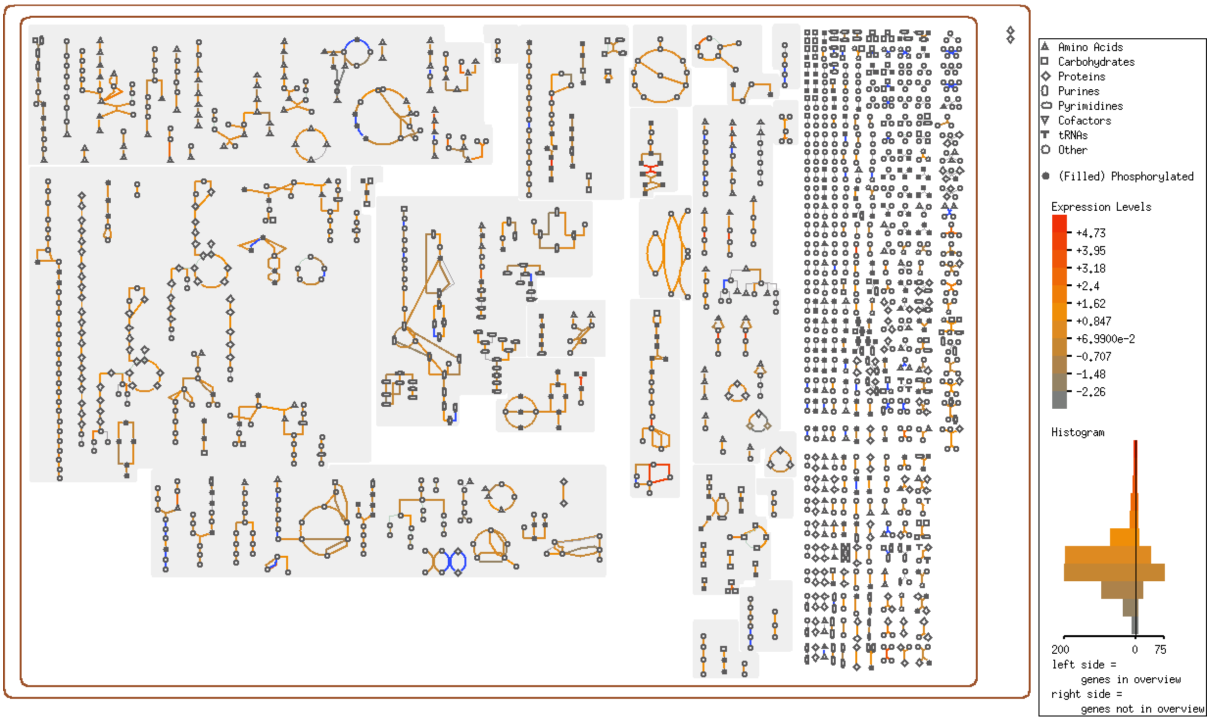
Supplementary information File 1 (SI File 1)

Title: Physiological and transcriptional response to *d*-limonene in *Saccharomyces cerevisiae* shows changes to the cell wall, not the plasma membrane

Authors: Timothy C. R. Brennan[1], Jens O. Krömer[2]#, Lars K. Nielsen[1]



SI Fig 1. Metabolic map of entire transcriptome dataset.

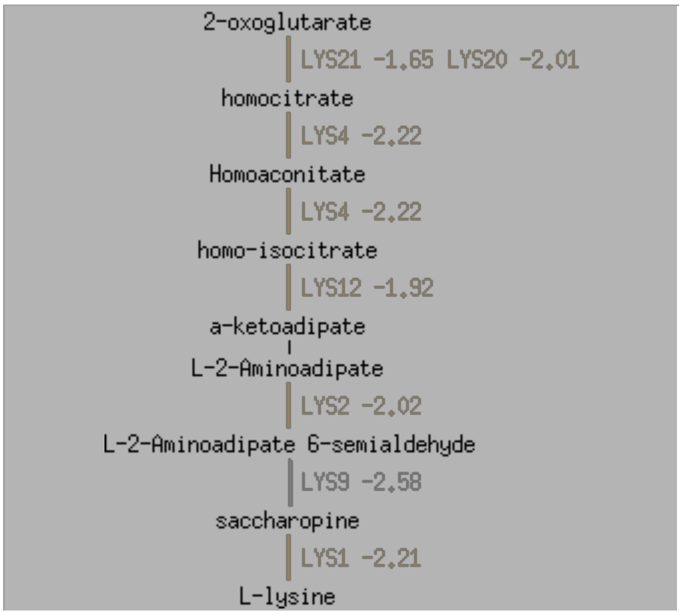
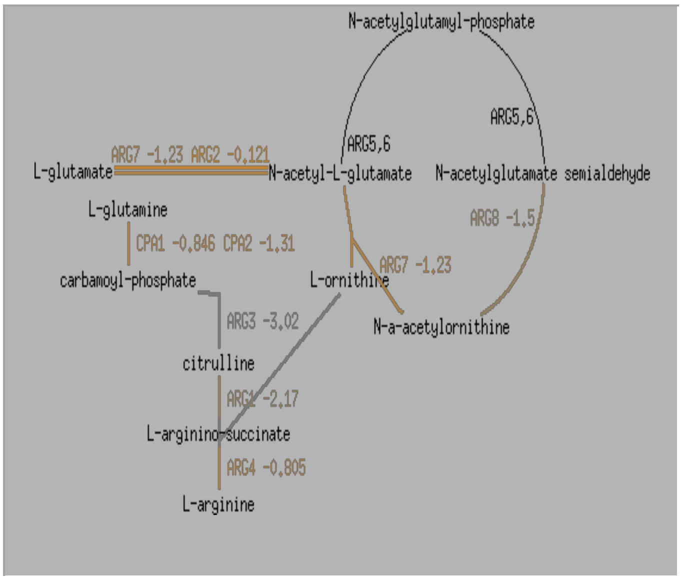
Total number of data rows (not including comment lines): 10563
Number of rows for which the gene could not be found: 9804
Number of rows for which the gene name was ambiguous: 0
Number of rows for which the gene is valid, but for which a data value was missing or malformed: 0

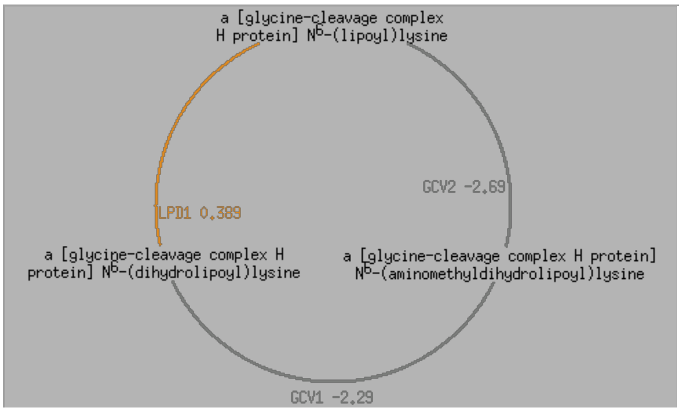
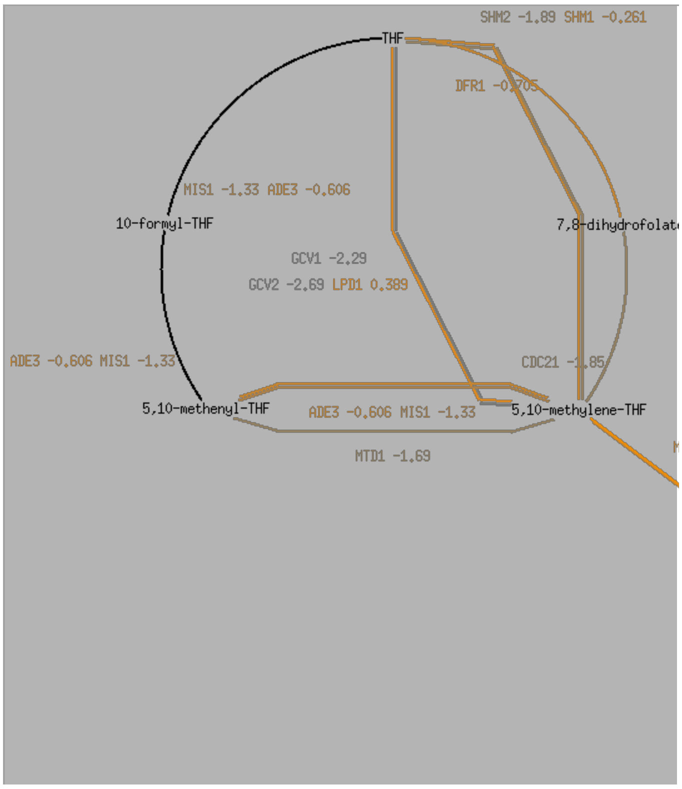
The table below shows statistics for the selected column/column ratio for all genes and for those genes that appear in the Overview (or in any of the selected overviews, if multiple were selected).

Data Statistics	All Genes	Overview Genes
Number of values:	759	619
Minimum value:	-3.037	-3.037

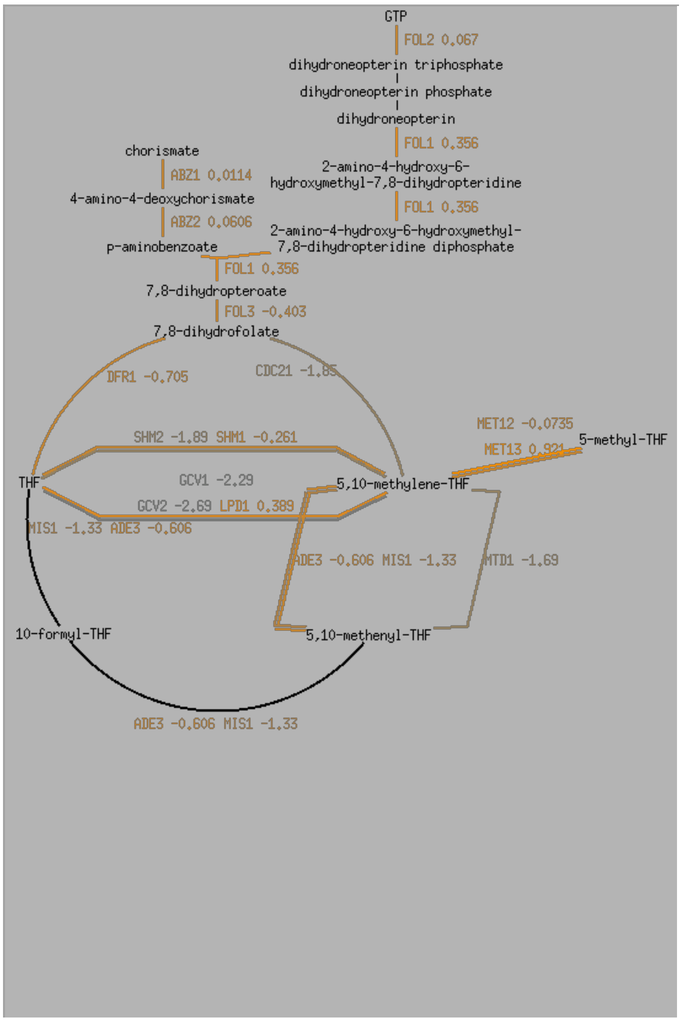
Maximum value:	5.5071	5.5071
Median:	-0.0144	0.032449998
Mean:	-0.0021671697	0.019628845
Standard deviation:	0.9757149	1.027266

SI Table 1. Metabolic pathway analysis of exposure to limonene. Values are $\log_2$ treatment/control ratio and only pathways exceeding threshold value of ±2 are shown.

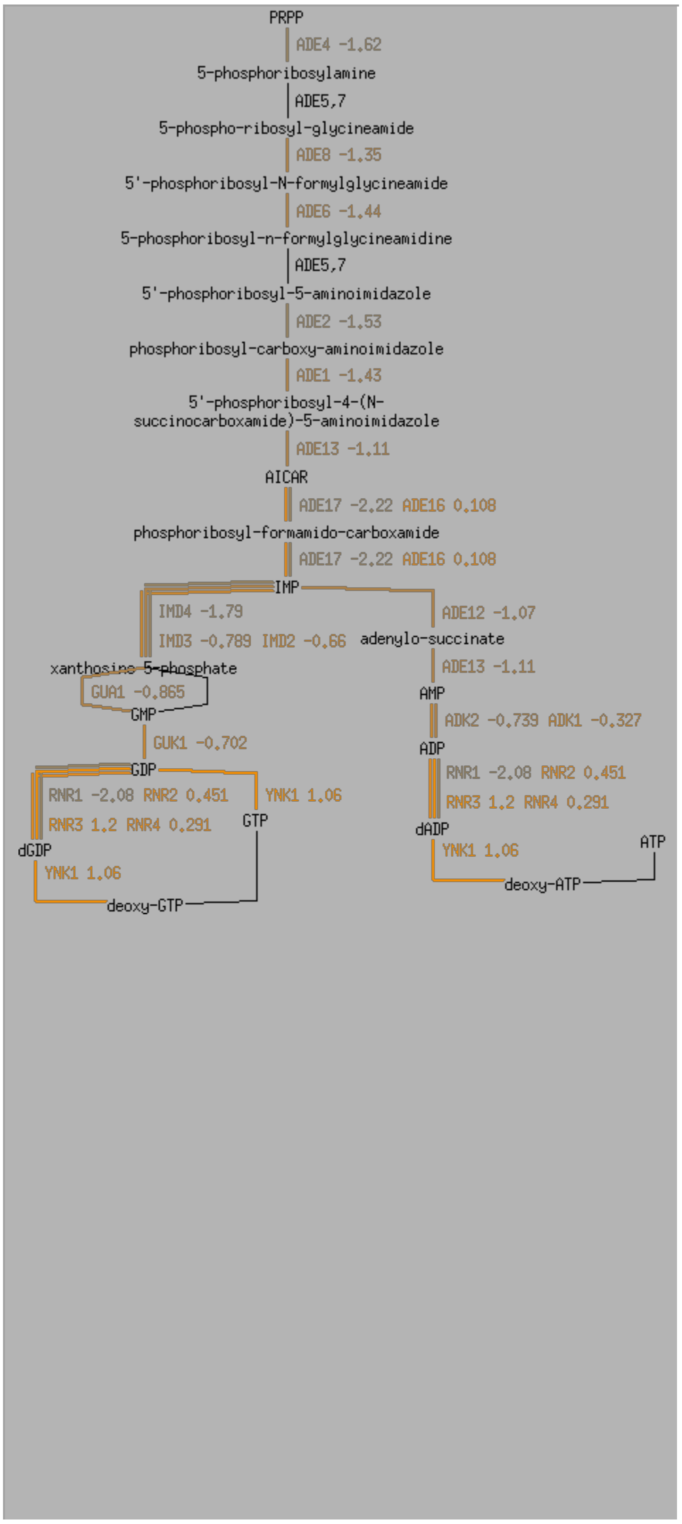
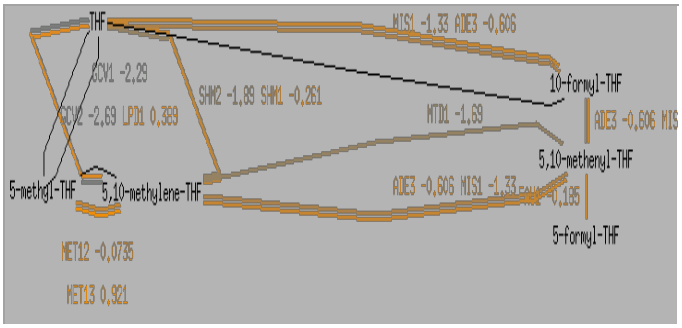
Pathway	Pathway Diagram	Enzymes, Genes, and Enzyme Cellular Locations
lysine biosynthesis		homocitrate synthase LYS20 homocitrate synthase LYS21 homoaconitase LYS4 homo-isocitrate dehydrogenase LYS12 alpha aminoadipate reductase LYS2 saccharopine dehydrogenase (NADP+, L-glutamate-forming) LYS9 saccharopine dehydrogenase (NAD+, L-lysine-forming) LYS1
arginine biosynthesis		ornithine carbamoyltransferase ARG3 acetylornithine aminotransferase ARG8 acetylglutamate kinase / N-acetyl-gamma-glutamyl-phosphate reductase ARG5,6 carbamoyl phosphate synthetase CPA1 CPA2 acetylglutamate synthase ARG2 acetylornithine acetyltransferase ARG7 arginosuccinate synthetase ARG1 argininosuccinate lyase ARG4

