

Additional file 3 – Regulated *P. pastoris* pathways in hypoxia vs. normoxia

Individual *P. pastoris* (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
2	aspartate biosynthesis		pyruvate carboxylase PYC2 pyruvate carboxylase PYC1 aspartate aminotransferase AAT1 aspartate aminotransferase AAT2
3	asparagine biosynthesis		aspartate aminotransferase AAT1 aspartate aminotransferase AAT2 ASN2 ASN2 ASN1 ASN1
4	pantothenate and coenzyme A biosynthesis		amine oxidase FMS1 aldehyde dehydrogenase (stress inducible cytoplasmic) ALD2 aldehyde dehydrogenase (stress inducible cytoplasmic) ALD3 3-methyl-2-oxobutanoate hydroxymethyltransferase ECM31 gluconate 5-dehydrogenase PAN5 pantoate-beta-alanine ligase PAN6 pantothenate kinase CAB1 phosphopantothenate-cysteine ligase CAB2 phosphopantothenoylcysteine decarboxylase CAB3 phosphopantothenoylcysteine decarboxylase VHS3 phosphopantothenoylcysteine decarboxylase SIS2 pantetheine-phosphate adenyltransferase CAB4 dephospho-CoA kinase CAB5

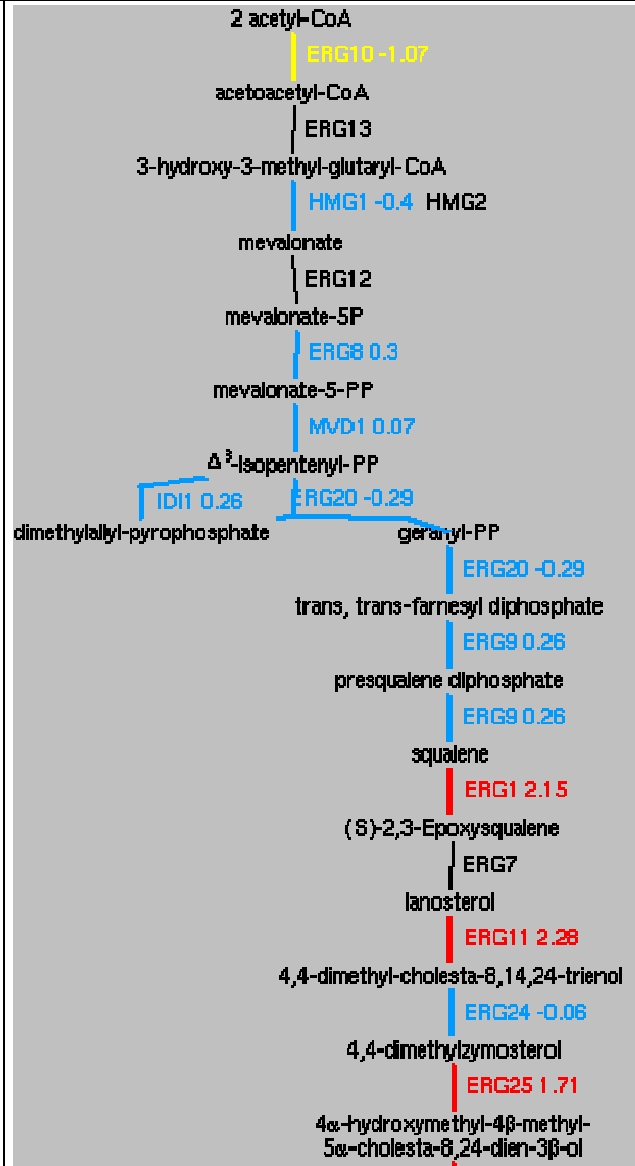
8	arginine biosynthesis	<p style="text-align: center;">L-glutamate N-ACETYLGLUTAMATE_SEMIALDEHYDE</p> <p style="text-align: center;"> ARG7 0.08 ARG2 -0.29</p> <p style="text-align: center;">N-acetyl-L-glutamate</p> <p style="text-align: center;"> ARG5,6 -0.26</p> <p style="text-align: center;">N-acetylglutamyl-phosphate</p> <p style="text-align: center;"> ARG5,6 -0.26</p> <p style="text-align: center;">N-acetylglutamate semialdehyde</p> <p style="text-align: center;"> ARG8 -0.79</p> <p style="text-align: center;">N-α-acetylornithine</p> <p style="text-align: center;"> ARG7 0.08</p> <p style="text-align: center;">L-ornithine</p> <p style="text-align: center;"> ARG3 0.04</p> <p style="text-align: center;">citrulline</p> <p style="text-align: center;"> ARG1 -0.84</p> <p style="text-align: center;">L-arginino-succinate</p> <p style="text-align: center;"> ARG4 -0.12</p> <p style="text-align: center;">L-arginine</p>	<p>acetylglutamate synthase ARG2</p> <p>acetylglutamate kinase / N-acetyl-gamma-glutamyl-phosphate reductase ARG5,6</p> <p>acetylornithine aminotransferase ARG8</p> <p>acetylornithine acetyltransferase ARG7</p> <p>ornithine carbamoyltransferase ARG3</p> <p>arginosuccinate synthetase ARG1</p> <p>argininosuccinate lyase ARG4</p>
9	arginine degradation (anaerobic)	<p style="text-align: center;">L-arginine</p> <p style="text-align: center;"> CAR1</p> <p style="text-align: center;">L-ornithine</p> <p style="text-align: center;"> CAR2 0.41</p> <p style="text-align: center;">L-glutamate γ-semialdehyde</p> <p style="text-align: center;">L-Δ^1-pyrroline-5-carboxylate</p> <p style="text-align: center;"> PRO3 0.63</p> <p style="text-align: center;">L-proline</p>	<p>arginase CAR1</p> <p>ornithine aminotransferase CAR2</p> <p>delta 1-pyrroline-5-carboxylate reductase PRO3</p>

