Supplementary Material

Figure S1. Distribution of differentially expressed cAMP-responsive genes according to Munich Information Centre for Protein Sequences (MIPS) functional categories.

Figure S2. Representation of MIPS functional categories amongst the differentially expressed genes common to *Candida pde2* at 25°C and 37°C data sets compared to that of *S. cerevisiae pde2*

Table S1. List of all differentially expressed genes in *pde2* at 25°C and 37°C

Table S2. Number of differentially expressed genes

Table S3. Down-regulated cAMP-responsive genes at both 25°C and 37°C

Table S4. Up-regulated cAMP-responsive genes at both 25°C and 37°C

Table S5. Common differentially transcribed genes in *pde2* mutants of *S. cerevisiae* and *C. albicans*

Table S6. Comparative analysis of differentially expressed genes upon deletion of *PDE2* (our data) and *CDC35*, *EFG1* and *RAS1* (Harcus *et al*., 2004).

Table S7. Differentially regulated genes involved in protein degradation, modification, folding, fate and targeting

Table S8. Plasmids used in this study

Table S9. Primers used in this study

Figure S1. Distribution of differentially expressed cAMP-responsive genes according to Munich Information Centre for Protein Sequences (MIPS) functional categories.

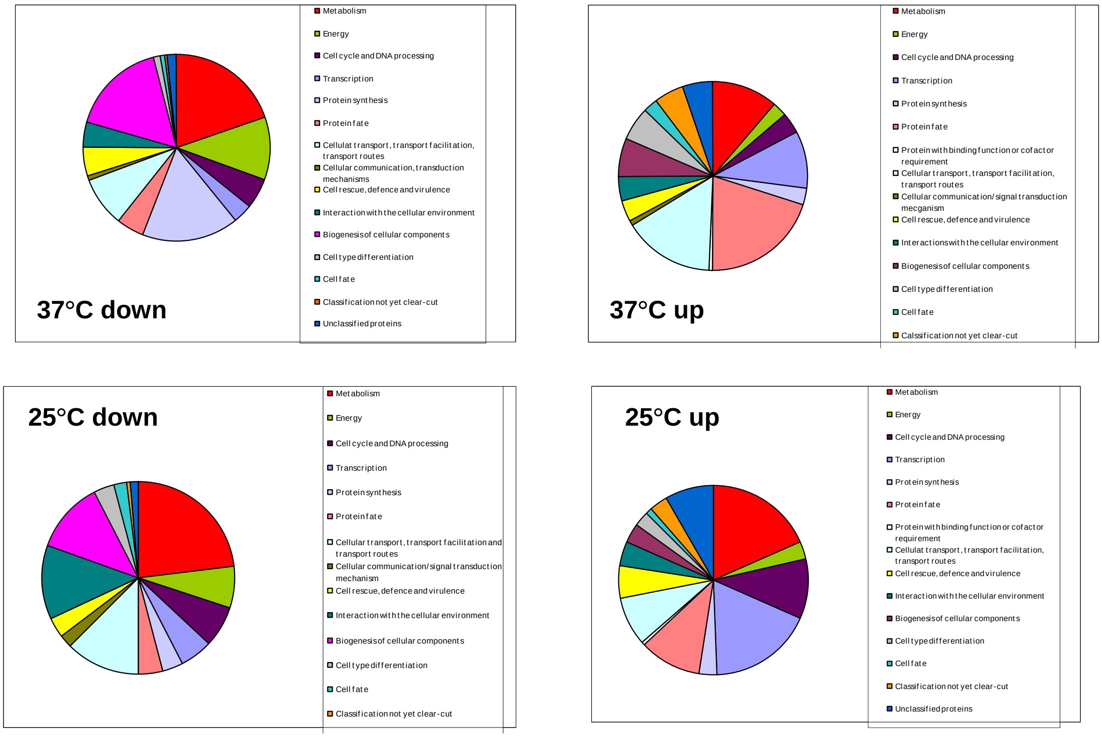
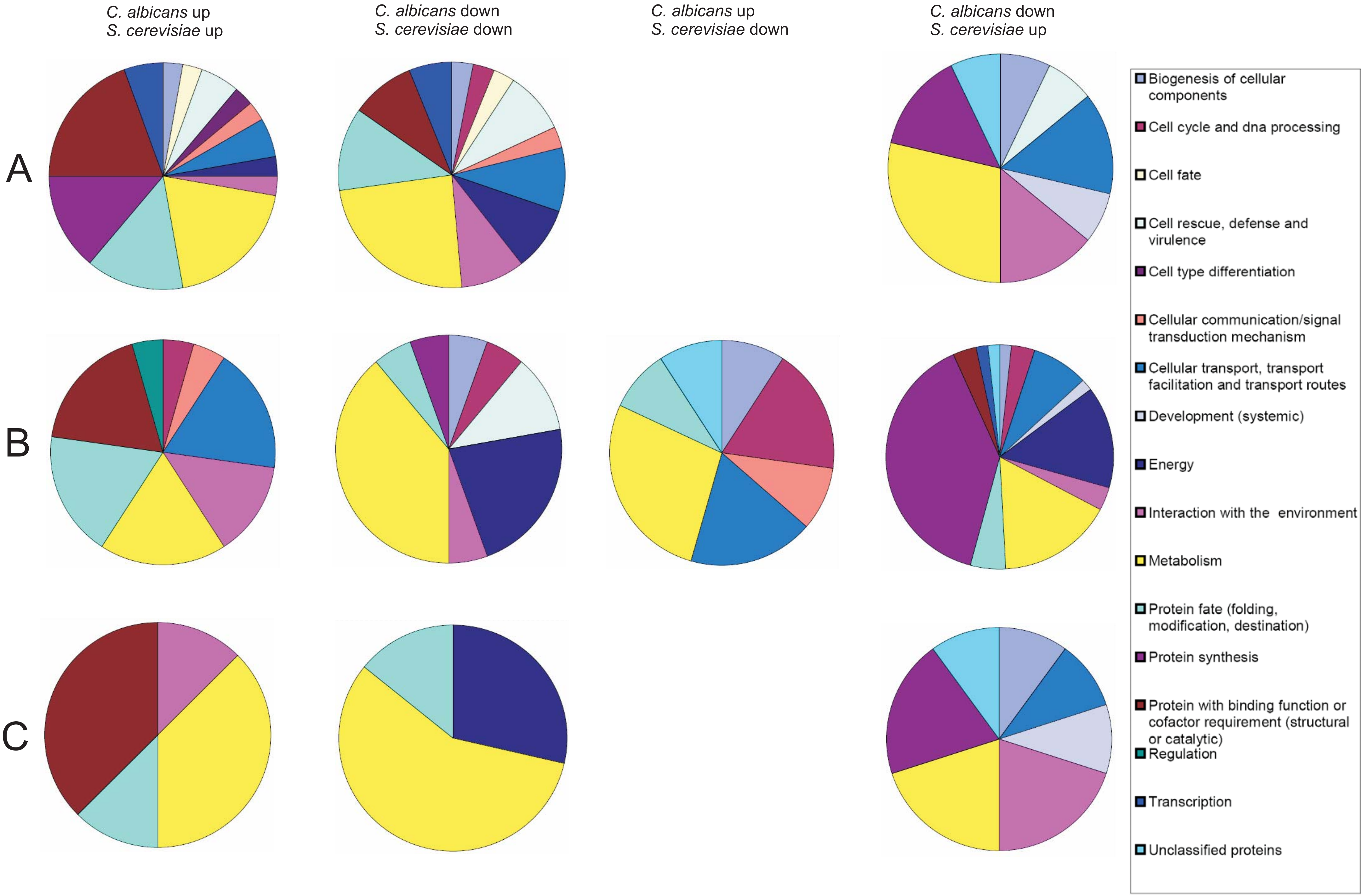


Figure 1. Distribution of differentially expressed cAMP-responsive genes according to Munich Information Centre for Protein Sequences (MIPS) functional categories. Differentially expressed genes in the *pde2* mutant are divided into up- and down-regulated at 25°C and 37°C, respectively. Some of the genes are assigned to more than one functional category by MIPS and this is reflected in the distribution.


C. albicans up
S. cerevisiae up
C. albicans down
S. cerevisiae down
C. albicans up
S. cerevisiae down
C. albicans down
S. cerevisiae up
A
B
C
Biogenesis of cellular components
Cell cycle and dna processing
Cell fate
Cell rescue, defense and virulence
Cell type differentiation
Cellular communication/signal transduction mechanism
Cellular transport, transport facilitation and transport routes
Development (systemic)
Energy
Interaction with the environment
Metabolism
Protein fate (folding, modification, destination)
Protein synthesis
Protein with binding function or cofactor requirement (structural or catalytic)
Regulation
Transcription
Unclassified proteins

Supplementary Figure S2. Representation of MIPS functional categories amongst the differentially expressed genes common to *Candida pde2* data sets compared to that of *S. cerevisiae pde2*

Panel A – comparison between *C.albicans pde2* at 25°C and *S. cerevisiae pde2*

Panel B – comparison between *C.albicans pde2* at 37°C and *S. cerevisiae pde2*

Panel C – comparison between *C.albicans* cAMP-responsive gene set (common to 25°C and 37°C) and *S. cerevisiae pde2*

Some of the genes are assigned to more than one functional category by MIPS and this is reflected in the distribution

Table S1. List of all differentially expressed genes

Orf.19	Suggested name	Expr level change	Product/Function
Down-regulated at 25°C			
orf19.7502		-25.53	hypothetical protein
orf19.3111	**PRA1**	-18.89	pH-regulated antigen
orf19.7219	**FTR1**	-6.53	plasma membrane iron permease
orf19.1716	**URA3**	-6.16	orotidine-5'-phosphate decarboxylase
orf19.566		-6.12	hypothetical protein
orf19.4737	**DHA12**	-5.62	membrane transporter of the MFS-MDR family
orf19.5383	**PMA1**	-5.53	plasma membrane H+-ATPase
orf19.4599	**PHO89**	-5.3	Na+/Pi symporter
orf19.1715	**IRO1**	-5.05	transcription factor
orf19.1585	**ZRT2**	-4.87	low affinity zinc transporter
orf19.3112	**ZRT1**	-4.85	high affininty zinc transporter
orf19.2835	**AOS1**	-4.65	protein-sumoylation function, part of activating enzyme for Smt3
orf19.5741	**ALS1-1**	-4.48	agglutinin like protein 1
orf19.3618	**YWP1**	-4.43	putative cell wall protein
orf19.3794	**SUR1**	-4.14	SUppressor of ROK1 | zinc finger transcription factor
orf19.4765	**CCW12**	-4.13	cell wall mannoprotein
orf19.2765		-3.94	hypothetical protein
orf19.5960	**NCE102**	-3.93	non-classical protein export pathway
orf19.7550		-3.92	ORF MSV011 leucine rich repeat gene family protein
orf19.2003	**HNM2**	-3.84	choline permease
orf19.6420		-3.76	hypothetical membrane protein with repeated hydrophobic/hydrophilic domains
orf19.288	**MET13**	-3.71	methylene tetrahydrofolate reductase
orf19.3618	**YWP1**	-3.69	putative cell wall protein
orf19.4211	**FET3**	-3.68	multicopper ferro-O2- oxidoreductase involved in high-affinity iron uptake
orf19.6817	**FCR1**	-3.56	zinc finger transcription factor involved in pleiotropic drug resistance
orf19.4885	**MIR1**	-3.48	mitochondrial phosphate transport protein

