Supplementary Table 2: Genes upregulated by the cAMP-signaling pathway during normal budding growth

Grouping	Name	ID or ORF6.	ID or ORF19.	WT/ cap1	pde2/ cap1	pde2/ WT	Function
Amino Acid Biosynthesis	*LYS12*	3372	2525	1.20	2.68	2.23	Predicted ORF in Assemblies 19 and 20
Amino Acid Biosynthesis	*MET15*	4514	5645	2.18	2.68	1.23	O-acetylhomoserine O-acetylserine sulfhydrylase; involved in sulfur amino acid biosynthesis; immunogenic; Hog1p; biofilm; possibly adherence-induced
Amino Acid Biosynthesis	*THR4*	6612	4233	0.99	3.10	3.12	Predicted ORF from Assembly 19; Gcn4p-regulated
Amino Acid Biosynthesis	*ARO8*	7457	2098	1.06	2.12	2.01	Protein abundance is affected by URA3 expression in the CAI-4 strain background; alkaline upregulated; Gcn4p-regulated
Amino Acid Biosynthesis	*AAT1*	4647	3554	1.13	2.31	2.04	Protein described as aspartate aminotransferase; soluble protein in hyphae; alkaline upregulated; amphotericin B repressed
Amino Acid Biosynthesis	*MAE1*	6106	3419	1.08	2.11	1.96	Malic enzyme, mitochondrial protein; transcription regulated by Mig1p and Tup1p; shows colony morphology-related gene regulation by Ssn6p
Amino Acid Biosynthesis	*HIS5*	6071	4177	1.04	2.85	2.73	Predicted ORF from Assembly 19; Gcn4p-regulated
Amino Acid Biosynthesis	*LYS2*	2119	2970	1.52	2.00	1.32	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
Amino Acid Catabolism	*GDH2*	3428	2192	1.44	5.38	3.74	Putative NAD-specific glutamate dehydrogenase; fungal-specific (no human or murine homolog); transcription is regulated by Nrg1p, Mig1p, Tup1p, and Gcn4p
Carbohydrate metabolism	YMR099C	1972	1946	1.19	2.75	2.31	Similar to an aldose 1-epimerase-related protein; antigenic during murine systemic infection
Carbohydrate metabolism	YMR099C	5593	1946	1.03	2.54	2.46	Similar to an aldose 1-epimerase-related protein; antigenic during murine systemic infection
Cell Surface Protein	*PGA7*	4504	5635	1.55	5.64	3.63	Protein described as a putative precursor of a hypha surface antigen; putative GPI-anchor; induced by ciclopirox olamine, ketoconazole, or by Rim101p at pH 8; regulated during planktonic growth; induced during cell wall regeneration
Cell Surface Protein	*RBT5*	4505	5636	1.37	5.58	4.07	GPI-anchored cell wall protein; has CRoW motif; not required for filamentous growth; expression is regulated by Rfg1p, Rim101p; repressed by Sfu1p, Hog1p, Tup1p; induced by serum, iron, alkaline pH, ketoconazole, or ciclopirox olamine
Cell Surface Protein	*FRE10*	6384		1.34	2.05	1.54	Major cell-surface ferric reductase under low-iron conditions; 7 transmembrane regions and a secretion signal predicted; repressed by Tup1p, Rim101p, Ssn6p, Hog1p, caspofungin; ciclopirox olamine induced; not required for filamentous growth
Cell Surface Protein	*RHD3*	8294	5305	2.48	3.35	1.35	Putative GPI-anchored protein that localizes to the cell wall; transcription is decreased upon yeast-hypha switch; transcriptionally regulated by iron; expression greater in high iron
Cell Surface Protein	*CSA1*	8439	7114	0.87	11.65	13.33	Surface antigen on elongating hyphae and buds; no obvious hypha defects in mutant; strain variation in number of repeat domains; upregulated in filaments; alkaline upregulated by Rim101p; ciclopirox induced; Efg1p- and Cph1p-regulated
Cytoskeleton/ Actin	*ARC19*	8251	3251	1.28	2.03	1.59	Predicted ORF in Assemblies 19 and 20
Cytoskeleton/ Microtubules	*STU2*	6222	6610	1.25	2.10	1.67	Predicted ORF in Assemblies 19 and 20
DNA repair	*RAD51*	4214	3752	1.37	3.73	2.71	Predicted ORF from Assembly 19; flucytosine induced
Ergosterol Biosynthesis and Lipid Metabolism	*ERG251* (*XJP2*)	2054	4631	1.41	3.38	2.39	Predicted ORF from Assembly 19; ketoconazole-induced; amphotericin B, caspofungin repressed
Ergosterol Biosynthesis and Lipid Metabolism	*ERG12*	5215	4809	1.11	2.36	2.12	Predicted ORF in Assemblies 19 and 20
