

<b>Supplemental Table S4. Gene Expression Responses to 6NDA in <i>C. albicans</i></b>					
<b>ORF</b>	<b>Gene symbol</b>	<b>Sc Ortholog</b>	<b>Oligo_ID*</b>	<b>Description</b>	<b>Fold Change</b>
orf19.1048	IFD6	YPL088W	opCaV0100001456	Aldo-keto reductase family member; similar to aryl alcohol dehydrogenases, <i>S. cerevisiae</i> Ypl088wp; increased protein	23.7
orf19.7504		RTS3	CA06011_01	Predicted ORF in Assemblies 19, 20 and 21; Plc1p-regulated; induced in core caspofungin response	20.2
orf19.320		YOR246C	CA03439_01	Predicted ORF in Assemblies 19, 20 and 21	17.8
orf19.4476		YPL088W	opCaV0100000273	Predicted ORF in Assemblies 19, 20 and 21	16.4
orf19.2724		MOT3	opCaV0100000730	Predicted ORF in Assemblies 19, 20 and 21	11.9
			CA02493_01		9.6
orf19.535	RBR1		opCaV0100001550	Glycosylphosphatidylinositol (GPI)-anchored cell wall protein required for filamentous growth at acidic pH; expression is	9.3
orf19.2344	ASR1	HPF1	opCaV0100000268	Protein described as similar to heat shock proteins; transcription regulated by cAMP, osmotic stress, ciclopirox	8.5
orf19.5113	ADH2	ADH1	CA10232_01	Putative alcohol dehydrogenase; soluble protein in hyphae; fungal-specific (no human or murine homolog); expression is	7.7
orf19.2241	PST1	PST2	opCaV0100001146	Protein described as 1,4-benzoquinone reductase; hyphal-induced expression, regulated by Cyr1p, Ras1p, Efg1p, Nrg1p,	6.8
orf19.23	RTA3	RSB1	opCaV0100000022	Similar to <i>S. cerevisiae</i> Rta1p (role in 7-aminosterol resistance) and Rsb1p (flippase); putative membrane protein;	6.6
orf19.3051		YJR116W	CA05177_01	Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related gene regulation by Ssn6p	6.4
orf19.7585	INO1	INO1	CA10179_01	Inositol-1-phosphate synthase; enzyme of inositol biosynthesis; antigenic in human; repressed by farnesol (in biofilm) or	6.2
			CA10170_01		5.9
orf19.4077	MIT1	SUR1 CSH1	CA01846_01	Protein involved in sphingolipid biosynthesis; required for mannosylation of inositol phosphoceramide (IPC) to form	5.7
orf19.6000	CDR1	PDR5	opCaV0100000146	Multidrug transporter of ATP-binding cassette (ABC) superfamily; transports phospholipids in an in-to-out direction;	5.6
orf19.4477	CSH1	YPL088W	opCaV0100000003	Member of aldo-keto reductase family, similar to aryl alcohol dehydrogenases; role in adhesion to fibronectin, cell surface	5.4
orf19.3249	LAG1	LAG1	CA05577_01	Predicted ORF in Assemblies 19, 20 and 21; amphotericin B repressed	5.3
orf19.2515			CA02303_01	Predicted ORF in Assemblies 19, 20 and 21	5.3
orf19.5431			CA05940_01	Predicted ORF in Assemblies 19, 20 and 21	5.2
orf19.4819			opCaV0100000885	Predicted ORF in Assemblies 19, 20 and 21	5.2
			CA10089_01		5.0
orf19.7166		YGR110W	CA05421_01	Predicted ORF in Assemblies 19, 20 and 21; increased transcription is observed in an azole-resistant strain that	4.9
orf19.4128		YOR059C	CA01434_01	Predicted ORF in Assemblies 19, 20 and 21	4.9
orf19.5759	SNQ2	SNQ2	CA03858_01	Protein similar to <i>S. cerevisiae</i> Ssq2p transporter; member of PDR subfamily of ABC family; transposon mutation affects	4.7
orf19.5295			CA02319_01	Predicted ORF in Assemblies 19, 20 and 21; transcription is induced in response to alpha pheromone in SpiderM medium	4.6
orf19.1287			CA02513_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	4.5
orf19.4818			CA01376_01	Predicted ORF in Assemblies 19, 20 and 21	4.4
orf19.5775.3			opCaV0100001488	ORF Predicted by Annotation Working Group; removed from Assembly 21	4.4

orf19.771	LPG20	YPL088W	opCaV0100000793	Protein of aldo-keto reductase family; nonessential; similar to aryl alcohol dehydrogenases, <i>S. cerevisiae</i> Ypl088wp, A.	4.4
orf19.3672	GAL10	GAL10	CA04058_01	UDP-glucose 4-epimerase, required for galactose utilization; mutant shows cell wall defects and increased filamentation;	4.3
orf19.2726		SFK1	CA01435_01	Predicted ORF in Assemblies 19, 20 and 21; Plc1p-regulated	4.2
orf19.4432		KSP1	CA01548_01	Predicted ORF in Assemblies 19, 20 and 21	4.2
			CA10131_01		4.2
orf19.689	PLB1	PLB3	opCaV0100001535	Phospholipase B; required for wild-type host cell penetration and for wild-type virulence in mouse model of systemic	4.1
orf19.909	STP4	STP3	CA02326_01	Putative transcription factor with zinc finger DNA-binding motif; induced in core caspofungin response; shows colony	4.1
orf19.1301			CA00851_01	Predicted ORF in Assemblies 19, 20 and 21	4.1
			CA05457_01		4.0
orf19.6489	FMP45	FMP45	CA00713_01	Protein induced during the mating process; alkaline downregulated; repressed in response to alpha pheromone in	4.0
orf19.4504		ADH1	opCaV0100000201	Predicted ORF in Assemblies 19, 20 and 21	3.9
orf19.7306		YPR127W	CA05692_01	Protein of aldo-keto reductase family; increased transcription is associated with MDR1 overexpression, benomyl or long-term	3.9
orf19.4155.12			opCaV0100000114	ORF Predicted by Annotation Working Group; removed from Assembly 20	3.8
orf19.5683		YHR140W	CA02723_01	Predicted ORF in Assemblies 19, 20 and 21	3.8
orf19.3250		PRP40	CA05578_01	Predicted ORF in Assemblies 19, 20 and 21	3.8
orf19.181			opCaV0100001090	Predicted ORF from Assembly 19; merged with orf19.4128 in Assembly 20	3.7
orf19.6068	SVF1	SVF1	CA05016_01	Predicted ORF in Assemblies 19, 20 and 21; fluconazole-induced; regulated by Gcn4p; repressed in response to amino	3.7
orf19.2768	AMS1	AMS1	CA04146_01	Putative alpha-mannosidase; transcription is regulated by Nrg1p; induced during cell wall regeneration	3.6
orf19.1945	AUR1	AUR1	opCaV0100000717	Inositolphosphorylceramide (IPC) synthase, catalyzes the key step in the synthesis of sphingolipids; potential target for	3.6
orf19.3544		YML131W	CA02551_01	Predicted ORF in Assemblies 19, 20 and 21	3.6
orf19.6229	CAT1	CTA1	CA10133_01	Catalase; role in resistance to oxidative stress, including neutrophils, peroxide; role in murine systemic virulence;	3.6
orf19.7441		BRR6	CA05879_01	Predicted ORF in Assemblies 19, 20 and 21	3.5
orf19.1783	YOR1	YOR1	CA01441_01	Protein similar to <i>S. cerevisiae</i> Yor1p, which is a plasma membrane transporter of the ATP-binding cassette (ABC)	3.5
