Supplemental Table 1

Expression of genes in the *efg1* mutant HLC52 relative to the wild-type CAF2-1. Cells were grown in non-inducing YPD-medium at 30 °C. The minimal FDR value calculated by the SAM program was 0.95 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes in mutant				
Citric acid cycle				
ACC1	CA5816	acetyl-coenzyme-A carboxylase	1.5	0.12
ACH1	CA0345	acetyl-coenzyme-A hydrolase	2.3	0.12
FUM12.3F	CA4351	Fumarate hydratase, 3-prime end	3.1	0.12
FUM12.5F	CA4349	Fumarate hydratase, 5-prime end	2.1	0.12
GDH3	CA1579	NADP-glutamate dehydrogenase	2.5	0.12
IPF4401	CA0903	Succinate dehydrogenase	1.7	0.12
KGD1	CA3149	2-oxoglutarate dehydrogenase	2	0.12
MDH1	CA5164	Mitochondrial malate dehydrogenase precursor	1.6	0.12
SDH12	CA2470	Succinate dehydrogenase	1.5	0.12
Respiration				
ATP1.EXON3	CA4457	F1F0-ATPase complex, F1 alpha subunit, exon 3	1.6	0.12
ATP17.3	CA5852	F1F0-ATPase complex, F1 delta subunit	1.6	0.75
STF2	CA2738	ATP synthase regulatory factor	2.5	0.12
NUBM	CA2326	nucleotide-binding respiratory complex I subunit	1.6	0.12
PET9	CA5388	ADP/ATP carrier protein	1.6	0.12
Histones				
HHF21	CA2862	histone H4	2	0.12
HHF22	CA3372	histone H4	3	0.12
HHT21	CA2861	Histone H3	2	0.12
HTA3	CA3382	histone H2A F/Z variant	1.5	0.12
HTB1	CA4697	Histone H2B	2	0.12
Cell wall				
IPF10153	CA3747	membrane transporter	1.5	0.12
ECM29.EXON2	CA5930	Involved in cell wall biogenesis and architecture	1.7	0.12
ECM14	CA2407	carboxypeptidase involved in cell wall biogenesis and architecture	1.6	0.12
Ribosomes				
MRPL16	CA0910	ribosomal protein	1.6	0.12
MRPL49	CA4434	ribosomal protein mitochondrial	1.5	0.12
MRPS5	CA3526	probable ribosomal protein S5, mitochondrial	2.6	0.53
RPS26A	CA4534	ribosomal protein S26.e.A, cytosolic	2	0.12
YST1.EXON2	CA5021	Ribosomal protein, exon 2	1.6	0.12
Transcription factors				
CAP1	CA2614	transcriptional acivator	1.9	0.20
CTA21	CA2615	transcriptional activation	1.9	0.12
CTA24	CA2495	transcriptional regulation	1.8	0.12
CTA241.EXON1	CA4358	transcriptional activator, exon 1	2.1	0.12
CTA241.EXON2	CA0183	transcriptional activator, exon 2	2.1	0.12
CTA26	CA6059	transcriptional activation	1.9	0.12
IPF6067	CA3851	putative transcription factor	1.6	0.12
Stress				
SOD22.3F	CA5588	superoxide dismutase, 3-prime end	1.6	0.12

SSC1	CA4474	mitochondrial heat shock protein 70-related protein	1.9	0.12
YHB1	CA0943	flavohemoglobin	2.9	0.12
Formate dehydrogenases				
FDH12	CA1846	formate dehydrogenase	2.1	0.12
FDH3.3F	CA1253	formate dehydrogenase, 3-prime end	1.5	0.12
FDH4.3F	CA0636	formate dehydrogenase, 3-prime end	1.5	0.60
Unknown and unclassified				
AMD1	CA4680	AMP deaminase	1.5	0.12
ARO8	CA4804	aromatic amino acid aminotransferase I	1.6	0.12
CDC55	CA4535	B subunit of protein phosphatase 2A	1.8	0.12
CDR11.3F	CA0609	multidrug resistance protein, 3-prime end	1.6	0.12
CDR3.5EOC	CA1545	ABC transporter, multidrug resistance protein	1.5	0.26
CHA12	CA3945	L-serine/L-threonine deaminase	1.7	0.12
CTR1	CA1496	copper transport protein	1.5	0.12
FAS2.3F	CA6107	fatty-acyl-CoA synthase, alpha chain, 3-prime end	1.8	0.12
FBP1	CA3199	fructose-1,6-bisphosphatase	1.5	0.75
FTR1	CA5345	high affinity iron permease	1.8	0.12
GCV2	CA3883	glycine decarboxylase P subunit	1.6	0.12
HRP1	CA6073	nuclear polyadenylated RNA-binding protein	1.7	0.26
IPF10138.3F	CA1355	unknown function	1.9	0.12
IPF10138.5F	CA1356	unknown function	1.8	0.12
IPF11	CA6074	unknown function	1.7	0.26
IPF1164	CA4810	Subunit NUHM	1.5	0.12
IPF11936.3F	CA3701	unknown function	1.5	0.12
IPF1210	CA4829	similar to *Saccharomyces cerevisiae* NFU1	2	0.12
IPF12316	CA1098	unknown function	1.7	0.12
IPF1239	CA0077	unknown function	1.6	0.12
IPF1292	CA5678	unknown function	1.9	0.12
IPF13319	CA1088	unknown function	1.8	0.12
IPF13943	CA5012	Unknown function	1.6	0.41
IPF14285	CA1962	unknown function	1.8	0.12
IPF14895	CA1987	unknown function	2	0.12
IPF17790	CA0030	unknown function	1.8	0.12
IPF2431	CA5714	similar to *Saccharomyces cerevisiae* Tsa1p	1.7	0.12
IPF2441	CA5719	unknown function	1.6	0.26
IPF2690.3F	CA5812	unknown function	2.1	1.04
IPF2795	CA5936	unknown function	1.5	0.12
IPF3309.3EOC	CA5696	unknown function	1.7	0.12
IPF3503	CA5952	similar to *Saccharomyces cerevisiae* Fcp1p	1.7	0.12
IPF3810	CA2784	unknown function	1.8	0.12
IPF4229	CA4695	unknown function	1.5	0.20
IPF4835	CA6071	zinc finger protein	1.6	0.12
IPF5457	CA2609	similar to *Saccharomyces cerevisiae* Sec28p	2.5	0.12
IPF5471	CA2603	unknown function	1.5	0.12
IPF5915	CA0670	phosphatidyl synthase	1.8	0.12
IPF5987	CA5544	unknown function	1.6	0.12
IPF6003	CA1345	similar to *Saccharomyces cerevisiae* Msb2p	1.5	0.20
IPF6505	CA3973	unknown function	1.6	0.12
IPF66	CA6100	unknown function	2	0.12
IPF7141	CA3986	unknown function	1.9	0.12
IPF7377	CA3750	unknown function	1.5	0.12
IPF8179	CA3836	putative esterase	3.1	0.75
IPF9251	CA3639	unknown function	2	0.12
IPF9401	CA5395	unknown function	1.6	0.12
IPF9632	CA3167	unknown function	1.5	0.20

KIP3	CA5651	kinesin-related protein required for nuclear migration	2.1	0.75
NCE102	CA6097	secretion of proteins that lack classical secretory signal sequence	2	0.12
NRD1	CA3436	involved in regulation of nuclear pre-mRNA abundance	1.7	0.12
PHO87.5EOC	CA0015	member of the phosphate permease family, 5-prime end	1.6	0.12
QCR9	CA0376	ubiquinol--cytochrome-c reductase subunit 9	1.6	0.12
RDH54	CA5519	helicase required for mitotic diploid-specific recombination and repair	2	0.53
RGA2	CA5154	rho-GTPase activating protein 2	1.9	0.60
RPS620A	CA3267	unknown function	2.7	0.12
RPS620B	CA3268	unknown function	3.4	0.12
TIM54	CA3631	translocase for the insertion of proteins into the mitochondrial inner membrane	1.5	0.26
UBI4	CA5932	polyubiquitin	1.8	0.12
YTA12	CA4838	protease of the *SEC18/CDC48/PAS1* family of ATPases (AAA)	1.6	0.12

Downregulated genes in mutant

Glycolysis

ENO1	CA3874	enolase I	0.66	1.04
FBA1	CA5180	fructose-bisphosphate aldolase	0.37	0.12
GLK1	CA0263	aldohexose specific glucokinase	0.40	0.12
GPM1	CA4671	phosphoglycerate mutase	0.40	0.12
PFK1	CA1834	6-phosphofructokinase, alpha subuni	0.46	0.12
PFK2	CA3112	6-phosphofructokinase, beta subunit	0.41	0.12
PGI1	CA3559	glucose-6-phosphate isomerase	0.50	0.12
TPI1	CA5950	triose phosphate isomerase	0.44	0.12
HXK2.3F	CA0127	hexokinase II, 3-prime end	0.36	0.12

Reserve carbohydrates

TPS2	CA5066	threalose-6-phosphate phosphatase	0.45	0.12
TPS3.3	CA5505	trehalose-phosphate synthase, regulatory subunit	0.41	0.12
IPF8321	CA2938	similar to *Saccharomyces cerevisiae* Glg2p	0.41	0.12
GSY1	CA5467	glycogen synthase	0.45	0.12
GPH1	CA5206	glycogen phosphorylase	0.35	0.12

