugar transporter; transcription is upregulated in response to treatment with ciclopirox olamine; alkaline downregulated; shows colony morphology-related gene regulation by Ssn6p
ACH1	orf19.3171	0	3.214033333	Protein not essential for viability; similar to S. cerevisiae Ach1p, which is acetyl-coA hydrolase required for acetate utilization; induced upon adherence to polystyrene; ketoconazole-induced; fungal-specific (no human or murine homolog)
GUT1	orf19.558	0	3.207855556	Putative glycerol kinase; downregulated upon adherence to polystyrene; greater mRNA abundance observed in a cyr1 homozygous null mutant than in wild type
-	orf19.6916	0	3.195788889	Ortholog(s) have unfolded protein binding activity, role in mitochondrial proton-transporting ATP synthase complex assembly and mitochondrion localization
-	orf19.95	1.259043568	3.194866667	Ortholog of *S. cerevisiae* : PRM5, *C. dubliniensis* CD36 : Cd36_60980, *C. parapsilosis* CDC317 : CPAR2_603060, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_113703 and *Debaryomyces hansenii* CBS767 : DEHA2F10032g
ICL1	orf19.6844	0	3.188044444	Isocitrate lyase; enzyme of glyoxylate cycle; required for wild-type virulence in murine systemic infection; no mammalian homolog; transcription induced upon phagocytosis by macrophage; farnesol regulated; putative peroxisome target signal
CIC1	orf19.124	0	3.186133333	Putative proteasome-interacting protein; rat catheter biofilm induced
MET15	orf19.5645	0	3.173466667	O-acetylhomoserine O-acetylserine sulfhydrylase; involved in sulfur amino acid biosynthesis; biofilm-, possibly adherence-induced; brown colony color of homozygous mutant in Pb(2+)-containing medium may be a useful visual selection marker
IPT1	orf19.4769	0.010562201	3.143288889	Inositol phosphoryl transferase, involved in sphingolipid biosynthesis; catalyzes the synthesis of the most abundant sphingolipid, mannose-(inositol-P)2-ceramide, M(IP)2C, from MIPC; required for wild-type membrane localization of Cdr1p
-	orf19.3154	0	3.141777778	Ortholog(s) have role in inner mitochondrial membrane organization and integral component of mitochondrial inner membrane localization
-	orf19.2650.1	0	3.087688889	Mitochondrial ribosomal protein of the small subunit; Spider biofilm repressed
-	orf19.334	0	3.073477778	Protein of unknown function; flow model biofilm induced; Spider biofilm induced; regulated by Sef1, Sfu1, and Hap43
-	orf19.733	0	3.058922222	Ortholog(s) have endoplasmic reticulum localization
-	orf19.6307	0.016622678	3.053955556	Ortholog of *C. dubliniensis* CD36 : Cd36_30250, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_98619, *Debaryomyces hansenii* CBS767 : DEHA2G22594g and *Pichia stipitis Pignal* : PICST_50168
-	orf19.5576	0	3.052544444	Protein similar to S. cerevisiae Ydr531wp; transposon mutation affects filamentous growth
-	orf19.3627	0	3.050877778	Ortholog of *C. dubliniensis* CD36 : Cd36_22640, *C. parapsilosis* CDC317 : CPAR2_406910, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_104937 and *Debaryomyces hansenii* CBS767 : DEHA2D02706g
-	orf19.6830	0	3.033277778	Putative enoyl-CoA hydratase
-	orf19.2320	0	3.018755556	Putative serine/threonine-protein kinase; possibly an essential gene, disruptants not obtained by UAU1 method
ISU1	orf19.6548	0	2.992333333	Similar to NifU; possible role in iron-sulfur cluster biogenesis; transcriptionally regulated by iron; expression greater in low iron

INO1	orf19.7585	0	2.991444444	Inositol-1-phosphate synthase; enzyme of inositol biosynthesis; farnesol-downregulated in biofilm; caspofungin repressed; regulated during planktonic growth; has upstream inositol/choline regulatory element; glycosylation predicted
-	orf19.4751	0	2.988588889	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization
ALK2	orf19.7513	0	2.979977778	N-Alkane inducible cytochrome P450
-	orf19.6556	0	2.964577778	Protein of unknown function; rat catheter, flow model and Spider biofilm induced
-	orf19.4161	0	2.944477778	Ortholog(s) have SUMO transferase activity, role in DNA repair and Smc5-Smc6 complex, nucleus localization
MPS1	orf19.7293	0	2.939666667	Monopolar spindle protein, putative spindle assembly checkpoint kinase; essential for growth; involved in oxidative stress response; periodic mRNA expression, peak at cell-cycle S/G2 phase
MAS2	orf19.6295	0.016622678	2.931977778	Putative processing peptidase, catalytic (alpha) subunit; protein level decreases in stationary phase cultures
SWE1	orf19.4867	0	2.881433333	Functional homolog of S. cerevisiae Swe1p; mutant cells are small, rounded, and sometimes binucleate; not required for filamentous growth
CHT1	orf19.7517	0	2.867944444	Chitinase; putative N-terminal catalytic domain; has secretory signal sequence; lacks S/T region and N-glycosylation motifs of Chs2p and Chs3p; alkaline downregulated; expression not detected in yeast-form or hyphal cells
-	orf19.4531	0	2.852866667	Putative PDR-subfamily ABC transporter
MLS1	orf19.4833	0	2.845444444	Malate synthase; enzyme of the glyoxylate cycle; no mammalian homolog; transcription is induced upon phagocytosis by macrophage; expression is regulated upon white-opaque switching; biofilm-repressed expression
-	orf19.1438	0	2.8274	Protein with homology to NADH dehydrogenase; regulated by Sef1p-, Sfu1p-, and Hap43p
ANT1	orf19.6254	0.034795801	2.788133333	Peroxisomal adenine nucleotide transporter; role in beta-oxidation of medium-chain fatty acid and peroxisome proliferation; rat catheter biofilm induced
POX1-3	orf19.1652	0	2.787444444	Predicted acyl-CoA oxidase; farnesol regulated
TRY4	orf19.5975	0	2.781433333	C2H2 transcription factor; fluconazole-repressed; induced in ssr1 mutant; required for yeast cell adherence to silicone substrate; Spider biofilm induced
IMG2	orf19.3777	0	2.769994444	Mitochondrial ribosomal protein of the large subunit; rat catheter biofilm induced
YOR1	orf19.1783	0	2.7685	Protein similar to S. cerevisiae Yor1; ABC-type plasma membrane transporter involved in resistance to aureobasidin A; white cell type-specific transcript; Spider biofilm induced
ERG6	orf19.1631	0.010562201	2.7631	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in ergosterol biosynthesis by methylating position C-24; mutation confers nystatin resistance; fluconazole-induced; transcription increased in azole-resistant strain
ARO8	orf19.2098	0	2.7544	Protein abundance is affected by URA3 expression in the CAI-4 strain background; alkaline upregulated; Gcn4p-regulated
OAC1	orf19.7411	0	2.752955556	Putative mitochondrial inner membrane transporter; rat catheter biofilm induced
-	orf19.4273	0	2.751033333	Putative mitochondrial membrane protein; ortholog of S. cerevisiae Sls1; coordinates expression of mitochondrially-encoded genes; Hap43-induced
-	orf19.3694	0	2.749188889	Ortholog of *C. dubliniensis* CD36 : Cd36_02210, *C. parapsilosis* CDC317 : CPAR2_106350, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_116785 and *Debaryomyces hansenii* CBS767 : DEHA2C01980g
LYS22	orf19.4506	0.034795801	2.746333333	Putative homocitrate synthase; fungal-specific (no human or murine homolog); repressed by nitric oxide
ARD	orf19.6322	0	2.739622222	D-arabitol dehydrogenase, NAD-dependent (ArDH); enzyme of D-arabitol and D-arabinose catabolism; D-arabitol is a marker for active infection in humans; has conserved YXXXK motif of short-chain alcohol-polyol-sugar dehydrogenases