orf19.251		HSP31	CA01159_01	Member of ThiJ/Pfpl protein family; antigenic (Cand a 3 allergen); binds human immunoglobulin E; 2 N-glycosylation	3.4
orf19.1964			CA03038_01	Decreased transcription is observed upon fluphenazine treatment; increased transcription is observed upon benomyl	3.4
orf19.1069	RPN4	RPN4	CA02955_01	DNA binding protein with Cys2-His2 zinc-finger; putative regulator of proteasome genes; DNA recognition sequence	3.4
orf19.2175		AIF1	CA03777_01	Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide	3.4
orf19.3369	MOH1	MOH1	opCaV0100000434	Protein similar to <i>S. cerevisiae</i> Moh1p; transcription is induced in response to alpha pheromone in SpiderM medium	3.3
orf19.7350		YNL208W	CA05803_01	Predicted ORF in Assemblies 19, 20 and 21; soluble protein in hyphae; fluconazole-induced; greater mRNA abundance	3.3
orf19.2458		SIP5	CA00493_01	Putative transcription factor with zinc finger DNA-binding motif	3.3
orf19.6169.2			opCaV0100001305	ORF Predicted by Annotation Working Group; fluconazole-downregulated; merged with orf19.2496 in Assembly 20	3.3

			CA05804_01		3.2
orf19.7330		PET18	CA05713_01	Predicted ORF in Assemblies 19, 20 and 21	3.2
orf19.1721	NCE103	NCE103	CA02907_01	Carbonic anhydrase involved in the conversion of carbon dioxide to bicarbonate; essential for pathogenesis in host	3.2
orf19.4658			CA02817_01	Protein not essential for viability	3.2
orf19.4082	DDR48	DDR48	CA04361_01	Immunogenic stress-associated protein; regulated by filamentous growth pathways; induced by benomyl,	3.2
orf19.2062	SOD4		opCaV0100001556	Copper- and zinc-containing superoxide dismutase, expression is regulated during white-opaque switching; ciclopirox olamine	3.2
orf19.6318		YJR085C	CA03348_01	Predicted ORF in Assemblies 19, 20 and 21	3.2
orf19.3340	SOD2	SOD2	CA10051_01	Mitochondrial manganese-containing superoxide dismutase; role in protection against oxidative stress; active as	3.2
orf19.4420		RRN6	CA02502_01	Predicted ORF in Assemblies 19, 20 and 21	3.2
			CA10099_01		3.2
orf19.7514	PCK1	PCK1	opCaV0100001484	Phosphoenolpyruvate carboxykinase; role in gluconeogenesis; regulated by hyphal switch, carbon source; repressed on	3.2
orf19.6957.3			opCaV0100000602	ORF Predicted by Annotation Working Group; removed from Assembly 20	3.2
orf19.4690		SMF1	opCaV0100000172	Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide in yhb1 mutant	3.1
orf19.4706		PIN2	opCaV0100000133	Predicted ORF in Assemblies 19, 20 and 21; greater mRNA abundance observed in a <i>cyr1</i> or <i>ras1</i> homozygous null mutant	3.1
orf19.55		ZH2 ZH1	opCaV0100001342	Predicted ORF in Assemblies 19, 20 and 21	3.1
orf19.6627			CA04095_01	Predicted ORF in Assemblies 19, 20 and 21; possibly transcriptionally regulated upon hyphal formation	3.0
orf19.3854		SAT4	CA03163_01	Protein similar to <i>S. cerevisiae</i> Sat4p; amphotericin B induced	3.0
orf19.4970		SRP40	CA01104_01	Predicted ORF in Assemblies 19, 20 and 21	3.0
orf19.3682	CWH8	CAX4	CA01426_01	Putative dolichyl pyrophosphate (Dol-P-P) phosphatase; ketoconazole-induced; expression is increased in a fluconazole-	3.0
orf19.4899	GCA1	ROT2	CA00339_01	Predicted extracellular or plasma membrane-associated glucoamylase; possible adhesin; gene is transcribed during rat	3.0
orf19.3364			opCaV0100000167	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	3.0
orf19.1369			CA03194_01	Predicted ORF in Assemblies 19, 20 and 21	3.0
			CA03037_01		3.0
orf19.1784			CA01442_01	Protein similar to <i>S. cerevisiae</i> Yor1p, a plasma membrane transporter of the ATP-binding cassette (ABC) family involved	2.9
orf19.6007		ELO1	CA06248_01	Predicted ORF in Assemblies 19, 20 and 21	2.9
orf19.6660		YHR131C	CA04291_01	Predicted ORF in Assemblies 19, 20 and 21	2.9
orf19.1979	GIT1	GIT1	opCaV0100000834	Putative glycerophosphoinositol permease; fungal-specific (no human or murine homolog); alkaline downregulated;	2.9
orf19.6601.1	YKE2	YKE2	opCaV0100001210	Possible cytoskeletal modulator; transcription induced upon yeast-to-hyphal switch; regulated by Nrg1p, Tup1p	2.9
orf19.1224	FRP3	ATO2	opCaV0100001195	Upregulated in the presence of human neutrophils; fluconazole-downregulated; repressed by nitric oxide	2.9
orf19.5194.1		YIR035C	opCaV0100000608	ORF Predicted by Annotation Working Group	2.8
orf19.3050	AGE1	AGE1	CA05176_01	Protein described as a GTPase activator; transcriptionally regulated by iron; expression greater in low iron	2.8

orf19.4780		YJR124C	CA00872_01	Predicted ORF in Assemblies 19, 20 and 21	2.8
orf19.7175	HLJ1	HLJ1	CA05428_01	Protein repressed during the mating process	2.8
orf19.4963		YDR161W	CA01613_01	Predicted ORF in Assemblies 19, 20 and 21	2.8
orf19.4135	PRC2	PRC1	CA01482_01	Protein described as a carboxypeptidase; upregulated in the presence of human neutrophils	2.8
orf19.6877			CA04613_01	Predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in response to treatment with caspofungin,	2.8
orf19.334			opCaV0100000480	Predicted ORF in Assemblies 19, 20 and 21	2.8
orf19.3607		ECM18	CA01413_01	Predicted ORF in Assemblies 19, 20 and 21	2.7
orf19.192			CA01683_01	Predicted ORF in Assemblies 19, 20 and 21	2.7
orf19.2802	PDR10		opCaV0100000958	Upregulated by Rim101p at pH 8; merged with orf19.918 in Assembly 20	2.7
orf19.2341		HNT1	CA02496_01	Predicted ORF in Assemblies 19, 20 and 21	2.7
orf19.4659		PRP21	CA02818_01	Predicted ORF in Assemblies 19, 20 and 21	2.7
orf19.4907		YCR061W	CA02195_01	Predicted ORF in Assemblies 19, 20 and 21; increased transcription is observed upon fluphenazine treatment; possibly	2.7
orf19.6769		YHL029C	CA06098_01	Predicted ORF in Assemblies 19, 20 and 21	2.7
orf19.4779		YKR105C	CA01113_01	Putative transporter; slightly similar to the Sit1p siderophore transporter; Gcn4p-regulated; fungal-specific (no human or	2.7
orf19.94			CA02162_01	Predicted ORF in Assemblies 19, 20 and 21	2.7
orf19.93		MIC17	opCaV0100000937	Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related gene regulation by Ssn6p	2.6
orf19.6869		AST2	CA04607_01	Predicted ORF in Assemblies 19, 20 and 21	2.6
			CA11012_01		2.6
