Supplemental Table 1A

Expression of genes in the wild-type CAF2-1 in hypoxic conditions relative to normoxic conditions. 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 on array	gene number	orf19 number	proposed function (according to CandidaDB: http://genolist.pasteur.fr/CandidaDB)	fold regulation	q-value
upregulation					
fatty acid metabolism					
ACC1	CA5816	orf19.7466	acetyl-coenzyme-A carboxylase	2.8	0.52
FAS1	CA5426	orf19.979	fatty-acyl-CoA synthase	2.8	2.29
FAS2.3F	CA6107	orf19.5949	fatty-acyl-CoA synthase	1.7	4.17
FAS2.5F	CA6105	orf19.5951	fatty-acyl-CoA synthase	1.5	0.52
OLE1	CA3921	orf19.5117	stearoyl-CoA desaturase	3.5	0.52
ergosterol metabolism					
ERG11	CA1387	orf19.922	cytochrome P450 lanosterol 14a-demethylase	2.5	0.52
ERG251	CA0875	orf19.4631	C-4 sterol methyl oxidase	1.6	0.52
ERG3	CA1956	orf19.767	C5,6 desaturase	2.4	0.52
ERG5	CA4418	orf19.5178	C-22 sterol desaturase by homology	2.2	0.52
orf19.391	CA3878	orf19.391	similar to *S. cerevisiae* Upc2p RNA polymerase II transcription factor (sterol uptake)	1.6	0.52
POT14	CA0290	orf19.1591	acetyl-CoA acetyltransferase	1.7	0.52
cell wall/ membrane					
ALG2.5	CA1530	orf19.1221	mannosyltransferase, 5-prime end	2.1	3.08
ECM33.3	CA3115	orf19.3010.1	cell wall biogenesis	2.5	0.52
PGA6	CA2625	orf19.4765	putative glycosylphosphatidylinositol-modified protein	1.6	0.52
PLB4.3F	CA0186	orf19.1443	phospholipase (3-prime end)	1.6	0.52
PLB4.5F	CA0185	orf19.1442	phospholipase (5-prime end)	1.8	1.43
SUN41	CA0883	orf19.3642	putative cell wall beta-glucosidase	1.9	0.52
SUN42	CA5232	orf19.5032	putative cell wall beta-glucosidase	2.1	0.52
glycolysis					
ENO1	CA3874	orf19.395	enolase I (2-phosphoglycerate dehydratase)	2.4	0.52
FBA1	CA5180	orf19.4618	fructose-bisphosphate aldolase	3.5	0.52
GAP1	CA5892	orf19.6814	glyceraldehyde-3-phosphate dehydrogenase	3.4	0.52
GLK1	CA0263	orf19.13	aldohexose specific glucokinase	2.9	0.52
GPM1	CA4671	orf19.903	phosphoglycerate mutase	2.9	0.52
PDC11	CA2474	orf19.2877	pyruvate decarboxylase	2.6	0.52
PFK2	CA3112	orf19.6540	6-phosphofructokinase	1.6	0.80
PGI1	CA3559	orf19.3888	glucose-6-phosphate isomerase	2.8	0.52
PGK1	CA1691	orf19.3651	phosphoglycerate kinase	4.2	0.52
PYC2.EXON2	CA1464	orf19.789	pyruvate carboxylase 2	1.6	2.29
TPI1	CA5950	orf19.6745	triose phosphate isomerase	2.5	0.52
TPS3.3	CA5505	orf19.5348	alpha,alpha-trehalose-phosphate synthase, regulatory subunit	2.3	0.52
fermentation					
ADH1	CA4765	orf19.3997	alcohol dehydrogenase	3.8	0.52
ADH2	CA3923	orf19.5113	alcohol dehydrogenase I	1.6	0.52
ADH5	CA2391	orf19.2608	probable alcohol dehydrogenase	1.5	0.52

stress response					
CTA1	CA3011	orf19.6229	catalase A, peroxisomal	3.6	1.83
GRP2	CA2644	orf19.4309	reductase	1.7	2.29
HSP12	CA0627	orf19.3160	heat shock protein	9.6	0.52
SSA1	CA2857	orf19.1065	heat shock protein of Hsp70 family	2.5	2.29
SSA4	CA1230	orf19.4980	cahsp70 mRNA for heat shock	1.6	0.52
SSC1	CA4474	orf19.1896	mitochondrial heat shock protein 70-related protein	1.7	4.17
SSU81	CA2188	orf19.4772	protein involved in the Hog1 high-osmolarity signal transduction pathway	1.7	4.17
hyphae specific genes					
ALS12.3F	CA0413	orf19.2122	agglutinin-like protein	8.5	0.52
DDR48	CA4336	orf19.4082	stress protein	2.3	0.52
HWP1	CA2825	orf19.1321	hyphal wall protein	4.1	2.29
RBT5	CA2558	orf19.5636	repressed by Tup1 protein	5.5	0.52
translation					
BEL1.EXON2	CA4589	orf19.6906.1	protein of the 40S ribosomal subunit (exon 2)	1.6	1.83
PRT1	CA4892	orf19.6584	translation initiation factor eIF3	5.3	3.08
RNR21	CA4155	orf19.5801	ribonucleoside-diphosphate reductase	1.7	0.80
RPL10E	CA5200	orf19.7015	ribosomal protein L10, cytosolic	2.0	2.29
RPL18.EXON2	CA6079	orf19.5981.1	ribosomal Protein Rpl18B (large subunit)	1.5	0.80
RPS7A	CA1502	orf19.1700	ribosomal protein	1.7	2.29
iron metabolism					
FRE5	CA2556	orf19.5634	ferric reductase transmembrane component	3.4	5.53
FTR1	CA5345	orf19.7219	high affinity iron permease	1.6	0.52
unknown and unclassified					
ACT1	CA5255	orf19.5007	actin	1.9	0.80
CBP1	CA5559	orf19.7323	corticosteroid binding protein	1.7	0.80
CDC5	CA2986	orf19.6010	cell-cycle protein kinase	1.6	0.80
CPY1.3F (PRC1)	CA0430	orf19.1339	carboxypeptidase Y precursor	1.6	0.52
FUN30	CA3229	orf19.6291	helicases of the Snf2/Rad54 family	2.0	0.52
GPH1	CA5206	orf19.7021	glycogen phosphorylase	1.7	1.83
HHT21	CA2861	orf19.1061	histone H3	2.0	1.41
HXK2.3F	CA0127	orf19.542	hexokinase II (3-prime end)	1.5	1.43
HXT62	CA1067	orf19.2023	sugar transporter	1.8	0.52
IFA6	CA4419	orf19.5177	unknown function	2.1	1.41
orf19.1151	CA1330	orf19.1151	unknown function	1.6	0.52
orf19.1573	CA0761	orf19.1573	P-type ATPase	1.6	2.29
orf19.1728	CA1644	orf19.1728	unknown function	1.7	0.80
orf19.1729	CA1643	orf19.1729	unknown function	3.5	0.52
orf19.1872	CA4490	orf19.1872	unknown function	2.2	0.52
orf19.1964	CA2947	orf19.1964	unknown function	2.4	0.52
orf19.1964	CA2302	orf19.1691	unknown function	6.9	0.52
orf19.2119	CA2727	orf19.2119	similar to *S. cerevisiae* Ndt80p, meiosis-specific protein	1.5	0.80
orf19.2296	CA0446	orf19.2296	similar to mucin proteins	1.7	0.52
orf19.2368	CA2748	orf19.2368	unknown function	8.6	5.53
orf19.2374	CA2752	orf19.2374	GAG protein of retrotransposon pCal	2.4	0.52
orf19.2451	CA0380	orf19.2451	unknown function	2.2	0.52
orf19.251	CA0828	orf19.251	unknown function	3.0	0.52
orf19.2758	CA1898	orf19.2758	unknown function	1.6	0.80
orf19.2762	CA4127	orf19.2762	unknown function	2.3	0.52
orf19.2825	CA0381	orf19.2825	unknown function	1.6	0.52
orf19.3037	CA5065	orf19.3037	similar to *S. cerevisiae* Pab1p, mRNA polyadenylate-	1.8	0.52