orf19.3911	**SAH1**	-3.42	S-adenosyl-L-homocysteine hydrolase
orf19.2659		-3.22	conserved hypothetical protein
orf19.1172	**PHO84**	-3.21	inorganic phosphate permease
orf19.2551	**MET6**	-3.21	methionine-synthesizing 5- methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
orf19.3713		-3.19	hypothetical protein
orf19.169	**CHO2**	-3.18	phosphatidyl- ethanolamine N-methyltransferase
orf19.1442	**PLB4**	-3.07	phospholipase B (lysophospholipase)
orf19.6844	**ICL1**	-3.02	isocitrate lyase
orf19.3700	**TOM70**	-2.98	mitochondrial outer membrane specialized import receptor
orf19.1979	**GIT3**	-2.95	glycerophosphoinositol permease
orf19.5591	**ADO1**	-2.93	adenosine kinase
orf19.6078		-2.93	conserved hypothetical protein
orf19.4833	**MLS1**	-2.9	malate synthase
orf19.4342		-2.9	conserved hypothetical protein
orf19.655	**PHO842**	-2.89	high-affinity inorganic phosphate/H+ symporter
orf19.7021	**GPH1**	-2.86	glycogen phosphorylase
orf19.7446	**OPI3**	-2.85	methylene-fatty-acyl-phospholipid synthase
orf19.1353		-2.83	hypothetical protein
orf19.5117	**OLE1**	-2.81	stearoyl-CoA desaturase
orf19.5288	**YAL60**	-2.78	Zn-containing alcohol dehydrogenase
orf19.251		-2.75	conserved hypothetical protein
orf19.4966		-2.74	probable mitochondrial carrier protein
orf19.1770	**CYC1**	-2.72	cytochrome-c isoform 1
orf19.6763	**SLK19**	-2.71	protein involved in control of spindle dynamics together with kar3p
orf19.1618	**GFA1**	-2.68	glucoseamine-6- phosphate synthase
orf19.3793		-2.66	hypothetical protein
orf19.2003	**HNM2**	-2.63	choline permease
orf19.3219		-2.63	phosphohydrolase
orf19.2432	**HAC1**	-2.63	transcription factor that binds to CRE motif
orf19.6983		-2.6	conserved hypothetical protein
orf19.3215		-2.59	hypothetical protein

orf19.6002	**RPL8B**	-2.57	ribosomal protein L8B (L4B) (rp6) (YL5)
orf19.979	**FAS1**	-2.57	fatty-acyl-CoA synthase, beta chain
orf19.1760	**RAS1**	-2.55	small monomeric GTPase involved in hyphae differentiation and the transmission of cAMP signals
orf19.2531	**CSP37**	-2.55	cell surface protein
orf19.657	**SAM2**	-2.5	S- adenosylmethionine synthetase
orf19.2841	**PGM2**	-2.48	phosphoglucomutase
orf19.85	**GPX1**	-2.48	glutathione peroxidase
orf19.2454	**PHO87**	-2.48	phosphate permease
orf19.238	**CCP1**	-2.44	cytochrome-c peroxidase
orf19.3414	**SUR7**	-2.41	potential membrane protein
orf19.3359	**ARP8**	-2.4	actin-related protein
orf19.334		-2.37	hypothetical protein
orf19.4959		-2.37	hypothetical protein
orf19.48	**RPM2**	-2.37	RNase P subunit
orf19.2972	**PDE2**	-2.36	nucleotide phosphodiesterase
orf19.646	**GLN1**	-2.36	glutamine synthetase
orf19.5741	**ALS1-1**	-2.36	agglutinin like protein 1
orf19.1862		-2.35	conserved hypothetical protein
orf19.7481	**MDH2**	-2.33	malate dehydrogenase
orf19.6837		-2.33	benzil reductase
orf19.4381	**VTC2**	-2.33	polyphosphate synthetase
orf19.238	**CCP1**	-2.32	cytochrome-c peroxidase
orf19.6070	**ENA5**	-2.31	Na+ ATPase
orf19.2644	**QCR2**	-2.3	ubiquinol--cytochrome-c reductase 40KD chain II
orf19.1378	**ERF3**	-2.29	translation release factor 3
orf19.4309	**GRP3**	-2.28	induced by osmotic stress
orf19.3149	**LSP1**	-2.27	Long chain base Stimulates Phosphorylation
orf19.2766		-2.26	hypothetical protein
orf19.3554	**AAT1**	-2.26	aspartate aminotransferase
orf19.2496	**FUN34**	-2.24	transporter involved in nitrogen utilization
orf19.7610	**PTP3**	-2.23	protein tyrosine phosphatase

orf19.4991	**MPT5**	-2.23	protein necessary for high temperature growth
orf19.7349	**CHS4**	-2.22	chitin synthase regulatory factor
orf19.2680	**DNF3**	-2.22	aminophospholipid-translocating ATPase
orf19.97	**CAN2**	-2.22	arginine permease
orf19.1680	**TFP1**	-2.22	vacuolar ATPase V1 domain catalytic subunit A
orf19.2767		-2.21	hypothetical protein
orf19.3603		-2.21	conserved hypothetical protein
orf19.7001	**YCK2**	-2.2	casein kinase I
orf19.1783	**YOR1**	-2.2	oligomycin resistance ATP-dependent permease | ABC transporter
orf19.4488	**SWI3**	-2.2	general RNA polymerase II transcription factor
orf19.7381	**LYS145**	-2.19	zinc finger transcription factor
orf19.178		-2.19	hypothetical protein
orf19.147	**YAK2**	-2.18	serine-threonine protein kinase, PKA suppressor
orf19.4495	**NUO51**	-2.18	NADH dehydrogenase complex I | nucleotide-binding respiratory complex I subunit
orf19.717	**HSP60**	-2.18	mitochondrial groEL-type heat shock protein
orf19.1995	**MNN5**	-2.17	alpha-1,2- mannosyltransferase
orf19.5063		-2.17	hypothetical protein
orf19.3793		-2.16	hypothetical protein
orf19.6556		-2.16	conserved hypothetical protein
orf19.1027	**PDR16**	-2.15	phosphatidylinositol transfer protein | drug resistance
orf19.173	**AZF1**	-2.15	DNA-binding transcription factor
orf19.1535		-2.15	hypothetical protein
orf19.4262	**JSN1**	-2.15	tubulin mutant, benomyl dependent
orf19.5113	**ADH2**	-2.14	alcohol dehydrogenase
orf19.522	**PIM1**	-2.14	mitochondrial ATP-dependent protease
orf19.3599	**TIF4631**	-2.13	mRNA cap binding protein eIF 4F
orf19.6197	**DHH1**	-2.13	RNA helicase of DEAD box family
orf19.4649		-2.13	zinc finger transcription factor
orf19.1709	**PXP18**	-2.13	sterol carrier protein
orf19.7392	**DED1**	-2.12	ATP-dependent RNA helicase of DEAD box family
orf19.3997	**ADH1**	-2.12	alcohol dehydrogenase 1
orf19.5541		-2.12	conserved hypothetical protein

orf19.7466	**ACC1**	-2.11	homologous to acetyl-coenzyme-A carboxylase
orf19.7053	**GAC1**	-2.11	regulatory subunit for phosphoprotein phosphatase type 1 (PP-1)
orf19.3984		-2.11	conserved hypothetical protein
orf19.1964		-2.11	conserved hypothetical protein
orf19.508	**QDR1**	-2.11	multidrug resistance transporter
orf19.6763	**SLK19**	-2.1	protein involved in control of spindle dynamics together with kar3p
orf19.5334	**TIS11**	-2.1	Zinc finger containing protein
orf19.5305	**RHD3**	-2.1	conserved protein reressed in hyphal development
orf19.6812	**PMT2**	-2.09	dolichyl-P-mannose-protein mannosyltransferase
orf19.6007		-2.08	similar to fatty acid elongating enzymes
orf19.7487	**RRT98**	-2.07	reverse transcriptase
orf19.4890	**CLA4**	-2.07	serine-threonine kinase involved in cytokinesis and maintenance of hyphal growth
orf19.4631	**ERG252**	-2.07	C-4 sterol methyl oxidase | membrane-bound non-heme di-iron oxygenase involved in lipid metabolism
orf19.1128	**MYO4**	-2.06	class II myosin | myosin-1 isoform (type II myosin) heavy chain
orf19.2170		-2.06	membrane transporter
orf19.230		-2.06	hypothetical protein
orf19.3010.1	**ECM33**	-2.05	3-prime end of ExtraCellular Mutant protein
orf19.4322	**DAP2**	-2.05	dipeptidyl aminopeptidase B
orf19.7153	**LOS1**	-2.03	tRNA transport receptor
orf19.2992	**RPA1**	-2.03	60S ribosomal protein
orf19.1112	**BUD7**	-2.03	involved in bud-site selection
orf19.5949	**FAS2**	-2.02	fatty acid synthase alpha subunit
orf19.7239	**CRP1**	-2.02	regulation of G-protein function
orf19.4635	**NIP1**	-2.02	subunit of translation initiation complex eIF3 | associated with 40s ribosomal subunit
orf19.1442	**PLB4**	-2.02	phospholipase B (lysophospholipase)
orf19.6763	**SLK19**	-2.01	protein involved in control of spindle dynamics together with kar3p
orf19.6281		-2.01	conserved hypothetical protein
orf19.4759	**COX5A**	-2.01	cytochrome-c oxidase subunit Va
orf19.5576	**PNK1**	-2.01	panthotenate kinase, 3- prime end
Up-regulated at 25°C			
orf19.5982	**RPL18**	56.47	ribosomal protein L18A (rp28A)

orf19.7265	**SAD1**	13.06	snRNP assembly defective
orf19.2672	**NCP1**	12.64	NADPH-cytochrome P450 reductase
orf19.3810	**MTD1**	12.5	methylenetetrahydrofolate dehydrogenase | NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase | NAD-dependent 5,10- methylenetetrahydrafolate dehydrogenase | methylenetetrahydrofolate dehydrogenase (NAD+)
orf19.3812	**SSZ1**	12.34	regulator protein involved in pleiotropic drug resistance that forms a ribosome-associated complex | DnaJ/HSP70 chaperone
orf19.6540	**PFK2**	10.89	PFK2
orf19.6548	**ISU1**	10.27	iron-sulfur cluster nifU-like
orf19.3130		9.98	highly conserved hypothetical protein
orf19.2669		8.55	rev product adjacent to gag/pol products
orf19.3120		8.52	highly conserved hypothetical protein, possible ABC transporter
orf19.2676	**IKI1**	8.4	RNA polymerase II elongator associated protein
orf19.3448		7.9	hypothetical protein
orf19.6506		7.6	conserved hypothetical protein
orf19.3817	**RTS2**	6.89	similar to mouse KIN7 protein
orf19.4203	**NDC1**	6.69	nuclear envelope protein
orf19.2678	**BUB1**	6.43	ser/thr protein kinase in mitosis checkpoint
orf19.3809	**BAS1**	6.1	transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
orf19.3127	**CZF1**	5.25	zinc finger protein
orf19.2410	**IMH1**	4.95	involved in vesicular transport
orf19.6357	**MAD1**	4.73	coiled-coil protein involved in the spindle-assembly checkpoint
orf19.2340	**CDC48**	4.18	microsomal ATPase involved in secretion, peroxisome formation and gene expression
orf19.3115		3.93	hypothetical protein
orf19.5139		3.81	hypothetical protein
orf19.2909	**ERG26**	3.46	C-3 sterol dehydrogenase
orf19.2667	**RPF1**	3.45	nucleolar protein involved in rRNA processing
orf19.2143		3.41	conserved hypothetical protein
orf19.4191	**RLP24**	3.39	similar to ribosomal protein L24.e.B
orf19.1083		3.33	conserved hypothetical protein
orf19.2774	**LIP12**	3.29	lipoic acid synthase
orf19.1932	**FRE5**	3.29	ferric reductase