10	arginine biosynthesis		<p>acetylglutamate synthase ARG2</p> <p>acetylglutamate kinase / N-acetyl-gamma-glutamyl-phosphate reductase ARG5,6</p> <p>acetylornithine aminotransferase ARG8</p> <p>acetylornithine acetyltransferase ARG7</p> <p>carbamyl phosphate synthase / aspartate transcarbamylase URA2</p> <p>carbamoyl phosphate synthetase CPA2 CPA1</p> <p>ornithine carbamoyltransferase ARG3</p> <p>arginosuccinate synthetase ARG1</p> <p>arginosuccinate lyase ARG4</p>
11	isoleucine biosynthesis		<p>threonine deaminase ILV1</p> <p>acetolactate synthase ILV6 ILV2</p> <p>acetohydroxyacid reductoisomerase ILV5</p> <p>dihydroxy-acid dehydratase ILV3</p> <p>branched-chain amino acid aminotransferase BAT1</p> <p>branched-chain amino acid transaminase BAT2</p>
11	valine biosynthesis		<p>acetolactate synthase ILV6 ILV2</p> <p>acetohydroxyacid reductoisomerase ILV5</p> <p>dihydroxy-acid dehydratase ILV3</p> <p>branched-chain amino acid aminotransferase BAT1</p> <p>branched-chain amino acid transaminase BAT2</p>

11	acetoin biosynthesis	<pre> graph TD A[pyruvate] -- ILV6 -0.47 --> B[2-aceto-lactate] B -- ILV2 -1.15 --> C[diacetyl] C -- BDH1 --> D[acetoin] </pre>	acetolactate synthase 2,3-butanediol dehydrogenase / diacetyl reductase	ILV6 ILV2 BDH1
11	leucine biosynthesis	<pre> graph TD A[2-keto-isovalerate] -- LEU9 0.14 --> B[2-isopropylmalate] B -- LEU1 -0.31 --> C[3-isopropylmalate] C -- LEU2 0.3 --> D[alpha-ketoisocaproate] D -- BAT2 BAT1 1.21 --> E[L-leucine] </pre>	alpha-isopropylmalate synthase alpha-isopropylmalate synthase, minor isozyme isopropylmalate isomerase beta-IPM dehydrogenase branched-chain amino acid aminotransferase branched-chain amino acid transaminase	LEU4 LEU9 LEU1 LEU2 BAT1 BAT2
12	serine biosynthesis from glyoxylate	<pre> graph TD A[L-glycine] -- SHM2 -0.45 SHM1 -0.83 --> B[L-serine] </pre>	Serine hydroxymethyltransferase, mitochondrial serine hydroxymethyltransferase	SHM1 SHM2
12	glycine biosynthesis from serine	<pre> graph TD A[L-serine] -- SHM2 -0.45 SHM1 -0.83 --> B[L-glycine] </pre>	Serine hydroxymethyltransferase, mitochondrial serine hydroxymethyltransferase	SHM1 SHM2
13	cysteine biosynthesis/homocysteine degradation	<pre> graph TD A[homocysteine] -- CYS4 1.17 --> B[cystathionine] B -- CYS3 2.68 --> C[L-cysteine] </pre>	cystathionine beta-synthase cystathionine gamma-lyase	CYS4 CYS3
13	sulfate assimilation pathway	<pre> graph TD A[SO4^2-] -- MET3 0.71 --> B[APS] B -- MET14 0.53 --> C[PAPS] C -- MET16 0.49 --> D[SO3] D -- MET5 -0.13 MET10 0.33 --> E[H2S] </pre>	ATP sulfurylase adenylylsulfate kinase 3'phosphoadenylylsulfate reductase sulfite reductase	MET3 MET14 MET16 MET5 MET10
17	glutamate biosynthesis from ammonia	<pre> graph TD A[2-oxoglutarate] -- GDH1 0.75 GDH3 -0.75 --> B[L-glutamate] </pre>	NADP-dependent glutamate dehydrogenase NADP-dependent glutamate dehydrogenase	GDH3 GDH1

17	glutamate biosynthesis from glutamine	<p>L-glutamine 2-oxoglutarate GLT1 -1.84 2 L-glutamate</p>	glutamate synthase (NADH)	GLT1
17	superpathway of glutamate biosynthesis	<p>isocitrate NH₃ IDP3 IDP2 -4.0 IDP1 2-oxoglutarate L-glutamate NH₃ 2-oxoglutarate GDH1 GDH3 -0.78 2 L-glutamate GLT1 -1.84</p>	NADP-dependent glutamate dehydrogenase NADP-dependent glutamate dehydrogenase glutamine synthetase NADP-dependent isocitrate dehydrogenase NADP-dependent isocitrate dehydrogenase NADP-dependent isocitrate dehydrogenase glutamate synthase (NADH)	GDH3 GDH1 GLN1 IDP1 IDP2 IDP3 GLT1
18	methionine salvage pathway	<p>5-methylthioadenosine MEU1 0.01 5-methylthioribose-1-phosphate MRI1 5-methylthioribulose-1-phosphate MDE1 0.81 5-(methylthio)-2,3-dioxopentyl phosphate UTR4 0.42 1,2-dihydroxy-3-keto-5-methylthiopentene ADI1 0.14 2-oxo-4-methylthiobutanoate BAT2 BAT1 1.21 ARO8 0.035 ARO9 -0.58 L-methionine</p>	5'-methylthioadenosine phosphorylase methylthioribose-1 P isomerase methylthioribulose-1-phosphate dehydratase 2,3-dioxomethiopentane-1-phosphate enolase/phosphatase acireductone dioxygenase aromatic amino acid aminotransferase II aromatic amino acid aminotransferase I branched-chain amino acid aminotransferase branched-chain amino acid transaminase	MEU1 MRI1 MDE1 UTR4 ADI1 ARO9 ARO8 BAT1 BAT2
19	proline biosynthesis	<p>L-glutamate PRO1 0.39 L-glutamate-5-phosphate PRO2 0.18 L-glutamate gamma-semialdehyde L-delta1-pyrroline-5-carboxylate PRO3 0.63 L-proline</p>	gamma-glutamyl kinase gamma-glutamyl phosphate reductase delta 1-pyrroline-5-carboxylate reductase	PRO1 PRO2 PRO3