			binding protein		
orf19.3261	CA5454	orf19.3261	member of the FRP family of proteins related to *Y. lipolytica* glyoxylate pathway regulator Gpr1p and *S. cerevisiae*Fun34p	3.5	0.52
orf19.3414	CA0055	orf19.3414	unknown function	1.6	0.80
orf19.3712	CA3141	orf19.3712	unknown function	1.5	0.80
orf19.4246	CA2186	orf19.4246	putative phosphatidyl synthase	2.3	1.43
orf19.4280	CA3067	orf19.4280	unknown function	2.5	0.52
orf19.5315	CA5482	orf19.5315	repeated protein (10 times) of unknown function	1.8	0.80
orf19.5372	CA2216	orf19.5372	*TCA2* retrotransposon	2.7	0.52
orf19.5525	CA0210	orf19.5525	unknown function	2.5	0.52
orf19.5539	CA1923	orf19.5539	unknown function	6.5	0.52
orf19.5667	CA4376	orf19.5667	unknown function	1.5	4.17
orf19.5976	CA6083	orf19.5976	unknown function	1.6	3.08
orf19.6608	CA3848	orf19.6608	unknown function	1.7	0.80
orf19.6614	CA5811	orf19.6614	unknown function	1.6	0.52
orf19.6882	CA4570	orf19.6882	similar to *S. cerevisiae* Osm1p, osmotic growth protein	1.6	3.08
orf19.7310	CA5547	orf19.7310	similar to *S.cerevisiae* Gin3p	2.3	3.08
orf19.7350	CA5650	orf19.7350	unknown function	1.5	0.52
orf19.842	CA2020	orf19.842	unknown function	1.7	2.29
PGA34	CA2548	orf19.2833	unknown function	4.7	1.43
PGA54	CA2769	orf19.2685	unknown function	1.7	2.29
PGA56	CA0171	orf19.1105.2	unknown function	1.9	2.29
PHO88	CA5563	orf19.7327	involved in phosphate transport	6.5	2.29
PMA1	CA2300	orf19.5383	plasma membrane H+-transporting ATPase	1.8	2.29
POL0	CA2217	orf19.5373	Pol polyprotein, reverse transcriptase	3.8	0.52
PRC1	CA0430	orf19.1339	carboxypeptidase Y precursor	1.8	0.52
QDR1	CA4501	orf19.508	putative antibiotic resistance proteins	2.0	0.52
RAT1	CA3242	orf19.4681	5´-3´-exoribonuclease	1.7	4.17
SBP1	CA2951	orf19.5854	RNA binding protein-like	1.5	5.53
SCS7	CA4852	orf19.3822	required for hydroxylation of ceramide	1.6	1.41
SCW1	CA0156	orf19.1779	glucanase	2.0	0.52
SIK1	CA5975	orf19.7569	nucleolar protein involved in pre-rRNA processing	6.3	2.29
SPB1	CA0443	orf19.76	putative methyltransferase by homology	5.1	4.17
SUR2	CA2225	orf19.5818	hydroxylation of C-4 of the sphingoid moiety of ceramide	1.6	0.80
TKL1	CA3924	orf19.5112	transketolase	8.2	0.80
TOS1	CA2303	orf19.1690	putative anchor subunit of a-agglutinin	1.7	0.52
UBI4	CA5932	orf19.6771	polyubiquitin	2.2	0.80

<u>downregulation</u>

respiratory chain

COX13	CA4536	orf19.1467	cytochrome-c oxidase chain VIa	0.62	0.52
CYT1	CA0864	orf19.3527	cytochrome-c1	0.64	1.43
orf19.2821	CA0540	orf19.2821	NADH dehydrogenase (ubiquinone)	0.67	1.83
orf19.4016	CA4783	orf19.4016	ubiquinol-cytochrome-c reductase	0.58	0.52
orf19.913.2	CA0118	orf19.913.2	similar to *S. cerevisiae* Qcr6p ubiquinol-cytochrome-c reductase 17K protein, 3-prime end	0.63	1.83
QCR2	CA2065	orf19.2644	ubiquinol--cytochrome-c reductase 40KD chain II	0.55	0.52
RIP1	CA6149	orf19.5893	ubiquinol cytochrome-c reductase	0.63	0.52

(ATP-synthesis)

ATP1.EXON3	CA4457	orf19.6853.3	F1F0-ATPase complex, F1 alpha subunit, exon 3	0.45	0.52
ATP2	CA4362	orf19.5653	F1F0-ATPase complex, F1 beta subunit	0.52	0.52

ATP3.3	CA1489	orf19.3223	F1F0-ATPase complex, F1 gamma subunit, 3-prime end	0.56	0.52
ATP5	CA5775	orf19.5419	F1F0-ATPase complex, OSCP subunit	0.52	0.52
ATP7	CA1907	orf19.2785	F1F0-ATPase complex, FO D subunit	0.56	0.52
orf19.5598.2	CA2973	orf19.5598.2	F1-ATPase epsilon subunit	0.63	2.29
MIR1	CA1513	orf19.4885	phosphate transport protein, mitochondrial (MCF)	0.39	0.52
orf19.5231.2	CA1107	orf19.5231.2	ATP19 subunit K of the dimeric form of mitochondrial F1F0-ATP synthase	0.62	0.52
orf19.5598.2	CA2973	orf19.5598.2	F1-ATPase epsilon subunit	0.64	2.29
PHO84.3EOC	CA1782	orf19.1172	Inorganic phosphate transport protein, 3-prime end	0.61	0.52
STF2	CA2738	orf19.2107.1	ATP synthase regulatory factor	0.67	1.83
citric acid cycle					
ACO1	CA3546	orf19.6385	aconitate hydratase	0.63	1.41
CIT1.EXON2	CA3909	orf19.4393	citrate synthase, exon 2	0.56	0.52
FUM12.3F	CA4351	orf19.6725	fumarate hydratase (3-prime end)	0.41	0.52
FUM12.5F	CA4349	orf19.6724	fumarate hydratase (5-prime end)	0.53	0.52
IDH1.3	CA4753	orf19.4826	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial, 3-prime end	0.54	0.52
IDH2	CA4148	orf19.5791	isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial	0.55	0.52
KGD2	CA2997	orf19.6126	2-oxoglutarate dehydrogenase complex, E2 component	0.65	0.52
unknown and unclassified					
DBF2	CA0205	orf19.1223	putative ser/thr protein kinase by homology	0.48	0.52
FRE30.3	CA3416	orf19.6139	strong similarity to ferric reductase Fre2p (3-prime end)	0.55	0.52
FRE30.53	CA3415	orf19.6140	strong similarity to ferric reductase (internal fragment)	0.56	0.52
GPX2	CA0558	orf19.85	glutathione peroxidase	0.63	0.80
IFE2	CA2075	orf19.5288	unknown function	0.51	0.52
FKH2	CA5754	orf19.5390	fork head protein-type transcription factor	0.64	2.29
OGG1	CA5318	orf19.7190	8-oxoguanine DNA glycosylase	0.60	0.80
orf19.1590	CA0289	orf19.1590	unknown function	0.61	0.52
orf19.1682	CA0216	orf19.1682	unknown function	0.63	0.52
orf19.26	CA3609	orf19.26	similar to *S. cerevisiae* Png1P, peptide:N-glycanase	0.64	1.83
orf19.2954	CA4178	orf19.2954	unknown function	0.66	2.29
orf19.3264	CA5456	orf19.3264	unknown function	0.54	3.08
orf19.3679	CA4048	orf19.3679	unknown function	0.33	0.52
orf19.3926	CA2231	orf19.3926	similar to *S. cerevisiae* Rny1p, ribonuclease from the T2 family of ribonucleases	0.66	1.83
orf19.6124	CA2996	orf19.6124	similar to *S. cerevisiae* Ace2p, transcription factor	0.50	3.08
orf19.6223	CA0400	orf19.6223	similar to *S. cerevisiae* Spo22p, involved in sporulation (3-prime end)	0.48	0.52
orf19.6474	CA0973	orf19.6474	unknown function	0.43	1.83
orf19.6493	CA1727	orf19.6493	unknown function	0.54	0.52
orf19.695	CA2209	orf19.695	unknown function	0.64	3.08
orf19.718	CA1240	orf19.718	similar to *S. cerevisiae* Rrn11p, involved in RNA polymerase I specific transcription	0.51	0.52
orf19.7386	CA5684	orf19.7386	unknown function	0.65	0.52
orf19.952	CA5408	orf19.952	unknown function	0.44	0.52
PDE2	CA3450	orf19.2972	nucleotide phosphodiesterase	0.65	2.29
YHB1	CA0943	orf19.3707	flavohemoglobin	0.27	0.52
YNK1	CA2645	orf19.4311	nucleoside diphosphate kinase	0.53	0.52