Ergosterol Biosynthesis and Lipid Metabolism	*EHT1*	7777		1.31	3.51	2.68	Protein similar to *S. cerevisiae* Eht1p; transcription is induced in response to alpha pheromone in Spider medium
Fermentation	*PDC11* (*PDC1*)	4386	2877	2.08	3.47	1.67	Protein similar to pyruvate decarboxylase; antigenic; at cell surface of hypha, but not yeast-form cells; soluble in hyphae; regulated by Gcn4p, Efg1p, Efh1p; fluconazole-induced; repressed upon amino acid starvation; biofilm-induced
Fermentation	*ADH2*	6337	5113	1.82	2.13	1.17	Putative alcohol dehydrogenase; soluble protein in hyphae; fungal-specific (no human or murine homolog); expression is regulated upon white-opaque switching; regulated by Ssn6p
Fermentation	*PDC12* (*PDC1*)	7907	4608	1.63	2.68	1.65	Putative pyruvate decarboxylase; fungal-specific (no human or murine homolog)
Gluconeogenesis	*PYC2*	2989	789	2.10	2.74	1.31	Putative pyruvate carboxylase, binds to biotin cofactor; gene is up-regulated in a mutant lacking the Ssk1p response regulator protein, upon benomyl treatment, or in an azole-resistant strain overexpressing MDR1
Glycolysis	*TYE7*	6049	4941	1.75	2.39	1.36	Putative bHLH (basic region, helix-loop-helix) transcription factor; hypha regulated via Cph1p, Cyr1p; flucytosine, Hog1p induced; amphotericin B, caspofungin repressed; downregulated in azole-resistant strain overexpressing MDR1
Glycolysis	*HXK2*	6754	542	1.96	2.55	1.30	Protein described as hexokinase II; antigenic in human; downregulated in the presence of human neutrophils; regulated by Efg1p; fluconazole-induced; shows colony morphology-related gene regulation by Ssn6p
Glycolysis/Gluconeogenesis	*PFK1*	3504	3967	2.14	2.39	1.12	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 hypha induction; phagocytosis-downregulated; fluconazole-induced
Glycolysis/Gluconeogenesis	*GPM1*	7274	903	1.44	2.19	1.52	Protein described as phosphoglycerate mutase; enzyme of glycolysis; antigenic during murine, human infection; biofilm-, fluconazole-, or amino acid starvation (3-aminotriazole treatment) induced; regulated by Efg1p, Gcn4p

Glycolysis/Gluconeogenesis	*TPI1*	8886	6745	1.49	2.54	1.70	Putative ortholog of *S. cerevisiae* Tpi1p, which is triose-phosphate isomerase involved in glycolysis and gluconeogenesis; antigenic in mouse or human; transposon mutation affects filamentous growth; biofilm-induced expression
Glycolysis/TCA cycle	*PDX1*	7988	5021	1.63	2.05	1.26	Predicted ORF in Assemblies 19 and 20
Histone Modifying Protein	*RPD3*	8830	6801	1.29	2.87	2.22	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.125	125	4167	0.84	1.97	2.36	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.1308	1308	1506	1.41	2.20	1.56	Predicted ORF in Assemblies 19 and 20; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.3941	3941	5293	1.17	2.04	1.75	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	YMR074C	407	713	1.36	2.00	1.48	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	YGR169C-A	4195	4503	1.57	2.14	1.36	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.4856	4856	5784	2.06	2.49	1.21	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.5494	5494	6301	1.16	3.55	3.05	Predicted ORF from Assembly 19; removed from Assembly 20
Hypothetical Protein	Orf6.5504	5504	6311	1.28	2.33	1.83	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	YLR251W	5916	22	1.42	3.00	2.11	Transcription is positively regulated by Sfu1p; possibly spurious ORF (Annotation Working Group prediction)
Hypothetical Protein	Orf6.6926	6926	3119	1.48	5.73	3.87	Predicted ORF from Assembly 19; merged with orf19.3117 in Assembly 20
Hypothetical Protein	*GYP5*	8329	5340	2.22	2.22	1.00	Predicted ORF in Assemblies 19 and 20
Hypothetical Protein	Orf6.8506	8506	7346	1.38	2.43	1.77	Predicted ORF from Assembly 19; removed from Assembly 20