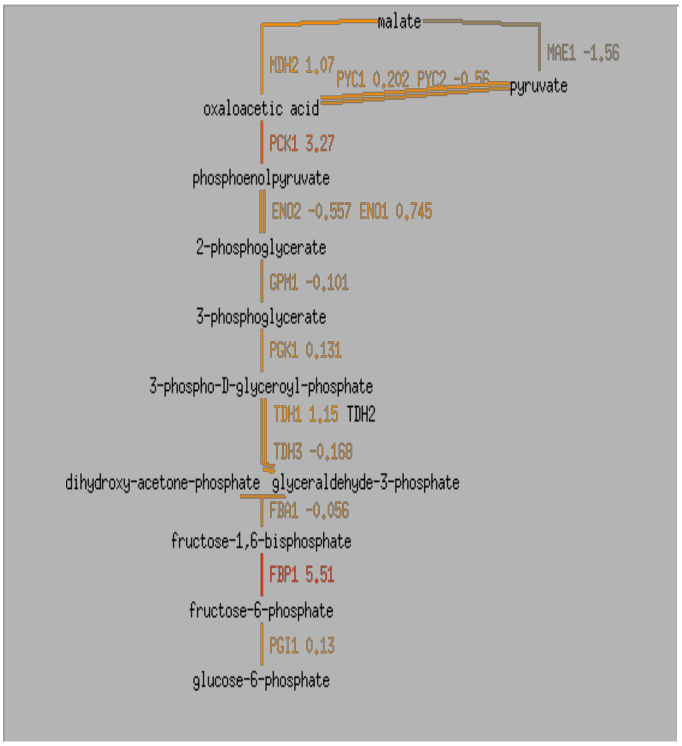
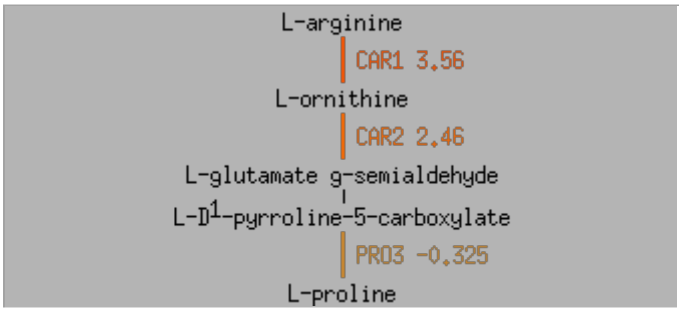
glycine cleavage complex		glycine decarboxylase complex P subunit	GCV2
		GCV1	GCV1
		dihydrolipoamide dehydrogenase	LPD1
folate interconversions		C1-tetrahydrofolate synthase	ADE3
		mitochondrial C1-tetrahydrofolate synthase	MIS1
		Serine hydroxymethyltransferase, mitochondrial	SHM1
		serine hydroxymethyltransferase	SHM2
		thymidylate synthase	CDC21
		dihydrofolate reductase	DFR1
		glycine cleavage complex	GCV1 GCV2 LPD1
		MTHFR	MET13
		MTHFR	MET12
		NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase	MTD1

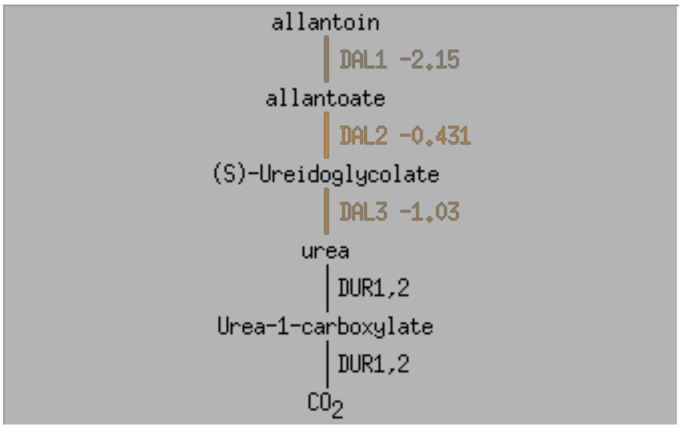
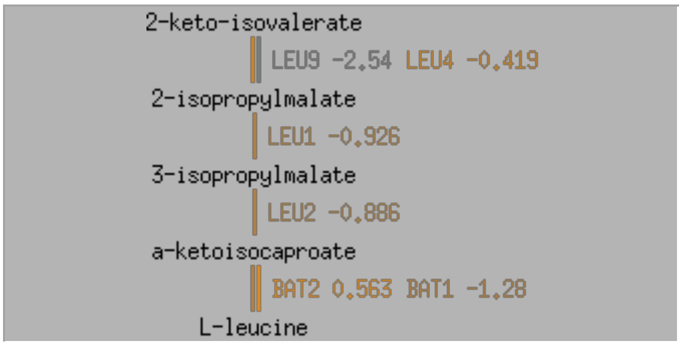
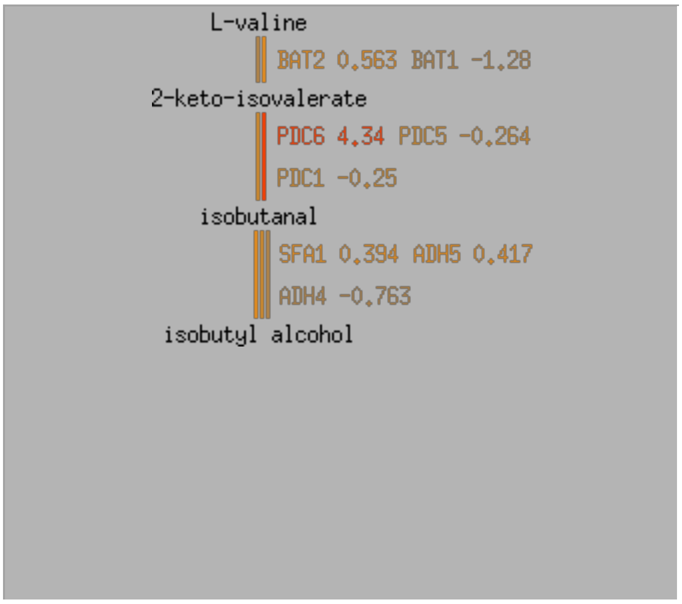
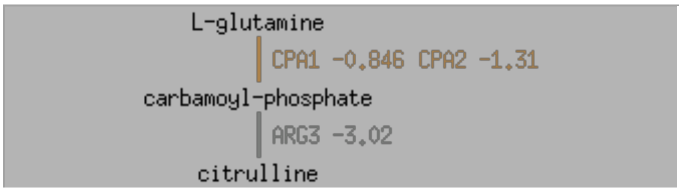
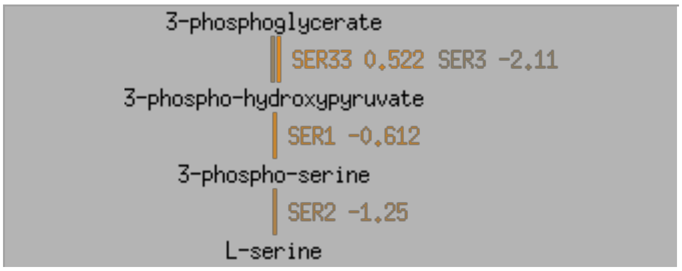
folate biosynthesis

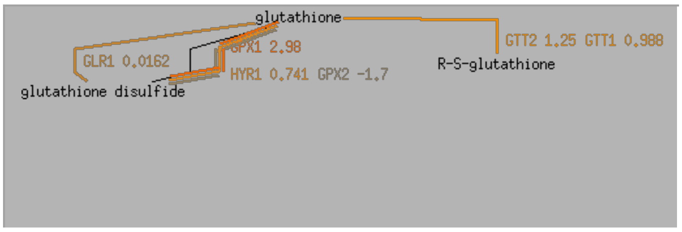
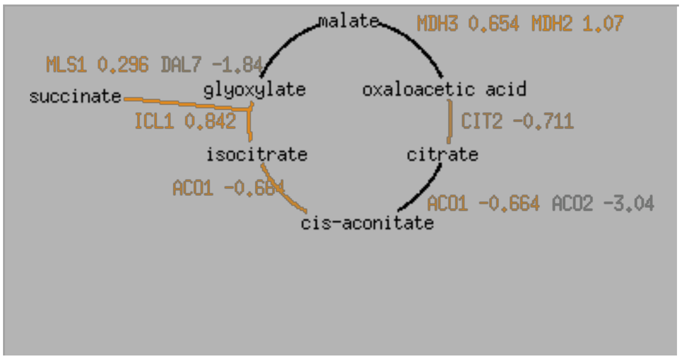
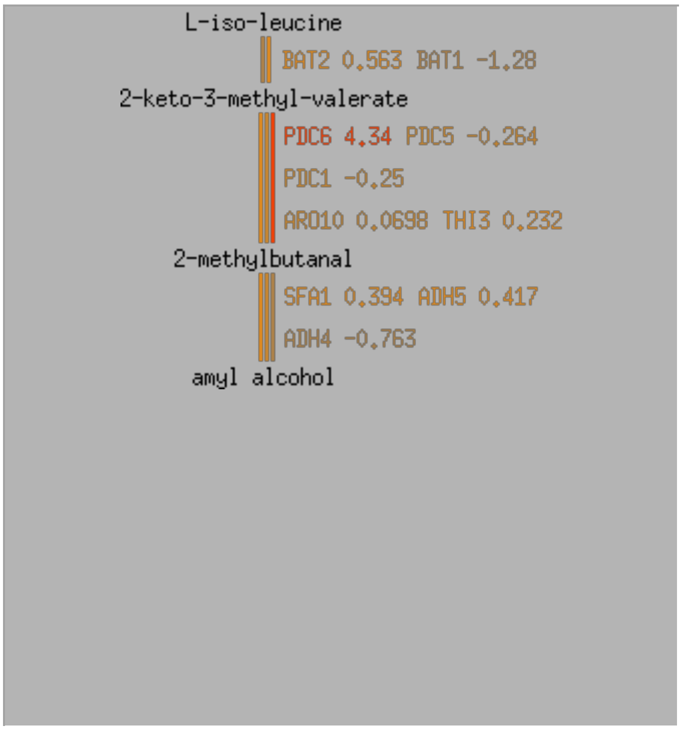


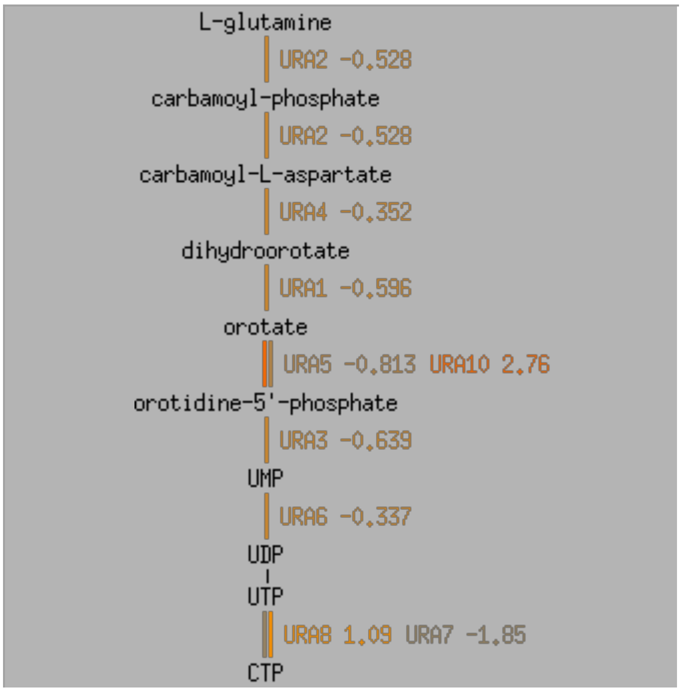
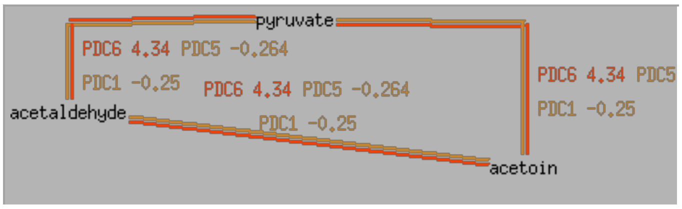
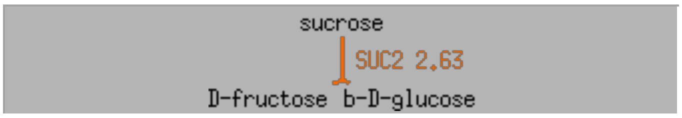
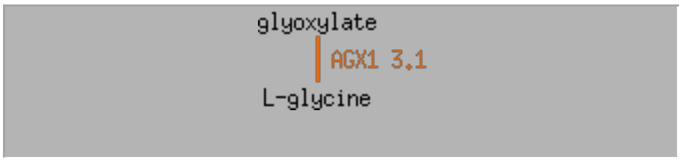
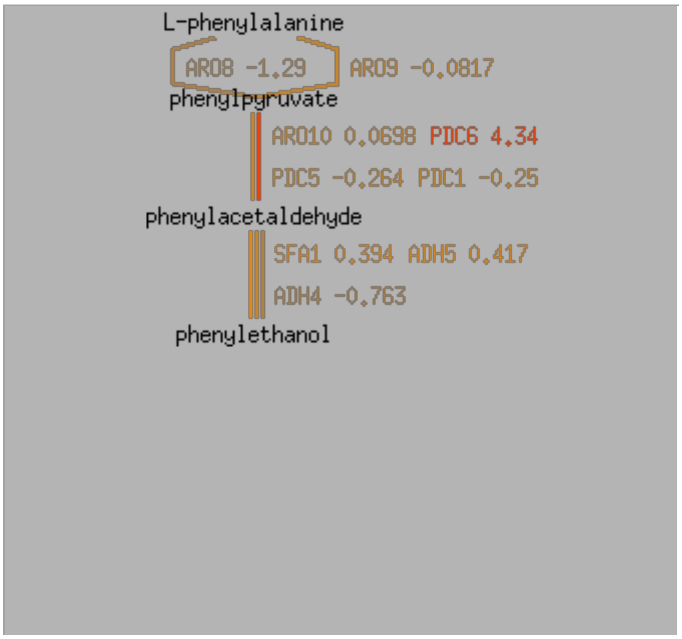
aminodeoxychorismate synthase	ABZ1
GTP-cyclohydrolase I	FOL2
aminodeoxychorismate lyase	ABZ2
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase [multifunctional]	FOL1
dihydrofolate synthase	FOL3
dihydrofolate reductase	DFR1
glycine cleavage complex	GCV1 GCV2 LPD1
Serine hydroxymethyltransferase, mitochondrial	SHM1
serine hydroxymethyltransferase	SHM2
thymidylate synthase	CDC21
MTHFR	MET13
MTHFR	MET12
NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase	MTD1
C1-tetrahydrofolate synthase	ADE3
mitochondrial C1-tetrahydrofolate synthase	MIS1