Supplemental Table 1B

Expression of genes in the *efg1* mutant HLC52 in hypoxic conditions relative to normoxic conditions. 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 on array	**gene number**	**orf 19 number**	**proposed function (according to CandidaDB: http://genolist.pasteur.fr/CandidaDB)**	**fold regulation**	**q-value**
upregulation					
fatty acid metabolism					
OLE1	CA3921	orf19.5117	stearoyl-CoA desaturase	1.7	1.08
orf19.4048	CA2493	orf19.4048	putative fatty acid desaturase	1.9	0.25
ergosterol metabolism					
ERG13	CA5549	orf19.7312	3-hydroxy-3-methylglutaryl coenzyme A synthase	1.5	0.25
ERG11	CA1387	orf19.922	cytochrome P450 lanosterol 14a-demethylase	3.1	0.25
ERG251	CA0875	orf19.4631	C-4 sterol methyl oxidase	1.9	0.25
ERG3	CA1956	orf19.767	C5,6 desaturase	8.1	0.25
ERG5	CA4418	orf19.5178	C-22 sterol desaturase by homology	2.4	0.25
ERG7	CA3994	orf19.1570	lanosterol synthase	1.6	4.45
orf19.391	CA3878	orf19.391	similar to *S. cerevisiae* Upc2p, RNA polymerase II transcription factor (sterol uptake)	2.0	0.25
POT14	CA0290	orf19.1591	acetyl-CoA acetyltransferase	1.9	0.25
cell wall/ membrane					
EXG1	CA0822	orf19.2990	glucan 1,3-beta-glucosidase	5.2	1.19
SUN41	CA0883	orf19.3642	putative cell wall beta-glucosidase	1.7	0.25
SUN42	CA5232	orf19.5032	putative cell wall beta-glucosidase	2.1	0.25
glycolysis					
ENO1	CA3874	orf19.395	enolase I (2-phosphoglycerate dehydratase)	1.9	0.25
FBA1	CA5180	orf19.4618	fructose-bisphosphate aldolase	4.0	0.25
GAP1	CA5892	orf19.6814	glyceraldehyde-3-phosphate dehydrogenase	2.0	0.25
GPM1	CA4671	orf19.903	phosphoglycerate mutase	3.7	0.25
PFK1	CA1834	orf19.3967	6-phosphofructokinase, alpha subunit	2.1	0.45
PGI1	CA3559	orf19.3888	glucose-6-phosphate isomerase	2.4	0.25
PGK1	CA1691	orf19.3651	phosphoglycerate kinase	2.2	0.82
TPI1	CA5950	orf19.6745	triose phosphate isomerase	2.2	0.25
fermentation					
ADH1	CA4765	orf19.3997	alcohol dehydrogenase	2.3	0.82
ADH2	CA3923	orf19.5113	alcohol dehydrogenase I	2.6	0.25
glycosylation					
ALG2.5	CA1530	orf19.1221	mannosyltransferase, 5-prime end	2.0	3.54
PMT2	CA5894	orf19.6812	O-D-mannosyltransferase	1.5	1.17
hyphae specific genes					
RBT5	CA2558	orf19.5636	repressed by Tup1p, protein 5	2.5	0.25
iron metabolism					
FET34.3EOC	CA1431	orf19.1206	iron transport multicopper oxidase (3-prime end)	8.1	0.25
FET5	CA2920	orf19.4215	multicopy oxidase	5.2	0.25
FTR1	CA5345	orf19.7219	high affinity iron permease	3.5	0.25

FTR2	CA5354	orf19.7231	high affinity iron permease	2.0	0.45
respiratory chain					
COX15	CA1688	orf19.3656	cytochrome oxidase assembly factor	1.9	0.82
CYB5	CA5645	orf19.7049	cytochrome b5	1.9	1.17
NCP1	CA3327	orf19.2672	NADPH-cytochrome P450 reductase	1.5	0.45
transcription					
GAL11	CA3928	orf19.5105	DNA-directed RNA polymerase II holoenzyme and Kornberg s mediator (SRB) subcomplex subunit	2.2	5.46
RPA49	CA0912	orf19.2017	DNA-directed RNA polymerase A	1.6	4.45
RPO26	CA2066	orf19.2643	DNA-directed RNA polymerase I, II, III 18 KD subunit	2.4	2.88
translation					
BEL1.EXON1	CA4588	orf19.6906.1	protein of the 40S ribosomal subunit, exon 1	1.6	1.59
BEL1.EXON2	CA4589	#NV	protein of the 40S ribosomal subunit, exon 2	2.0	2.46
CDC61.3F	CA2060	orf19.2560	cytosolic leucyl-tRNA synthetase, 3-prime end	1.8	0.83
HCR1	CA6012	orf19.7613	putative translation initiation factor 3 subunit	1.8	1.59
HTS1	CA2494	orf19.4051	histidine tRNA synthetase	1.6	0.93
KRS1	CA5947	orf19.6749	lysyl-tRNA synthetase	1.6	1.17
MRPL16	CA0910	orf19.2019	ribosomal protein	1.6	2.88
MRPL38	CA2607	orf19.5684	ribosomal protein of the large subunit (L14), mitochondrial, by homology	1.6	3.54
MRPL9	CA5830	orf19.7485	mitochondrial ribosomal protein of the large subunit	1.5	4.45
orf19.3341	CA2720	orf19.3341	arginyl-tRNA synthetase	1.7	1.59
RPL82	CA3304	orf19.2311	60S ribosomal protein L7a.e.B	1.9	0.82
RPS13.3	CA1304	orf19.4193.1	ribosomal protein (3-prime end)	1.5	1.17
RPS19A.3	CA6068	orf19.5996.1	ribosomal protein S19.e (3-prime end)	1.7	3.54
RPS21	CA1715	orf19.3334	ribosomal protein	1.5	0.83
SES1	CA1598	orf19.269	seryl-tRNA synthetase	1.9	0.25
SUI3	CA5298	orf19.7161	translation initiation factor eIF2 beta subunit	1.7	2.08
TIF3	CA3754	orf19.3423	translation initiation factor eIF4B	2.0	0.25
TIF34	CA4166	orf19.2967	translation initiation factor eIF3, p39 subunit	1.9	1.59
TIF35	CA5359	orf19.7236	translation initiation factor eIF3, p33 subunit	1.5	1.59
TIF5	CA0667	orf19.4261	translation initiation factor eIF5	1.8	0.25
TRM1	CA5457	orf19.3265	N2,N2-dimethylguanine tRNA methyltransferase	1.8	4.45
DNA replication					
MCM3	CA4471	orf19.1901	replication initiation protein	1.7	2.46
RNR21	CA4155	orf19.5801	ribonucleoside-diphosphate reductase	1.8	1.59
RNR22	CA4492	orf19.1868	ribonucleoside-diphosphate reductase	2.3	0.45
GTP-binding					
ARF22	CA6093	orf19.5964	GTP-binding protein of the ARF family	1.5	0.93
FUN11	CA3893	orf19.5083	putative GTP-binding protein	5.2	2.88
GSP1	CA2675	orf19.5493	GTP-binding protein	1.8	1.08
GTR1	CA1677	orf19.3617	GTP-binding protein by homology	2.8	3.54
orf19.3977	CA3401	orf19.3977	putative GTP-binding protein	1.6	0.25
SAR1.3	CA2029	orf19.3462	GTP-binding protein of the ARF family, 3-prime end	1.7	2.88
unknown and unclassified					
ARO2	CA0398	orf19.1986	chorismate synthase	1.7	2.08
BAT22	CA5040	orf19.6994	branched chain amino acid aminotransferase	1.6	3.54
CC43	CA3005	orf19.6237	homologue of Cdc42p	1.8	5.46
COS162	CA4134	orf19.4240	involved in manganese homeostasis	1.8	3.54
CYS3	CA5127	orf19.6402	cystathionine gamma-lyase by homology	1.9	1.17
DAK2.3EOC	CA0776	orf19.4777	dihydroxyacetone kinase (3-prime end)	1.6	3.54
DBP2.EXON2	CA1415	orf19.171	ATP-dependent RNA helicase of DEAD box family, exon 2	1.9	0.25

