

SUPPLEMENTAL INFORMATION

Identification of lysine succinylation substrates and the succinylation regulatory enzyme **CobB** in *E. coli*

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Running title: Lysine succinylome and its regulatory enzyme in *E. coli*.

SUPPLEMENTAL MATERIALS AND METHODS

Estimation of absolute stoichiometry of lysine succinylation and acetylation sites— We modified a previously reported algorithm (37) and used it to calculate absolute stoichiometries of the Ksucc (or Kac) peptides, either in Light or Heavy media. This calculation was based on the quantification data (intensity of MS signals) for the Ksucc (or Kac) peptides, the corresponding protein, and the corresponding unmodified peptide, with the assumption that only one type of PTM occurs at a given site (stoichiometry calculated using this method is approximately accurate, even if a second type of PTM in the peptide is present and has low stoichiometry). The completely digested fragment of the peptide sequence containing the site of Ksucc (or Kac) modification was selected as the unmodified peptide. This peptide contained no other modifications. Quantification ratios of Ksucc or Kac peptides (x) to corresponding unmodified peptides (y) and proteins (z) were used to calculate the absolute stoichiometry using the previously reported algorithm (37). If the peptide contains no other PTM and tryptic digestion is complete, this method provides a good estimate of stoichiometry for a modified peptide.

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Fig. S1. The SILAC distribution of proteins identified with more than 2 quantifiable Ksucc sites. The x axis shows individual proteins with more than 2 quantifiable Ksucc sites. The yellow line (left y axis) shows the range of Ksucc sites SILAC ratios (H/L) in each individual protein. The blue line (right y axis) shows SILAC ratio fold of changes among the Ksucc sites in each individual protein (the maximum SILAC ratio (H/L) divided by the minimum SILAC ratio (H/L)).

Supplemental Fig. S2. Illustrations of the top ten enriched metabolic pathways from the KEGG database. Each individual figure is drawn by using DAVID software. Below the pathway map, all the enzymes that participate in each pathway are listed with weblinks that provide information. Identified succinylated proteins are listed in red (presented with DAVID gene names). In addition, the detailed explanation of KEGG Pathway Maps in the figure can be obtained from http://www.genome.jp/kegg/document/help_pathway.html. **A.** Ribosomal RNAs and ribosomal proteins. **B.** Purine Metabolism. **C.** Aminoacyl-tRNA biosynthesis. **D.** Glycolysis and gluconeogenesis. **E.** Pyrimidine metabolism. **F.** Pyruvate metabolism. **G.** Pentose phosphate pathway. **H.** Citrate cycle (TCA cycle). **I.** Glutathione metabolism. **J.** Fatty acid biosynthesis.

Supplemental Fig. S3. The complete Ksucc interaction network was obtained from the STRING 9.05 database with confidence score ≥ 0.7 , and visualized in Cytoscape. The resulting interactome had 403 nodes and 5,624 edges. The top 7 highly interconnected clusters identified by MCODE are shown in different colors (see also Fig. 5 for detail).

Supplemental Fig. S4. Profiling of *E. coli* lysine acetylome (related to Fig. 6). **A.** The total number of lysine-acetylated sites per protein. **B.** The sequence motif surrounding the acetylated lysine residue generated by iceLogo software.

Supplemental Fig. S5. Distribution of the SILAC ratios of Kac sites. **A.** The peptide intensities (y-axis, summed precursor-ion intensities of each peptide derived from MaxQuant) of the quantifiable Kac peptides in relation to their \log_2 Ratio(H/L) (x-axis) between high- and no-glucose media. Blue: $-6 \leq \log_2$ Ratio (H/L) ≤ -1 , green: $-1 \leq \log_2$ Ratio(H/L) ≤ 1 , red: $1 \leq \log_2$ Ratio(H/L) ≤ 6 . **B.** Distributions of the SILAC ratios of acetyllysine sites between high- and no-glucose media. The y-axis represents the number of Ksucc peptides in each category.

Supplemental Fig. S6. The distributions of normalized SILAC ratios of Ksucc over Kac. The normalized ratio of Ksucc (\log_2 H/L) over Kac (\log_2 H/L) of the peptides that contain both Ksucc and Kac modifications at the same lysine residue.

Supplemental Fig. S7. The SILAC ratio distribution of quantifiable *E. coli* proteins. Histogram showing the distribution of the SILAC ratios of *E. coli* proteins in high-glucose (Heavy) over no-glucose medium (Light). The y-axis represents the number of proteins in each category.

SUPPLEMENTAL TABLE LEGENDS

Supplemental Table S1. List of identified Ksucc peptides. **A.** All identified Ksucc peptides. **B.** Ksucc peptides identified only in cells grown in Heavy (high-glucose) medium. **C.** Ksucc peptides identified only in cells grown in Light (no-glucose) medium. **D.** Quantifiable Ksucc peptides. **E.** Ksucc sites with absolute stoichiometries in Light (no-glucose) medium and Heavy (high-glucose) medium.

Supplemental Table S2. KEGG pathway enrichment analysis of lysine-succinylated proteins.

Supplemental Table S3. Gene Ontology (GO) analysis of lysine-succinylated proteins. **A.** Succinylation-enriched biological processes (BP). **B.** Succinylation-enriched cellular compartments (CC). **C.** Succinylation-enriched molecular functions (MF).

Supplemental Table S4. Enrichment analysis for Pfam domains of lysine-succinylated proteins.

Supplemental Table S5. Protein interaction networks of succinylated proteins using the STRING database by MCODE. The top 14 MCODE networks are listed.