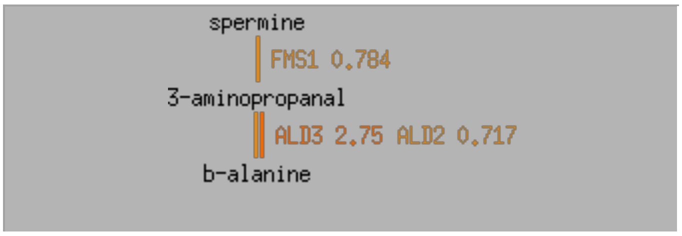
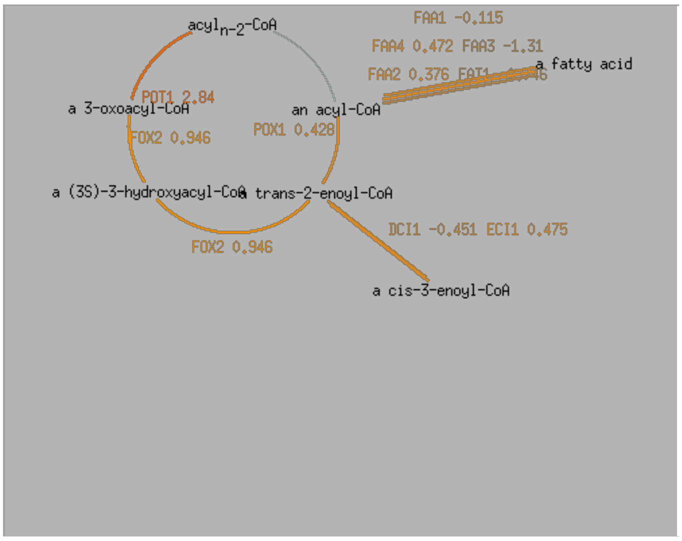
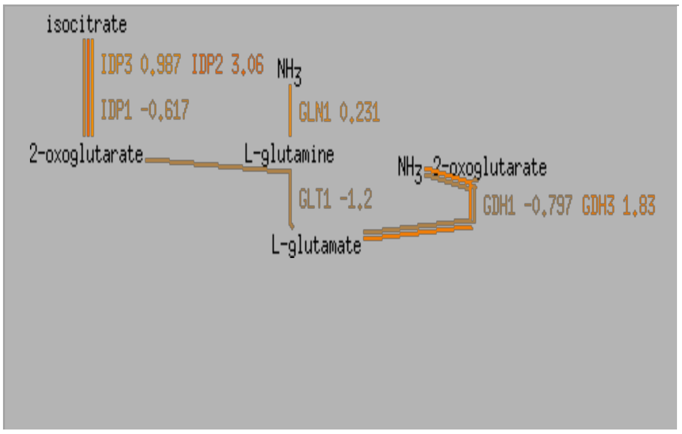
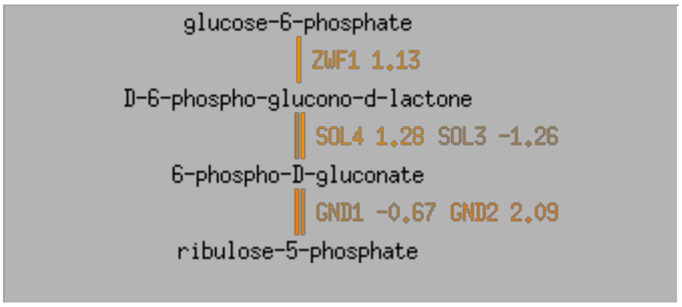
<table>
<tr><td rowspan="15">de novo biosynthesis of purine nucleotides</td><td rowspan="15"> </td><td>phosphoribosylpyrophosphate amidotransferase</td><td>ADE4</td></tr>
<tr><td>glycinamide ribotide transformylase</td><td>ADE8</td></tr>
<tr><td>5'-phosphoribosylformyl glycinamidine synthetase</td><td>ADE6</td></tr>
<tr><td>phosphoribosylglycinamidine synthetase / phopshoribosylaminoimidazole synthetase</td><td>ADE5,7</td></tr>
<tr><td>phosphoribosylaminoimidazole-carboxylase</td><td>ADE2</td></tr>
<tr><td>phosphoribosyl amino imidazolesuccinocarbozamide synthetase</td><td>ADE1</td></tr>
<tr><td>inosine monophosphate cyclohydrolase [multifunctional]</td><td>ADE16</td></tr>
<tr><td>inosine monophosphate cyclohydrolase [multifunctional]</td><td>ADE17</td></tr>
<tr><td>IMP dehydrogenase</td><td>IMD2</td></tr>
<tr><td>IMP dehydrogenase</td><td>IMD3</td></tr>
<tr><td>IMP dehydrogenase</td><td>IMD4</td></tr>
<tr><td>GMP synthase</td><td>GUA1</td></tr>
<tr><td>guanylate kinase</td><td>GUK1</td></tr>
<tr><td>adenylosuccinate synthetase</td><td>ADE12</td></tr>
<tr><td>adenylosuccinate lyase</td><td>ADE13</td></tr>
<tr><td></td><td></td><td>adenylate kinase</td><td>ADK1</td></tr>
<tr><td></td><td></td><td>mitochondrial GTP:AMP phosphotransferase</td><td>ADK2</td></tr>
<tr><td></td><td></td><td>ribonucleotide reductase</td><td>RNR1 RNR2 RNR3RNR4</td></tr>
<tr><td></td><td></td><td>nucleoside diphosphate kinase</td><td>YNK1</td></tr>
<tr><td rowspan="5">folate transformations</td><td rowspan="5"> </td><td>Serine hydroxymethyltransferase, mitochondrial</td><td>SHM1</td></tr>
<tr><td>serine hydroxymethyltransferase</td><td>SHM2</td></tr>
<tr><td>MTHFR</td><td>MET13</td></tr>
<tr><td>MTHFR</td><td>MET12</td></tr>
<tr><td>glycine cleavage</td><td>GCV1 GCV2 L</td></tr>
</table>

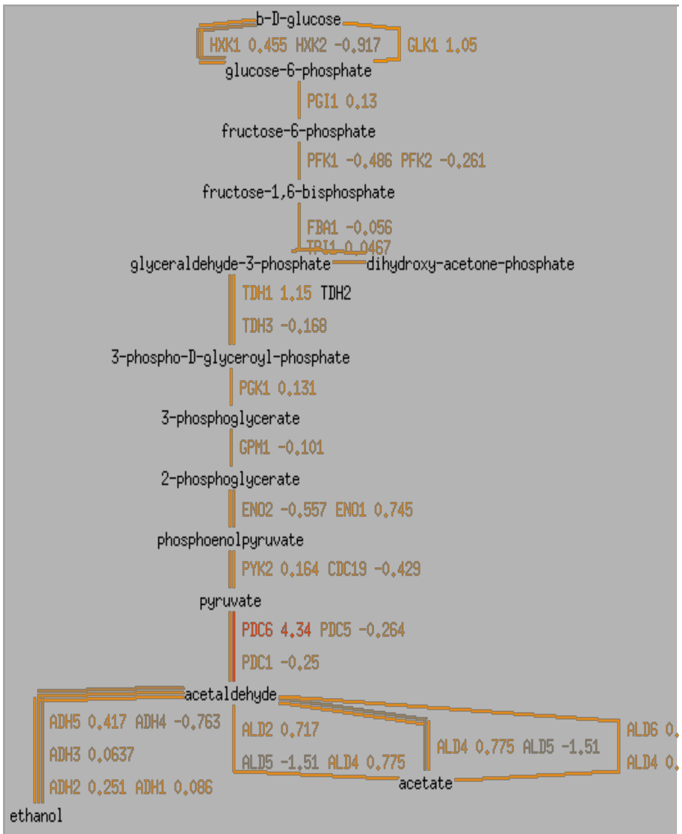
<table>
<tr><td></td><td></td><td>complex
NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase
mitochondrial C1-tetrahydrofolate synthase
C1-tetrahydrofolate synthase
5,10-methenyltetrahydrofolate synthetase</td><td>PD1
MTD1
MIS1
ADE3
FAU1</td></tr>
<tr><td>gluconeogenesis</td><td>
</td><td>malic enzyme
pyruvate carboxylase
pyruvate carboxylase
cytosolic malate dehydrogenase
phosphoenolpyruvate carboxylkinase
enolase I
enolase
phosphoglycerate mutase
3-phosphoglycerate kinase
glyceraldehyde-3-phosphate dehydrogenase
glyceraldehyde 3-phosphate dehydrogenase
glyceraldehyde-3-phosphate dehydrogenase
aldolase
fructose-1,6-bisphosphatase
glucose-6-phosphate isomerase</td><td>MAE1
PYC2
PYC1
MDH2
PCK1
ENO1
ENO2
GPM1
PGK1
TDH3
TDH2
TDH1
FBA1
FBP1
PGI1</td></tr>
<tr><td>arginine degradation (anaerobic)</td><td>
</td><td>arginase
ornithine aminotransferase
delta 1-pyrroline-5-carboxylate reductase</td><td>CAR1
CAR2
PRO3</td></tr>
</table>

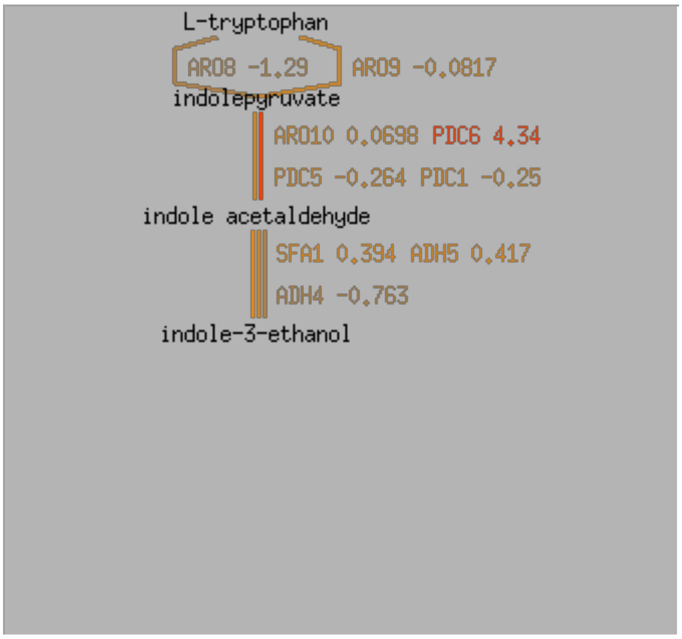
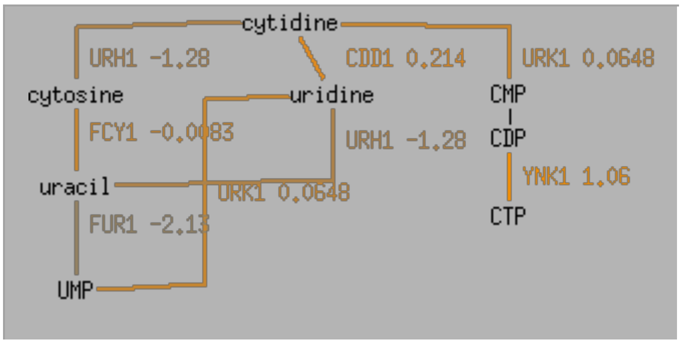
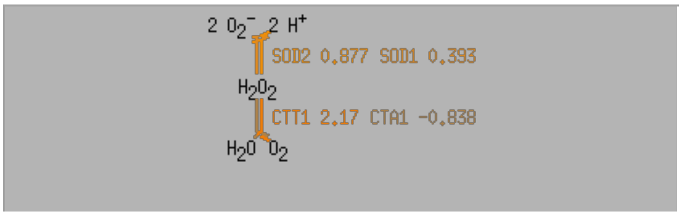
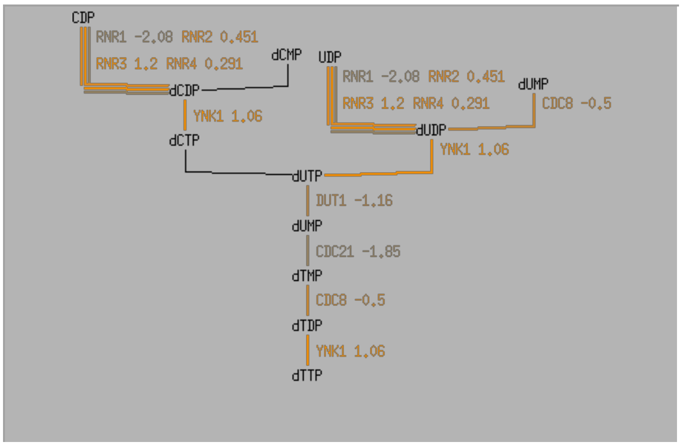
allantoin degradation		allantoinase	DAL1
		allantoicase	DAL2
		ureidoglycolate hydrolase	DAL3
		urea carboxylase / allophanate hydrolase	DUR1,2
leucine biosynthesis		alpha-isopropylmalate synthase	LEU4
		alpha-isopropylmalate synthase, minor isozyme	LEU9
		isopropylmalate isomerase	LEU1
		beta-IPM dehydrogenase	LEU2
		branched-chain amino acid aminotransferase	BAT1
		branched-chain amino acid transaminase	BAT2
valine degradation		branched-chain amino acid aminotransferase	BAT1
		branched-chain amino acid transaminase	BAT2
		pyruvate decarboxylase / decarboxylase	PDC1
		pyruvate decarboxylase / decarboxylase	PDC5
		pyruvate decarboxylase / decarboxylase	PDC6
		alcohol dehydrogenase	ADH1
		alcohol dehydrogenase	ADH2
		alcohol dehydrogenase	ADH3
		alcohol dehydrogenase	ADH4
		alcohol dehydrogenase	ADH5
		formaldehyde dehydrogenase / alcohol dehydrogenase	SFA1
citrulline biosynthesis		carbamoyl phosphate synthetase	CPA1 CPA2
		ornithine carbamoyltransferase	ARG3
serine biosynthesis from 3-phosphoglycerate		3-phosphoglycerate dehydrogenase	SER3
		3-phosphoglycerate dehydrogenase	SER33
		phosphoserine transaminase	SER1
		phosphoserine phosphatase	SER2