20 ergosterol biosynthesis

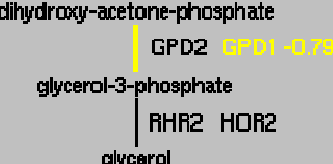
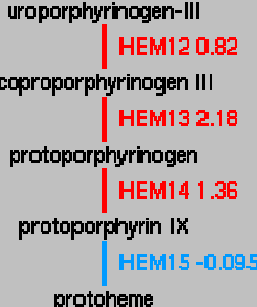
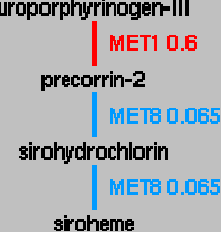
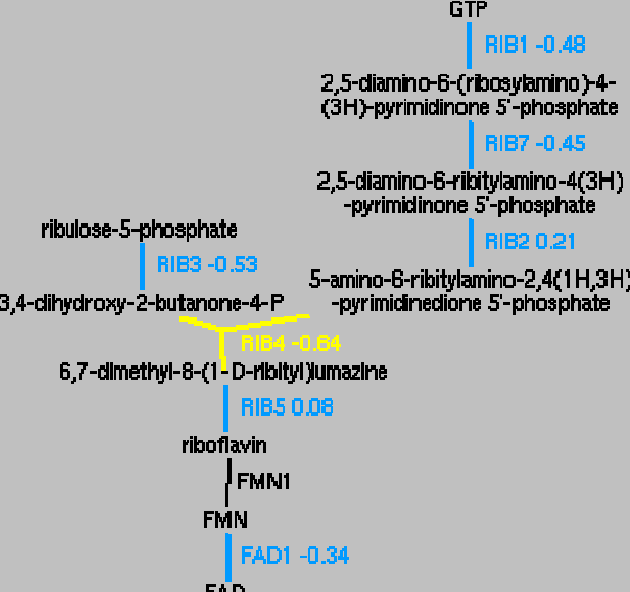


acetoacetyl CoA thiolase	ERG10
3-hydroxy-3-methylglutaryl coenzyme A synthase	ERG13
3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)	HMG2
3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)	HMG1
mevalonate kinase	ERG12
phosphomevalonate kinase	ERG8
mevalonate pyrophosphate decarboxylase	MVD1
isopentenyl diphosphate:dimethylallyl diphosphate isomerase	IDI1
farnesyl diphosphate synthetase	ERG20
squalene synthetase	ERG9
squalene monooxygenase	ERG1
2,3-oxidosqualene-lanosterol cyclase	ERG7
cytochrome P450 lanosterol 14α-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

		<p>4α-hydroxymethyl-4β-methyl-5α-cholesta-8,24-dien-3β-ol</p> <p>ERG25 1.71</p> <p>4α-formyl-4β-methyl-5α-cholesta-8,24-dien-3β-ol</p> <p>ERG25 1.71</p> <p>4α-carboxy-4β-methyl-5α-cholesta-8,24-dien-3β-ol</p> <p>ERG26 0.045</p> <p>3-keto-4-methylzymosterol</p> <p>ERG27 -0.08</p> <p>4-α-methylzymosterol</p> <p>ERG25 1.71</p> <p>4α-hydroxymethyl-5α-cholesta-8,24-dien-3β-ol</p> <p>ERG25 1.71</p> <p>4α-formyl-5α-cholesta-8,24-dien-3β-ol</p> <p>ERG25 1.71</p> <p>4α-carboxy-5α-cholesta-8,24-dien-3β-ol</p> <p>ERG26 0.045</p> <p>5α-cholesta-8,24-dien-3-one</p> <p>ERG27 -0.08</p> <p>zymosterol</p> <p>ERG6 -0.57</p> <p>fecosterol</p> <p>ERG2 -0.57</p> <p>episterol</p> <p>ERG3 1.33</p> <p>5,7,24(28)-ergostatrienol</p> <p>ERG5 0.69</p> <p>5,7,22,24(28)-ergostetraenol</p> <p>ERG4 0.32</p> <p>ergosterol</p>	
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20	mevalonate pathway		<p>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</p>
26	sphingolipid metabolism		<p>serine palmitoyltransferase LCB2 serine palmitoyltransferase LCB1 3-ketosphinganine reductase TSC10 dihydrospingosine C-4 hydroxylase SUR2 PHS kinase / DHS kinase LCB4 PHS kinase / DHS kinase LCB5 PHS-1-P phosphatase / DHS-1-P phosphatase YSR3 PHS-1-P phosphatase / DHS-1-P phosphatase LCB3 ceramide synthase LIP1 LAG1 LAC1 ceramidase YPC1 ceramidase YDC1 desaturase SCS7 IPC synthase AUR1 inositol phosphorylceramide mannosyltransferase SUR1 CSG2 inositolphosphotransferase IPT1 dihydrospingosine phosphate lyase DPL1</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>
31	phosphatidate biosynthesis I (the dihydroxyacetone pathway)		<p>dihydroxyacetone phosphate acyltransferase [multifunctional] GPT2</p> <p>dihydroxyacetone phosphate acyltransferase [multifunctional] SCT1</p> <p>1-acyl dihydroxyacetone phosphate reductase AYR1</p> <p>1-acyl-sn-glycerol-3-phosphate acyl transferase SLC1</p>
31	phosphatidate biosynthesis II (the glycerol-3-phosphate pathway)		<p>glycerol 3-phosphate dehydrogenase GPD1</p> <p>glycerol-3-phosphate dehydrogenase (NAD+) GPD2</p> <p>dihydroxyacetone phosphate acyltransferase [multifunctional] GPT2</p> <p>dihydroxyacetone phosphate acyltransferase [multifunctional] SCT1</p> <p>1-acyl-sn-glycerol-3-phosphate acyl transferase SLC1</p>
31	triglyceride biosynthesis		<p>dihydroxyacetone phosphate acyltransferase [multifunctional] GPT2</p> <p>dihydroxyacetone phosphate acyltransferase [multifunctional] SCT1</p> <p>1-acyl-sn-glycerol-3-phosphate acyl transferase SLC1</p> <p>phosphatidate phosphatase PAH1</p> <p>Lecithin cholesterol acyl transferase LRO1</p> <p>Diacylglycerol Acyltransferase DGA1</p>