FRE7	orf19.6139	0	2.737033333	Protein similar to ferric reductase Fre10p; transcription is downregulated in response to treatment with ciclopirox olamine, amphotericin B; alkaline upregulated; transcriptionally induced by interaction with macrophage
YHM1	orf19.685	0	2.731911111	Putative mitochondrial carrier protein; fungal-specific (no human or murine homolog)
MTM1	orf19.417	0	2.730411111	Ortholog(s) have metallochaperone activity, pyridoxal phosphate binding activity, role in manganese ion transport, pyridoxal phosphate transport and mitochondrion localization
GPR1	orf19.1944	0	2.7223	Putative G-protein-coupled receptor of plasma membrane; required for wild-type hyphal growth; acts in cAMP-PKA pathway; reports differ on role in cAMP-mediated glucose signaling; Gpr1p C terminus binds Gpa2p; regulates HWP1 and ECE1
-	orf19.2891	0	2.695211111	Ortholog(s) have role in cellular response to oxidative stress, misfolded or incompletely synthesized protein catabolic process, protein import into peroxisome matrix and mitochondrial inner membrane localization
-	orf19.5611	0.034795801	2.693666667	Predicted 3-methylbutanol:NAD(P) oxidoreductase and methylglyoxal reductase (NADPH-dependent); role in ergosterol metabolic process; early stage flow model biofilm induced; Spider biofilm induced
-	orf19.281	0	2.6858	Ortholog of *C. dubliniensis* CD36 : Cd36_82880, *C. parapsilosis* CDC317 : CPAR2_102370, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_118463 and *Pichia stipitis Pignal* : PICST_32241
-	orf19.345	0	2.685	Succinate semialdehyde dehydrogenase; for utilization of gamma-aminobutyrate (GABA) as a nitrogen source; part of 4-aminobutyrate and glutamate degradation pathways; rat catheter biofilm induced
-	orf19.3328	0	2.678116667	Putative transcription factor; S. cerevisiae ortholog Hot1 is required for the transient induction of glycerol biosynthetic genes GPD1 and GPP2 in response to high osmolarity; filament induced
HGT15	orf19.3526	0	2.657677778	Putative glucose transporter of major facilitator superfamily;*C. albicans* glucose transporter family comprises 20 members; 12 probable transmembrane motifs; expressed in rich medium with 2% glucose; fluconazole, caspofungin downregulated
-	orf19.445	0	2.642788889	Protein of unknown function; repressed by prostaglandins
-	orf19.3501	0.010562201	2.6334	S. cerevisiae ortholog Pxl1 localizes to sites of polarized growth and is required for selection and/or maintenance of polarized growth sites; Hog1p-repressed
-	orf19.6639	0	2.631733333	Ortholog of S. cerevisiae Mdm36; mitochondrial distribution and morphology protein; Hap43-repressed gene
MTO1	orf19.5050	0	2.631288889	Putative mitochondrial protein; rat catheter biofilm induced
NCE103	orf19.1721	0	2.580822222	Protein similar to carbonic anhydrase; induced upon biofilm formation
-	orf19.4377	0	2.580388889	ORF Predicted by Annotation Working Group
-	orf19.320	0	2.577511111	Predicted short chain dehydrogenase; Spider biofilm induced
-	orf19.6790	0	2.574933333	Ortholog(s) have mRNA binding activity, role in 3'-UTR-mediated mRNA destabilization, mitochondrion organization and cytoplasmic mRNA processing body, cytoplasmic stress granule, cytosol, perinuclear region of cytoplasm localization
-	orf19.4122	0	2.565022222	Ortholog(s) have acyl-CoA hydrolase activity, role in fatty acid beta-oxidation and mitochondrion, peroxisome localization
-	orf19.5843	0	2.553911111	Predicted ORF from Assembly 19; Plc1p-regulated; greater mRNA abundance observed in a cyr1 homozygous null mutant than in wild type
-	orf19.4100	0	2.552588889	Predicted ORF from Assembly 19
APN2	orf19.1836	0	2.550966667	Predicted ORF from Assembly 19; flucytosine induced
-	orf19.996	3.011327416	2.545566667	Protein with a predicted leucine-rich repeat domain; possibly an essential gene, disruptants not obtained by UAU1 method
-	orf19.828	0	2.543855556	Putative ribosomal protein, large subunit, mitochondrial precursor; repressed by prostaglandins; Spider biofilm repressed

-	orf19.2825	0	2.533744444	Putative cytosolic Fe-S protein assembly protein; a-specific transcript; regulated by Sef1, Sfu1, and Hap43; rat catheter and Spider biofilm induced
-	orf19.4701	0	2.524733333	Ortholog(s) have ATPase activity, tRNA binding activity, role in protein urmylation, regulation of transcription from RNA polymerase II promoter, tRNA wobble uridine modification and Elongator holoenzyme complex localization
-	orf19.1562	0	2.519933333	Protein of unknown function; flow model biofilm induced; Spider biofilm induced; repressed by alpha pheromone in SpiderM medium
-	orf19.6586	0	2.5044	Predicted ORF from Assembly 19; increased transcription is observed upon benomyl treatment or in an azole-resistant strain that overexpresses MDR1; shows colony morphology-related gene regulation by Ssn6p; induced by nitric oxide
-	orf19.192	0	2.502133333	Predicted ORF from Assembly 19
CDR2	orf19.5958	0	2.495333333	Multidrug transporter, ATP-binding cassette (ABC) superfamily; transports phospholipids, in-to-out direction; low mRNA level; overexpressed in azole-resistant isolates; expression confers multidrug resistance to S. cerevisiae pdr5 mutant
-	orf19.4932	0	2.478933333	Ortholog of *C. dubliniensis* CD36 : Cd36_19320, *C. parapsilosis* CDC317 : CPAR2_209670, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_113478 and *Debaryomyces hansenii* CBS767 : DEHA2C15136g
FLU1	orf19.6577	0	2.463088889	Multidrug efflux pump of the plasma membrane; member of the MDR family of the MFS (major facilitator superfamily) of transporters; preferred substrate may be mycophenolic acid; fungal-specific (no human or murine homolog)
CAS1	orf19.1135	0	2.459833333	Putative transcription factor with Ku70/Ku80 beta-barrel DNA-binding motif; involved in telomerase regulation and telomere protection; mutation causes marginal increase in caspofungin sensitivity
-	orf19.1765	0	2.459155556	Secreted protein; fluconazole-induced
AOX2	orf19.4773	0.010562201	2.454722222	Alternative oxidase; induced by antimycin A, some oxidants; growth- and carbon-source-regulated; one of two isoforms (Aox1p and Aox2p); involved in cyanide-resistant respiratory pathway that is absent from S. cerevisiae
MNN11	orf19.2927	0.010562201	2.45255	Protein with similarity to mannosyltransferases
-	orf19.670.2	0	2.449888889	ORF Predicted by Annotation Working Group
-	orf19.7504	0.010562201	2.4389	Predicted ORF from Assembly 19; Plc1p-regulated
PPT1	orf19.1673	0.034795801	2.432477778	Protein described as serine/threonine phosphatase; transcriptionally regulated by iron; expression greater in high iron
-	orf19.5785	0	2.430488889	Predicted ORF from Assembly 19; greater mRNA abundance observed in a cyr1 or ras1 homozygous null mutant than in wild type; induced by nitric oxide
-	orf19.73	0	2.411144444	Putative metalloprotease; associates with ribosomes and is involved in ribosome biogenesis; Spider biofilm induced
BUD23	orf19.1966	0	2.409466667	Putative methyltransferase; Hap43-induced; repressed by prostaglandins
ERG2	orf19.6026	0	2.393755556	C-8 sterol isomerase; enzyme of ergosterol biosynthesis pathway; converts fecosterol to episterol; mutant is hypersensitive to multiple drugs; ketoconazole-induced
MSB1	orf19.1133	0	2.3919	Putative regulator of transcription; expression in S. cerevisiae flo8 and flo11 mutants suggests a role in regulation of adhesion factors
-	orf19.3205	0.010562201	2.382511111	Mitochondrial ribosomal protein of the large subunit; rat catheter biofilm induced
-	orf19.264	0	2.381055556	Has domain(s) with predicted protein kinase binding activity and role in regulation of cyclin-dependent protein serine/threonine kinase activity

-	orf19.1794	0	2.378677778	Ortholog(s) have RNA binding, translation regulator activity and role in Group I intron splicing, mitochondrial respiratory chain complex IV biogenesis, positive regulation of mitochondrial translation
YMX6	orf19.5713	0	2.372944444	Putative NADH dehydrogenase; macrophage-downregulated gene; induced by nitric oxide; rat catheter biofilm induced
PCL2	orf19.403	0	2.367222222	Cyclin homolog; reduced expression observed upon depletion of Cln3p; farnesol regulated
-	orf19.6869	0	2.360666667	Putative lipid raft associated protein; Spider biofilm induced
-	orf19.4121	0.010562201	2.356283333	Predicted thioesterase/thiol ester dehydrase-isomerase; Spider biofilm induced
RSM22	orf19.414	0	2.352988889	Predicted mitochondrial small ribosomal subunit; rat catheter and Spider biofilm induced
KGD2	orf19.6126	0	2.337588889	Protein described as dihydrolipoamide S-succinyltransferase; transcriptionally regulated by iron; expression greater in high iron
CTN1	orf19.4551	0	2.332988889	Predicted carnitine acetyl transferase; similar to S. cerevisiae Yat1p; transcriptionally induced in macrophage; macrophage/pseudohyphal-repressed after 16h
-	orf19.1486	0	2.329888889	Protein with a life-span regulatory factor domain; regulated by Sef1, Sfu1, and Hap43; flow model biofilm induced; Spider biofilm induced
LYS9	orf19.7448	0.010562201	2.325855556	Predicted ORF from Assembly 19; amphotericin B repressed; Gcn4p-regulated; shows colony morphology-related gene regulation by Ssn6p
AAP1	orf19.2810	0	2.321777778	Putative amino acid permease; fungal-specific (no human or murine homolog)
RTA3	orf19.23	0	2.317033333	Similar to S. cerevisiae Rta1p (role in 7-aminocholesterol resistance) and Rsb1p (flippase); putative membrane protein; putative drug-responsive regulatory site; induced by fluphenazine, estradiol, ketoconazole, caspofungin
TBF1	orf19.801	0.010562201	2.316766667	Essential transcription factor; induces ribosomal protein genes and the rDNA locus; acts with Cbf1 at subset of promoters; recruits Fhl1 and Ifh1 to promoters; role is analogous to that of S. cerevisiae Rap1; Spider biofilm induced
-	orf19.7077	0	2.311033333	Protein of unknown function; Plc1p-regulated; transcription is negatively regulated by Rim101p
MEF2	orf19.6208	0	2.307722222	Predicted ORF from Assembly 19; caspofungin induced
-	orf19.3070.1	0.010562201	2.307466667	ORF Predicted by Annotation Working Group
-	orf19.6769	0	2.302833333	Ortholog(s) have cytoplasm localization
-	orf19.1344	0	2.298977778	Protein of unknown function; fluconazole-induced; Spider biofilm induced
ABC1	orf19.3331	0	2.295066667	Protein described as ubiquinol-cytochrome-c reductase; induced upon adherence to polystyrene
FRP3	orf19.1224	0.010562201	2.2868	Upregulated in the presence of human neutrophils; fluconazole-downregulated; repressed by nitric oxide
LCB4	orf19.5257	0.010562201	2.284166667	Putative sphingosine kinase; Tac1p-regulated expression; rat catheter biofilm induced
CIT1	orf19.4393	0	2.283555556	Protein described as citrate synthase; transcriptionally regulated by iron; expression greater in high iron; upregulated upon phagocytosis; regulated by Efg1p under yeast-form but not hyphal growth conditions
RPN4	orf19.1069	0	2.283183333	C2H2 transcription factor; putative regulator of proteasome genes; DNA recognition sequence (GAAGGCAAAA) enriched in regions upstream of proteasome genes; induced in core stress response; Hap43-induced; Spider biofilm induced
-	orf19.1447	0	2.281366667	Has domain(s) with predicted sequence-specific DNA binding, transcription factor activity, sequence-specific DNA binding activity and role in regulation of transcription, DNA-templated
-	orf19.4933	0	2.278744444	Predicted ORF from Assembly 19; caspofungin induced; Plc1p-regulated; shows colony morphology-related gene regulation by Ssn6p
-	orf19.3255	0	2.276388889	Transcription is regulated upon yeast-hyphal switch