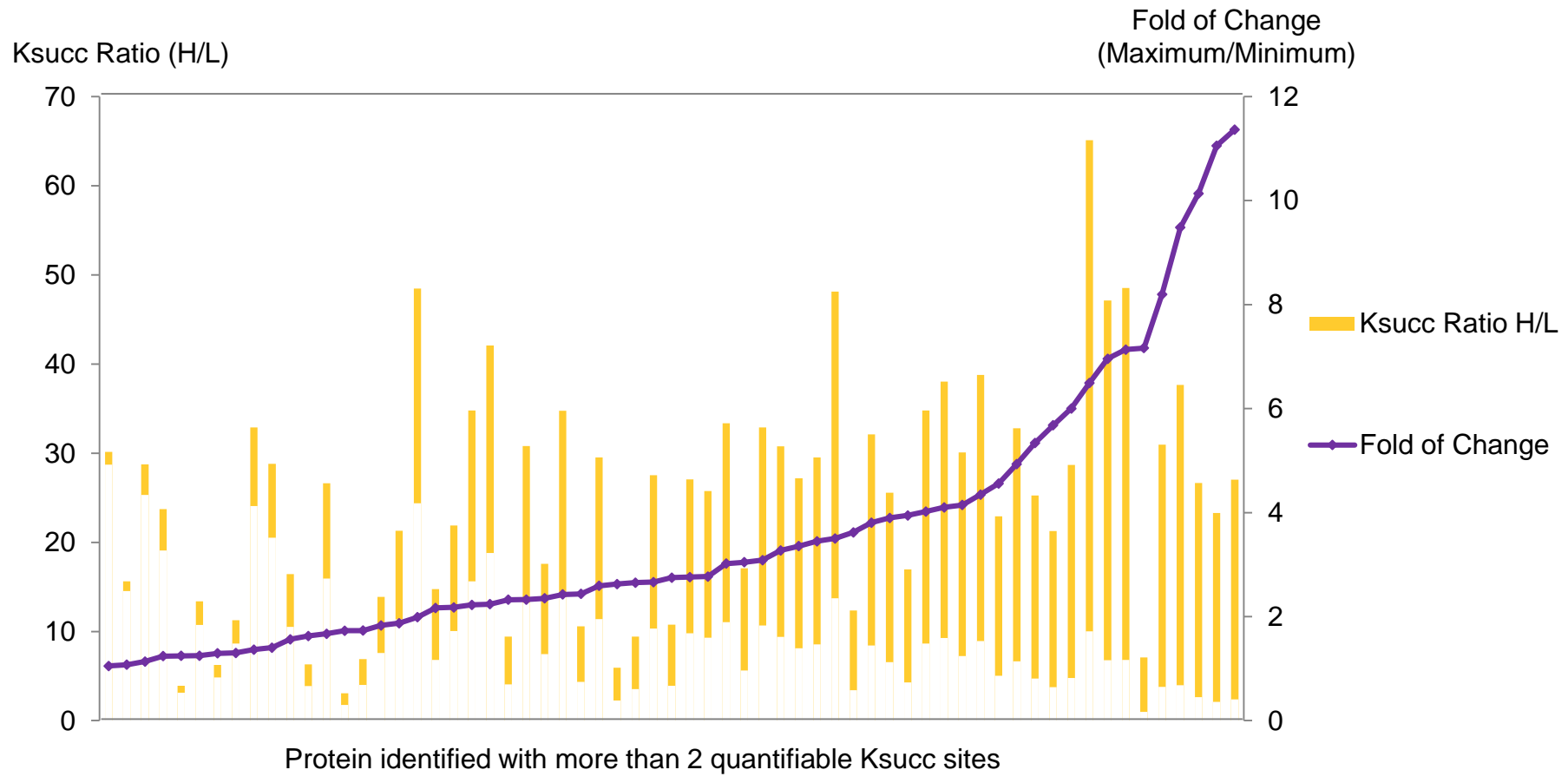
Supplemental Table S6. List of identified Kac peptides. **A.** All identified Kac peptides. **B.** Kac peptides identified only in cells grown in Heavy (high-glucose) medium. **C.** Kac peptides identified only in cells grown in Light (no-glucose) medium. **D.** The list of quantifiable Kac peptides. **E.** The list of Kac peptides and their calculated stoichiometries in Light (no-glucose) medium and Heavy (high-glucose) medium.

Supplemental Table S7. List of protein quantification results.

Supplemental Table S8. List of sites quantifiable for both Kac and Ksucc. **Column A:** Normalized Kac SILAC ratio (H/L). **Column F:** Normalized Ksucc SILAC ratio (H/L) **Column**

J: The ratios of the normalized K_{succ} (H/L) divided by the normalized K_{ac} (H/L) in the same peptide sequence bearing either an acetyllysine or a succinyllysine residue.

Supplemental Figure S1



Supplemental Figure S2 A

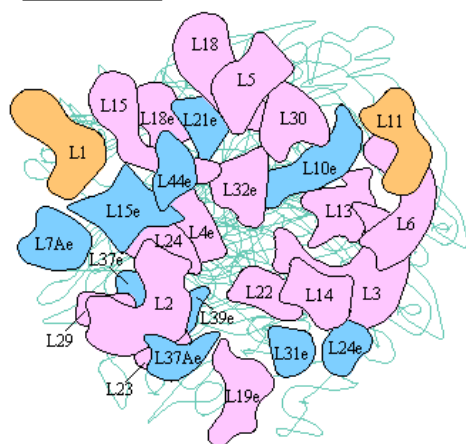
Pathway: Ribosome

Pathway information generated by [KEGG](#).

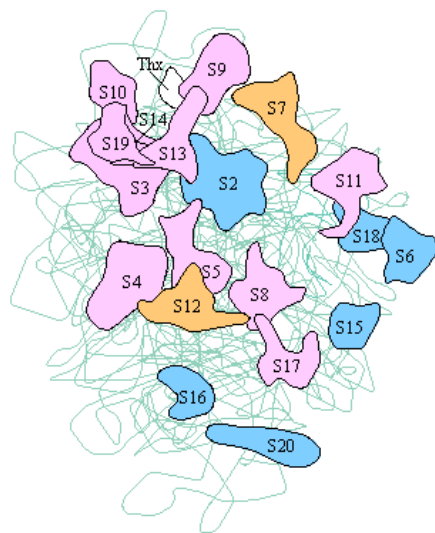
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RIBOSOME



