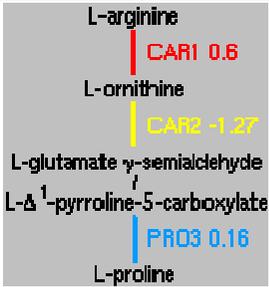
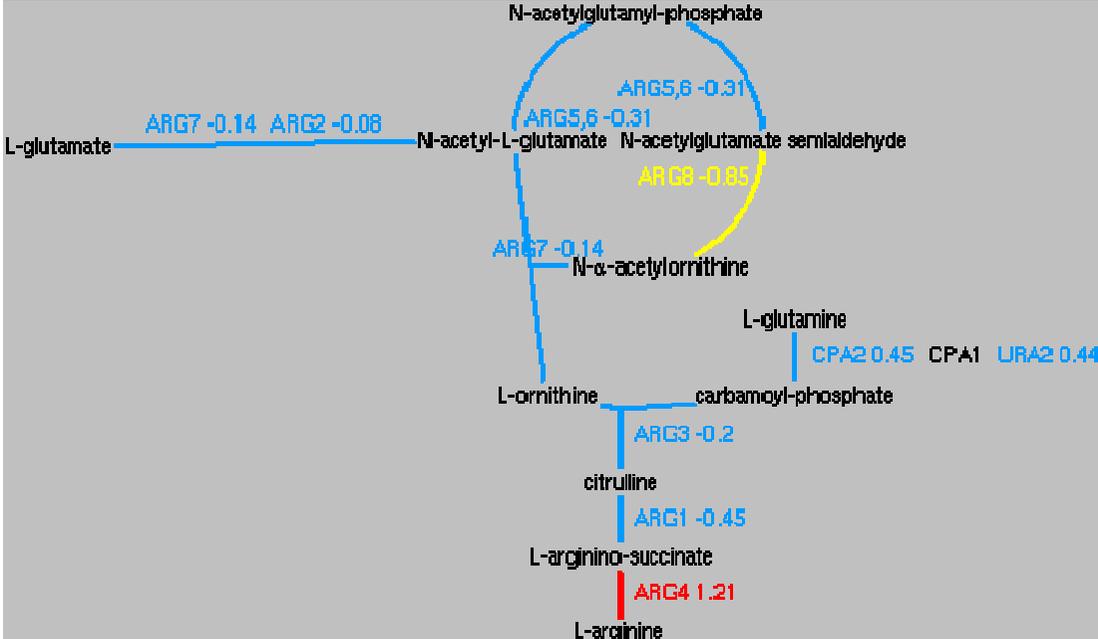
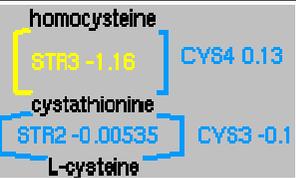
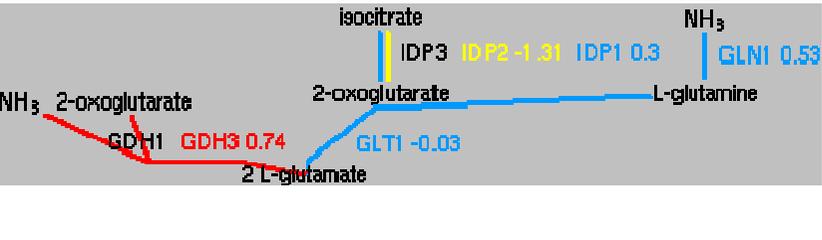
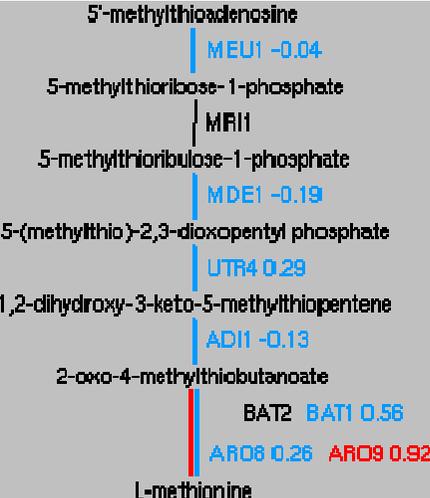


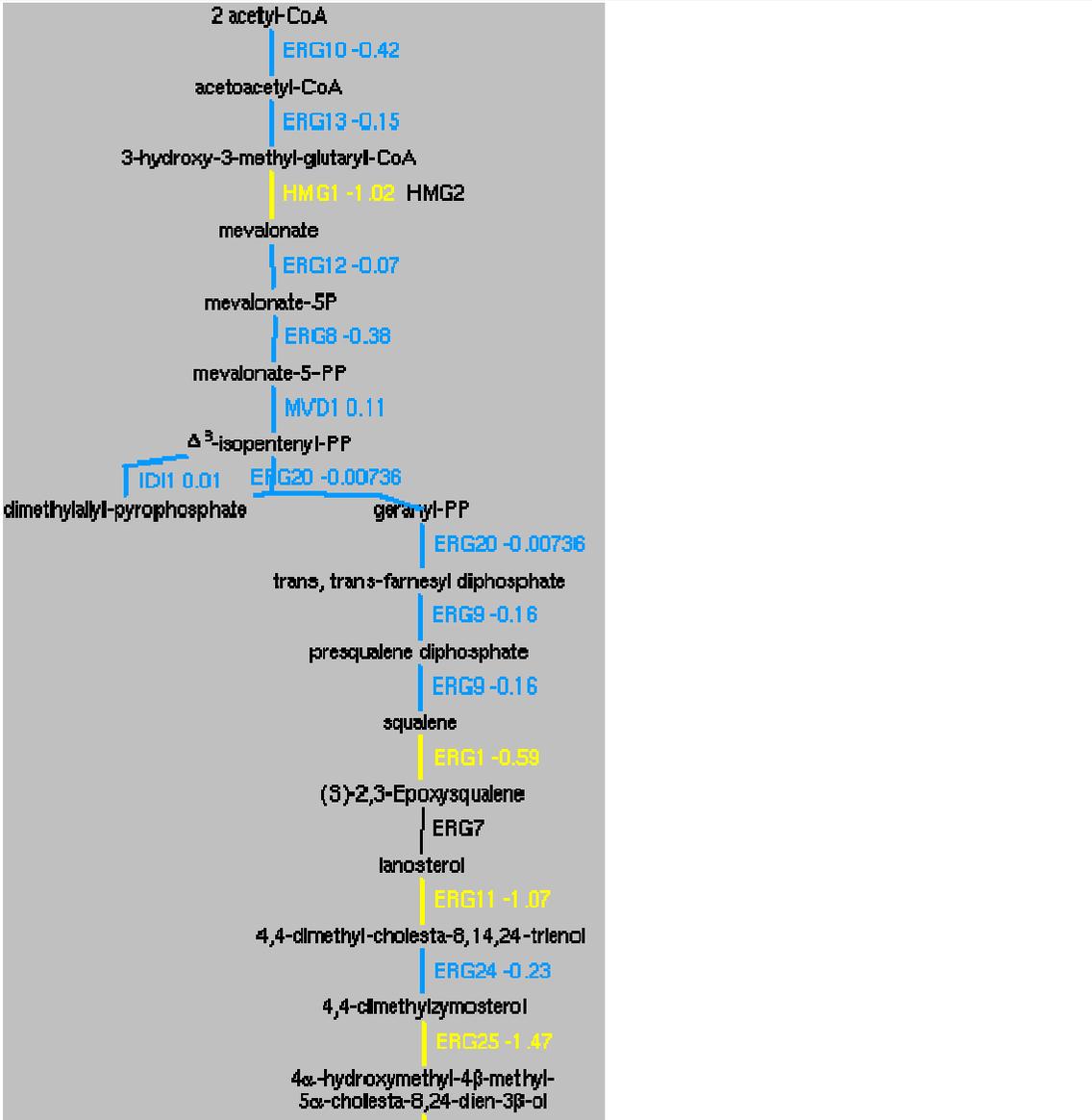
Additional file 2 – Regulated *S.cerevisiae* pathways in hypoxia vs. normoxia