DBP3	CA1202	orf19.4870	ATP-dependent RNA helicase (CA3) by homology	3.3	0.25
DIP2	CA3927	orf19.5106	beta transducin	1.7	2.08
EBP4	CA4030	orf19.3433	NADPH dehydrogenase	1.8	1.17
ENP1	CA2449	orf19.5507	essential nuclear protein	1.7	0.25
FUR1	CA2069	orf19.2640	uracil phosphoribosyltransferase	1.8	5.46
GAA1	CA2612	orf19.5693	required for attachment of GPI anchor onto proteins by homology	2.8	2.88
GAP3	CA2638	orf19.4304	general amino acid permease	1.7	2.08
GAP6	CA4265	orf19.6659	general amino acid permease	1.5	1.17
GAP7.5EOC	CA0160	orf19.3195	general amino acid permease (5-prime end)	1.6	2.08
GOG5	CA2980	orf19.1232	GDP-mannose transporter	1.6	0.25
HEM15	CA4484	orf19.1880	ferrochelatase precursor	1.9	5.46
HIS7	CA2447	orf19.5505	histidine biosynthesis	4.0	1.19
HPT1	CA3787	orf19.5832	hypoxanthine guanine phosphoribosy transferase	1.8	2.46
HSH49	CA3579	orf19.2261	spliceosome-associated essential protein	1.6	0.25
ICL1	CA4446	orf19.6844	isocitrate lyase (glyoxylate cycle)	1.5	0.25
IFO3	CA1393	orf19.1766	similar to *Streptomyces coelicolor* putative hydrolase	3.6	0.45
ILV2	CA0428	orf19.1613	acetolactate synthase	2.8	1.59
IMH3.EXON1	CA1246	orf19.19	IMP dehydrogenase, exon 1	1.5	1.17
IPF3767	CA0057	unknown	unknown fuction	1.7	2.88
LYS2	CA0916	orf19.2970	L-aminoadipate-semialdehyde dehydrogenase, large subunit	1.7	5.46
MAK11	CA2461	orf19.1791	involved in cell growth and replication of M1 dsRNA virus	2.7	3.54
MIS12	CA5869	orf19.7534	mitochondrial C1-tetrahydrofolate synthase precursor	2.4	5.46
MRT4	CA2283	orf19.5550	required for mRNA decay	1.7	1.08
NOG2.EXON2	CA2848	orf19.5733	unknown function nuclear/nucleolar GTP-binding protein, by homology	1.5	1.19
NOP1	CA3570	orf19.3138	fibrillarin	1.6	0.25
NOP2	CA4505	orf19.501	nucleolar protein	1.5	1.17
NUP2	CA4270	orf19.6665	nuclear pore protein	1.5	4.45
orf19.1086	CA0372	orf19.1086	unknown fuction	1.6	0.25
orf19.1168	CA1786	orf19.1168	unknown fuction	3.1	0.45
orf19.150	CA0010	orf19.150	similar to *S. cerevisiae* Tim17p, mitochondrial inner membrane import translocase subunit	1.6	2.08
orf19.1518.3	CA1749	orf19.1518.3	unknown fuction	2.0	1.17
orf19.1566	CA3990	orf19.1566	beta-transducin	2.2	1.59
orf19.1569	CA3993	orf19.1569	unknown fuction	1.5	2.08
orf19.1573	CA0761	orf19.1573	P-type ATPase	1.7	1.59
orf19.1595	CA0295	orf19.1595	unknown fuction	1.6	1.08
orf19.1679	CA0837	orf19.1679	unknown fuction	1.7	2.08
orf19.1691	CA2302	orf19.1691	unknown fuction	4.9	0.25
orf19.1697	CA1500	orf19.1697	unknown fuction	1.6	4.45
orf19.1729	CA1643	orf19.1729	unknown fuction	1.6	0.25
orf19.1800	CA0982	orf19.1800	unknown fuction	1.7	1.17
orf19.1802	CA0984	orf19.1802	unknown fuction	1.9	0.25
orf19.1865	CA4495	orf19.1865	aldehyde dehydrogenase	1.9	0.25
orf19.1917	CA0812	orf19.1917	unknown fuction	2.1	1.19
orf19.2119	CA2727	orf19.2119	similar to *S. cerevisiae* Ndt80p meiosis-specific protein	1.5	0.83
orf19.2286	CA1114	orf19.2286	unknown fuction	2.3	0.25
orf19.2314	CA3301	orf19.2314	unknown fuction	2.6	0.82
orf19.2374	CA2752	orf19.2374	GAG protein of retrotransposon pCal	1.9	0.25
orf19.2503	CA1040	orf19.2503	unknown fuction	1.8	1.08
orf19.2810	CA2619	orf19.2810	amino acid permease	2.9	5.46
orf19.2998	CA2814	orf19.2998	unknown fuction	1.5	0.25

orf19.3034	CA5063	orf19.3034	putative member of nontransporter group of ATP-binding cassette (ABC) superfamily	1.8	0.25
orf19.3063	CA5088	orf19.3063	similar to *S. cerevisiae* Dpb3p, DNA-directed DNA polymerase epsilon, subunit C	1.8	3.54
orf19.3159	CA1268	orf19.3159	unknown fuction	1.8	4.45
orf19.319	CA3389	orf19.319	unknown fuction	2.6	2.08
orf19.3261	CA5454	orf19.3261	member of the FRP family of proteins related to *Y. lipolytica* glyoxylate pathway regulator Gpr1p and *S. cerevisiae* Fun34p	3.7	0.82
orf19.3350	CA0986	orf19.3350	similar to *S. cerevisiae* Mrp20p, ribosomal protein of the large subunit, mitochondrial	1.6	1.17
orf19.3463	CA2030	orf19.3463	unknown fuction	1.6	1.17
orf19.3799	CA1423	orf19.3799	unknown fuction	1.6	1.19
orf19.3859	CA3097	orf19.3859	unknown fuction	3.3	2.46
orf19.3876	CA3551	orf19.3876	unknown fuction	1.5	2.08
orf19.3914	CA3016	orf19.3914	unknown fuction	1.6	1.19
orf19.3969	CA1309	orf19.3969	unknown fuction	1.6	2.08
orf19.4002	CA4770	orf19.4002	similar to *S. cerevisiae* Dun1p, protein kinase (3-prime end)	1.6	1.59
orf19.4013	CA4780	orf19.4013	unknown fuction	1.6	1.08
orf19.4030	CA4795	orf19.4030	similar to *S. cerevisiae* Pri1p, DNA-directed DNA polymerase alpha 48kDa subunit (DNA primase)	1.7	1.08
orf19.4068	CA1140	orf19.4068	unknown fuction	1.5	1.17
orf19.4070	CA1142	orf19.4070	unknown fuction	2.3	0.25
orf19.4219	CA1318	orf19.4219	nuclear valosin-containing protein-like	1.6	1.59
orf19.4282	CA3065	orf19.4282	unknown fuction	3.5	0.25
orf19.4283	CA3064	orf19.4283	unknown fuction	1.5	3.54
orf19.4330	CA0646	orf19.4330	unknown fuction	4.8	3.54
orf19.4612	CA5175	orf19.4612	similar to *Legionella pneumophila* SbpA	6.5	2.88
orf19.4742	CA1947	orf19.4742	starvation protein -like	7.0	3.54
orf19.4831	CA4749	orf19.4831	unknown fuction	1.5	5.46
orf19.494	CA4511	orf19.494	unknown fuction	1.9	1.19
orf19.506	CA4502	orf19.506	Similar to DnaJ proteins	1.6	1.17
orf19.5067	CA0533	orf19.5067	unknown fuction	2.0	5.46
orf19.5103	CA3931	orf19.5103	unknown fuction	1.6	2.08
orf19.5246	CA5001	orf19.5246	unknown fuction	1.9	5.46
orf19.5279	CA4973	orf19.5279	unknown fuction	2.0	1.17
orf19.5305	CA5476	orf19.5305	unknown fuction	1.7	1.19
orf19.5356	CA5510	orf19.5356	unknown fuction	1.5	3.54
orf19.5372	CA2216	orf19.5372	Tca2 retrotransposon	2.4	0.25
orf19.5884	CA6155	orf19.5884	unknown fuction	3.3	2.46
orf19.5885	CA6154	orf19.5885	similar to *S. cerevisiae* Snu13p, U4/U6.U5 snRNP associated protein	1.9	1.19
orf19.6227	CA3012	orf19.6227	unknown fuction	1.7	0.25
orf19.6234	CA3007	orf19.6234	unknown fuction	2.4	0.25
orf19.6379	CA3543	orf19.6379	unknown fuction	2.7	3.54
orf19.6686	CA4289	orf19.6686	unknown fuction	1.6	0.25
orf19.6705	CA4305	orf19.6705	unknown fuction	1.5	1.17
orf19.6710	CA4339	orf19.6710	unknown fuction	1.6	1.59
orf19.6723	CA4348	orf19.6723	unknown fuction	1.6	4.45
orf19.6803	CA5903	orf19.6803	transmembrane sugar transporter	1.5	0.93
orf19.6862	CA4465	orf19.6862	unknown fuction	1.5	3.54
orf19.6882	CA4570	orf19.6882	similar to *S. cerevisiae* Osm1p, osmotic growth protein	2.0	1.59
orf19.6955	CA4718	orf19.6955	unknown fuction	1.8	5.46
orf19.6984	CA5030	orf19.6984	unknown fuction	2.5	3.54
orf19.7098	CA5601	orf19.7098	transcriptional regulator	1.5	1.19