Metabolism

ADH1	CA4765	alcohol dehydrogenase	0.48	0.12
ADH4	CA2333	alcohol dehydrogenase	0.52	0.60
DAK2.3EOC	CA0311	dihydroxyacetone kinase, 3-prime end	0.45	0.12
GPD1	CA2263	glycerol-3-phosphate dehydrogenase	0.55	0.12
GPD2	CA0824	glycerol 3-phosphate dehydrogenase	0.38	0.12
PDC11	CA2474	pyruvate decarboxylase	0.63	0.12

Transporter & cell wall

AGP3	CA1525	amino acid-permease	0.59	0.12
BPT1.3F	CA3544	membrane transporter of the ATP-binding cassette (ABC) superfamily, 3-prime end	0.61	0.20
BPT1.5F	CA3545	membrane transporter of the ATP-binding cassette (ABC) superfamily, 5-prime end	0.60	0.26
DUR35.3F	CA6133	urea transport protein, 3-prime end	0.48	0.75
IPF1954	CA5295	putative transporter	0.35	0.20
IPF5185 (FLO1)	CA1678	putative cell wall protein	0.20	0.12
STL1	CA0472	sugar transporter	0.66	0.26

Lipid and fatty acid metabolism

ERG13	CA5549	3-hydroxy-3-methylglutaryl coenzyme A synthase	0.62	0.12
ERG251	CA0875	C-4 sterol methyl oxidase	0.51	0.12
SUR2	CA2225	hydroxylation of C-4 of the sphingoid moiety of ceramide	0.28	0.12
Stress				
HSP12	CA0627	heat shock protein	0.56	0.12
RHR2	CA5788	DL-glycerol phosphatase	0.23	0.12
SSA4	CA1230	Cahsp70 mRNA for heat shock	0.55	0.12
IPF13836	CA2342	probable heat shock protein	0.66	0.12
unknown and unclassified				
CAF16	CA3880	ABC ATPase	0.57	0.12
CBK1	CA2022	serine/threonine protein kinase	0.62	0.12
CBP3	CA2518	involved in cytochrome-c reductase assembly	0.58	0.75
CDR4	CA3895	multidrug resistance protein	0.55	0.12
CHL4	CA4453	chromosome segregation protein	0.67	0.12
CMK1	CA6135	Ca2+/calmodulin-dependent ser/thr protein kinase	0.61	0.20
CNH1.3F	CA0878	Na+/H+ antiporter, 3-prime end	0.55	0.12
CRD1	CA2832	Cu-transporting P1-type ATPase	0.63	0.12
CYP1	CA0972	cyclophilin (peptidylprolyl isomerase), mitochondrial	0.64	0.60
DAL53	CA2957	allantoate permease	0.60	1.04
DLD1	CA4905	D-lactate ferricytochrome C oxidoreductase	0.66	1.04
DLD2	CA5942	D-lactate ferrycytochrome C oxidoreductase	0.64	1.04
EBP4	CA4030	NADPH dehydrogenase	0.67	1.04
ETF1	CA0510	ETF-ubiquinonen oxidoreductase	0.61	0.12
GIM5	CA2888	Gim complex component	0.64	0.12
GLN4	CA5631	glutaminyl-tRNA synthetase	0.54	0.12
HIS6	CA1480	5 Pro-FAR isomerase	0.62	0.41
HNT1	CA2345	similarity to protein kinase C inhibitor-I	0.55	0.20
IFB2	CA2451	unknown function	0.59	0.12
IFE2	CA2075	unknown function	0.41	0.12
IFF1.3EOC	CA0344	unknown function, 3-prime end	0.21	0.75
IFQ3	CA2597	unknown function	0.60	0.12
IPF10555.3EOC	CA0688	unknown function, 3-prime end	0.55	0.12
IPF10727	CA4611	unknown function	0.55	0.12
IPF10864	CA1968	similar to *Saccharomyces cerevisiae* Rex4p	0.61	0.26
IPF11081	CA4032	unknown function	0.53	0.12
IPF11667	CA2187	unknown function	0.58	0.12
IPF11688	CA2867	similar to Saccharomyces cerevisiae Apl4p	0.46	0.12
IPF11714	CA1331	unknown function	0.48	0.12
IPF11759	CA1943	unknown function	0.60	0.12
IPF12138	CA0820	unknown function	0.65	0.41
IPF12303	CA4392	glutathione-S-transferase	0.63	0.12
IPF1261	CA5668	unknown function	0.65	0.60
IPF1264	CA5669	unknown function	0.56	0.12
IPF13081	CA0588	unknown function	0.65	0.53
IPF13678	CA0370	unknown function	0.62	0.12
IPF13683	CA0260	unknown function	0.62	0.60
IPF13944	CA5011	unknown function	0.27	0.12
IPF14083	CA1008	similarity to *Saccharomyces cerevisiae* carrier protein Flx1p	0.43	0.12
IPF14282	CA0446	Similar to mucin proteins	0.59	0.12
IPF14438	CA2282	unknown function	0.58	0.12
IPF14540	CA1615	putative multidrug resistance protein	0.03	0.26
IPF14545	CA2314	unknown function	0.46	0.12
IPF14550	CA2822	unknown function	0.63	0.41
IPF14554	CA2823	similar to *Saccharomyces cerevisiae* Osh3p	0.62	0.26

IPF14559.3F	CA1758	unknown function, 3-prime end	0.56	0.12
IPF14603	CA0785	unknown function	0.64	1.04
IPF14864	CA0572	unknown function	0.56	0.12
IPF15033	CA0295	unknown function	0.61	1.04
IPF15160	CA4454	unknown function	0.58	0.20
IPF15225	CA0402	Sorting nexin-like protein	0.54	0.20
IPF15297	CA5078	unknown function	0.60	0.12
IPF1548	CA5407	unknown function	0.59	0.12
IPF15601	CA0458	unknown function	0.65	0.20
IPF16662	CA1648	unknown function	0.67	0.12
IPF16901	CA2020	unknown function	0.48	0.12
IPF16924	CA2544	unknown function	0.65	0.12
IPF17026	CA2828	unknown function	0.66	0.12
IPF1798	CA5264	unknown function	0.50	0.12
IPF18207	CA4516	unknown function	0.57	0.12
IPF18474	CA2383	unknown function	0.32	0.75
IPF18561.3	CA2028	unknown function, 3-prime end	0.36	0.53
IPF1882	CA6140	unknown function	0.61	0.53
IPF18822	CA0961	unknown function	0.55	0.53
IPF18924	CA0619	unknown function	0.63	0.12
IPF19974	CA3178	unknown function	0.63	0.20
IPF19980	CA3245	putative lipase	0.60	0.20
IPF19983	CA3336	unknown function	0.60	0.12
IPF20161	CA4125	unknown function	0.59	0.12
IPF20169	CA4381	unknown function	0.52	0.12
IPF2147	CA5320	unknown function	0.59	0.26
IPF2167	CA5310	unknown function	0.57	0.12
IPF2180	CA5303	unknown function	0.64	1.04
IPF2223	CA4587	unknown function	0.57	0.12
IPF2283	CA4266	unknown function	0.65	0.12
IPF2471	CA5728	maltose acetyltransferase	0.63	0.12
IPF2555	CA4075	unknown function	0.61	0.12
IPF2560	CA4072	unknown function	0.60	0.26
IPF257.3	CA5454	similar to *Saccharomyces cerevisiae* Fun34p	0.60	0.12
IPF2857	CA5526	unknown function	0.64	0.12
IPF3121	CA4651	unknown function	0.67	0.12
IPF3506	CA5953	unknown function	0.59	0.26
IPF351	CA5868	unknown function	0.50	0.12
IPF3597	CA5071	similar to Saccharomyces cerevisiae Ald4p	0.42	0.12
IPF3937	CA1203	Unknown function	0.66	0.12
IPF4039	CA4487	similar to Saccharomyces cerevisiae Nam8p	0.59	0.26
IPF4122	CA3641	unknown function	0.57	0.12
IPF420	CA5841	unknown function	0.66	0.26
IPF4288	CA4253	unknown function	0.61	0.20
IPF4305	CA4244	unknown function	0.59	0.26
IPF4328	CA0210	unknown function	0.45	0.12
IPF4450	CA0684	unknown function	0.62	0.12
IPF448	CA5643	unknown function	0.65	0.60
IPF4696	CA4970	unknown Function	0.45	0.12
IPF4959	CA6057	D-xylulose reductase	0.52	0.12
IPF5078	CA1469	unknown function	0.62	0.26
IPF511	CA5620	unknown function	0.55	0.12
IPF5149	CA4948	unknown function	0.37	0.41
IPF5356	CA3122	unknown function	0.48	0.12
IPF5363	CA3117	unknown function	0.60	0.26
IPF549	CA5604	unknown function	0.62	0.12

