Supplementary Table 4: Genes downregulated by the cAMP-signaling pathway during normal budding growth

17-Aug-07

			Fold Change				
Grouping	**Name**	**ID or ORF6.**	**ID or ORF19.**	**cap1/ WT**	**cap1/ pde2**	**WT/ pde2**	**Function**
Cell Surface Protein	*IFF6* (Orf6.2490)	2490	4072	1.86	2.10	1.13	Putative GPI-anchored protein of unknown function; opaque-specific transcription
Cell Surface Protein	*ECE99*	2929	3384	2.10	3.83	1.82	Putative cell wall protein with C-terminal similarity to Hwp1p; alkaline upregulated; alpha factor induced; Rim101p-regulated; merged with orf19.1327 in Assembly 20
Cell Surface Protein	*MUC1*	3075	4556	4.05	21.33	5.27	Putative GPI-anchored protein, member of the ALS gene family; ketoconazole induced; caspofungin repressed; merged with orf19.4555 in Assembly 20
Cell Surface Protein	*YWP1*	3288	3618	1.39	2.10	1.51	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
Cell Surface Protein	*RBR3*	3407	5124	1.76	2.67	1.52	Cell wall protein; expression is repressed by Rim101p
Cell Surface Protein	*ECM331*	3969	4255	2.01	2.11	1.05	Putative GPI-anchored protein; caspofungin induced; Plc1p-regulated; repressed by Rim101p, Hog1p; shows colony morphology-related gene regulation by Ssn6p; increased mRNA abundance in cyr1 homozygous null mutant yeast-form cells
Cell Surface Protein	*PGA18*	4292	301	1.30	3.08	2.36	Putative GPI-anchored protein of unknown function; regulated by Nrg1p, Tup1p
Cell Surface Protein	RBR1 (*SNF5*)	450	535	2.79	4.94	1.77	GPI-anchored cell wall protein required for filamentous growth at acidic pH; expression is repressed by Rim101p and activated by Nrg1p
Cell Surface Protein	*PGA6*	4590	4765	1.72	2.38	1.39	Putative GPI-anchored cell wall protein of unknown function; similar to *S. cerevisiae* Ccw12p/Ylr110cp; transcriptionally regulated by iron; expression greater in high iron; upregulated upon Als2p depletion
Cell Surface Protein	*RBT1*	4889	1327	1.79	2.22	1.24	Putative cell wall protein with similarity to Hwp1p, required for virulence; predicted to be cell-wall attached and glycosylated; Tup1p repressed; serum, hypha and alkaline induced; farnesol, alpha factor induced; Rfg1p-, Rim101p-regulated
Cell Surface Protein	*PGA25*	5529	6336	1.36	2.09	1.54	Putative GPI-anchored protein of unknown function; fluconazole-downregulated
Cell Surface Protein	*RBR1* (*SNF5*)	6747	535	2.90	4.43	1.53	GPI-anchored cell wall protein required for filamentous growth at acidic pH; expression is repressed by Rim101p and activated by Nrg1p
Cell Surface Protein	*SSR1*	7956	7030	1.38	2.12	1.53	Beta-glucan associated cell wall protein with role in cell wall structure; S/T rich protein, GPI-anchor; similar mRNA abundance in yeast-form and germ tube; detected at germ tube plasma membrane by mass spec; similar to *S. cerevisiae* Ssr1p
Cell Surface Protein	*PGA52* (YJL171C)	799		1.91	2.06	1.08	Putative GPI-anchored protein of unknown function; fluconazole-induced
Cell Surface Protein	*HYR1* (YIL169C)	857	4975	1.31	2.15	1.64	Nonessential, GPI-anchored, predicted cell wall protein; possible N- and O-glycosylation; induced in hyphae; induction associated with azole resistance; regulated by Rfg1p, Efg1p, Nrg1p, Tup1p, Cyr1p
Cell Surface Protein	*IFF6*	3209	4072	1.70	2.20	1.29	Putative GPI-anchored protein of unknown function; opaque-specific transcription
Cell Wall Biosynthesis	*GSC1*	3785	2929	1.42	2.01	1.41	Subunit of beta-1,3-glucan synthase; essential; gsc1 allele determines resistance/sensitivity to echinocandin antifungals; 16 predicted membrane-spanning regions; mRNA abundance declines after yeast-to-hypha transition; fungal-specific