orf19.7053	GAC1	GAC1	CA05795_01	Protein described as similar to regulatory subunit of serine/threonine phosphoprotein phosphatase 1; fluconazole-	2.5
			CA06100_01		2.5
			CA00697_01		2.5
orf19.4279	MNN1	MNN1	CA01775_01	Putative alpha-1,3-mannosyltransferase, a component of mannosyltransferase complex; transcription is negatively	2.5
orf19.5576		YDR531W	CA01022_01	Protein similar to <i>S. cerevisiae</i> Ydr531wp; transposon mutation affects filamentous growth; downregulated in core stress	2.5
orf19.4056	GAT2	GAT2	CA01405_01	Putative DNA-binding transcription factor; similar to <i>S. cerevisiae</i> Gat2p; transposon mutation affects filamentous	2.5
orf19.6833.2			opCaV0100001200	ORF Predicted by Annotation Working Group	2.5
orf19.753		MNT4 MNT2	CA02118_01	Predicted ORF in Assemblies 19, 20 and 21	2.5
orf19.5192			CA02043_01	Predicted ORF from Assembly 19; removed from Assembly 20	2.4
orf19.851		MNN4	CA00938_01	Protein of unknown function; transcription is negatively regulated by Rim101p	2.4
orf19.35		SKY1	CA01070_01	Predicted ORF in Assemblies 19, 20 and 21	2.4
orf19.941	SEC14	SEC14	CA10295_01	Essential protein; functional homolog of <i>S. cerevisiae</i> Sec14p, which is a Golgi phosphatidylinositol/phosphatidylcholine	2.4
orf19.2244		YJR096W	CA00695_01	Similar to oxidoreductases and to <i>S. cerevisiae</i> Yjr096wp; transcription is negatively regulated by Sfu1p; increased	2.4

orf19.1149	MRF1	ETR1	CA01586_01	Protein similar to mitochondrial respiratory proteins; increased transcription is observed upon benomyl treatment; induced by	2.4
orf19.7229		IML2	CA05473_01	Predicted ORF in Assemblies 19, 20 and 21	2.4
orf19.2608	ADH5	ADH5	CA02540_01	Putative alcohol dehydrogenase; soluble protein in hyphae; expression is regulated upon white-opaque switching;	2.4
orf19.2432	HAC1	HAC1	CA00857_01	Putative transcription factor with bZIP DNA-binding motif; induced during the mating process; caspofungin induced	2.4
orf19.4263			CA00693_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	2.4
orf19.1225			CA00825_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	2.4
orf19.3994		OST3	CA04829_01	Predicted ORF in Assemblies 19, 20 and 21	2.3
orf19.2903			CA03797_01	Predicted ORF in Assemblies 19, 20 and 21; hyphal-induced expression, regulated by Cyr1p, Ras1p, Efg1p, Nrg1p, Tup1p	2.3
orf19.1505			CA02065_01	Predicted ORF in Assemblies 19, 20 and 21	2.3
orf19.6043		DLD1	CA04991_01	Predicted ORF in Assemblies 19, 20 and 21	2.3
orf19.4943	PSA2	PSA1	CA03747_01	Predicted ORF in Assemblies 19, 20 and 21; macrophage-downregulated gene	2.3
orf19.3171	ACH1	ACH1	CA00752_01	Soluble protein in hyphae; similar to <i>S. cerevisiae</i> Ach1p, which is acetyl-coA hydrolase required for acetate utilization;	2.3
orf19.1671	UTR2	UTR2	CA00977_01	Putative cell-surface glycosidase, role in adhesion; required for hyphal growth on Spider (not serum) medium; chitin-binding,	2.3
orf19.3649		FES1	CA00596_01	Predicted ORF in Assemblies 19, 20 and 21	2.3
orf19.4262		JSN1	CA00692_01	Predicted ORF in Assemblies 19, 20 and 21	2.3
orf19.7030	SSR1	CCW14	CA05328_01	Beta-glucan associated cell-wall protein with role in cell wall structure; S/T rich protein, GPI anchor; similar mRNA	2.2
orf19.2686		CPS1	CA02878_01	Predicted ORF in Assemblies 19, 20 and 21	2.2
orf19.2232	RPL11	RPL11A  RPL11B	CA01100_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.2
orf19.3465	RPL10A	RPL1A  RPL1B	opCaV0100000672	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.2
orf19.5904	RPL19A	RPL19A  RPL19B	CA06338_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.2
orf19.4447	YMC1	YMC1	CA04715_01	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced	-2.2
orf19.5838		SER2	CA03814_01	Predicted ORF in Assemblies 19, 20 and 21	-2.2
orf19.4013		YHR045W	CA04846_01	Predicted ORF in Assemblies 19, 20 and 21	-2.2
orf19.1700	RPS7A	RPS7A	CA01734_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.2
orf19.4193.1	RPS13	RPS13	opCaV0100000796	Putative ribosomal protein; ORF predicted by Annotation Working Group	-2.2
orf19.3341		YDR341C	CA02831_01	Putative tRNA-Arg synthetase; essential; <i>S. cerevisiae</i> ortholog is essential; genes encoding ribosomal subunits, translation	-2.2
orf19.687.1	RPL25	RPL25	opCaV0100001569	ORF Predicted by Annotation Working Group; shows colony morphology-related gene regulation by Ssn6p	-2.2
orf19.3942.1	RPL43A	RPL43A  RPL43B	opCaV0100000001	Downregulated in the presence of human whole blood or polymorphonuclear (PMN) cells; shows colony morphology-	-2.2
orf19.5225.2	RPL27A	RPL27A	opCaV0100001307	Predicted ribosomal protein	-2.2
orf19.5982	RPL18	RPL18A  RPL18B	CA06267_01	Predicted ribosomal protein; Plc1p-regulated; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA	-2.2
orf19.4632	RPL20B	RPL20B  RPL20A	CA01082_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.2

orf19.6253	RPS23A	RPS23B  RPS23A	opCaV0100001636	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.3
orf19.2864.1	RPL28	RPL28	opCaV0100001003	Putative ribosomal protein; Plc1p-regulated; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA	-2.3
orf19.6085	RPL16A	RPL16A	CA03900_01	Protein similar to <i>S. cerevisiae</i> ribosomal protein Rpl16Ap; transposon mutation affects filamentous growth; genes	-2.3
orf19.5809		BNA3	CA04180_01	Predicted ORF in Assemblies 19, 20 and 21; Gcn4p-regulated	-2.3
orf19.667.1	RPL37B	RPL37B	opCaV0100000159	Predicted ribosomal protein	-2.3
orf19.2994	RPL13	RPL13A	CA10240_01	Protein described as ribosomal subunit; antigenic during murine systemic infection; genes encoding cytoplasmic	-2.3
orf19.6415.1		RPS29A	opCaV0100001563	ORF Predicted by Annotation Working Group; intron in 5'-UTR	-2.3
orf19.2560	CDC60	CDC60	CA02223_01	Cytosolic leucyl tRNA synthetase; has conserved amino acid and ATP binding class I signature, tRNA binding, and	-2.3
orf19.3789	RPL24A	RPL24B	opCaV0100001310	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.3
orf19.3222		YGR125W	CA01043_01	Predicted ORF in Assemblies 19, 20 and 21; fungal-specific (no human or murine homolog)	-2.3