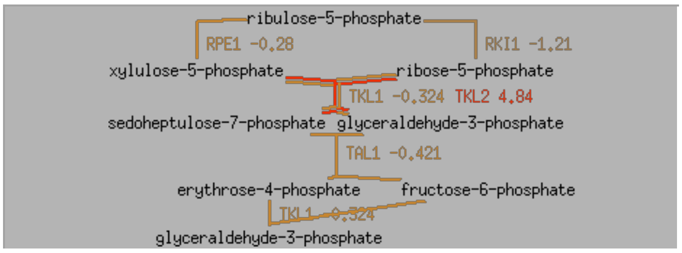
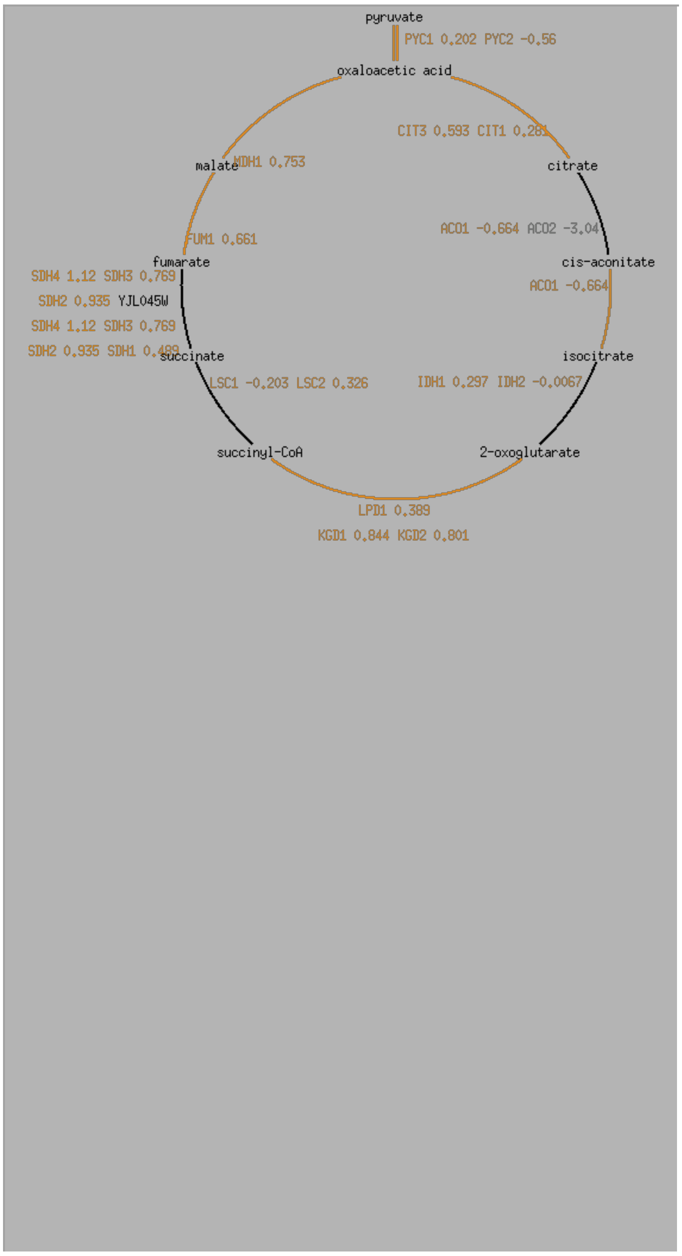
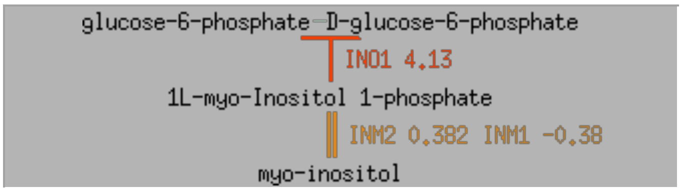
glutathione-glutaredoxin redox reactions		glutathione oxidoreductase	GLR1
		glutathione transferase	GTT1
		glutathione transferase	GTT2
		Glutathione peroxidase	GPX2
		glutathione-peroxidase	HYR1
		Glutathione peroxidase	GPX1
glyoxylate cycle		cytosolic malate dehydrogenase	MDH2
		peroxisome malate dehydrogenase	MDH3
		citrate synthase	CIT2
		aconitate hydratase	ACO2
		aconitase	ACO1
		isocitrate lyase	ICL1
		malate synthase 2	DAL7
		malate synthase	MLS1
isoleucine degradation		branched-chain amino acid aminotransferase	BAT1
		branched-chain amino acid transaminase	BAT2
		ketoisocaproate decarboxylase / decarboxylase	THI3
		decarboxylase	ARO10
		pyruvate decarboxylase / decarboxylase	PDC1
		pyruvate decarboxylase / decarboxylase	PDC5
		pyruvate decarboxylase / decarboxylase	PDC6
		alcohol dehydrogenase	ADH1
		alcohol dehydrogenase	ADH2
		alcohol dehydrogenase	ADH3
		alcohol dehydrogenase	ADH4
		alcohol dehydrogenase	ADH5
		formaldehyde dehydrogenase / alcohol dehydrogenase	SFA1

de novo biosynthesis of pyrimidine ribonucleotides		carbamyl phosphate synthase / aspartate transcarbamylase dihydrooratase dihydroorotate dehydrogenase orotate phosphoribosyltransferase orotate phosphoribosyltransferase orotidine-5'-phosphate decarboxylase uridylate kinase CTP synthase CTP synthase	URA2 URA4 URA1 URA10 URA5 URA3 URA6 URA7 URA8
acetoin biosynthesis II		pyruvate decarboxylase / decarboxylase pyruvate decarboxylase / decarboxylase pyruvate decarboxylase / decarboxylase	PDC1 PDC5 PDC6
sucrose degradation		invertase	SUC2
glycine biosynthesis from glyoxylate		alanine:glyoxylate aminotransferase	AGX1
phenylalanine degradation		aromatic amino acid aminotransferase I aromatic amino acid aminotransferase II pyruvate decarboxylase / decarboxylase pyruvate decarboxylase / decarboxylase pyruvate decarboxylase / decarboxylase decarboxylase alcohol dehydrogenase alcohol dehydrogenase alcohol dehydrogenase alcohol dehydrogenase alcohol dehydrogenase formaldehyde dehydrogenase / alcohol dehydrogenase	ARO8 ARO9 PDC1 PDC5 PDC6 ARO10 ADH1 ADH2 ADH3 ADH4 ADH5 SFA1

beta-alanine biosynthesis		amine oxidase aldehyde dehydrogenase (stress inducible cytoplasmic) aldehyde dehydrogenase (stress inducible cytoplasmic)	FMS1 ALD2 ALD3
fatty acid oxidation pathway		fatty acid transporter acyl-CoA synthetase acyl-CoA synthase long chain fatty acyl:CoA synthetase long chain fatty acyl:CoA synthetase d3,d2-Enoyl-CoA Isomerase delta(3,5)-delta(2,4)-dienoyl-CoA isomerase fatty-acyl coenzyme A oxidase 3-hydroxyacyl-CoA dehydrogenase 3-oxoacyl CoA thiolase	FAT1 FAA2 FAA3 FAA4 FAA1 ECI1 DCI1 POX1 FOX2 POT1
superpathway of glutamate biosynthesis		NADP-dependent isocitrate dehydrogenase NADP-dependent isocitrate dehydrogenase NADP-dependent isocitrate dehydrogenase glutamine synthetase NADP-dependent glutamate dehydrogenase NADP-dependent glutamate dehydrogenase glutamate synthase (NADH)	IDP1 IDP2 IDP3 GLN1 GDH3 GDH1 GLT1
oxidative branch of the pentose phosphate pathway		glucose-6-phosphate dehydrogenase 6-phosphogluconolactonase 6-phosphogluconolactonase 6-phosphogluconate dehydrogenase 6-phosphogluconate dehydrogenase, decarboxylating	ZWF1 SOL3 SOL4 GND2 GND1

superpathway of glucose fermentation		hexokinase II	HXK2
		hexokinase I	HXK1
		glucokinase	GLK1
		glucose-6-phosphate isomerase	PGI1
		phosphofructokinase	PFK1 PFK2
		aldolase	FBA1
		triosephosphate isomerase	TPI1
		glyceraldehyde-3-phosphate dehydrogenase	TDH3
		glyceraldehyde 3-phosphate dehydrogenase	TDH2
		glyceraldehyde-3-phosphate dehydrogenase	TDH1
		3-phosphoglycerate kinase	PGK1
		phosphoglycerate mutase	GPM1
		enolase I	ENO1
		enolase	ENO2
		pyruvate kinase	CDC19
		pyruvate kinase	PYK2
		pyruvate decarboxylase / decarboxylase	PDC1
		pyruvate decarboxylase / decarboxylase	PDC5
		pyruvate decarboxylase / decarboxylase	PDC6
		aldehyde dehydrogenase (stress inducible cytoplasmic)	ALD2
		aldehyde dehydrogenase (major mitochondrial)	ALD4
		aldehyde dehydrogenase (minor mitochondrial)	ALD5
		aldehyde dehydrogenase (major cytoplasmic)	ALD6
		alcohol dehydrogenase	ADH1
		alcohol dehydrogenase	ADH2
		alcohol dehydrogenase	ADH3
		alcohol dehydrogenase	ADH4
		alcohol dehydrogenase	ADH5

tryptophan degradation		aromatic amino acid aminotransferase I aromatic amino acid aminotransferase II pyruvate decarboxylase / decarboxylase pyruvate decarboxylase / decarboxylase pyruvate decarboxylase / decarboxylase decarboxylase alcohol dehydrogenase alcohol dehydrogenase alcohol dehydrogenase alcohol dehydrogenase alcohol dehydrogenase formaldehyde dehydrogenase / alcohol dehydrogenase	ARO8 ARO9 PDC1 PDC5 PDC6 ARO10 ADH1 ADH2 ADH3 ADH4 ADH5 SFA1
salvage pathways of pyrimidine ribonucleotides		cytidine deaminase deoxycytidine kinase / cytidine kinase / uridine kinase nicotinic acid riboside hydrolase [multifunctional] cytosine deaminase UPRTase nucleoside diphosphate kinase	CDD1 URK1 URH1 FCY1 FUR1 YNK1
removal of superoxide radicals		cytoplasmic superoxide dismutase mitochondrial superoxide dismutase catalase A catalase T	SOD1 SOD2 CTA1 CTT1
de novo biosynthesis of pyrimidine deoxyribonucleotides		ribonucleotide reductase dUTP pyrophosphatase thymidylate synthase uridylate kinase / thymidylate kinase nucleoside diphosphate kinase	RNR1 RNR2 RNR3 RNR4 DUT1 CDC21 CDC8 YNK1

non-oxidative branch of the pentose phosphate pathway		D-ribulose-5-Phosphate 3-epimerase	RPE1
		ribose-5-phosphate ketol-isomerase	RKI1
		transketolase	TKL2
		transaldolase	TAL1
		transketolase	TKL1
TCA cycle, aerobic respiration		pyruvate carboxylase	PYC2
		pyruvate carboxylase	PYC1
		mitochondrial malate dehydrogenase	MDH1
		citrate synthase	CIT1
		citrate synthase	CIT3
		aconitate hydratase	ACO2
		aconitase	ACO1
		NAD-dependent isocitrate dehydrogenase	IDH1 IDH2
		2-ketoglutarate dehydrogenase complex	LPD1 KGD1 KGD2
		succinyl-CoA ligase	LSC1 LSC2
		succinate dehydrogenase (ubiquinone)	SDH4 SDH3 SDH2 SDH1
		minor succinate dehydrogenase (ubiquinone)	SDH4 SDH3 SDH2 YJL045W
		fumarate hydralase	FUM1
myo-inositol biosynthesis		L-myo-inositol-1-phosphate synthase	INO1
		inositol monophosphatase	INM1
		inositol monophosphate	INM2

SI Table 2. Differentially expressed genes 2 h after limonene exposure. Genes are categorized based on either cellular compartments and/or biological processes.