Endocytosis	*FMP45* (YDL222C)	1074	6489	2.42	3.84	1.59	Protein induced during the mating process; alkaline downregulated; repressed in response to alpha pheromone in Spider medium
Endocytosis	*LSP1*	1659	3149	1.34	2.10	1.57	Predicted ORF from Assembly 19; caspofungin repressed; fungal-specific (no human or murine homolog)
Endocytosis	*SUR7*	360	3414	1.75	2.62	1.50	Predicted ORF in Assemblies 19 and 20
ER Protein	*ROT1*	3157	6029	2.15	2.16	1.00	Similar to *S. cerevisiae* Rot1p, which is involved in cell wall 1,6-beta-glucan biosynthesis; has predicted transmembrane region
ER Protein	*YET3*	6421	1564	1.55	2.18	1.41	Predicted ORF in Assemblies 19 and 20
ER Protein	*PER1*	6605	4240	1.88	3.80	2.02	Predicted ORF in Assemblies 19 and 20
Ergosterol Biosynthesis	*CYB5*	8504	7049	1.48	2.84	1.92	Cytochrome b(5); not essential for viability; similar to *S. cerevisiae* Cyb5p; transcriptionally regulated by iron; expression greater in high iron; fluconazole-induced; shows colony morphology-related gene regulation by Ssn6p
Ergosterol biosynthesis and lipid metabo	*ERG5*	6958	5178	1.28	2.39	1.86	Putative C-22 sterol desaturase; fungal C-22 sterol desaturases are cytochrome P450 enzymes of ergosterol biosynthesis, catalyze formation of the C-22(23) double bond in the sterol side chain; transposon mutation affects filamentous growth
Fatty Acid Biosynthesis	*FGR22*	5334	1586	1.91	2.08	1.09	Putative phosphatidylinositol-specific phospholipase C (PI-PLC); predicted type 2 membrane protein; role in, and regulated by, filamentation; no mouse systemic virulence role; almost identical to orf19.5797
Fatty Acid Catabolism	*SOU1*	6126	2896	1.29	3.51	2.71	Enzyme involved in utilization of L-sorbose; has sorbitol dehydrogenase, fructose reductase, and sorbose reductase activities; has NAD-binding site motif; transcriptional regulation affected by chromosome 5 copy number
Galactose Metabolism	*GAL10*	6483	3672	1.28	2.12	1.66	Protein described as similar to UDP-glucose 4-epimerase; fluconazole-induced
Glucoside Hydrolysis	YBR056W	8114	7214	1.38	2.14	1.55	Protein described as similar to glucan 1,3-beta-glucosidase; regulated by Nrg1p, Tup1p; possibly regulated by Tac1p; induced upon biofilm formation; induced by nitric oxide; induced during cell wall regeneration
Glutamate Biosynthesis	*GLT1*	2272	6257	1.24	2.79	2.25	Alkaline downregulated
Glycogen catabolism	*GPH1*	7947	7021	1.16	4.94	4.25	Putative glycogen phosphorylase; gene regulated by Ssk1p, Mig1p, and Tup1p; fluconazole-induced; localizes to cell surface of hypha cells, but not yeast-form cells; *S. cerevisiae* Gph1p is a stress-regulated protein of glycogen metabolism
Glycogen Synthesis	*GLG2*	8594	7434	1.31	3.29	2.50	Protein described as self-glucosylating initiator of glycogen synthesis; expression is regulated upon white-opaque switching
Glycolysis Detoxification	*GLO2*	6848	4088	1.67	2.19	1.31	Predicted ORF in Assemblies 19 and 20
Glycosylation	*MNT1*	5740	1665	1.28	2.25	1.75	Alpha-1,2-mannosyl transferase; adds second mannose during cell wall mannoprotein biosynthesis; required for wild-type virulence and adherence to epithelial cells; predicted type II membrane protein of Golgi; fungal-specific
Golgi Protein	YER113C	3027	3228	1.23	3.01	2.45	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.1072	1072	1594	1.94	2.23	1.15	Predicted ORF from Assembly 19; possibly spurious ORF (Annotation Working Group prediction); merged with orf19.792 in Assembly 20