33	glycerol biosynthesis	 <pre> graph TD A[dihydroxy-acetone-phosphate] -- GPD2 GPD1 -0.79 --> B[glycerol-3-phosphate] B -- RHR2 HOR2 --> C[glycerol] </pre>	glycerol 3-phosphate dehydrogenase glycerol-3-phosphate dehydrogenase (NAD+) DL-glycerol-3-phosphatase DL-glycerol-3-phosphatase	GPD1 GPD2 HOR2 RHR2
37	heme biosynthesis	 <pre> graph TD A[uroporphyrinogen-III] -- HEM12 0.92 --> B[coproporphyrinogen III] B -- HEM13 2.18 --> C[protoporphyrinogen] C -- HEM14 1.36 --> D[protoporphyrin IX] D -- HEM15 -0.095 --> E[protoheme] </pre>	uroporphyrinogen decarboxylase aerobic coproporphyrinogen oxidase protoporphyrinogen oxidase protoheme ferredoxin	HEM12 HEM13 HEM14 HEM15
37	siroheme biosynthesis	 <pre> graph TD A[uroporphyrinogen-III] -- MET1 0.6 --> B[precorrin-2] B -- MET8 0.065 --> C[sirohydrochlorin] C -- MET8 0.065 --> D[siroheme] </pre>	uroporphyrinogen III transmethylase ferrochelatase / precorrin-2 dehydrogenase	MET1 MET8
38	riboflavin, FMN and FAD biosynthesis	 <pre> graph TD A[GTP] -- RIB1 -0.48 --> B["2,5-diamino-6-(ribosylamino)-4-(3H)-pyrimidinone 5'-phosphate"] B -- RIB7 -0.45 --> C["2,5-diamino-6-ribitylamino-4(3H)-pyrimidinone 5'-phosphate"] C -- RIB2 0.21 --> D["5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidinone 5'-phosphate"] D -- RIB3 -0.53 --> E[3,4-dihydroxy-2-butanone-4-P] E -- RIB4 -0.64 --> F[6,7-dimethyl-8-(1-D-ribityl)lumazine] F -- RIB5 0.08 --> G[riboflavin] G -- FMN1 --> H[FMN] H -- FAD1 -0.34 --> I[FAD] </pre>	GTP cyclohydrolase II diaminohydroxyphosphoribosylaminopyrimidine deaminase DRAP deaminase 3,4-dihydroxy-2-butanone-4-phosphate synthase lumazine synthase riboflavine synthetase riboflavin kinase FAD synthetase	RIB1 RIB7 RIB2 RIB3 RIB4 RIB5 FMN1 FAD1

40	tryptophan degradation via kynurenine	<p>CPD-250 L-tryptophan</p> <p style="text-align: center;"> BNA2 1.24</p> <p>L-Formylkynurenine</p> <p style="text-align: center;"> BNA7</p> <p>kynurenine</p> <p style="text-align: center;"> BNA4 -0.02</p> <p>3-hydroxy-L-kynurenine</p> <p style="text-align: center;"> BNA5 -0.05</p> <p>3-hydroxy-anthranilate</p> <p style="text-align: center;"> BNA1 1.31</p> <p>2-amino-3-carboxymuconate semialdehyde</p> <p style="text-align: center;"> </p> <p>quinolinate</p> <p style="text-align: center;"> BNA6 0.16</p> <p>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>
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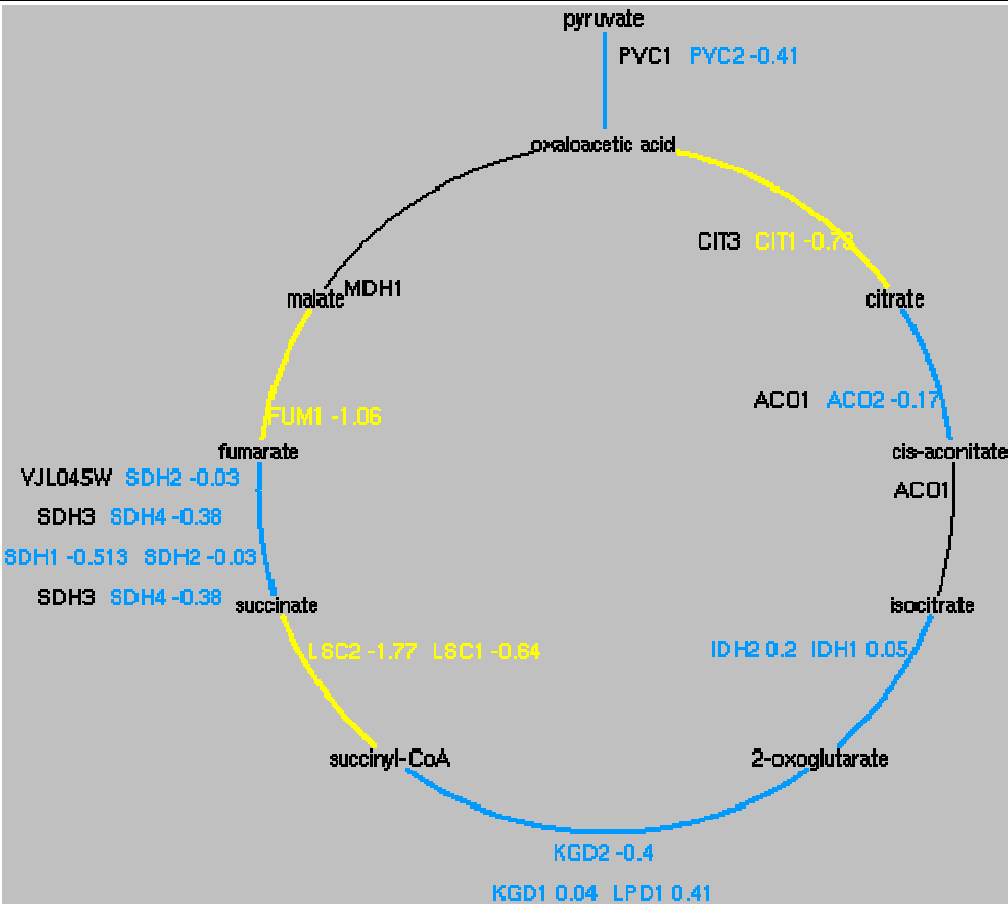
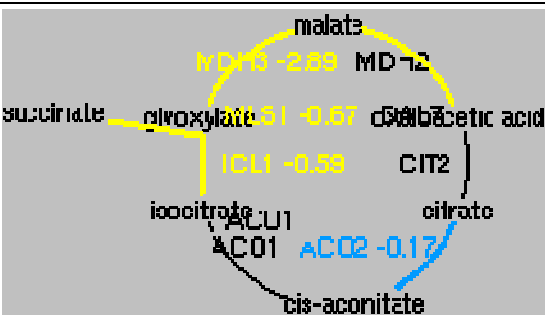
41	folate polyglutamylati on		<p>dihydrofolate reductase DFR1</p> <p>Serine hydroxymethyltransferase, mitochondrial SHM1</p> <p>serine hydroxymethyltransferase SHM2</p> <p>MTHFR MET13</p> <p>MTHFR MET12</p> <p>C1-tetrahydrofolate synthase ADE3</p> <p>mitochondrial C1-tetrahydrofolate synthase MIS1</p> <p>folylpolyglutamate synthetase MET7</p>
42	folate interconversion s		<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>
43	biotin biosynthesis		<p>7,8-diamino-pelargonic acid aminotransferase BIO3</p> <p>dethiobiotin synthetase BIO4</p> <p>biotin synthase BIO2</p>