orf19.1566	**UTP21**	3.21	U3 snoRNP protein | strong similarity to S. pombe beta-transducin
orf19.1248	**RPB3**	3.2	45 kDa subunit of RNA polymerase II
orf19.1234		3.19	hypothetical protein
orf19.5299	**ECM1**	3.14	cell wall structure or biosynthesis
orf19.42		3.08	transport protein
orf19.5678	**DPH3**	3	conserved hypothetical protein | similar to diphteria toxin resistance protein
orf19.1217		2.89	conserved hypothetical protein
orf19.6402	**CYS3**	2.87	cystathionine gamma-lyase
orf19.1642	**LOC1**	2.86	nuclear mRNA binding protein
orf19.3103	**RPO31**	2.84	RNA polymerase III large subunit
orf19.3778		2.82	WD-repeat protein
orf19.6109	**TUP1**	2.79	general transcription repressor
orf19.5106	**DIP2**	2.77	beta transducin
orf19.3401	**VPS60**	2.77	involved in vacuolar protein sorting
orf19.2607	**PMU2**	2.76	phosphomutase homolog
orf19.5090	**TAD3**	2.75	tRNA-specific adenosine-34 deaminase subunit
orf19.6469	**TCA99**	2.74	reverse transcriptase
orf19.2146	**HAT2**	2.74	histone acetyltransferase subunit
orf19.3396	**HCH1**	2.74	high copy Hsp90 suppressor
orf19.3540	**MAK5**	2.73	ATP-dependent RNA helicase
orf19.6614		2.71	DEAD/DEAH box helicase
orf19.6114		2.7	hypothetical protein
orf19.5912	**MAK21**	2.63	required for 60S ribosomal subunit biogenesis
orf19.3125		2.62	conserved hypothetical protein
orf19.6718		2.62	conserved hypothetical protein
orf19.4611	**PRS4**	2.61	ribose-phosphate pyrophosphokinase
orf19.1913		2.61	hypothetical protein
orf19.5796	**SHE9**	2.6	causes growth arrest when overexpressed
orf19.1388	**NOP16**	2.6	nucleolar protein involved in ribosome biogenesis
orf19.4605	**TYR1**	2.59	prephenate dehydrogenase | tyrosine biosynthesis
orf19.5764	**SKI8**	2.58	antiviral protein
orf19.2098	**ARO8**	2.58	aromatic amino acid aminotransferase

orf19.1250		2.58	conserved hypothetical protein
orf19.6753		2.57	conserved hypothetical protein
orf19.5597	**POL5**	2.57	DNA polymerase V, 5-prime end
orf19.5634	**FRP1**	2.57	ferric reductase
orf19.6073	**HMX1**	2.54	heme binding protein
orf19.1412		2.54	hypothetical protein
orf19.5732	**NOG2**	2.54	nuclear/nucleolar GTP-binding protein 2
orf19.4666		2.54	hypothetical protein
orf19.1265	**TRS130**	2.53	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic
orf19.2393	**YTH2**	2.52	polyadenylation factor subunit
orf19.7601		2.51	conserved hypothetical protein
orf19.5639	**HIS4**	2.51	histidinol dehydrogenase
orf19.4181	**SPC2**	2.5	subunit of signal peptidase complex
orf19.6828	**RRP1**	2.49	protein Involved in processing rRNA precursor species to mature rRNAs
orf19.367	**CNH1**	2.49	Na+/H+ antiporter
orf19.6314	**RPB8**	2.48	16-kDa RNA polymerase subunit (common to polymerases I, II and III)
orf19.4171		2.47	conserved hypothetical protein
orf19.7675	**MRPL25**	2.46	mitochondrial ribosomal protein MRPL25
orf19.1996	**CHA2**	2.46	catabolic serine/threonine dehydratase
orf19.5768	**SNF4**	2.46	nuclear protein
orf19.1220	**RVS167**	2.46	cytoskeletal binding and regulatory protein
orf19.3370	**UBP10**	2.46	ubiquitin-specific protease
orf19.2917	**NUG1**	2.45	GTPase involved in ribosome biogenesis
orf19.124	**CIC1**	2.44	protease substrate recruitment factor
orf19.5732	**NOG2**	2.43	nuclear/nucleolar GTP-binding protein 2
orf19.7258	**DDI1**	2.42	response to DNA alkylation
orf19.43		2.42	hypothetical protein
orf19.4401	**YVH1**	2.42	protein-tyrosine phosphatase
orf19.5519	**GCV1**	2.42	glycine cleavage T protein
orf19.5182	**CDC2**	2.42	DNA-directed DNA polymerase delta, catalytic 125 KD subunit
orf19.3099	**TRP4**	2.41	anthranilate phosphoribosyltransferase
orf19.4193		2.41	cofilin/tropomyosin-type actin-binding protein

orf19.5066		2.41	conserved hypothetical protein
orf19.6324	**VID27**	2.4	vacuole import and degradation
orf19.1915	**MPP10**	2.39	component of the U3 small nucleolar ribonucleoprotein (snoRNP)
orf19.2708		2.39	highly conserved hypothetical protein, involved in 35S rRNA processing
orf19.1923	**RRN3**	2.38	RNA polymerase I transcription factor
orf19.6074	**FAP7**	2.37	nuclear protein involved in oxidative stress response
orf19.6730		2.36	conserved hypothetical protein
orf19.4079	**SLP2**	2.35	potential SPFH domain | possible regulator of cation conductance
orf19.2107	**MUQ1**	2.35	choline phosphate cytidylyltransferase | phosphoethanolamine cytidylyltransferase
orf19.6213	**SUI2**	2.34	translation initiation factor eIF2, alpha chain
orf19.2742		2.33	hypothetical protein
orf19.4118	**NNT1**	2.31	concentrative Na+-nucleoside cotransporter
orf19.3564	**RPC40**	2.31	RNA polymerase III (C) subunit
orf19.7286	**RPN7**	2.29	subunit of the regulatory particle of the proteasome
orf19.5720		2.29	monocarboxylate transporter proteins
orf19.3370	**UBP10**	2.29	ubiquitin-specific protease
orf19.3415	**PTK2**	2.27	putative serine/threonine protein kinase
orf19.2251	**AAH1**	2.27	adenine aminohydrolase | adenine deaminase
orf19.3978		2.27	conserved hypothetical protein
orf19.2143		2.27	conserved hypothetical protein
orf19.5607		2.26	hypothetical protein
orf19.7422	**LCP5**	2.26	nucleolar protein required for ribosomal RNA processing
orf19.59		2.26	zinc finger protein with unknown function
orf19.5517	**ADH6**	2.26	alcohol dehydrogenase
orf19.2873	**TOP2**	2.26	DNA topoisomerase II
orf19.5660	**PEX10**	2.25	peroxisomal biogenesis protein
orf19.3366	**CSH3**	2.25	ER chaperone required for proper uptake and sensing of extracellular amino acids
orf19.4089	**SGT1**	2.24	subunit of SCF ubiquitin ligase complex | regulator of cell cycle
orf19.2251	**AAH1**	2.24	adenine aminohydrolase | adenine deaminase
orf19.1249	**HIS6**	2.24	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
orf19.38		2.24	hypothetical protein
orf19.2030		2.23	hypothetical protein

orf19.1797		2.23	conserved hypothetical protein
orf19.3505	LIT1	2.23	putative transcription factor
orf19.4029	SQT1	2.22	ribosomal assembly
orf19.500	GCD10	2.22	translation initiation factor 3 (eIF-3) zeta subunit
orf19.5666	SUB1	2.22	transcriptional coactivator
orf19.1428		2.22	hypothetical protein
orf19.2688	NAN1	2.22	U3 snoRNP protein in ribosomal small subunit (SSU) processosome
orf19.157		2.21	hypothetical protein
orf19.386	SAM4	2.21	AdoMet-homocysteine methyltransferase
orf19.4167		2.21	hypothetical protein
orf19.1923	RRN3	2.21	RNA polymerase I transcription factor
orf19.4447	YMC1	2.2	mitochondrial carrier protein
orf19.6710		2.2	hypothetical protein
orf19.366	RAD17	2.2	3'-5'exonuclease
orf19.5440		2.19	26S proteasome subunit
orf19.3128	SLY1	2.18	t-SNARE- interacting protein that functions in ER-to-Golgi traffic
orf19.5765	NUP82	2.18	nuclear pore protein
orf19.6312	RPS3	2.18	ribosomal protein S3 (rp13) (YS3)
orf19.5772		2.17	actin overexpression resistant
orf19.3091		2.17	hypothetical protein
orf19.93		2.17	conserved hypothetical protein
orf19.5614	RNH2	2.16	ribonuclease H
orf19.1562		2.16	hypothetical protein
orf19.4718	TRP5	2.16	tryptophan synthetase
orf19.2630	RAD59	2.16	involved in mitotic recombination and DNA repair
orf19.7605	PUP1	2.15	20S proteasom ebeta2 subunit
orf19.2871	SDH3	2.15	succinate dehydrogenase
orf19.3797	MPRL11	2.14	mitochondrial ribosomal protein (YmL11)
orf19.5767	CUS2	2.13	cold sensitive U2 snRNA Suppressor
orf19.6321		2.13	hypothetical protein
orf19.5989	HRP1	2.12	nuclear polyadenylated-RNA- binding protein
orf19.6959	HOM32	2.12	first step in common pathway for methionine and threonine biosynthesis | aspartate kinase (L-

			aspartate 4-P-transferase) | L-aspartate 4-P-transferase
orf19.4399		2.12	conserved hypothetical protein
orf19.5515	**CBP3**	2.12	involved in cytochrome-c reductase assembly
orf19.5461		2.11	hypothetical protein
orf19.5658	**MNN10**	2.11	galactosyltransferase
orf19.6648	**SDA1**	2.11	required for normal organization of the actin cytoskeleton and passage through Start
orf19.6190	**PSA1**	2.11	GDP-mannose pyrophosphorylase
orf19.2385	**KTI12**	2.11	RNA polymerase II Elongator associated protein
orf19.6751	**TRM7**	2.1	tRNA methyltransferase
orf19.5793	**RPT3**	2.1	26S proteasome regulatory subunit
orf19.3409	**SED4**	2.1	involved in vesicle formation at the endoplasmic reticulum
orf19.105	**MET22**	2.1	3'(2')5'-bisphosphate nucleotidase , possibly involved in salt tolerance and methionine synthesis
orf19.3089		2.1	possibly involved in intramitochondrial sorting
orf19.2711	**ELP2**	2.1	RNA polymerase II Elongator subunit
orf19.2154	**HXK1**	2.1	hexokinase I
orf19.6570	**NUP3**	2.09	purine nucleoside permease
orf19.3123	**RPT5**	2.09	26S proteasome regulatory subunit
orf19.3449		2.09	highly conserved hypothetical protein
orf19.6297	**DEG1**	2.09	pseudouridine synthase | rRNA methyltransferase
orf19.2604		2.09	highly conserved hypothetical protein
orf19.2920		2.09	highly conserved hypothetical protein
orf19.4627	**NUP120**	2.08	nuclear pore protein
orf19.5665		2.08	conserved hypothetical protein
orf19.2889	**IES6**	2.08	conserved hypothetical protein
orf19.2320	**RIO1**	2.08	protein serine kinase
orf19.5564	**RNH1**	2.08	ribonuclease H, exon 2
orf19.7552		2.07	conserved hypothetical protein
orf19.3126	**CCT6**	2.07	cytoplasmic chaperonin of the Cct ring complex
orf19.52	**MMT2**	2.07	mitochondrial protein with role in iron accumulation
orf19.3080	**SCC2**	2.07	sister chromatid cohesion protein
orf19.6014	**RRS1**	2.07	regulator of ribosome synthesis

orf19.7657	POP3	2.06	RNase P and RNase MRP subunit
orf19.5009	KEL3	2.06	Kelch-repeat containing protein
orf19.4183		2.06	Pro/Ser-rich protein
orf19.4676		2.06	conserved hypothetical protein
orf19.2131	TUL1	2.06	transmembrane ubiquitin ligase
orf19.4639.1	PWP1	2.06	beta-transducin superfamily with periodic tryptophan residues
orf19.3827		2.05	conserved hypothetical protein
orf19.4004	CCT3	2.05	chaperonin
orf19.5768	SNF4	2.05	nuclear protein
orf19.1261	CEG1	2.05	mRNA capping enzyme alpha subunit and guanylyltransferase
orf19.3967	PFK1	2.05	6-phosphofructokinase, alpha subunit
orf19.3775	SSK2	2.05	MAP kinase kinase kinase | Activator of Pbs2p
orf19.6862		2.04	conserved hypothetical protein
orf19.7618		2.03	conserved hypothetical protein
orf19.7109		2.03	ankyrin repeat protein
orf19.3055	SRB4	2.03	subunit of RNA polymerase II holoenzyme
orf19.4177	HIS5	2.03	histidinol-phosphate aminotransferase
orf19.6369	RIO2	2.03	conserved protein of unknown function
orf19.789	PYC2	2.03	pyruvate carboxylase
orf19.962		2.02	hypothetical protein
orf19.3076	TVP15	2.02	conserved hypothetical protein
orf19.156		2.01	hypothetical protein
orf19.7658	RFC4	2.01	DNA replication factor C
orf19.3244		2.01	conserved hypothetical protein
orf19.3846	LYS4	2.01	homoaconitase
orf19.6955	NOB1	2.01	Nin1 (One) Binding protein
orf19.2465		2.01	hypothetical protein
orf19.5710	NSP2	2.01	nuclear pore protein
orf19.364	VMA6	2.01	vacuolar ATPase
orf19.5753	STL1	2.01	sugar transporter
orf19.5812		2	conserved hypothetical protein
orf19.4940	HIP1	2	histidine permease