Individual *S. cerevisiae* (Fab-producing strain) pathways transcriptionally regulated (*i.e.* exceeding log2 FC threshold of 0.59) in the comparison hypoxic vs. normoxic conditions, as resulting from MetaCyc analysis (see Figure 3). Pathway numbers are referred to Figure 3 legend.

N°	Pathway	Pathway Diagram	Enzymes, Genes
8	lysine biosynthesis	<p>2-oxoglutarate LYS21 -0.12 LYS20 homocitrate LYS4 -0.01 Homoaconitate LYS4 -0.01 homo-isocitrate LYS12 0.76 α-ketoadipate L-2-Amino adipate LYS2 0.28 L-2-Amino adipate 6-semialdehyde LYS9 -0.04 saccharopine LYS1 0.25 L-lysine</p>	homocitrate synthase LYS20 homocitrate synthase LYS21 homoaconitase LYS4 homo-isocitrate dehydrogenase LYS12 alpha amino adipate reductase LYS2 saccharopine dehydrogenase (NADP+, L-glutamate-forming) LYS9 saccharopine dehydrogenase (NAD+, L-lysine-forming) LYS1
8	arginine biosynthesis	<p>L-glutamate N-ACETYLGlutamate_SEMIALDEHYDE ARG7 -0.14 ARG2 -0.08 N-acetyl-L-glutamate ARG5,6 -0.31 N-acetylglutamyl-phosphate ARG5,6 -0.31 N-acetylglutamate semialdehyde ARG9 -0.85 N-α-acetylornithine ARG7 -0.14 L-ornithine ARG3 -0.2 citrulline ARG1 -0.45 L-arginino-succinate ARG4 1.21 L-arginine</p>	acetylglutamate synthase ARG2 acetylglutamate kinase / N-acetyl-gamma-glutamyl-phosphate reductase ARG5,6 acetylornithine aminotransferase ARG8 acetylornithine acetyltransferase ARG7 ornithine carbamoyltransferase ARG3 arginosuccinate synthetase ARG1 argininosuccinate lyase ARG4

9	arginine degradation (anaerobic)		arginase ornithine aminotransferase delta 1-pyrroline-5-carboxylate reductase	CAR1 CAR2 PRO3
10	arginine biosynthesis		acetylglutamate synthase acetylglutamate kinase / N-acetyl-gamma-glutamyl-phosphate reductase acetylornithine aminotransferase acetylornithine acetyltransferase carbamyl phosphate synthase / aspartate transcarbamylase carbamoyl phosphate synthetase ornithine carbamoyltransferase arginosuccinate synthetase arginosuccinate lyase	ARG2 ARG5,6 ARG8 ARG7 URA2 CPA2 CPA1 ARG3 ARG1 ARG4
12	serine biosynthesis from 3-phosphoglycerate		3-phosphoglycerate dehydrogenase 3-phosphoglycerate dehydrogenase phosphoserine transaminase phosphoserine phosphatase	SER3 SER33 SER1 SER2
12	serine biosynthesis from glyoxylate		Serine hydroxymethyltransferase, mitochondrial serine hydroxymethyltransferase	SHM1 SHM2
12	glycine biosynthesis from serine		Serine hydroxymethyltransferase, mitochondrial serine hydroxymethyltransferase	SHM1 SHM2