IPF5604	CA2815	unknown function	0.55	0.12
IPF6032	CA5168	unknown function	0.31	0.12
IPF6156	CA1625	similar to *C.elegans* LIM homeobox protein	0.66	0.12
IPF6235	CA2216	*Candida albicans* Tca2 retrotransposon	0.45	0.12
IPF6238	CA2752	GAG protein of retrotransposon pCal	0.35	0.60
IPF6342	CA1458	unknown function	0.59	0.12
IPF6629	CA4127	unknown function	0.38	0.12
IPF6803.5F	CA2503	unknown function	0.66	0.12
IPF6881	CA2186	putative phosphatidyl synthase	0.50	0.12
IPF6898	CA3320	similar to *Saccharomyces cerevisiae BUB1*	0.65	0.75
IPF7081	CA4121	unknown function	0.55	0.12
IPF7289	CA3878	similar to *Saccharomyces cerevisiae UPC2*	0.47	0.12
IPF7333	CA0731	unknown function	0.59	0.26
IPF7400	CA0984	unknown function	0.67	0.12
IPF7644	CA1864	unknown function	0.65	0.12
IPF7760	CA3558	unknown function	0.46	1.04
IPF7804.5F	CA3567	unknown function	0.65	0.12
IPF7970	CA3259	unknown function	0.56	0.12
IPF8889	CA3758	putative arginase	0.56	0.12
IPF9160	CA4485	similar to *Saccharomyces cerevisiae MED4*	0.60	0.12
IPF946	CA5968	unknown function	0.64	0.12
IPF9550	CA4570	similar to *Saccharomyces cerevisiae OSM1*	0.33	0.12
IPF9995	CA1114	unknown function	0.64	0.12
IPT1	CA0228	mannosyl diphosphorylinositol ceramide	0.61	0.12
MNT1	CA3469	mannosyltransferase involved in N-linked and O-linked glycosylation	0.65	0.20
MSS116	CA1945	RNA helicase of the DEAD box family	0.58	0.12
MYO1	CA3233	myosin-1 isoform (type II myosin) heavy chain	0.60	0.12
NCB2	CA3794	transcriptional repressor by homology	0.55	0.12
NMT1	CA1063	N-myristoyltransferase	0.62	0.26
PTC1	CA2833	protein serine/threonine phosphatase 2c	0.56	0.12
QDR1	CA4501	putative antibiotic resistance proteins	0.65	0.12
REV3.3F	CA5689	DNA-directed DNA polymerase zeta subunit	0.62	0.26
RNR22	CA4492	ribonucleoside-diphosphate reductase	0.19	0.20
RPS27A	CA2130	ribosomal protein S27	0.65	0.53
RSR1.3	CA2385	GTP-binding protein	0.65	0.60
SEC14	CA5398	phosphatidylinositol-phosphatidylcholine transfer	0.62	0.12
SNF7	CA4903	class E Vps protein	0.65	0.60
SNU114	CA0350	snRNP-specific protein	0.67	0.12
SPE4	CA1249	spermine synthase	0.61	0.12
SPS20	CA1225	peroxisomal 2,4-dienoyl-CoA reductase	0.66	0.53
SSN6	CA5907	transcriptional repressor	0.65	1.04
TAL1	CA2582	transaldolase	0.66	0.12
UBP2	CA0476	ubiquitin-specific proteinase	0.64	0.12
UGA11.EXON2	CA0772	4-aminobutyrate aminotransferase, exon 2	0.48	0.12
URA1	CA4745	dihydroorotate dehydrogenase	0.59	0.12
URK1	CA2961	uridine kinase	0.59	0.12
YEA4	CA2315	Golgi uridine diphosphate-N-acetylglucosamine transporter	0.57	0.12
YSA1	CA5909	sugar-nucleotide hydrolase	0.62	0.26

Supplemental Table 2

Expression of genes in the *efg1* mutant HLC52 relative to the wild-type CAF2-1. Cells were grown in hyphae inducing conditions (30 min 10 % serum at 37 °C). The minimal FDR value calculated by the SAM program was 4.6 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes in mutant				
Metabolism				
ICL1	CA4446	isocitrate lyase	1.6	3.21
IPF8806	CA3309	6-phosphofructose-2-kinase	1.6	0.80
Histones				
HHF21	CA2862	histone H4	3.2	3.49
HHT21	CA2861	histone H3	3.2	3.21
HTB1	CA4697	histone H2B	2.2	3.21
Cell wall and transporter				
ECM2	CA5930	involved in cell wall biogenesis and architecture	1.8	0.51
GSL21	CA2043	1,3-beta-D-glucan synthase subunit	1.5	1.03
IPF8796	CA4800	putative GPI-anchhored protein related to Phr1, Phr2 and Phr3	1.8	0.51
OPT2.3F	CA2871	oligopeptide transporter, 3-prime end	2.6	4.63
Ribosomes				
IPF8752	CA4226	similar to *Saccharomyces cerevisiae* Mrpl24p	3.0	3.21
RPL14B.3	CA3602	ribosomal protein L14B, 3-prime end	3.4	0.80
RPL19A.3	CA6141	ribosomal protein L19.e, 3-prime end	1.8	3.71
RPL38	CA2734	ribosomal protein L38	1.7	3.21
RPL42.3	CA2023	ribosomal protein L36a, 3-prime end	1.7	0.51
RPL6.3	CA3123	ribosomal protein, 3-prime end	1.5	1.03
RPL81	CA6064	60S ribosomal protein L7a.e.B	1.6	3.49
RPN4	CA2854	26S proteasome subunit	1.7	0.80
RPS12	CA5920	acidic ribosomal protein S12	1.8	0.51
RPS15.3	CA6123	40S ribosomal protein S15, 3-prime end	1.7	0.80
RPS19A.3	CA6068	ribosomal protein S19.e, 3-prime end	1.5	1.03
RPS26A	CA4534	ribosomal protein S26.e.A, cytosolic	2.1	0.51
RPS6A	CA2708	ribosomal protein S6	1.6	0.51
YST1.EXON2	CA5021	ribosomal protein, exon 2	2.1	0.51
Stress				
IPF1218	CA4835	similar to superoxide dismutase	2.4	0.80
MXR1	CA0123	methionine sulfoxide reductase	1.7	3.21
SSA1	CA2857	heat shock protein of Hsp70 family	2.6	0.51
SSE1	CA1911	heat shock protein of Hsp70 family	1.6	0.51
unknown and unclassified				
ADE12	CA4752	adenylosuccinate synthetase	3.3	2.77
ADE2	CA6139	phosphoribosylaminoimidazole carboxylase	1.7	3.49
AIP2	CA2406	actin interacting protein 2	1.8	0.51
BET5	CA2508	targeting and fusion of ER to Golgi transport vesicles	2.0	0.51
BNI1	CA3597	regulator of budding	1.9	0.80
CCN1	CA2479	G1 cyclin	1.5	3.21
CDC55	CA4535	B subunit of protein phosphatase 2A	1.5	0.51

CHA12	CA3945	L-serine/L-threonine deaminase	2.6	0.51
CMK1	CA6135	Ca2+/calmodulin-dependent ser/thr protein kinase	1.5	0.51
COX13	CA4536	cytochrome-c oxidase chain VIa	1.9	2.77
ERG12	CA3072	mevalonate kinase	1.5	1.95
FTR1	CA5345	high affinity iron permease	2.0	0.80
GCV2	CA3883	glycine decarboxylase P subunit	2.0	0.51
HIK1.5EOC	CA0108	histidine kinase, 5-prime end	1.8	0.51
HOM2	CA3984	aspartate-semialdehyde dehydrogenase	2.8	0.51
HPR5	CA6088	ATP-dependent DNA helicase	1.7	3.99
HRP1	CA6073	nuclear polyadenylated RNA-binding protein	1.6	0.51
IFA12	CA2755	unknown function	1.9	0.51
IFC3	CA2349	unknown function	1.6	3.21
IFC4	CA0442	unknown function	1.5	3.71
IFU1.5F	CA2267	unknown function	3.8	1.03
ILV5	CA1983	ketol-acid reducto-isomerase	2.5	2.77
IMH3.EXON1	CA1246	IMP dehydrogenase, exon 1	2.6	1.03
IPF10003	CA3219	similar to *Saccharomyces cerevisiae* Rnh70p	1.8	3.21
IPF10021	CA3017	unknown function	1.5	1.49
IPF10029	CA3015	unknown function	2.3	3.21
IPF10045	CA1622	similar to *Saccharomyces cerevisiae* Taf61p	2.6	4.63
IPF10391	CA4502	Similar to dnaJ proteins	2.4	3.21
IPF10919	CA2625	Similar to Flo1p	2.2	3.99
IPF10929	CA2232	unknown function	1.6	3.21
IPF11045	CA1517	unknown function	1.8	3.99
IPF11262	CA3083	unknown function	1.6	3.21
IPF11460	CA1060	unknown function	1.6	3.49
IPF11802	CA2005	unknown function	2.2	3.49
IPF11814	CA1233	unknown function	2.7	3.21
IPF11817	CA1231	unknown function	3.0	3.49
IPF11936.3F	CA3701	unknown function	1.5	3.62
IPF12662	CA0973	unknown function	2.6	0.51
IPF12782	CA2530	unknown function	1.5	3.21
IPF13582	CA3338	unknown function	2.2	0.51
IPF13756.3F	CA2414	unknown function	1.5	2.77
IPF14094	CA5482	repeated protein (10 times) of unknown function	1.7	0.80
IPF14448	CA2970	unknown function	1.9	4.63
IPF14562	CA1756	unknown function	2.3	3.62
IPF14676	CA2976	unknown function	4.3	3.49
IPF14706	CA1777	unknown function	1.8	1.03
IPF15870	CA2769	unknown function	2.1	0.51
IPF1660	CA4879	unknown function	1.8	4.63
IPF17186	CA0828	unknown function	3.5	0.51
IPF17881	CA0918	cyclin	2.0	0.51
IPF18316.3F	CA3628	unknown function	4.3	0.51
IPF19168	CA0162	unknown function	1.9	3.21
IPF19195.3F	CA0144	putative amino acid or GABA permease, 3-prime end	4.2	3.49
IPF19724	CA1182	similar to *Saccharomyces cerevisiae* Tbf1p	1.6	3.21
IPF20030	CA5740	unknown function	2.5	1.03
IPF20152	CA3975	unknown function	2.5	3.49
IPF2280	CA4264	unknown function	1.6	3.99
IPF276	CA5459	unknown function	2.7	3.21
IPF2822	CA5924	unknown function	1.6	3.21
IPF2954	CA3057	unknown function	1.5	0.51
IPF3491	CA5944	unknown function	1.6	0.51
IPF3616	CA4338	unknown function	1.6	0.51
IPF3631	CA4344	unknown function	1.7	3.49