-	orf19.5012	0	2.273433333	Ortholog of *C. dubliniensis* CD36 : Cd36_12740, *C. parapsilosis* CDC317 : CPAR2_201620, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_107586 and *Debaryomyces hansenii* CBS767 : DEHA2D04994g
SFL1	orf19.454	0	2.256744444	Transcription factor involved in negative regulation of morphogenesis, flocculation and virulence; induced in core caspofungin response; Spider biofilm induced
-	orf19.4600	0	2.2558	Protein of unknown function; possible mitochondrial protein; Spider biofilm induced
ARG1	orf19.7469	0.010562201	2.255455556	Similar to argininosuccinate synthase; enzyme of arginine biosynthesis; increased transcription is observed upon benomyl treatment; regulated by Gcn4p, Rim101p; induced in response to amino acid starvation (3-aminotriazole treatment)
-	orf19.6829	0	2.253266667	Protein with a predicted mitochondrial ATPase expression domain; possibly an essential gene, disruptants not obtained by UAU1 method
-	orf19.3560	0	2.250733333	S. cerevisiae ortholog Mrps35p is a structural constituent of ribosome and localizes to mitochondrial small ribosomal subunit; the snoRNA CD39 is encoded within the MRPS35 intron
LYS2	orf19.2970	0	2.250361111	Large subunit of heterodimeric alpha-aminoadipate reductase; enzyme of lysine biosynthesis; contains predicted binding sites for AMP and alpha-aminoadipate; feedback inhibited by lysine or thialysine; regulated by Gcn2p and Gcn4p
-	orf19.6805	0.034795801	2.246344444	Protein of unknown function; Spider biofilm induced
-	orf19.7344	0	2.244355556	Ortholog(s) have DNA binding, chromatin binding, histone deacetylase activity
-	orf19.6899	0	2.241766667	Putative oxidoreductase; mutation confers hypersensitivity to toxic ergosterol analog; rat catheter and Spider biofilm induced
MRP17	orf19.947	0.073554382	2.239866667	Predicted mitochondrial ribosomal protein
-	orf19.3988	0	2.239311111	Putative adhesin-like protein; induced by Mnl1 under weak acid stress; rat catheter and Spider biofilm induced
-	orf19.6871	0	2.238188889	Protein of unknown function; Hap43-induced; flow model biofilm repressed
TAC1	orf19.3188	0	2.236561111	Transcriptional activator of drug-responsive genes including CDR1 and CDR2; has Zn(2)-Cys(6) binuclear cluster; binds DRE element; gene in zinc cluster region near MTL locus; resequencing indicates that TAC1 spans orf19.3188 and orf19.3189
RTG3	orf19.2315	0.016622678	2.234222222	Putative transcription factor with bZIP DNA-binding motif; mutants are sensitive to cations and antifungal drugs, and defective in filamentous growth
TAZ1	orf19.4096	0	2.232566667	Putative lyso-phosphatidylcholine acyltransferase, required for normal phospholipid content of mitochondrial membranes; rat catheter biofilm induced
-	orf19.2478	0.016622678	2.232411111	Ortholog of *C. dubliniensis* CD36 : Cd36_05410, *C. parapsilosis* CDC317 : CPAR2_107480, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_94695 and *Debaryomyces hansenii* CBS767 : DEHA2D02288g
SHA3	orf19.3669	0.010562201	2.229488889	Protein similar to S. cerevisiae Sha3p, which is a serine/threonine kinase involved in glucose transport; transposon mutation affects filamentous growth; fluconazole-induced; ketoconazole-repressed
ECI1	orf19.6445	0	2.229044444	Protein similar to S. cerevisiae Eci1p, which is involved in fatty acid oxidation; transposon mutation affects filamentous growth; expression is regulated upon white-opaque switching
MET3	orf19.5025	0	2.226566667	Putative ATP sulfurlyase, enzyme of sulfate assimilation; repressed by methionine or cysteine, Sfu1p, or in fluconazole-resistant isolate; strongly induced on biofilm formation, even in presence of Met and Cys; possibly adherence-induced
CRC1	orf19.2599	0	2.225311111	Mitochondrial carnitine carrier protein
CUP9	orf19.6514	0	2.214344444	Transcription reduced upon yeast-hyphal switch; ketoconazole-induced; Plc1p-regulated; shows colony morphology-related gene regulation by Ssn6p

-	orf19.2236	0.010562201	2.2143	Protein with forkhead domain; similar to Fhl1p
-	orf19.5921	0	2.203755556	Ortholog(s) have glyoxysome localization
IFR1	orf19.1763	0	2.201211111	Predicted oxidoreductase/dehydrogenase; induced by nitric oxide; rat catheter and Spider biofilm induced
ALD5	orf19.5806	0.010562201	2.200266667	Protein described as an aldehyde dehydrogenase; decreased expression in a fluconazole-resistant isolate, or in hyphae; fluconazole-downregulated; protein abundance is affected by URA3 expression in the CAI-4 strain background
DLD1	orf19.5805	0	2.198777778	Transcription is specific to white cell type; shows colony morphology-related gene regulation by Ssn6p
-	orf19.3797	0	2.196311111	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization
-	orf19.6066	0	2.1961	Hexadecenal dehydrogenase; involved in the conversion of sphingosine 1-phosphate breakdown product hexadecenal to hexadecenoic acid; Spider biofilm induced
PDK2	orf19.7281	0.010562201	2.193511111	Putative pyruvate dehydrogenase kinase; mutation confers hypersensitivity to amphotericin B
TES15	orf19.5215	0	2.193344444	Putative acyl-CoA thioesterase; Hap43-repressed; Spider biofilm induced
SFU1	orf19.4869	0	2.178355556	Transcriptional regulator of iron-responsive genes; represses some iron utilization genes when iron is present; not required for wild-type hyphal growth; has two GATA1-like zinc fingers separated by Cys-rich iron-sensing region
-	orf19.4476	0	2.170222222	Protein with a NADP-dependent oxidoreductase domain; transcript induced by ketoconazole; rat catheter and Spider biofilm induced
CTN2	orf19.4591	0	2.167788889	Predicted carnitine acetyl transferase; similar to S. cerevisiae Cat2p; transcriptionally induced in macrophage; farnesol-upregulated in biofilm
-	orf19.1174	0	2.166666667	Ortholog(s) have role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine and cytoplasm localization
BCR1	orf19.723	0	2.1589	Transcription factor required for wild-type biofilm formation; not required for hyphal growth; regulates cell-surface-associated genes; has C2H2 zinc finger; similar to S. cerevisiae Ypl230Wp; filament induced; Tup1p-, Tec1p-regulated
-	orf19.86	0	2.1587	Putative glutathione peroxidase; induced by peroxide, exposure to neutrophils and macrophage blood fractions; repressed during infection of macrophages; Spider biofilm induced; flow model biofilm repressed
-	orf19.4166	0	2.156866667	Predicted zinc-finger protein of unknown function
PMC1	orf19.1727	0	2.156522222	Vacuolar calcium P-type ATPase; transcript regulated by calcineurin and fluconazole; mutant shows increased resistance to fluconazole, lithium; increased sensitivity to calcium; Spider biofilm induced
-	orf19.3435	0.010562201	2.149522222	Ortholog of *Candida albicans* WO-1 : CAWG_05215
-	orf19.4159	0	2.148522222	Ortholog(s) have magnesium ion transmembrane transporter activity, role in magnesium ion export from mitochondrion, magnesium ion transport and mitochondrial inner membrane localization
-	orf19.2175	0.016622678	2.144922222	Putative mitochondrial cell death effector; induced by nitric oxide; Spider biofilm induced; rat catheter biofilm repressed
-	orf19.1499	0	2.144566667	Predicted zinc-finger protein of unknown function; has similarity to S. cerevisiae transcription factors
-	orf19.3644	0	2.1441	Protein of unknown function; Cyr1-repressed; rat catheter and Spider biofilm induced
REI1	orf19.59	0.034795801	2.135577778	Putative cytoplasmic pre-60S factor; Hap43-induced; repressed by prostaglandins
ALD6	orf19.742	0.016622678	2.131233333	Expression is regulated upon white-opaque switching
-	orf19.5577	0.010562201	2.1289	Protein similar to S. cerevisiae Ydr531wp; transposon mutation affects filamentous growth
MET10	orf19.4076	0	2.128733333	Predicted enzyme of sulfur amino acid metabolism; biofilm-induced expression; upregulated in the presence of human whole blood or polymorphonuclear (PMN) cells; possibly adherence-induced