Hypothetical Protein	Orf6.8556	8556	7396	2.51	4.38	1.75	Predicted ORF in Assemblies 19 and 20
Inositol Biosynthesis	*INO1*	8933	7585	1.21	2.04	1.68	Inositol-1-phosphate synthase; enzyme of inositol biosynthesis; antigenic in human; repressed by farnesol (in biofilm) or caspofungin; regulated during planktonic growth; upstream inositol/choline regulatory element; glycosylation predicted
Iron Reduction	*CFL2* (*FRE4*)	5731	1264	1.84	3.48	1.89	Iron utilization protein; similar to an *S. cerevisiae* oxidoreductase, Ynr060wp; regulated by Sfu1p, Nrg1p, Tup1p; alkaline (via Rim101p, low iron, fluphenazine, ciclopirox olamine, flucytosine, induced; caspofungin, amphotericin B repressed
Iron Regulated	Orf6.2096	2096	411	1.30	2.66	2.05	Similar to GTPase regulators; transcriptionally regulated by iron; expression greater in low iron; possibly spurious ORF (Annotation Working Group prediction)
Iron Regulated	*FET35*	2939	1206	1.81	2.30	1.27	Similar to multicopper ferroxidase; transcriptionally regulated by iron; expression greater in low iron; transcription is negatively regulated by Sfu1p; merged with orf19.4215 in Assembly 20
Iron Regulated	*FRP1*	4503	5634	1.23	2.17	1.76	Protein similar to ferric reductases; transcription is positively regulated by Rim101p; expression greater in low iron; fluconazole-downregulated; ciclopirox olamine induced; colony morphology-related gene regulation by Ssn6p
Mitochondrion/ATP synthesis	*ATP2*	6893	5653	1.21	2.00	1.65	Protein described as a similar to F1 beta subunit of F1F0 ATPase complex; antigenic in human; transcription upregulated in response to ciclopirox olamine; flucytosine induced; caspofungin repressed; macrophage/pseudohypha-induced
Mitochondrion/ATP synthesis	*ATP16*	9026	7678	1.27	2.05	1.62	Predicted ORF in Assemblies 19 and 20
Nitrogen Catabolism	*AAH1*	5895	2251	1.06	3.31	3.11	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; Hog1p-, biofilm-induced
Oxidoreductase	YJR096W	1037	2244	1.50	2.48	1.65	Similar to oxidoreductases and to *S. cerevisiae* Yjr096wp; transcription is negatively regulated by Sfu1p; increased transcription is observed upon benomyl treatment; decreased expression observed in an ssr1 homozygous null mutant
Pentose-Phosphate Shunt	*RKI1*	3042	1701	1.67	2.06	1.24	Predicted ORF in Assemblies 19 and 20
Protein Degradation	*RPN8*	2670	3168	1.14	2.23	1.95	Predicted ORF from Assembly 19; transcription is regulated by Mig1p; regulated by Gcn2p and Gcn4p
Protein Degradation	*RPN13*	4931	1058	1.23	2.28	1.85	Predicted ORF in Assemblies 19 and 20
Protein Degradation	*PR26* (*RPT3*)	6627	5793	1.27	2.07	1.62	Protein with similarity to proteasomal 26S regulatory subunit of *S. cerevisiae, H. sapiens, Methanobacterium thermoautotrophicum* (Archaebacterium)
Protein Degradation	*LAP3*	6751	539	1.24	2.08	1.69	Protein described as an aminopeptidase; transcription is positively regulated by Sfu1p; transcription is repressed in response to alpha pheromone in Spider medium
Protein Folding	*EGD2*	5050	5858	1.64	2.00	1.23	Predicted ORF from Assembly 19; soluble protein in hyphae; macrophage/pseudohypha-induced
Reverse Transcription	*POL93*	1756	6078	1.33	4.04	3.03	Putative gypsy-like reverse transcriptase; transcription is downregulated in response to treatment with ciclopirox olamine; induced upon biofilm formation
Riboflavin Biosynthesis	*RIB3*	2440	5228	1.32	2.40	1.81	3,4-Dihydroxy-2-butanone 4-phosphate synthase; homodimeric enzyme of riboflavin biosynthesis; converts ribulose 5-phosphate to L-3,4-dihydroxy-2-butanone 4-phosphate; transcription regulated on yeast-hypha switch; macrophage interaction
Sphingolipid Biosynthesis	*IPT1*	927	4769	1.13	2.02	1.79	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