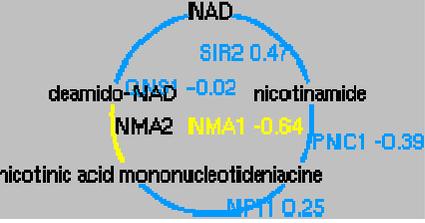
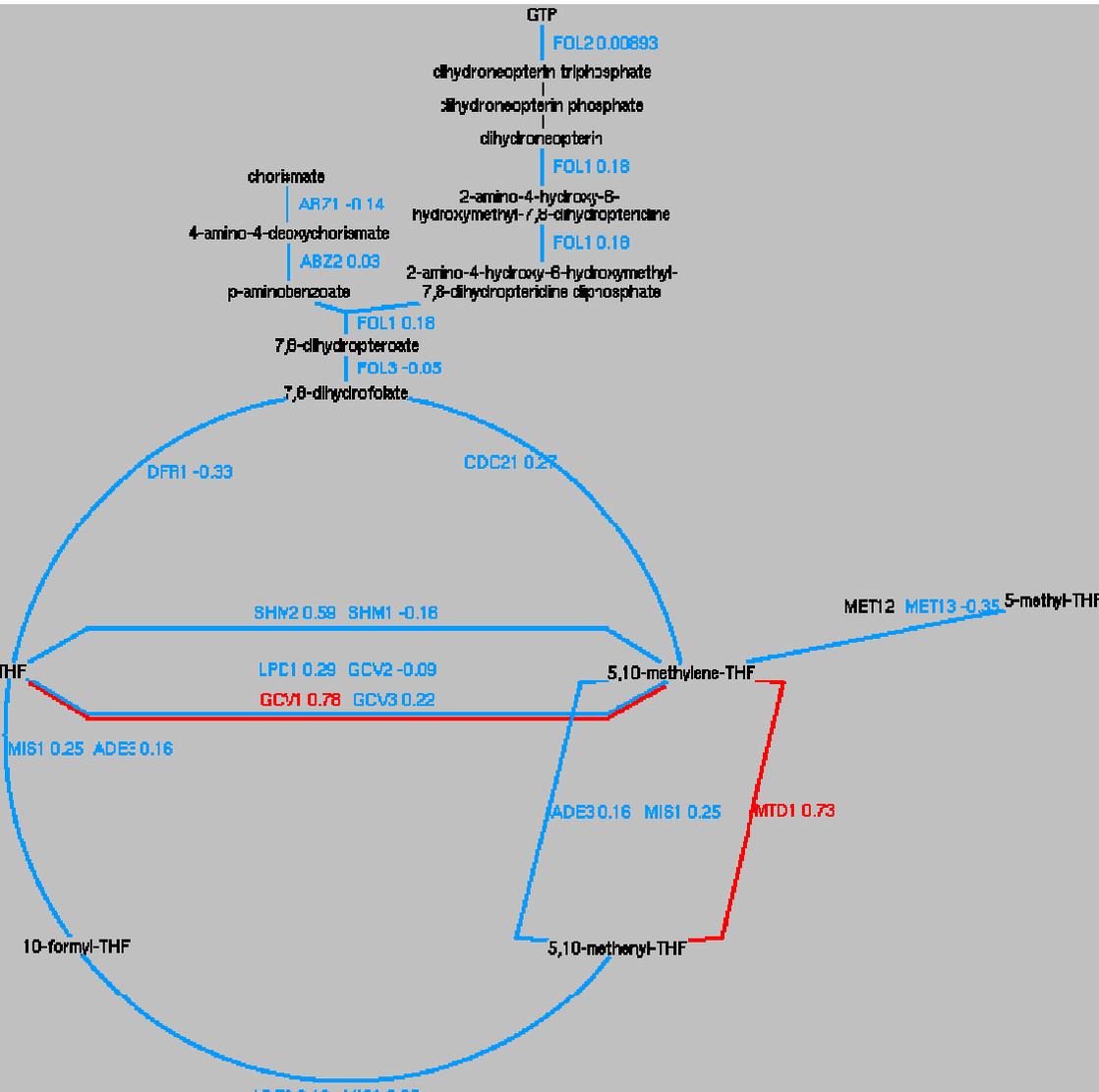
13	homocysteine and cysteine interconversion		cystathionine gamma-synthase STR2 cystathionine beta-lyase STR3 cystathionine beta-synthase CYS4 cystathionine gamma-lyase CYS3
17	glutamate biosynthesis from ammonia		NADP-dependent glutamate dehydrogenase GDH3 NADP-dependent glutamate dehydrogenase GDH1
17	superpathway of glutamate biosynthesis		NADP-dependent glutamate dehydrogenase GDH3 NADP-dependent glutamate dehydrogenase GDH1 glutamine synthetase GLN1 NADP-dependent isocitrate dehydrogenase IDP1 NADP-dependent isocitrate dehydrogenase IDP2 NADP-dependent isocitrate dehydrogenase IDP3 glutamate synthase (NADH) GLT1
18	methionine salvage pathway		5'-methylthioadenosine phosphorylase MEU1 methylthioribose-1 P isomerase MRI1 methylthioribulose-1-phosphate dehydratase MDE1 2,3-dioxomethiopentane-1-phosphate enolase/phosphatase UTR4 acireductone dioxygenase ADI1 aromatic amino acid aminotransferase II ARO9 aromatic amino acid aminotransferase I ARO8 branched-chain amino acid aminotransferase BAT1 branched-chain amino acid transaminase BAT2