Gene	**Description**	**FC** [a]	**P value** [b]
Cell wall cellular compartment			
Cytokinesis			
XBP1	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, and late in meiosis; member of the Swi4p/Mbp1p family; potential Cdc28p substrate, XBP1	2.1	2.58E-05
AFR1	Alpha-factor pheromone receptor regulator, negatively regulates pheromone receptor signaling; required for normal mating projection (shmoo) formation; required for Spa2p to recruit Mpk1p to shmoo tip during mating; interacts with Cdc12p, AFR1	1.9	1.81E-04
MET30	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin ligase complex; interacts with and regulates Met4p, localizes within the nucleus, MET30	1.6	2.18E-03
DSE4	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother, DSE4	-1.9	2.50E-04
GAS2	1,3-beta-glucanosyltransferase, involved with Gas4p in spore wall assembly; has similarity to Gas1p, GAS2	-2.0	8.47E-04
EGT2	Glycosylphosphatidylinositol (GPI)-anchored cell wall endoglucanase required for proper cell separation after cytokinesis, expression is activated by Swi5p and tightly regulated in a cell cycle-dependent manner, EGT2	-2.1	7.20E-03
SUN4	Cell wall protein related to glucanases, possibly involved in cell wall septation; member of the SUN family, SUN4	-2.2	1.47E-04
GAS3	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall, GAS3	-2.3	6.04E-04
CTS1	Endochitinase, required for cell separation after mitosis; transcriptional activation during late G and early M cell cycle phases is mediated by transcription factor Ace2p, CTS1	-2.4	9.10E-04
UTR2	Cell wall protein that functions in the transfer of chitin to beta(1-6)glucan; putative chitin transglycosidase; glycosylphosphatidylinositol (GPI)-anchored protein localized to the bud neck; has a role in cell wall maintenance, UTR2	-2.6	3.22E-04
SCW11	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on its regulation by Ste12p, SCW11	-3.0	3.29E-04
DSE1	Daughter cell-specific protein, may participate in	-3.1	1.03E-

	pathways regulating cell wall metabolism; deletion affects cell separation after division and sensitivity to drugs targeted against the cell wall, DSE1		03
DSE2	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother; expression is repressed by cAMP, DSE2	-3.2	7.35E-04
SPS4	Protein whose expression is induced during sporulation; not required for sporulation; heterologous expression in E. coli induces the SOS response that senses DNA damage, SPS4	-3.7	3.24E-06
Cell wall organization			
YGP1	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved in adaptation prior to stationary phase entry; has similarity to Sps100p, YGP1	4.0	1.13E-07
PIR3	O-glycosylated covalently-bound cell wall protein required for cell wall stability; expression is cell cycle regulated, peaking in M/G1 and also subject to regulation by the cell integrity pathway, PIR3	5.0	9.39E-07
FIT2	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall, FIT2	2.0	6.39E-05
TIP1	Major cell wall mannoprotein with possible lipase activity; transcription is induced by heat- and cold-shock; member of the Srp1p/Tip1p family of serine-alanine-rich proteins, TIP1	2.1	1.44E-04
YPK2	Protein kinase with similarityto serine/threonine protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; homolog of mammalian kinase SGK, YPK2	1.8	5.36E-04
SPI1	GPI-anchored cell wall protein involved in weak acid resistance; basal expression requires Msn2p/Msn4p; expression is induced under conditions of stress and during the diauxic shift; similar to Sed1p, SPI1	4.7	8.17E-04
SNA3	Integral membrane protein localized to vacuolar intralumenal vesicles, computational analysis of large-scale protein-protein interaction data suggests a possible role in either cell wall synthesis or protein-vacuolar targeting, SNA3	1.2	8.98E-04
FRT2	Tail-anchored endoplasmic reticulum membrane protein, interacts with homolog Frt1p but is not a substrate of calcineurin (unlike Frt1p), promotes growth in conditions of high Na+, alkaline pH, or cell wall stress; potential Cdc28p substrate, FRT2	1.7	3.36E-03
USV1	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes	1.2	4.26E-03

	involved in protein folding, ATP binding, and cell wall biosynthesis, USV1		
PST1	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell integrity pathway, as mediated by Rlm1p; upregulated by cell wall damage via disruption of FKS1, PST1	1.9	4.73E-03
ECM4	Omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ECM4	1.4	2.94E-04
TDH1	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell wall [Source:SGD;Acc:S000003588]	1.1	5.38E-03
FIT3	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall, FIT3	1.7	5.54E-03
Hsp150	O-mannosylated heat shock protein that is secreted and covalently attached to the cell wall via beta-1,3-glucan and disulfide bridges; required for cell wall stability; induced by heat shock, oxidative stress, and nitrogen limitation, HSP150	1.0	6.70E-03
CWP1	Cell wall mannoprotein, linked to a beta-1,3- and beta-1,6-glucan heteropolymer through a phosphodiester bond; involved in cell wall organization, CWP1	1.1	7.41E-03
YPS6	Putative GPI-anchored aspartic protease, YPS6	1.2	8.35E-03
GSC2	Catalytic subunit of 1,3-beta-glucan synthase, involved in formation of the inner layer of the spore wall; activity positively regulated by Rho1p and negatively by Smk1p; has similarity to an alternate catalytic subunit, Fks1p (Gsc1p), GSC2	1.6	1.04E-03
RIM21	Component of the RIM101 pathway, has a role in cell wall construction and alkaline pH response; has similarity to A. nidulans PalH, RIM21	1.1	5.03E-03
SLT2	Serine/threonine MAP kinase involved in regulating the maintenance of cell wall integrity and progression through the cell cycle; regulated by the PKC1-mediated signaling pathway,	0.9	0.057308
MLP1	Protein kinase implicated in the Slt2p mitogen-activated (MAP) kinase signaling pathway; associates with Rlm1p, ---	2.1	1.38E-03
ECM4	Omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ECM4	1.4	2.94E-04
FBP26	Fructose-2,6-bisphosphatase, required for glucose metabolism	1.4	7.85E-04
Transmembrane transport			

AGP3	Low-affinity amino acid permease, may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation, AGP3	5.1	3.92E-06
MUP1	High affinity methionine permease, integral membrane protein with 13 putative membrane-spanning regions; also involved in cysteine uptake, MUP1	4.6	1.75E-04
YCT1	High-affinity cysteine-specific transporter with similarity to the Dal5p family of transporters; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YCT1 is not an essential gene, YCT1	4.3	3.25E-04
HXT5	Hexose transporter with moderate affinity for glucose, induced in the presence of non-fermentable carbon sources, induced by a decrease in growth rate, contains an extended N-terminal domain relative to other HXTs,	3.9	8.32E-06
STL1	Glycerol proton symporter of the plasma membrane, subject to glucose-induced inactivation, strongly but transiently induced when cells are subjected to osmotic shock, STL1	3.9	2.35E-03
PDR15	Plasma membrane ATP binding cassette (ABC) transporter, multidrug transporter and general stress response factor implicated in cellular detoxification; regulated by Pdr1p, Pdr3p and Pdr8p; promoter contains a PDR responsive element, PDR15	3.2	4.08E-04
MMP1	High-affinity S-methylmethionine permease, required for utilization of S-methylmethionine as a sulfur source; has similarity to S-adenosylmethionine permease Sam3p, MMP1	2.3	1.05E-03
SAM3	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p, SAM3	2.2	1.71E-03
JEN1	Lactate transporter, required for uptake of lactate and pyruvate; phosphorylated; expression is derepressed by transcriptional activator Cat8p during respiratory growth, and repressed in the presence of glucose, fructose, and mannose, JEN1	2.2	2.20E-03
JEN1	Lactate transporter, required for uptake of lactate and pyruvate; phosphorylated; expression is derepressed by transcriptional activator Cat8p during respiratory growth, and repressed in the presence of glucose, fructose, and mannose, JEN1	2.2	2.20E-03
CSR2	Nuclear protein with a potential regulatory role in utilization of galactose and nonfermentable carbon sources; overproduction suppresses the lethality at high temperature of a chs5 spa2 double null mutation; potential Cdc28p substrate, CSR2	2.1	3.02E-05
PDR5	Plasma membrane ATP-binding cassette (ABC) transporter, short-lived multidrug transporter actively regulated by Pdr1p; also involved in steroid transport,	2.0	3.66E-03

	cation resistance, and cellular detoxification during exponential growth, PDR5		
MUP3	Low affinity methionine permease, similar to Mup1p, MUP3	1.9	8.15E-04
YOR1	Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter mediates export of many different organic anions including oligomycin, YOR1	1.7	8.81E-03
ALP1	Arginine transporter; expression is normally very low and it is unclear what conditions would induce significant expression, ALP1	1.2	3.81E-03
ZRT1	High-affinity zinc transporter of the plasma membrane, responsible for the majority of zinc uptake; transcription is induced under low-zinc conditions by the Zap1p transcription factor, ZRT1	-1.1	7.69E-03
PDR12	Plasma membrane ATP-binding cassette (ABC) transporter, weak-acid-inducible multidrug transporter required for weak organic acid resistance; induced by sorbate and benzoate and regulated by War1p; mutants exhibit sorbate hypersensitivity, PDR12	-1.5	8.27E-04
Redox processes			
JLP1	Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase, involved in sulfonate catabolism for use as a sulfur source, contains sequence that closely resembles a J domain (typified by the E. coli DnaJ protein), JLP1	6.7	1.80E-05
OYE3	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye2p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism, OYE3	3.6	9.43E-05
IDP2	Cytosolic NADP-specific isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate; levels are elevated during growth on non-fermentable carbon sources and reduced during growth on glucose, IDP2	3.1	1.51E-04
GPX1	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress, GPX1	3.0	8.70E-03
IRC15	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; null mutant displays increased levels of spontaneous Rad52 foci, ---	2.9	5.70E-05
NDE2	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic NADH to the mitochondrial respiratory chain, NDE2	2.7	9.11E-06
HMX1	ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme oxygenases; expression	2.5	9.76E-03

	regulated by AFT1, HMX1		
FMO1	Flavin-containing monooxygenase, localized to the cytoplasmic face of the ER membrane; catalyzes oxidation of biological thiols to maintain the ER redox buffer ratio for correct folding of disulfide-bonded proteins, FMO1	2.4	1.45E-04
GRE2	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway, GRE2	2.2	3.38E-03
GTO1	Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization, GTO1	2.2	9.17E-05
CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide, CTT1	2.2	1.98E-04
GND2	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone, GND2	2.1	1.28E-04
FRE5	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies, FRE5	2.1	9.73E-04
FMP46	Putative redox protein containing a thioredoxin fold; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies, FMP46	2.0	5.29E-03
YHB1	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses, YHB1	1.9	4.92E-03
OLE1	Delta(9) fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal distribution of mitochondria, OLE1	1.9	3.32E-04
MET8	Bifunctional dehydrogenase and ferrochelatase, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis, MET8	1.9	4.47E-04
GDH3	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh1p; expression regulated by nitrogen and carbon sources, GDH3	1.8	5.97E-04
MXR1	Peptide methionine sulfoxide reductase, reverses the oxidation of methionine residues; involved in oxidative damage repair, providing resistance to oxidative stress and regulation of lifespan, MXR1	1.8	1.94E-03
BDH2	Putative medium-chain alcohol dehydrogenase with similarity to BDH1; transcription induced by constitutively active PDR1 and PDR3; BDH2 is an essential gene, BDH2	1.7	3.83E-03
YKL107W	Putative protein of unknown function, ---	1.6	5.03E-

			04
TRX3	Mitochondrial thioredoxin, highly conserved oxidoreductase required to maintain the redox homeostasis of the cell, forms the mitochondrial thioredoxin system with Trr2p, redox state is maintained by both Trr2p and Glr1p, TRX3	1.6	2.39E-03
HBN1	Putative protein of unknown function; similar to bacterial nitroreductases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus, HBN1	1.5	2.10E-04
YDL124W	NADPH-dependent alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; member of the aldo-keto reductase (AKR) family, ---	1.5	4.20E-04
ECM4	Omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ECM4	1.4	2.94E-04
GUT2	Mitochondrial glycerol-3-phosphate dehydrogenase; expression is repressed by both glucose and cAMP and derepressed by non-fermentable carbon sources in a Snf1p, Rsf1p, Hap2/3/4/5 complex dependent manner, GUT2	1.3	4.40E-03
MCR1	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis, MCR1	1.3	1.58E-03
RPH1	JmjC domain-containing histone demethylase which can specifically demethylate H3K36 tri- and dimethyl modification states; transcriptional repressor of PHR1; Rph1p phosphorylation during DNA damage is under control of the MEC1-RAD53 pathway, RPH1	1.3	7.43E-03
AAD6	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response, AAD6	1.2	7.73E-03
RNR3	Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits, RNR3	1.2	8.96E-03
GDH2	NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen catabolite repression and intracellular ammonia levels, GDH2	1.1	1.67E-03
OYE2	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye3p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism, OYE2	1.1	4.40E-03
FRE6	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels, FRE6	1.1	7.08E-03
UGA2	Succinate semialdehyde dehydrogenase involved in the utilization of gamma-aminobutyrate (GABA) as a nitrogen source; part of the 4-aminobutyrate and	1.1	5.39E-03

	glutamate degradation pathways; localized to the cytoplasm, UGA2		
FAS2	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; phosphorylated, FAS2	1.1	6.48E-03
PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; induced during respiratory growth and under conditions of oxidative stress; phosphorylated, PRX1	1.1	2.76E-03
GTT1	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT1	1.0	9.16E-03
HTD2	Mitochondrial 3-hydroxyacyl-thioester dehydratase involved in fatty acid biosynthesis, required for respiratory growth and for normal mitochondrial morphology, HTD2	1.0	3.55E-03
LOT6	FMN-dependent NAD(P)H:quinone reductase that may be involved in quinone detoxification; gene expression increases in cultures shifted to a lower temperature, LOT6	0.9	5.86E-03
Biosynthesis of secondary metabolites			
FBP1	Fructose-1,6-bisphosphatase, key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism, FBP1	5.5	7.81E-05
PDC6	Minor isoform of pyruvate decarboxylase, decarboxylates pyruvate to acetaldehyde, involved in amino acid catabolism; transcription is glucose- and ethanol-dependent, and is strongly induced during sulfur limitation, PDC6	4.3	3.70E-04
INO1	Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other phospholipid biosynthetic genes by Ino2p and Ino4p, which bind the UASINO DNA element, INO1	4.1	7.39E-07
AGX1	Alanine:glyoxylate aminotransferase (AGT), catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast; has similarity to mammalian and plant alanine:glyoxylate aminotransferases, AGX1	3.1	8.96E-06
IDP2	Cytosolic NADP-specific isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate; levels are elevated during growth on non-fermentable carbon sources and reduced during growth on glucose, IDP2	3.1	1.51E-04
IRC15	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; null mutant displays increased levels of spontaneous Rad52	2.9	5.70E-05

	foci, ---		
POT1	3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids, POT1	2.8	5.84E-04
CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide, CTT1	2.2	1.98E-04
GND2	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone, GND2	2.1	1.28E-04
MET8	Bifunctional dehydrogenase and ferrochelatase, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis, MET8	1.9	4.47E-04
GAL3	Transcriptional regulator involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p inhibition of Gal4p; binds galactose and ATP but does not have galactokinase activity, GAL3	1.3	2.31E-03
MCR1	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis, MCR1	1.3	1.58E-03
ACS1	Acetyl-coA synthetase isoform which, along with Acs2p, is the nuclear source of acetyl-coA for histone acetlyation; expressed during growth on nonfermentable carbon sources and under aerobic conditions, ACS1	1.2	2.15E-03
SDH4	Membrane anchor subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone, SDH4	1.1	4.66E-03
YNK1	Nucleoside diphosphate kinase, catalyzes the transfer of gamma phosphates from nucleoside triphosphates, usually ATP, to nucleoside diphosphates by a mechanism that involves formation of an autophosphorylated enzyme intermediate, YNK1	1.1	4.62E-03
SAM2	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p), SAM2	0.9	8.18E-03
Small metobolic processes			
PDC6	Minor isoform of pyruvate decarboxylase, decarboxylates pyruvate to acetaldehyde, involved in amino acid catabolism; transcription is glucose- and ethanol-dependent, and is strongly induced during sulfur limitation, PDC6	4.3	3.70E-04
INO1	Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other phospholipid biosynthetic genes by Ino2p and Ino4p, which bind the UASINO DNA element, INO1	4.1	7.39E-07