PGA13	orf19.6420	0	2.128688889	Putative GPI-anchored protein; described as similar to mucins; greater mRNA abundance observed in a cyr1 homozygous null mutant than in wild type; regulated by Tsa1p, Tsa1Bp in minimal media at 37 deg and by Nrg1p, Tup1p
MRV8	orf19.3908	0	2.125822222	Protein of unknown function; Spider biofilm induced
GDH3	orf19.4716	0	2.121666667	Protein described as similar to NADP-glutamate dehydrogenase; hyphal downregulated expression; transcription is regulated by Nrg1p, Plc1p; downregulated by Efg1p; upregulated by Rim101p at pH 8; ciclopirox olamine induced
-	orf19.4592	0	2.1189	Putative glucosyl transferase of sphingolipid metabolism
AOX1	orf19.4774	0	2.118388889	Alternative oxidase; low abundance; constitutively expressed; one of two isoforms (Aox1p and Aox2p); involved in a cyanide-resistant respiratory pathway present in plants, protists, and some fungi, although absent from S. cerevisiae
-	orf19.5216	0	2.111644444	Ortholog of *C. parapsilosis* CDC317 : CPAR2_209840, *C. dubliniensis* CD36 : Cd36_20380, Lodderomyces elongisporus NRLL YB-4239 : LELG_00983 and *Candida orthopsilosis* Co 90-125 : CORT_0A09100
SWD2	orf19.2790	0	2.110633333	Ortholog(s) have histone methyltransferase activity (H3-K4 specific) activity
-	orf19.643	0	2.110216667	Ortholog(s) have role in apoptotic process, mitotic spindle assembly checkpoint, mitotic spindle elongation, sister chromatid biorientation
PHR1	orf19.3829	0	2.106666667	Glycosidase of hyphal 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
IDP2	orf19.3733	0	2.097477778	Putative isocitrate dehydrogenase; expression is regulated upon white-opaque switching; shows colony morphology-related gene regulation by Ssn6p
-	orf19.4883	0	2.094377778	Protein of unknown function; S. cerevisiae ortholog Cos111 confers resistance to the antifungal drug ciclopirox olamine; constitutive expression independent of MTL or white-opaque status; Spider biofilm induced
MCD1	orf19.7634	0	2.094188889	Alpha-kleisin cohesin complex subunit; for sister chromatid cohesion in mitosis and meiosis; repressed by alpha pheromone in SpiderM medium; periodic cell-cycle expression; Hap43-repressed; rat catheter and Spider biofilm repressed
CLA4	orf19.4890	0	2.090044444	S/T kinase of Ste20p family; required for wild-type filamentous growth and for wild-type organ colonization and virulence in mouse systemic infection; role in chlamydospore formation; functional homolog of S. cerevisiae Cla4p
-	orf19.7042	0	2.088655556	Increased transcription is observed upon benomyl treatment or in an azole-resistant strain that overexpresses MDR1; induced by nitric oxide
TOP1	orf19.96	3.011327416	2.0885	DNA topoisomerase I; required for wild-type growth and for wild-type mouse virulence; sensitive to camptothecin; induced upon adherence to polystyrene
-	orf19.5905	0.034795801	2.086544444	Predicted ORF from Assembly 19; induced upon biofilm formation
FRE7	orf19.6140	0	2.083988889	Protein similar to ferric reductase Fre10p; transcription is downregulated in response to treatment with ciclopirox olamine, amphotericin B; alkaline upregulated; transcriptionally induced by interaction with macrophage
-	orf19.2247	0	2.0796	Ortholog of *C. parapsilosis* CDC317 : CPAR2_406700, *C. dubliniensis* CD36 : Cd36_21220, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_127772 and *Candida orthopsilosis* Co 90-125 : CORT_0C06120
FAA2-3	orf19.7156	0.016622678	2.0775	Predicted acyl CoA synthetase
FAA2	orf19.7379	0	2.074633333	Predicted acyl CoA synthetase; expression is regulated upon white-opaque switching
-	orf19.7166	0	2.073666667	Predicted ORF from Assembly 19; increased transcription is observed in an azole-resistant strain that overexpresses MDR1
-	orf19.449	0.034795801	2.071422222	Predicted ORF from Assembly 19; possible phosphatidyl synthase; transcription reduced upon yeast-hyphal switch

GTT12	orf19.359	0	2.071111111	Ortholog(s) have glutathione peroxidase activity, glutathione transferase activity, role in glutathione metabolic process and endoplasmic reticulum, mitochondrial outer membrane, plasma membrane localization
-	orf19.6838	0	2.071077778	Putative protein of unknown function, transcript upregulated in clinical isolates from HIV+ patients with oral candidiasis; Spider biofilm induced
-	orf19.2520	0	2.070711111	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization
PSF3	orf19.7065	0	2.068455556	Putative GINS complex subunit; cell-cycle regulated periodic mRNA expression; Spider biofilm induced
-	orf19.5223	0	2.067311111	Ortholog of *Candida albicans* WO-1 : CAWG_00199
-	orf19.4459	0	2.065755556	Predicted ORF from Assembly 19; similar to S. cerevisiae Ynl234wp, which is a putative heme-binding stress-related protein; transposon mutation affects filamentous growth
-	orf19.732	0	2.061233333	Possible dehydrogenase; flow model biofilm induced; rat catheter biofilm induced; Spider biofilm induced
HIS3	orf19.183	0	2.058244444	Protein described as imidazoleglycerol-phosphate dehydratase; hyphal-induced expression; regulated by Gcn2p and Gcn4p; fungal-specific (no human or murine homolog)
MAC1	orf19.7068	0	2.0559	Transcriptional regulator of CTR1, which encodes a copper transporter; activates CTR1 transcription under low-copper conditions
-	orf19.660	0.010562201	2.054544444	Protein of unknown function; mRNA binds She3
PUT2	orf19.3974	0.010562201	2.049866667	Alkaline upregulated
-	orf19.6918	0.010562201	2.045766667	Protein of unknown function; Hap43-induced gene; Spider biofilm induced
FUM12	orf19.6725	0	2.045355556	Protein described as similar to fumarate hydratase, enzyme of citric acid cycle; fluconazole-downregulated; downregulated by Efg1p
TIM23	orf19.1361	0	2.044655556	Protein involved in mitochondrial matrix protein import
NRG1	orf19.7150	0.010562201	2.043466667	Transcriptional repressor; regulates hyphal genes, virulence genes, chlamydospore development, and genes involved in rescue and stress responses; effects both Tup1p-dependent (major) and -independent (minor) regulation
FAA2-2	orf19.272	0	2.041977778	Predicted acyl CoA synthetase; upregulated upon phagocytosis
-	orf19.3938	0	2.0404	Putative mitochondrial ribosomal protein of the small subunit; mutation confers hypersensitivity to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)
-	orf19.3635	0	2.040377778	Ortholog of *C. dubliniensis* CD36 : Cd36_22580, *C. parapsilosis* CDC317 : CPAR2_406960, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_113677 and *Debaryomyces hansenii* CBS767 : DEHA2D03608g
DIP5	orf19.2943	0.010562201	2.039566667	Putative permease for dicarboxylic amino acids; transcriptionally induced upon phagocytosis by macrophage; Gcn4p-regulated; upregulated by Rim101p at pH 8
POT1	orf19.7520	0	2.0386	Putative peroxisomal 3-oxoacyl CoA thiolase; transcription is regulated by Nrg1p and Mig1p; farnesol regulated
-	orf19.1086	0	2.033822222	Ortholog(s) have mRNA binding activity and role in protein deubiquitination, regulation of ER to Golgi vesicle-mediated transport, regulation of retrograde vesicle-mediated transport, Golgi to ER, ribophagy
CTN3	orf19.2809	0	2.028122222	Predicted peroxisomal carnitine acetyl transferase; required for filamentous growth in macrophage and on solid media; transcriptionally induced early upon macrophage engulfment, by induction of hyphal growth, by starvation conditions
TAC1	orf19.3189	0.010562201	2.027988889	Zn(2)-Cys(6) transcriptional activator of drug-responsive genes (CDR1 and CDR2); binds DRE element; gene in zinc cluster region near MTL locus; resequencing indicates that TAC1 spans orf19.3188 and orf19.3189; Spider biofilm induced
-	orf19.1363	0	2.024533333	Predicted ORF from Assembly 19; Plc1p-regulated

-	orf19.5037	0	2.024155556	Protein not essential for viability
MAK16	orf19.5500	0	2.022966667	Putative constituent of 66S pre-ribosomal particles; Hap43-induced; repressed by prostaglandins; Spider biofilm induced
MET14	orf19.946	3.011327416	2.0226	Predicted ORF from Assembly 19; predicted role in sulfur metabolism; induced upon biofilm formation; possibly adherence-induced
RLI1	orf19.3034	0	2.021344444	RLI-subfamily ABC family protein, predicted not to be a transporter
SFC1	orf19.3931	0	2.018644444	Alkaline upregulated
-	orf19.585	0	2.018533333	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization
-	orf19.344	0.010562201	2.018133333	Predicted ORF from Assembly 19; increased transcription is observed upon fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2; possibly transcriptionally regulated by Tac1p
-	orf19.3854	0.016622678	2.015322222	Protein similar to S. cerevisiae Sat4p; amphotericin B induced
LYS4	orf19.3846	0	2.014988889	Protein described as homoaconitase; regulated by Gcn4p, Gcn2p; induced in response to amino acid starvation (3-aminotriazole treatment); upregulated in the presence of human whole blood or polymorphonuclear (PMN) cells
-	orf19.5777	0	2.012577778	Protein of unknown function; F-12/CO2 early biofilm induced
-	orf19.93	0	2.0123	Predicted ORF from Assembly 19; shows colony morphology-related gene regulation by Ssn6p
-	orf19.5433	0.010562201	2.009666667	Ortholog(s) have protein binding involved in protein folding activity, role in mitochondrial respiratory chain complex III assembly and mitochondrial matrix localization
-	orf19.2724	0	2.007555556	Protein of unknown function; flow model, rat catheter and Spider biofilm induced; Hap43-repressed
-	orf19.94	0.138372782	2.006688889	Protein of unknown function; Spider biofilm induced
ADH3	orf19.4505	0	2.003266667	Expression is regulated upon white-opaque switching; induced by nitric oxide in yhb1 mutant