20	ergosterol biosynthesis		<table border="0"> <tr> <td>acetoacetyl CoA thiolase</td> <td>ERG10</td> </tr> <tr> <td>3-hydroxy-3-methylglutaryl coenzyme A synthase</td> <td>ERG13</td> </tr> <tr> <td>3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)</td> <td>HMG2</td> </tr> <tr> <td>3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)</td> <td>HMG1</td> </tr> <tr> <td>mevalonate kinase</td> <td>ERG12</td> </tr> <tr> <td>phosphomevalonate kinase</td> <td>ERG8</td> </tr> <tr> <td>mevalonate pyrophosphate decarboxylase</td> <td>MVD1</td> </tr> <tr> <td>isopentenyl diphosphate:dimethylallyl diphosphate isomerase</td> <td>IDI1</td> </tr> <tr> <td>farnesyl diphosphate synthetase</td> <td>ERG20</td> </tr> <tr> <td>squalene synthetase</td> <td>ERG9</td> </tr> <tr> <td>squalene monooxygenase</td> <td>ERG1</td> </tr> <tr> <td>2,3-oxidosqualene-lanosterol cyclase</td> <td>ERG7</td> </tr> <tr> <td>cytochrome P450 lanosterol 14a-demethylase</td> <td>ERG11</td> </tr> <tr> <td>C-14 sterol reductase</td> <td>ERG24</td> </tr> <tr> <td>C-4 sterol methyl oxidase</td> <td>ERG25</td> </tr> <tr> <td>C-3 sterol dehydrogenase</td> <td>ERG26</td> </tr> <tr> <td>3-keto sterol reductase</td> <td>ERG27</td> </tr> <tr> <td>SAM:C-24 sterol methyltransferase</td> <td>ERG6</td> </tr> <tr> <td>C-8 sterol isomerase</td> <td>ERG2</td> </tr> <tr> <td>C-5 sterol desaturase</td> <td>ERG3</td> </tr> <tr> <td>C-22 sterol desaturase</td> <td>ERG5</td> </tr> <tr> <td>C-24 sterol reductase</td> <td>ERG4</td> </tr> </table>	acetoacetyl CoA thiolase	ERG10	3-hydroxy-3-methylglutaryl coenzyme A synthase	ERG13	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)	HMG2	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)	HMG1	mevalonate kinase	ERG12	phosphomevalonate kinase	ERG8	mevalonate pyrophosphate decarboxylase	MVD1	isopentenyl diphosphate:dimethylallyl diphosphate isomerase	IDI1	farnesyl diphosphate synthetase	ERG20	squalene synthetase	ERG9	squalene monooxygenase	ERG1	2,3-oxidosqualene-lanosterol cyclase	ERG7	cytochrome P450 lanosterol 14a-demethylase	ERG11	C-14 sterol reductase	ERG24	C-4 sterol methyl oxidase	ERG25	C-3 sterol dehydrogenase	ERG26	3-keto sterol reductase	ERG27	SAM:C-24 sterol methyltransferase	ERG6	C-8 sterol isomerase	ERG2	C-5 sterol desaturase	ERG3	C-22 sterol desaturase	ERG5	C-24 sterol reductase	ERG4
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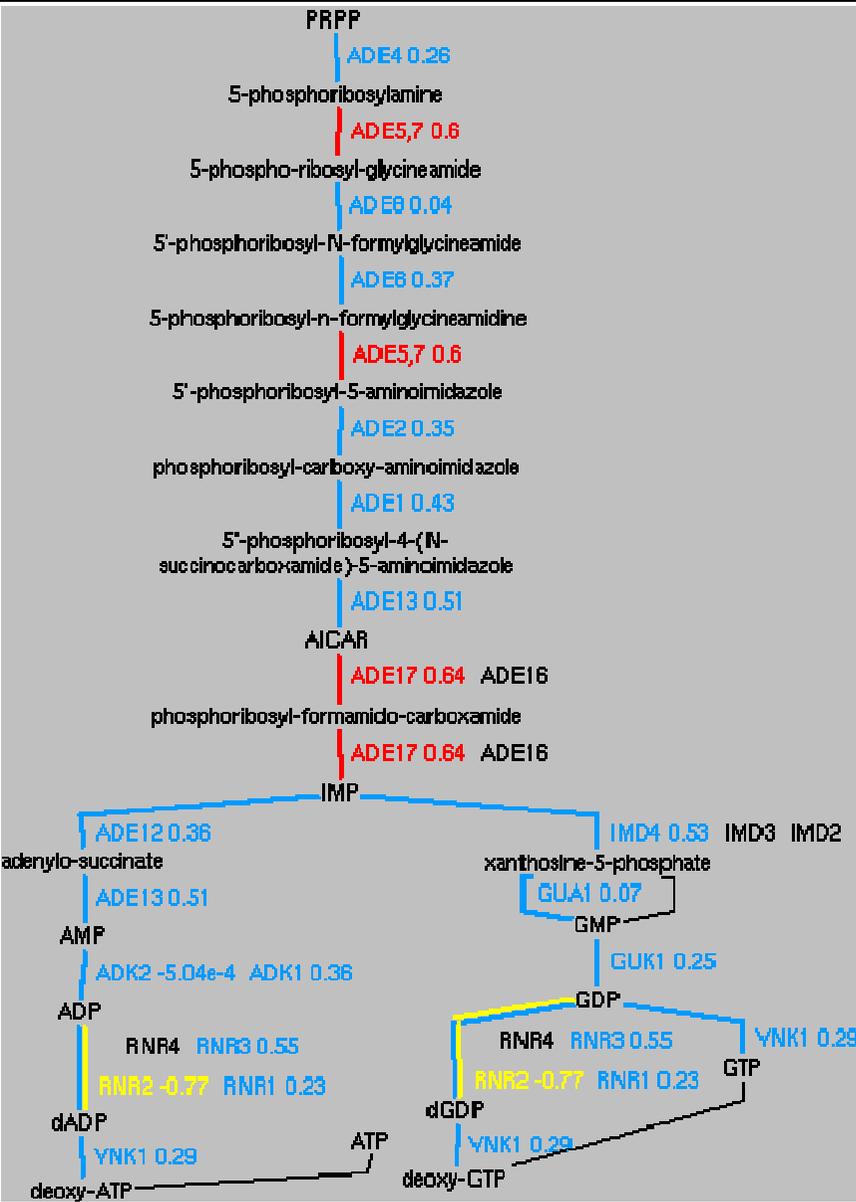
		<p>4α-hydroxymethyl-4β-methyl-5α-cholesta-8,24-dien-3β-ol ERG25 -1.47</p> <p>4α-formyl-4β-methyl-5α-cholesta-8,24-dien-3β-ol ERG25 -1.47</p> <p>4α-carboxy-4β-methyl-5α-cholesta-8,24-dien-3β-ol ERG26 -0.41</p> <p>3-keto-4-methylzymosterol ERG27 -0.89</p> <p>4-α-methylzymosterol ERG25 -1.47</p> <p>4α-hydroxymethyl-5α-cholesta-8,24-dien-3β-ol ERG25 -1.47</p> <p>4α-formyl-5α-cholesta-8,24-dien-3β-ol ERG25 -1.47</p> <p>4α-carboxy-5α-cholesta-8,24-dien-3β-ol ERG26 -0.41</p> <p>5α-cholesta-8,24-dien-3-one ERG27 -0.89</p> <p>zymosterol ERG6 -1.28</p> <p>fecosterol ERG2 -0.52</p> <p>episterol ERG3 -1.12</p> <p>5,7,24(28)-ergostatrienol ERG5 -0.46</p> <p>5,7,22,24(28)-ergostetraenol ERG4 -0.8</p> <p>ergosterol</p>		
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20	mevalonate pathway		<p>acetoacetyl CoA thiolase ERG10</p> <p>3-hydroxy-3-methylglutaryl coenzyme A synthase ERG13</p> <p>3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) HMG2</p> <p>3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) HMG1</p> <p>mevalonate kinase ERG12</p> <p>phosphomevalonate kinase ERG8</p> <p>mevalonate pyrophosphate decarboxylase MVD1</p> <p>isopentenyl diphosphate:dimethylallyl diphosphate isomerase IDI1</p>
30	phospholipid biosynthesis		<p>phosphatidylserine synthase CHO1</p> <p>phosphatidylserine decarboxylase, golgi/vacuole PSD2</p> <p>phosphatidylserine decarboxylase, mitochondria PSD1</p> <p>CHO2 CHO2</p> <p>OPI3 OPI3</p> <p>phosphatidylglycerolphosphate synthase PGS1</p> <p>cardiolipin synthase CRD1</p>
35	phosphatidylinositol biosynthesis		<p>phosphatidylinositol synthase PIS1</p>

40	de novo NAD biosynthesis	<p>CPD-250 L-tryptophan</p> <p style="text-align: center;"> BNA2 1.31</p> <p style="text-align: center;">L-Formylkynurenine</p> <p style="text-align: center;"> BNA7</p> <p style="text-align: center;">kynurenine</p> <p style="text-align: center;"> BNA4 1.04</p> <p style="text-align: center;">3-hydroxy-L-kynurenine</p> <p style="text-align: center;"> BNA5 1.24</p> <p style="text-align: center;">3-hydroxy-anthranilate</p> <p style="text-align: center;"> BNA1 1.05</p> <p style="text-align: center;">2-amino-3-carboxymuconate semialdehyde</p> <p style="text-align: center;"> quinolinate</p> <p style="text-align: center;"> BNA6 0.48</p> <p style="text-align: center;">nicotinic acid mononucleotide</p> <p style="text-align: center;"> NMA2 NMA1 -0.54</p> <p style="text-align: center;">deamido-NAD</p> <p style="text-align: center;"> QNS1 -0.02</p> <p style="text-align: center;">NAD</p>	<p>Tryptophan 2,3-dioxygenase BNA2</p> <p>Arylformamidase BNA7</p> <p>Kynurenine 3-mono oxygenase BNA4</p> <p>Kynureninase BNA5</p> <p>3-hydroxyanthranilic acid dioxygenase BNA1</p> <p>Quinolinate phosphoribosyl transferase BNA6</p> <p>Nicotinamide/nicotinic acid mononucleotide adenylyltransferase NMA1</p> <p>Nicotinamide/nicotinic acid mononucleotide adenylyltransferase NMA2</p> <p>glutamine-dependent NAD synthase QNS1</p>
40	tryptophan degradation via kynurenine	<p>CPD-250 L-tryptophan</p> <p style="text-align: center;"> BNA2 1.31</p> <p style="text-align: center;">L-Formylkynurenine</p> <p style="text-align: center;"> BNA7</p> <p style="text-align: center;">kynurenine</p> <p style="text-align: center;"> BNA4 1.04</p> <p style="text-align: center;">3-hydroxy-L-kynurenine</p> <p style="text-align: center;"> BNA5 1.24</p> <p style="text-align: center;">3-hydroxy-anthranilate</p> <p style="text-align: center;"> BNA1 1.05</p> <p style="text-align: center;">2-amino-3-carboxymuconate semialdehyde</p> <p style="text-align: center;"> quinolinate</p> <p style="text-align: center;"> BNA6 0.48</p> <p style="text-align: center;">nicotinic acid mononucleotide</p>	<p>Tryptophan 2,3-dioxygenase BNA2</p> <p>Arylformamidase BNA7</p> <p>Kynurenine 3-mono oxygenase BNA4</p> <p>Kynureninase BNA5</p> <p>3-hydroxyanthranilic acid dioxygenase BNA1</p> <p>Quinolinate phosphoribosyl transferase BNA6</p>
40	nicotinamide riboside salvage pathway I	<p>nicotinamide ribose</p> <p style="text-align: center;"> NRK1 0.22</p> <p style="text-align: center;">nicotinamide nucleotide</p> <p style="text-align: center;"> NMA1 -0.54 NMA2</p> <p style="text-align: center;">NAD</p>	<p>nicotinic acid riboside kinase / nicotinamide ribose kinase NRK1</p> <p>Nicotinamide/nicotinic acid mononucleotide adenylyltransferase NMA2</p> <p>Nicotinamide/nicotinic acid mononucleotide adenylyltransferase NMA1</p>