Stress Associated Protein	*PHO15* (*PHO13*)	7257	4444	2.52	4.47	1.78	Protein described as 4-nitrophenyl phosphatase; hypha downregulated; induced in core stress response; induced by heavy metal (cadmium) stress via Hog1p
Stress Associated Protein	*SOD4* (*SOD1*)	7493	2062	2.41	4.55	1.89	Copper- and zinc-containing superoxide dismutase, expression is regulated during white-opaque switching; ciclopirox olamine induced; caspofungin repressed; member of a gene family that includes *SOD1*, *SOD4*, *SOD5*, and *SOD6*
Stress Associated Protein	YNL168C	8144	7244	1.08	2.04	1.89	Predicted ORF in Assemblies 19 and 20; induced by nitric oxide in yhb1 mutant

Stress Associated Protein	*TSA1*	8577	7417	1.12	2.54	2.28	Protein of TSA/alkyl hydroperoxide peroxidase C (AhPC) family; similar to thiol-dependent peroxidases, roles in oxidative stress signaling; immunogenic; on hypha surface, nucleus; yeast-form nucleus, cytoplasm; neutrophil, peroxide induced
Stress Associated Protein	*ALO1*	8899	7551	1.03	2.36	2.30	D-Arabinono-1,4-lactone oxidase, involved in biosynthesis of D-erythroascorbic acid, which has a protective role against oxidative damage; required for full virulence in a mouse model of systemic infection
Stress Associated Protein	*TRX1*	8959	7611	1.50	2.06	1.37	Similar to thioredoxin; increased transcription is observed upon benomyl treatment; flucytosine induced; amphotericin B repressed; caspofungin repressed; peroxide-induced; upregulated in the presence of human neutrophils
SUMO	*SMT3*	6563	670	1.53	2.28	1.49	SUMO, small ubiquitin-like protein; Smt3p-conjugated proteins localize to septation site and mother side of bud neck; *C. albicans* septins appear not to be Smt3p-modified, in contrast to *S. cerevisiae* septins; similar to *S. cerevisiae* Smt3p
TCA cycle	*LSC2*	1730	710	1.85	2.81	1.52	Protein described as beta subunit of succinate-CoA ligase; transcription regulated by Mig1p and Tup1p; transcriptionally regulated by iron; expression greater in high iron; merged with orf19.1860 in Assembly 20
TCA cycle	*IDP1*	3902	5211	1.41	2.11	1.50	Protein described as isocitrate dehydrogenase; transcriptionally induced by interaction with macrophage; alkaline upregulated
Transcription	*CRZ2*	1328	2356	1.42	2.09	1.47	Putative transcription factor; zinc finger; similar to *S. cerevisiae* Crz1p; homozygous crz1, not crz2, null mutation suppresses fluconazole resistance of homozygous cka2 null (defective in CK2 kinase); Rim101p-downregulated at pH 8
Transcription	*POB3*	6417	1560	1.49	2.11	1.42	Protein similar to *S. cerevisiae* Pob3p, which is involved in chromatin assembly and disassembly; transposon mutation affects filamentous growth
Transcription	*MBF1*	7189	3294	1.37	2.29	1.68	Predicted ORF from Assembly 19; caspofungin repressed
Transcription	*FCP1*	8889	6742	2.78	3.45	1.24	Predicted ORF in Assemblies 19 and 20
Transporter	YKR105C	1908	4779	1.05	2.02	1.92	Putative transporter; slightly similar to the Sit1p siderophore transporter; Gcn4p-regulated; fungal-specific (no human or murine homolog)
Transporter	*PHO91*	2133	3663	2.17	2.65	1.22	Putative low-affinity phosphate transporter; fungal-specific (no human or murine homolog)
Transporter	*HAK1*	2201	6249	2.67	3.40	1.27	Putative potassium transporter; similar to *Schwanniomyces occidentalis* Hak1p; amphotericin B induced; transcriptionally induced upon phagocytosis by macrophage
Transporter	*TPO4*	2283	473	1.76	2.91	1.66	Putative sperimidine transporter; fungal-specific (no human or murine homolog)
Transporter	*HGT7 (HXT6)*	2376	2023	2.28	3.97	1.74	Putative glucose transporter, major facilitator superfamily; glucose-, fluconazole-, Snf3p-induced, expressed at high glucose; upregulated in biofilm; *C. albicans* glucose transporter family comprises 20 members; 12 TM regions predicted