orf19.5466	RPS24	RPS24B  RPS24A	CA05972_01	Predicted ribosomal protein; hyphal downregulated; genes encoding cytoplasmic ribosomal subunits, translation factors,	-2.3
orf19.7217	RPL4B	RPL4B	CA05463_01	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.3
orf19.4616	POL30	POL30	CA05292_01	Protein described as proliferating cell nuclear antigen (PCNA); RNA abundance regulated by tyrosol and cell density;	-2.3
orf19.2329.1	RPS17B	RPS17B	opCaV0100000177	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.3
orf19.1601	RPL3	RPL3	CA00983_01	Putative ribosomal protein; similar to <i>S. cerevisiae</i> Rpl3p; gene induced by ciclopirox olamine treatment; genes encoding	-2.3
orf19.6689	ARG4	ARG4	CA10030_01	Argininosuccinate lyase, catalyzes the final step in the arginine biosynthesis pathway; alkaline downregulated	-2.3
orf19.5408		HRK1	CA05917_01	Predicted ORF in Assemblies 19, 20 and 21	-2.3
orf19.6286.2	RPS27	RPS27B	opCaV0100001419	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.3
orf19.3690.2		RPL26B	opCaV0100000387	ORF Predicted by Annotation Working Group	-2.3
orf19.6265	RPS22A	RPS22A	CA03726_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.3
orf19.7278			opCaV0100000011	Similar to a region of the Tca2 (pCal) retrotransposon, which is present in strain hOG1042 as 50 to 100 copies of a linear	-2.3
orf19.2309.2		RPL2A  RPL2B	opCaV0100000147	ORF Predicted by Annotation Working Group	-2.3
orf19.4623.3	NHP6A	NHP6B	CA00170_01	Protein described as nonhistone chromatin component; RNA abundance regulated by tyrosol and cell density; amphotericin	-2.4
			CA10053_01		-2.4
orf19.7297		YHR112C	CA05686_01	Predicted ORF in Assemblies 19, 20 and 21; Hog1p-induced; Gcn4p-regulated	-2.4
orf19.3572.3		RPL31B  RPL31A	opCaV0100000884	ORF Predicted by Annotation Working Group	-2.4
orf19.3334	RPS21	RPS2	CA01931_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.4
orf19.3415.1	RPL32	RPL32	opCaV0100001058	Predicted ribosomal protein	-2.4
			CA10037_01		-2.4
orf19.18	IMH3	IMD4	CA10062_01	Inosine monophosphate (IMP) dehydrogenase; enzyme of GMP biosynthesis; target of mycophenolic acid and mizoribine	-2.4
orf19.6265.1	RPS14B	RPS14B  RPS14A	opCaV0100000975	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.4

orf19.3752	RAD51	RAD51	CA02498_01	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced	-2.4
orf19.5094	BUL1	BSC5	CA03918_01	Protein not essential for viability; macrophage/pseudohyphal-induced; similar to <i>S. cerevisiae</i> Bul1p, which may be involved	-2.4
orf19.3354		RPS4A  RPS4B	CA10098_01	Predicted ORF in Assemblies 19, 20 and 21	-2.4
orf19.6975	YST1	RPS0A	CA00283_01	Ribosome-associated protein; complements viability of <i>S. cerevisiae</i> yst1 yst2 mutant; similar to laminin-binding proteins,	-2.4
orf19.5719			CA03576_01	Predicted ORF from Assembly 19; removed from Assembly 20	-2.4
orf19.4650	ILV6	ILV6	CA01936_01	Putative regulatory subunit of acetolacetate synthase ; fungal-specific (no human or murine homolog); alkaline upregulated;	-2.4
orf19.1756	GPD1	GPD1	CA02416_01	Protein similar to <i>S. cerevisiae</i> glycerol-3-phosphate dehydrogenase (enzyme of glycerol biosynthesis); biofilm-	-2.4
orf19.5996.1	RPS19A	RPS19A	opCaV0100000795	Putative ribosomal protein; ORF Predicted by Annotation Working Group	-2.4
orf19.4149.1		RPS11A  RPS11B	opCaV0100001496	ORF Predicted by Annotation Working Group	-2.4
orf19.3066	ENG1	DSE4	opCaV0100000640	Endo-1,3-beta-glucanase required for cell separation after division, orthologous to <i>S. cerevisiae</i> Dse4p; caspofungin	-2.5
orf19.6220.4		RPL34B	opCaV0100001534	ORF Predicted by Annotation Working Group	-2.5
orf19.2179.2	RPS10	RPS10A	opCaV0100001524	Predicted ribosomal protein; downregulated in the presence of human whole blood or polymorphonuclear (PMN) cells	-2.5
orf19.7015	RPP0	RPP0	CA05314_01	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.5
orf19.840	RPL21A	RPL21A	opCaV0100000493	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.5
orf19.5635	PGA7	TIR1	CA02680_01	Protein described as a putative precursor of a hyphal surface antigen; putative GPI-anchor; induced by ciclopirox olamine,	-2.5
orf19.7238	NPL3	NPL3	CA05480_01	Putative RNA-binding protein, ortholog of <i>S. cerevisiae</i> Npl3p; nuclear export is facilitated by Hmt1p	-2.5
orf19.5927	RPS15	RPS15	CA06318_01	Putative ribosomal protein; macrophage/pseudohyphal-induced after 16 h; genes encoding cytoplasmic ribosomal subunits,	-2.5
orf19.6541	RPL5	RPL5	opCaV0100000431	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.5
orf19.1701		RK11	CA01735_01	Predicted ORF in Assemblies 19, 20 and 21	-2.5
orf19.3475		DEF1	opCaV0100001199	Described as a Gag-related protein; hyphal induced; downregulation correlates with clinical development of	-2.5
orf19.85	GPX2	HYR1	opCaV0100000692	Similar to glutathione peroxidase; expression greater in high iron; alkaline upregulated by Rim101p; transcriptionally induced	-2.5
orf19.3846	LYS4	LYS4	CA04948_01	Protein described as homoacnitase; regulated by Gcn4p, Gcn2p; induced in response to amino acid starvation (3-	-2.5
orf19.7502			opCaV0100000636	Predicted ORF in Assemblies 19, 20 and 21; greater mRNA abundance observed in a <i>cyr1</i> homozygous null mutant than in	-2.5
orf19.1033	STR2	STR2	CA01851_01	Protein not essential for viability; similar to <i>S. cerevisiae</i> Str2p, which is cystathionine gamma-synthase involved in sulfur	-2.5
orf19.5673	OPT7	OPT2	CA04411_01	Putative oligopeptide transporter; possibly transports GSH and related compounds; induced upon biofilm formation; Hog1p-	-2.5
			CA10060_01		-2.5
orf19.4040	ILV3	ILV3	CA04870_01	Putative dihydroxyacid dehydratase; fungal-specific (no human or murine homolog); upregulated in biofilm; <i>S. cerevisiae</i>	-2.5
orf19.712	KIP1	CIN8	CA01501_01	Non-essential kinesin from the bipolar (Kinesis-5) family; involved in formation of the mitotic spindle	-2.5
orf19.1358	GCN4	GCN4	CA00423_01	Transcriptional activator of general amino acid control response; required for Efg1p-dependent pseudohyphal filament	-2.6