Hypothetical Protein	Orf6.1220	1220	1830	1.86	3.06	1.65	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	*HEH2*	1358	5569	2.23	2.32	1.04	Predicted ORF in Assemblies 19 and 20

Hypothetical Protein	Orf6.1513	1513	3621	1.55	2.08	1.34	Possible pseudogene; similar to Ywp1p; ORF extended upstream from the initiating Met of orf19.3621 has a stop codon in the region corresponding to the Ywp1p signal peptide; disruption causes no apparent phenotype; no expression detected
Hypothetical Protein	Orf6.1762	1762	5592	1.06	2.44	2.31	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	*DAG7* (Orf6.1768)	1768	4688	1.44	2.33	1.61	Predicted ORF from Assembly 19; a-specific transcription; alpha-factor induced
Hypothetical Protein	Orf6.1793	1793	682	1.81	3.66	2.02	Predicted ORF from Assembly 19; ketoconazole-induced; fluconazole-downregulated; induced in a cyr1 homozygous null mutant; shows colony morphology-related gene regulation by Ssn6p; merged with orf19.2296 in Assembly 20
Hypothetical Protein	*SNA2*	2615	4132	1.36	2.35	1.73	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.2644	2644	1344	1.15	2.85	2.47	Predicted ORF in Assemblies 19 and 20; fluconazole-induced; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.282	282	1873	1.81	2.10	1.16	Predicted ORF in Assemblies 19 and 20; repressed by nitric oxide; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.2999	2999	1098	2.69	18.93	7.04	Predicted ORF from Assembly 19; merged with orf19.1097 in Assembly 20
Hypothetical Protein	*ADH5*	4277	2608	1.18	2.01	1.70	Putative alcohol dehydrogenase; soluble protein in hyphae; expression is regulated upon white-opaque switching; fluconazole-induced; antigenic during murine systemic infection; regulated by Nrg1p, Tup1p
Hypothetical Protein	*AVT1*	4661	5496	1.03	2.44	2.36	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.4929	4929	1060	1.21	3.11	2.57	Predicted ORF in Assemblies 19 and 20; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.5070	5070	5602	2.17	2.40	1.10	Predicted ORF in Assemblies 19 and 20; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.5548	5548	2302	1.36	3.07	2.26	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	YGR026W	5843	3872	2.41	3.53	1.47	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.5961	5961	5137	1.34	2.33	1.74	Predicted ORF in Assemblies 19 and 20; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.5969	5969	2030	2.29	2.37	1.03	Predicted ORF in Assemblies 19 and 20; greater mRNA abundance observed in a cyr1 or ras1 homozygous null mutant than in wild-type
Hypothetical Protein	*PHM7*	6093	2170	1.20	2.76	2.31	Putative transporter; fungal-specific (no human or murine homolog); Hog1p-downregulated; downregulated in response to 17-beta-estradiol, ethynyl estradiol
Hypothetical Protein	Orf6.6095	6095	3430	1.86	2.07	1.11	Predicted ORF in Assemblies 19 and 20; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	*FMP27*	6103	3422	1.74	2.33	1.34	Predicted ORF from Assembly 19; fungal-specific (no human or murine homolog)
Hypothetical Protein	*MET13* (YMR295C)	6135	2887	1.31	2.19	1.66	Predicted ORF from Assembly 19; ketoconazole-induced; amphotericin B repressed
Hypothetical Protein	Orf6.6662	6662	2954	1.18	2.65	2.24	Predicted ORF in Assemblies 19 and 20; repressed by nitric oxide; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	YKR049	6978	5158	1.46	2.54	1.74	Protein with slight similarity to a human gene associated with colon cancer and to orf19.5158; regulated by Gcn4p, Cyr1p; induced in response to amino acid starvation (3-aminotriazole treatment)