(B) Down-regulated genes in the combination group cells

Name	**sequence_id**	**q-value(%)**	**Fold Change**	**Description**
-	orf19.4665	0	0.065255556	Protein of unknown function; Spider biofilm induced
PTR2	orf19.6937	0	0.078633333	Putative oligopeptide transporter; regulated by Stp2p and Stp3p; transcriptionally induced upon phagocytosis by macrophage; downregulated by Rim101p at pH 8
ARO10	orf19.1847	0	0.117866667	Protein described as pyruvate decarboxylase; alkaline downregulated; protein abundance is affected by URA3 expression in the CAI-4 strain background
GPX3	orf19.4436	0	0.133577778	Putative glutathione peroxidase involved in Cap1p-dependent oxidative stress response, required for Cap1p oxidation in response to H2O2; planktonic growth-induced
-	orf19.1619	0	0.133611111	Putative kinase subunit of RNA polymerase II carboxy-terminal domain kinase I; possibly an essential gene, disruptants not obtained by UAU1 method
CRZ2	orf19.2356	0	0.141444444	Protein similar to S. cerevisiae Crz1p transcription factor; homozygous crz1, but not crz2, null mutation suppresses fluconazole resistance of a homozygous cka2 null mutant, which is defective in CK2 kinase; downregulated by Rim101p at pH 8
-	orf19.341	0	0.152511111	Putative spermidine export pump; fungal-specific (no human or murine homolog)

TPS3	orf19.5348	0	0.154422222	Protein described as regulatory subunit of trehalose-phosphate synthase; regulated by Efg1p; biofilm-repressed expression; regulated by Tsa1p, Tsa1Bp under H2O2 stress conditions
PGA10	orf19.5674	0	0.163611111	Plasma membrane protein involved in heme-iron utilization; allows utilization of hemin and hemoglobin as iron sources in host tissues; predicted GPI anchor; ketoconazole, ciclopirox olamine, or hyphal-induced; upregulated by Rim101p at pH 8
-	orf19.6354	0	0.163822222	Ortholog of *C. dubliniensis* CD36 : Cd36_11870, *C. parapsilosis* CDC317 : CPAR2_201650, *Candida tenuis* NRRL Y-1498 : cten_CGOB_00224 and *Debaryomyces hansenii* CBS767 : DEHA2D04884g
WSC4	orf19.7251	0	0.167122222	Transcription is specific to white cell type
-	orf19.5070	0	0.182111111	Predicted ORF from Assembly 19; transcriptionally regulated by iron; expression greater in low iron; similar to cell-wall mannoproteins; greater mRNA abundance observed in a cyr1 homozygous null mutant than in wild type
-	orf19.6239	0	0.188566667	Putative serine/threonine protein kinase; possibly an essential gene, disruptants not obtained by UAU1 method
EBP1	orf19.125	0	0.190022222	NADPH oxidoreductase; interacts with phenolic substrates, such as 17beta-estradiol; possible role in response to estrogen; increased transcription is observed upon benomyl treatment; induced by nitric oxide; no human or murine homolog
-	orf19.5527	0	0.192866667	Protein with a predicted role in 5.8S rRNA processing; flow model biofilm induced
-	orf19.5451	0	0.1957	ORF Predicted by Annotation Working Group
-	orf19.7459	0	0.211044444	Predicted ORF from Assembly 19; fluconazole-induced; ketoconazole-repressed
-	orf19.2583.2	0	0.217388889	ORF Predicted by Annotation Working Group
TPI1	orf19.6745	0	0.219977778	Putative ortholog of S. cerevisiae Tpi1p, which is triose-phosphate isomerase involved in glycolysis and gluconeogenesis; antigenic during murine systemic infection; transposon mutation affects filamentous growth; biofilm-induced expression
RNR22	orf19.1868	0	0.224744444	Protein described as ribonucleoside diphosphate reductase; shows colony morphology-related gene regulation by Ssn6p; RNA abundance regulated by tyrosol and cell density
-	orf19.5475	0	0.224822222	ORF Predicted by Annotation Working Group
-	orf19.5812	0	0.229433333	Ortholog of S. cerevisiae Ett1, a nuclear protein that inhibits replication of Brome mosaic virus; early-stage flow model biofilm induced
-	orf19.2335	0	0.232155556	Putative aspartyl aminopeptidase; stationary phase enriched protein; mutation confers hypersensitivity to 5-fluorouracil (5-FU); Hog1-induced; planktonic growth-induced; rat catheter and Spider biofilm repressed
-	orf19.3755	0	0.2341	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization
LIP6	orf19.4823	0	0.235855556	Secreted lipase, member of family of lipase genes expressed differentially in response to carbon source and during infection; may have a role in nutrition and/or in creating an acidic microenvironment; induced on adherence to polystyrene
-	orf19.3395	0	0.239522222	Predicted MFS membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family; induced by nitric oxide, oxidative stress, alpha pheromone; fungal-specific; Hap43-repressed; Spider biofilm induced
PDX3	orf19.550	0	0.242766667	Transcription is regulated upon yeast-hyphal switch; regulated by Nrg1p, Mig1p, and Tup1p; caspofungin repressed
-	orf19.5251	0	0.244466667	Predicted zinc-finger protein of unknown function; not essential for viability; decreased transcription is observed upon fluphenazine treatment
-	orf19.6189	0	0.249055556	Chalcone related protein family; flow model biofilm induced
-	orf19.3214	0	0.254633333	Alpha/beta-HydrolasE superfamily protein; membrane-localized

-	orf19.3806	0	0.255544444	Ortholog(s) have role in negative regulation of gluconeogenesis, proteasome-mediated ubiquitin-dependent protein catabolic process, traversing start control point of mitotic cell cycle and GID complex, cytoplasm, nucleus localization
GOR1	orf19.2989	0	0.2609	Ortholog(s) have glyoxylate reductase activity, role in glyoxylate catabolic process and cytosol, extracellular region, mitochondrion, nucleus localization
MDR1	orf19.5604	0	0.262244444	Multidrug efflux pump of plasma membrane; member of the MDR family of major facilitator transporter superfamily; methotrexate is preferred substrate; overexpression in drug-resistant clinical isolates confers fluconazole resistance
-	orf19.1116	0	0.266033333	Protein of unknown function; planktonic growth-induced gene
RHR2	orf19.5437	0	0.270455556	Putative glycerol 3-phosphatase; roles in osmotic tolerance and glycerol accumulation in response to salt; regulated by salt stress, yeast-hyphal switch, Gcn4p, Hog1p, Nrg1p and Tup1p; antigenic during murine systemic infection
OFD1	orf19.1802	0	0.271544444	Putative prolyl hydroxylase family member; regulates Ume6p stability in response to oxygen; inhibited by hypoxia; repressed by prostaglandins; Spider biofilm induced
FCR1	orf19.6817	0	0.2752	Putative zinc cluster transcription factor; negative regulator of fluconazole, ketoconazole, brefeldin A resistance; transposon mutation affects filamentous growth; partially suppresses S. cerevisiae pdr1 pdr3 mutant fluconazole sensitivity
-	orf19.1368	0	0.279266667	Protein of unknown function; flow model biofilm induced; Spider biofilm induced
CDC19	orf19.3575	0	0.281233333	Putative pyruvate kinase; on yeast-form, not hyphal, cell surface; elicits host antibody response during infection; Gcn4p-regulated; induced on adherence to polystyrene; downregulated upon phagocytosis; mutation affects filamentation
-	orf19.6056	0	0.2817	Ortholog(s) have phosphatase activity, role in dephosphorylation and cytosol, nucleus localization
SPR3	orf19.1524	0	0.285822222	Septin; mutant has no obvious phenotype
CRP1	orf19.4784	0	0.288022222	Copper transporter of the plasma membrane; P1-type ATPase (CPx type); mediates copper resistance; similar to proteins of Menkes and Wilson disease; copper-induced; suppresses copper sensitivity of an S. cerevisiae cup1 null mutant
-	orf19.1672	0	0.2884	Alpha subunit of COPI vesicle coatomer complex; role in ER to Golgi vesicle-mediated transport, retrograde vesicle-mediated transport, Golgi to ER transport; flow model biofilm repressed
-	orf19.4577	0	0.288411111	Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity, signal transducer activity
ERG1	orf19.406	0	0.290188889	Squalene epoxidase, catalyzes epoxidation of squalene to 2,3(S)-oxidosqualene in the ergosterol biosynthetic pathway; essential; target of allylamine antifungal drugs; uses NADH as a reducing cofactor, while S. cerevisiae Erg1p uses NADPH
-	orf19.7499	0	0.299744444	Putative nicotinic acid mononucleotide adenylyltransferase, involved in NAD salvage pathway; Spider biofilm repressed
TERT	orf19.5089	0	0.300244444	Telomerase reverse transcriptase; catalytic protein subunit of telomere synthesis; essential for telomerase activity; has telomerase-specific motif T and other conserved reverse transcriptase motifs
-	orf19.6905	0	0.309333333	Ortholog of *S. cerevisiae* : YNL011C, *C. glabrata* CBS138 : CAGL0H03619g, *C. dubliniensis* CD36 : Cd36_71090, *C. parapsilosis* CDC317 : CPAR2_300420 and *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_111980
-	orf19.296	0	0.311544444	Ortholog of *C. dubliniensis* CD36 : Cd36_82980, *C. parapsilosis* CDC317 : CPAR2_102360, *Candida tenuis* NRRL Y-1498 : cten_CGOB_00165 and *Debaryomyces hansenii* CBS767 : DEHA2G00990g
-	orf19.2106	0	0.313188889	Putative protein of unknown function; Hap43p-repressed gene
HGT6	orf19.2020	0	0.314288889	Putative glucose transporter of the major facilitator superfamily;*C. albicans* glucose transporter family comprises 20 members; 12 probable membrane-spanning segments; fluconazole-induced; expressed in rich medium with 2% glucose
-	orf19.280	0	0.315366667	Ortholog of *C. dubliniensis* CD36 : Cd36_82875 and *Candida albicans* WO-1 : CAWG_02609