IPF3647	CA4354	unknown function	1.6	0.80
IPF4398	CA4527	unknown function	1.5	1.03
IPF4764	CA3938	unknown function	1.5	0.80
IPF4835	CA6071	zinc finger protein	1.5	4.63
IPF5198	CA1128	unknown function	2.2	1.03
IPF5681	CA1100	unknown function	4.8	0.51
IPF6076.3	CA3594	unknown function	2.2	3.21
IPF6101.3	CA3076	unknown function	2.1	1.95
IPF6105	CA3075	similar to *Saccharomyces cerevisiae* Gua1p	1.6	1.95
IPF661	CA6002	unknown function	1.6	3.21
IPF6712.5F	CA3955	unknown function	1.5	3.21
IPF7030	CA1210	unknown function	1.8	3.21
IPF7133.3	CA3983	unknown function	1.6	3.62
IPF7575	CA1097	putative endo-exonuclease	1.6	3.21
IPF7891	CA3712	unknown function	2.2	2.77
IPF7927	CA0431	putative aldose reductase	1.8	0.51
IPF7940	CA3848	unknown function	2.2	3.49
IPF8746	CA1548	putative alpha-1,3-mannosyltransferase	1.7	0.51
IPF8811	CA3313	unknown function	1.5	3.21
IPF89.3	CA6109	unknown function	1.6	0.51
IPF9401	CA5395	unknown function	1.5	0.51
IPF9562	CA3357	similar to *Saccharomyces cerevisiae* Nuf2p	2.5	1.03
IPF963	CA5964	unknown function	1.5	3.62
IPF9785	CA0717	unknown function	1.6	1.03
KIP3	CA5651	kinesin-related protein required for nuclear migration	1.6	3.49
MRT4	CA2283	required for mRNA decay	1.6	3.21
MSH3	CA1127	DNA mismatch repair	2.6	3.21
MTR10	CA1811	Involved in nuclear protein import	2.4	3.71
NAB3	CA0084	polyadenylated RNA-binding protein	2.0	2.77
NAG2	CA1131	N-acetyl-glucosamine-6-phosphate deacetylase	1.6	3.49
PHO87	CA0548	member of the phosphate permease family	1.5	4.63
PHR1	CA4857	GPI-anchored pH responsive glycosyl transferase.7	1.6	0.51
POB3	CA3985	binds DNA polymerase delta	2.2	3.21
POT1	CA1505	acetyl-CoA C-acyltransferase, peroxisomal	2.4	0.51
POT11	CA5862	peroxysomal 3-ketoacyl-CoA thiolase A	1.8	3.99
PRO2	CA5926	proline biosynthetic enzyme	1.6	3.21
PUT4	CA4186	proline permease	1.6	3.49
RIB7	CA3495	HTP reductase	2.3	1.49
RNH1	CA0277	ribonuclease H	2.6	0.51
RNH1.EXON2	CA1651	ribonuclease H, exon 2	1.7	1.95
RNR21	CA4155	ribonucleoside-diphosphate reductase	2.7	0.51
SBA1	CA0896	Hsp90-associated Co-chaperone	1.9	0.51
SHM2	CA0895	serine hydroxymethyltransferase precursor	2.8	0.51
TBP1	CA2369	TATA-binding protein	1.7	0.51
TUB2.3	CA4897	beta-tubulin, 3-prime end	1.5	1.95
UFE1	CA5284	endoplasmic reticulum t-SNARE	1.7	3.71
VID21	CA0604	unknown function	2.0	1.03
YPT521	CA5342	GTP-binding protein of the Rab/Ypt family	1.8	3.49

Downregulated genes in mutant

Glycolysis

ENO1	CA3874	enolase I (2-phosphoglycerate dehydratase)	0.59	0.80
FBA1	CA5180	fructose-bisphosphate aldolase	0.58	1.49
GLK1	CA0263	aldohexose specific glucokinase	0.43	0.51

GPM1	CA4671	phosphoglycerate mutase	0.52	0.51
HXK2.3F	CA0127	hexokinase II, 3-prime end	0.58	0.80
PFK1	CA1834	6-phosphofructokinase, alpha subunit	0.54	0.51
PFK2	CA3112	6-phosphofructokinase, beta subunit	0.65	1.49
PGI1	CA3559	glucose-6-phosphate isomerase	0.42	0.51
Reserve-carbohydrates				
IPF8321	CA2938	similar to *Saccharomyces cerevisiae* Glg2p	0.49	0.51
TPS2	CA5066	threalose-6-phosphate phosphatase	0.48	0.51
GSY1	CA5467	glycogen synthase	0.64	3.21
Metabolism				
ADH1	CA4765	alcohol dehydrogenase	0.67	3.21
ADH5	CA2391	probable alcohol dehydrogenase	0.45	0.51
GAD1	CA1564	glutamate decarboxylase	0.65	0.51
GDH2	CA1775	NAD-specific glutamate dehydrogenase (NAD)	0.53	0.51
MDH1	CA5164	mitochondrial malate dehydrogenase precursor	0.62	0.51
PGK1	CA1691	phosphoglycerate kinase	0.55	0.51
Cell wall and transporter				
ALS1.3EOC	CA0316	agglutinin-like protein	0.31	0.51
ALS10	CA0448	agglutinin like protein	0.46	0.51
ALS12.3F	CA0413	agglutinin-like protein	0.42	0.51
ALS4.3F	CA1528	agglutinin-like protein	0.43	0.51
BPT1.5F	CA3545	membrane transporter of the ATP-binding cassette	0.63	1.49
FET34.3EOC	CA1431	iron transport multicopper oxidase, 3-prime end	0.60	0.51
HWP1	CA2825	hyphal wall protein	0.64	4.63
IPF20169	CA4381	*RBT5*-like:Mycelial surfaceantigen precursor	0.45	0.51
IPF19766	CA2746	unknown function	0.57	0.51
RBT5	CA2558	repressed by Tup1 protein 5	0.43	0.51
Transcription factors				
EFG1	CA2787	enhanced filamentous growth factor	0.53	0.51
IPF3912	CA4960	*CUP9*-homeodomain protein	0.59	0.51
TYE7	CA3707	basic helix-loop-helix transcription factor	0.67	2.77
Stress				
HSP12	CA0627	heat shock protein	0.38	0.51
DDR48	CA4336	stress protein	0.63	0.51
GPX2	CA0558	glutathione peroxidase	0.47	0.51
Unknown and unclassified				
ACT1	CA5255	actin	0.58	3.49
AQY1	CA2873	similarity to plasma membrane and water channel proteins	0.59	0.51
COF1	CA5409	cofilin	0.61	3.21
DLH1.3F	CA1007	meiotic recombination protein, 3-prime end	0.57	2.77
HAM1	CA1460	Controls 6-N-hydroxylaminopurine sensitivity and mutagenesis	0.59	3.71
HRD3	CA2651	involved in HMG-CoA reductase degradation	0.65	3.21
IFE2	CA2075	unknown function	0.65	4.63
IPF10138.5F	CA1356	unknown function	0.64	0.51
IPF10179	CA1634	unknown function	0.65	0.51
IPF10662	CA3827	IHD1	0.30	0.51
IPF11363	CA2802	unknown function	0.65	0.80
IPF11667	CA2187	unknown function	0.66	0.51
IPF11702	CA2806	unknown function	0.67	2.77

IPF11713	CA1330	unknown function	0.67	3.21
IPF11858	CA1411	unknown function	0.53	0.51
IPF12303	CA4392	glutathione-S-transferase	0.67	3.21
IPF12611	CA1854	unknown function	0.65	1.49
IPF13522	CA0566	unknown function	0.60	1.49
IPF13782	CA3301	unknown function	0.67	3.99
IPF14282	CA0446	Similar to mucin proteins	0.57	0.51
IPF14598	CA1360	unknown function	0.64	0.51
IPF15297	CA5078	unknown function	0.64	0.51
IPF1634	CA4886	unknown function	0.65	3.99
IPF1649	CA4883	similar to *Saccharomyces cerevisiae* Bem2p	0.56	0.51
IPF16646	CA1167	unknown function	0.58	0.51
IPF16662	CA1648	unknown function	0.61	3.21
IPF16947	CA5473	unknown function	0.66	1.49
IPF16981	CA1870	unknown function	0.67	3.71
IPF17840	CA0059	unknown function	0.67	0.51
IPF1798	CA5264	unknown function	0.32	0.51
IPF18587	CA1925	putative methyltransferase	0.53	0.51
IPF18853	CA0843	unknown function	0.65	3.49
IPF19801	CA4566	unknown function	0.66	0.51
IPF19897	CA1050	unknown function	0.64	4.63
IPF19953	CA2562	unknown function	0.51	0.51
IPF19977	CA3211	unknown function	0.65	1.49
IPF20056	CA0495	unknown function	0.54	0.51
IPF3336	CA4771	unknown function	0.62	3.21
IPF3897.5F	CA1954	unknown function	0.66	3.71
IPF3937	CA1203	unknown function	0.62	0.51
IPF3964	CA4111	unknown function	0.55	0.51
IPF4065	CA0386	unknown function	0.63	0.51
IPF4293	CA4249	similar to *Saccharomyces cerevisiae* Gpi2p	0.66	4.63
IPF4696	CA4970	unknown function	0.52	0.51
IPF4959	CA6057	D-xylulose reductase	0.48	0.51
IPF5217	CA5382	unknown function	0.67	3.49
IPF5806	CA4216	unknown function	0.33	0.51
IPF6342	CA1458	unknown function	0.35	0.51
IPF6518	CA2302	unknown function	0.66	4.63
IPF652	CA6006	unknown function	0.01	1.49
IPF6881	CA2186	putative phosphatidyl synthase	0.63	1.49
IPF7109	CA5650	unknown function	0.62	0.51
IPF7666	CA1120	unknown function	0.59	0.80
IPF7715	CA0706	unknown function	0.65	0.80
IPF9057	CA2649	unknown function	0.62	0.80
IPF9145	CA0962	unknown function	0.59	0.51
IPF9167	CA2697	unknown function	0.64	0.51
IPF946	CA5968	unknown function	0.60	0.51
IPF9995	CA1114	unknown function	0.55	0.51
LPI9	CA3110	microtubule-associated protein	0.67	0.80

