

**Supplemental Table 2. Genes differently expressed during hypoxia in wild-type and *efg1* mutant**

hypoxic regulation, type <sup>1</sup>	gene on array	orf19 number	proposed function (according to CandidaDB: <a href="http://genolist.pasteur.fr/CandidaDB">http://genolist.pasteur.fr/CandidaDB</a> )	fold regulation <sup>2</sup>				class <sup>3</sup>	
				wt h/n	<i>efg1</i> h/n	<i>efg1</i> /wt h	<i>efg1</i> /wt n		
<b>in wt, not in <i>efg1</i> strain</b>	<i>ACC1</i>	<i>orf19.7466</i>	acetyl-coenzyme-A carboxylase	2.8	1	0.49	1.5	E	
	<i>PDE2</i>	<i>orf19.2972</i>	nucleotide phosphodiesterase	0.65	1	1.5	1	E	
	<i>PHO84</i>	<i>orf19.1172</i>	inorganic phosphate transport protein (3-prime end)	0.61	1	1.7	1	E	
	<i>RIP1</i>	<i>orf19.5893</i>	ubiquinol cytochrome-c reductase	0.63	1	1.7	1	E	
	<i>ADH5</i>	<i>orf19.2608</i>	probable alcohol dehydrogenase	1.5	1	0.59	1	E	
	<i>CPY1.3F</i> ( <i>PRC1</i> )	<i>orf19.1339</i>	carboxypeptidase Y precursor	1.6	1	0.64	1	E	
	<i>CTA1</i>	<i>orf19.6229</i>	catalase A, peroxisomal	3.6	1	0.48	1	E	
	<i>DDR48</i>	<i>orf19.4082</i>	stress protein	2.3	1	0.46	1	E	
	<i>GRP2</i>	<i>orf19.4309</i>	reductase	1.7	1	0.65	1	E	
	<i>PRC1</i>	<i>orf19.1339</i>	carboxypeptidase Y precursor	1.8	1	0.41	1	E	
	<i>orf19.1728</i>	<i>orf19.1728</i>	unknown function	1.7	1	0.65	1	E	
	<i>orf19.7350</i>	<i>orf19.7350</i>	unknown function	1.5	1	0.49	1	E	
	<i>GLK1</i>	<i>orf19.13</i>	aldohexose specific glucokinase	2.9	1	0.44	0.40	E	
	<i>GPH1</i>	<i>orf19.7021</i>	glycogen phosphorylase	1.7	1	0.38	0.34	E	
	<i>SSA4</i>	<i>orf19.4980</i>	hsp70 heat shock protein	1.6	1	0.52	0.56	E	
	<i>HSP12</i>	<i>orf19.3160</i>	heat shock protein	9.6	1	0.27	0.56	E	
	<i>orf19.2296</i>	<i>orf19.2296</i>	Similar to mucin proteins	1.7	1	0.61	0.59	E	
	<i>orf19.2762</i>	<i>orf19.2762</i>	unknown function	2.3	1	0.25	0.38	E	
	<i>HHT21</i>	<i>orf19.1061</i>	histone H3	2.0	1	1	2.0	C	
	<i>UBI4</i>	<i>orf19.6771</i>	polyubiquitin	2.2	1	1	1.8	C	
	<i>SSC1</i>	<i>orf19.1896</i>	mitochondrial heat shock protein 70-related protein	1.7	1	1	1.9	C	
	<b>in <i>efg1</i>, not in wt strain</b>	<i>GAD1</i>	<i>orf19.1153</i>	glutamate decarboxylase	1	0.51	0.59	1	F
		<i>NRG1</i>	<i>orf19.7150</i>	transcriptional repressor	1	0.56	0.56	1	F
		<i>PDA1</i>	<i>orf19.3097</i>	pyruvate dehydrogenase alpha chain	1	0.32	0.67	1	F
		<i>orf19.3335</i>	<i>orf19.3335</i>	unknown function	1	0.58	0.56	1	F