Hypothetical Protein	*STU1*	7247	4435	1.07	3.09	2.89	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.7464	7464	2091	2.11	2.30	1.09	Predicted ORF in Assemblies 19 and 20; repressed by nitric oxide
Hypothetical Protein	Orf6.7997	7997	5012	1.28	2.17	1.70	Predicted ORF in Assemblies 19 and 20; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.8375	8375	7294	2.72	2.91	1.07	Predicted ORF from Assembly 19; removed from Assembly 20
Hypothetical Protein	Orf6.8635	8635	5399	2.16	3.06	1.42	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.8756	8756	7504	1.77	2.20	1.24	Predicted ORF in Assemblies 19 and 20; Plc1p-regulated; induced in core caspofungin response
Hypothetical Protein	Orf6.968	968	3888.2	1.19	2.76	2.31	ORF Predicted by Annotation Working Group
Kinase activity	*CRK1*	2037	3524	1.24	2.51	2.02	Protein kinase of the Cdc2 subfamily involved in hypha development and virulence; promotes hypha development independently of Cph1 and Efg1; complements *S. cerevisiae* sgv1 mutant; merged with orf19.3523 in Assembly 20
Kinase activity	YDR109C	4693	2737	1.45	2.61	1.80	Predicted ORF in Assemblies 19 and 20
Lipid Binding Protein	*TCB3*	5286	3003	2.82	2.86	1.01	Predicted ORF in Assemblies 19 and 20
Membrane Protein	*CSH3*	2577	3366	2.53	2.96	1.17	Functional homolog of *S. cerevisiae* Shr3p, which is a chaperone specific for amino acid permeases; localized to ER; required for wild-type amino-acid responsive hypha growth and for mouse systemic virulence; regulated by Gcn2p and Gcn4p
Metabolism	*MAM33*	8087	7187	1.08	2.18	2.03	Predicted ORF from Assembly 19; regulated by Ssn6p
Methylation	*SPE2*	4718	568	1.07	2.99	2.80	Predicted ORF from Assembly 19; possibly adherence-induced
Mitochondrial Protein	*MRPS5*	1598	989	1.36	3.42	2.51	Predicted ORF in Assemblies 19 and 20
Mitochondrial Protein	*CYT1*	2040	3527	1.73	2.83	1.64	Protein described as cytochrome c1; transcriptionally regulated by iron; expression greater in high iron; alkaline downregulated
Mitochondrial Protein	*CYC1*	244	1770	1.99	2.03	1.02	Cytochrome c; complements defects of an *S. cerevisiae* cyc1 cyc7 double mutant; transcriptionally regulated by iron; expression greater in high iron; alkaline downregulated; repressed by nitric oxide
Mitochondrial Protein	*COX15*	3305	3656	1.45	2.29	1.58	Transcription is regulated by Nrg1p and Tup1p; alkaline downregulated
Mitochondrial Protein	Orf6.4597	4597	4758	1.53	2.09	1.37	Predicted ORF in Assemblies 19 and 20; alkaline downregulated
Mitochondrial Protein	*QCR7*	4788	5629	1.87	2.33	1.25	Predicted ORF in Assemblies 19 and 20
Mitochondrial Protein	YER053C	5348	1395	1.49	2.03	1.36	Predicted ORF in Assemblies 19 and 20
Mitochondrial Protein	*COX4*	7102	1471	1.59	2.03	1.28	Predicted ORF from Assembly 19; transcription is regulated by Mig1p; macrophage/pseudohypha-induced; repressed by nitric oxide
Mitochondrial Protein	*COR1*	7429	4016	1.36	2.01	1.47	Predicted ORF in Assemblies 19 and 20; amphotericin B induced; repressed by nitric oxide
Mitochondrial Protein	*NUC2*	7629	6531	1.92	3.25	1.69	Protein described as NADH-ubiquinone oxidoreductase; identified in detergent-resistant membrane fraction (possible lipid raft component); alkaline downregulated
Mitochondrial Protein	*YML6*	7945	7019	1.82	2.06	1.13	Protein described as a mitochondrial ribosomal protein; induced upon adherence to polystyrene
Mitochondrial Protein	*FESUR1*	8837	6794	1.78	2.03	1.14	Protein described as ubiquinone reductase; transcriptionally induced by interaction with macrophage; alkaline downregulated; repressed by nitric oxide