MAL31	CA3404	maltose permease	0.52	0.51
MNN22	CA0752	Golgi alpha-1,2-mannosyltransferase	0.64	0.51
NEM1	CA2705	required for nuclear morphology	0.58	0.51
PET191.3	CA5759	assembly of cytochrome oxidase, 3-prime end	0.62	0.80
PHO8.5	CA0892	repressible alkaline phosphatase, 5-prime end	0.62	0.80
PUT1	CA1552	proline oxidase	0.65	0.51
RPC31	CA2546	DNA-directed RNA polymerase III	0.64	0.80
RSP5	CA1279	ubiquitin-protein ligase	0.66	3.21
SOK1	CA1536	high copy suppressor of a cyclic AMP-dependent protein kinase mutant	0.67	1.95
TAF90	CA4247	probable transcription-associated factor protein	0.63	4.63
TFS1	CA0748	cdc25-dependent nutrient- and ammonia-response cell-cycle regulator	0.61	3.62
UNG1	CA5720	uracil-DNA glycosylase	0.59	3.49

Supplemental Table 3

Expression of genes in the *efh1* mutant C4/d6-3 relative to the wild-type CAF2-1. Cells were grown in non-inducing YPD-medium at 30 °C. The minimal FDR value calculated by the SAM program was 4.8 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes				
IPF4696	CA4970	unknown function	1.7	1.59
Downregulated genes				
IPF10277	CA0946	unknown function	0.5	1.44
IPF17064	CA3496	unknown function	0.63	4.69
IPF17186	CA0828	unknown function	0.61	1.44
IPF4328	CA0210	unknown function	0.67	1.44
IPF6493	CA0193	unknown function	0.64	4.83
IPF7109	CA5650	unknown function	0.58	1.44
IPF9901	CA2426	similar to *S. cerevisiae* Rad18p DNA repair protein	0.52	4.69
KRE9	CA2958	cell wall synthesis protein	0.65	4.42

Supplemental Table 4

Expression of genes in the *efh1* mutant C4/d6-3 relative to the wild-type CAF2-1. Cells were grown in hyphae inducing conditions (30 min 10 % serum at 37 °C). The minimal FDR value calculated by the SAM program was 5.0 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes				
Ribosomes				
RPL42.3	CA2023	ribosomal protein L36a, 3-prime end	1.67	2.37
RPS12	CA5920	acidic ribosomal protein S12	1.56	0.90
RPS30.3	CA2587	40S ribosomal protein S30, 3-prime end	1.67	0.90
RPS6A	CA2708	ribosomal protein S6	1.59	0.90
Unknown and unclassified				
CSE1.3F	CA2982	importin-beta-like protein, 3-prime	1.59	1.10
ECE1	CA1402	cell elongation protein	1.60	0.90
FRP2	CA3153	member of the FRP family of proteins related to Y. lipolytica glyoxylate pathway regulator Gpr1p and S. cerevisiae Fun34p	1.67	0.90
FTR1	CA5345	high affinity iron permease	1.68	3.85
GAL1	CA4040	galactokinase	1.75	0.90
GFA1	CA4016	glutamine:fructose-6-phosphate amidotransferase	1.60	0.90
IDP2	CA0643	isocitrate dehydrogenase, cytosolic	1.55	0.90
IPF15870	CA2769	unknown function	1.64	0.90
IPF17237	CA1716	unknown function	1.80	0.90
IPF20016	CA4514	similar to *S. cerevisiae* Sec63p ER protein-translocation complex subunit	1.51	5.04
IPF3416	CA2015	unknown function	3.51	3.85
IPF3647	CA4354	unknown function	1.58	0.90
IPF3870	CA1247	similar to Saccharomyces cerevisiae Rts1p potential regulatory subunit of protein phosphatase 2A	1.60	0.90
IPF4481	CA4749	unknown function	1.51	3.85
IPF6117	CA3069	unknown function	1.60	0.90
IPF8806	CA3309	6-phosphofructose-2-kinase	1.52	0.90
KRR1	CA4096	involved in cell division and spore germination	1.50	0.90
MSB3	CA2717	GTPase-activating protein for Sec4p	1.61	1.10
PET9	CA5388	ADP/ATP carrier protein	1.78	3.85
PMT1	CA4424	mannosyltransferase	1.70	0.90
POT11	CA5862	peroxysomal 3-ketoacyl-CoA thiolase A	1.54	0.90
POX4	CA1572	peroxisomal fatty acyl-CoA oxidase	1.56	0.90
SEC26	CA4242	beta chain of secretory vesicles coatomer complex	1.51	0.90
SHM2	CA0895	Serine hydroxymethyltransferase precursor, mitochondrial	2.03	0.90
SPC2	CA3731	signal peptidase 18 kDa subunit	1.60	0.90
STL2.3F	CA5606	sugar transporter, 3-prime end	1.54	5.04
TUB2.3	CA4897	beta-tubulin, 3-prime end	1.60	0.90

Downregulated genes

Unknown and unclassidfied

COS161	CA0490	involved in manganese homeostasis	0.56	0.90
HSH49	CA3579	spliceosome-associated essential protein	0.66	0.90
IPF15013	CA2761	pyruvate decarboxylase regulatory protein	0.66	3.85
IPF3920	CA4964	unknown function	0.66	3.85
IPF4303	CA4245	unknown function	0.65	5.04
IPF4959	CA6057	D-xylulose reductase	0.64	3.85
STF2	CA2738	ATP synthase regulatory factor	0.62	0.90
TRX2	CA0467	thioredoxin	0.67	3.85

Supplemental Table 5

Expression of genes in the *efg1 efh1* mutant H/1.22 relative to the wild-type CAF2-1. Cells were grown in non-inducing YPD-medium at 30 °C. The minimal FDR value calculated by the SAM program was 5.1 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes				
Metabolism				
ACH1	CA0345	acetyl-coenzyme-A hydrolase	1.8	0.83
ACS2	CA2858	acetyl-coenzyme-A synthetase	1.5	0.83
IPF15013	CA2761	pyruvate decarboxylase regulatory protein	1.6	0.83
Histones				
HHF21	CA2862	histone H4	2.0	0.83
HHF22	CA3372	histone H4	2.2	0.83
HHT21	CA2861	histone H3	2.0	0.83
RPD31	CA2549	histone deacetylase B	3.5	0.83
Transcription factors				
CTA25	CA0050	transcriptional activation	1.6	0.83
SEF1	CA2346	putative transcription factor1	1.6	1.40
TYE7	CA3707	basic helix-loop-helix transcription factor	2.5	0.83
Stress				
SSA1	CA2857	heat shock protein of HSP70 family	1.6	4.89
YHB1	CA0943	flavohemoglobin	3.3	0.83
Format-dehydrogenases				
FDH11.3	CA6000	glutathione-dependent formaldehyde dehydrogenase, 3-prime end	1.6	0.83
FDH12	CA1846	formate dehydrogenase	4.0	0.83
FDH3.3F	CA1253	formate dehydrogenase, 3-prime end	1.7	0.83
FDH4.3F	CA0636	Formate dehydrogenase, 3-prime end	3.2	0.83
Iron uptake				
FET33	CA2924	cell surface ferroxidase	1.5	0.83
FRE7	CA5621	ferric reductase transmembrane component	2.0	0.83
CFL1	CA3460	ferric reductase	1.9	0.83
unknown and unclassified				
CDR1	CA6066	multidrug resistance protein	2.5	0.83
DBP2.EXON2	CA1415	ATP-dependent RNA helicase of DEAD box family, exon 2	1.6	3.22
DDC1	CA0391	DNA damage checkpoint protein	2.2	1.40
EBP7	CA2227	NADPH dehydrogenase	2.6	0.83
GRP3	CA2963	dihydroflavonol-4-reductases	2.1	0.83
IFC4	CA0442	unknown function	1.5	4.89
IPF10138.5F	CA1356	unknown function	2.0	2.09
IPF10355	CA4841	unknown function	2.2	0.83
IPF10391	CA4502	similar to dnaJ proteins	1.7	0.83
IPF10429	CA0721	unknown function	1.5	0.83
IPF11262	CA3083	unknown function	1.6	0.83
IPF11725	CA2903	unknown function	1.7	0.83
IPF11998	CA1898	unknown function	1.5	1.40
IPF1239	CA0077	unknown function	1.5	0.83
IPF1286	CA5677	unknown function	3.3	2.09