Large subunit



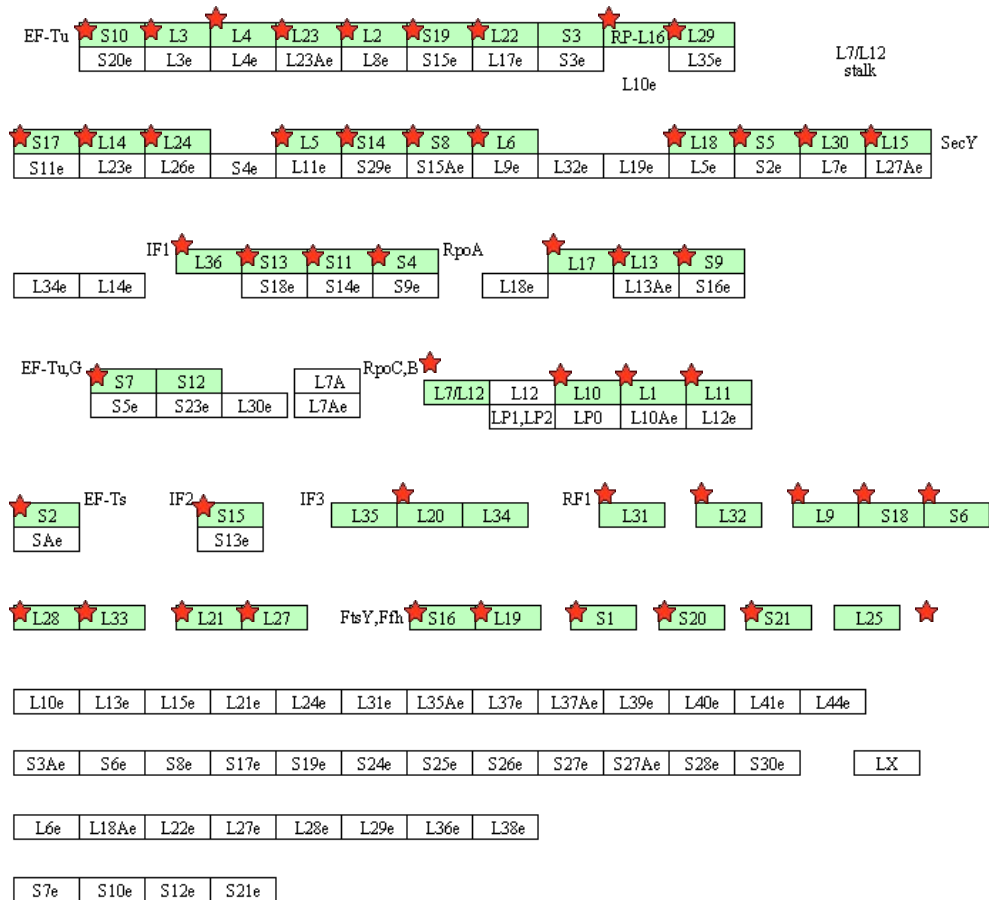
Small subunit

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Ribosomal RNAs

23S	5S		16S
25S	5S	5.8S	18S

Ribosomal proteins



List genes are shown in red

DAVID Gene Name
30S ribosomal protein S1
30S ribosomal protein S10
30S ribosomal protein S11
30S ribosomal protein S13: 30S ribosomal protein
30S ribosomal protein S14
30S ribosomal protein S15
30S ribosomal protein S16
30S ribosomal protein S17
30S ribosomal protein S18
30S ribosomal protein S19
30S ribosomal protein S2
30S ribosomal protein S20
30S ribosomal protein S21
30S ribosomal protein S4
30S ribosomal protein S5
30S ribosomal protein S6
30S ribosomal protein S7
30S ribosomal protein S8
30S ribosomal protein S9
50S ribosomal protein L1
50S ribosomal protein L10
50S ribosomal protein L11
50S ribosomal protein L13
50S ribosomal protein L14
50S ribosomal protein L15
50S ribosomal protein L16

50S ribosomal protein L17
50S ribosomal protein L18
50S ribosomal protein L19
50S ribosomal protein L2
50S ribosomal protein L20
50S ribosomal protein L21
50S ribosomal protein L22
50S ribosomal protein L23
50S ribosomal protein L24
50S ribosomal protein L25
50S ribosomal protein L27
50S ribosomal protein L28
50S ribosomal protein L29
50S ribosomal protein L3
50S ribosomal protein L30
50S ribosomal protein L31 type B 2: 50S ribosomal protein L31 type B 1: 50S ribosomal protein L31 type B: 50S ribosomal protein L31
50S ribosomal protein L31
50S ribosomal protein L32
50S ribosomal protein L33
50S ribosomal protein L34
50S ribosomal protein L35
50S ribosomal protein L36 2: 50S ribosomal protein L36: 50S ribosomal protein L36 1
50S ribosomal protein L4
50S ribosomal protein L5
50S ribosomal protein L6
50S ribosomal protein L7/L12
50S ribosomal protein L9
Stationary-phase-induced ribosome-associated protein