orf19.3129	**RVB1**	2	RUVB-like protein
orf19.5734	**POP2**	2	glucose derepression
orf19.5526	**SEC20**	2	secretory pathway protein
orf19.1791	**MAK11**	2	involved in cell growth and viral replication
orf19.3921	**FSH3**	2	dihydrofolate reductase
orf19.2135	**TAF2**	2	component of TFIID complex
orf19.494	**NAF1**	2	nuclear snoRNA binding and assembly factor
Down-regulated at 37°C			
orf19.2767		-20.48	hypothetical protein
orf19.7219	**FTR1**	-16.75	plasma membrane iron permease
orf19.2020	**HXT6**	-14.22	hexose transporter
orf19.2765		-12.28	hypothetical protein
orf19.6133	**PIF1**	-9.99	DNA helicase, mitochondrial
orf19.6814	**TDH3**	-9.72	GLYCERALDEHYDE 3- PHOSPHATE DEHYDROGENASE
orf19.1321	**HWP1**	-9.56	hyphal wall protein
orf19.2765		-9.43	hypothetical protein
orf19.1321	**HWP1**	-9.34	hyphal wall protein
orf19.1321	**HWP1**	-9.11	hyphal wall protein
orf19.5383	**PMA1**	-8.03	plasma membrane H+-ATPase
orf19.1353		-7.77	hypothetical protein
orf19.5741	**ALS1-1**	-7.43	agglutinin like protein 1
orf19.2355	**ALS2**	-7.35	agglutinin-like protein 2
orf19.3384	**RBT12**	-6.94	repressed by TUP1 protein 1
orf19.4885	**MIR1**	-6.38	mitochondrial phosphate transport protein
orf19.2766		-6.37	hypothetical protein
orf19.5960	**NCE102**	-5.97	non-classical protein export pathway
orf19.1097	**ALS4**	-5.79	agglutinin like protein 4
orf19.2023	**HXT3**	-5.54	hexose transporter
orf19.4216	**HSP122**	-5.5	heat shock protein
orf19.5117	**OLE1**	-5.45	stearoyl-CoA desaturase
orf19.2659		-5.39	conserved hypothetical protein
orf19.4618	**FBA1**	-5.31	fructose-bisphosphate aldolase

orf19.6375	**RPS20**	-5.2	ribosomal protein S20
orf19.4216	**HSP122**	-5.06	heat shock protein
orf19.6906	**ASC1**	-5.03	WD repeat protein that interacts with the translational machinery
orf19.1435	**TEF2**	-5.01	translational elongation factor EF- 1 alpha
orf19.5741	**ALS1-1**	-4.93	agglutinin like protein 1
orf19.5117	**OLE1**	-4.88	stearoyl-CoA desaturase
orf19.1715	**IRO1**	-4.88	transcription factor
orf19.566		-4.55	hypothetical protein
orf19.6785	**RPS12**	-4.41	acidic ribosomal protein S12
orf19.5119	**TEF1**	-4.39	elongation factor 1- alpha
orf19.657	**SAM2**	-4.39	S- adenosylmethionine synthetase
orf19.930	**PET9**	-4.35	ATP/ADP translocator
orf19.4215	**FET35**	-4.31	multicopper ferro-O2- oxidoreductase involved in high-affinity iron uptake
orf19.7217	**RPL4**	-4.16	ribosomal protein L4B
orf19.4309	**GRP3**	-4.13	induced by osmotic stress
orf19.4941	**TYE7**	-4.08	basic helix-loop-helix transcription factor
orf19.5927	**RPS15**	-4	ribosomal protein S15 (S21) (rp52) (RIG protein)
orf19.3997	**ADH1**	-4	alcohol dehydrogenase 1
orf19.2531	**CSP37**	-3.92	cell surface protein
orf19.2685		-3.88	hypothetical protein
orf19.5007	**ACT1**	-3.87	actin
orf19.2021	**HXT5**	-3.8	hexose transporter
orf19.6608		-3.79	transposase
orf19.2013	**KAR2**	-3.73	dnaK/HSP70/ BiP family ATPase and chaperone involved in translocation of nascent polypeptides across the ER membrane
orf19.7015	**RPP0**	-3.72	ribosomal protein P0 (A0) (L10E)
orf19.2478.1	**RPL7B**	-3.7	60S large subunit ribosomal protein
orf19.1601	**RPL3**	-3.67	60S large subunit ribosomal protein L3.e
orf19.236	**RPL9B**	-3.65	ribosomal protein L9B
orf19.4959		-3.62	hypothetical protein
orf19.2168		-3.61	hypothetical membrane protein
orf19.1868	**RNR3**	-3.6	small subunit of ribonucleotide reductase

orf19.4649		-3.56	zinc finger transcription factor
orf19.4765	**CCW12**	-3.55	cell wall mannoprotein
orf19.6403.1	**RPP2A**	-3.48	60S acidic ribosomal protein P2A (L44) (A2) (YP2alpha)
orf19.1770	**CYC1**	-3.43	cytochrome-c isoform 1
orf19.5982	**RPL18**	-3.42	ribosomal protein L18A (rp28A)
orf19.979	**FAS1**	-3.41	fatty-acyl-CoA synthase, beta chain
orf19.7030	**CCW14**	-3.38	cell wall mannoprotein | secretory Stress Response protein
orf19.7021	**GPH1**	-3.36	glycogen phosphorylase
orf19.493	**RPL15A**	-3.34	ribosomal protein L15B
orf19.2021	**HXT5**	-3.31	hexose transporter
orf19.6745	**TPI1**	-3.3	triose phosphate isomerase
orf19.1862		-3.28	conserved hypothetical protein
orf19.7610	**PTP3**	-3.27	protein tyrosine phosphatase
orf19.3911	**SAH1**	-3.27	S-adenosyl-L-homocysteine hydrolase
orf19.3149	**LSP1**	-3.27	Long chain base Stimulates Phosphorylation
orf19.395	**ENO1**	-3.25	enolase I
orf19.655	**PHO842**	-3.23	high-affinity inorganic phosphate/H+ symporter
orf19.1051	**HTA2**	-3.22	histone 2A
orf19.6873	**RPS8**	-3.21	ribosomal protein S8E
orf19.7606		-3.2	hypothetical protein
orf19.778	**PIL1**	-3.19	conserved protein
orf19.3354	**S4**	-3.18	40S ribosomal protein
orf19.2841	**PGM2**	-3.18	phosphoglucomutase
orf19.3575	**CDC19**	-3.16	pyruvate kinase
orf19.3475		-3.12	Gag protein
orf19.3642	**SUN4**	-3.11	beta-glucosidase
orf19.1206	**FET34**	-3.1	iron transport multicopper oxidase
orf19.3414	**SUR7**	-3.09	potential membrane protein
orf19.3074	**CTA2**	-3.08	hypothetical protein
orf19.6253	**RPS23**	-3.08	ribosomal protein S23A
orf19.7585	**INO1**	-3.06	myo-inositol-1- phosphate synthase
orf19.4490	**RPL17B**	-3.05	ribosomal protein L17B

orf19.5928	**RPP2B**	-3.04	acidic ribosomal protein P2B | ribosomal protein P2B (YP2beta) (L45)
orf19.6146	**CLG1**	-3.04	cyclin-like protein
orf19.227	**COX7**	-3.04	cytochrome-c oxidase, subunit VII
orf19.2551	**MET6**	-3.03	methionine-synthesizing 5- methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
orf19.493	**RPL15A**	-3	ribosomal protein L15B
orf19.6562	**RNH35**	-2.97	ribonuclease H
orf19.3334	**RPS2**	-2.95	ribosomal protein
orf19.6002	**RPL8B**	-2.94	ribosomal protein L8B (L4B) (rp6) (YL5)
orf19.1327	**RBT1**	-2.92	repressed by Tup1, related to HWP1
orf19.7481	**MDH2**	-2.89	malate dehydrogenase
orf19.2803	**HEM13**	-2.89	coprophyrinogen oxidase | heme biosynthesis
orf19.6253	**RPS23**	-2.88	ribosomal protein S23A
orf19.1470	**RPS26A**	-2.86	40S small subunit ribosomal protein S26A
orf19.4152	**EFT3**	-2.86	translation elongation factor
orf19.1052	**HTB2**	-2.84	histone 2B
orf19.251		-2.84	conserved hypothetical protein
orf19.5341	**RPS4**	-2.83	ribosomal protein S4
orf19.3895	**CHT2**	-2.83	chitinase 2 precursor
orf19.683	**ADK1**	-2.8	adenylate kinase
orf19.1340		-2.78	aldose reductase
orf19.646	**GLN1**	-2.75	glutamine synthetase
orf19.7502		-2.74	hypothetical protein
orf19.5293		-2.74	conserved hypothetical protein
orf19.6791	**HHT3**	-2.72	histone H3
orf19.2992	**RPA1**	-2.7	60S ribosomal protein
orf19.4456	**GAP4**	-2.69	amino acid permease
orf19.717	**HSP60**	-2.69	mitochondrial groEL-type heat shock protein
orf19.2644	**QCR2**	-2.68	ubiquinol--cytochrome-c reductase 40KD chain II
orf19.3335		-2.68	hypothetical protein
orf19.3038	**TPS2**	-2.66	threalose-6-phosphate phosphatase
orf19.2355	**ALS2**	-2.63	agglutinin-like protein 2

orf19.3215		-2.62	hypothetical protein
orf19.1738	**UGP1**	-2.6	UTP-glucose-1-phosphate uridylyltransferase
orf19.5741	**ALS1-1**	-2.6	agglutinin like protein 1
orf19.712	**KIP1**	-2.59	kinesin-related protein involved in mitotic spindle assembly
orf19.1738	**UGP1**	-2.57	UTP-glucose-1-phosphate uridylyltransferase
orf19.4848	**SKI3**	-2.56	antiviral protein with tetratricopeptide repeats
orf19.3700	**TOM70**	-2.56	mitochondrial outer membrane specialized import receptor
orf19.1618	**GFA1**	-2.56	glucoseamine-6- phosphate synthase
orf19.3156	**MEDA**	-2.55	developmental regulator medusa
orf19.7053	**GAC1**	-2.53	regulatory subunit for phosphoprotein phosphatase type 1 (PP-1)
orf19.903	**GPM1**	-2.51	phosphoglycerate mutase
orf19.2935	**RPL10**	-2.5	ribosomal protein L10
orf19.6472	**CPR1**	-2.5	peptidyl-prolyl cis-trans isomerase
orf19.5024	**GND1**	-2.48	6-phosphogluconate dehydrogenase
orf19.2778		-2.48	conserved hypothetical protein
orf19.3156	**MEDA**	-2.47	developmental regulator medusa
orf19.508	**QDR1**	-2.47	multidrug resistance transporter
orf19.1471	**COX4**	-2.46	cytochrome c oxidase subunit IV
orf19.5788	**EFT2**	-2.43	translation elongation factor 2 (EF-2)
orf19.922	**ERG11**	-2.43	cytochrome P450 lanosterol 14a-demethylase
orf19.1716	**URA3**	-2.42	orotidine-5'-phosphate decarboxylase
orf19.4980	**HSP70**	-2.42	heat shock protein 70
orf19.3599	**TIF4631**	-2.41	mRNA cap binding protein eIF 4F
orf19.236	**RPL9B**	-2.39	ribosomal protein L9B
orf19.4311	**YNK1**	-2.39	nucleoside diphosphate kinase
orf19.7514	**PCK1**	-2.37	phosphoenolpyruvate carboxykinase
orf19.1896	**SSC1**	-2.37	mitochondrial heat shock protein of the HSP70 family
orf19.85	**GPX1**	-2.37	glutathione peroxidase
orf19.7323	**CBP1**	-2.36	corticosteroid- binding protein
orf19.6663	**RPS25**	-2.36	ribosomal protein S25
orf19.2994	**RPL13**	-2.36	ribosomal protein
orf19.3651	**PGK1**	-2.36	phosphoglycerate kinase