orf19.7200	CA5326	orf19.7200	unknown fuction	2.0	1.19
orf19.7307	CA5545	orf19.7307	similar to cytochrome-b5- and nitrate reductases	1.9	5.46
orf19.7310	CA5547	orf19.7310	similar to *S. cerevisiae* Gin3p	2.8	2.88
orf19.7463	CA5814	orf19.7463	putative protease	1.8	0.45
orf19.853	CA0771	orf19.853	asaprtic proteinase	2.9	5.46
orf19.927	CA1383	orf19.927	unknown fuction	4.5	1.17
PAN3	CA4777	orf19.4010	component of the Pab1p-dependent poly(A) ribonuclease	1.7	2.46
PGA26	CA2885	orf19.2475	unknown fuction	2.0	0.93
PGA50	CA1777	orf19.1824	unknown fuction	2.0	3.54
PGA54	CA2769	orf19.2685	unknown fuction	1.6	0.83
PHO85	CA4448	orf19.6846	negative regulator of *PHO* genes	1.5	2.88
PHO88	CA5563	orf19.7327	involved in phosphate transport	1.5	1.19
POL0	CA2217	orf19.5373	pol polyprotein, reverse transcriptase	2.5	0.25
POL30	CA5178	orf19.4616	proliferating cell nuclear antigen	1.6	2.08
PRY2	CA5344	orf19.7218	putative pathogen related proteins	3.0	1.08
RAT1	CA3242	orf19.4681	5´-3´-exoribonuclease	3.4	2.46
RCK2	CA1881	orf19.2268	Ca/calmodulin-dependent ser/thr protein kinase	4.1	1.17
RHR2	CA5788	orf19.5437	DL-glycerol phosphatase	1.6	0.25
RRP9	CA2545	orf19.2830	U3 small nucleolar ribonucleoprotein-associated protein involved in pre-ribosomal RNA processing	1.7	0.25
SBH1	CA1072	orf19.2533.1	involved in translocation into the ER	1.7	3.54
SCS7	CA4852	orf19.3822	required for hydroxylation of ceramide	1.8	4.45
SOU2	CA3770	orf19.2897	sorbitol utilization protein Sou2p	1.7	0.45
SPO70.5F	CA6102	orf19.5954	involved in meiosis and sporulation (5-prime end)	2.0	2.08
SSH1.3	CA0898	orf19.412	involved in co-translational pathway of protein transport (3-prime end)	1.6	2.88
SUR2	CA2225	orf19.5818	hydroxylation of C-4 of the sphingoid moiety of ceramide by homology	1.7	2.88
THR4	CA4139	orf19.4233	threonine synthase	1.8	4.45
TOS1	CA2303	orf19.1690	putative anchor subunit of a-agglutinin	1.6	0.45
UGA6.3EOC	CA3798	orf19.5820	GABA-specific transport protein (3-prime end)	2.0	0.25
URA7	CA1635	orf19.3941	CTP synthase 1	1.6	0.45
YBN5	CA1927	orf19.754	putative purine nucleotide-binding protein	1.6	3.54
YRB1	CA5822	orf19.7477	GTPase-activating protein	1.5	1.08

downregulation

fatty acid metabolism					
FAS2.3F	CA6107	orf19.5949	fatty-acyl-CoA synthase, alpha chain (3-prime end)	0.57	0.25
(acetyl-CoA-synthesis)					
ACH1	CA0345	orf19.3171	acetyl-coenzyme-A hydrolase	0.62	0.82
PDA1	CA4412	orf19.3097	pyruvate dehydrogenase alpha chain	0.32	0.25
PDX1	CA5242	orf19.5021	pyruvate dehydrogenase complex protein X	0.51	0.25
citric acid cycle					
ACO1	CA3546	orf19.6385	aconitate hydratase	0.27	0.25
CIT1.EXON2	CA3909	orf19.4393	citrate synthase (exon 2)	0.50	0.25
FUM12.3F	CA4351	orf19.6725	fumarate hydratase (3-prime end)	0.29	0.25
FUM12.5F	CA4349	orf19.6724	fumarate hydratase (5-prime end)	0.38	0.25
IDH1.3	CA4753	orf19.4826	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial (3-prime end)	0.36	0.25
IDH2	CA4148	orf19.5791	isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial	0.59	0.25
IDP1	CA2131	orf19.5211	isocitrate dehydrogenase, cytosolic	0.62	0.25

IDP2	CA0643	orf19.3733	isocitrate dehydrogenase, cytosolic	0.34	0.25
KGD1	CA3149	orf19.6165	2-oxoglutarate dehydrogenase	0.47	0.25
KGD2	CA2997	orf19.6126	2-oxoglutarate dehydrogenase complex E2 component	0.62	0.45
LSC1	CA0791	orf19.3358	succinate-CoA ligase / synthetase	0.64	0.25
MDH1	CA5164	orf19.4602	mitochondrial malate dehydrogenase precursor	0.33	0.25
gluconeogenesis					
FBP26	CA5110	orf19.6423	fructose-2,6-bisphosphatase	0.65	5.46
PCK1	CA5857	orf19.7514	phosphoenolpyruvate carboxykinase	0.28	0.25
fermentation					
ALD5	CA4159	orf19.5806	aldehyde dehydrogenase (NAD+)	0.44	0.25
transcription					
CAP1	CA0183	orf19.1623	transcriptional acivator	0.58	0.25
CTA24.3	CA5387	orf19.7276.1	transcriptional activator (3-prime end)	0.51	0.25
CTA241.EXON1	CA2615	orf19.5700	transcriptional activator (exon 1)	0.53	0.25
MRPL8	CA2999	orf19.6129	mitochondrial 60s ribosomal subunit	0.48	0.25
orf19.5338	CA5497	orf19.5338	transcriptional activator	0.59	0.25
respiratory chain					
COX4	CA4533	orf19.1471	cytochrome-c oxidase	0.62	0.25
CYT1	CA0864	orf19.3527	cytochrome-c1	0.66	2.88
MCR1	CA2457	orf19.3507	NADH-cytochrome-b5 reductase	0.52	0.25
NDH1	CA4633	orf19.339	mitochondrial NADH dehydrogenase	0.45	0.25
orf19.2091	CA4810	orf19.2091	subunit NUHM of NADH:Ubiquinone Oxidoreductase	0.57	0.25
orf19.2821	CA0540	orf19.2821	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor	0.47	0.25
QCR2	CA2065	orf19.2644	ubiquinol--cytochrome-c reductase 40KD chain II	0.51	0.25
QCR9	CA0376	orf19.2707.1	ubiquinol--cytochrome-c reductase subunit 9	0.59	1.08
ATP-synthesis					
ATP1.EXON3	CA4457	orf19.6853.3	F1F0-ATPase complex, F1 alpha subunit (exon 3)	0.41	0.25
ATP2	CA4362	orf19.5653	F1F0-ATPase complex, F1 beta subunit	0.30	0.25
ATP3.3	CA1489	orf19.3223	F1F0-ATPase complex, F1 gamma subunit (3-prime end)	0.62	0.82
ATP5	CA5775	orf19.5419	F1F0-ATPase complex, OSCP subunit	0.59	1.08
ATP7	CA1907	orf19.2785	F1F0-ATPase complex, FO D subunit	0.45	0.25
ATP8.EXON2	CA4830	orf19.2066.1	F1F0-ATPase complex, Atp8 subunit (exon 2)	0.65	1.59
orf19.5231.2	CA1107	orf19.5231.2	ATP19 subunit K of the dimeric form of mitochondrial F1F0-ATP synthase	0.46	0.25
orf19.5598.2	CA2973	orf19.5598.2	F1-ATPase epsilon subunit	0.59	0.25
STF2	CA2738	orf19.2107.1	ATP synthase regulatory factor	0.35	0.25
stress					
HSP104	CA5135	orf19.6389	heat shock protein	0.61	0.82
SOD22.3F	CA5588	orf19.7111.2	superoxide dismutase (3-prime end)	0.41	0.25
YHB1	CA0943	orf19.3707	flavohemoglobin	0.22	0.25
GTP-Binding					
TEM1	CA2812	orf19.3001	GTP-binding protein of the Ras superfamily	0.64	2.08
unknown and unclassified					
ADE2	CA6139	orf19.5906	phosphoribosylaminoimidazole carboxylase	0.51	0.25
AIP2	CA2406	orf19.300	actin interacting protein 2	0.59	0.25
AMI3	CA5025	orf19.6979	protein required for normal mitochondrial structure	0.66	1.08
AOX2	CA2189	orf19.4773	alternative oxidase	0.33	0.25
BUB3	CA0526	orf19.2655	cell cycle arrest protein	0.56	0.25
CAN2	CA1191	orf19.111	amino acid permease	0.65	1.19
CBF1	CA2473	orf19.2876	putative centromere binding factor 1	0.53	0.25
CDC55	CA4535	orf19.1468	B subunit of protein phosphatase 2A	0.58	0.25
CDR11.3F	CA0609	orf19.919	multidrug resistance protein (3-prime end)	0.66	0.25