44	folate transformations	<p>Metabolic pathway diagram for folate transformations. Key components include: <ul style="list-style-type: none"> THF (Tetrahydrofolate) at the top left. Enzymes and their values: LPD1 (0.41), GCV2 (-0.39), SHM2 (-0.45), SHM1 (-0.83), MTD1 (0.18), ADE3 (-0.18), MIS1, GCV1, GCV3 (-0.11), MET12, MET13 (-0.37), FAU1 (0.33). Products: 10-formyl-THF, 5,10-methenyl-THF, 5-formyl-THF, 5-methyl-THF, 10-methylene-THF. </p>	<p>Serine hydroxymethyltransferase, mitochondrial SHM1 serine hydroxymethyltransferase SHM2 MTHFR MET13 MTHFR MET12 glycine cleavage complex LPD1 GCV2 GCV1 GCV3 NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase MTD1 mitochondrial C1-tetrahydrofolate synthase MIS1 C1-tetrahydrofolate synthase ADE3 5,10-methenyltetrahydrofolate synthetase FAU1</p>
45	glutathione degradation	<p>Metabolic pathway diagram for glutathione degradation. Key components include: <ul style="list-style-type: none"> glutathione at the top. Enzymes and their values: ECM38 (-0.62), DUG1. Products: L-cysteinylglycine, L-cysteine. </p>	<p>γ-glutamyltransferase ECM38 Cys-Gly metallopeptidase DUG1</p>
45	superpathway of glutathione metabolism (truncated γ -glutamyl cycle)	<p>Metabolic pathway diagram for the superpathway of glutathione metabolism. Key components include: <ul style="list-style-type: none"> L-glycine at the top left. Enzymes and their values: GSH1 (0.5), ECM38 (-0.62), DUG1. Products: glutathione, L-cysteine. </p>	<p>gamma-glutamylcysteine synthetase GSH1 glutathione synthetase GSH2 γ-glutamyltransferase ECM38 Cys-Gly metallopeptidase DUG1</p>
46	pyridoxal 5'-phosphate salvage pathway	<p>Metabolic pathway diagram for the pyridoxal 5'-phosphate salvage pathway. Key components include: <ul style="list-style-type: none"> pyridoxine and pyridoxamine at the top. Enzymes and their values: BUD16 (-0.06), PDX3 (1.82). Products: pyridoxine-5'-phosphate, pyridoxamine 5'-phosphate, pyridoxal, pyridoxal 5'-phosphate. </p>	<p>pyridoxal kinase / pyridoxamine kinase / pyridoxine kinase BUD16 pyridoxine phosphate oxidase PDX3</p>
52	salvage pathways of purines and their nucleosides	<p>Metabolic pathway diagram for the salvage pathways of purines and their nucleosides. Key components include: <ul style="list-style-type: none"> inosine, adenine, and guanine at the top. Enzymes and their values: PNP1, AAH1, APT1 (-0.01), APT2, ADO1 (0.655), GUD1 (0.14), HPT1 (0.02), XPT1 (0.25), AMD1 (0.48). Products: hypoxanthine, AMP, IMP, xanthosine-5-phosphate, GMP. </p>	<p>purine nucleoside phosphorylase PNP1 guanine deaminase GUD1 xanthine phosphoribosyl transferase XPT1 adenine aminohydrolase AAH1 hypoxanthine guanine phosphoribosyltransferase HPT1 adenine phosphoribosyltransferase APT2 adenine phosphoribosyltransferase APT1 adenosine kinase ADO1 AMD1 AMD1</p>

52	salvage pathways of adenine, hypoxanthine and their nucleosides		adenosine kinase ADO1 purine nucleoside phosphorylase PNP1 adenine phosphoribosyltransferase APT2 adenine phosphoribosyltransferase APT1 AMD1 AMD1 adenine aminohydrolase AAH1 hypoxanthine guanine phosphoribosyltransferase HPT1
53	salvage pathways of pyrimidine deoxyribonucleotides		deoxycytidine kinase / cytidine kinase / uridine kinase URK1 nicotinic acid riboside hydrolase [multifunctional] URH1 cytidine deaminase CDD1
54	salvage pathways of pyrimidine ribonucleotides		cytosine deaminase FCY1 nucleoside diphosphate kinase YNK1 cytidine deaminase CDD1 deoxycytidine kinase / cytidine kinase / uridine kinase URK1 nicotinic acid riboside hydrolase [multifunctional] URH1 UPRTase FUR1