IPF13582	CA3338	unknown function	1.6	2.98
IPF14285	CA1962	unknown function	1.5	2.98
IPF16047	CA0381	unknown function	2.3	3.22
IPF18474	CA2383	unknown function	1.6	2.98
IPF1848	CA6154	similar to S. cerevisiae Snu13p	1.5	4.89
IPF2178	CA5304	unknown function	2.0	0.83
IPF2392	CA5893	unknown function	1.9	1.40
IPF3309.3EOC	CA5696	unknown function	1.7	2.09
IPF3406	CA2093	unknown function	1.7	0.83
IPF4835	CA6071	zinc finger protein	1.6	0.83
IPF5376	CA2288	unknown function	1.7	0.83
IPF538	CA5609	unknown function	1.6	0.83
IPF564	CA5596	unknown function	1.5	1.40
IPF6266	CA3277	unknown function	2.0	2.98
IPF6561	CA4661	unknown function	1.6	0.83
IPF6654	CA4305	unknown function	1.9	0.83
IPF676	CA5995	unknown function	1.5	4.89
IPF8210	CA5480	unknown function	4.4	1.40
IPF8336	CA2839	unknown function	2.1	0.83
IPF8404	CA2797	putative helicase	2.5	0.83
IPF8423	CA1384	similar to *S. cerevisiae* Dhs1p exonuclease	1.6	4.89
IPF8527	CA5476	unknown function	2.8	0.83
IPF8537	CA2157	similar to *S. cerevisiae* Cne1p calnexin	2.1	1.40
IPF856	CA5352	unknown function	2.2	2.09
KEM1.3	CA0767	multifunctional nuclease, 3-prime end	2.5	0.83
MOT1	CA2331	transcriptional accessory protein	1.5	0.83
MVP1.EXON2	CA5220	required for vacuolar protein sorting	1.9	0.83
NDH2	CA2659	NADH dehydrogenase	4.3	0.83
OST2	CA2260	oligosaccharyltransferase epsilon subunit	1.7	2.98
PLB3	CA3834	phospholipase B	2.8	4.89
RPB11.3	CA2987	DNA-directed RNA polymerase II subunit	2.1	2.09
RPB140	CA0987	DNA-dependent RNA polymerase II RPB140	6.0	1.40
RPS31	CA2011	ubiquitin fusion protein	1.6	2.09
RPS620A	CA3267	unknown function	2.8	0.83
RPS620B	CA3268	unknown function	2.3	0.83
SBH1	CA1072	involved in translocation into the ER	1.6	0.83
SKP1	CA1285	kinetochore protein complex CBF3	1.5	0.83
SKS1	CA4039	serine/threonine kinase	2.4	0.83
STT3	CA4528	oligosaccharyl transferase	2.5	3.22
UBP12	CA1124	ubiquitin C-terminal hydrolase	1.9	0.83

Downregulated genes

Glycolysis

ENO1	CA3874	enolase I (2-phosphoglycerate dehydratase)	0.60	0.83
FBA1	CA5180	fructose-bisphosphate aldolase	0.46	0.83
GLK1	CA0263	aldohexose specific glucokinase	0.54	0.83
GPM1	CA4671	phosphoglycerate mutase	0.56	0.83
PFK1	CA1834	6-phosphofructokinase, alpha subunit	0.53	0.83
PFK2	CA3112	6-phosphofructokinase, beta subunit	0.65	2.98
PGI1	CA3559	glucose-6-phosphate isomerase	0.64	0.83
TPI1	CA5950	Triose phosphate isomerase	0.58	0.83
HXK2.3F	CA0127	hexokinase II, 3-prime end	0.49	0.83

Reserve carbohydrates

GPH1	CA5206	glycogen phosphorylase	0.57	0.83
GSY1	CA5467	glycogen synthase	0.51	0.83
IPF8321	CA2938	similar to *Saccharomyces cerevisiae* Glg2p	0.53	0.83
TPS3.3	CA5505	alpha,alpha-trehalose-phosphate synthase	0.49	0.83
Unknown and unclassified				
AGP1	CA1373	asparagine and glutamine permease	0.57	0.83
CBP3	CA2518	involved in cytochrome-c reductase assembly	0.44	0.83
DAK2.3EOC	CA0311	dihydroxyacetone kinase, 3-prime end	0.50	0.83
EFG1	CA2787	enhanced filamentous growth factor	0.64	0.83
HSP12	CA0627	heat shock protein	0.48	0.83
IFE2	CA2075	unknown function	0.48	0.83
IPF11759	CA1943	unknown function	0.66	0.83
IPF2857	CA5526	unknown function	0.66	1.40
IPF351	CA5868	unknown function	0.52	0.83
IPF3937	CA1203	unknown function	0.61	0.83
IPF4328	CA0210	unknown function	0.56	0.83
IPF4959	CA6057	D-xylulose reductase	0.67	2.98
IPF5185	CA1678	putative cell wall protein	0.25	0.83
IPF6235	CA2216	Candida albicans Tca2 retrotransposon	0.62	0.83
IPF6238	CA2752	GAG protein of retrotransposon pCal	0.71	1.40
IPF6518	CA2302	unknown function	0.41	0.83
IPF6629	CA4127	unknown function	0.50	0.83
IPF6881	CA2186	putative phosphatidyl synthase	0.67	3.22
IPF7289	CA3878	similar to *Saccharomyces cerevisiae* Upc2p	0.54	0.83
IPF9550	CA4570	similar to *Saccharomyces cerevisiae* Osm1p	0.52	0.83
PRA1	CA4399	pH-regulated antigen	0.64	1.40
RHR2	CA5788	DL-glycerol phosphatase	0.60	0.83
SUR2	CA2225	hydroxylation of C-4 of the sphingoid moiety of ceramide	0.37	0.83
TFC1	CA5163	transcription initiation factor TFIIIC 95 kD subunit	0.54	0.83
URA1	CA4745	dihydroorotate dehydrogenase	0.61	0.83

Supplemental Table 6

Expression of genes in the *efg1 efh1*mutant H/1.22 relative to the wild-type CAF2-1. Cells were grown in hyphae inducing conditions (30 min 10 % serum at 37 °C). The minimal FDR value calculated by the SAM program was 5.1 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes				
Metabolism				
ARD8	CA3288	D-arabinitol dehydrogenase	1.51	1.43
CHA12	CA3945	L-serine/L-threonine deaminase	1.76	1.05
MLS1	CA4748	malate synthase	1.51	1.05
Stress				
HSP60	CA1239	heat shock protein 60	1.51	1.43
SSA1	CA2857	heat shock protein of HSP70 family	1.68	1.43
Format-dehydrogenases				
FDH12	CA1846	formate dehydrogenase	1.90	1.43
FDH13.3F	CA0639	putative formate dehydrogenase, 3-prime end	1.68	1.05
FDH4.3F	CA0636	formate dehydrogenase, 3-prime end	1.76	1.43
Iron-uptake				
FTR1	CA5345	high affinity iron permease	2.41	1.43
FTR2	CA5354	high affinity iron permease	1.89	2.96
Unknown and unclassified				
ARG81.3EOC	CA2624	transcription factor possibly involved in arginine metabolism, 3-prime end	2.04	1.43
GCV2	CA3883	glycine decarboxylase P subunit	1.51	2.84
HIK1.5EOC	CA0108	histidine kinase, 5-prime end	1.51	2.84
IPF10911	CA2629	unknown function	1.64	4.21
IPF10929	CA2232	unknown function	1.56	2.84
IPF11262	CA3083	unknown function	1.51	1.05
IPF12824	CA2594	unknown function	1.51	2.84
IPF14614	CA0288	unknown function	1.53	4.21
IPF14624	CA1343	unknown function	3.94	5.07
IPF15706	CA2831	unknown function	1.63	2.84
IPF18393	CA3028	unknown function	1.65	2.84
IPF18512	CA2209	unknown function	2.02	4.21
IPF18579.5F	CA1970	unknown function	4.50	2.84
IPF19195.3F	CA0144	putative amino acid or GABA permease, 3-prime end	3.18	2.96
IPF19980	CA0093	putative lipase	1.58	2.84
IPF20163	CA4135	unknown function	1.57	2.84
IPF3394	CA2088	unknown function	4.26	4.02
IPF3603	CA5073	unknown function	1.51	2.85
IPF3621	CA4340	unknown function	1.55	2.84
IPF4899	CA2129	unknown function	1.64	2.99
IPF6108	CA3073	putative tricarboxylate carrier	1.69	1.43
IPF662	CA6001	unknown function	2.32	5.07
IPF8069	CA1399	unknown function	3.96	2.96
IPF823	CA5366	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1.52	1.05