PRM1	orf19.669	0	0.318155556	Protein induced during the mating process
-	orf19.411	0	0.318577778	Similar to GTPase regulators; transcriptionally regulated by iron; expression greater in low iron
INT1	orf19.4257	0	0.320133333	Integrin-like protein; role in morphogenesis, adhesion, and mouse cecal colonization and systemic virulence; similar to S. cerevisiae Bud4p (has role in bud site selection); structurally similar to alpha-subunit of human leukocyte integrins
-	orf19.6722	0	0.323911111	Predicted ORF from Assembly 19; similar to S. cerevisiae Rad4p; down-regulation associated with azole resistance
FGR23	orf19.1616	0	0.324055556	Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth; transcriptionally repressed by A1p and Alpha2p in white-phase cells, a-specific and induced by alpha factor
AAH1	orf19.2251	0	0.328544444	Protein not essential for viability; similar to S. cerevisiae Aah1p, which is an adenine deaminase involved in purine salvage and nitrogen catabolism; shows colony morphology-related gene regulation by Ssn6p; induced upon biofilm formation
-	orf19.3021	0	0.3296	Putative protein of unknown function; Hap43-repressed gene; Spider biofilm induced
-	orf19.1434	0	0.3322	Ortholog(s) have protein complex scaffold, protein kinase activator activity
ALK6	orf19.6574	0	0.336066667	Putative cytochrome P-450 of N-alkane-induced detoxification; macrophage-induced gene
GPX2	orf19.85	0	0.33625	Similar to glutathione peroxidase; transcriptionally regulated by iron and by Efg1p; expression greater in high iron; alkaline upregulated by Rim101p; transcriptionally induced by interaction with macrophage; caspofungin repressed
PSF2	orf19.57	0	0.337077778	Ortholog(s) have role in double-strand break repair via break-induced replication, mitotic DNA replication and GINS complex, cytosol, nuclear chromatin, replication fork protection complex localization
MAE1	orf19.3419	0	0.3447	Malic enzyme, mitochondrial; transcription regulated by Mig1p and Tup1p; shows colony morphology-related gene regulation by Ssn6p
NTH1	orf19.7479	0	0.345088889	Neutral trehalase; hyphal induction in homozygous null mutant is delayed but not reduced overall; not required for virulence in mouse systemic infection; homodimeric enzyme; possible regulatory cAMP-dependent phosphorylation at S10 and S213
HEM13	orf19.2803	0	0.346333333	Homolog of S. cerevisiae coproporphyrinogen III oxidase; not transcriptionally regulated by Rfg1p; localizes to cell surface of yeast-form cells, but not hyphae; transcriptionally regulated by iron; expression greater in high iron
HSP70	orf19.4980	0	0.347566667	Putative chaperone of the Hsp70 family; transcription is activated by heat shock; farnesol-downregulated in biofilm; amphotericin B, ketoconazole-induced; localizes to surface of yeast-form and hyphal cells; antigenic in host
-	orf19.1654	0	0.349622222	Predicted membrane protein; induced by prostaglandins
ATC1	orf19.6214	0	0.351	Cell wall acid trehalase; catalyzes hydrolysis of the disaccharide trehalose; similar to S. cerevisiae vacuolar acid trehalase (Ath1p)
-	orf19.1867	0	0.357388889	Putative malate permease; induced during macrophage infection; regulated by Gcn2p and Gcn4p; has putative peroxisome targeting signal
NAG3	orf19.2158	0	0.358477778	Putative transporter of the major facilitator superfamily (MFS); similar to Nag4p; required for wild-type mouse virulence and cycloheximide resistance; in gene cluster that includes genes encoding enzymes of GlcNAc catabolism
ASM3	orf19.6037	0	0.365	Putative secreted acid sphingomyelin phosphodiesterase; induced upon biofilm formation; possible Kex2p substrate
-	orf19.5339	0	0.366877778	Ortholog of S. cerevisiae Spg5; required for proteasome assembly during quiescence; transcript detected on high-resolution tiling arrays; Spider biofilm induced
GAP4	orf19.4456	0	0.367222222	Putative amino acid permease; hyphal induced; regulated by Gcn2p and Gcn4p; shows colony morphology-related gene regulation by Ssn6p

TPS1	orf19.6640	0	0.371011111	Trehalose-6-phosphate synthase; required for trehalose synthesis; role in hyphal growth and virulence in a mouse systemic infection; upregulated in the presence of human neutrophils; macrophage/pseudohyphal-repressed after 16 h
-	orf19.3820	0	0.375388889	Protein with DNA binding domain, an endonuclease domain; adjacent to CEN4, the centromere region of Chr 4; clade-associated gene expression
VID21	orf19.3077	0	0.376433333	Subunit of the NuA4 histone acetyltransferase complex; soluble protein in hyphae; Spider biofilm repressed
PTH2	orf19.4231	0	0.378611111	Putative cAMP-independent regulatory protein; constitutive expression independent of MTL or white-opaque status; Spider biofilm induced
-	orf19.3499	0	0.379155556	Secreted potein; Hap43-repressed; fluconazole-induced; regulated by Tsa1, Tsa1B under H2O2 stress conditions; induced by Mnl1p under weak acid stress; Spider biofilm induced
ALS2	orf19.1097	0	0.385488889	ALS family protein; role in adhesion, biofilm formation, wild-type germ tube induction; expressed during infection of human buccal epithelial cells, not under laboratory growth conditions; ALS family includes cell-surface glycoproteins
-	orf19.2047	0	0.387944444	Putative protein of unknown function; Hap43p-repressed gene; mutation confers hypersensitivity to toxic ergosterol analog, and to amphotericin B
-	orf19.5692	0	0.389988889	Ortholog(s) have ubiquitin-protein transferase activity and role in anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process, protein ubiquitination
SNG3	orf19.1333	0	0.391894444	Predicted ORF from Assembly 19; shows colony morphology-related gene regulation by Ssn6p
ERG1	orf19.406	0	0.392944444	Squalene epoxidase, catalyzes epoxidation of squalene to 2,3(S)-oxidosqualene in the ergosterol biosynthetic pathway; essential; target of allylamine antifungal drugs; uses NADH as a reducing cofactor, while S. cerevisiae Erg1p uses NADPH
-	orf19.5136	0	0.396655556	Putative pyridoxamine 5'-phosphate oxidase; planktonic growth and early-stage flow model biofilm induce
-	orf19.4581	0	0.396811111	Predicted ORF from Assembly 19; regulated by Tsa1p, Tsa1Bp under H2O2 stress conditions
-	orf19.3649	0	0.397677778	Ortholog(s) have adenyl-nucleotide exchange factor activity, role in cytoplasm-associated proteasomal ubiquitin-dependent protein catabolic process, cytoplasmic translation and cytosolic ribosome, nucleus localization
-	orf19.915	0	0.398025	Protein of unknown function; Spider biofilm induced
-	orf19.5532	0	0.398033333	Protein of unknown function; Spider biofilm induced
LTP1	orf19.5104	0	0.400222222	Putative protein phosphatase of the PTP family (tyrosine-specific), similar to S. cerevisiae Ltp1p
IHD1	orf19.5760	0	0.400577778	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
-	orf19.7196	0	0.401388889	Protein described as a vacuolar protease; upregulated in the presence of human neutrophils
CBP1	orf19.7323	0	0.401833333	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
-	orf19.4617	0	0.40345	Predicted peptide alpha-N-acetyltransferase; flow model biofilm induced
FTR1	orf19.7219	0	0.405622222	High-affinity iron permease (ferric citrate, ferrioxamines E or B, transferrin); required for mouse virulence, low-iron growth; iron, amphotericin B, caspofungin, ciclopirox regulated; complements S. cerevisiae ftr1 iron transport defect
-	orf19.6077	0	0.406033333	Predicted ORF from Assembly 19; shows colony morphology-related gene regulation by Ssn6p
-	orf19.3444	0.010562201	0.408777778	Predicted membrane transporter, member of the drug:proton antiporter (14 spanner) (DHA2) family, major facilitator superfamily (MFS); Hap43p-repressed gene