59	lipid-linked oligosaccharide biosynthesis	<p>dolichol-phosphate</p> <p>ALG7 0.34</p> <p>GlcNAc-PP-Dol</p> <p>ALG14 -0.53 ALG13 -0.21</p> <p>GlcNAc(2)-PP-Dol</p> <p>ALG1 -0.16</p> <p>Man(1)GlcNAc(2)-PP-Dol</p> <p>ALG2 0.82</p> <p>Man(2)GlcNAc(2)-PP-Dol</p> <p>ALG2 0.82</p> <p>Man(3)GlcNAc(2)-PP-Dol</p> <p>ALG11</p> <p>Man(4)GlcNAc(2)-PP-Dol</p> <p>ALG11</p> <p>Man(5)GlcNAc(2)-PP-Dol</p> <p>ALG3 -0.02</p> <p>Man(6)GlcNAc(2)-PP-Dol</p> <p>ALG9 0.135</p> <p>Man(7)GlcNAc(2)-PP-Dol</p> <p>ALG12 -0.19</p> <p>Man(8)GlcNAc(2)-PP-Dol</p> <p>ALG9 0.135</p> <p>Man(9)GlcNAc(2)-PP-Dol</p> <p>ALG6 0.09</p> <p>Glc(1)Man(9)GlcNAc(2)-PP-Dol</p> <p>ALG8 0.08</p> <p>Glc(2)Man(9)GlcNAc(2)-PP-Dol</p> <p>DIE2 0.11</p> <p>Glc(3)Man(9)GlcNAc(2)-PP-Dol</p>	<p>Dol-PP-GlcNAc-1-P-transferase ALG7</p> <p>UDP-N-acetylglucosamine: N-acetylglucosaminyl-diphosphodolichol N-acetylglucosaminyltransferase ALG14 ALG13</p> <p>Dol-PP-GlcNAc2:Man transferase ALG1</p> <p>Dol-PP-GlcNAc2:Man2:Man transferase ALG2</p> <p>alpha-1,2-mannosyltransferase ALG11</p> <p>Dol-PP-GlcNAc2:Man5:Man transferase ALG3</p> <p>Dol-PP-GlcNAc2:Man7:Man transferase ALG12</p> <p>Dol-PP-GlcNAc2:Man6:Man transferase ALG9</p> <p>Dol-PP-GlcNAc2:Man9:Glc transferase ALG6</p> <p>Dol-PP-GlcNAc2:Man9:Glc transferase ALG8</p> <p>Dol-PP-GlcNAc2:Man9:Glc transferase DIE2</p>
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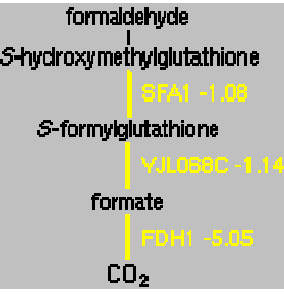
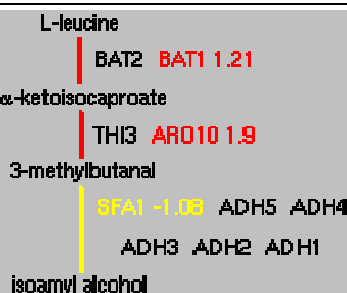
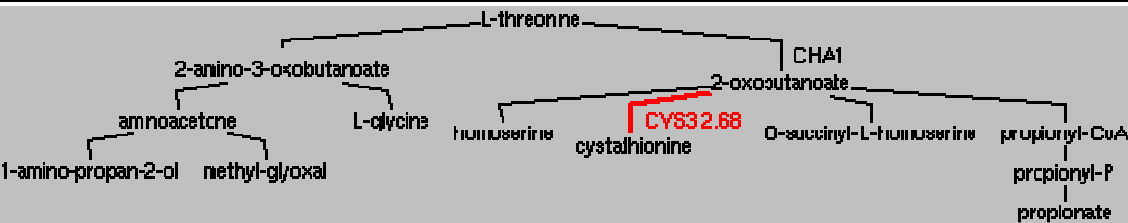
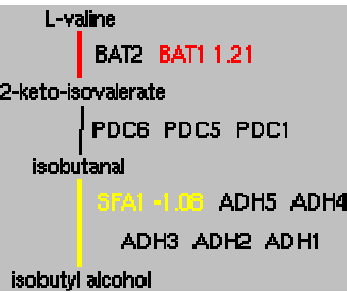
61	gluconeogenesis	<p>The diagram illustrates the gluconeogenesis pathway. Intermediates are listed vertically: malate, pyruvate, oxaloacetic acid, phosphoenolpyruvate, 2-phosphoglycerate, 3-phosphoglycerate, 3-phospho-D-glyceroyl-phosphate, dihydroxy-acetone-phosphate, fructose-1,6-bisphosphate, fructose-5-phosphate, and glucose-6-phosphate. Enzymes and their activities are shown as follows: MDH2 (malate to oxaloacetic acid), PYC1 and PYC2 (-0.41) (pyruvate to oxaloacetic acid), MAE1 (0.83) (malate to pyruvate), PCK1 (-0.485) (oxaloacetic acid to phosphoenolpyruvate), ENO2 and ENO1 (2.05) (phosphoenolpyruvate to 2-phosphoglycerate), GPM1 (1.58) (2-phosphoglycerate to 3-phosphoglycerate), PGK1 (1.55) (3-phosphoglycerate to 3-phospho-D-glyceroyl-phosphate), TDH1, TDH2, and TDH3 (1.6) (3-phospho-D-glyceroyl-phosphate to dihydroxy-acetone-phosphate), FBA1 (0.93) (dihydroxy-acetone-phosphate to fructose-1,6-bisphosphate), FBP1 (-0.06) (fructose-1,6-bisphosphate to fructose-5-phosphate), and PGI1 (1.2) (fructose-5-phosphate to glucose-6-phosphate). Red lines indicate the main pathway, while blue lines indicate bypass reactions.</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>The diagram shows the biosynthesis of trehalose. It starts with glucose-6-phosphate and UDP-D-glucose, which are converted to α,α-trehalose 6-phosphate by the enzyme TPS1 (0.09). This intermediate is then converted to trehalose by the enzyme TPS2 (1.03).</p>	<p>trehalose-6-phosphate synthase TPS1</p> <p>trehalose-6-phosphate phosphatase TPS2</p>