Transporter	*SMF1*	3571	2270	1.15	2.62	2.27	Protein not essential for viability; similar to *S. cerevisiae* Smf1p, which is a manganese transporter; Gcn4p-regulated; alkaline upregulated; caspofungin repressed
Transporter	*OPT1*	3597	2606	1.52	3.26	2.15	Oligopeptide transporter; transports 3-to-5-residue peptides; alleles are distinct, one has intron; not ABC or PTR type transporter; suppresses *S. cerevisiae* ptr2-2 mutant defects; induced by BSA or peptides; Stp3p, Hog1p regulated
Transporter	*SEO1*	4008	1855	1.33	2.06	1.55	Predicted ORF in Assemblies 19 and 20; Gcn4p-regulated; flucytosine induced; ketoconazole-repressed; oxidative stress-induced via Cap1p
Transporter	*ZRT2*	5335	1585	3.65	5.41	1.48	Protein described as predicted zinc transporter; ciclopirox olamine, fluconazole, or alkaline downregulated; transcriptionally induced by interaction with macrophage; amphotericin B induced
Transporter	*DUR3*	6765	6656	1.62	2.14	1.32	Alkaline downregulated; amphotericin B induced; shows colony morphology-related gene regulation by Ssn6p
Transporter	*GAP6* (*GAP1*)	6768	6659	1.06	3.70	3.50	Putative general amino acid permease; Plc1p-regulated; Gcn4p-regulated; fungal-specific (no human or murine homolog)
Transporter	*PTR2*	7323	6937	1.04	2.63	2.52	Putative oligopeptide transporter; regulated by Stp2p and Stp3p; transcriptionally induced upon phagocytosis by macrophage; downregulated by Rim101p at pH 8
Unknown	Orf6.1150	1150	3378	1.25	2.42	1.93	Predicted ORF in Assemblies 19 and 20; regulated by Tsa1p, Tsa1Bp in minimal media at 37ºC
Unknown	YER067W	1464	1354	4.69	6.62	1.41	Transcriptionally regulated by iron or by yeast-hypha switch; expression greater in high iron, decreased upon yeast-hypha switch; downregulation correlates with clinical development of fluconazole resistance; Ras1p-regulated
Unknown	Orf6.1609	1609	5063	2.22	3.95	1.78	Predicted ORF in Assemblies 19 and 20; ciclopirox olamine induced; regulated by Ssn6p; induced by nitric oxide in yhb1
Unknown	Orf6.1618	1618	4905	1.43	2.12	1.48	Predicted ORF in Assemblies 19 and 20; decreased expression observed in an ssr1 homozygous null mutant
Unknown	Orf6.2443	2443	2283	1.13	2.22	1.97	Predicted ORF in Assemblies 19 and 20; ketoconazole-repressed
Unknown	YNR018W	2819	409	1.36	2.73	2.00	Predicted membrane protein; similar to *S. cerevisiae* Ynr018wp
Unknown	*ECM21*	3331	4887	1.13	2.27	2.02	Protein not essential for viability; similar to *S. cerevisiae* Ecm21p (may have cell wall role); alkaline upregulated by Rim101p; fluconazole induced; caspofungin repressed; downregulated in azole-resistant strain overexpressing MDR1
Unknown	YNL010W	3572	2269	2.05	2.55	1.24	Putative 3-phosphoserine phosphatase; fungal-specific (no human or murine homolog); increased transcription is observed upon benomyl treatment or in an azole-resistant strain that
Unknown	Orf6.6220	6220	6608	1.38	2.04	1.48	Predicted ORF in Assemblies 19 and 20; downregulation correlates with clinical development of fluconazole resistance

Unknown	*SHA3*	6480	3669	1.72	3.01	1.74	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; induced in response to alpha pheromone
Unknown	*HRT2*	7923	4624	2.63	4.49	1.71	Protein described as having a role in Ty3 transposition; decreased expression in hyphae compared to yeast-form cells
Unknown	*RBE1*	8118	7218	2.42	2.86	1.18	Putative cell wall protein; transcription is negatively regulated by Rim101p, Efg1p, Ssn6p; alkaline downregulated; predicted signal sequence, O-glycosylation
Unknown	*PAA1*	8169	7269	1.19	2.06	1.73	Predicted ORF in Assemblies 19 and 20
Unknown	YMR259C	8354	5365	1.03	2.71	2.64	Predicted ORF in Assemblies 19 and 20; decreased transcription is observed upon fluphenazine treatment or in an azole-resistant strain that overexpresses *CDR1* and *CDR2*
Unknown	YBR238C	8619	7459	1.51	2.90	1.92	Predicted ORF in Assemblies 19 and 20; fluconazole-induced; ketoconazole-repressed