Mitochondrial Protein	*RIP1*	9144	5893	1.66	2.31	1.39	Protein described as subunit of ubiquinol cytochrome c-reductase; transcriptionally regulated by iron; expression greater in high iron; alkaline downregulated; repressed by nitric oxide
Nucleotide Biosynthesis	*URA2*	2755	2360	2.02	2.25	1.11	Predicted ORF from Assembly 19; flucytosine induced; macrophage/pseudohyphal-induced
Phosphatase activity	*CWH8*	2497	3682	1.62	3.09	1.91	Putative dolichyl pyrophosphate (Dol-P-P) phosphatase; ketoconazole-induced; expression is increased in a fluconazole-resistant isolate
Phosphatase activity	*UGP1*	346	1738	1.62	2.01	1.24	Protein similar to UTP-glucose-1-phosphaturidyl transferase; localizes to cell surface of yeast-form cells, but not hypha cells; Hog1p-downregulated

Phospholipid Synthesis	*CHO1*	6570	677	2.17	2.77	1.27	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
Protein catabolism	YOL098C	6802	6693	1.26	3.04	2.42	Predicted ORF in Assemblies 19 and 20
Protein Folding	*PAC10*	9052	5985	2.16	2.20	1.02	Predicted ORF in Assemblies 19 and 20
Protein Modification	*VRG4*	5085	1232	1.15	2.17	1.89	GDP-mannose transporter; essential gene; required for glycosylation, hypha growth; functional homolog of *S. cerevisiae* Vrg4p, which imports GDP-mannose from cytoplasm to Golgi for protein and lipid mannosylation; no mammalian homolog
Protein Secretion	*NCE102*	9077	5960	1.09	2.14	1.96	Predicted ORF in Assemblies 19 and 20
Protein Sorting	*BRO1*	5745	1670	1.53	3.57	2.33	Protein involved in transport from multivesicular body to vacuole; similar to *S. cerevisiae* Bro1p, which is a class E vacuolar protein sorting (VPS) factor; not involved in *RIM101* pathway; macrophage/pseudohypha-repressed
Protein Synthesis	*ALA1*	2925	5746	1.73	2.95	1.70	Alanyl-tRNA synthetase; translational regulation generates cytoplasmic and mitochondrial forms; regulated by Gcn4p; repressed upon amino acid starvation (3-AT); translation-related genes downregulated upon phagocytosis by murine macrophage
Ribosomal Formation	*YTM1*	5221	4815	1.11	3.01	2.72	Protein similar to *S. cerevisiae* Ytm1p, which is involved in biogenesis of the large ribosomal subunit; transposon mutation affects filamentous growth
Ribosomal Formation	*EMG1*	6558	665	2.72	2.98	1.09	Protein of unknown function; ortholog of *S. cerevisiae* Emg1p, which is involved in ribosome biogenesis
Ribosomal Formation/ Transporter	*KAP120*	8077	7177	0.99	2.46	2.48	Predicted ORF in Assemblies 19 and 20
RNA metabolism	Orf6.1932	1932	551	1.17	2.61	2.22	Predicted ORF in Assemblies 19 and 20
Secreted Protein	*SAP8*	2688	242	1.97	2.03	1.03	Secreted aspartyl proteinase; regulated by growth phase, temperature, and white-opaque switch; highly expressed in opaque cells; expressed upon deep epidermal invasion; greater expression during vaginal infection than oral infection
Splicing	*CWC2*	6567	674	0.83	2.79	3.36	Predicted ORF in Assemblies 19 and 20
Stress Associated Protein	Orf6.2780	2780	1152	1.58	3.30	2.09	Predicted ORF in Assemblies 19 and 20; regulated by Gcn2p and Gcn4p; induced in core stress response
Stress Associated Protein	YDR533C	1991	251	1.80	2.46	1.37	Member of ThiJ/PfpI protein family; antigenic (C and a 3 allergen); binds human immunoglobulin E; 2 N-glycosylation motifs; alkaline, fluconazole, Hog1p-downregulated; induced in core stress response or by oxidative stress (via Cap1p); possibly benomyl induced
Stress Associated Protein	*GRP2* (*GRE2*)	3162	4309	1.64	2.91	1.78	Similar to *S. cerevisiae* Gre2p (methylglyoxal reductase); antigenic in human; regulation associated with azole resistance; induced in core stress response or by oxidative stress (via Cap1p), fluphenazine, benomyl, or fluconazole (long term)