orf19.7048.1	RPS28B	RPS28B	opCaV0100000453	Putative ribosomal protein S28B; ORF Predicted by Annotation Working Group	-2.6
orf19.4931.1		RPL14A  RPL14B	opCaV0100001471	ORF Predicted by Annotation Working Group	-2.6

orf19.1115	GUK1	GUK1	CA02023_01	Putative guanylate kinase; identified in extracts from biofilm and planktonic cells	-2.6
orf19.5528	MOB1	MOB1	CA02658_01	Predicted ORF in Assemblies 19, 20 and 21	-2.6
orf19.4060	ARO4	ARO4	opCaV0100001326	3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase; enzyme of aromatic amino acid biosynthesis; GCN-regulated;	-2.6
orf19.5062			opCaV0100000963	Predicted ORF from Assembly 19; merged with orf19.5061 in Assembly 20	-2.6
orf19.6779	PRO2	PRO2	CA06089_01	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p	-2.6
orf19.5245		BUL2	CA05095_01	Predicted ORF in Assemblies 19, 20 and 21	-2.6
orf19.7634	MCD1	MCD1	CA06204_01	Protein similar to <i>S. cerevisiae</i> Mcd1p; transcription is repressed in response to alpha pheromone in SpiderM medium	-2.6
orf19.6124	ACE2	ACE2	CA03076_01	Putative transcription factor involved in regulation of morphogenesis; required for wild-type cell separation,	-2.6
orf19.3616	ERG9	ERG9	CA00372_01	Putative farnesyl-diphosphate farnesyl transferase (squalene synthase) involved in the sterol biosynthesis pathway; likely to	-2.6
orf19.4945	MSH6	MSH6	CA03745_01	Protein similar to <i>S. cerevisiae</i> Msh6p, which is involved in mismatch repair; repressed under Cdc5p depletion	-2.6
orf19.1613	ILV2	ILV2	CA00834_01	Protein described as acetolactate synthase; regulated by Gcn4p; induced in response to amino acid starvation (3-	-2.6
orf19.6312	RPS3	RPS3	CA03342_01	Putative ribosomal protein; Hog1p-induced; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA	-2.6
orf19.493	RPL15A	RPL15B  RPL15A	CA04555_01	Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.6
orf19.4617		MAK3	CA05293_01	Predicted ORF in Assemblies 19, 20 and 21	-2.6
orf19.6645	HMO1	HMO1	CA04111_01	High mobility group-like protein; activates pseudohyphal growth when expressed in <i>S. cerevisiae</i> ; decreased expression in	-2.6
orf19.6755		DLD1	CA06110_01	Predicted ORF in Assemblies 19, 20 and 21	-2.6
orf19.4675			CA03312_01	Predicted ORF in Assemblies 19, 20 and 21	-2.7
orf19.5006		GCV3	CA05367_01	Predicted ORF in Assemblies 19, 20 and 21	-2.7
orf19.2618	MET2	MET2	CA00985_01	Putative homoserine acetyltransferase; Gcn4p-regulated; macrophage/pseudohyphal-repressed; not greatly induced by	-2.7
orf19.6644			CA04110_01	Predicted ORF in Assemblies 19, 20 and 21	-2.7
orf19.3641			CA01202_01	Expression is regulated upon white-opaque switching; merged with orf19.84 in Assembly 20	-2.7
orf19.4630	CPA1	CPA1	CA01189_01	Alkaline downregulated	-2.7
orf19.6002	RPL8B	RPL8B	opCaV0100000272	Predicted ribosomal protein; transcription is regulated upon yeast-hyphal switch; genes encoding cytoplasmic ribosomal	-2.7
orf19.5750	SHM2	SHM2	CA10044_01	Cytoplasmic serine hydroxymethyltransferase; complements the glycine auxotrophy of an <i>S. cerevisiae</i> shm1 null shm2 null	-2.7
orf19.7095		YOR390W	CA05757_01	Predicted ORF in Assemblies 19, 20 and 21	-2.7
orf19.6936	RAD53	RAD53	CA04767_01	Protein involved in regulation of DNA-damage-induced filamentous growth; putative component of cell cycle	-2.7
orf19.6882.1		RPL33A	opCaV0100000854	ORF Predicted by Annotation Working Group	-2.7
orf19.1116			CA02024_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	-2.7
orf19.2512			CA02300_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	-2.7
orf19.5928	RPP2B	RPP2B	CA06317_01	Conserved acidic ribosomal protein, likely to be involved in regulation of translation elongation; interacts with Rpp1Ap; one	-2.8
orf19.2525	LYS12	LYS12	CA01954_01	Protein described as mitochondrial homoisocitrate dehydrogenase	-2.8



orf19.3146			CA00987_01	Predicted ORF from Assembly 19; merged with orf19.2227 in Assembly 20	-2.8
orf19.4704	ARO1	ARO1	CA02054_01	Putative pentafunctional arom enzyme; fungal-specific (no human or murine homolog); Gcn2p-, Gcn4p-regulated	-2.8
orf19.1679			CA01167_01	Predicted ORF in Assemblies 19, 20 and 21	-2.8
orf19.6403.1	RPP2A	RPP2B	opCaV0100000556	Conserved acidic ribosomal protein, likely to be involved in regulation of translation elongation; interacts with Rpp1Bp; one	-2.8
orf19.4192	CDC14	CDC14	CA01560_01	Protein involved in exit from mitosis and morphogenesis; ortholog of <i>S. cerevisiae</i> Cdc14p, which is a dual-specificity	-2.8
orf19.2360	URA2	URA2	CA00584_01	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; macrophage/pseudohyphal-induced; intron in 5'-UTR	-2.8
orf19.2374			opCaV0100001509	Predicted ORF from Assembly 19; removed from Assembly 20	-2.8
orf19.2607		PMU1	CA02541_01	Predicted ORF in Assemblies 19, 20 and 21	-2.8
orf19.3969		SFL1	CA01563_01	Predicted ORF in Assemblies 19, 20 and 21	-2.9
orf19.5591	ADO1	ADO1	opCaV0100001425	Predicted ORF in Assemblies 19, 20 and 21; ketoconazole-induced	-2.9
orf19.6702	DED81	DED81	CA04325_01	Putative tRNA-Asn synthetase; genes encoding ribosomal subunits, translation factors, and tRNA synthetases are	-2.9
orf19.1799		GAP1	opCaV0100001313	Putative general amino acid permease; fungal-specific (no human or murine homolog)	-2.9
orf19.236	RPL9B	RPL9B	CA00673_01	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases	-2.9
orf19.2372			CA10283_01	Predicted ORF from Assembly 19; orf19.2371, orf19.2372, and orf19.2375 are similar to the Tca2 (pCal) retrotransposon,	-2.9
orf19.3591	APE3	APE3	CA01187_01	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p	-2.9
orf19.926		EXO1	CA01626_01	Predicted ORF in Assemblies 19, 20 and 21	-2.9
orf19.6632	ACO2	ACO2	CA04099_01	Protein described as aconitate hydratase 2; regulated by Gcn4p; repressed in response to amino acid starvation (3-	-2.9
orf19.2179	SIT1	ARN1	CA03773_01	Transporter of ferrichrome siderophores, but not ferrioxamine B; required for wild-type invasion of human epithelial cells in	-2.9
orf19.2992	RPP1A	RPP1A	CA10241_01	Conserved acidic ribosomal protein, likely to be involved in regulation of translation elongation; interacts with Rpp2Bp; one	-2.9