orf19.1896	**SSC1**	-2.35	mitochondrial heat shock protein of the HSP70 family
orf19.5806	**ALD5**	-2.34	aldehyde dehydrogenase
orf19.915	**LRR**	-2.34	leucine rich repeat protein
orf19.2992	**RPA1**	-2.34	60S ribosomal protein
orf19.1172	**PHO84**	-2.34	inorganic phosphate permease
orf19.7239	**CRP1**	-2.33	regulation of G-protein function
orf19.1806		-2.32	hypothetical protein
orf19.6701		-2.31	proline-tRNA ligase
orf19.3618	**YWP1**	-2.31	putative cell wall protein
orf19.273		-2.31	conserved hypothetical protein
orf19.48	**RPM2**	-2.31	RNase P subunit
orf19.5949	**FAS2**	-2.3	fatty acid synthase alpha subunit
orf19.4118	**NNT1**	-2.29	concentrative Na+-nucleoside cotransporter
orf19.3010.1	**ECM33**	-2.29	3-prime end of ExtraCellular Mutant protein
orf19.5788	**EFT2**	-2.28	translation elongation factor 2 (EF-2)
orf19.815		-2.27	DOCK180 protein
orf19.1700	**RPS7A**	-2.27	ribosomal protein S7A
orf19.3590	**IPP1**	-2.27	inorganic pyrophosphatase
orf19.6604		-2.26	hypothetical protein
orf19.4660	**RPS6A**	-2.26	ribosomal protein S6A (S10A) (rp9) (YS4)
orf19.4737	**DHA12**	-2.26	membrane transporter of the MFS-MDR family
orf19.18	**IMD3**	-2.25	inosine-5'- monophosphate dehydrogenase | guanosine nucleotide biosynthesis
orf19.3554	**AAT1**	-2.25	aspartate aminotransferase
orf19.1613	**ILV2**	-2.25	acetolactate synthase
orf19.3599	**TIF4631**	-2.24	mRNA cap binding protein eIF 4F
orf19.646	**GLN1**	-2.24	glutamine synthetase
orf19.7417	**TSA1**	-2.22	thiol-specific antioxidant protein
orf19.3097	**PDA1**	-2.22	alpha subunit of pyruvate dehydrogenase
orf19.4646		-2.22	hypothetical protein
orf19.1152		-2.21	hypothetical protein
orf19.989	**MRPS5**	-2.21	mitochondrial ribosomal protein S5
orf19.238	**CCP1**	-2.2	cytochrome-c peroxidase

orf19.913.2	**QCR6**	-2.2	ubiquinol-cytochrome c oxidoreductase subunit 6
orf19.1779	**SCW10**	-2.2	soluble cell wall protein similar to mannoprotein MP65
orf19.5544	**SAC6**	-2.19	actin filament bundling protein - fibrim homolog
orf19.3426	**HYP2**	-2.18	translation initiation factor eIF5A.1
orf19.6197	**DHH1**	-2.17	RNA helicase of DEAD box family
orf19.6529	**CDC34**	-2.16	ubiquitin-conjugating enzyme
orf19.1378	**ERF3**	-2.15	translation release factor 3
orf19.4784	**CRD1**	-2.15	copper-transporting P1-type ATPase
orf19.1591	**ERG10**	-2.15	acetyl-CoA acetyltransferase | acetoacetyl CoA thiolase
orf19.4262	**JSN1**	-2.14	tubulin mutant, benomyl dependent
orf19.7247	**RIM101**	-2.13	Zn finger transcription factor | regulator of pH response
orf19.4632	**RPL20B**	-2.13	ribosomal protein L20
orf19.3268		-2.12	translationally controlled tumor protein
orf19.1635	**RPL12**	-2.12	large subunit ribosomal protein L12.e
orf19.1743	**ACS1**	-2.12	acetyl-coenzyme A synthetase
orf19.1331	**HSM3**	-2.11	MutS family (putative) | mismatch repair
orf19.150	**TIM17**	-2.11	mitochondrial inner membrane import translocase subunit
orf19.3599	**TIF4631**	-2.11	mRNA cap binding protein eIF 4F
orf19.3603		-2.11	conserved hypothetical protein
orf19.178		-2.11	hypothetical protein
orf19.7483	**CRM1**	-2.1	nuclear export factor
orf19.1442	**PLB4**	-2.1	phospholipase B (lysophospholipase)
orf19.3997	**ADH1**	-2.1	alcohol dehydrogenase 1
orf19.5351	**TIF11**	-2.09	translation initiation factor eIF1A
orf19.7239	**CRP1**	-2.09	regulation of G-protein function
orf19.7550		-2.09	ORF MSV011 leucine rich repeat gene family protein
orf19.736	**SRB8**	-2.09	subunit of activation mediator subcomplex of RNA polymerase II holoenzyme
orf19.1048	**IFD1**	-2.09	conserved aryl-alcohol dehydrogenase
orf19.3219		-2.08	phosphohydrolase
orf19.2241	**PST1**	-2.08	1,4-benzoquinone reductase | brefeldin A resistance protein | Protoplast-SecreTed protein
orf19.1433		-2.08	predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold
orf19.7214		-2.07	glucan 1,3-beta-glucosidase

orf19.5233		-2.07	hypothetical protein
orf19.147	**YAK2**	-2.07	serine-threonine protein kinase, PKA suppressor
orf19.1853	**HHT2**	-2.07	histone H3
orf19.3475		-2.07	Gag protein
orf19.409		-2.07	conserved hypothetical protein
orf19.4607		-2.07	conserved hypothetical protein
orf19.1742	**HEM3**	-2.07	phorphobilinogen deaminase (uroporphyrinogen synthase) | heme biosynthesis
orf19.6420		-2.06	hypothetical membrane protein with repeated hydrophobic/hydrophilic domains
orf19.5113	**ADH2**	-2.06	alcohol dehydrogenase
orf19.4317	**GRE3**	-2.06	aldose reductase
orf19.5949	**FAS2**	-2.05	fatty acid synthase alpha subunit
orf19.6112	**CTA2**	-2.05	putative transcriptional activator
orf19.4772	**SHO1**	-2.04	transmembrane osmosensor | involved in the HOG1 high-osmolarity signal transduction pathway
orf19.3599	**TIF4631**	-2.04	mRNA cap binding protein eIF 4F
orf19.3618	**YWP1**	-2.04	putative cell wall protein
orf19.7231	**FTR2**	-2.03	plasma membrane iron permease
orf19.7188	**RP1B**	-2.02	60S large subunit acidic ribosomal protein a1
orf19.6197	**DHH1**	-2.02	RNA helicase of DEAD box family
orf19.911	**TOM12**	-2.02	E3 ubiqitin ligase required for G2/M transition
orf19.3599	**TIF4631**	-2.02	mRNA cap binding protein eIF 4F
orf19.4211	**FET3**	-2.02	multicopper ferro-O2- oxidoreductase involved in high-affinity iron uptake
Up-regulated at 37°C			
orf19.2672	**NCP1**	18.7	NADPH-cytochrome P450 reductase
orf19.3812	**SSZ1**	16.63	regulator protein involved in pleiotropic drug resistance that forms a ribosome-associated complex | DnaJ/HSP70 chaperone
orf19.6540	**PFK2**	11.99	PFK2
orf19.3810	**MTD1**	9.78	methylenetetrahydrofolate dehydrogenase | NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase | NAD-dependent 5,10- methylenetetrahydrafolate dehydrogenase | methylenetetrahydrofolate dehydrogenase (NAD+)
orf19.1263	**FRE1**	9.72	ferric reductase
orf19.6548	**ISU1**	9.34	iron-sulfur cluster nifU-like
orf19.4181	**SPC2**	8.22	subunit of signal peptidase complex

orf19.3117	**CSA2**	7.42	mycelial surface antigen, similar to RBT5
orf19.3117	**CSA2**	7.37	mycelial surface antigen, similar to RBT5
orf19.3448		6.76	hypothetical protein
orf19.4203	**NDC1**	6.03	nuclear envelope protein
orf19.3710	**YHB3**	5.79	flavohemoglobin | dihydropteridine reductase
orf19.3817	**RTS2**	5.59	similar to mouse KIN7 protein
orf19.2676	**IKI1**	5.53	RNA polymerase II elongator associated protein
orf19.2678	**BUB1**	5.34	ser/thr protein kinase in mitosis checkpoint
orf19.3893	**SCW11**	4.81	Soluble Cell Wall protein
orf19.1562		4.73	hypothetical protein
orf19.5635	**RBT6**	4.64	glycosyl- phosphatidylinositol protein | similar to RBT5
orf19.5634	**FRP1**	4.51	ferric reductase
orf19.6837		4.38	benzil reductase
orf19.6321		4.21	hypothetical protein
orf19.4910		4.1	hypothetical protein
orf19.3396	**HCH1**	3.9	high copy Hsp90 supressor
orf19.3438	**SCJ1**	3.67	dnaJ homolog in endoplasmic reticulum
orf19.5139		3.57	hypothetical protein
orf19.3127	**CZF1**	3.57	zinc finger protein
orf19.6073	**HMX1**	3.56	heme binding protein
orf19.4210		3.54	epoxide hydrolase
orf19.7504		3.5	conserved hypothetical protein
orf19.1418	**SEC15**	3.49	exocyst complex component
orf19.4183		3.4	Pro/Ser-rich protein
orf19.6192		3.39	hypothetical protein
orf19.3815	**UBP7**	3.32	ubiquitin-specific protease
orf19.3505	**LIT1**	3.32	putative transcription factor
orf19.4208	**RAD52**	3.27	recombination and DNA repair protein
orf19.5597	**POL5**	3.21	DNA polymerase V, 5-prime end
orf19.1797		3.19	conserved hypothetical protein
orf19.3753	**SEF1**	3.17	zinc finger transcription factor
orf19.6506		3.16	conserved hypothetical protein

orf19.4180	**SEC72**	3.14	signal recognition particle receptor involved in membrane protein insertion into the ER
orf19.6840		3.12	hypothetical protein
orf19.2909	**ERG26**	3.12	C-3 sterol dehydrogenase
orf19.3809	**BAS1**	3.11	transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
orf19.747	**NBP35**	3.08	nuclear ATPase
orf19.2107	**MUQ1**	3.05	choline phosphate cytidylyltransferase | phosphoethanolamine cytidylyltransferase
orf19.6522		3.02	allantoate permease
orf19.2038		2.97	hypotheticalprotein
orf19.5299	**ECM1**	2.94	cell wall structure or biosynthesis
orf19.2768	**AMS1**	2.92	vacuolar alpha mannosidase
orf19.6818		2.91	RNA helicase
orf19.42		2.87	transport protein
orf19.5952		2.84	hypothetical protein
orf19.4676		2.82	conserved hypothetical protein
orf19.7285		2.81	conserved hypothetical protein
orf19.6077		2.81	conserved hypothetical protein
orf19.2146	**HAT2**	2.81	histone acetyltransferase subunit
orf19.5296		2.81	conserved hypothetical protein
orf19.4163		2.79	conserved hypothetical protein
orf19.1323	**APL6**	2.79	clathrin assembly complex beta adaptin component
orf19.2135	**TAF2**	2.79	component of TFIID complex
orf19.2320	**RIO1**	2.77	protein serine kinase
orf19.2337	**ALP1**	2.73	high-affinity permease for basic amino acids
orf19.4683	**MLP1**	2.73	myosin-like protein involved in translocation of macromolecules between the nucleoplasm and the NPC
orf19.1234		2.73	hypothetical protein
orf19.1186		2.73	hypothetical protein
orf19.7286	**RPN7**	2.68	subunit of the regulatory particle of the proteasome
orf19.62		2.68	zinc aminopeptidase
orf19.7085		2.63	hypothetical protein
orf19.5710	**NSP2**	2.62	nuclear pore protein