-	orf19.5210	0	0.410122222	Putative Xbp1 transcriptional repressor; binds to cyclin gene promoters in S. cerevisiae; Hap43-repressed; possibly essential, disruptants not obtained by UAU1 method
-	orf19.4550	0	0.411777778	Predicted MFS membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family; flow model biofilm induced
-	orf19.2048	0.016622678	0.413177778	Transcription is positively regulated by Sfu1p
PFK1	orf19.3967	0	0.413311111	Alpha subunit of phosphofructokinase (PFK), which is Pfk1p, Pfk2p heteromultimer; PFK is activated by fructose 2,6-bisphosphate or AMP, inhibited by ATP; activity reduced on hyphal induction; phagocytosis-downregulated; fluconazole-induced
-	orf19.2132	0	0.415077778	Ortholog of *C. dubliniensis* CD36 : Cd36_65220, *C. parapsilosis* CDC317 : CPAR2_213740, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_92162 and *Debaryomyces hansenii* CBS767 : DEHA2A01056g
YKE2	orf19.6601.1	0	0.420133333	Possible cytoskeletal modulator; transcription induced upon yeast-to-hyphal switch; regulated by Nrg1p, Tup1p
-	orf19.5474	0	0.420333333	Protein of unknown function; induced by Mnl1 under weak acid stress; transcript detected on high-resolution tiling arrays; Spider biofilm repressed
ALS12	orf19.2122	0	0.421088889	ALS family protein; ALS family includes cell-surface glycoproteins, some with adhesin function; putative GPI-anchor; ketoconazole-induced; expression greater in low iron; transcription is positively regulated by Sfu1p
-	orf19.4742	0	0.421216667	Putative SH3-domain-containing protein
CDG1	orf19.7314	0	0.421677778	Protein described as similar to cysteine dioxygenases; expression is regulated upon white-opaque switching
-	orf19.6353	0	0.4223	Ortholog of *Candida albicans* WO-1 : CAWG_00172
-	orf19.5573	0	0.423588889	Predicted ORF from Assembly 19; decreased expression observed in an ssr1 homozygous null mutant
-	orf19.1999	0	0.423922222	Protein of unknown function; transcript detected on high-resolution tiling arrays
FCA1	orf19.4195.1	0	0.424055556	Cytosine deaminase; enzyme of pyrimidine salvage; functional homolog of S. cerevisiae Fcy1p; mutation is associated with resistance to flucytosine (5-FC) in a clinical isolate; hyphal downregulated; gene has intron
-	orf19.2751	0	0.4247	Predicted membrane transporter; member of the monocarboxylate porter (MCP) family, major facilitator superfamily; Hap43-induced gene; alkaline upregulated by Rim101; possibly an essential gene, disruptants not obtained by UAU1 method
-	orf19.4593.1	0	0.425611111	ORF Predicted by Annotation Working Group
PHO89	orf19.4599	0	0.427566667	Putative phosphate permease; expression is regulated upon white-opaque switching; alkaline upregulated by Rim101p; induced upon biofilm formation; possibly adherence-induced
RPF1	orf19.2667	0	0.428777778	Putative nucleolar protein with a predicted role in the assembly and export of the large ribosomal subunit; essential for growth; rat catheter and Spider biofilm induced
-	orf19.6055	0.010562201	0.428866667	Ortholog of *C. dubliniensis* CD36 : Cd36_00460, *C. parapsilosis* CDC317 : CPAR2_800010, *Candida tenuis* NRRL Y-1498 : CANTEDRAFT_125085 and *Debaryomyces hansenii* CBS767 : DEHA2D09086g
-	orf19.1200	0	0.430677778	Protein of unknown function; Spider biofilm induced
-	orf19.7596	0.010562201	0.431188889	Protein with a phosphoglycerate mutase family domain; Hap43-repressed gene
-	orf19.4391	0	0.431288889	Ortholog of *C. dubliniensis* CD36 : Cd36_28730, *Candida tropicalis* MYA-3404 : CTRG_00749 and *Candida albicans* WO-1 : CAWG_01683
LIP4	orf19.2133	0	0.435366667	Secreted lipase, member of a differentially expressed lipase gene family with possible roles in nutrition and/or in creating an acidic microenvironment; expressed more strongly during mucosal infections than during systemic infections

-	orf19.1034	0	0.435555556	Protein with a predicted cytochrome b5-like Heme/Steroid binding domain; Hap43, caspofungin repressed; flow model biofilm induced
ECM3	orf19.1563	0	0.4361	Ortholog(s) have endoplasmic reticulum localization
-	orf19.3720	0	0.437333333	Ortholog(s) have role in positive regulation of endo-1,4-beta-xylanase activity and SCF ubiquitin ligase complex, cytoplasm localization
-	orf19.1796	0	0.437422222	Putative glyoxylate reductase; acts on glyoxylate and hydroxypyruvate substrates; Spider biofilm repressed
-	orf19.4185	0	0.4379	Ortholog(s) have phosphoprotein phosphatase activity, thiosulfate sulfurtransferase activity, role in protein dephosphorylation and cytosol, nucleus localization
PHO15	orf19.4444	0	0.438244444	Protein described as 4-nitrophenyl phosphatase; hyphal downregulated
-	orf19.4607	0.010562201	0.438577778	Predicted ORF from Assembly 19; hyphal induced
-	orf19.2745	0	0.440722222	Predicted zinc-finger protein of unknown function; has similarity to S. cerevisiae Ume6p, which is a transcription factor involved in the regulation of meiotic genes
RIM9	orf19.101	0	0.4422	Protein required for alkaline pH response via the Rim101 signaling pathway; ortholog of S. cerevisiae Rim9 and A. nidulans palI; Spider biofilm induced
-	orf19.3143	0	0.442877778	Has domain(s) with predicted DNA binding, nucleic acid binding activity
-	orf19.3902	0	0.445022222	Predicted ORF from Assembly 19; decreased transcription is observed upon fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2
-	orf19.5326	0	0.449266667	Putative transcription factor with zinc finger DNA-binding motif; possible ortholog of S. cerevisiae Mig2p
CLB2	orf19.1446	0	0.451644444	B-type mitotic cyclin (cyclin-dependent protein kinase regulatory subunit); essential; required for wild-type mitotic exit; role in cell polarization; interacts with catalytic subunit Cdk1p
LAP3	orf19.539	0	0.452522222	Protein described as an aminopeptidase; transcription is positively regulated by Sfu1p
DAL52	orf19.3208	0	0.453622222	Putative allantoate permease; fungal-specific (no human or murine homolog); not essential for viability; similar to S. cerevisiae Dal5p
-	orf19.4580	0	0.454622222	Protein of unknown function; Hap43-repressed gene
PEX4	orf19.4041	0	0.454888889	Putative peroxisomal ubiquitin conjugating enzyme; regulated by Sef1, Sfu1, and Hap43; rat catheter biofilm induced; Spider biofilm induced
-	orf19.5400	0	0.454966667	ORF Predicted by Annotation Working Group
-	orf19.775	0	0.45625	Ortholog of *C. dubliniensis* CD36 : Cd36_04450, *C. parapsilosis* CDC317 : CPAR2_105460, *Debaryomyces hansenii* CBS767 : DEHA2D07128g and *Pichia stipitis Pignal* : PICST_80203
-	orf19.7396	0	0.4584	Protein of unknown function; Spider biofilm induced; Hap43-repressed
FCY2	orf19.333	0	0.458933333	Putative purine-cytosine permease of pyrimidine salvage; similar to S. cerevisiae Fcy2p; mutation associated with resistance to flucytosine in clinical isolates; transposon mutation affects filamentation; farnesol-upregulated in biofilm
FMP27	orf19.3422	0	0.459911111	Predicted ORF from Assembly 19; fungal-specific (no human or murine homolog)
HRK1	orf19.5408	0	0.461822222	Putative serine/threonine kinase; predicted role in cellular ion homeostasis; Spider biofilm repressed
UBA4	orf19.2324	0	0.462955556	Putative ubiquitin activating protein; Hap43-repressed; induced by prostaglandins; clade-associated gene expression

GCY1	orf19.6757	0	0.465966667	Aldo/keto reductase; mutation confers hypersensitivity to toxic ergosterol analog; farnesol-repressed; stationary phase enriched protein; flow model biofilm induced; Spider biofilm repressed
SOD5	orf19.2060	0	0.466888889	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
TRY3	orf19.1971	0	0.469744444	RING-finger transcription factor; regulator of yeast form adherence; required for yeast cell adherence to silicone substrate; Spider biofilm induced
ALS9	orf19.5742	0	0.470422222	ALS family protein; expressed during infection of human epithelial cells; confers laminin adhesion to S. cerevisiae; sequence is highly variable; ALS family includes cell-surface glycoproteins, some with adhesin function
-	orf19.3577.1	0	0.470444444	ORF Predicted by Annotation Working Group
CAF16	orf19.388	0	0.470677778	ABC family protein, predicted not to be a transporter; caspofungin repressed
-	orf19.5761	0	0.471022222	Protein not essential for viability; transcription is alkaline upregulated
PHO113	orf19.2619	0	0.471644444	Putative constitutive acid phosphatase; Rim101-repressed; DTT-extractable; N-glycosylated; possibly an essential gene, disruptants not obtained by UAU1 method
RVS162	orf19.6349	0	0.472144444	Protein containing a BAR domain, which is found in proteins involved in membrane curvature; null mutant does not display the endocytic, hyphal growth, virulence, or cell wall defects exhibited by mutants in related genes RVS161 and RVS167
GZF3	orf19.2842	0	0.472777778	GATA-type transcription factor; oxidative stress-induced via Cap1; mutant has abnormal colony morphology and altered sensitivity to fluconazole, LiCl, and copper; Spider biofilm induced
URA1	orf19.4836	0	0.475066667	Dihydroorotate dehydrogenase; de novo pyrimidine biosynthesis; regulated by yeast-hypha switch, Nrg1/Mig1/Tup1; flow model biofilm induced; rat catheter and Spider biofilm repressed
-	orf19.3281	0	0.475611111	Ortholog(s) have histone demethylase activity (H3-K36 specific), methylated histone binding activity and role in histone demethylation, positive regulation of transcription elongation from RNA polymerase II promoter
-	orf19.1961	0.016622678	0.476	Planktonic growth-induced gene
SIT1	orf19.2179	0	0.476455556	Transporter of ferrichrome siderophores, but not ferrioxamine B; required for wild-type invasion of human epithelial cells in vitro, but not for wild-type systemic virulence in mouse; transcription regulated by iron, Sfu1p, Rfg1p, Tup1p
-	orf19.4612	0.034795801	0.478588889	Protein with a dienelactone hydrolase domain; Hap43-repressed gene
ZRT2	orf19.1585	0	0.479188889	Protein described as predicted zinc transporter; ciclopirox olamine, fluconazole, or alkaline downregulated; transcriptionally induced by interaction with macrophage; amphotericin B induced
-	orf19.846	0	0.479383333	Predicted protein kinase similar to S. cerevisiae Nnk1; implicated in proteasome function in S. cerevisiae; induced by Mnl1 under weak acid stress
RAD1	orf19.5318	0	0.4796	Putative single-stranded DNA endonuclease; transcript regulated by Nrg1; macrophage-induced gene
GPD1	orf19.1756	0	0.481733333	Protein described as similar to glycerol-3-phosphate dehydrogenase; predicted enzyme of carbohydrate metabolism; biofilm-induced expression; regulated by Efg1p; regulated by Tsa1p, Tsa1Bp under H2O2 stress conditions
-	orf19.3378	0	0.482888889	Protein of unknown function; regulated by Tsa1, Tsa1B in minimal media at 37 degrees C
-	orf19.2073	0	0.4849	Protein with a multidrug and toxin extrusion protein domain; induced by Mnl1 under weak acid stress
AQY1	orf19.2849	0	0.487066667	Aquaporin water channel; mutant has increased resistance to osmotic shock; required for wild-type tolerance of freezing; not required for virulence in a mouse model of systemic infection; flucytosine repressed