orf19.2371			opCaV0100001532	Predicted ORF from Assembly 19; orf19.2371, orf19.2372, and orf19.2375 are similar to the Tca2 (pCal) retrotransposon,	-2.9
orf19.3893	SCW11	SCW11	CA01345_01	Cell wall protein; transcription is decreased in mutant lacking ACE2; downregulated in core caspofungin response;	-2.9
orf19.944	IFG3		CA05524_01	Putative D-amino acid oxidase	-2.9
orf19.3957		FOL2	CA00734_01	Predicted ORF in Assemblies 19, 20 and 21	-3.0
orf19.4827	ADE12	ADE12	CA04817_01	Predicted enzyme of adenine biosynthesis; upregulated in biofilm; decreased expression in hyphae compared to yeast-	-3.0
orf19.668		TOS4	CA04127_01	Predicted ORF in Assemblies 19, 20 and 21	-3.0
orf19.780	DUR1,2	DUR1,2	CA02433_01	Transcription is regulated by Nrg1p	-3.0
orf19.5877			CA06359_01	Predicted ORF in Assemblies 19, 20 and 21; caspofungin repressed	-3.0
orf19.2196		CUE3	CA02581_01	Predicted ORF in Assemblies 19, 20 and 21	-3.0
orf19.5372			opCaV0100000291	Predicted ORF from Assembly 19; orf19.5372 and orf19.5373 are similar to the Tca2 (pCal) retrotransposon, which is present	-3.0
orf19.7244		YNL168C	CA05486_01	Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide in yhb1 mutant	-3.0
orf19.7534		MIS1	CA06036_01	Predicted ORF in Assemblies 19, 20 and 21	-3.0

orf19.6086	LEU4	LEU4	CA03899_01	Putative 2-isopropylmalalate synthase; regulated by Nrg1p, Mig1p, Tup1p, Gcn4p; upregulated in the presence of human	-3.0
			CA04954_01		-3.0
orf19.5178	ERG5	ERG5	CA04447_01	Putative C-22 sterol desaturase; fungal C-22 sterol desaturases are cytochrome P450 enzymes of ergosterol	-3.0
orf19.1235	HOM3	HOM3	opCaV0100000213	Putative L-aspartate 4-P-transferase; fungal-specific (no human or murine homolog); regulated by Gcn2p and Gcn4p	-3.0
orf19.3115			CA04427_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	-3.0
orf19.4012	PCL5		CA04845_01	Protein similar to <i>S. cerevisiae</i> Pcl5p and other cyclins for Pho85p kinase; Gcn4p-induced; suppresses toxicity of C.	-3.0
orf19.1743	ACS1	ACS1	opCaV0100000858	Putative acetyl-CoA synthetase, similar to <i>S. cerevisiae</i> Acs2p; upregulated in the presence of human neutrophils; fluconazole-	-3.0
orf19.6899			CA04629_01	Predicted ORF in Assemblies 19, 20 and 21	-3.0
orf19.1857		SPT10	CA03426_01	Protein not essential for viability	-3.0
orf19.1375	LEU42	LEU4	CA02461_01	Putative alpha-isopropylmalate synthase; fungal-specific (no human or murine homolog); upregulated in the presence of	-3.0
orf19.2375			opCaV0100000169	Predicted ORF from Assembly 19; orf19.2371, orf19.2372, and orf19.2375 are similar to the Tca2 (pCal) retrotransposon,	-3.1
orf19.5784			CA02918_01	Predicted ORF in Assemblies 19, 20 and 21	-3.1
orf19.2759			opCaV0100000280	Putative GPI-anchored protein of unknown function; repressed during cell wall regeneration; merged with orf19.2758 in	-3.1
orf19.1272		YGR111W	CA01255_01	Predicted ORF in Assemblies 19, 20 and 21	-3.1
orf19.4513			opCaV0100000427	Protein not essential for viability; possibly spurious ORF (Annotation Working Group prediction)	-3.1
orf19.3489	ARO22		opCaV0100001129	Putative chorismate synthase; fungal-specific (no human or murine homolog); merged with orf19.1986 in Assembly 20	-3.1
			CA01474_01		-3.1
orf19.1587	HGT20	YBR241C	CA03214_01	Putative glucose transporter of the major facilitator superfamily; the <i>C. albicans</i> glucose transporter family comprises 20	-3.1
orf19.5188	CHS1	CHS2	CA00376_01	Chitin synthase; essential; required for primary septum synthesis in yeast-form cells and hyphae; one of multiple chitin	-3.1
orf19.4304	GAP1	GAP1	CA02765_01	General amino acid permease; antigenic in human; 10-12 transmembrane regions; regulated by nitrogen source; alkaline,	-3.1
orf19.3142			CA01085_01	Predicted ORF in Assemblies 19, 20 and 21	-3.1
orf19.557			CA01234_01	Predicted ORF in Assemblies 19, 20 and 21	-3.1
orf19.6451			opCaV0100001319	Predicted ORF from Assembly 19; similar to a region of the Tca2 (pCal) retrotransposon, which is present in strain	-3.2
orf19.5243	TRP3	TRP3	CA05097_01	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p	-3.2
orf19.5061	ADE5,7	ADE5,7	opCaV0100000430	Enzyme of adenine biosynthesis; interacts with Vps34p; required for hyphal growth and virulence; flucytosine induced;	-3.2
orf19.1832	FCY23	TPN1	CA02526_01	Putative transporter; Gcn4p-regulated; more similar to <i>S. cerevisiae</i> Tpn1p, which is a vitamin B6 transporter, than to	-3.2
			CA10144_01		-3.2
orf19.3612	PST2	PST2	CA01891_01	Putative NADH:quinone oxidoreductase; similar to 1,4-benzoquinone reductase; immunogenic in mouse; increased	-3.2
orf19.3895	CHT2	CTS1	CA10176_01	Chitinase; putative N-terminal catalytic domain, GPI anchor, O-mannosylated region, signal peptide; 3 N-glycosylation motifs;	-3.2
orf19.2551	MET6	MET6	CA01016_01	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase (cobalamin-independent methionine	-3.3
			CA00152_01		-3.4

orf19.2758	PGA38	AGA1	opCaV0100000511	Putative GPI-anchored protein of unknown function; repressed during cell wall regeneration	-3.4
orf19.7313	SSU1	SSU1	CA05698_01	Protein similar to <i>S. cerevisiae</i> Ssu1p sulfite transport protein; transposon mutation affects filamentous growth; regulated by	-3.4
orf19.3722		FAP1	CA01078_01	Predicted ORF in Assemblies 19, 20 and 21	-3.4
orf19.2583.2		OPT2	opCaV0100000904	ORF Predicted by Annotation Working Group	-3.4
orf19.5263	SER33	SER3	CA05077_01	Predicted enzyme of amino acid biosynthesis; Gcn4p-regulated; upregulated in biofilm; <i>S. cerevisiae</i> ortholog is	-3.4
orf19.4631	ERG251	ERG25	opCaV0100000418	Predicted ORF in Assemblies 19, 20 and 21; ketoconazole-induced; amphoterin B, caspofungin repressed	-3.4
orf19.5779	RNR1	RNR1	CA02913_01	Protein similar <i>S. cerevisiae</i> Rnr1p, large subunit of ribonucleotide reductase; expression greater in low iron;	-3.4
orf19.2283	DQD1		opCaV0100000775	Predicted ORF in Assemblies 19, 20 and 21; ketoconazole-repressed; macrophage-downregulated protein abundance	-3.4