orf19.5630	**APA2**	2.58	ATP adenylyltransferase II
orf19.2667	**RPF1**	2.57	nucleolar protein involved in rRNA processing
orf19.1254	**SEC23**	2.56	component of COPII coat of ER- golgi vesicles
orf19.3578		2.54	hypothetical protein
orf19.5804	**HYU1**	2.53	5-oxoprolinase | hydantoin utilization protein A
orf19.1294		2.52	coiled coil protein similar to myosin
orf19.4145	**HAP1**	2.52	zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
orf19.1185		2.51	conserved hypothetical protein
orf19.3055	**SRB4**	2.5	subunit of RNA polymerase II holoenzyme
orf19.6163	**CSE4**	2.5	histone H3 variant
orf19.1191	**HRD3**	2.49	responsible for ER-associated degradation (ERAD) of numerous ER-resident proteins
orf19.2889	**IES6**	2.47	conserved hypothetical protein
orf19.1265	**TRS130**	2.47	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic
orf19.6840		2.46	hypothetical protein
orf19.3462	**SAR1**	2.46	GTP-binding protein of the ARF family | component of COPII coat of vesicles | required for ER to Golgi protein transport
orf19.3066	**ACF3**	2.45	endo-1,3-beta-glucanase
orf19.3818		2.44	hypothetical protein
orf19.3130		2.43	highly conserved hypothetical protein
orf19.2182	**BLM3**	2.42	integral membrane protein possibly involved in bleomycin resistance
orf19.3401	**VPS60**	2.42	involved in vacuolar protein sorting
orf19.7218	**PRY2**	2.41	homology to plant PR-1 class of proteins
orf19.6544	**MHP1**	2.4	microtubule-interacting protein
orf19.3344	**VPS17**	2.38	vacuolar sorting protein
orf19.3659		2.38	conserved hypothetical protein
orf19.3811	**GYP1**	2.37	GTPase activating protein
orf19.2983	**CDC73**	2.37	accessory factor associated with RNA polymerase II
orf19.2771	**BEM3**	2.36	rho GTPase activating protein (GAP)
orf19.2180		2.35	calcium-binding protein
orf19.5730		2.35	3-polyprenyl-4-hydroxybenzoate decarboxylase
orf19.4167		2.35	hypothetical protein
orf19.7265	**SAD1**	2.34	snRNP assembly defective

orf19.4191	**RLP24**	2.34	similar to ribosomal protein L24.e.B
orf19.2875		2.33	hypothetical protein, possibly related to DNAJ
orf19.5732	**NOG2**	2.32	nuclear/nucleolar GTP-binding protein 2
orf19.1792	**CDC16**	2.32	subunit of anaphase-promoting complex (cyclosome)
orf19.3123	**RPT5**	2.31	26S proteasome regulatory subunit
orf19.4079	**SLP2**	2.31	potential SPFH domain | possible regulator of cation conductance
orf19.5658	**MNN10**	2.3	galactosyltransferase
orf19.5595	**SHE3**	2.3	mother-specific HO expression
orf19.5584	**PEP3**	2.3	vacuolar membrane protein
orf19.2886	**CEK1**	2.3	MAP kinase involved in pheromone signal transduction
orf19.7101	**TEL2**	2.29	involved in controlling telomere length
orf19.2964	**RSC1**	2.29	Member of RSC complex, which remodels the structure of chromatin
orf19.3457		2.29	WD domain protein likely involved in chromatin remodeling
orf19.2465		2.28	hypothetical protein
orf19.1437		2.28	conserved hypothetical protein
orf19.1667	**RAD15**	2.27	DNA-dependent ATPase of the nucleotide excision repair factor 4 complex
orf19.5783		2.27	conserved hypothetical protein
orf19.7295	**SCD5**	2.26	multicopy suppressor of clathrin deficiency
orf19.3678		2.26	hypothetical protein
orf19.4201	**NHX1**	2.26	NA+/H+ antiporter
orf19.2143		2.25	conserved hypothetical protein
orf19.1290	**XKS2**	2.24	xylulokinase
orf19.7602		2.23	conserved hypothetical protein
orf19.4591	**CAT2**	2.23	carnitine acetyltransferase
orf19.5666	**SUB1**	2.23	transcriptional coactivator
orf19.4167		2.23	hypothetical protein
orf19.3132	**MSC2**	2.23	transmembrane cation antiporter involved in zinc ion homeostatis and meiotic recombination
orf19.2774	**LIP12**	2.22	lipoic acid synthase
orf19.2970	**LYS2**	2.22	L-aminoadipate-semialdehyde dehydrogenase, large subunit
orf19.2739	**RLF2**	2.22	chromatin assembly complex, subunit p90
orf19.2731		2.22	hypothetical protein
orf19.4373	**FMN1**	2.22	riboflavin kinase

orf19.1259	**SNT2**	2.21	conserved hypothetical protein
orf19.2131	**TUL1**	2.21	transmembrane ubiquitin ligase
orf19.6692	**MNN7**	2.2	alpha-1,2- mannosyltransferase
orf19.4230	**PRE4**	2.2	B-type subunit of proteasome
orf19.401	**TCP1**	2.2	component of chaperonin-containing T-complex
orf19.2671	**NDI1**	2.2	NADH dehydrogenase
orf19.538	**GPI2**	2.19	N-acetylglucosaminyl-phosphatidylinositol (GPI) biosynthetic protein
orf19.2039	**MSF1**	2.19	phenylalanyl-tRNA synthetase alpha subunit, mitochondrial
orf19.5765	**NUP82**	2.19	nuclear pore protein
orf19.100	**LIP11**	2.19	triacylglycerol lipase
orf19.1324	**RAD2**	2.18	structure-specific nuclease of the nucleotide excision repairosome
orf19.789	**PYC2**	2.18	pyruvate carboxylase
orf19.7328	**CAP100**	2.17	Candida albicans p100 homolog
orf19.6861	**APC5**	2.17	anaphase-promoting complex
orf19.5171	**PMT1**	2.16	mannosyltransferase
orf19.6584	**PRT1**	2.15	translation initiation factor eIF3 subunit
orf19.5676		2.15	conserved hypothetical protein
orf19.5772		2.15	actin overexpression resistant
orf19.4603	**ARL1**	2.14	GTP-binding protein of the ARF family | ADP-ribosylation factor
orf19.6359	**SOM1**	2.14	peptidase of the protein sorting machinery
orf19.2684	**SLK192**	2.14	conserved coiled-coil protein
orf19.101	**RIM9**	2.14	low similarity to a regulator of sporulation
orf19.7583		2.13	potential fungal Zn(2)-Cys(6) binuclear cluster domain
orf19.3091		2.13	hypothetical protein
orf19.2605	**ARK1**	2.13	serine/threonine protein kinase involved in regulation of actin cytoskeleton organization
orf19.1180		2.12	conserved hypothetical protein
orf19.539	**LAP3**	2.12	DNA-binding cysteine-type protease; bleomycin hydrolase
orf19.5106	**DIP2**	2.11	beta transducin
orf19.2417	**SMC5**	2.11	structural maintenance of chromosomes protein
orf19.5640	**PEX5**	2.11	peroxisomal protein receptor
orf19.1336	**PUP3**	2.11	20S proteasome subunit beta3
orf19.3646	**CTR1**	2.11	copper transport protein

orf19.1440		2.11	hypothetical protein
orf19.5370		2.1	conserved hypothetical protein
orf19.3040	**EHT1**	2.1	alcohol acyl transferase
orf19.5725		2.1	hypothetical protein
orf19.133		2.1	hypothetical protein
orf19.2770		2.09	hypothetical protein
orf19.5830	**LHS1**	2.09	translocation of protein precursors across ER | Hsp70 family chaperone
orf19.3442	**OYE3**	2.08	NADPH dehydrogenase
orf19.5768	**SNF4**	2.08	nuclear protein
orf19.3428	**IOC4**	2.08	chromatin component
orf19.2411	**SYN8**	2.08	SNARE protein releated to mammalian syntaxin
orf19.6965	**MRS107**	2.08	hypothetical protein
orf19.1301		2.08	hypothetical protein
orf19.2244		2.08	aldo/keto reductase
orf19.6417	**TSR1**	2.07	conserved protein possibly involved in ribosome biogenesis
orf19.3415	**PTK2**	2.07	putative serine/threonine protein kinase
orf19.4930	**SPC3**	2.07	signal peptidase subunit
orf19.6357	**MAD1**	2.07	coiled-coil protein involved in the spindle-assembly checkpoint
orf19.6183	**TIM8**	2.07	mitochondrial protein import machinery subunit
orf19.4792		2.07	hypothetical protein
orf19.992		2.06	putative aminopeptidase
orf19.1260	**LEA1**	2.06	similar to human U2AsnRNP protein
orf19.6136	**MRPL4**	2.06	mitochondrial ribosome protein L4
orf19.2301	**NAS2**	2.06	putative proteasome modulator
orf19.2737		2.06	kinase
orf19.687		2.06	hypothetical protein
orf19.3658		2.06	conserved hypothetical protein
orf19.7332	**ELF1**	2.05	elongation-like factor
orf19.3021		2.05	hypothetical protein
orf19.3126	**CCT6**	2.05	cytoplasmic chaperonin of the Cct ring complex
orf19.6630		2.05	membrane protein confirmed by cDNA cloning
orf19.3449		2.05	highly conserved hypothetical protein

orf19.5599	**MDL2**	2.05	ATP-binding transporter, 3- prime end
orf19.1796		2.05	similar to glycerate dehydrogenases
orf19.714	**YPT6**	2.05	GTP binding protein involved in vesicle fusion in the secretory pathway
orf19.5723	**POX2**	2.05	acyl-coenzyme A oxidase
orf19.559		2.05	reverse transcriptase
orf19.3387	**RRT**	2.05	reverse transcriptase
orf19.1814	**STT4**	2.05	phosphatidylinositol-4- kinase involved in protein kinase C pathway
orf19.7321		2.04	conserved hypothetical protein
orf19.3103	**RPO31**	2.04	RNA polymerase III large subunit
orf19.4683	**MLP1**	2.04	myosin-like protein involved in translocation of macromolecules between the nucleoplasm and the NPC
orf19.1560	**POB3**	2.04	DNA polymerase delta binding protein
orf19.1419	**SEC15**	2.04	exocyst complex component
orf19.593	**SWA2**	2.04	auxilin-like clathrin-binding protein required for normal clathrin function
orf19.6326		2.04	hypothetical protein
orf19.2690	**MGM1**	2.04	mitochondrial dynamin-like GTP-ase
orf19.2611	**MCM6**	2.04	involved in replication
orf19.5440		2.03	26S proteasome subunit
orf19.7335	**PRE8**	2.03	20S proteasome subunit Y7
orf19.4625	**TOA2**	2.03	transcription factor IIA, small chain
orf19.5164	**ECM39**	2.03	alpha-1,6- mannosyltransferase
orf19.5771	**PBP2**	2.03	PAB1 binding protein
orf19.3129	**RVB1**	2.03	RUVB-like protein
orf19.6345	**RPG1**	2.03	translation initiation factor eIF3
orf19.1261	**CEG1**	2.03	mRNA capping enzyme alpha subunit and guanylyltransferase
orf19.3402		2.03	conserved hypothetical protein
orf19.745	**VAC8**	2.03	vacuole memebrane protein required for vacuole inheritance
orf19.3787	**KAE1**	2.03	glycoprotease | kinase-associated endopeptidase
orf19.1249	**HIS6**	2.02	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
orf19.7313	**SSU1**	2.01	sulfite sensitivity protein
orf19.6864		2.01	conserved hypothetical protein
orf19.2769		2.01	hypothetical protein

orf19.2484		2.01	highly conserved hypothetical protein
orf19.3128	**SLY1**	2.01	t-SNARE- interacting protein that functions in ER-to-Golgi traffic
orf19.6177		2.01	hypothetical protein
orf19.2128	**YLF2**	2.01	putative GTP-binding protein
orf19.1578	**RRP5**	2.01	processing of pre-rRNA to 18S and 5.8S rRNA
orf19.1584	**MCH**	2.01	similarity to monocarboxylate transporters
orf19.1514	**UBP1**	2.01	ubiquitin-dependent protease
orf19.1195	**OCT1**	2.01	mitochondrial intermediate peptidase involved in protein import
orf19.2081	**POM152**	2	nuclear pore membrane glycoprotein
orf19.1893		2	hypothetical protein
orf19.3737		2	hypothetical membrane protein
orf19.1396	**AGE2**	2	zinc finger protein | putative GTPase actiovating protein
orf19.5734	**POP2**	2	glucose derepression
orf19.2873	**TOP2**	2	DNA topoisomerase II
orf19.4184	**YAP180**	2	clathrin coat assembly protein