IPF8746	CA1548	putative alpha-1,3-mannosyltransferase	1.52	2.96
IPF8810	CA3312	unknown function	1.59	2.84
IPF8921.5EOC	CA3125	unknown function	2.11	1.43
KIP3	CA5651	kinesin-related protein required for nuclear migration	1.64	1.43
LIP6	CA4756	Secretory lipase	1.92	2.85
MIS11	CA2250	mitochondrial C1-tetrahydrofolate synthase precursor	1.62	2.84
MSB3	CA2717	GTPase-activating protein for Sec4p	2.65	1.43
NUP49	CA5273	nuclear pore protein	1.51	1.05
PRY2	CA5344	putative pathogen related proteins	1.89	1.43
PWP2	CA5466	periodic tryptophan protein	3.35	2.84
RNR21	CA4155	ribonucleoside-diphosphate reductase	1.56	1.05
RPL14B.3	CA3602	ribosomal protein L14B, 3-prime end	1.62	2.84
SGD1.3F	CA2034	Involved in HOG pathway, 3-prime end	1.85	4.02
SHM2	CA0895	serine hydroxymethyltransferase precursor, mitochondrial	1.72	2.84
SNF31	CA5605	high-affinity glucose transporter	1.53	1.43

Downregulated genes

Glykolysis

ENO1	CA3874	enolase I (2-phosphoglycerate dehydratase)	0.63	1.43
GAP1	CA5892	glyceraldehyde-3-phosphate dehydrogenase	0.42	1.05
GLK1	CA0263	aldohexose specific glucokinase	0.46	1.05
GPM1	CA4671	phosphoglycerate mutase	0.62	1.05
HXK2.3F	CA0127	hexokinase II, 3-prime end	0.48	1.05
PFK1	CA1834	6-phosphofructokinase, alpha subunit	0.65	1.05
PFK2	CA3112	6-phosphofructokinase, beta subunit	0.57	1.05
PGI1	CA3559	glucose-6-phosphate isomerase	0.66	2.85
PGK1	CA1691	phosphoglycerate kinase	0.42	1.43
TPI1	CA5950	triose phosphate isomerase	0.55	1.05

Reserve-carbohydrates

GPH1	CA5206	glycogen phosphorylase	0.56	1.05
GSY1	CA5467	glycogen synthase	0.67	1.05
IPF8321	CA2938	similar to S. cerevisiae Glg2p	0.58	1.43
TPS1	CA4084	trehalose-6-phosphat synthase	0.66	2.96
TPS2	CA5066	threalose-6-phosphate phosphatase	0.50	1.05

Metabolism

ADH5	CA2391	probable alcohol dehydrogenase	0.57	1.05
GDH2	CA1775	NAD-specific glutamate dehydrogenase (NAD)	0.68	1.43
FAS1	CA5426	fatty-acyl-CoA synthase, beta chain	0.43	2.84
FAS2.3F	CA6107	fatty-acyl-CoA synthase, alpha chain, 3-prime end	0.68	1.43

Cell wall and transporter

ALS1.3EOC	CA0316	agglutinin-like protein, 3-prime end	0.21	1.05
ALS10	CA0448	agglutinin like protein	0.52	2.84
ALS12.3F	CA0413	agglutinin-like protein, 3-prime end	0.33	1.05
ALS4.3F	CA1528	agglutinin-like protein, 3-prime end	0.34	1.05
ECE1	CA1402	cell elongation Protein	0.63	2.84
IPF5185	CA1678	putative cell wall protein	0.43	1.05

Stress

DDR48	CA4336	stress protein	0.53	1.05
HSP12	CA0627	heat shock protein	0.64	1.05
GPX2	CA0558	glutathione peroxidase	0.63	1.05

Transcription factors

EFG1	CA2787	enhanced filamentous growth factor	0.69	2.84
TYE7	CA3707	basic helix-loop-helix transcription factor	0.59	1.05

Unknown and unclassified

APR1	CA4476	aspartyl protease	0.60	2.84
ARC40	CA3549	subunit of the Arp2/3 complex involved in the control of actin polymerization	0.66	2.84
CYB1	CA4553	G2/Mitotic-specific cyclin	0.57	2.84
FCR1	CA5890	zinc cluster transcription factor	0.63	2.84
IPF10662	CA3827	unknown function	0.22	1.05
IPF11713	CA1330	unknown function	0.52	1.05
IPF11858	CA1411	unknown function	0.62	1.47
IPF15604	CA0457	transcription factor	0.64	2.85
IPF1798	CA5264	unknown function	0.60	1.05
IPF18690	CA1377	unknown function	0.67	1.43
IPF19766	CA2746	unknown function	0.52	1.43
IPF3592	CA5068	unknown function	0.65	1.05
IPF3937	CA1203	unknown function	0.61	1.05
IPF3964	CA4111	unknown function	0.67	2.84
IPF4303	CA4245	unknown function	0.48	1.43
IPF4696	CA4970	unknown function	0.58	1.43
IPF5806	CA4216	unknown function	0.47	1.05
IPF6881	CA2186	putative phosphatidyl synthase	0.65	2.85
IPF7109	CA5650	unknown function	0.53	1.05
IPF7666	CA1120	unknown function	0.57	1.05
IPF8762	CA4220	unknown function	0.68	1.05
IPF9550	CA4570	similar to S. cerevisiae Osm1p	0.63	1.43
NDH1	CA4633	mitochondrial NADH dehydrogenase	0.50	2.84
SAP5	CA2499	secreted aspartyl proteinase 5	0.57	2.84
SEC61	CA3197	ER protein-translocation complex subunit	0.61	1.43
SNF4	CA0122	nuclear regulatory protein	0.67	1.05
SRP72	CA2519	signal recognition particle protein SRP72	0.65	2.84
STF2	CA2738	ATP synthase regulatory factor	0.53	1.05
TUB1.3	CA5546	alpha-1 tubulin, 3-prime end	0.56	2.84
UGP1	CA0435	UTP-glucose-1-phosphate uridylyltransferase	0.64	1.05

Supplemental Table 7

Expression of genes in the *EFG1*-overexpressing strain CAI4[pRC2312P-H] relative to the control strain CAI4[pBI-1]. Cells were grown in *PCK1p*-inducing SCAA medium. The minimal FDR value calculated by the SAM program was 4.9 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	Accession	description (CandidaDB)	fold regulation	q-value
Upregulated genes				
Metabolism				
ACH1	CA0345	acetyl-coenzyme-A hydrolase	1.5	0.45
ACS1	CA0848	acetyl-coenzyme-A synthetase	1.8	0.45
ACS2	CA2858	acetyl-coenzyme-A synthetase	1.5	0.45
ADH5	CA2391	probable alcohol dehydrogenase	1.5	4.95
FBA1	CA5180	fructose-bisphosphate aldolase	1.5	0.76
Cell wall and transporter				
ALS10	CA0448	agglutinin like protein	2.5	0.45
ECE1	CA1402	cell elongation Protein	1.7	0.45
HWP1	CA2825	hyphal wall protein	19.1	0.45
PHR1	CA4857	GPI-anchored pH responsive glycosyl transferase	1.5	1.25
RBT1	CA2830	repressed by Tup1 protein	2.9	0.45
Stress				
DDR48	CA4336	stress protein	2.1	0.45
IPF1222	CA4836	similar to superoxide dismutase	6.7	0.45
Unknown and unclassified				
ADO1	CA0685	adenosine kinase	1.6	0.45
CHT2	CA1051	chitinase 2 precursor	1.6	0.45
CTR1	CA1496	copper transport protein	1.6	0.45
EGD2	CA2956	nascent polypeptide associated complex protein alpha subunit	1.5	2.07
FET34.3EOC	CA1431	iron transport multicopper oxidase, 3-prime end	1.7	0.45
FET5	CA2920	multicopy oxidase	1.9	0.45
FRE30.53	CA3415	strong similarity to ferric reductase, internal fragment	1.6	0.45
FRP2	CA3153	member of the FRP family of proteins related to *Yarrowia lipolytica* glyoxylate pathway regulator Gpr1p and *Saccharomyces cerevisiae* Fun34p	1.6	0.45
IFE2	CA2075	unknown function	1.6	0.45
IPF15604	CA0457	transcription factor	1.7	4.95
IPF15781	CA1238	unknown function	1.6	0.45
IPF15870	CA2769	unknown function	1.5	0.45
IPF4450	CA0684	unknown function	1.5	0.76
IPF5196	CA1672	unknown function	1.5	4.48
IPF5198	CA1128	unknown function	1.6	4.95
MET10	CA1620	sulfite reductase flavin-binding subunit	1.5	0.76
MET15	CA2565	O-acetylhomoserine O-acetylserine sulphydrylase	1.6	0.45
MET6	CA0653	methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	1.8	0.45
RIB7	CA3495	HTP reductase	1.6	1.25
YKE2.3	CA3842	Gim complex component, 3-prime end	1.5	0.45

Downregulated genes

Cell wall and transporter

ALS1.3EOC	CA0316	agglutinin-like protein, 3-prime end	0.61	0.76
STL1	CA0472	sugar transporter	0.65	0.76

Secreted

SAP1	CA2660	secreted aspartyl proteinase	0.67	4.60
SAP2	CA3138	aspartic protease	0.63	4.26
SAP4	CA2055	secreted aspartyl proteinase	0.60	1.25