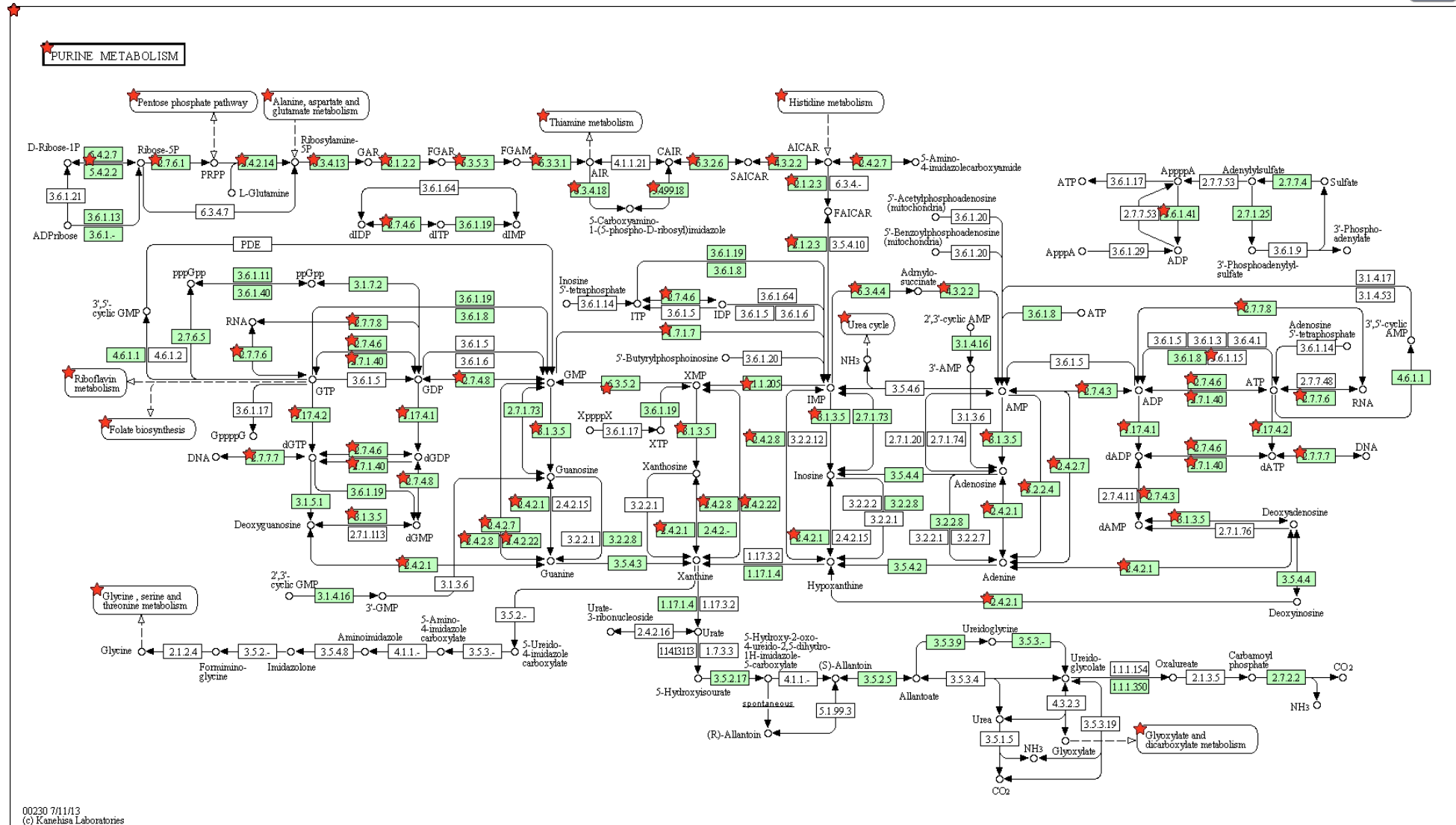
Supplemental Figure S2 B

Pathway: Purine metabolism

Pathway information generated by KEGG.

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Help



List genes are shown in red

DAVID Gene Name
5-nucleotidase yjjG
ADP compounds hydrolase nudE
ADP-ribose pyrophosphatase
AMP nucleosidase
Adenine deaminase
Adenine phosphoribosyltransferase
Adenosine deaminase
Adenylyl cyclase
Adenylyl kinase
Adenylosuccinate lyase
Adenylosuccinate synthetase
Adenylyl-sulfate kinase
Allantoate amidohydrolase
Amidophosphoribosyltransferase
Anaerobic ribonucleoside-triphosphate reductase
Bifunctional purine biosynthesis protein purH
Bis(5'-nucleosyl)-tetraphosphatase, symmetrical: Bis(5'-nucleosyl)-tetraphosphatase [symmetrical]
Carbamate kinase
Carbamate kinase

Carbamate kinase-like protein yahl
Carbamate kinase-like protein yqeA
DNA polymerase I
DNA polymerase III subunit alpha
DNA polymerase III subunit beta
DNA polymerase III subunit chi
DNA polymerase III subunit delta
DNA polymerase III subunit delta'
DNA polymerase III subunit epsilon
DNA polymerase III subunit psi
DNA polymerase III subunit tau
DNA polymerase III subunit theta
DNA-directed RNA polymerase subunit alpha
DNA-directed RNA polymerase subunit beta
DNA-directed RNA polymerase subunit omega
DNA-directed RNA polymerase: DNA-directed RNA polymerase subunit beta'
Deoxyguanosinetriphosphate triphosphohydrolase
ECs5191: ECP_4467: ECSE_4519: EcSMS35_4692: ECUMN_4750: Z5824: EcoIC_3793: EGS88_4807: F2348C_4544: EC55989_4773: ECDH10B_4408: ECED1_5072: ECH74115_5730: ECIA11_4447: b4213: ECIA139_4685: UTI89_C4822: EcHS_A4467: APECO1_2173: EcE24377A_4783
Exopolyphosphatase
GMP reductase
GMP synthase [glutamine-hydrolyzing]
GTP pyrophosphokinase
Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase
Guanosine-5'-triphosphate 3'-diphosphate pyrophosphatase
Guanylate kinase
Hypoxanthine phosphoribosyltransferase
Inosine-5'-monophosphate dehydrogenase
Inosine-guanosine kinase
Multifunctional protein surF
Nucleoside diphosphate kinase
Nucleoside-triphosphatase: Nucleoside-triphosphatase rdgB
Phosphopentomutase
Phosphoribosylamine-glycine ligase
Phosphoribosylaminoimidazole carboxylase ATPase subunit
Phosphoribosylaminoimidazole carboxylase catalytic subunit
Phosphoribosylaminoimidazole-succinocarboxamide synthase
Phosphoribosylformylglycinamide cyclo-ligase
Phosphoribosylformylglycinamide synthase
Phosphoribosylglycinamide formyltransferase 2
Phosphoribosylglycinamide formyltransferase
Polyribonucleotide nucleotidyltransferase
Protein mazG
Purine nucleoside phosphorylase deoD-type
Pyrimidine-specific ribonucleoside hydrolase rihB
Pyruvate kinase I: Pyruvate kinase
Pyruvate kinase II: Pyruvate kinase
Ribonucleoside-diphosphate reductase 1 subunit beta
Ribonucleoside-diphosphate reductase 2 subunit beta
Ribonucleoside-diphosphate reductase: Ribonucleoside-diphosphate reductase 1 subunit alpha
Ribonucleoside-diphosphate reductase: Ribonucleoside-diphosphate reductase 2 subunit alpha
Ribose-phosphate pyrophosphokinase
Sulfate adenyltransferase subunit 1
Sulfate adenyltransferase subunit 2
UPF0207 protein yfbR: 5'-nucleotidase yfbR
Ureidoglycolate dehydrogenase
Xanthine phosphoribosyltransferase
Xanthosine phosphorylase