<i>orf19.4907</i>	<i>orf19.4907</i>	unknown function	1	0.35	0.52	1	F
<i>orf19.6757</i>	<i>orf19.6757</i>	aldo/keto reductase	1	0.66	0.61	1	F
<i>BAT22</i>	<i>orf19.6994</i>	branched chain amino acid aminotransferase	1	1.6	1.7	1	F
<i>DBP2</i>	<i>orf19.170</i>	ATP-dependent RNA helicase of DEAD box family	1	1.9	1.5	1	F
<i>FET34</i>	<i>orf19.1206</i>	iron transport multicopper oxidase	1	8.1	3.6	1	F
<i>FTR2</i>	<i>orf19.7231</i>	high affinity iron permease	1	2.0	2.5	1	F
<i>GTR1</i>	<i>orf19.3617</i>	GTP-binding protein	1	2.8	1.5	1	F
<i>HPT1</i>	<i>orf19.5832</i>	hypoxanthine guanine phosphoribosyl transferase	1	1.8	1.6	1	F
<i>KRS1</i>	<i>orf19.6749</i>	lysyl-tRNA synthetase	1	1.6	1.6	1	F
<i>URA7</i>	<i>orf19.3941</i>	CTP synthase 1	1	1.6	1.6	1	F
<i>orf19.3876</i>	<i>orf19.3876</i>	unknown function	1	1.5	1.5	1	F
<i>orf19.3969</i>	<i>orf19.3969</i>	unknown function	1	1.6	2.0	1	F
<i>orf19.4282</i>	<i>orf19.4282</i>	unknown function	1	3.5	1.6	1	F
<i>orf19.4612</i>	<i>orf19.4612</i>	Similar to <i>Legionella pneumophila</i> sbpA	1	6.5	1.7	1	F
<i>orf19.5305</i>	<i>orf19.5305</i>	unknown function	1	1.7	3.8	1	F
<i>MDH1</i>	<i>orf19.4602</i>	mitochondrial malate dehydrogenase precursor	1	0.33	0.61	1.6	F
<i>TAL1</i>	<i>orf19.4371</i>	transaldolase	1	0.56	0.65	0.66	F
<i>DAK2</i>	<i>orf19.4777</i>	dihydroxyacetone kinase, 3-prime end	1	1.6	1	0.44	B
<i>EBP4</i>	<i>orf19.3433</i>	NADPH dehydrogenase	1	1.8	1	0.67	B
<i>PFK1</i>	<i>orf19.3967</i>	6-phosphofructokinase, alpha subunit	1	2.1	1	0.46	B
<i>RHR2</i>	<i>orf19.5437</i>	DL-glycerol phosphatase	1	1.6	1	0.23	B
<i>RNR22</i>	<i>orf19.1868</i>	ribonucleoside-diphosphate reductase	1	2.3	1	0.24	B
<i>orf19.1595</i>	<i>orf19.1595</i>	unknown function, 5-prime end	1	1.6	1	0.61	B
<i>orf19.1802</i>	<i>orf19.1802</i>	unknown function	1	1.9	1	0.67	B
<i>orf19.2286</i>	<i>orf19.2286</i>	unknown function	1	2.3	1	0.64	B
<i>ACH1</i>	<i>orf19.3171</i>	acetyl-coenzyme-A hydrolase	1	0.62	1	2.3	B
<i>CAP1</i>	<i>orf19.1623</i>	transcriptional activator	1	0.58	1	2.1	B
<i>CDC55</i>	<i>orf19.1468</i>	B subunit of protein phosphatase 2A	1	0.58	1	1.8	B
<i>CDR11.3f</i>	<i>orf19.919</i>	multidrug resistance protein, 3-prime end	1	0.66	1	1.6	B
<i>CTA241.3</i>	<i>orf19.5700</i>	transcriptional activator, 3-prime end	1	0.53	1	1.9	B
<i>FDH12</i>	<i>orf19.638</i>	formate dehydrogenase	1	0.41	1	2.1	B