Table S2. Number of differentially expressed genes

Temperature	25°C				37°C			
Differentially expressed genes	Up		Down		Up		Down	
	Annotated	HP	Annotated	HP	Annotated	HP	Annotated	HP
	161	67	113	36	164	79	195	41
Total	228		149		243		236	

Table S3. Down-regulated cAMP-responsive genes at both 25°C and 37°C

Gene name	**Gene function**
AAT1	aspartate aminotransferase
ADH1	alcohol dehydrogenase 1
ADH2	alcohol dehydrogenase
ALS1-1	agglutinin like protein 1
CCP1	cytochrome-c peroxidase
CCW12	cell wall mannoprotein
CRP1	regulation of G-protein function
CSP37	cell surface protein
CYC1	cytochrome-c isoform 1
DHA12	membrane transporter of the MFS-MDR family
DHH1	RNA helicase of DEAD box family
ECM33	3-prime end of ExtraCellular Mutant protein
ERF3	translation release factor 3
FAS1	fatty-acyl-CoA synthase, beta chain
FAS2	fatty acid synthase alpha subunit
FET3	multicopper ferro-O2- oxidoreductase involved in high-affinity iron uptake
FTR1	plasma membrane iron permease
GAC1	regulatory subunit for phosphoprotein phosphatase type 1 (PP-1)
GFA1	glucoseamine-6- phosphate synthase
GLN1	glutamine synthetase
GPH1	glycogen phosphorylase
GPX1	glutathione peroxidase
GRP3	induced by osmotic stress
HSP60	mitochondrial groEL-type heat shock protein
IRO1	transcription factor
JSN1	tubulin mutant, benomyl dependent
LSP1	Long chain base Stimulates Phosphorylation
MDH2	malate dehydrogenase
MET6	methionine-synthesizing 5- methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
MIR1	mitochondrial phosphate transport protein
NCE102	non-classical protein export pathway
OLE1	stearoyl-CoA desaturase
PGM2	phosphoglucomutase

PHO84	inorganic phosphate permease
PHO842	high-affinity inorganic phosphate/H+ symporter
PLB4	phospholipase B (lysophospholipase)
PMA1	plasma membrane H+-ATPase
PTP3	protein tyrosine phoisphatase
QCR2	ubiquinol--cytochrome-c reductase 40KD chain II
QDR1	multidrug resistance transporter
RPA1	60S ribosomal protein
RPL8B	ribosomal protein L8B (L4B) (rp6) (YL5)
RPM2	RNase P subunit
SAH1	S-adenosyl-L-homocysteine hydrolase
SAM2	S- adenosylmethionine synthetase
SUR7	potential membrane protein
TIF4631	mRNA cap binding protein eIF 4F
TOM70	mitochondrial outer membrane specialized import receptor
URA3	orotidine-5'-phosphate decarboxylase
YAK2	serine-threonine protein kinase, PKA suppressor
YWP1	putative cell wall protein

Table S4. Up-regulated cAMP-responsive genes at both 25°C and 37°C

Gene	**Gene function**
BAS1	transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
BUB1	ser/thr protein kinase in mitosis checkpoint
CCT6	cytoplasmic chaperonin of the Cct ring complex
CEG1	mRNA capping enzyme alpha subunit and guanylyltransferase
CZF1	zinc finger protein
DIP2	beta transducin
ECM1	cell wall structure or biosynthesis
ERG26	C-3 sterol dehydrogenase
FRP1	ferric reductase
HAT2	histone acetyltransferase subunit
HCH1	high copy Hsp90 supressor
HIS6	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
HMX1	heme binding protein
IES6	conserved hypothetical protein
IKI1	RNA polymerase II elongator associated protein
ISU1	iron-sulfur cluster nifU-like
LIP12	lipoic acid synthase
LIT1	putative transcription factor
MAD1	coiled-coil protein involved in the spindle-assembly checkpoint
MNN10	galactosyltransferase
MTD1	methylenetetrahydrofolate dehydrogenase | NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase | NAD-dependent 5,10- methylenetetrahydrafolate dehydrogenase | methylenetetrahydrofolate dehydrogenase (NAD+)
MUQ1	choline phosphate cytidylyltransferase | phosphoethanolamine cytidylyltransferase
NCP1	NADPH-cytochrome P450 reductase
NDC1	nuclear envelope protein
NOG2	nuclear/nucleolar GTP-binding protein 2
NSP2	nuclear pore protein
NUP82	nuclear pore protein

PFK2	6-phosphofructokinase, alpha subunit
POL5	DNA polymerase V, 5-prime end
POP2	glucose derepression
PTK2	putative serine/threonine protein kinase
PYC2	pyruvate carboxylase
RIO1	protein serine kinase
RLP24	similar to ribosomal protein L24.e.B
RPF1	nucleolar protein involved in rRNA processing
RPN7	subunit of the regulatory particle of the proteasome
RPO31	RNA polymerase III large subunit
RPT5	26S proteasome regulatory subunit
RTS2	similar to mouse KIN7 protein
RVB1	RUVB-like protein
SAD1	snRNP assembly defective
SLP2	potential SPFH domain | possible regulator of cation conductance
SLY1	t-SNARE- interacting protein that functions in ER-to-Golgi traffic
SNF4	nuclear protein
SPC2	subunit of signal peptidase complex
SRB4	subunit of RNA polymerase II holoenzyme
SSZ1	regulator protein involved in pleiotropic drug resistance that forms a ribosome-associated complex | DnaJ/HSP70 chaperone
SUB1	transcriptional coactivator
TAF2	component of TFIID complex
TOP2	DNA topoisomerase II
TRS130	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic
TUL1	transmembrane ubiquitin ligase
VPS60	involved in vacuolar protein sorting

Table S5. Common differentially transcribed genes in *pde2* mutants of *S. cerevisiae* and *C. albicans*

Genes with identical differential transcription pattern*		**Genes with opposite differential transcription pattern***	
C.albicans* at 25°C and *S. cerevisiae			
Up	**Down**	**Up *Candida* Down *Saccharomyces***	**Down *Candida* Up *Saccharomyces***
MRPL25	*YOR1*	*STL1*	*PDR16*
LIP12	*ENA5*		*ADO1*
RPN7	***FAS1***		***MIR1***
MTD1	***GPH1***		***URA3***
LCP5	***FAS2***		***GLN1***
CYS3	*MLS1*		***RPL8B***
YKR087C	***PGM2***		***YLR110C***
PRS4	*PIM1*		***YDR134C***
YNL119W	*MPT5*		***RPA1***
RPL18	*PDE2*		
RPS3	*PMT2*		
SAM4			
ISU1			
CSH3			
TYR1			
CBP3			
LOC1			
C.albicans* 37°C and *S. cerevisiae			
LIP12	***GPH1***	*YOR161C*	*RPL17B*
RPN7	***FAS1***	*STT4*	*ENO1*
MTD1	***FAS2***	*ACF3*	*RPL3*
CEK1	***PGM2***	*AMS1*	*PET9*
TIM8	*EFT2*		*HYP2*
CTR1	*TPS2*		*RPS23*
ISU1	*ACS1*		*RPS12*
SAR1	*HSP122*		*TPI1*
SYN8			*COX4*
			RPS26A
			TIM17
			YKL056C
			MIR1
			RPL9B
			RPS6A
			RPS25
			GPM1
			URA3
			RPP2B
			ASC1
			RPS15
			GLN1
			CDC19
			RPS20
			ERG10
			FBA1
			RPL10
			RPS8
			TEF1
			RPL8B

			HTA2
			RPS2
			RPL18
			RPS7A
			YLR110C
			YDR134C
			RPA1
			TDH3
			RPL12
			RPL13

*The genes shown in bold are common to both 25°C and 37°C C.albicans data sets, which we refer to cAMP-responsive genes

Supplementary Table S6. Comparative analysis of differentially expressed genes upon deletion of *PDE2* (our data) and *CDC35*, *EFG1* and *RAS1* (Harcus *et al*., 2004).

pde2 up Harcus up *	*pde2* down Harcus down *	*pde2* up Harcus down *	*pde2* down Harcus up *
Candida* at 25°C versus *cdc35			
HAT2	*DED1*	*ADH6*	***CCP1***
VMA6	*IFE2*	*CCT3*	***CSP37***
orf19.1234	***MIR1***	*CIC1*	***DHA12***
orf19.2030	*PHO87*	*CYS3*	***GPH1***
	PIM1	*HIS4*	***GRP3***
	RPA1	*HIS5*	*MLS1*
		KEL3	***NCE102***
		LOC1	***PLB4***
		LYS4	*SLK19*
		MAK21	***SUR7***
		MAK5	orf19.2170
		MTD1	**orf19.2765**
		NUG1	orf19.3793
		PFK1	**orf19.6420**
		PFK2	orf19.6983
		PRS4	**orf19.7502**
		RNH1	
		RPF1	
		RPL18	
		RPS3	
		SDA1	
		SDH3	
		SUI2	
		TRP5	
		YMC1	
		orf19.3089	
		orf19.3115	
		orf19.5066	
		orf19.6710	
		orf19.6718	
		orf19.6730	
		orf19.7601	
		orf19.962	
Candida* at 37°C versus *cdc35			
CAT2	*ASC1*	*EHT1*	*ACS1*
CTR1	*CHT2*	*ELF1*	*ALD5*
HAT2	*EFT3*	*FMN1*	***CCP1***
HYU1	*FTR2*	*MRPL4*	*CCW14*
RBT6	*HXT3*	***MTD1***	*CLG1*
orf19.1234	*HYP2*	***PFK2***	***CSP37***
orf19.2769	***MIR1***	***RPF1***	***DHA12***
	MRPS5	*YHB3*	***GPH1***
	RPA1	orf19.1301	*GRE3*

	RPL13	orf19.7602	***GRP3***
	RPL15A		*IFD1*
	RPL18		***NCE102***
	RPL20B		*PIL1*
	RPL9B		***PLB4***
	RPS12		*PST1*
	RPS15		*SCW10*
	RPS6A		*SHO1*
	RPS7A		***SUR7***
	TYE7		orf19.1152
	YNK1		orf19.2685
	orf19.1340		**orf19.2765**
			orf19.6420
			orf19.6604
			orf19.7214
			orf19.7502
Candida **at 25°C versus** ***efg1***			
ISU1	***ADH1***	*PFK1*	*FUN34*
RNH2	***CCP1***	***PFK2***	*RHD3*
	CSP37		
	DHA12		
	ERG252		
	FCR1		
	GPH1		
	IFE2		
	QDR1		
	TIS11		
	YWP1		
	orf19.1353		
	orf19.1862		
	orf19.2659		
Candida **at 37°C versus** ***efg1***			
CAT2	***ADH1***	*EHT1*	orf19.2685
ISU1	***CCP1***	***PFK2***	orf19.4607
YHB3	*CDC19*	orf19.7085	
	CSP37		
	DHA12		
	FBA1		
	GPH1		
	HEM13		
	HXT3		
	HXT6		
	PGK1		
	QDR1		
	TPI1		
	TPS2		
	YWP1		
	orf19.1353		
	orf19.1862		
	orf19.2659		
Candida **at 25°C versus** ***ras1***			
DDI1	*PHO87*	*MAK21*	***DHA12***
RPB3	*DED1*	*NOP16*	***GPH1***
VMA6	*NIP1*		***GRP3***
orf19.2030	*ERG252*		***PLB4***
orf19.4183	*RHD3*		***SUR7***
	TIS11		***YWP1***

			orf19.2765
			orf19.3793
			orf19.6983
Candida* at 37°C versus *ras1			
CAT2	*RPL9B*		***GPH1***
orf19.2769			*CCW14*
orf19.4183			***DHA12***
			GRP3
			HSP70
			IFD1
			PLB4
			SCW10
			SUR7
			YWP1
			orf19.1152
			orf19.2765