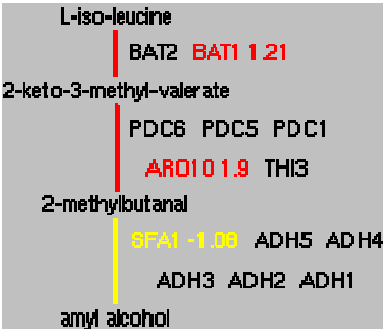
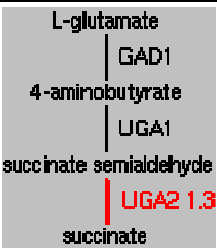
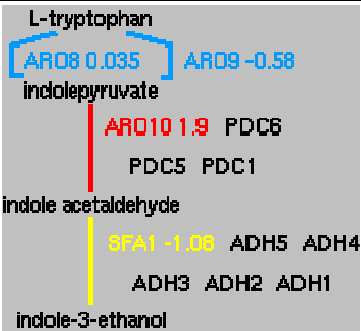
66	TCA cycle, aerobic respiration	 <p>The diagram illustrates the TCA cycle with the following intermediates and associated enzymes/genes:</p> <ul style="list-style-type: none"> pyruvate → oxaloacetic acid: PYC1, PYC2 -0.41 oxaloacetic acid + citrate → isocitrate: CIT3, CIT1 -0.73 isocitrate → 2-oxoglutarate: IDH2 0.2, IDH1 0.05 2-oxoglutarate → succinyl-CoA: KGD2 -0.4, KGD1 0.04, LPD1 0.41 succinyl-CoA → succinate: LSC2 -1.77, LSC1 -0.84 succinate → fumarate: SDH3, SDH4 -0.38; SDH1 -0.513, SDH2 -0.03 fumarate → malate: FUM1 -1.05 malate → oxaloacetic acid: MDH1 Additional enzymes: AC01, ACO2 -0.17, ACO1, ACO2 	<table border="0"> <tbody> <tr><td>pyruvate carboxylase</td><td>PYC2</td></tr> <tr><td>pyruvate carboxylase</td><td>PYC1</td></tr> <tr><td>citrate synthase</td><td>CIT1</td></tr> <tr><td>citrate synthase</td><td>CIT3</td></tr> <tr><td>aconitate hydratase</td><td>ACO2</td></tr> <tr><td>aconitase</td><td>ACO1</td></tr> <tr><td>NAD-dependent isocitrate dehydrogenase</td><td>IDH2 IDH1</td></tr> <tr><td>2-ketoglutarate dehydrogenase complex</td><td>KGD2 KGD1 LPD1</td></tr> <tr><td>succinyl-CoA ligase</td><td>LSC2 LSC1</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>fumarate hydralase</td><td>FUM1</td></tr> <tr><td>mitochondrial malate dehydrogenase</td><td>MDH1</td></tr> </tbody> </table>	pyruvate carboxylase	PYC2	pyruvate carboxylase	PYC1	citrate synthase	CIT1	citrate synthase	CIT3	aconitate hydratase	ACO2	aconitase	ACO1	NAD-dependent isocitrate dehydrogenase	IDH2 IDH1	2-ketoglutarate dehydrogenase complex	KGD2 KGD1 LPD1	succinyl-CoA ligase	LSC2 LSC1	succinate dehydrogenase (ubiquinone)	SDH1 SDH2 SDH3 SDH4	minor succinate dehydrogenase (ubiquinone)	YJL045W SDH2 SDH3 SDH4	fumarate hydralase	FUM1	mitochondrial malate dehydrogenase	MDH1
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66	glyoxylate cycle	 <p>The diagram illustrates the glyoxylate cycle with the following intermediates and associated enzymes/genes:</p> <ul style="list-style-type: none"> malate → oxaloacetic acid: MDH2 -2.69, MDH3 oxaloacetic acid + citrate → isocitrate: CIT2 isocitrate → cis-aconitate: ICL1 -0.59, AC01 cis-aconitate → citrate: ACO2 -0.17 citrate → oxaloacetic acid: CIT2 oxaloacetic acid + succinate → malate: MDH2, MDH3 Additional enzymes: AC01, ACO2 	<table border="0"> <tbody> <tr><td>cytosolic malate dehydrogenase</td><td>MDH2</td></tr> <tr><td>peroxisome malate dehydrogenase</td><td>MDH3</td></tr> <tr><td>citrate synthase</td><td>CIT2</td></tr> <tr><td>aconitate hydratase</td><td>ACO2</td></tr> <tr><td>aconitase</td><td>ACO1</td></tr> <tr><td>isocitrate lyase</td><td>ICL1</td></tr> <tr><td>malate synthase 2</td><td>DAL7</td></tr> <tr><td>malate synthase</td><td>MLS1</td></tr> </tbody> </table>	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										
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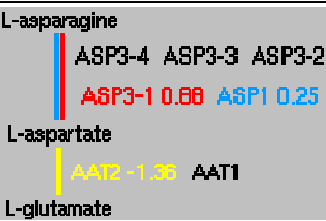