YGP1	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved in adaptation prior to stationary phase entry; has similarity to Sps100p, YGP1	4.0	1.13E-07
PDR15	Plasma membrane ATP binding cassette (ABC) transporter, multidrug transporter and general stress response factor implicated in cellular detoxification; regulated by Pdr1p, Pdr3p and Pdr8p; promoter contains a PDR responsive element, PDR15	3.2	4.08E-04
AGX1	Alanine:glyoxylate aminotransferase (AGT), catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast; has similarity to mammalian and plant alanine:glyoxylate aminotransferases, AGX1	3.1	8.96E-06
IDP2	Cytosolic NADP-specific isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate; levels are elevated during growth on non-fermentable carbon sources and reduced during growth on glucose, IDP2	3.1	1.51E-04
POT1	3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids, POT1	2.8	5.84E-04
URA10	One of two orotate phosphoribosyltransferase isozymes (see also URA5) that catalyze the fifth enzymatic step in the de novo biosynthesis of pyrimidines, converting orotate into orotidine-5'-phosphate, URA10	2.8	2.39E-03
NDE2	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic NADH to the mitochondrial respiratory chain, NDE2	2.7	9.11E-06
GRE2	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway, GRE2	2.2	3.38E-03
GTO1	Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization, GTO1	2.2	9.17E-05
GND2	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone, GND2	2.1	1.28E-04
MHT1	S-methylmethionine-homocysteine methyltransferase, functions along with Sam4p in the conversion of S-adenosylmethionine (AdoMet) to methionine to control the methionine/AdoMet ratio, MHT1	2.0	8.18E-04
PDR5	Plasma membrane ATP-binding cassette (ABC) transporter, short-lived multidrug transporter actively regulated by Pdr1p; also involved in steroid transport, cation resistance, and cellular detoxification during exponential growth, PDR5	2.0	3.66E-03

OLE1	Delta(9) fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal distribution of mitochondria, OLE1	1.9	3.32E-04
MET8	Bifunctional dehydrogenase and ferrochelatase, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis, MET8	1.9	4.47E-04
GDH3	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh1p; expression regulated by nitrogen and carbon sources, GDH3	1.8	5.97E-04
CAT2	Carnitine acetyl-CoA transferase present in both mitochondria and peroxisomes, transfers activated acetyl groups to carnitine to form acetylcarnitine which can be shuttled across membranes, CAT2	1.7	1.13E-04
YOR1	Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter mediates export of many different organic anions including oligomycin, YOR1	1.7	8.81E-03
MET32	Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine biosynthetic genes, similar to Met31p, MET32	1.6	4.12E-04
TRX3	Mitochondrial thioredoxin, highly conserved oxidoreductase required to maintain the redox homeostasis of the cell, forms the mitochondrial thioredoxin system with Trr2p, redox state is maintained by both Trr2p and Glr1p, TRX3	1.6	2.39E-03
THI4	Thiazole synthase, catalyzes formation of the thiazole moiety of thiamin pyrophosphate; required for thiamine biosynthesis and for mitochondrial genome stability, THI4	1.6	1.27E-04
MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism, MET28	1.6	1.74E-04
UBC8	Ubiquitin-conjugating enzyme that negatively regulates gluconeogenesis by mediating the glucose-induced ubiquitination of fructose-1,6-bisphosphatase (FBPase); cytoplasmic enzyme that catalyzes the ubiquitination of histones in vitro, UBC8	1.6	4.67E-03
MET30	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin ligase complex; interacts with and regulates Met4p, localizes within the nucleus, MET30	1.6	2.18E-03
YKL151C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ---	1.6	2.19E-03
DAP1	Heme-binding protein involved in regulation of cytochrome P450 protein Erg11p; damage response	1.5	8.74E-03

	protein, related to mammalian membrane progesterone receptors; mutations lead to defects in telomeres, mitochondria, and sterol synthesis, DAP1		
MET2	L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic pathway, MET2	1.5	1.79E-04
YDL124W	NADPH-dependent alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; member of the aldo-keto reductase (AKR) family, ---	1.5	4.20E-04
ECM4	Omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ECM4	1.4	2.94E-04
GSP2	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; interacts with Kap121p, Kap123p and Pdr6p (karyophilin betas); Gsp1p homolog that is not required for viability, GSP2	1.4	6.29E-04
STF1	Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p act as stabilizing factors that enhance inhibitory action of the Inh1p protein, STF1	1.3	1.16E-03
GUT2	Mitochondrial glycerol-3-phosphate dehydrogenase; expression is repressed by both glucose and cAMP and derepressed by non-fermentable carbon sources in a Snf1p, Rsf1p, Hap2/3/4/5 complex dependent manner, GUT2	1.3	4.40E-03
GSH1	Gamma glutamylcysteine synthetase catalyzes the first step in glutathione (GSH) biosynthesis; expression induced by oxidants, cadmium, and mercury, GSH1	1.3	5.85E-04
CKI1	Choline kinase, catalyzing the first step in phosphatidylcholine synthesis via the CDP-choline (Kennedy pathway); exhibits some ethanolamine kinase activity contributing to phosphatidylethanolamine synthesis via the CDP-ethanolamine pathway, CKI1	1.3	3.23E-03
MCR1	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis, MCR1	1.3	1.58E-03
GTT2	Glutathione S-transferase capable of homodimerization; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT2	1.2	1.15E-03
VHS3	Functionally redundant (see also SIS2) inhibitory subunit of Ppz1p, a PP1c-related ser/thr protein phosphatase Z isoform; synthetically lethal with sis2; putative phosphopantothenoylcysteine decarboxylase involved in coenzyme A biosynthesis, VHS3	1.2	3.03E-03
CAT8	Zinc cluster transcriptional activator necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements, CAT8	1.2	7.90E-03
PCA1	Cadmium transporting P-type ATPase; may also have a role in copper and iron homeostasis; S288C and most	1.2	7.40E-03

	other lab strains contain a G970R mutation which eliminates normal cadmium transport function, PCA1		
GDE1	Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to choline and glycerolphosphate, for use as a phosphate source and as a precursor for phosphocholine synthesis; may interact with ribosomes, GDE1	1.2	8.96E-03
RNR3	Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits, RNR3	1.2	8.96E-03
YNL200C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies, ---	1.2	1.16E-03
ACS1	Acetyl-coA synthetase isoform which, along with Acs2p, is the nuclear source of acetyl-coA for histone acetlyation; expressed during growth on nonfermentable carbon sources and under aerobic conditions, ACS1	1.2	2.15E-03
CHO1	Phosphatidylserine synthase, functions in phospholipid biosynthesis; catalyzes the reaction CDP-diaclyglycerol + L-serine = CMP + L-1-phosphatidylserine, transcriptionally repressed by myo-inositol and choline, CHO1	1.1	1.53E-03
CHO2	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis, CHO2	1.1	3.97E-03
MSB3	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of polarized growth, MSB3	1.1	2.29E-03
GDH2	NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen catabolite repression and intracellular ammonia levels, GDH2	1.1	1.67E-03
UGA2	Succinate semialdehyde dehydrogenase involved in the utilization of gamma-aminobutyrate (GABA) as a nitrogen source; part of the 4-aminobutyrate and glutamate degradation pathways; localized to the cytoplasm, UGA2	1.1	5.39E-03
FAS2	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; phosphorylated, FAS2	1.1	6.48E-03
YNK1	Nucleoside diphosphate kinase, catalyzes the transfer of gamma phosphates from nucleoside triphosphates, usually ATP, to nucleoside diphosphates by a mechanism that	1.1	4.62E-03

	involves formation of an autophosphorylated enzyme intermediate, YNK1		
MET3	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine metabolism, MET3	1.1	9.38E-03
ROM1	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP, ROM1	1.0	5.61E-03
GTT1	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT1	1.0	9.16E-03
HTD2	Mitochondrial 3-hydroxyacyl-thioester dehydratase involved in fatty acid biosynthesis, required for respiratory growth and for normal mitochondrial morphology, HTD2	1.0	3.55E-03
OPI3	Phospholipid methyltransferase (methylene-fatty-acyl-phospholipid synthase), catalyzes the last two steps in phosphatidylcholine biosynthesis, OPI3	1.0	6.83E-03
EHT1	Acyl-coenzymeA:ethanol O-acyltransferase that plays a minor role in medium-chain fatty acid ethyl ester biosynthesis; contains esterase activity; localizes to lipid particles and the mitochondrial outer membrane, EHT1	0.9	6.13E-03
INH1	Protein that inhibits ATP hydrolysis by the F1F0-ATP synthase, inhibitory function is enhanced by stabilizing proteins Stf1p and Stf2p; has similarity to Stf1p and both Inh1p and Stf1p exhibit the potential to form coiled-coil structures, INH1	0.9	8.93E-03
SAM2	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p), SAM2	0.9	8.18E-03
Stress			
Multiple stress response			
SPI1	GPI-anchored cell wall protein involved in weak acid resistance; basal expression requires Msn2p/Msn4p; expression is induced under conditions of stress and during the diauxic shift; similar to Sed1p, SPI1	4.7	8.17E-04
PDR15	Plasma membrane ATP binding cassette (ABC) transporter, multidrug transporter and general stress response factor implicated in cellular detoxification; regulated by Pdr1p, Pdr3p and Pdr8p; promoter contains a PDR responsive element, PDR15	3.2	4.08E-04
DDR2	Multistress response protein, expression is activated by a variety of xenobiotic agents and environmental or physiological stresses, DDR2	2.7	1.11E-05
GRE2	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic,	2.2	3.38E-03

	ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway, GRE2		
CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide,	2.2	1.98E-04
SRL3	Cytoplasmic protein that, when overexpressed, suppresses the lethality of a rad53 null mutation; potential Cdc28p substrate	2.0	0.003542
DCS2	Non-essential, stress induced regulatory protein containing a HIT (histidine triad) motif; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway, similar to Dcs1p., DCS2	1.9	6.80E-04
FRT2	Tail-anchored endoplasmic reticulum membrane protein, interacts with homolog Frt1p but is not a substrate of calcineurin (unlike Frt1p), promotes growth in conditions of high Na+, alkaline pH, or cell wall stress; potential Cdc28p substrate, FRT2	1.7	3.36E-03
RPN4	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback control mechanism; RPN4 is transcriptionally regulated by various stress responses, RPN4	1.5	8.18E-03
MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants, MBR1	1.5	7.49E-03
UBI4	Ubiquitin, becomes conjugated to proteins, marking them for selective degradation via the ubiquitin-26S proteasome system; essential for the cellular stress response; encoded as a polyubiquitin precursor comprised of 5 head-to-tail repeats, UBI4	1.2	1.98E-03
HSP150	O-mannosylated heat shock protein that is secreted and covalently attached to the cell wall via beta-1,3-glucan and disulfide bridges; required for cell wall stability; induced by heat shock, oxidative stress, and nitrogen limitation, HSP150	1.0	6.70E-03
NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p, NTH1	1.0	5.36E-03
Osmolarity stress			
SIP18	Protein of unknown function whose expression is induced by osmotic stress, SIP18	5.4	5.69E-08
STL1	Glycerol proton symporter of the plasma membrane, subject to glucose-induced inactivation, strongly but transiently induced when cells are subjected to osmotic shock, STL1	3.9	2.35E-03
PAI3	Cytop\lasmic proteinase A (Pep4p) inhibitor, dependent on Pbs2p and Hog1p protein kinases for osmotic induction; intrinsically unstructured, N-terminal half	3.7	5.86E-06

	becomes ordered in the active site of proteinase A upon contact, PAI3		
SMP1	Putative transcription factor involved in regulating the response to osmotic stress; member of the MADS-box family of transcription factors, SMP1	1.7	2.70E-03
GPH1	Non-essential glycogen phosphorylase required for the mobilization of glycogen, activity is regulated by cyclic AMP-mediated phosphorylation, expression is regulated by stress-response elements and by the HOG MAP kinase pathway, GPH1	1.4	2.25E-03
SSK22	MAP kinase kinase kinase of the HOG1 mitogen-activated signaling pathway; functionally redundant with, and homologous to, Ssk2p; interacts with and is activated by Ssk1p; phosphorylates Pbs2p, SSK22	1.2	5.15E-03
Heat shock			
HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; oligomer activation requires a heat-induced conformational change; not expressed in unstressed cells, HSP26	4.4	2.95E-07
GAC1	Regulatory subunit for Glc7p type-1 protein phosphatase (PP1), tethers Glc7p to Gsy2p glycogen synthase, binds Hsf1p heat shock transcription factor, required for induction of some HSF-regulated genes under heat shock, GAC1	2.2	9.99E-05
TIP1	Major cell wall mannoprotein with possible lipase activity; transcription is induced by heat- and cold-shock; member of the Srp1p/Tip1p family of serine-alanine-rich proteins, TIP1	2.1	1.44E-04
HSP12	Plasma membrane localized protein that protects membranes from desiccation; induced by heat shock, oxidative stress, osmostress, stationary phase entry, glucose depletion, oleate and alcohol; regulated by the HOG and Ras-Pka pathways, HSP12	1.9	5.34E-04
UBC5	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins, central component of the cellular stress response; expression is heat inducible, UBC5	1.3	4.99E-04
Oxidative stress			
OYE3	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye2p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism, OYE3	3.6	9.43E-05
GPX1	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress, GPX1	3.0	8.70E-03
GTO1	Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization, GTO1	2.2	9.17E-05

CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide,	2.2	1.98E-04
YHB1	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses, YHB1	1.9	4.92E-03
MXR1	Peptide methionine sulfoxide reductase, reverses the oxidation of methionine residues; involved in oxidative damage repair, providing resistance to oxidative stress and regulation of lifespan, MXR1	1.8	1.94E-03
gsh1	Gamma glutamylcysteine synthetase catalyzes the first step in glutathione (GSH) biosynthesis; expression induced by oxidants, cadmium, and mercury, GSH1	1.3	5.85E-04
GTT2	Glutathione S-transferase capable of homodimerization; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT2	1.2	1.15E-03
AAD6	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response, AAD6	1.2	7.73E-03
PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; induced during respiratory growth and under conditions of oxidative stress; phosphorylated, PRX1	1.1	2.76E-03
YAP5	Basic leucine zipper (bZIP) transcription factor	1.0	0.00598
GTT1	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT1	1.0	9.16E-03
Cell wall integrity and PKC-pathway			
PIR3	O-glycosylated covalently-bound cell wall protein required for cell wall stability; expression is cell cycle regulated, peaking in M/G1 and also subject to regulation by the cell integrity pathway	5.0	9.39E-07
KDX1(MLP1)	Protein kinase implicated in the Slt2p mitogen-activated (MAP) kinase signaling pathway; associates with Rlm1p, ---	2.1	1.38E-03
BAG7	Rho GTPase activating protein (RhoGAP), stimulates the intrinsic GTPase activity of Rho1p, which plays a role in actin cytoskeleton organization and control of cell wall synthesis; structurally and functionally related to Sac7p	2.0	0.43253
HSP12	Plasma membrane localized protein that protects membranes from desiccation; induced by heat shock, oxidative stress, osmostress, stationary phase entry, glucose depletion, oleate and alcohol; regulated by the HOG and Ras-Pka pathways, HSP12	1.9	5.34E-04
DCS2	Non-essential, stress induced regulatory protein containing a HIT (histidine triad) motif; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway, similar to Dcs1p.	1.9	6.80E-04

AFR1	Alpha-factor pheromone receptor regulator, negatively regulates pheromone receptor signaling; required for normal mating projection (shmoo) formation; required for Spa2p to recruit Mpk1p to shmoo tip during mating; interacts with Cdc12p, AFR1	1.9	1.81E-04
SLT2	Serine/threonine MAP kinase involved in regulating the maintenance of cell wall integrity and progression through the cell cycle; regulated by the PKC1-mediated signaling pathway	1.9	0.004729
PST1	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell integrity pathway, as mediated by Rlm1p; upregulated by cell wall damage via disruption of FKS1	1.9	0.004729
GSC2	Catalytic subunit of 1,3-beta-glucan synthase, involved in formation of the inner layer of the spore wall; activity positively regulated by Rho1p and negatively by Smk1p; has similarity to an alternate catalytic subunit, Fks1p (Gsc1p), GSC2	1.6	1.04E-03
RLM1	MADS-box transcription factor, component of the protein kinase C-mediated MAP kinase pathway involved in the maintenance of cell integrity; phosphorylated and activated by the MAP-kinase Slt2p, RLM1	1.2	1.44E-03
VHS3	Functionally redundant (see also SIS2) inhibitory subunit of Ppz1p, a PP1c-related ser/thr protein phosphatase Z isoform; synthetically lethal with sis2; putative phosphopantothenoylcysteine decarboxylase involved in coenzyme A biosynthesis, VHS3	1.2	3.03E-03
MTL1	Protein with both structural and functional similarity to Mid2p, which is a plasma membrane sensor required for cell integrity signaling during pheromone-induced morphogenesis; suppresses rgd1 null mutations	1.2	0.503124
ROM1	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP, ROM1	1.0	5.61E-03
SDP1	Stress-inducible dual-specificity MAP kinase phosphatase, negatively regulates Slt2p MAP kinase by direct dephosphorylation, diffuse localization under normal conditions shifts to punctate localization after heat shock	1.0	0.695198
PTP2	Phosphotyrosine-specific protein phosphatase involved in the inactivation of mitogen-activated protein kinase (MAPK) during osmolarity sensing; dephosporylates Hog1p MAPK and regulates its localization; localized to the nucleus,	1.0	0.027224
SLT2	Serine/threonine MAP kinase involved in regulating the maintenance of cell wall integrity and progression through the cell cycle; regulated by the PKC1-mediated signaling pathway	0.9	0.057308
BCK2	Protein rich in serine and threonine residues involved in	0.8	0.03723

	protein kinase C signaling pathway, which controls cell integrity; overproduction suppresses pkc1 mutations		1
WSC3	Partially redundant sensor-transducer of the stress-activated PKC1-MPK1 signaling pathway involved in maintenance of cell wall integrity; involved in the response to heat shock and other stressors; regulates 1,3-beta-glucan synthesis	0.7	0.116598
PRM5	Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell integrity signaling	0.7	1
PKH2	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling cascade required for maintenance of cell wall integrity; redundant with Pkh1p	0.6	0.600569
PKH3	Protein kinase with similarity to mammalian phosphoinositide-dependent kinase 1 (PDK1) and yeast Pkh1p and Pkh2p, two redundant upstream activators of Pkc1p; identified as a multicopy suppressor of a pkh1 pkh2 double mutant	0.6	0.822118
ROM2	GDP/GTP exchange protein (GEP) for Rho1p and Rho2p; mutations are synthetically lethal with mutations in rom1, which also encodes a GEP	0.6	1
GFA1	Glutamine-fructose-6-phosphate amidotransferase, catalyzes the formation of glucosamine-6-P and glutamate from fructose-6-P and glutamine in the first step of chitin biosynthesis	0.5	1
MID2	O-glycosylated plasma membrane protein that acts as a sensor for cell wall integrity signaling and activates the pathway; interacts with Rom2p, a guanine nucleotide exchange factor for Rho1p, and with cell integrity pathway protein Zeo1p	0.5	1
PTP3	Phosphotyrosine-specific protein phosphatase involved in the inactivation of mitogen-activated protein kinase (MAPK) during osmolarity sensing; dephosporylates Hog1p MAPK and regulates its localization; localized to the cytoplasm	0.4	1
TUS1	Guanine nucleotide exchange factor (GEF) that functions to modulate Rho1p activity as part of the cell integrity signaling pathway; multicopy suppressor of tor2 mutation and ypk1 ypk2 double mutation; potential Cdc28p substrate	0.4	1
BCK1	Mitogen-activated protein (MAP) kinase kinase kinase acting in the protein kinase C signaling pathway, which controls cell integrity; upon activation by Pkc1p phosphorylates downstream kinases Mkk1p and Mkk2p	0.3	1
RHO5	Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely involved in protein kinase C (Pkc1p)-dependent signal transduction pathway that controls cell integrity	0.3	1

PKH1	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling cascade required for maintenance of cell wall integrity; redundant with Pkh2p	0.3	1
PKC1	Protein serine/threonine kinase essential for cell wall remodeling during growth; localized to sites of polarized growth and the mother-daughter bud neck; homolog of the alpha, beta, and gamma isoforms of mammalian protein kinase C (PKC)	0.3	1
BNI1	Formin, nucleates the formation of linear actin filaments, involved in cell processes such as budding and mitotic spindle orientation which require the formation of polarized actin cables, functionally redundant with BNR1	0.3	1
SWI4	DNA binding component of the SBF complex (Swi4p-Swi6p), a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including cyclins and genes required for DNA synthesis and repair	0.2	1
MKK1	Mitogen-activated kinase kinase involved in protein kinase C signaling pathway that controls cell integrity; upon activation by Bck1p phosphorylates downstream target, Slt2p; functionally redundant with Mkk2p	0.2	1
MSG5	Dual-specificity protein phosphatase required for maintenance of a low level of signaling through the cell integrity pathway; regulates and is regulated by Slt2p; dephosphorylates Fus3p; required for adaptive response to pheromone	0.1	1
SEC3	Non-essential subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p) which mediates targeting of post-Golgi vesicles to sites of active exocytosis; Sec3p specifically is a spatial landmark for secretion	0.1	1
FKS3	Protein involved in spore wall assembly, has similarity to 1,3-beta-D-glucan synthase catalytic subunits Fks1p and Gsc2p; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studie	0.0	1
SAC7	GTPase activating protein (GAP) for Rho1p, involved in signaling to the actin cytoskeleton, null mutations suppress tor2 mutations and temperature sensitive mutations in actin; potential Cdc28p substrate	-0.1	1
BNR1	Formin, nucleates the formation of linear actin filaments, involved in cell processes such as budding and mitotic spindle orientation which require the formation of polarized actin cables, functionally redundant with BNI1	-0.2	1
BEM2	Rho GTPase activating protein (RhoGAP) involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence	-0.2	1
SKN7	Nuclear response regulator and transcription factor, part of a branched two-component signaling system; required	-0.3	1

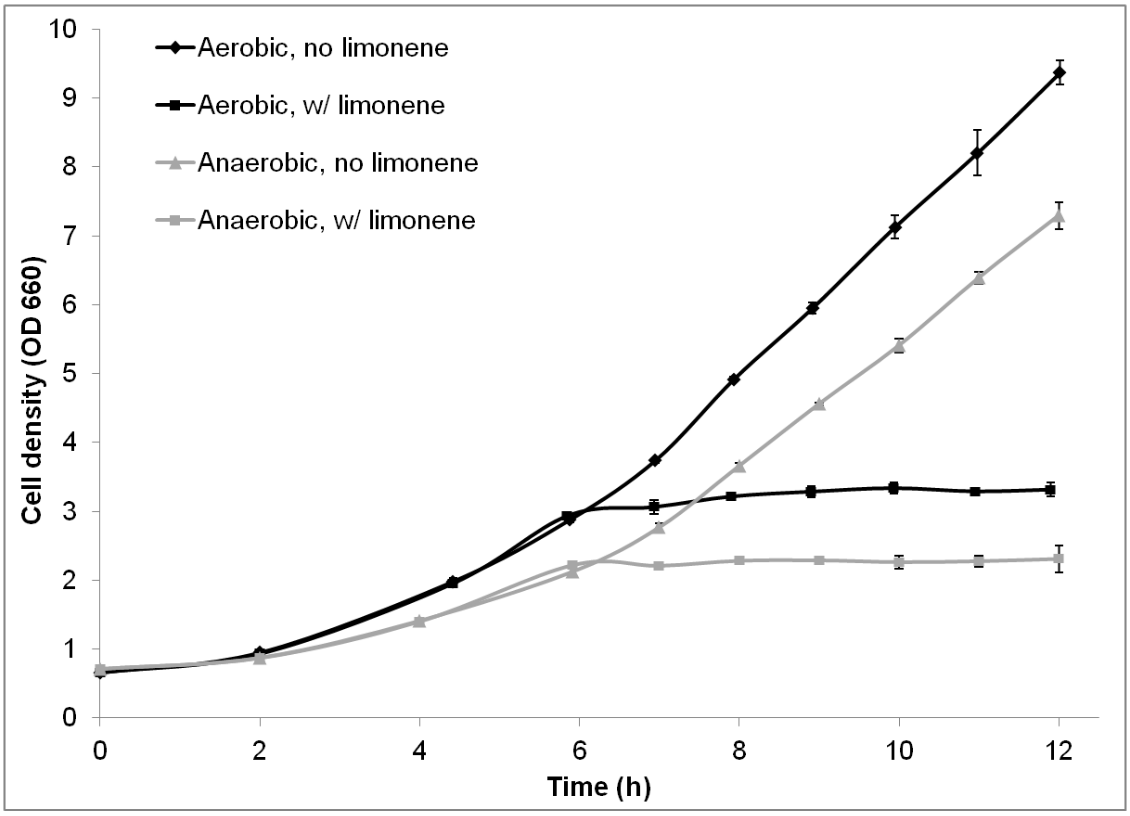
	for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation		
RHO1	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p)	-0.3	1
SWI6	Transcription cofactor, forms complexes with DNA-binding proteins Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; localization regulated by phosphorylation; potential Cdc28p substrate	-0.5	0.686307
FKS1	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling	-0.6	1
LRG1	Putative GTPase-activating protein (GAP) involved in the Pkc1p-mediated signaling pathway that controls cell wall integrity; appears to specifically regulate 1,3-beta-glucan synthesis	-0.8	0.185367
WSC2	Partially redundant sensor-transducer of the stress-activated PKC1-MPK1 signaling pathway involved in maintenance of cell wall integrity and recovery from heat shock; secretory pathway Wsc2p is required for the arrest of secretion response,	-1.2	0.454214
Sulfur metabolism			
JLP1	Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase, involved in sulfonate catabolism for use as a sulfur source, contains sequence that closely resembles a J domain (typified by the E. coli DnaJ protein), JLP1	6.7	1.80E-05
AGP3	Low-affinity amino acid permease, may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation, AGP3	5.1	3.92E-06
PDC6	Minor isoform of pyruvate decarboxylase, decarboxylates pyruvate to acetaldehyde, involved in amino acid catabolism; transcription is glucose- and ethanol-dependent, and is strongly induced during sulfur limitation, PDC6	4.3	3.70E-04
BDS1	Bacterially-derived sulfatase required for use of alkyl- and aryl-sulfates as sulfur sources, BDS1	3.2	7.60E-05
GTO1	Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization, GTO1	2.2	9.17E-05
MHT1	S-methylmethionine-homocysteine methyltransferase, functions along with Sam4p in the conversion of S-adenosylmethionine (AdoMet) to methionine to control the methionine/AdoMet ratio, MHT1	2.0	8.18E-04
MET8	Bifunctional dehydrogenase and ferrochelatase, involved	1.9	4.47E-

	in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis, MET8		04
YLL058W	Putative protein of unknown function with similarity to Str2p, which is a cystathionine gamma-synthase important in sulfur metabolism; YLL058W is not an essential gene, ---	1.8	3.34E-03
MET32	Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine biosynthetic genes, similar to Met31p, MET32	1.6	4.12E-04
THI4	Thiazole synthase, catalyzes formation of the thiazole moiety of thiamin pyrophosphate; required for thiamine biosynthesis and for mitochondrial genome stability, THI4	1.6	1.27E-04
MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism, MET28	1.6	1.74E-04
MET30	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin ligase complex; interacts with and regulates Met4p, localizes within the nucleus, MET30	1.6	2.18E-03
MET2	L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic pathway, MET2	1.5	1.79E-04
ECM4	Omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ECM4	1.4	2.94E-04
GSH1	Gamma glutamylcysteine synthetase catalyzes the first step in glutathione (GSH) biosynthesis; expression induced by oxidants, cadmium, and mercury, GSH1	1.3	5.85E-04
GTT2	Glutathione S-transferase capable of homodimerization; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT2	1.2	1.15E-03
YHR112C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, ---	1.2	1.65E-03
MET3	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine metabolism, MET3	1.1	9.38E-03
GTT1	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p, GTT1	1.0	9.16E-03
SAM2	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p), SAM2	0.9	8.18E-03