<i>KGD1</i>	<i>orf19.6165</i>	2-oxoglutarate dehydrogenase	1	0.47	1	2.0	B
<i>NCE102</i>	<i>orf19.5960</i>	secretion of proteins that lack classical secretory signal sequence	1	0.63	1	2.0	B
<i>PET9</i>	<i>orf19.930</i>	ADP/ATP carrier protein	1	0.35	1	1.6	B
<i>QCR9</i>	<i>orf19.2707.1</i>	ubiquinol--cytochrome-c reductase subunit 9	1	0.59	1	1.6	B
<i>SOD22.3f</i>	<i>orf19.7111.2</i>	superoxide dismutase	1	0.41	1	1.6	B
<i>orf19.1562</i>	<i>orf19.1562</i>	unknown function	1	0.60	1	1.9	B
<i>orf19.2091</i>	<i>orf19.2091</i>	subunit NUHM of NADH:ubiquinone oxidoreductase	1	0.57	1	1.5	B
<i>orf19.2398</i>	<i>orf19.2398</i>	unknown function	1	0.45	1	1.8	B
<i>orf19.449</i>	<i>orf19.449</i>	phosphatidyl synthase	1	0.35	1	1.8	B
<i>orf19.5069</i>	<i>orf19.5069</i>	unknown function	1	0.45	1	1.7	B
<i>orf19.6763</i>	<i>orf19.6763</i>	unknown function	1	0.63	1	1.5	B
<i>orf19.7306</i>	<i>orf19.7306</i>	unknown function	1	0.49	1	1.6	B
<i>orf19.93</i>	<i>orf19.93</i>	unknown function	1	0.63	1	2.0	B

---

<b>differently in wt and <i>efg1</i> strain</b>	<i>OLE1</i>	<i>orf19.5117</i>	stearoyl-CoA desaturase	3.5	1.7	0.63	1	G
	<i>RBT5</i>	<i>orf19.5636</i>	repressed by TUP1 protein 5	5.5	2.5	0.63	1	G
	<i>orf19.1729</i>	<i>orf19.1729</i>	unknown function	3.5	1.6	0.56	1	G
	<i>ENO1</i>	<i>orf19.395</i>	enolase I	2.4	1.9	0.65	0.66	G
	<i>orf19.3261</i>	<i>orf19.3261</i>	member of the FRP family of proteins related to <i>Yarrowia lipolytica</i> glyoxylate pathway regulator Gpr1p and <i>S. cerevisiae</i> Fun34p, 3-prime end	3.5	3.7	1.6	0.6	G
	<i>FAS2.3f</i>	<i>orf19.5949</i>	fatty-acyl-CoA synthase, alpha chain,	1.7	0.57	0.56	1.8	G
	<i>PGA54</i>	<i>orf19.2685</i>	unknown function	1.7	1.6	1.8	1	G
	<i>FTR1</i>	<i>orf19.7219</i>	high affinity iron permease	1.6	3.5	3.6	1.8	G
	<i>orf19.251</i>	<i>orf19.251</i>	unknown function	3.0	0.65	0.48	1	G
	<i>orf19.4246</i>	<i>orf19.4246</i>	putative phosphatidyl synthase	2.3	0.63	0.52	0.50	G