Unknown and unclassified

APN2	CA2370	AP endonuclease, exonuclease III homologue	0.66	4.26
ARO4	CA1484	3-dehydro-deoxyphosphoheptonate aldolase, tyrosine-inhibited	0.67	3.10
DAL52	CA2478	allantoate permease	0.67	4.71
DYN2.3	CA4550	dynein light chain 1, cytosolic, 3-prime end	0.62	0.45
FRE7	CA5621	ferric reductase transmembrane component	0.50	0.76
GIM5	CA2888	Gim complex component	0.62	3.90
HIS6	CA1480	5 Pro-FAR isomerase	0.56	3.10
IFA2	CA0335	unknown function	0.61	3.10
IFF10.5	CA5763	unknown function	0.59	1.50
IPF10864	CA1968	similar to *Saccharomyces cerevisiae* Rex4p	0.63	3.90
IPF10884	CA1747	unknown function	0.58	2.07
IPF11694	CA0164	similar to *Saccharomyces cerevisiae* Tna1p	0.66	4.60
IPF11766	CA0890	unknown function	0.62	2.07
IPF1261	CA5668	unknown function	0.65	3.90
IPF12662	CA0973	unknown function	0.51	3.10
IPF12676	CA1681	unknown function	0.65	0.76
IPF13139	CA3759	unknown function	0.58	2.07
IPF13626	CA2890	putative methyltransferase	0.55	3.10
IPF13667	CA3673	unknown function	0.55	0.76
IPF15575	CA1482	unknown function	0.58	2.22
IPF1882	CA6140	unknown function	0.67	3.10
IPF19195.3F	CA0144	putative amino acid or GABA permease, 3-prime end	0.41	3.10
IPF19974	CA3178	unknown function	0.67	2.07
IPF19980	CA3245	putative lipase	0.66	3.90
IPF2053	CA4983	unknown function	0.66	0.76
IPF2167	CA5310	unknown function	0.56	2.22
IPF2334	CA5199	unknown function	0.60	3.90
IPF3101	CA4654	unknown function	0.61	1.50
IPF3239	CA2472	unknown function	0.65	3.10
IPF4704	CA4974	unknown function	0.65	2.07
IPF5673	CA1103	similar to Saccharomyces cerevisiae Rex3p	0.67	4.95
IPF5865	CA2132	unknown function	0.60	3.90
IPF6889	CA3326	unknown function	0.57	2.07
IPF721.3F	CA5517	unknown function	0.66	1.50
IPF7493	CA3241	putative permease	0.62	0.45
IPF7819	CA3563	unknown function	0.65	2.07
IPF9825	CA3089	unknown function	0.63	3.10
MSC2	CA3565	probable membrane protein	0.66	3.10
MYO1	CA3233	myosin-1 isoform (type II myosin) heavy chain	0.60	4.60
NMT1	CA1063	N-myristoyltransferase	0.56	3.90
PET127	CA3308	component of mitochondrial translation	0.61	2.07
PHO11	CA0616	secreted acid phosphatase	0.61	2.07

RRS1	CA2992	regulator for ribosome synthesis	0.61	3.10
RTA1	CA0401	unknown function	0.66	4.60
SAS2	CA4814	zinc finger protein involved in silencing	0.33	4.71
TOA1	CA2767	transcription initiation factor IIA	0.66	4.60
URA2.5EOC	CA1315	multifunctional pyrimidine biosynthesis protein	0.65	0.45
YSA1	CA5909	sugar-nucleotide hydrolase	0.65	2.73

Supplemental Table 8

Expression of genes in the *EFH1*-overexpressing strain CAI4[pDB35] relative to the control strain CAI4[pBI-1]. Cells were grown in *PCK1p*-inducing SCAA medium. The minimal FDR value calculated by the SAM program was 5.5 %. Only genes regulated at least by a factor 1.5 are shown.

Gene-Name	**Accesion**	**description (CandidaDB)**	**fold regulation**	**q-value**
Upregulated genes				
Metabolism				
ACS1	CA0848	acetyl-coenzyme-A synthetase	1.9	0.89
ADH5	CA2391	probable alcohol dehydrogenase	2.0	0.89
MET13	CA2785	methylene tetrahydrofolate reductase	1.6	0.89
MET6	CA0653	methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	2.2	0.89
PDC11	CA2474	pyruvate decarboxylase	1.5	0.89
PFK2	CA3112	6-phosphofructokinase, beta subunit	1.7	3.72
Cell wall and transporter				
ALS10	CA0448	agglutinin like protein	1.5	0.89
ECE1	CA1402	cell elongation protein	2.2	0.89
HWP1	CA2825	hyphal wall protein	3.0	0.89
HYR1.53	CA0557	hyphally regulated protein	1.7	0.89
Stress				
SOD22.3F	CA5588	superoxide dismutase, 3-prime end	1.9	0.89
YHB1	CA0943	flavohemoglobin	2.5	0.89
Transcription factors				
EFH1	CA2672	transcription regulator	1.6	0.89
IPF15604	CA0457	transcription factor	2.3	3.72
Unknown and unclassified				
CAR2	CA2561	ornithine aminotransferase	1.5	0.89
CLN21	CA1582	G1 cyclin	1.5	4.73
CSE1.3F	CA2982	importin-beta-like protein, 3-prime end	1.5	4.73
DOC1	CA0002	component of the anaphase promoting complex	1.7	0.89
GIT1	CA3615	glycerophosphoinositol transporter	1.5	4.73
GLC3	CA2758	1,4-glucan branching enzyme	1.7	2.12
IFG3.3	CA5402	probable d-amino acid oxidase, 3-prime end	1.6	0.89
IPF10645	CA1944	unknown function	1.7	4.07
IPF10651	CA3823	unknown function	1.6	2.72
IPF10662	CA3827	unknown function	1.5	2.12
IPF1067	CA5757	putative glutamate decarboxylase	1.7	0.89
IPF11344	CA1341	unknown function	1.8	1.47
IPF11363	CA2802	unknown function	1.6	0.89
IPF12253	CA4727	unknown function	1.9	1.47
IPF12312	CA1099	unknown function	1.7	4.73
IPF13467	CA3768	putative peroxisomal 2,4-dienoyl-CoA reductase	1.8	0.89
IPF15543	CA5654	unknown function	1.5	3.72
IPF16253	CA0782	unknown function	1.9	1.84
IPF1833	CA6162	similar to opaque phase protein OP4	1.6	2.72
IPF1837	CA6159	unknown function	1.6	2.72
IPF4902	CA0897	unknown function	1.5	0.89
IPF4972	CA0461	unknown function	1.7	1.84

IPF525	CA5613	unknown function	2.8	0.89
IPF5806	CA4216	unknown function	1.9	0.89
IPF635	CA6013	unknown function	1.6	3.72
IPF6662	CA4288	similar to S. cerevisiae Isy1p	1.7	4.07
IPF7715	CA0706	unknown function	1.6	4.73
IPF7717	CA4058	unknown function	1.8	0.89
IPF7970	CA3259	unknown function	1.7	4.73
IPF8321	CA2938	similar to S. cerevisiae Glg2p	1.9	0.89
IPF8814	CA3315	unknown function	1.5	2.12
IPF9238	CA3412	long chain fatty alcohol oxidase	1.5	3.72
IPF995	CA5155	unknown function	2.6	4.07
LOC1	CA3997	putative double-stranded RNA-binding protein	1.6	4.73
NIT3	CA2338	nitrilase	1.6	2.12
RIB4.3	CA0054	6,7-dimethyl-8-ribityllumazine synthase, 3-prime end	1.6	2.72
SEC24	CA0958	component of COPII coat of ER-Golgi vesicles	1.6	3.72
STF2	CA2738	ATP synthase regulatory factor	1.5	2.72
UBC9	CA5109	E2 ubiquitin-conjugating enzyme	1.8	0.89

Downregulated genes

Cell wall and transporter

ALS4.3F	CA1528	agglutinin-like protein, 3-prime end	0.48	0.89
HGT11	CA1506	hexose transporter	0.36	0.89
HGT12	CA4038	hexose transporter	0.36	0.89
IPF331	CA5873	GPI-anchored cell surface protein	0.54	0.89
IPF5185	CA1678	putative cell wall protein	0.40	0.89
IPF7493	CA3241	putative permease	0.45	0.89
IPF4181	CA5798	putative permease	0.57	0.89
JEN1	CA5737	carboxylic acid transporter protein	0.63	1.47
JEN2	CA5478	carboxylic acid transporter protein	0.56	0.89

Unknown and unclassified

ARG81.3EOC	CA2624	transcription factor possibly involved in arginine metabolism, 3-prime end	0.61	3.72
CMK1	CA6135	Ca2+/calmodulin-dependent ser/thr protein kinase	0.65	0.89
FRP1	CA3813	member of the FRP family of proteins related to Y. lipolytica glyoxylate pathway regulator Gpr1p and S. cerrevisiae Fun34p	0.37	0.89
FUN34.5EOC	CA3154	unknown function	0.59	1.47
GAL10	CA4041	UDP-glucose 4-epimerase by homology	0.65	0.89
GCD2	CA5929	Translation initiation factor eIF2B	0.66	4.73
HEM14	CA1951	Mitochondrial protoporphyrinogen oxidase	0.65	2.72
IMH3.EXON2	CA1245	IMP dehydrogenase, exon 2	0.61	0.89
IPF11182.3EOC	CA0174	unknown function	0.65	2.72
IPF12540	CA2974	unknown function	0.60	0.89
IPF1390	CA5093	unknown function	0.63	4.80
IPF14710	CA1080	unknown function	0.64	3.72
IPF17283	CA2021	unknown function	0.65	1.47
IPF4182	CA5797	unknown function	0.64	0.89
IPF4859	CA3700	unknown function	0.65	0.89
IPF5330	CA1339	unknown function	0.65	2.72
IPF6105	CA3075	similar to S. cerevisiae Gua1p GMP synthase	0.60	2.72
RRP6	CA2593	involved in 5.8S rRNA processing	0.65	2.72
TIM23	CA3130	mitochondrial inner membrane import translocase	0.61	4.73