40	NAD salvage pathway		<p>Nicotinamide/nicotinic acid mononucleotide adenyltransferase NMA1</p> <p>Nicotinamide/nicotinic acid mononucleotide adenyltransferase NMA2</p> <p>glutamine-dependent NAD synthase QNS1</p> <p>NAD-dependent histone deacetylase SIR2</p> <p>nicotinamidase PNC1</p> <p>nicotinate phosphoribosyl transferase NPT1</p>
36 - 42	folate biosynthesis		<p>GTP-cyclohydrolase I FOL2</p> <p>aminodeoxychorismate synthase ABZ1</p> <p>aminodeoxychorismate lyase ABZ2</p> <p>2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase [multifunctional] FOL1</p> <p>dihydrofolate synthase FOL3</p> <p>dihydrofolate reductase DFR1</p> <p>glycine cleavage complex LPD1 GCV2 GCV1 GCV3</p> <p>Serine hydroxymethyltransferase, mitochondrial SHM1</p> <p>serine hydroxymethyltransferase SHM2</p> <p>thymidylate synthase CDC21</p> <p>MTHFR MET13</p> <p>MTHFR MET12</p> <p>NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase MTD1</p> <p>C1-tetrahydrofolate synthase ADE3</p> <p>mitochondrial C1-tetrahydrofolate synthase MIS1</p>

41	folate polyglutamylaton		<p>dihydrofolate reductase DFR1</p> <p>Serine hydroxymethyltransferase, mitochondrial SHM1</p> <p>serine hydroxymethyltransferase SHM2</p> <p>MTHFR MET13</p> <p>MTHFR MET12</p> <p>C1-tetrahydrofolate synthase ADE3</p> <p>mitochondrial C1-tetrahydrofolate synthase MIS1</p> <p>folylpolyglutamate synthetase MET7</p>
42	folate interconversions		<p>C1-tetrahydrofolate synthase ADE3</p> <p>mitochondrial C1-tetrahydrofolate synthase MIS1</p> <p>Serine hydroxymethyltransferase, mitochondrial SHM1</p> <p>serine hydroxymethyltransferase SHM2</p> <p>thymidylate synthase CDC21</p> <p>dihydrofolate reductase DFR1</p> <p>glycine cleavage complex LPD1 GCV2 GCV1 GCV3</p> <p>MTHFR MET13</p> <p>MTHFR MET12</p> <p>NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase MTD1</p>
44	folate transformations		<p>Serine hydroxymethyltransferase, mitochondrial SHM1</p> <p>serine hydroxymethyltransferase SHM2</p> <p>MTHFR MET13</p> <p>MTHFR MET12</p> <p>glycine cleavage complex LPD1 GCV2 GCV1 GCV3</p> <p>NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase MTD1</p> <p>mitochondrial C1-tetrahydrofolate synthase MIS1</p> <p>C1-tetrahydrofolate synthase ADE3</p> <p>5,10-methenyltetrahydrofolate synthetase FAU1</p>

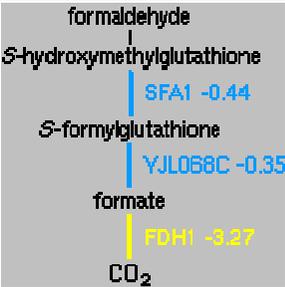
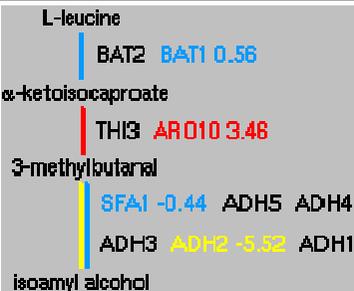
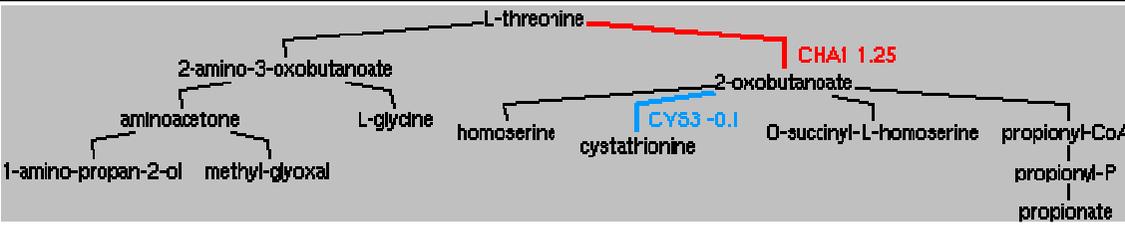
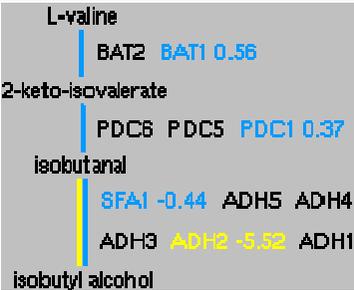
48	glutathione-glutaredoxin redox reactions		<p>glutathione oxidoreductase GLR1</p> <p>glutathione transferase GTT1</p> <p>glutathione transferase GTT2</p> <p>Glutathione peroxidase GPX2</p> <p>glutathione-peroxidase HYR1</p> <p>Glutathione peroxidase GPX1</p>
49	de novo biosynthesis of purine nucleotides		<p>phosphoribosylpyrophosphate amidotransferase ADE4</p> <p>glycinamide ribotide transformylase ADE8</p> <p>5'-phosphoribosylformyl glycinamide synthetase ADE6</p> <p>phosphoribosylglycinamide synthetase / phosphoribosylaminoimidazole synthetase ADE5,7</p> <p>phosphoribosylaminoimidazole-carboxylase ADE2</p> <p>phosphoribosyl amino imidazolesuccinocarboxamide synthetase ADE1</p> <p>inosine monophosphate cyclohydrolase [multifunctional] ADE16</p> <p>inosine monophosphate cyclohydrolase [multifunctional] ADE17</p> <p>IMP dehydrogenase IMD2</p> <p>IMP dehydrogenase IMD3</p> <p>IMP dehydrogenase IMD4</p> <p>GMP synthase GUA1</p> <p>guanylate kinase GUK1</p> <p>adenylosuccinate synthetase ADE12</p> <p>adenylosuccinate lyase ADE13</p> <p>adenylate kinase ADK1</p> <p>mitochondrial GTP:AMP phosphotransferase ADK2</p> <p>ribonucleotide reductase RNR4 RNR3 RNR2 RNR1</p> <p>nucleoside diphosphate kinase YNK1</p>