CSA1	CA5585	orf19.7114	mycelial surface antigen by homology	0.58	0.83
DBF2	CA0205	orf19.1223	putative ser/thr protein kinase by homology	0.55	0.25
DPH52.3EOC	CA4284	orf19.6682	diphthamide methyltransferase (3-prime end)	0.55	2.88
ECM21.3	CA1707	orf19.4887	Involved in cell wall biogenesis and architecture	0.47	0.25
FDH11.3	CA6000	orf19.7600	glutathione-dependent formaldehyde dehydrogenase (3-prime end)	0.60	0.25
FDH12	CA1846	orf19.638	formate dehydrogenase	0.41	0.25
FRE7	CA5621	orf19.7077	ferric reductase transmembrane component	0.46	0.25
FTI1	CA2642	orf19.4307	Rad52 inhibitor	0.64	2.88
FUN34.5EOC	CA3154	orf19.6169.2	unknown function	0.65	0.25
GAD1	CA1564	orf19.1153	glutamate decarboxylase	0.51	0.25
GAL1	CA4040	orf19.3670	galactokinase	0.54	0.25
GAL10	CA4041	orf19.3672	UDP-glucose 4-epimerase by homology	0.63	0.25
GDH2	CA1775	orf19.2192	NAD-specific glutamate dehydrogenase	0.34	0.25
IFE2	CA2075	orf19.5288	unknown function	0.57	0.25
IFN1	CA1137	orf19.1979	glycerophosphoinositol transporter	0.54	0.25
IFQ1.3F	CA2241	orf19.4674	unknown function	0.60	1.19
IFR2	CA1964	orf19.2396	unknown function	0.41	0.25
IFS4	CA2891	orf19.2467	pirin protein	0.58	0.25
IPF17799	CA0019	unknown	unknown function	0.52	0.25
IPF18859	CA0827	unknown	unknown function	0.64	1.08
MAF1	CA3745	orf19.2173	nuclear protein by homology	0.53	0.45
MEP3	CA0302	orf19.1614	low affinity high capacity ammonium permease	0.48	0.25
MIR1	CA1513	orf19.4885	phosphate transport protein, mitochondrial	0.49	0.25
MTD1	CA4842	orf19.3810	methylenetetrahydrofolate dehydrogenase	0.34	0.45
NCE102	CA6097	orf19.5960	secretion of proteins that lack classical secretory signal sequence	0.63	0.93
NRG1	CA5289	orf19.7150	transcriptional repressor	0.56	0.25
orf19.1151	CA1330	orf19.1151	unknown function	0.66	0.82
orf19.1277	CA1411	orf19.1277	unknown function	0.59	0.25
orf19.1306	CA1326	orf19.1306	unknown function	0.62	1.19
orf19.1356	CA0258	orf19.1356	thiosulfate sulfurtransferase	0.60	0.25
orf19.1562	CA3986	orf19.1562	unknown function	0.60	0.25
orf19.1664	CA3468	orf19.1664	beta-glucosidase	0.66	0.25
orf19.1785	CA1168	orf19.1785	unknown function	0.49	0.25
orf19.1795	CA2465	orf19.1795	unknown function	0.61	0.25
orf19.1861	CA0385	orf19.1861	unknown function	0.60	0.25
orf19.204	CA3621	orf19.204	unknown function	0.64	0.25
orf19.2397.3	CA0026	orf19.2397.3	unknown function	0.61	0.25
orf19.2398	CA1962	orf19.2398	unknown function	0.45	0.25
orf19.2414	CA0005	orf19.2414	unknown function	0.57	0.25
orf19.2439.1	CA1916	orf19.2439.1	unknown function	0.65	2.46
orf19.251	CA0828	orf19.251	unknown function	0.65	0.25
orf19.26	CA3609	orf19.26	similar to *S. cerevisiae* Png1p, peptide:N-glycanase	0.62	0.25
orf19.2647	CA1726	orf19.2647	unknown function	0.57	0.25
orf19.2659	CA0495	orf19.2659	unknown function	0.28	0.25
orf19.2730	CA1163	orf19.2730	unknown function	0.64	0.25
orf19.2749	CA1170	orf19.2749	unknown function	0.55	0.25
orf19.2753	CA1892	orf19.2753	similarity to transcription factors	0.43	0.25
orf19.279	CA2779	orf19.279	unknown function	0.54	0.25
orf19.285	CA2782	orf19.285	unknown function	0.55	0.25
orf19.2954	CA4178	orf19.2954	unknown function	0.66	2.46
orf19.3007.2	CA3119	orf19.3007.2	unknown function	0.67	0.25
orf19.3071	CA0578	orf19.3071	similar to *S. cerevisiae* Mih1p, M-phase inducing	0.63	0.25

			protein, tyrosine phosphatase		
orf19.3233	CA5431	orf19.3233	unknown function	0.52	0.25
orf19.3335	CA1716	orf19.3335	unknown function	0.58	0.25
orf19.3364	CA1196	orf19.3364	unknown function	0.47	0.25
orf19.3378	CA0338	orf19.3378	unknown function	0.66	0.25
orf19.3406	CA2427	orf19.3406	probable formate dehydrogenase	0.66	0.25
orf19.3782.2	CA1184	orf19.3782.2	unknown function	0.62	0.93
orf19.3926	CA2231	orf19.3926	similar to *S. cerevisiae* Rny1p, ribonuclease of the T2 family of ribonucleases	0.65	1.59
orf19.3963	CA1838	orf19.3963	unknown function	0.48	0.25
orf19.4127	CA1158	orf19.4127	unknown function	0.65	2.08
orf19.4246	CA2186	orf19.4246	putative phosphatidyl synthase	0.63	1.08
orf19.4347	CA2193	orf19.4347	probable ser/thr protein kinase	0.65	0.25
orf19.4424	CA1363	orf19.4424	acid phosphatase	0.59	0.45
orf19.4430	CA1287	orf19.4430	unknown function	0.54	1.19
orf19.449	CA0670	orf19.449	phosphatidyl synthase	0.35	0.25
orf19.4544	CA4202	orf19.4544	unknown function	0.38	0.25
orf19.4579	CA5142	orf19.4579	similar to *S. cerevisiae* Erv29p, ER-Golgi transport vesicle protein	0.63	0.83
orf19.4684.2	CA3239	orf19.4684.2	unknown function	0.66	4.45
orf19.4698	CA0641	orf19.4698	unknown function	0.59	0.83
orf19.4811	CA3073	orf19.4811	putative tricarboxylate carrier	0.44	0.25
orf19.4897	CA2360	orf19.4897	unknown function	0.66	1.17
orf19.4907	CA2021	orf19.4907	unknown function	0.35	0.25
orf19.5008.1	CA5254	orf19.5008.1	unknown function	0.54	0.83
orf19.5069	CA1098	orf19.5069	unknown function	0.45	0.25
orf19.5193	CA1761	orf19.5193	oxidoreductase	0.46	0.25
orf19.5282	CA4970	orf19.5282	unknown function	0.41	0.25
orf19.5513	CA2516	orf19.5513	unknown function	0.61	2.88
orf19.5552	CA2285	orf19.5552	unknown function	0.62	0.82
orf19.5917	CA6131	orf19.5917	similar to *S. cerevisiae* Stp2p, involved in pre-tRNA splicing	0.41	0.25
orf19.5961	CA6096	orf19.5961	similar to *S. cerevisiae* Nas6p, subunit of 26S proteasome	0.65	0.25
orf19.6223	CA0400	orf19.6223	similar to *S. cerevisiae* Spo22p, involved in sporulation (3-prime end)	0.39	0.25
orf19.6225	CA3014	orf19.6225	similar to *S. cerevisiae* Pcl7p, cyclin-like protein interacting with Pho85p	0.64	4.45
orf19.6435	CA5104	orf19.6435	unknown function	0.65	0.25
orf19.6580	CA4888	orf19.6580	unknown function	0.61	0.25
orf19.6713	CA4341	orf19.6713	unknown function	0.46	0.25
orf19.6720	CA4346	orf19.6720	unknown function	0.64	0.45
orf19.6757	CA5940	orf19.6757	aldo/keto reductase	0.66	2.46
orf19.6763	CA5936	orf19.6763	unknown function	0.63	0.93
orf19.6807	CA5899	orf19.6807	unknown function	0.64	2.08
orf19.6918	CA4599	orf19.6918	unknown function	0.57	5.46
orf19.6971	CA5018	orf19.6971	unknown function	0.61	1.17
orf19.7006	CA5194	orf19.7006	unknown function	0.59	0.25
orf19.7085	CA5613	orf19.7085	unknown function	0.53	0.25
orf19.7209	CA5335	orf19.7209	unknown function	0.29	0.25
orf19.7306	CA5544	orf19.7306	unknown function	0.49	0.25
orf19.7341	CA5574	orf19.7341	unknown function	0.65	1.17
orf19.7381	CA5678	orf19.7381	unknown function	0.62	0.25
orf19.93	CA1987	orf19.93	unknown function	0.63	0.25
orf19.952	CA5408	orf19.952	unknown function	0.50	0.25

PCL2	CA1351	orf19.403	G1/S specific cyclin	0.24	0.25
PET9	CA5388	orf19.930	ADP/ATP carrier protein	0.35	0.25
PGA16	CA2015	orf19.848	unknown function	0.51	0.25
PTC5	CA3540	orf19.6376	type 2C protein phosphatase	0.58	1.08
RPS31	CA2011	orf19.3087	ubiquitin fusion protein	0.64	0.25
SDS24	CA3920	orf19.5118	similar to *S. cerevisiae YBR214w*	0.43	0.25
SHM2	CA0895	orf19.5750	serine hydroxymethyltransferase precursor, mitochondrial	0.63	1.17
SKS1	CA4039	orf19.3669	serine/threonine kinase	0.59	0.93
SNC2.EXON2	CA5257	orf19.5006.2	strong similarity to synaptobrevin, exon 2	0.67	0.83
SPC19	CA2420	orf19.4473	spindle pole body protein	0.61	0.25
SPT16	CA1409	orf19.2884	general chromatin factor	0.49	0.25
SRB10	CA1468	orf19.794	cyclin-dependent kinase by homology	0.66	0.25
STE23	CA1653	orf19.5561	protease involved in a-factor processing by homology	0.66	0.25
TAL1	CA2582	orf19.4371	transaldolase	0.56	0.25
TPS2	CA5066	orf19.3038	threalose-6-phosphate phosphatase	0.55	0.45
UGT51	CA0618	orf19.2616	UDP-glucose:sterol glucosyltransferase	0.64	1.08
YDC1	CA4406	orf19.3104	alkaline dihydroceramidase	0.56	2.88
YNK1	CA2645	orf19.4311	nucleoside diphosphate kinase	0.37	0.25