Supplemental Figure S2 C

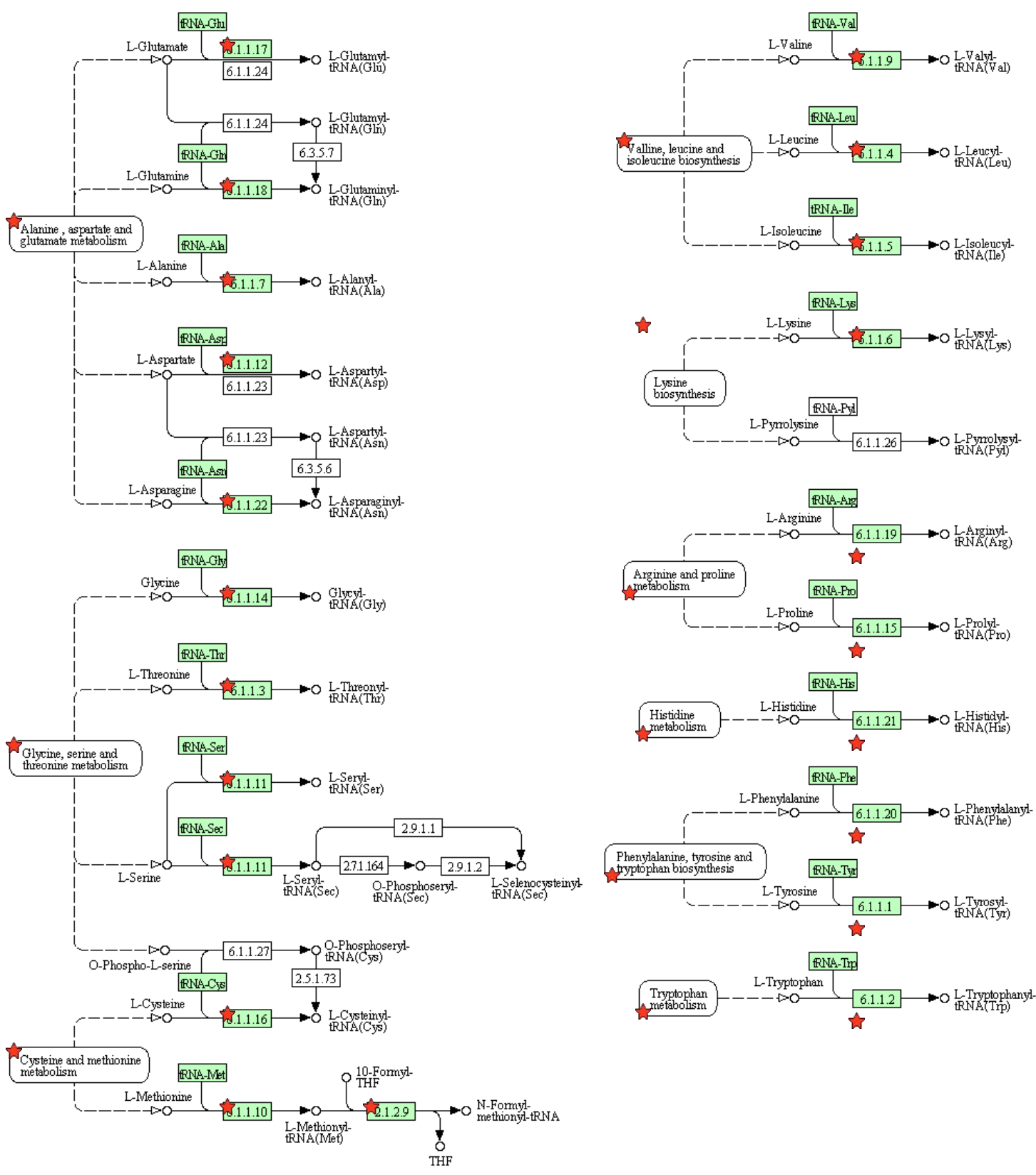
Pathway: Aminoacyl-tRNA biosynthesis

Pathway information generated by KEGG.

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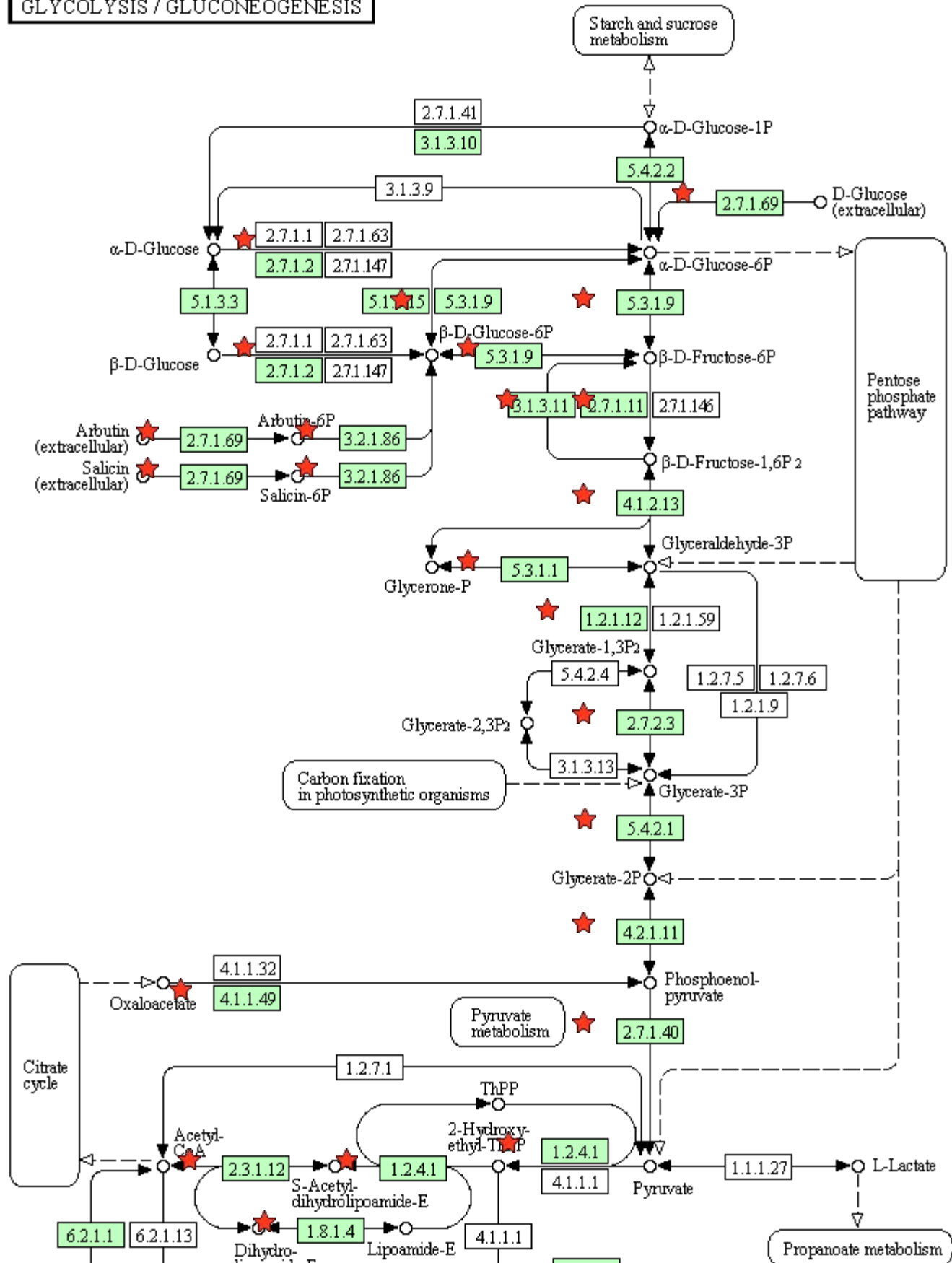
AMINOACYL-tRNA BIOSYNTHESIS