51	de novo biosynthesis of pyrimidine deoxyribonucleotides		<p>ribonucleotide reductase RNR4 RNR3 RNR2 RNR1</p> <p>dUTP pyrophosphatase DUT1</p> <p>thymidylate synthase CDC21</p> <p>uridylate kinase / thymidylate kinase CDC8</p> <p>nucleoside diphosphate kinase YNK1</p>
58	myo-inositol biosynthesis		<p>L-myo-inositol-1-phosphate synthase INO1</p> <p>inositol monophosphatase INM1</p> <p>inositol monophosphate INM2</p>
60	chitosan biosynthesis		<p>chitin deacetylase CDA2</p> <p>chitin deacetylase CDA1</p>

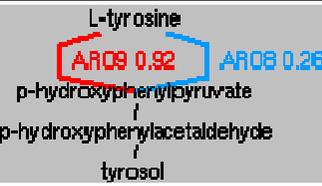
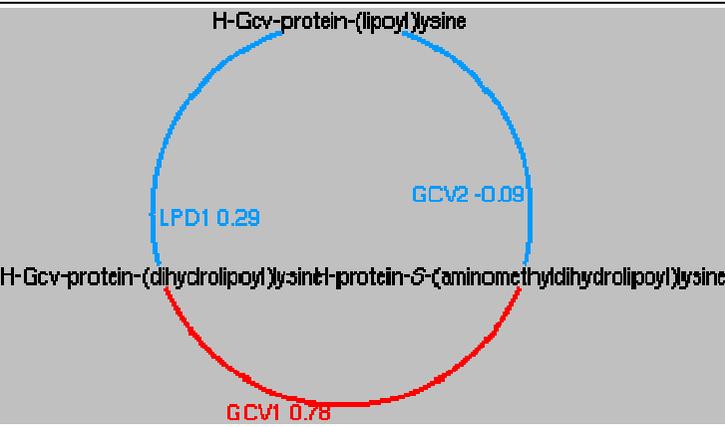
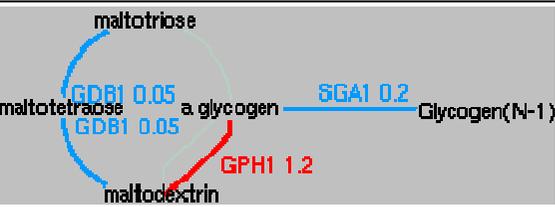
61	gluconeogenesis	<p>malate</p> <p>MDH2 MDH3 -0.38 MDH2</p> <p>pyruvate MAE1 0.25</p> <p>oxaloacetic acid</p> <p>PCK1 1.14</p> <p>phosphoenolpyruvate</p> <p>ENO2 ENO1 -0.31</p> <p>2-phosphoglycerate</p> <p>GPM1 0.32</p> <p>3-phosphoglycerate</p> <p>PGK1 0.05</p> <p>3-phospho-D-glyceroyl-phosphate</p> <p>TDH1 TDH2 TDH3 0.04</p> <p>dihydroxy-acetone-phosphate glyceraldehyde-3-phosphate</p> <p>FBA1 -0.00549</p> <p>fructose-1,6-bisphosphate</p> <p>FBP1 -0.29</p> <p>fructose-6-phosphate</p> <p>PGI1 0.33</p> <p>glucose-6-phosphate</p>	<p>malic enzyme MAE1</p> <p>pyruvate carboxylase PYC2</p> <p>pyruvate carboxylase PYC1</p> <p>cytosolic malate dehydrogenase MDH2</p> <p>phosphoenolpyruvate carboxylkinase PCK1</p> <p>enolase I ENO1</p> <p>enolase ENO2</p> <p>phosphoglycerate mutase GPM1</p> <p>3-phosphoglycerate kinase PGK1</p> <p>glyceraldehyde-3-phosphate dehydrogenase TDH3</p> <p>glyceraldehyde 3-phosphate dehydrogenase TDH2</p> <p>glyceraldehyde-3-phosphate dehydrogenase TDH1</p> <p>aldolase FBA1</p> <p>fructose-1,6-bisphosphatase FBP1</p> <p>glucose-6-phosphate isomerase PGI1</p>
64	trehalose biosynthesis	<p>glucose-6-phosphate UDP-D-glucose</p> <p>TPS1 -0.26</p> <p>α,α-trehalose 6-phosphate</p> <p>TPS2 -0.75</p> <p>trehalose</p>	<p>trehalose-6-phosphate synthase TPS1</p> <p>trehalose-6-phosphate phosphatase TPS2</p>
66	glyoxylate cycle	<p>malate</p> <p>MDH3 -0.38 MDH2</p> <p>succinate glyoxylate ICL1 -1.25 CIT2</p> <p>isocitrate ACO1 0.55 citrate ACO2 0.3</p> <p>cis-acconitate</p> <p>malate</p> <p>MDH3 -0.38 MDH2</p> <p>oxaloacetate DAL7</p> <p>malate</p> <p>MDH3 -0.38 MDH2</p>	<p>cytosolic malate dehydrogenase MDH2</p> <p>peroxisome malate dehydrogenase MDH3</p> <p>citrate synthase CIT2</p> <p>aconitate hydratase ACO2</p> <p>aconitase ACO1</p> <p>isocitrate lyase ICL1</p> <p>malate synthase 2 DAL7</p> <p>malate synthase MLS1</p>
67	oxidative branch of the pentose phosphate pathway	<p>glucose-6-phosphate</p> <p>ZWF1 -0.09</p> <p>D-6-phospho-glucono-δ-lactone</p> <p>SOL4 SOL3 -1.08</p> <p>6-phospho-D-gluconate</p> <p>GND1 GND2 -1.33</p> <p>ribulose-5-phosphate</p>	<p>glucose-6-phosphate dehydrogenase ZWF1</p> <p>6-phosphogluconolactonase SOL3</p> <p>6-phosphogluconolactonase SOL4</p> <p>6-phosphogluconate dehydrogenase GND2</p> <p>6-phosphogluconate dehydrogenase, decarboxylating GND1</p>