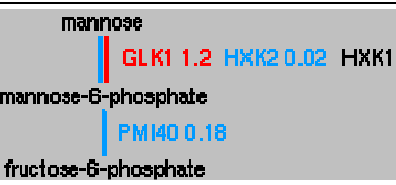
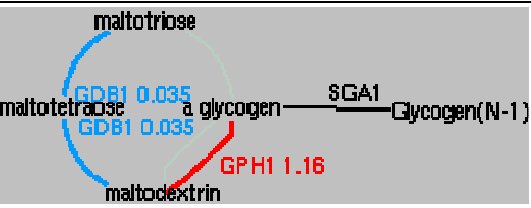
67	non-oxidative branch of the pentose phosphate pathway		<table border="0"> <tr> <td>ribose-5-phosphate ketol-isomerase</td> <td>RKI1</td> </tr> <tr> <td>D-ribulose-5-Phosphate 3-epimerase</td> <td>RPE1</td> </tr> <tr> <td>transketolase</td> <td>TKL2</td> </tr> <tr> <td>transaldolase</td> <td>TAL1</td> </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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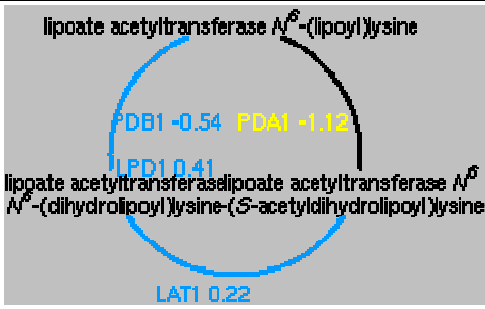
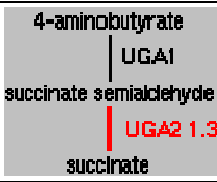
69	glycolysis	<pre> graph TD G6P[glucose-6-phosphate] -- PGI 1.2 --> F6P[fructose-6-phosphate] F6P -- PFK2 1.5 PFK1 1.71 --> F16BP[fructose-1,6-bisphosphate] F16BP -- FBA1 0.93 --> GAP[glyceraldehyde-3-phosphate] F16BP -- TPI 1.3 --> DHAP[dihydroxy-acetone-phosphate] GAP -- TDH1 TDH2 TDH3 1.6 --> P3GDP[3-phospho-D-glyceroyl-phosphate] P3GDP -- PGK1 1.55 --> P3G[3-phosphoglycerate] P3G -- GPM1 1.58 --> P2G[2-phosphoglycerate] P2G -- ENO2 ENO1 2.05 --> PEP[phosphoenolpyruvate] PEP -- PYK2 CDC19 2.39 --> P[pyruvate] </pre>	<p>glucose-6-phosphate isomerase PGI1</p> <p>phosphofructokinase PFK2 PFK1</p> <p>aldolase FBA1</p> <p>triosephosphate isomerase TPI1</p> <p>glyceraldehyde-3-phosphate dehydrogenase TDH3</p> <p>glyceraldehyde 3-phosphate dehydrogenase TDH2</p> <p>glyceraldehyde-3-phosphate dehydrogenase TDH1</p> <p>3-phosphoglycerate kinase PGK1</p> <p>phosphoglycerate mutase GPM1</p> <p>enolase I ENO1</p> <p>enolase ENO2</p> <p>pyruvate kinase CDC19</p> <p>pyruvate kinase PYK2</p>
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69	superpathway of glucose fermentation	<p>Metabolic pathway diagram for glucose fermentation. The pathway starts with β-D-glucose, which is converted to glucose-6-phosphate (enzymes: HXK1, HXK2 0.02, GLK1 1.2). Glucose-6-phosphate is then converted to fructose-6-phosphate (enzyme: PGI1 1.2). Fructose-6-phosphate is converted to fructose-1,6-bisphosphate (enzymes: PFK2 1.5, PFK1 1.71). Fructose-1,6-bisphosphate is converted to glyceraldehyde-3-phosphate (enzyme: FBA1 0.93) and dihydroxy-acetone-phosphate (enzyme: TPI1 1.3). Glyceraldehyde-3-phosphate is converted to dihydroxy-acetone-phosphate (enzymes: TDH1, TDH2, TDH3 1.6). Dihydroxy-acetone-phosphate is converted to 3-phospho-D-glyceroyl-phosphate (enzyme: PGK1 1.55). 3-phospho-D-glyceroyl-phosphate is converted to 3-phosphoglycerate (enzyme: GPM1 1.58). 3-phosphoglycerate is converted to 2-phosphoglycerate (enzyme: ENO2, ENO1 2.05). 2-phosphoglycerate is converted to phosphoenolpyruvate (enzyme: ENO2, ENO1 2.05). Phosphoenolpyruvate is converted to pyruvate (enzymes: PYK2, CDC19 2.38). Pyruvate is converted to acetaldehyde (enzymes: PDC6, PDC5, PDC1). Acetaldehyde is converted to ethanol (enzymes: ADH5, ADH4, ADH3, ADH2, ADH1) and acetate (enzymes: ALD5 3.24, ALD4, ALD4, ALD5 3.24, ALD6, ALD5 3.24, ALD4).</p>	<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>phosphofruktokinase</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	phosphofruktokinase	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, which is converted to an acyl-CoA (enzymes: FAA1 2.08, FAA4, FAA3). An acyl-CoA is converted to 3-oxoacyl-CoA (enzyme: FAT1 -0.1). 3-oxoacyl-CoA is converted to a (3S)-3-hydroxyacyl-CoA (enzyme: POT1). A (3S)-3-hydroxyacyl-CoA is converted to a trans-2-enoyl-CoA (enzyme: FOX2 -2.71). A trans-2-enoyl-CoA is converted to a cis-3-enoyl-CoA (enzyme: FOX1 -2.39). A cis-3-enoyl-CoA is converted to an acyl-CoA (enzyme: DCII, ECI1 -2.52). A (3S)-3-hydroxyacyl-CoA is also converted to an acyl-CoA (enzyme: FOX2 -2.71).</p>	<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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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																																																								

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 1.21 2-keto-3-methyl-valerate PDC6 PDC5 PDC1 ARO10 1.9 THI3 2-methylbutanal SFA1 -1.08 ADH5 ADH4 ADH3 ADH2 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
80	glutamate degradation I	 <p>L-glutamate GAD1 4-aminobutyrate UGA1 succinate semialdehyde UGA2 1.3 succinate</p>	glutamate decarboxylase GAD1 gamma-aminobutyrate (GABA) transaminase UGA1 succinate semialdehyde dehydrogenase UGA2
81	tryptophan degradation	 <p>L-tryptophan ARO8 0.035 ARO9 -0.58 indolepyruvate ARO10 1.9 PDC6 PDC5 PDC1 indole acetaldehyde SFA1 -1.08 ADH5 ADH4 ADH3 ADH2 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		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
84	asparagine degradation		asparaginase I ASP1 asparaginase II ASP3-1 asparaginase II ASP3-2 asparaginase II ASP3-3 asparaginase II ASP3-4 aspartate aminotransferase AAT1 aspartate aminotransferase AAT2
89	alanine degradation		alanine aminotransferase ALT1
89	alanine biosynthesis		alanine aminotransferase ALT1
91	mannose degradation		hexokinase I HXK1 hexokinase II HXK2 glucokinase GLK1 mannose-6-phosphate isomerase PMI40
93	glycogen catabolism		glucoamylase SGA1 glycogen phosphorylase GPH1 glucanotranferase GDB1

99	pyruvate dehydrogenase complex		dihydrolipoamide dehydrogenase LPD1 pyruvate dehydrogenase PDA1 pyruvate dehydrogenase PDB1 dihydrolipoamide acetyltransferase LAT1
100	allantoin degradation		allantoinase DAL1 allantoicase DAL2 ureidoglycolate hydrolase DAL3 urea carboxylase / allophanate hydrolase DUR1,2
101	4-aminobutyrate degradation		gamma-aminobutyrate (GABA) transaminase UGA1 succinate semialdehyde dehydrogenase UGA2
102	glycerol degradation		glycerol kinase GUT1 glycerol-3-phosphate dehydrogenase GUT2

glycogen biosynthesis	<pre> glucose-6-phosphate PGM2 0.135 PGM1 glucose-1-phosphate UGP1 YHL012W UDP-D-glucose GLG2 GLG1 α-glucosyl-glycogenin GLG2 GLG1 (1,4-α-D-glucosyl)_n-glucosyl glycogenin GLG2 GLG1 (1,4-α-D-glucosyl)_(n) glycogenin GSY2 -1.71 GSY1 α-glucosylated glycogenin GLC3 -0.04 glycogen </pre>	<pre> phosphoglucomutase PGM1 phosphoglucomutase PGM2 UTP glucose-1-phosphate uridylyltransferase YHL012W uridinephosphoglucose pyrophosphorylase UGP1 glycogenin glucosyltransferase GLG1 glycogenin glucosyltransferase GLG2 UDP-glucose-starch glucosyltransferase GSY1 UDP-glucose-starch glucosyltransferase GSY2 1,4-glucan-6-(1,4-glucano)-transferase GLC3 </pre>
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