Stress Associated Protein	*IST2*	3721	2792	1.33	2.03	1.53	Predicted ORF in Assembly 19
Stress Associated Protein	*ASR1*	4208	2344	2.99	5.43	1.82	Protein described as similar to heat shock proteins; transcription regulated by cAMP, osmotic stress, ciclopirox olamine, ketoconazole; negatively regulated by Cyr1p, Ras1p; shows colony morphology-related gene regulation by Ssn6p
Stress Associated Protein	*GRP2* (*GRE2*)	4614	4309	1.58	2.30	1.46	Similar to *S. cerevisiae* Gre2p (methylglyoxal reductase); antigenic in human; regulation associated with azole resistance; induced in core stress response or by oxidative stress (via Cap1p), fluphenazine, benomyl, or fluconazole (long term)
Stress Associated Protein	*AQY1*	4943	2849	1.64	2.75	1.68	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
Stress Associated Protein	*CAT1*	5127	6229	2.40	6.84	2.85	Catalase; role in resistance to oxidative stress, including neutrophils, peroxide; role in murine systemic virulence; regulated by iron, ciclopirox olamine, fluconazole, growth, carbon source, pH, Rim101p, Ssn6p, Hog1p, core stress response
Stress Associated Protein	YEL077C	6568	675	2.07	2.18	1.05	Similar to cell wall proteins; induced in core stress response, core caspofungin response; iron-regulated; amphotericin B induced; regulated by Cyr1p, Ssn6p; possibly spurious ORF (Annotation Working Group prediction)
Stress Associated Protein	*DDR48*	6854	4082	3.16	4.52	1.43	Immunogenic stress-associated protein; regulated by filamentous growth pathways; induced by benomyl, caspofungin, or in azole-resistant strain; Hog1p, alkaline downregulated; similar to *S. cerevisiae* Ddr48p (ATP/GTPase, role in DNA repair)
Stress Associated Protein	*HSP12* (*WHS11*)	2761	4216	2.63	25.29	9.60	Predicted ORF in Assemblies 19 and 20; decreased expression in hyphae compared to yeast-form cells; transcription is increased in populations of cells exposed to fluconazole over multiple generations
Stress Associated Protein, Mitochondria	*CCP1*	957	238	2.11	2.68	1.27	Similar to cytochrome-c peroxidase N terminus; transcription is negatively regulated by Rim101p or alkaline pH; transcription induced by interaction with macrophage or low iron; oxygen-induced activity
Stress Associated Protein, Mitochondria	*SOD2*	4731	3340	1.24	2.35	1.89	Mitochondrial manganese-containing superoxide dismutase; role in protection against oxidative stress; active as homotetramer; N-terminal 34 amino acids removed upon import into mitochondria; H_2O_2-induced via Cap1p; alkaline downregulated
TCA Cycle	*ACO1*	5837	6385	1.33	2.60	1.96	Protein described as aconitase; regulated by Gcn4p; induced by amino acid starvation (3-AT treatment) or amphotericin B, phagocytosis; fluconazole-downregulated; expression greater in high iron; antigenic in human or murine infection
Transcription	*EFG1*	2978	610	2.64	2.74	1.04	Transcriptional repressor; required for white-phase cell type; hypha growth, metabolism, cell-wall gene regulator; roles in adhesion, virulence; Cph1p and Efg1p have role in host cytokine response; bHLH; binds E-box; T206 phosphorylated
Transcription	*ZCF29*	5965	5133	1.27	2.12	1.66	Predicted zinc-finger protein of unknown function
Transcription	*FCR1*	8814	6817	2.15	5.43	2.53	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
Transcription / Biofilm Formation	*BCR1*	6020	723	1.12	2.45	2.20	Transcription factor required for wild-type biofilm formation; not required for hypha growth; regulates cell surface associated genes; has C2H2 zinc finger; similar to *S. cerevisiae* Ypl230wp; filament induced; Tup1p-, Tec1p-regulated