orf19.9		LAS17	CA00553_01	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction)	-3.5
orf19.1394		YCR090C	opCaV0100000238	Protein not essential for viability	-3.5
orf19.4664		NAT4	CA02822_01	Predicted ORF in Assemblies 19, 20 and 21	-3.5
orf19.4581		GPI14	CA05258_01	Predicted ORF in Assemblies 19, 20 and 21; regulated by Tsa1p, Tsa1Bp under H <sub>2</sub> O <sub>2</sub> stress conditions	-3.5
orf19.1986	ARO2	ARO2	opCaV0100000584	Putative chorismate synthase; fungal-specific (no human or murine homolog)	-3.5
orf19.3099	TRP4	TRP4	CA04440_01	Predicted enzyme of amino acid biosynthesis; upregulated in biofilm; regulated by Gcn2p and Gcn4p; <i>S. cerevisiae</i> ortholog	-3.5
orf19.1815		TIF6	opCaV0100001631	Predicted ORF in Assemblies 19, 20 and 21	-3.5
orf19.1295	VAS1	VAS1	CA00661_01	Putative tRNA-Val synthetase; genes encoding ribosomal subunits, translation factors, and tRNA synthetases are	-3.6
orf19.6559		TFC7	opCaV0100001589	Predicted ORF in Assemblies 19, 20 and 21	-3.6
orf19.2951	HOM6	HOM6	CA04201_01	Protein described as homoserine dehydrogenase; regulated by Gcn4p; induced in response to amino acid starvation (3-	-3.6
orf19.2351	NIT3	NIT3	CA02488_01	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p	-3.6
orf19.2849	AQY1	AQY1	CA02971_01	Aquaporin water channel; mutant has increased resistance to osmotic shock; required for wild-type tolerance of freezing; not	-3.6
			CA10001_01		-3.6
			CA02682_01		-3.6
orf19.6317	ADE6	ADE6	CA03347_01	Enzyme of adenine biosynthesis; not induced during GCN response, in contrast to the <i>S. cerevisiae</i> ortholog	-3.6
orf19.2284			opCaV0100000996	Predicted ORF in Assemblies 19, 20 and 21	-3.7
orf19.5636	RBT5		CA02681_01	GPI-anchored cell wall protein; has CRoW motif, not required for filamentous growth; expression is regulated by Rfg1p,	-3.7
orf19.5211	IDP1	IDP1	CA02287_01	Protein described as isocitrate dehydrogenase; transcriptionally induced by interaction with macrophage; alkaline upregulated	-3.7
orf19.7312	ERG13	ERG13	CA05697_01	Protein similar to <i>S. cerevisiae</i> Erg13p, which is involved in ergosterol biosynthesis; transposon mutation affects	-3.7
orf19.3810		MTD1	CA04915_01	Predicted ORF in Assemblies 19, 20 and 21	-3.7
orf19.4211	FET3	FET3	CA03015_01	Multicopper oxidase; required for growth under low-iron conditions; null mutant shows decreased prostaglandin E <sub>2</sub>	-3.8
orf19.5480	ILV1	ILV1	CA02470_01	Protein described as threonine dehydratase; regulated by Gcn4p and Gcn2p; induced in response to amino acid	-3.8
orf19.300	AIP2	DLD2	CA02554_01	Protein described as an actin interacting protein; regulated by Gcn4p; induced in response to amino acid starvation (3-	-3.8

orf19.1585	ZRT2	ZRT2	CA03215_01	Protein described as predicted zinc transporter; ciclopirox olamine, fluconazole, or alkaline downregulated;	-3.8
orf19.4718	TRP5	TRP5	CA01809_01	Predicted tryptophan synthase; Gcn4p-regulated; upregulated in biofilm; identified in detergent-resistant membrane fraction	-3.8
orf19.198	ASN1	ASN2	CA03658_01	Protein described as asparagine synthetase; soluble protein in hyphae; regulated by Rim101p; decreased expression at pH 4	-3.9
orf19.5664	HOF1		CA04402_01	Protein not essential for viability; similar to <i>S. cerevisiae</i> Hof1p, which is a protein localized to the bud neck and required for	-3.9
orf19.7638	PRO1	PRO1	CA06208_01	Transcription is regulated by Nrg1p; regulated by Gcn2p and Gcn4p	-3.9
orf19.3549	CDC21	CDC21	CA00384_01	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced	-3.9
orf19.5137.1	HHO1	HHO1	opCaV0100001469	Protein described at histone H1; farnesol regulated	-3.9
orf19.2546	TRP2	TRP2	CA01353_01	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p	-3.9
orf19.1853	HHT2	HHT2 HHT1	opCaV0100001007	Protein described as histone H3; farnesol regulated	-4.0
orf19.3365	DAO2		opCaV0100000901	Putative D-amino acid oxidase	-4.0
orf19.1061	HHT21	HHT2 HHT1	opCaV0100001390	Putative histone H3; amphotericin B repressed; regulated by Efg1p; farnesol regulated	-4.0
orf19.4910	FGR41	DSE2	CA02198_01	Putative GPI-anchored protein; transposon mutation affects filamentous growth; possibly spurious ORF (Annotation	-4.1
orf19.797	BAT21	BAT2	CA00741_01	Protein described as a branched chain amino acid aminotransferase; regulated by Gcn4p, Gcn2p; induced in	-4.1
orf19.2292			opCaV0100000630	Oligopeptide transporter; transcriptionally induced upon phagocytosis by macrophage; fungal-specific (no human or	-4.1
orf19.7637	YHB4	YHB1	CA06207_01	Protein related to flavohemoglobins; not required for wild-type nitric oxide resistance; has predicted globin, FAD-binding, and	-4.2
orf19.923	THR1	THR1	CA01629_01	Putative homoserine kinase; fungal-specific (no human or murine homolog); transcription is regulated by Tup1p;	-4.2
orf19.1789.1	LYS1	LYS1	CA00241_01	Saccharopine dehydrogenase (biosynthetic); enzyme of alpha-aminoacidipate lysine biosynthesis pathway; functionally	-4.2
orf19.7484	ADE1	ADE1	CA10191_01	Phosphoribosylaminoimidazole succinocarboxamide synthetase, enzyme of adenine biosynthesis; not induced	-4.2
orf19.6924	HTA1	HTA1	CA04758_01	Putative histone H2A; reduced mRNA abundance detected in homozygous fkh2 null mutant; amphotericin B repressed;	-4.3
orf19.2446		YDL144C	CA01119_01	Predicted ORF in Assemblies 19, 20 and 21	-4.3
orf19.2364	MIS11	MIS1	CA02406_01	Protein described as similar to precursor of mitochondrial C1-tetrahydrofolate synthase; putative protein of glycine	-4.3
orf19.1559	HOM2	HOM2	CA04011_01	Putative aspartate-semialdehyde dehydrogenase; fungal-specific (no human or murine homolog); ketoconazole-	-4.3
orf19.3770	ARG8	ARG8	opCaV0100000423	Predicted ORF in Assemblies 19, 20 and 21; Gcn2p-, Gcn4p-regulated	-4.3
tE(UUC)1			CAF0007147	tRNA-Glu predicted by tRNAscan-SE	-4.3
orf19.3870	ADE13	ADE13	opCaV0100001066	Enzyme of adenine biosynthesis; soluble protein in hyphae; not induced during GCN response, in contrast to the <i>S. cerevisiae</i>	-4.3
orf19.288		MET13	CA02891_01	Predicted ORF in Assemblies 19, 20 and 21	-4.4
orf19.2988			CA03489_01	Predicted ORF in Assemblies 19, 20 and 21	-4.4