*The genes shown in bold are common to both 25°C and 37°C *C.albicans* data sets, which we refer to cAMP-responsive genes

Table S7. Differentially regulated genes involved in protein degradation, modification, folding, fate and targeting

25°C		**37°C**	
Gene name	**Function**	**Gene name**	**Function**
Protein degradation			
AOS1	protein-sumoylation function	***APC5***	anaphase-promoting complex
CDC48	microsomal ATPase	***CDC16***	subunit of anaphase-promoting complex (cyclosome)
PUP1	20S proteasome beta 2 subunit	***CDC34***	ubiquitin-conjugating enzyme
RPN7	subunit of the regulatory particle of the proteasome	***LAP3***	DNA-binding cysteine-type protease; bleomycin hydrolase
RPT3	26S proteasome regulatory subunit	***NAS2***	putative proteasome modulator
SGT1	subunit of SCF ubiquitin ligase complex	***PRE4***	B-type subunit of proteasome
		PRE8	20S proteasome subunit Y7
		PUP3	20S proteasome subunit beta3
		RPT5	26S proteasome regulatory subunit
		UBP1	ubiquitin-dependent protease
		UBP7	ubiquitin-specific protease
Protein fate			
AOS1	protein-sumoylation function	***APC5***	anaphase-promoting complex
CBP3	involved in cytochrome-c reductase assembly	***ARL1***	GTP-binding protein
CCT6	cytoplasmic chaperonin of the Cct ring complex	***CDC16***	subunit of anaphase-promoting complex (cyclosome)

CDC48	microsomal ATPase	***CDC34***	ubiquitin-conjugating enzyme
FAS2	fatty-acyl-CoA synthase, beta chain	***CPR1***	regulation of G-protein function
HSP60	mitochondrial groEL-type heat shock protein	***FAS2***	fatty-acyl-CoA synthase, beta chain
MNN10	galactosyltransferase	***HAT2***	histone acetyltransferase subunit
PEX10	peroxisomal biogenesis protein	***HRD3***	responsible for ER-associated degradation (ERAD) of ER-resident proteins
PIM1	mitochondrial ATP-dependent protease	***HSP60***	mitochondrial groEL-type heat shock protein
PMT2	dolichyl-P-mannose-protein mannosyltransferase	***KAE1***	glycoprotease | kinase-associated endopeptidase
PUP1	20S proteasome beta 2 subunit	***KAR2***	dnaK/HSP70/BiP family ATPase
QCR2	ubiquinol-cytochrome-c reductase 40KD chain II	***LAP3***	DNA-binding cysteine-type protease; bleomycin hydrolase
RPN7	subunit of the regulatory particle of the proteasome	***LEA1***	similar to human U2AsnRNP protein
RPT3	26S proteasome regulatory subunit	***LHS1***	translocation of protein precursors across ER | Hsp70 family chaperone
RPT5	26S proteasome regulatory subunit	***MNN10***	galactosyltransferase
SEC20	secretory pathway protein	***MSF1***	phenylalanyl-tRNA synthetase alpha subunit, mitochondrial
SGT1	subunit of SCF ubiquitin ligase complex	***NAS2***	putative proteasome modulator
SPC2	subunit of signal peptidase complex	***PEP3***	vacuolar membrane protein
SQT1	ribosomal assembly	***PEX5***	peroxisomal protein receptor

TFP1	vacuolar ATPase V1 domain catalytic subunit A	***PMT1***	mannosyltransferase
TOM70	mitochondrial outer membrane specialized import receptor	***PRE4***	B-type subunit of proteasome
UBP10	ubiquitin-specific protease	***PRE8***	20S proteasome subunit Y7
VMA6	vacuolar ATPase	***PUP3***	20S proteasome subunit beta3
		QCR2	ubiquinol--cytochrome-c reductase 40KD chain II
		RLF2	chromatin assembly complex, subunit p90
		RPL10	ribosomal protein L10
		RPN7	subunit of the regulatory particle of the proteasome
		RPT5	26S proteasome regulatory subunit
		SCD5	multicopy suppressor of clathrin deficiency
		SCJ1	dnaJ homolog in endoplasmic reticulum
		SEC72	signal recognition particle receptor
		SOM1	peptidase of the protein sorting machinery
		SPC2	subunit of signal peptidase complex
		SPC3	signal peptidase subunit
		SSC1	mitochondrial heat shock protein of the HSP70 family
		SYN8	SNARE protein releated to mammalian syntaxin
		TCP1	component of chaperonin-containing T-complex

		TIM17	mitochondrial inner membrane import translocase subunit
		TIM8	mitochondrial protein import machinery subunit
		TOM70	mitochondrial outer membrane import receptor
		TUL1	transmembrane ubiquitin ligase
		UBP1	ubiquitin-dependent protease
		UBP7	ubiquitin-specific protease
		UGP1	UTP-glucose-1-phosphate uridylyltransferase
		VAC8	vacuole memebrane protein
		VPS17	vacuolar sorting protein
Protein modification			
AOS1	protein-sumoylation function	***APC5***	anaphase-promoting complex
MNN10	galactosyltransferase	***ARL1***	anaphase-promoting complex
PMT2	dolichyl-P-mannose-protein mannosyltransferase	***CDC16***	subunit of anaphase-promoting complex (cyclosome)
SPC2	subunit of signal peptidase complex	***CDC34***	ubiquitin-conjugating enzyme
UBP10	ubiquitin-specific protease	***HAT2***	histone acetyltransferase subunit
		MNN10	galactosyltransferase
		PMT1	mannosyltransferase
		SPC2	subunit of signal peptidase complex

		SPC3	signal peptidase subunit
		TUL1	transmembrane ubiquitin ligase
		UGP1	UTP-glucose-1-phosphate uridylyltransferase
Protein folding			
CCT3	chaperonin	***CCT6***	cytoplasmic chaperonin of the Cct ring complex
CCT6	cytoplasmic chaperonin of the Cct ring complex	***CPR1***	regulation of G-protein function
HSP60	mitochondrial groEL-type heat shock protein	***HSP60***	mitochondrial groEL-type heat shock protein
		KAR2	dnaK/HSP70/BiP family ATPase
		LHS1	translocation of protein precursors across ER | Hsp70 family chaperone
		SSC1	mitochondrial heat shock protein of the HSP70 family
		TCP1	component of chaperonin-containing T-complex
		TIM8	mitochondrial protein import machinery subunit
Protein targeting			
SEC20	secretory pathway protein	***KAR2***	dnaK/HSP70/BiP family ATPase
TOM70	mitochondrial outer membrane specialized import receptor	***LHS1***	translocation of protein precursors across ER | Hsp70 family chaperone
		MSF1	phenylalanyl-tRNA synthetase alpha subunit, mitochondrial
		PEP3	vacuolar membrane protein

		PEX5	peroxisomal protein receptor
		SCD5	multicopy suppressor of clathrin deficiency
		SCJ1	dnaJ homolog in endoplasmic reticulum
		SEC72	signal recognition particle receptor involved in membrane protein insertion into the ER
		SOM1	peptidase of the protein sorting machinery
		TIM17	mitochondrial inner membrane import translocase subunit
		TIM8	mitochondrial protein import machinery subunit
		TOM70	mitochondrial outer membrane specialized import receptor
		VAC8	vacuole memebrane protein required for vacuole inheritance
		VPS17	vacuolar sorting protein

Table S8. Plasmids used in this study.

Plasmid	Details	Reference or source
pBluescript	Expression vector, *Amp*^{r}, MCS, *lacZ* allowing blue-white selection	Stratagene
pDDB57	Cloning vector for gene disruption in *C. albicans*, *Amp*^{r}, *URA3-dpl200*	Wilson *et al*., 2000
pLUBP	Vector containing *C.albicans URA3* as a 4.9kb *Bgl*II-*Pst*I fragment	Ramon and Fonzi, 2003
p4	pBluescript derivative containing 1.8 kb *CaPDE1*, *Amp*^{r}	Steffen Rupp
pWH-P2MB	pWHPDE2 derivative containing *hisG-URA3-hisG* flanked by 5' and 3' *PDE2* homologous sequences; *Amp*^{r}	Jung and Stateva, 2003
pWHP2-R	pWH18P2-F-URA3 derivative containing 3' homologous *PDE2* sequence	Jung and Stateva, 2003
pDWURA3	pBluescript derivative containing *URA3*, *Amp*^{r}	This study
pDWURA3-3'P1	pDURA21 derivative containing 3'-*PDE1*, *Amp*^{r}	This study
pDWPDE1	pBluescript derivative containing 1.8 kb *CaPDE1* (in the opposite orientation in comparison to p4); *Amp*^{r}	This study
pDWR1	pDPDE1 derivative containing the *URA3*-3'*PDE1* fragment of pDURA::3'P1, *Amp*^{r}	This study

Table S9. Primers used in this study

Primer name	**Sequence 5’-3’**	**Purpose**
ADHF	GATTACCCAGTTCCAACTCC	Amplification of *ADH1*
ADHR	ATTTTAGCGGCTTGGACAGC	Amplification of *ADH1*
PFK2F	TGG TGGCTACTCTGCATTAG	Amplification of *PFK2*
PFK2R	TGTCCAACCCTAATCTGTCG	Amplification of *PFK2*
PMA1F	GCTGCCACAGTCAATGAAGC	Amplification of *PMA1*
PMA1R	CAGACAAACCTGGGGCCAAG	Amplification of *PMA1*
RPL18F	ATCCGGTCACAGAACCGCTC	Amplification of *RPL18*
RPL18R	ATGCTGCTCGAGTCTCTATG	Amplification of *RPL18*
SAH1F	AGAACGGTCGTCACGTTATC	Amplification of *SAH1*
SAH1R	ATGTCAGCCTTGTATGGACC	Amplification of *SAH1*
PDE1-SF1	CACCGGATCCCGCAAAACTAAAATGTCATTTG	Confirmation of *pde1* mutants
PDE1-SR1	GTATTTCTAGAGTGGCGTTATTTCCAATACTCTA	Confirmation of *pde1* mutants
PDE1-PF1	GATTAACTGTGACACGACGCAC	Confirmation of *pde1* mutants
PDE1-TR1	CCAATAGATATGACAAGGAAGAGG	Confirmation of *pde1* mutants
PDE1DWF1	GTATAGGTCGACGGAAATAACGCCACTACAGAAATA	Amplification of 3’*PDE1*sequence
PDE1DWR1	GTTTCGGGCCCTGACGATGAAGAATCATTACC	Amplification of 3’*PDE1* sequence
PDE1F	AACATATGAACTAAAATGTCATTTG	Amplification of *PDE1*
PDE1hisR	GGGGATCCCTAGTGATGGTGGTGGTGATGTACTATAATTGAGGTGCCACTAAG	Amplification of *PDE1*
PDE2TF	AACATATGAGATATTATGGCAGAA	Amplification of *PDE2*
PDE2-P2-RF	GGATATGGTTGTTAATTCTTGTGTC	*PDE2* reintegration
PDE2hisR	GGGGATCCCTAGTGATGGTGGTGGTGATGTTTCTTTGCTCTTTCCAACCAAAA	Amplification of *PDE2*
HWP1-F	TCAACTTATTGCTATCGCTTATTAC	RT-PCR of *HWP1*
HWP1-R	GGTGGATTGTCGCAAGG	RT-PCR of *HWP1*
CZF1-F	GTATCTCCCCCTAATAGCAG	RT-PCR of *CZF1*
CZF1-R	GTTTATCGCCGCTTCTC	RT-PCR of *CZF1*
URA3-F	ACCAGTAGCACAACGA	RT-PCR of *URA3*
URA3-R	CTCCATTCCCAGTGACA	RT-PCR of *URA3*
EFB1-F	AGCTGATGTCACTGTCT	RT-PCR of *EFB1*
EFB1-R	CCTTCCATTTCGATAGCTT	RT-PCR of *EFB1*
URA3 INTF	ATCAGTAGCATCATCCTCAGCG	Reintegration of *URA3*
URA3INTR	TAGTGATCACTTCTCCTACTCCG	Reintegration of *URA3*
URA3-INF1	GGATTTGATTGGCTTATTATGACACC	*URA3* integration
URA3-INR1	CATTCCCAGTGACACCATGAGCATTG	*URA3* integration