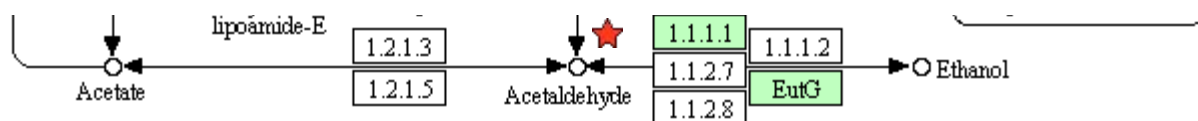


List genes are shown in red

DAVID Gene Name
Alanyl-tRNA synthetase
Arginyl-tRNA synthetase
Asparaginyl-tRNA synthetase: Regulatory protein asnC
Aspartyl-tRNA synthetase
Cysteinyl-tRNA synthetase
Glutaminyl-tRNA synthetase
Glutamyl-tRNA synthetase
Glycyl-tRNA synthetase beta subunit
Histidyl-tRNA synthetase
Isoleucyl-tRNA synthetase
Leucyl-tRNA synthetase
Lysyl-tRNA synthetase: Lysyl-tRNA synthetase, heat inducible
Lysyl-tRNA synthetase: Lysyl-tRNA synthetase, heat inducible
Methionyl-tRNA formyltransferase
Methionyl-tRNA synthetase
Phenylalanyl-tRNA synthetase alpha chain
Phenylalanyl-tRNA synthetase beta chain
Prolyl-tRNA synthetase
Putative lysyl-tRNA synthetase
Seryl-tRNA synthetase
Threonyl-tRNA synthetase
Tryptophanyl-tRNA synthetase
Tyrosyl-tRNA synthetase
Valyl-tRNA synthetase

GLYCOLYSIS / GLUCONEOGENESIS





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List genes are shown in red

DAVID Gene Name
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
2,3-bisphosphoglycerate-independent phosphoglycerate mutase
6-phospho-beta-glucosidase ascB
6-phospho-beta-glucosidase bglA
6-phospho-beta-glucosidase bglB
6-phospho-beta-glucosidase
6-phosphofructokinase isozyme 2
6-phosphofructokinase; 6-phosphofructokinase isozyme 1
Acetyl-coenzyme A synthetase
Aldehyde-alcohol dehydrogenase
Aldose 1-epimerase
Dihydrolipoyl dehydrogenase
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
Enolase
Ethanolamine utilization protein eutG
Fructose-1,6-bisphosphatase class 1
Fructose-1,6-bisphosphatase class 2
Fructose-bisphosphate aldolase class 1
Fructose-bisphosphate aldolase class 2
Glucokinase
Glucose-1-phosphatase
Glucose-6-phosphate isomerase
Glucose-specific phosphotransferase enzyme IIA component
Glyceraldehyde-3-phosphate dehydrogenase A
PTS system arbutin-, cellobiose-, and salicin-specific EIIBC component
PTS system glucose-specific EIICB component
PTS system maltose- and glucose-specific EIICB component
Phosphoenolpyruvate carboxykinase [ATP]
Phosphoglucomutase
Phosphoglycerate kinase
Probable phosphoglycerate mutase gpmB
Pyruvate dehydrogenase E1 component
Pyruvate kinase I; Pyruvate kinase
Pyruvate kinase II; Pyruvate kinase
S-(hydroxymethyl)glutathione dehydrogenase
Triosephosphate isomerase