orf19.1631	ERG6	ERG6	CA10112_01	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in ergosterol biosynthesis by methylating position C-	-4.4
orf19.1790			opCaV0100001145	Predicted ORF from Assembly 19; merged with orf19.1789.1 in Assembly 20	-4.5
orf19.1854	HHF2	HHF2 HHF1	opCaV0100001490	Putative histone H4; regulated by Efg1p; flucytosine, fluconazole-induced; amphotericin B, caspofungin repressed;	-4.5
orf19.1059	HHF1	HHF2 HHF1	opCaV0100000137	Putative histone H4; reduced mRNA in homozygous fkh2 null mutant; regulated by Efg1p; fluconazole induced; amphotericin	-4.6

orf19.7586	CHT3	CTS1	CA10175_01	Chitinase, major; functional homolog of <i>S. cerevisiae</i> Cts1p; 4 N-glycosylation motifs; possible O-mannosylated region;	-4.6
orf19.4506	LYS22	LYS21	opCaV0100000820	Putative homocitrate synthase; fungal-specific (no human or murine homolog); repressed by nitric oxide	-4.7
orf19.406	ERG1	ERG1	CA10278_01	Squalene epoxidase, catalyzes epoxidation of squalene to 2,3(S)-oxidosqualene in the ergosterol biosynthetic pathway;	-4.7
orf19.2947	SNZ1	SNZ1	CA04205_01	Similar to stationary-phase-related proteins; soluble in hyphae; induced on yeast to hyphal switch, in response to 3-	-4.8
orf19.5267			CA05073_01	Putative cell wall protein; downregulated in core caspofungin response; transcription is repressed in response to alpha	-4.8
orf19.2970	LYS2	LYS2	opCaV0100000598	Large subunit of heterodimeric alpha-amino acid reductase; enzyme of lysine biosynthesis; contains predicted binding sites	-4.8
orf19.5505	HIS7	HIS7	CA02589_01	Putative imidazole glycerol phosphate synthase; enzyme of histidine biosynthesis; fungal-specific (no human or murine	-4.9
orf19.176	OPT4	OPT2	opCaV0100000116	Oligopeptide transporter; detected at germ tube plasma membrane by mass spectrometry; transcriptionally induced	-4.9
orf19.5484		SER1	CA02473_01	Predicted ORF in Assemblies 19, 20 and 21	-4.9
orf19.1347			opCaV0100000389	Predicted ORF from Assembly 19; gene fragment (probable assembly 19 error); 3' end of OPT5 (oligopeptide transporter);	-5.0
orf19.385	GCV2	GCV2	opCaV0100000658	Putative protein of glycine catabolism; downregulated by Efg1p; Hog1p-induced; upregulated by Rim101p at acid pH	-5.0
orf19.1108	HAM1	HAM1	CA01696_01	Predicted ORF in Assemblies 19, 20 and 21; caspofungin repressed; regulated by Gcn2p and Gcn4p	-5.0
orf19.5672	MEP2	MEP2	CA04410_01	Ammonium permease and regulator of nitrogen starvation-induced filamentation; 11 predicted transmembrane regions; in	-5.1
orf19.4026	HIS1	HIS1	CA10076_01	ATP phosphoribosyl transferase; enzyme of histidine biosynthesis; fungal-specific (no human, murine homolog);	-5.1
orf19.767	ERG3	ERG3	CA10061_01	C-5 sterol desaturase; introduces C-5(6) double bond into episterol in ergosterol biosynthesis; clinically-isolated	-5.2
orf19.3554	AAT1	AAT1	CA02783_01	Protein described as aspartate aminotransferase; soluble protein in hyphae; macrophage-induced protein; alkaline	-5.2
orf19.922	ERG11	ERG11	CA10287_01	Lanosterol 14-alpha-demethylase, member of cytochrome P450 family that functions in ergosterol biosynthesis; target of	-5.2
orf19.1052		HTB1	opCaV0100000617	Predicted histone H2B	-5.4
orf19.4177	HIS5	HIS5	CA03761_01	Predicted ORF in Assemblies 19, 20 and 21; Gcn4p-regulated	-5.4
orf19.1051	HTA2	HTA1	CA01171_01	Protein described as histone H2A; farnesol regulated	-5.5
			CA00295_01		-5.5
orf19.5639	HIS4	HIS4	CA10274_01	Multifunctional enzyme that catalyzes three steps of histidine biosynthesis, with phosphoribosyl-AMP cyclohydrolase,	-5.5
orf19.3749	IFC3	OPT2	opCaV0100000282	Oligopeptide transporter; transcriptionally induced upon phagocytosis by macrophage; induced by BSA or peptides;	-5.5
			CA10244_01		-5.5
orf19.1517	ARO3	ARO3	opCaV0100000128	3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase; enzyme of aromatic amino acid biosynthesis; GCN-regulated;	-5.6
orf19.3175		YOR356W	CA00901_01	Predicted ORF in Assemblies 19, 20 and 21; alkaline downregulated; repressed by nitric oxide	-5.6
orf19.6925	HTB1	HTB1	opCaV0100000540	Putative histone H2B; induced upon adherence to polystyrene; amphotericin B or caspofungin repressed; flucytosine or	-5.6
orf19.6993	GAP2	GAP1	CA05132_01	Protein similar to amino acid permeases; ketoconazole, flucytosine repressed; induced by histidine, and induction	-6.1
orf19.6994	BAT22	BAT2	CA05133_01	Protein described as a branched chain amino acid aminotransferase; regulated by Gcn4p; induced in response to	-6.3
			CA01465_01		-6.4
orf19.5870	CTP1	CTP1	opCaV0100000501	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; amphotericin B repressed, caspofungin repressed	-6.5

orf19.5720		MCH4	CA02217_01	Predicted ORF in Assemblies 19, 20 and 21; ketoconazole or caspofungin repressed	-6.7
orf19.2098	ARO8	ARO8	CA04872_01	Protein abundance is affected by URA3 expression in the CAI-4 strain background; alkaline upregulated; Gcn4p-regulated	-6.8
orf19.386	SAM4	SAM4	CA03915_01	Alkaline upregulated	-7.2
orf19.4335	TNA1	TNA1	CA00613_01	Putative nicotinic acid transporter; fungal-specific (no human or murine homolog); detected at germ tube plasma membrane by	-7.3
orf19.2948	SNO1	SNO1	CA04204_01	Protein of unknown function expressed during stationary phase; transcription is regulated by Tup1p, Efg1p	-7.7
orf19.6570	NUP		CA10093_01	Nucleoside permease; adenosine and guanosine are substrates, whereas cytidine, adenine, guanine, uridine, uracil	-8.0
orf19.2584	OPT9	OPT1	opCaV0100001143	Probable pseudogene similar to fragments of OPT1 oligopeptide transporter gene; decreased expression in hyphae	-8.7
orf19.5674	PGA10	FIT1	CA04412_01	Plasma membrane protein involved in heme-iron utilization; allows utilization of heme and hemoglobin as iron sources in	-9.4
orf19.2602	OPT1	OPT1	CA02102_01	Oligopeptide transporter; transports 3-to-5-residue peptides; alleles are distinct, one has intron; not ABC or PTR type	-12.2
*Oligo_ID is based on database provided by the array manufacturer (Microarrays Inc., Nashville, TN, <a href="http://www.microarrays.com">www.microarrays.com</a> )					