Supplemental Table 1C

Expression of genes in the *efg1* mutant HLC52 in hypoxic conditions, relative to wild-type CAF2-1 in hypoxic conditions. The minimal FDR value calculated by the SAM program was 5.2 %. Only genes regulated at least by a factor 1.5 are shown.

gene on array	**gene number**	**orf19 number**	**proposed function (according to CandidaDB: http://genolist.pasteur.fr/CandidaDB)**	**fold regulation**	**q-value**
upregulation					
respiratory chain					
RIP1	CA6149	orf19.5893	ubiquinol cytochrome-c reductase	1.7	1.84
ergosterol synthesis					
ERG1	CA1353	orf19.406	squalene epoxidase	1.5	4.40
glycosylation					
KTR2	CA1444	orf19.4494	mannosyltransferase	1.6	3.17
MNN9	CA5681	orf19.7383	required for N-glycosylation	1.5	0.53
gluconeogenisis					
FBP1	CA3199	orf19.6178	fructose-1,6-bisphosphatase	1.6	0.53
iron metabolism					
FET31	CA2922	orf19.4213	cell surface ferroxidase	1.6	4.40
FET32	CA2923	orf19.4212	cell surface ferroxidase	1.8	0.53
FET34.3EOC	CA1431	orf19.1206	iron transport multicopper oxidase, 3-prime end	3.6	0.53
FET5	CA2920	orf19.4215	multicopy oxidase	2.2	4.40
FTR1	CA5345	orf19.7219	high affinity iron permease	3.6	0.53
FTR2	CA5354	orf19.7231	high affinity iron permease	2.5	1.76
translation					
ATE1	CA2736	orf19.2110	arginyl tRNA transferase	1.9	4.40
KRS1	CA5947	orf19.6749	lysyl-tRNA synthetase	1.6	0.53
RPS15.3	CA6123	orf19.5927	40S ribosomal protein S15 (3-prime end)	2.0	0.53
SEN15	CA0857	orf19.4464	tRNA splicing endonuclease delta subunit	1.5	0.80
transcription					
CTA4	CA5671	orf19.7374	probable transcription factor	1.5	1.69
HOS1	CA1453	orf19.4411	putative histon deacetylase	1.6	0.80
JA2	CA1155	orf19.107	ATP-dependent RNA helicases-like	1.6	0.80
MBP1	CA2953	orf19.5855	transcription factor (by homologgy)	2.4	0.80
MED8	CA2328	orf19.4497	transcriptional regulation mediator	1.5	4.40
RPC53	CA1275	orf19.2715	DNA-directed RNA polymerase III	1.5	5.24
ATP synthesis					
CRD1	CA2832	orf19.4784	Cu-transporting P1-type ATPase	1.9	1.69
ENA21.3	CA4425	orf19.5170	P-type ATPase (3-prime end)	1.5	2.77
ENA22	CA4929	orf19.6070	P-type ATPase involved in Na+ efflux	1.8	0.53
PHO84.3EOC	CA1782	orf19.1172	inorganic phosphate transport protein (3-prime end)	1.7	1.27
GTP-binding					
GTR1	CA1677	orf19.3617	GTP-binding protein by homology	1.5	2.52
unknown and unclassified					
AOX2	CA2189	orf19.4773	alternative oxidase	1.5	0.53
APN1	CA5723	orf19.7428	AP endonuclease, exonuclease III homologue	1.9	1.84
BAT22	CA5040	orf19.6994	branched chain amino acid aminotransferase	1.7	0.53

CAN2	CA1191	orf19.111	amino acid permease	1.9	1.76
CCT2	CA3174	orf19.1402	chaperonin of the Tcp1 ring complex, cytosolic	2.3	4.40
CDR1	CA6066	orf19.6000	multidrug resistance protein	1.6	0.53
CTK1	CA4014	orf19.1619	probable cell division protein kinase	1.9	3.51
DBP2.EXON2	CA1415	orf19.171	ATP-dependent RNA helicase of DEAD box family, exon 2	1.5	0.53
FDH3.3F	CA1253	orf19.1774	formate dehydrogenase (3-prime end)	2.2	1.27
HGT11	CA1506	orf19.4527	hexose transporter	1.5	3.51
HOM2	CA3984	orf19.1559	aspartate-semialdehyde dehydrogenase	1.7	0.53
HPT1	CA3787	orf19.5832	hypoxanthine guanine phosphoribosy transferase	1.6	4.40
HUB1	CA1206	orf19.3774.1	ubiquitin-like modifier	1.8	5.24
IFA12	CA2755	orf19.5619	unknown function	1.6	1.27
IFA5	CA3506	orf19.6353	unknown function	1.6	3.17
IFC4	CA0442	orf19.2292	unknown function	1.8	2.77
KRE1	CA2589	orf19.4377	secretory pathway protein	1.9	0.53
NOG2	CA2847	orf19.5733	unknown function	1.5	0.53
NPR2	CA3381	orf19.328	nitrogen permease regulator	1.8	1.84
orf19.1049	CA0925	orf19.1049	unknown function	1.5	0.53
orf19.138	CA1815	orf19.138	unknown function	1.6	3.17
orf19.1418	CA3959	orf19.1418	similar to *S. cerevisiae* Sec15p, component of the exocyst complex	1.5	1.84
orf19.1490	CA1345	orf19.1490	similar to *S. cerevisiae* Msb2p, multicopy suppressor of a *cdc24* bud emergence defect	1.6	1.76
orf19.1539	CA1028	orf19.1539	unknown function	2.0	1.76
orf19.1588	CA3157	orf19.1588	unknown function	1.9	2.77
orf19.1708	CA1559	orf19.1708	unknown function	1.8	0.53
orf19.1863	CA4497	orf19.1863	unknown function	1.6	4.40
orf19.1885	CA4481	orf19.1885	similar to *S. cerevisiae* Mpt1p, required for protein synthesis	1.5	0.53
orf19.1902	CA4470	orf19.1902	unknown function	1.8	4.40
orf19.2041	CA3650	orf19.2041	unknown function	1.5	0.53
orf19.2049	CA3657	orf19.2049	unknown function	1.5	1.76
orf19.2333	CA3338	orf19.2333	unknown function	1.8	0.53
orf19.2459	CA1872	orf19.2459	unknown function	1.9	1.27
orf19.2685	CA2769	orf19.2685	unknown function	1.8	0.53
orf19.284	CA2781	orf19.284	unknown function	4.6	0.53
orf19.286	CA2783	orf19.286	unknown function	2.8	1.05
orf19.3245	CA5442	orf19.3245	unknown function	1.7	5.24
orf19.3261	CA5454	orf19.3261	member of the FRP family of proteins, related to *Y. lipolytica* glyoxylate pathway regulator Gpr1p and *S. cerevisiae* Fun34p	1.6	3.17
orf19.3475	CA2903	orf19.3475	unknown function	1.7	0.53
orf19.3852	CA1032	orf19.3852	unknown function	2.3	3.51
orf19.3876	CA3551	orf19.3876	unknown function	1.5	4.40
orf19.3969	CA1309	orf19.3969	unknown function	2.0	1.76
orf19.4191.2	CA1307	orf19.4191.2	unknown function	2.2	1.84
orf19.4193	CA1305	orf19.4193	unknown function	2.2	4.40
orf19.4282	CA3065	orf19.4282	unknown function	1.6	1.76
orf19.454	CA0475	orf19.454	unknown function	1.5	4.40
orf19.4612	CA5175	orf19.4612	similar to *Legionella pneumophila* SbpA	1.7	1.05
orf19.4792	CA2839	orf19.4792	unknown function	3.1	0.53
orf19.5019	CA5244	orf19.5019	unknown function	2.1	0.53
orf19.5065	CA0535	orf19.5065	similar to *S. cerevisiae* Erd1p, required for retention of luminal ER proteins	1.7	0.53
orf19.5297	CA2159	orf19.5297	similar to *S. cerevisia*, Tfb1p, transcription initiation factor	1.6	1.84