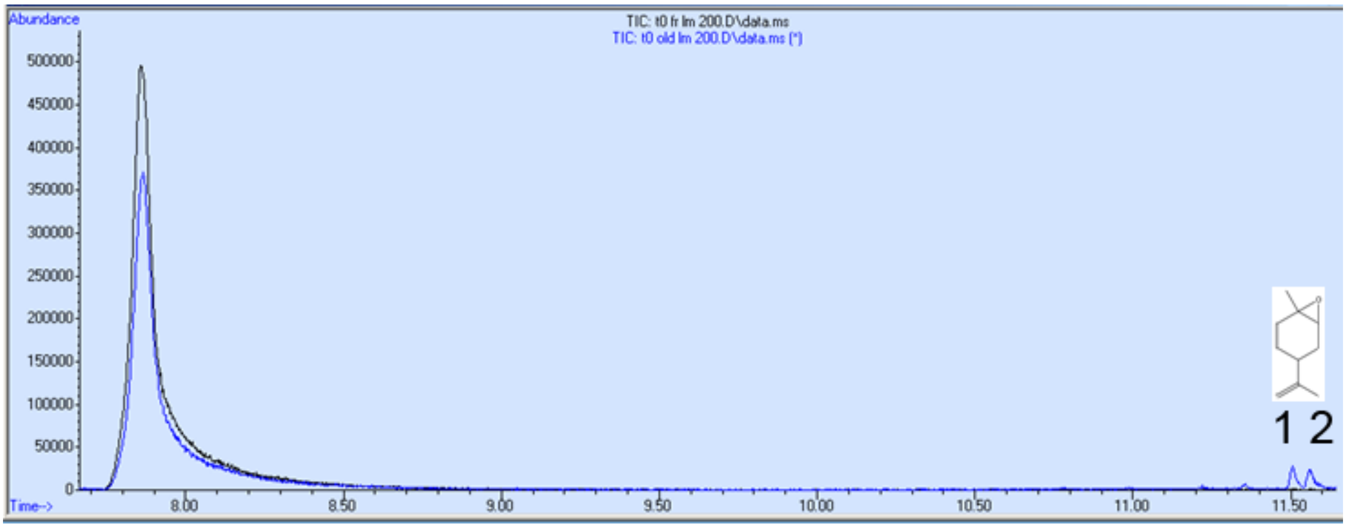
Iron ion homeostasis			
HMX1	ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme oxygenases; expression regulated by AFT1, HMX1	2.5	9.76E-03
SIT1	Ferrioxamine B transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; transcription is induced during iron deprivation and diauxic shift; potentially phosphorylated by Cdc28p, SIT1	2.3	1.28E-03
FIT2	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall, FIT2	2.0	6.39E-05
ARN2	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to the siderophore triacetylfusarinine C, ARN2	1.9	1.38E-03
FIT3	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall, FIT3	1.7	5.54E-03
TIS11	mRNA-binding protein expressed during iron starvation; binds to a sequence element in the 3'-untranslated regions of specific mRNAs to mediate their degradation; involved in iron homeostasis, TIS11	1.4	3.07E-03
PCA1	Cadmium transporting P-type ATPase; may also have a role in copper and iron homeostasis; S288C and most other lab strains contain a G970R mutation which eliminates normal cadmium transport function, PCA1	1.2	7.40E-03
FRE6	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels, FRE6	1.1	7.08E-03
ATX1	Cytosolic copper metallochaperone that transports copper to the secretory vesicle copper transporter Ccc2p for eventual insertion into Fet3p, which is a multicopper oxidase required for high-affinity iron uptake, ATX1	1.1	9.51E-03

[a] The $\log_2$ ratio of treated/control.

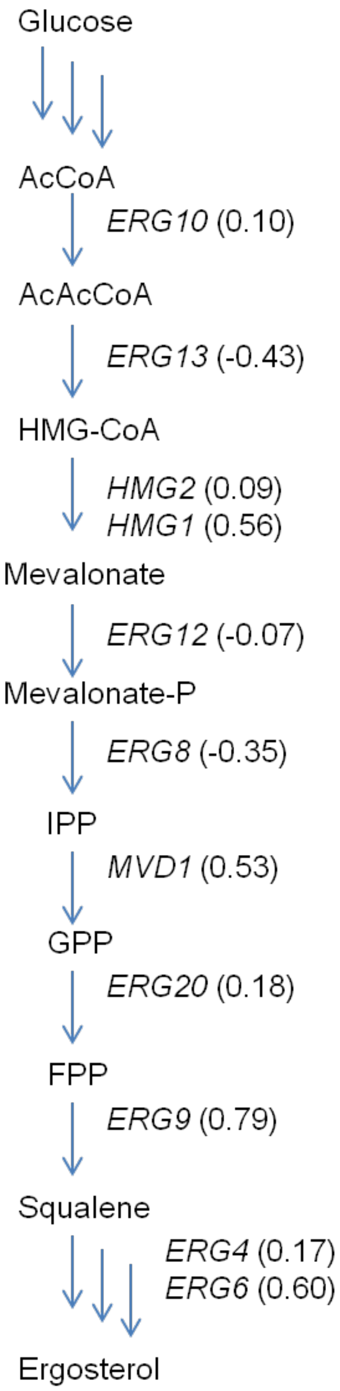
[b] The Bonferroni-corrected p values.



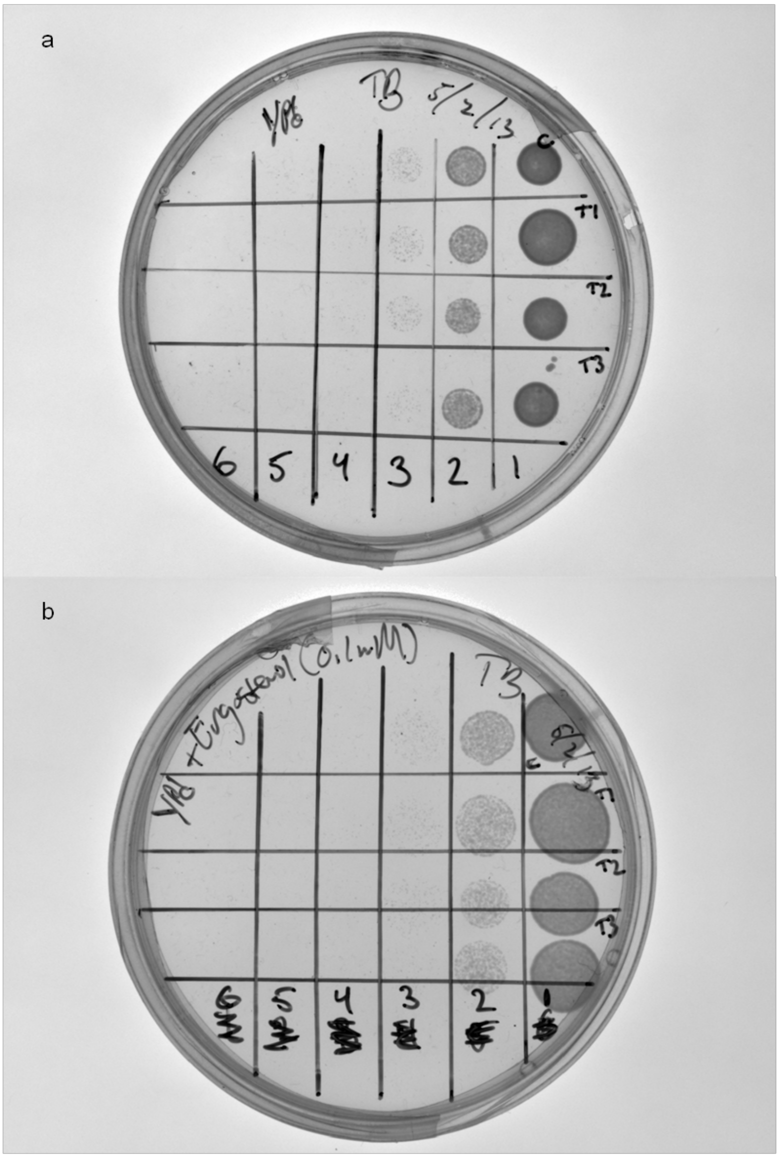
SI Fig 2. Anaerobic vs. aerobic growth curves. 107 mg/L of limonene was added at mid-exponential phase. Error bars represent one SD above and below the mean for biological triplicates.



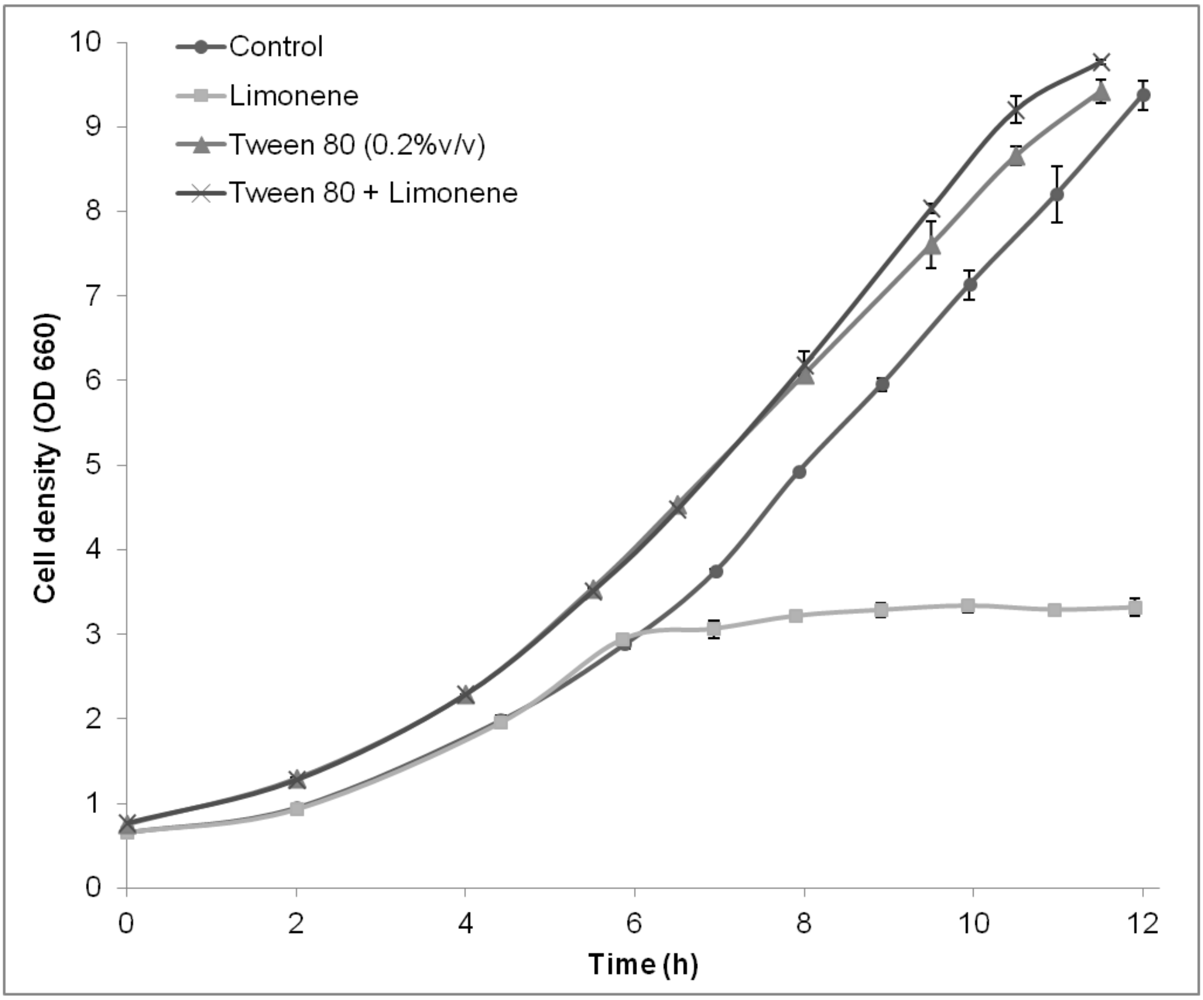
SI Fig 3. GC-MS chromatogram of limonene (RT = 7.9 min) sampled from challenged cultures after 6 h incubation at 30°C. The black line is limonene from anaerobic flasks (with no limonene oxide formation) and the blue line represents limonene from aerobic cultures (limonene oxide compounds at 11.5 min, peak 1 = limonene oxide, cis and peak 2 = limonene oxide, trans.). At 12 after inoculation (6 h after limonene addition), 1 mL of isopropyl myristate (IPM) was added to the culture (~ 22 ml), vortexed and harvested (1 min, 4025 rcf). The top IPM phase containing limonene was removed and 1 µL was resuspended in 1 mL of a 1:4 toluene:hexane solution. The GC-MS analysis was carried out using the setting described in the Materials and Methods section with the following changes: 1 µL of sample was injected and the oven temperature was set to 70°C, held for 10 min then followed by a temperature ramp of 40 °C/min to 300°C and held for 3 min. Detection was achieved in scan mode at 9.26 scans/sec from 30-300 amu.



SI Fig 4. Transcript levels of genes associated with ergosterol biosynthesis. Numbers in the parenthesis represent the $\log_2$ fold changes of that particular gene (treated/control). None of these genes were differentially expressed (Bonferroni-corrected $p < 0.01$).



SI Fig 5. Effect of exogenous ergosterol on the growth and viability. Yeast cultures were dosed with limonene as described in the Materials and Methods. Cells were harvested and washed and diluted on rich medium (YPD) plates as described by Liu, et al (1). (a) YPD and (b) YPD + 0.1 mM ergosterol/Tween 80 (0.25% v/v). The top row of each plate is the untreated control and rows 2-4 represent biological replicates for limonene-treated cells at varying dilutions (10^{-1}-10^{-6}). Image was taken at 24 h. Tween 80 did cause spreading of the culture droplet on the surface in the ergosterol supplemented plate causing an increase in the diameter.



SI Fig 6. Dose response growth curves in the presence of limonene and limonene + surfactant. 107 mg/L of limonene was added at mid-exponential phase. Limonene was administered in the presence and absence of Tween 80 (0.2% v/v). Error bars represent one SD above and below the mean for biological triplicates.

References:

1. **Liu, J., Y. Zhu, G. Du, J. Zhou, and J. Chen.** 2013. Exogenous ergosterol protects *Saccharomyces cerevisiae* from d-limonene stress. J. Appl. Microbiol. **114:**482-491.