HIP1	orf19.3195	0	0.487077778	Alkaline upregulated; flucytosine induced; regulated by Plc1p, Gcn2p and Gcn4p; fungal-specific (no human or murine homolog)
NAT4	orf19.4664	0	0.49	Putative histone acetyltransferase; involved in regulation of white-opaque switch; early-stage flow model biofilm induced; Spider biofilm induced
RBT7	orf19.2681	0.010562201	0.491144444	Protein with similarity to RNase T2 enzymes, has putative secretion signal; expression is Tup1p-repressed
HSP104	orf19.6389	0	0.491411111	Heat-shock protein; roles in biofilm and virulence; complements chaperone, prion activity in S. cerevisiae; guanidine-insensitive; heat shock/stress induced; repressed in farnesol-treated biofilm; sumoylation target; Spider biofilm induced
-	orf19.5523	0	0.492166667	Ortholog of *C. dubliniensis* CD36 : Cd36_62780, *C. parapsilosis* CDC317 : CPAR2_601690, Candida tenuis NRRL Y-1498 : CANTEDRAFT_113271 and Debaryomyces hansenii CBS767 : DEHA2A06644g
-	orf19.2059	0	0.4926	Protein with homology to magnesium-dependent endonucleases and phosphatases; regulated by Sef1, Sfu1, and Hap43; Spider biofilm induced
-	orf19.3459	0	0.494566667	Putative serine/threonine/tyrosine (dual-specificity) kinase; disruptants not obtained by UAU1 method
ALS2	orf19.1097	0	0.494855556	ALS family protein; role in adhesion, biofilm formation, germ tube induction; expressed at infection of human buccal epithelial cells; putative GPI-anchor; induced by ketoconazole, low iron and at cell wall regeneration; regulated by Sfu1p
CRP1	orf19.4784	0	0.495325	Copper transporter of the plasma membrane; P1-type ATPase (CPx type); mediates copper resistance; similar to proteins of Menkes and Wilson disease; copper-induced; suppresses copper sensitivity of an S. cerevisiae cup1 null mutant
YWP1	orf19.3618	0.016622678	0.496322222	Protein with suggested role in dispersal in host; mutation causes increased adhesion and biofilm formation; putative GPI-anchor; cell wall and secreted; has stable propeptide; regulated by growth phase, phosphate, Ssk1p, Ssn6p, Efg1p, Efh1p
-	orf19.3448	0.010562201	0.496966667	Predicted ORF from Assembly 19; ketoconazole-repressed
GPM2	orf19.1067	0	0.498155556	Protein described as phosphoglycerate mutase; decreased expression in hyphae compared to yeast-form cells; macrophage/pseudohyphal-repressed
-	orf19.21	0	0.4985	Ortholog(s) have role in ethanol metabolic process and mitochondrial inner membrane localization
FCA1	orf19.4195.1	0	0.499322222	Cytosine deaminase; enzyme of pyrimidine salvage; functional homolog of S. cerevisiae Fcy1p; mutation is associated with resistance to flucytosine (5-FC) in a clinical isolate; hyphal downregulated; gene has intron
FGR17	orf19.5729	0.010562201	0.499455556	Putative DNA-binding transcription factor; lacks an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
-	orf19.3336	0	0.499911111	Ortholog of *Candida albicans* WO-1 : CAWG_01228

Table S3 Interaction of osthole and azoles against 30 fluconazole-resistant *C. albicans* by microdilution assay

Clinical Isolates	MIC$_{50}$ (μg/ml) alone					MIC$_{50}$ (μg/ml) in combination				FICI			
	FLC	MCZ	KCZ	ICZ	OST	FLC/OST	MCZ/OST	KCZ/OST	ICZ/OST	FLC/OST	MCZ/OST	KCZ/OST	ICZ/OST
0304103	>64	>16	>16	2	>64	8/8	0.5/2	0.125/4	0.0625/4	0.13	0.03	0.04	0.06
100	>64	>16	16	4	>64	2/16	0.5/4	0.125/2	0.125/2	0.14	0.05	0.02	0.05
102	>64	>16	16	8	>64	2/8	0.5/4	0.125/4	0.25/4	0.08	0.05	0.04	0.06
311	>64	>16	16	4	>64	2/4	0.5/2	0.0625/4	0.125/4	0.05	0.03	0.04	0.06
0710922	>64	16	8	4	>64	2/16	0.25/2	0.0625/2	0.0625/4	0.14	0.03	0.02	0.05
0710497	>64	8	8	4	>64	4/16	0.5/4	0.125/4	0.125/2	0.16	0.09	0.05	0.05
19	>64	8	4	4	>64	4/4	0.25/4	0.0625/4	0.125/2	0.06	0.06	0.05	0.05
305	>64	>16	>16	>16	>64	4/8	1/4	1/2	0.5/8	0.09	0.06	0.05	0.08
385	>64	16	>16	16	>64	4/8	2/8	0.125/2	0.125/4	0.09	0.19	0.02	0.04
395	>64	16	8	4	>64	4/16	2/4	0.5/4	0.125/8	0.16	0.16	0.09	0.09
540	>64	4	4	2	>64	1/4	1/4	0.0625/4	0.0625/4	0.04	0.28	0.05	0.06
103101	>64	16	4	8	>64	4/8	0.5/2	0.125/4	0.0625/4	0.09	0.05	0.06	0.04
103102	>64	8	4	2	>64	2/8	0.5/4	0.0625/2	0.5/8	0.08	0.09	0.03	0.31
1034	>64	8	8	2	>64	2/8	0.25/8	0.0625/8	0.0625/4	0.08	0.09	0.07	0.06
23	>64	>16	16	4	>64	8/16	2/4	1/4	1/4	0.19	0.09	0.09	0.28
0710418	>64	>16	16	4	>64	4/8	4/4	1/2	0.5/8	0.09	0.16	0.08	0.19
0710452	>64	8	2	4	>64	4/16	2/8	0.0625/4	0.125/4	0.16	0.31	0.06	0.06
0710448	>64	16	8	4	>64	2/4	2/4	0.5/8	0.125/4	0.05	0.16	0.13	0.06
646	>64	16	8	1	>64	2/8	1/2	0.125/8	0.0625/8	0.08	0.08	0.08	0.13
31	16	4	2	0.5	>64	1/16	0.25/1	0.0625/4	0.0625/8	0.19	0.07	0.06	0.19
33	>64	>16	>16	16	>64	4/4	4/8	2/8	1/4	0.06	0.19	0.13	0.09
29	8	2	1	1	>64	2/8	0.5/4	0.0625/8	0.125/8	0.31	0.28	0.13	0.19
538	>64	4	8	4	>64	8/16	1/2	0.0625/4	0.0625/4	0.19	0.27	0.04	0.05

379	>64	>16	16	16	>64	4/4	4/8	2/8	2/8	0.06	0.19	0.19	0.19
18	>64	>16	16	8	>64	4/16	4/8	0.5/4	0.25/16	0.16	0.19	0.06	0.16
#2	>64	16	8	4	>64	8/16	4/8	2/8	1/8	0.19	0.31	0.31	0.31
#3	>64	8	4	4	>64	16/16	1/2	1/8	0.5/8	0.25	0.14	0.31	0.19
#4	>64	>16	16	8	>64	16/8	0.5/2	0.0625/4	0.125/4	0.19	0.03	0.04	0.05
OCA33	>64	>16	>16	>16	>64	4/8	0.5/8	0.125/8	0.25/8	0.09	0.08	0.07	0.07
B16	>64	>16	>16	>16	>64	8/16	2/8	2/8	2/4	0.19	0.13	0.13	0.09
ZC-B1	>64	>16	>16	>16	>64	4/8	4/8	0.5/4	0.125/4	0.09	0.19	0.05	0.04

Table S4 Interaction of fluconazole and osthole against 10 fluconazole-sensitive *C. albicans*

Clinical Isolates	MIC_{50} (μg/ml) alone		MIC_{50} (μg/ml) in combination		FICI
	fluconazole	osthole	fluconazole	osthole	
Y0109	0.25	>64	0.25	1	1.01
#5	0.25	>64	0.5	1	2.01
13	0.125	>64	0.125	1	1.01
14	1	>64	0.5	1	0.51
21	0.25	>64	0.5	1	2.01
28	0.25	>64	0.25	1	1.01
805	0.125	>64	0.25	1	2.01
OCA-1	0.5	>64	0.5	1	1.01
OCA-34	1	>64	1	1	1.01
OCA-42	0.5	>64	0.25	1	0.51