67	non-oxidative branch of the pentose phosphate pathway		<table border="0"> <tr> <td>ribose-5-phosphate ketol-isomerase</td> <td>RKI1</td> </tr> <tr> <td>D-ribulose-5-Phosphate 3-epimerase</td> <td>RPE1</td> </tr> <tr> <td>transketolase</td> <td>TKL2</td> </tr> <tr> <td>transaldolase</td> <td>TAL1</td> </tr> <tr> <td>transketolase</td> <td>TKL1</td> </tr> </table>	ribose-5-phosphate ketol-isomerase	RKI1	D-ribulose-5-Phosphate 3-epimerase	RPE1	transketolase	TKL2	transaldolase	TAL1	transketolase	TKL1
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68	aerobic respiration, electron transport chain		<table border="0"> <tr> <td>cytochrome c oxidase</td> <td>COX1 COX2 COX3 COX4 COX5A COX6 COX7 COX8 COX9 COX12 COX13</td> </tr> <tr> <td>ubiquinol cytochrome c reductase complex</td> <td>COB RIP1 CYT1 COR1 QCR2 QCR6 QCR7 QCR8 QCR9 QCR10</td> </tr> <tr> <td>succinate dehydrogenase (ubiquinone)</td> <td>SDH1 SDH2 SDH3 SDH4</td> </tr> <tr> <td>minor succinate dehydrogenase (ubiquinone)</td> <td>YJL045W SDH2 SDH3 SDH4</td> </tr> <tr> <td>NADH dehydrogenase (ubiquinone)</td> <td>NDI1</td> </tr> </table>	cytochrome c oxidase	COX1 COX2 COX3 COX4 COX5A COX6 COX7 COX8 COX9 COX12 COX13	ubiquinol cytochrome c reductase complex	COB RIP1 CYT1 COR1 QCR2 QCR6 QCR7 QCR8 QCR9 QCR10	succinate dehydrogenase (ubiquinone)	SDH1 SDH2 SDH3 SDH4	minor succinate dehydrogenase (ubiquinone)	YJL045W SDH2 SDH3 SDH4	NADH dehydrogenase (ubiquinone)	NDI1
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69	superpathway of glucose fermentation	<p>Metabolic pathway diagram for glucose fermentation. The pathway starts with β-D-glucose and proceeds through the following intermediates and enzymes:</p> <ul style="list-style-type: none"> β-D-glucose → glucose-6-phosphate (Enzymes: HXK1, HXK2 -0.11, GLK1 -0.19) glucose-6-phosphate → fructose-6-phosphate (Enzyme: PGI1 0.33) fructose-6-phosphate → fructose-1,6-bisphosphate (Enzymes: PFK2 0.16, PFK1 0.28) fructose-1,6-bisphosphate → glyceraldehyde-3-phosphate (Enzymes: FBA1 -0.00549, TPI1 0.54) glyceraldehyde-3-phosphate → dihydroxy-acetone-phosphate (Enzymes: TDH1, TDH2, TDH3 0.04) dihydroxy-acetone-phosphate → 3-phospho-D-glyceroyl-phosphate (Enzyme: PGK1 0.05) 3-phospho-D-glyceroyl-phosphate → 3-phosphoglycerate (Enzyme: GPM1 0.32) 3-phosphoglycerate → 2-phosphoglycerate (Enzymes: ENO2, ENO1 -0.31) 2-phosphoglycerate → phosphoenolpyruvate (Enzymes: PYK2, CDC19 0.11) phosphoenolpyruvate → pyruvate (Enzymes: PDC6, PDC5, PDC1 0.37) pyruvate → acetaldehyde (Enzymes: ADH5, ADH4, ADH3, ADH2 -5.52, ADH1) acetaldehyde → ethanol (Enzymes: ALD5 0.2, ALD4 -0.91, ALD4 -0.91, ALD5 0.2, ALD6, ALD5 0.2, ALD4 -0.91) 	<table border="0"> <tbody> <tr><td>glucokinase</td><td>GLK1</td></tr> <tr><td>hexokinase II</td><td>HXK2</td></tr> <tr><td>hexokinase I</td><td>HXK1</td></tr> <tr><td>glucose-6-phosphate isomerase</td><td>PGI1</td></tr> <tr><td>phosphofructokinase</td><td>PFK2 PFK1</td></tr> <tr><td>aldolase</td><td>FBA1</td></tr> <tr><td>triosephosphate isomerase</td><td>TPI1</td></tr> <tr><td>glyceraldehyde-3-phosphate dehydrogenase</td><td>TDH3</td></tr> <tr><td>glyceraldehyde-3-phosphate dehydrogenase</td><td>TDH2</td></tr> <tr><td>glyceraldehyde-3-phosphate dehydrogenase</td><td>TDH1</td></tr> <tr><td>3-phosphoglycerate kinase</td><td>PGK1</td></tr> <tr><td>phosphoglycerate mutase</td><td>GPM1</td></tr> <tr><td>enolase I</td><td>ENO1</td></tr> <tr><td>enolase</td><td>ENO2</td></tr> <tr><td>pyruvate kinase</td><td>CDC19</td></tr> <tr><td>pyruvate kinase</td><td>PYK2</td></tr> <tr><td>pyruvate decarboxylase / decarboxylase</td><td>PDC1</td></tr> <tr><td>pyruvate decarboxylase / decarboxylase</td><td>PDC5</td></tr> <tr><td>pyruvate decarboxylase / decarboxylase</td><td>PDC6</td></tr> <tr><td>aldehyde dehydrogenase (major mitochondrial)</td><td>ALD4</td></tr> <tr><td>aldehyde dehydrogenase (minor mitochondrial)</td><td>ALD5</td></tr> <tr><td>aldehyde dehydrogenase (major cytoplasmic)</td><td>ALD6</td></tr> <tr><td>alcohol dehydrogenase</td><td>ADH1</td></tr> <tr><td>alcohol dehydrogenase</td><td>ADH2</td></tr> <tr><td>alcohol dehydrogenase</td><td>ADH3</td></tr> <tr><td>alcohol dehydrogenase</td><td>ADH4</td></tr> <tr><td>alcohol dehydrogenase</td><td>ADH5</td></tr> </tbody> </table>	glucokinase	GLK1	hexokinase II	HXK2	hexokinase I	HXK1	glucose-6-phosphate isomerase	PGI1	phosphofructokinase	PFK2 PFK1	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 (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
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71	fatty acid oxidation pathway	<p>Metabolic pathway diagram for fatty acid oxidation. The pathway starts with a fatty acid and proceeds through the following intermediates and enzymes:</p> <ul style="list-style-type: none"> a fatty acid → acyl_{n-2}-CoA (Enzymes: FAA1 -0.24, FAA4, FAA3, FAA3 -1.31, FAT1 0.43) acyl_{n-2}-CoA → 3-oxoacyl-CoA (Enzyme: POX1 -1.29) 3-oxoacyl-CoA → an acyl-CoA (Enzyme: POX2 -2.05) an acyl-CoA → a (3S)-3-hydroxyacyl-CoA (Enzyme: POX3 -2.05) a (3S)-3-hydroxyacyl-CoA → a trans-2-enoyl-CoA (Enzymes: DCII, ECI1 -1.33) a trans-2-enoyl-CoA → a cis-3-enoyl-CoA 	<table border="0"> <tbody> <tr><td>d3,d2-Enoyl-CoA Isomerase</td><td>ECI1</td></tr> <tr><td>delta(3,5)-delta(2,4)-dienoyl-CoA isomerase</td><td>DCI1</td></tr> <tr><td>fatty acid transporter</td><td>FAT1</td></tr> <tr><td>acyl-CoA synthetase</td><td>FAA2</td></tr> <tr><td>acyl-CoA synthase</td><td>FAA3</td></tr> <tr><td>long chain fatty acyl:CoA synthetase</td><td>FAA4</td></tr> <tr><td>long chain fatty acyl:CoA synthetase</td><td>FAA1</td></tr> <tr><td>fatty-acyl coenzyme A oxidase</td><td>POX1</td></tr> <tr><td>3-hydroxyacyl-CoA dehydrogenase</td><td>FOX2</td></tr> <tr><td>3-oxoacyl CoA thiolase</td><td>POT1</td></tr> </tbody> </table>	d3,d2-Enoyl-CoA Isomerase	ECI1	delta(3,5)-delta(2,4)-dienoyl-CoA isomerase	DCI1	fatty acid transporter	FAT1	acyl-CoA synthetase	FAA2	acyl-CoA synthase	FAA3	long chain fatty acyl:CoA synthetase	FAA4	long chain fatty acyl:CoA synthetase	FAA1	fatty-acyl coenzyme A oxidase	POX1	3-hydroxyacyl-CoA dehydrogenase	FOX2	3-oxoacyl CoA thiolase	POT1																																		
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72	formaldehyde oxidation II (glutathione-dependent)		formaldehyde dehydrogenase / alcohol dehydrogenase SFA1 S-formylglutathione hydrolase YJL068C formate dehydrogenases FDH1
76	leucine degradation		branched-chain amino acid aminotransferase BAT1 branched-chain amino acid transaminase BAT2 decarboxylase ARO10 ketoisocaproate decarboxylase / decarboxylase THI3 alcohol dehydrogenase ADH1 alcohol dehydrogenase ADH2 alcohol dehydrogenase ADH3 alcohol dehydrogenase ADH4 alcohol dehydrogenase ADH5 formaldehyde dehydrogenase / alcohol dehydrogenase SFA1
77	threonine degradation		serine/threonine dehydratase CHA1 cystathionine gamma-lyase CYS3
78	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