[DNA polymerase III subunit delta'](#)
[DNA polymerase III subunit epsilon](#)
[DNA polymerase III subunit psi](#)
[DNA polymerase III subunit tau](#)
[DNA polymerase III subunit theta](#)
[DNA-directed RNA polymerase subunit alpha](#)
[DNA-directed RNA polymerase subunit beta](#)
[DNA-directed RNA polymerase subunit omega](#)
[DNA-directed RNA polymerase: DNA-directed RNA polymerase subunit beta'](#)
[Deoxycytidine triphosphate deaminase](#)
[Deoxyuridine 5'-triphosphate nucleotidohydrolase](#)
[Dihydroorotate](#)
[Dihydroorotate dehydrogenase](#)
[ECs5191: ECP_4467: ECSE_4519: EcSMS35_4692: ECUMN_4750: Z5824: EcolC_3793: ECS88_4807: E2348C_4544: EC55989_4773: ECDH10B_4408: ECED1_5072: ECH74115_5730: ECIAI1_4447: b4213: ECIAI39_4685: UTI89_C4822: EcHS_A4467: APECO1_2173: EcE24377A_4783](#)
[Multifunctional protein surE](#)
[Nucleoside diphosphate kinase](#)
[Orotate phosphoribosyltransferase](#)
[Orotidine 5'-phosphate decarboxylase](#)
[Polyribonucleotide nucleotidyltransferase](#)
[Protein mazG](#)
[Protein ushA](#)
[Purine nucleoside phosphorylase deoD-type](#)
[Pyrimidine-specific ribonucleoside hydrolase rihB](#)
[Ribonucleoside-diphosphate reductase 1 subunit beta](#)
[Ribonucleoside-diphosphate reductase 2 subunit beta](#)
[Ribonucleoside-diphosphate reductase: Ribonucleoside-diphosphate reductase 1 subunit alpha](#)
[Ribonucleoside-diphosphate reductase: Ribonucleoside-diphosphate reductase 2 subunit alpha](#)
[Thioredoxin reductase](#)
[Thymidine kinase](#)
[Thymidine phosphorylase](#)
[Thymidylate kinase](#)
[Thymidylate synthase](#)
[UPF0207 protein yfbR: 5'-nucleotidase yfbR](#)
[Uracil phosphoribosyltransferase](#)
[Uridine kinase](#)
[Uridine phosphorylase](#)
[Uridylate kinase](#)

Supplemental Figure S2 F

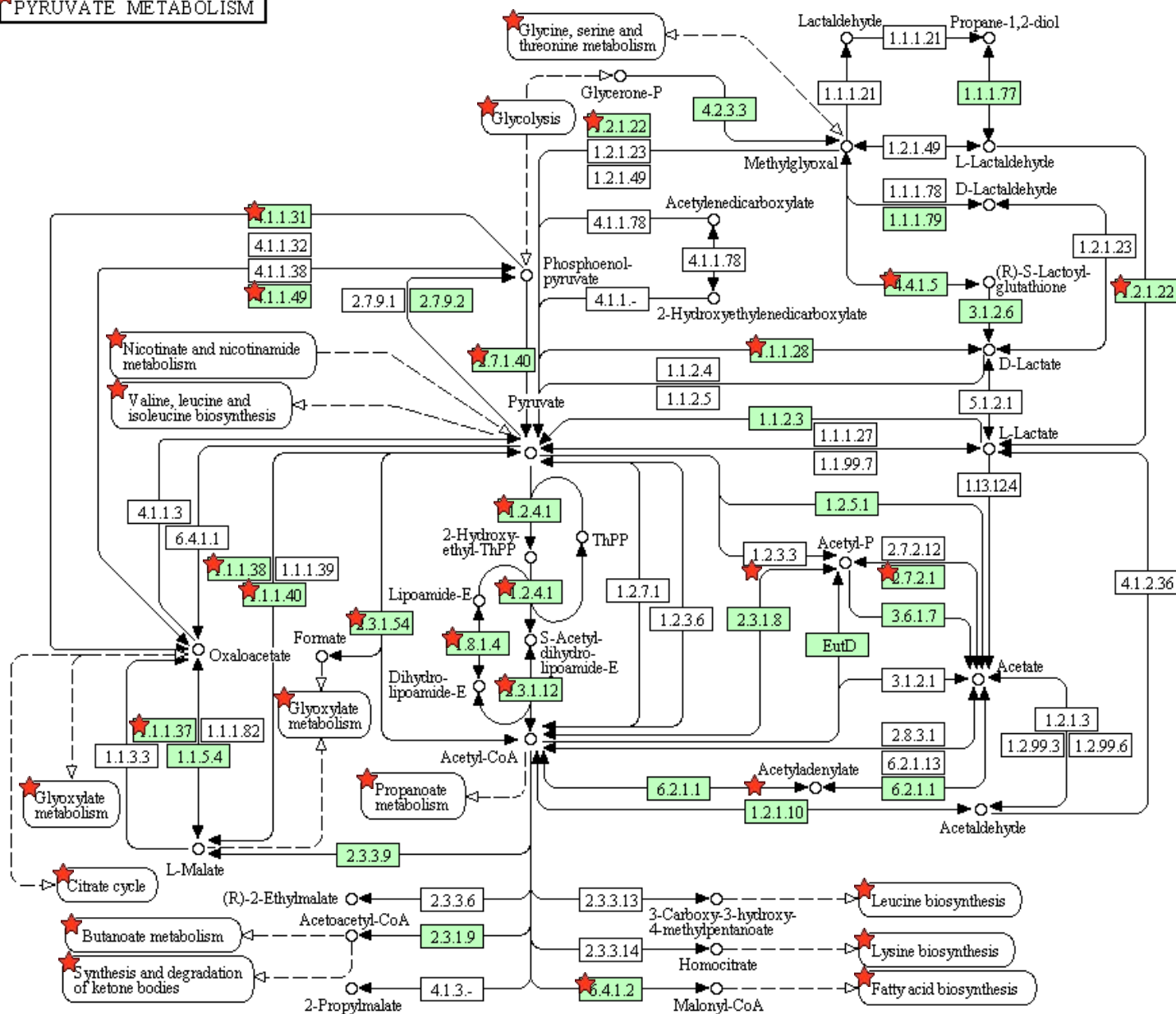
Pathway: Pyruvate metabolism

Pathway information generated by [KEGG](http://www.kegg.jp/).