<i>YHB1</i>	<i>orf19.3707</i>	flavo-hemoglobin	0.27	0.22	2.0	2.9	G
<i>ADH1</i>	<i>orf19.3997</i>	alcohol dehydrogenase	3.8	2.3	1	0.48	A
<i>GPM1</i>	<i>orf19.903</i>	phosphoglycerate mutase	2.9	3.7	1	0.40	A
<i>ERG251</i>	<i>orf19.4631</i>	C-4 sterol methyl oxidase	1.6	1.9	1	0.51	A
<i>FBA1</i>	<i>orf19.4618</i>	fructose-bisphosphate aldolase	3.5	4.0	1	0.37	A
<i>PGI1</i>	<i>orf19.3888</i>	glucose-6-phosphate isomerase	2.8	2.4	1	0.50	A
<i>SUR2</i>	<i>orf19.5818</i>	hydroxylation of C-4 of the sphingoid moiety of ceramide by homology	1.6	1.7	1	0.28	A
<i>TPI1</i>	<i>orf19.6745</i>	triose phosphate isomerase	2.5	2.2	1	0.44	A
<i>orf19.2374</i>	<i>orf19.2374</i>	GAG protein of retrotransposon pCal	2.4	1.9	1	0.35	A
<i>orf19.391</i>	<i>orf19.391</i>	similar to <i>S. cerevisiae</i> Upc2p RNA polymerase II transcription factor	1.6	2.0	1	0.47	A
<i>orf19.5372</i>	<i>orf19.5372</i>	<i>C. albicans</i> Tca2 retrotransposon	2.7	2.4	1	0.45	A
<i>orf19.6882</i>	<i>orf19.6882</i>	similar to <i>S. cerevisiae</i> Osm1p osmotic growth protein	1.6	2.0	1	0.33	A
<i>ADH2</i>	<i>orf19.5113</i>	alcohol dehydrogenase I	1.6	2.6	1	1	A
<i>ALG2.5</i>	<i>orf19.1221</i>	mannosyltransferase, 5-prime end	2.1	2.0	1	1	A
<i>BEL1.exon2</i>	<i>orf19.6906.1</i>	protein of the 40S ribosomal subunit	1.6	2.0	1	1	A
<i>ERG3</i>	<i>orf19.767</i>	C5,6 desaturase	2.4	8.1	1	1	A
<i>ERG5</i>	<i>orf19.5178</i>	C-22 sterol desaturase	2.2	2.4	1	1	A
<i>ERG16</i>	<i>orf19.922</i>	cytochrome P450 lanosterol 14a-demethylase	2.5	3.1	1	1	A
<i>GAP1</i>	<i>orf19.6814</i>	glyceraldehyde-3-phosphate dehydrogenase	3.4	2.0	1	1	A
<i>PGK1</i>	<i>orf19.3651</i>	phosphoglycerate kinase	4.2	2.2	1	1	A
<i>PHO88</i>	<i>orf19.7327</i>	involved in phosphate transport	6.5	1.5	1	1	A
<i>POL0</i>	<i>orf19.5373</i>	pol polyprotein, reverse transcriptase	3.8	2.5	1	1	A
<i>POT14</i>	<i>orf19.1591</i>	acetyl-CoA acetyltransferase	1.7	1.9	1	1	A
<i>RAT1</i>	<i>orf19.4681</i>	5'-3' Exoribonuclease	1.7	3.4	1	1	A
<i>RNR21</i>	<i>orf19.5801</i>	ribonucleoside-diphosphate reductase	1.7	1.8	1	1	A
<i>SCS7</i>	<i>orf19.3822</i>	required for hydroxylation of ceramide	1.6	1.8	1	1	A
<i>SUN41</i>	<i>orf19.3642</i>	putative cell wall beta-glucosidase	1.9	1.7	1	1	A
<i>SUN42</i>	<i>orf19.5032</i>	putative cell wall beta-glucosidase	2.1	2.1	1	1	A
<i>TOS1</i>	<i>orf19.1690</i>	putative Anchor subunit of a-agglutinin	1.7	1.6	1	1	A
<i>orf19.1573</i>	<i>orf19.1573</i>	P-type ATPase	1.6	1.7	1	1	A
<i>orf19.1691</i>	<i>orf19.1691</i>	unknown function	6.9	1.8	1	1	A