Transcription / Iron Regulated	YNL227C	229	2399	1.03	2.88	2.80	Putative transcription factor with zinc finger DNA-binding motif; similar to bacterial DnaJ; transcriptionally regulated by iron; expression greater in low iron
Transcription / Iron Regulated	YLR401C	6422	1565	1.27	2.73	2.16	Putative transcription factor with zinc finger DNA-binding motif
Transporter	*EPT1*	2143	3695	0.77	1.82	2.36	Predicted ORF in Assemblies 19 and 20

Transporter	*GAP6*	2231	1799	1.51	2.75	1.82	Putative general amino acid permease; fungal-specific (no human or murine homolog)
Transporter	*GIT1*	2481	1979	1.36	2.23	1.64	Putative glycerophosphoinositol permease; fungal-specific (no human or murine homolog); alkaline downregulated; transcription is specific to white cell type; caspofungin repressed; macrophage/pseudohypha-repressed
Transporter	*YHC3*	3016	4059	1.46	2.06	1.41	Predicted ORF in Assemblies 19 and 20
Transporter	*CCC1*	7334	6948	1.18	4.52	3.84	Protein described as predicted manganese transporter; alkaline downregulated; shows colony morphology-related gene regulation by Ssn6p; repressed by nitric oxide
Transporter	*HGT19*	8683	5447	1.54	2.10	1.36	Putative glucose/myo-inositol transporter of major facilitator superfamily; 12 transmembrane segments, extended N-terminus; expressed in rich medium, 2% glucose; phagocytosis-induced; *C. albicans* glucose transporter family has 20 members
tRNA_formation	YHR020W	6810	6701	1.64	2.47	1.51	Predicted ORF in Assemblies 19 and 20
Ubiquitination	*APC11*	8992	7644	1.99	2.83	1.42	Predicted ORF in Assemblies 19 and 20
Ubiquitination	*TOM1*	3950	911	1.38	4.63	3.35	Predicted ORF from Assembly 19; merged with orf19.5776 in Assembly 20
Unknown	Orf6.162	162	8979	1.68	2.67	1.60	Transcriptionally regulated by iron; expression greater in high iron; similar to GPI-linked cell wall proteins; slight similarity to mucins; removed from Assembly 20
Unknown	Orf6.1914	1914	3932	1.95	2.33	1.19	Predicted ORF in Assemblies 19 and 20; induced in core caspofungin response; increased expression observed in an ssr1 homozygous null mutant; induced by nitric oxide in yhb1 mutant
Unknown	YPL184C	2205	5541	1.02	2.10	2.05	Predicted ORF in Assemblies 19 and 20; similar to *S. pombe* Nrd1p; transcription is induced upon induction of hypha growth; regulated by Cph1p, Efg1p, Cph2p; low-level expression; alkaline upregulated; fungal-specific (no human or murine homolog)
Unknown	Orf6.3342	3342	3335	1.39	2.68	1.93	Predicted ORF in Assemblies 19 and 20; shows colony morphology-related gene regulation by Ssn6p; repressed by nitric oxide
Unknown	Orf6.3569	3569	2272	1.24	2.12	1.71	Predicted ORF in Assemblies 19 and 20
Unknown	YFL043C	3702	90	1.22	2.22	1.82	Predicted ORF in Assemblies 19 and 20
Unknown	*PRM5*	3707	95	1.66	2.30	1.39	Predicted ORF in Assemblies 19 and 20
Unknown	*XJP5*	4148	1691	1.29	15.40	11.96	Predicted ORF in Assemblies 19 and 20; fluconazole-induced; filament induced; Hog1p-induced; regulated by Nrg1p, Tup1p
Unknown	*RHD1*	4552	54	1.26	2.14	1.69	Putative transmembrane protein with hydrophobic N- and C- termini and a Ser-Gly rich region; transcription is decreased upon yeast-hypha switch; expression is regulated upon white-opaque switching
Unknown	*FMP42*	6763	1179	1.15	2.64	2.29	Predicted ORF in Assemblies 19 and 20
Unknown	Orf9.819	819	1179	1.38	2.13	1.55	Transcriptionally regulated by iron; expression greater in high iron; possibly subject to Kex2p processing