orf19.5305	CA5476	orf19.5305	unknown function	3.8	0.53
orf19.5314	CA0097	orf19.5314	unknown function	2.9	4.40
orf19.5340	CA5498	orf19.5340	unknown function	1.5	0.53
orf19.5491	CA2678	orf19.5491	unknown function	1.5	2.77
orf19.5725	CA2049	orf19.5725	unknown function	1.7	4.40
orf19.5840	CA3780	orf19.5840	unknown function	1.6	1.76
orf19.5890	CA6151	orf19.5890	unknown function	1.6	1.76
orf19.5919	CA6128	orf19.5919	unknown function	3.0	2.52
orf19.6175	CA3196	orf19.6175	unknown function	1.7	1.69
orf19.6736	CA4359	orf19.6736	unnown function	1.6	4.40
orf19.6742	CA5952	orf19.6742	similar to *S. cerevisiae* Fcp1p, TFIIF-interacting component of CTD phosphatase	1.5	0.80
orf19.6824	CA5885	orf19.6824	unknown function	1.8	2.52
orf19.7050	CA5644	orf19.7050	unknown function	1.5	3.17
orf19.7576	CA5980	orf19.7576	unknown function	1.5	3.51
orf19.938	CA5395	orf19.938	unknown function	1.5	3.17
PDE2	CA3450	orf19.2972	nucleotide phosphodiesterase	1.5	5.24
PTR21	CA4707	orf19.6937	peptide transporter	1.6	0.53
PUB1	CA5666	orf19.7368	major polyadenylated RNA-binding protein	1.5	1.27
RFG1.3f	CA0346	orf19.2824	regulator of filamentous growth and virulence (3- prime end)	1.5	1.76
RIM1	CA3804	orf19.2483	telomere-binding protein	1.5	0.53
RIM9	CA1150	orf19.101	regulator for sporulation and invasive growth	2.5	2.52
SPE2	CA2712	orf19.568	by homology to *S. cerevisiae* adenosylmethionine decarboxylase precurser	2.4	0.80
SRP40	CA1666	orf19.2859	RNA I and II supressor	2.9	4.40
URA7	CA1635	orf19.3941	CTP synthase 1	1.6	0.53
YHB1	CA0943	orf19.3707	flavohemoglobin	2.0	0.53
ZRC1	CA1030	orf19.1537	Zinc and cadmium resistance protein	1.8	3.17

downregulation

fatty acid metabolism					
ACB1.EXON2	CA5225	orf19.7043.1	acyl-coenzyme-A-binding protein	0.57	0.53
ACC1	CA5816	orf19.7466	acetyl-coenzyme-A carboxylase	0.49	0.53
FAS2.3F	CA6107	orf19.5949	fatty-acyl-CoA synthase, alpha chain	0.56	0.53
OLE1	CA3921	orf19.5117	stearoyl-CoA desaturase	0.63	1.69
PDA1	CA4412	orf19.3097	pyruvate dehydrogenase alpha chain	0.65	0.80
PDB1	CA2162	orf19.5294	pyruvate dehydrogenase	0.51	1.69
glycolysis					
ENO1	CA3874	orf19.395	enolase I	0.65	0.53
GLK1	CA0263	orf19.13	aldohexose specific glucokinase	0.44	0.53
GPH1	CA5206	orf19.7021	glycogen phosphorylase	0.38	0.53
GSY1	CA5467	orf19.3278	glycogen synthase	0.49	0.53
citric acid cycle					
GAD1	CA1564	orf19.1153	glutamate decarboxylase	0.58	0.53
MDH1	CA5164	orf19.4602	mitochondrial malate dehydrogenase precursor	0.61	0.53
stress response					
CTA1	CA3011	orf19.6229	catalase A, peroxisomal	0.48	1.05
GRP2	CA2644	orf19.4309	reductase	0.65	0.53
HSP104	CA5135	orf19.6389	heat shock protein	0.65	1.05
HSP12	CA0627	orf19.3160	heat shock protein	0.27	0.53
SOD1.3	CA4120	orf19.2770.1	Cu, Zn-superoxide dismutase	0.62	1.05
SSA4	CA1230	orf19.4980	Hsp70p, heat shock protein	0.52	0.53

hyphae specific genes					
ALS4.3F	CA1528	orf19.4556	agglutinin-like protein	0.38	0.53
DDR48	CA4336	orf19.4082	stress protein	0.46	0.53
NRG1	CA5289	orf19.7150	transcriptional repressor Nrg1p/Nrg2p	0.56	0.53
RBT5	CA2558	orf19.5636	repressed by Tup1p, protein 5	0.63	2.77
fermentation					
ADH5	CA2391	orf19.2608	probable alcohol dehydrogenase	0.59	0.53
unknown and unclassified					
ADE1	CA5829	orf19.7484	phosphoribosyl-amidoimidazole-succinocarboxamide synthetase	0.66	0.80
CPY1.3F (PRC1)	CA0430	orf19.1339	carboxypeptidase Y precursor	0.64	0.53
CWH8	CA1146	orf19.3682	putative required protein for full levels of dolichol-linked oligosaccharides in the ER	0.59	0.53
EFG1	CA2787	orf19.610	enhanced filamentous growth factor	0.65	1.84
IFQ3	CA2597	orf19.54	unknown function	0.55	0.53
IFU6.3F	CA2687	unknown	unknown function	0.67	0.53
MSW1	CA2636	orf19.4299	mitochondrial tryptophanyl-tRNA synthetase	0.65	0.53
orf19.1122	CA0360	orf19.1122	unknown function	0.64	0.53
orf19.1721	CA2796	orf19.1721	Nce103p, involved in non-classical protein export pathway	0.61	0.53
orf19.1728	CA1644	orf19.1728	unknown function	0.65	1.84
orf19.1729	CA1643	orf19.1729	unknown function	0.56	0.80
orf19.1862	CA0386	orf19.1862	unknown function	0.61	0.80
orf19.1889	CA4478	orf19.1889	unknown function	0.63	0.53
orf19.2071	CA4825	orf19.2071	unknown function	0.64	0.53
orf19.2296	CA0446	orf19.2296	similar to mucin proteins	0.61	1.05
orf19.2344	CA2342	orf19.2344	probable heat shock protein	0.61	0.80
orf19.251	CA0828	orf19.251	unknown function	0.48	4.40
orf19.260	CA0109	orf19.260	unknown function	0.65	0.80
orf19.2607	CA2392	orf19.2607	unknown function	0.63	0.80
orf19.2762	CA4127	orf19.2762	unknown function	0.25	0.53
orf19.28	CA3611	orf19.28	unknown function	0.52	0.53
orf19.3139	CA3571	orf19.3139	unknown function	0.64	0.53
orf19.3325	CA2938	orf19.3325	Glg2p, self-glucosylating initiator of glycogen synthesis	0.65	2.52
orf19.3335	CA1716	orf19.3335	unknown function	0.56	0.53
orf19.424	CA4049	orf19.424	unknown function	0.62	1.05
orf19.4246	CA2186	orf19.4246	putative phosphatidyl synthase	0.52	0.53
orf19.4390	CA3912	orf19.4390	unknown function	0.52	0.53
orf19.4907	CA2021	orf19.4907	unknown function	0.52	0.53
orf19.5145	CA3629	orf19.5145	related to flavin-containing monooxygenase	0.16	0.53
orf19.5232.1	CA1105	orf19.5232.1	unknown function	0.60	0.80
orf19.5267	CA4983	orf19.5267	unknown function	0.56	0.53
orf19.5334	CA5494	orf19.5334	Tis11p, tRNA-specific adenosine deaminase 3	0.66	0.53
orf19.5431	CA5784	orf19.5431	unknown function	0.64	2.52
orf19.566	CA0059	orf19.566	unknown function	0.62	0.53
orf19.5689	CA2609	orf19.5689	Sec28p, epsilon-COP coatomer subunit	0.67	0.53
orf19.6024	CA2152	orf19.6024	unknown function	0.65	2.52
orf19.6313	CA3279	orf19.6313	unknown function	0.61	0.80
orf19.6407	CA5121	orf19.6407	unknown function	0.66	0.80
orf19.675	CA4111	orf19.675	unknown function	0.61	1.05
orf19.6757	CA5940	orf19.6757	aldo/keto reductase	0.61	0.53
orf19.6816	CA5891	orf19.6816	putative aldehyde reductase	0.65	0.53
orf19.7350	CA5650	orf19.7350	unknown function	0.49	0.53
orf19.868	CA1203	orf19.868	unknown function	0.58	0.53

PET8	CA5616	orf19.7082	mitochondrial carrier protein	0.46	0.53
PHR2	CA3867	orf19.6081	pH-regulated protein 2	0.67	2.77
PRC1	CA0430	orf19.1339	carboxypeptidase Y precursor	0.41	0.53
PST2	CA1673	orf19.3612	1,4-benzoquinone reductase	0.59	0.53
RIB2	CA2531	orf19.3177	DRAP deaminase	0.66	0.53
SKI2	CA5108	orf19.6425	antiviral protein and putative helicase	0.65	2.77
SNZ1	CA4184	orf19.2947	stationary phase protein	0.63	0.80
SOU1	CA3771	orf19.2896	Sou1p, sorbitol utilization protein	0.67	5.24
TAL1	CA2582	orf19.4371	transaldolase	0.65	1.84
TFS1	CA0748	orf19.1974	Cdc25p-dependent nutrient- and ammonia-response, cell-cycle regulator	0.64	1.27
URA3	CA2801	orf19.1716	orotidine-5 -monophosphate decarboxylase	0.47	0.53
ZORRO2B.5F	CA5386	orf19.7277	putative gag protein (5-prime end)	0.66	1.69