79	isoleucine degradation	<p>L-iso-leucine BAT2 BAT1 0.56 2-keto-3-methyl-valerate PDC6 PDC5 PDC1 0.37 ARO10 3.46 THI3 2-methylbutanal SFA1 -0.44 ADH5 ADH4 ADH3 ADH2 -3.52 ADH1 amyl alcohol</p>	branded-chain amino acid aminotransferase BAT1 branded-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
81	tryptophan degradation	<p>L-tryptophan ARO8 0.26 ARO9 0.92 indolepyruvate ARO10 3.46 PDC6 PDC5 PDC1 0.37 indole acetaldehyde SFA1 -0.44 ADH5 ADH4 ADH3 ADH2 -3.52 ADH1 indole-3-ethanol</p>	aromatic amino acid aminotransferase II ARO9 aromatic amino acid aminotransferase I ARO8 pyruvate decarboxylase / decarboxylase PDC1 pyruvate decarboxylase / decarboxylase PDC5 pyruvate decarboxylase / decarboxylase PDC6 decarboxylase ARO10 alcohol dehydrogenase ADH1 alcohol dehydrogenase ADH2 alcohol dehydrogenase ADH3 alcohol dehydrogenase ADH4 alcohol dehydrogenase ADH5 formaldehyde dehydrogenase / alcohol dehydrogenase SFA1
82	phenylalanine degradation	<p>L-phenylalanine ARO8 0.26 ARO9 0.92 phenylpyruvate ARO10 3.46 PDC6 PDC5 PDC1 0.37 phenylacetaldehyde SFA1 -0.44 ADH5 ADH4 ADH3 ADH2 -3.52 ADH1 phenylethanol</p>	aromatic amino acid aminotransferase II ARO9 aromatic amino acid aminotransferase I ARO8 pyruvate decarboxylase / decarboxylase PDC1 pyruvate decarboxylase / decarboxylase PDC5 pyruvate decarboxylase / decarboxylase PDC6 decarboxylase ARO10 alcohol dehydrogenase ADH1 alcohol dehydrogenase ADH2 alcohol dehydrogenase ADH3 alcohol dehydrogenase ADH4 alcohol dehydrogenase ADH5 formaldehyde dehydrogenase / alcohol dehydrogenase SFA1

83	tyrosine degradation		aromatic amino acid aminotransferase II ARO9 aromatic amino acid aminotransferase I ARO8
85	glycine cleavage complex		glycine decarboxylase complex P subunit GCV2 GCV1 dihydrolipoamide dehydrogenase LPD1
87	L-serine degradation		serine/threonine dehydratase CHA1
88	glutamate degradation IX		NAD-dependent glutamate dehydrogenase GDH2
93	glycogen catabolism		glucoamylase SGA1 glycogen phosphorylase GPH1 glucanotranferase GDB1
97	trehalose degradation		neutral trehalase NTH1 acid trehalase ATH1

100	allantoin degradation		allantoinase DAL1 allantoicase DAL2 ureidoglycolate hydrolase DAL3 urea carboxylase / allophanate hydrolase DUR1,2
	phenylalanine biosynthesis		chorismate mutase ARO7 prephenate dehydratase PHA2 aromatic amino acid aminotransferase II ARO9 aromatic amino acid aminotransferase I ARO8
	tyrosine biosynthesis		chorismate mutase ARO7 prephenate dehydrogenase (NADP+) TYR1 aromatic amino acid aminotransferase II ARO9 aromatic amino acid aminotransferase I ARO8