<i>orf19.2119</i>	<i>orf19.2119</i>	similar to <i>S. cerevisiae</i> Ndt80p meiosis-specific protein	1.5	1.5	1	1	A
<i>orf19.7310</i>	<i>orf19.7310</i>	similar to <i>S. cerevisiae</i> Gin3p	2.3	2.8	1	1	A
<i>ACO1</i>	<i>orf19.6385</i>	aconitate hydratase	0.63	0.27	1	1	A
<i>ATP2</i>	<i>orf19.5653</i>	F1F0-ATPase complex, F1 beta subunit	0.52	0.30	1	1	A
<i>ATP3.3f</i>	<i>orf19.3223</i>	F1F0-ATPase complex, F1 gamma subunit	0.56	0.62	1	1	A
<i>ATP5</i>	<i>orf19.5419</i>	F1F0-ATPase complex, OSCP subunit	0.52	0.59	1	1	A
<i>ATP7</i>	<i>orf19.2785</i>	F1F0-ATPase complex, FO D subunit	0.56	0.45	1	1	A
<i>CIT1.exon2</i>	<i>orf19.4393</i>	Citrate synthase	0.56	0.50	1	1	A
<i>CYT1</i>	<i>orf19.3527</i>	cytochrome-c1	0.64	0.66	1	1	A
<i>DBF2</i>	<i>orf19.1223</i>	putative ser/thr protein kinase	0.48	0.55	1	1	A
<i>IDH1.3</i>	<i>orf19.4826</i>	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial	0.54	0.36	1	1	A
<i>IDH2</i>	<i>orf19.5791</i>	isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial	0.55	0.59	1	1	A
<i>KGD2</i>	<i>orf19.6126</i>	2-oxoglutarate dehydrogenase complex E2 component	0.65	0.47	1	1	A
<i>MIR1</i>	<i>orf19.4885</i>	phosphate transport protein, mitochondrial (MCF)	0.39	0.49	1	1	A
<i>QCR2</i>	<i>orf19.2644</i>	ubiquinol--cytochrome-c reductase 40KD chain II	0.55	0.51	1	1	A
<i>YNK1</i>	<i>orf19.4311</i>	nucleoside diphosphate kinase	0.53	0.37	1	1	A
<i>orf19.26</i>	<i>orf19.26</i>	similar to <i>S. cerevisiae</i> Png1P peptide:N-glycanase	0.64	0.62	1	1	A
<i>orf19.2821</i>	<i>orf19.2821</i>	NADH dehydrogenase (ubiquinone) 22K chain precursor	0.67	0.47	1	1	A
<i>orf19.2954</i>	<i>orf19.2954</i>	unknown function	0.66	0.66	1	1	A
<i>orf19.3926</i>	<i>orf19.3926</i>	similar to <i>S. cerevisiae</i> Rny1 ribonuclease from the T2 family of ribonucleases	0.66	0.65	1	1	A
<i>orf19.5231.2</i>	<i>orf19.5231.2</i>	by homology to <i>S. cerevisiae</i> : ATP19 subunit K of the dimeric form of mitochondrial F1F0-ATP synthase	0.62	0.46	1	1	A
<i>orf19.5598.2</i>	<i>orf19.5598.2</i>	F1-ATPase epsilon subunit respiration	0.63	0.59	1	1	A
<i>orf19.6223</i>	<i>orf19.6223</i>	similar to <i>S. cerevisiae</i> Spo22 involved in sporulation, 3-prime end	0.48	0.39	1	1	A
<i>orf19.952</i>	<i>orf19.952</i>	unknown function	0.44	0.50	1	1	A
<i>ATP1.exon3</i>	<i>orf19.6853.3</i>	F1F0-ATPase complex, F1 alpha subunit	0.45	0.41	1	1.6	A
<i>FUM12.3f</i>	<i>orf19.6725</i>	fumarate hydratase, 3-prime end	0.41	0.29	1	3.1	A
<i>FUM12.5f</i>	<i>orf19.6724</i>	fumarate hydratase, 5-prime end	0.53	0.38	1	2.1	A
<i>STF2</i>	<i>orf19.2107.1</i>	ATP synthase regulatory factor	0.67	0.35	1	2.5	A

---

<i>IFE2</i>	<i>orf19.5288</i>	unknown function	0.51	0.57	1	0.41	A
-------------	-------------------	------------------	------	------	---	------	---

---

<sup>1</sup>Transcript ratios of strain CAF2-1 (wt) or *efg1* mutant HLC52 were determined and classes of genes regulated in the indicated manner were selected (Fig. 1, Supplemental table 1). Only genes are shown, in which 4-way comparisons of transcriptomal data (Fig. 1; Doedt *et al.*, 2004) resulted in a consistent scheme of regulation.

<sup>2</sup>Strains had been grown in the presence of air (n) or in hypoxic conditions (h) before transcriptomal analysis.

<sup>3</sup>Classes of genes according to the Venn diagram of Fig. 1.