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★ PYRUVATE METABOLISM



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List genes are shown in red

DAVID Gene Name
Acetate kinase
Acetyl-CoA acetyltransferase
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
Acetyl-coenzyme A synthetase
Acylphosphatase
Aldehyde-alcohol dehydrogenase
Biotin carboxyl carrier protein of acetyl-CoA carboxylase
Biotin carboxylase
D-lactate dehydrogenase
D-lactate dehydrogenase
Dihydrolipoyl dehydrogenase
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
Ethanolamine utilization protein eutE
Formate acetyltransferase 1

Formate acetyltransferase 2
Glyoxylate/hydroxypyruvate reductase A
Hydroxyacylglutathione hydrolase
Keto-acid formate acetyltransferase
L-lactate dehydrogenase [cytochrome]
Lactaldehyde dehydrogenase
Lactaldehyde reductase
Lactoylglutathione lyase
Malate dehydrogenase
Malate synthase A: Malate synthase
Malate synthase G
Malate:quinone oxidoreductase: Probable malate:quinone oxidoreductase
Methylglyoxal synthase
NAD-dependent malic enzyme
NADP-dependent malic enzyme
Phosphate acetyltransferase
Phosphoenolpyruvate carboxykinase [ATP]
Phosphoenolpyruvate carboxylase
Phosphoenolpyruvate synthase
Probable acetyl-CoA acetyltransferase
Putative formate acetyltransferase 3
Pyruvate dehydrogenase E1 component
Pyruvate dehydrogenase [cytochrome]
Pyruvate kinase I: Pyruvate kinase
Pyruvate kinase II: Pyruvate kinase
Uncharacterized oxidoreductase ybiC

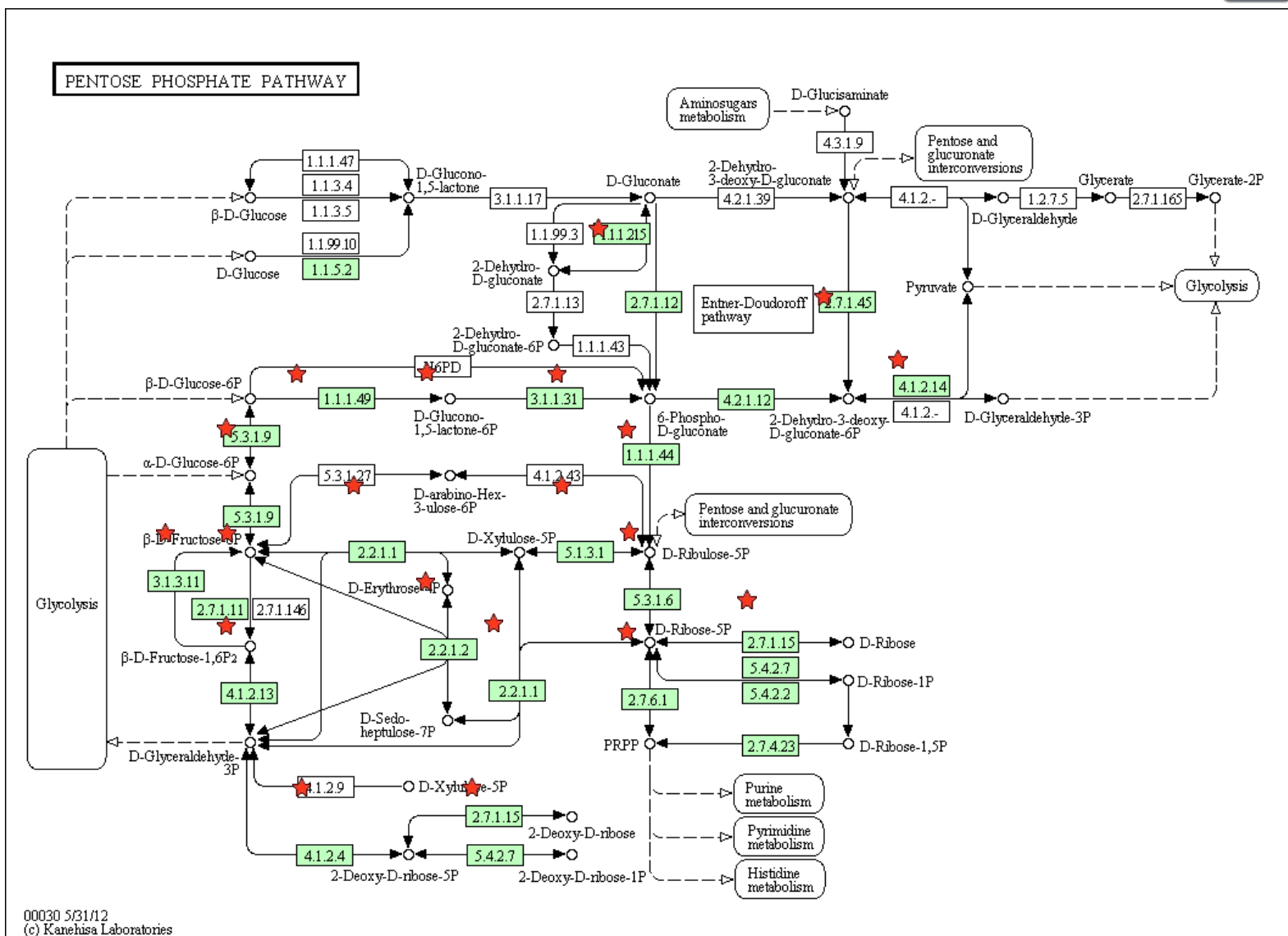
Supplemental Figure S1 G

Pathway: Pentose phosphate pathway

Pathway information generated by KEGG.

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DAVID Gene Name
2-dehydro-3-deoxygluconokinase
6-phosphofruktokinase isozyyme 2
6-phosphofruktokinase: 6-phosphofruktokinase isozyyme 1
6-phosphogluconate dehydrogenase, decarboxylating
6-phosphogluconolactonase
ATP-binding protein phnN
Deoxyribose-phosphate aldolase
Fructose-1,6-bisphosphatase class 1
Fructose-1,6-bisphosphatase class 2
Fructose-bisphosphate aldolase class 1
Fructose-bisphosphate aldolase class 2
Glucose-6-phosphate 1-dehydrogenase
Glucose-6-phosphate isomerase
Glyoxylate/hydroxypyruvate reductase B
KHG/KDPG aldolase
Phosphoglucomutase
Phosphogluconate dehydratase
Phosphopentomutase
Quinoprotein glucoase dehydrogenase
Ribokinase
Ribose-5-phosphate isomerase A
Ribose-5-phosphate isomerase B
Ribose-phosphate pyrophosphokinase
Ribulose-phosphate 3-epimerase
Thermoresistant gluconokinase
Thermosensitive gluconokinase
Transaldolase A: Transaldolase
Transaldolase B: Transaldolase
Transketolase 1

[Transketolase 2](#)

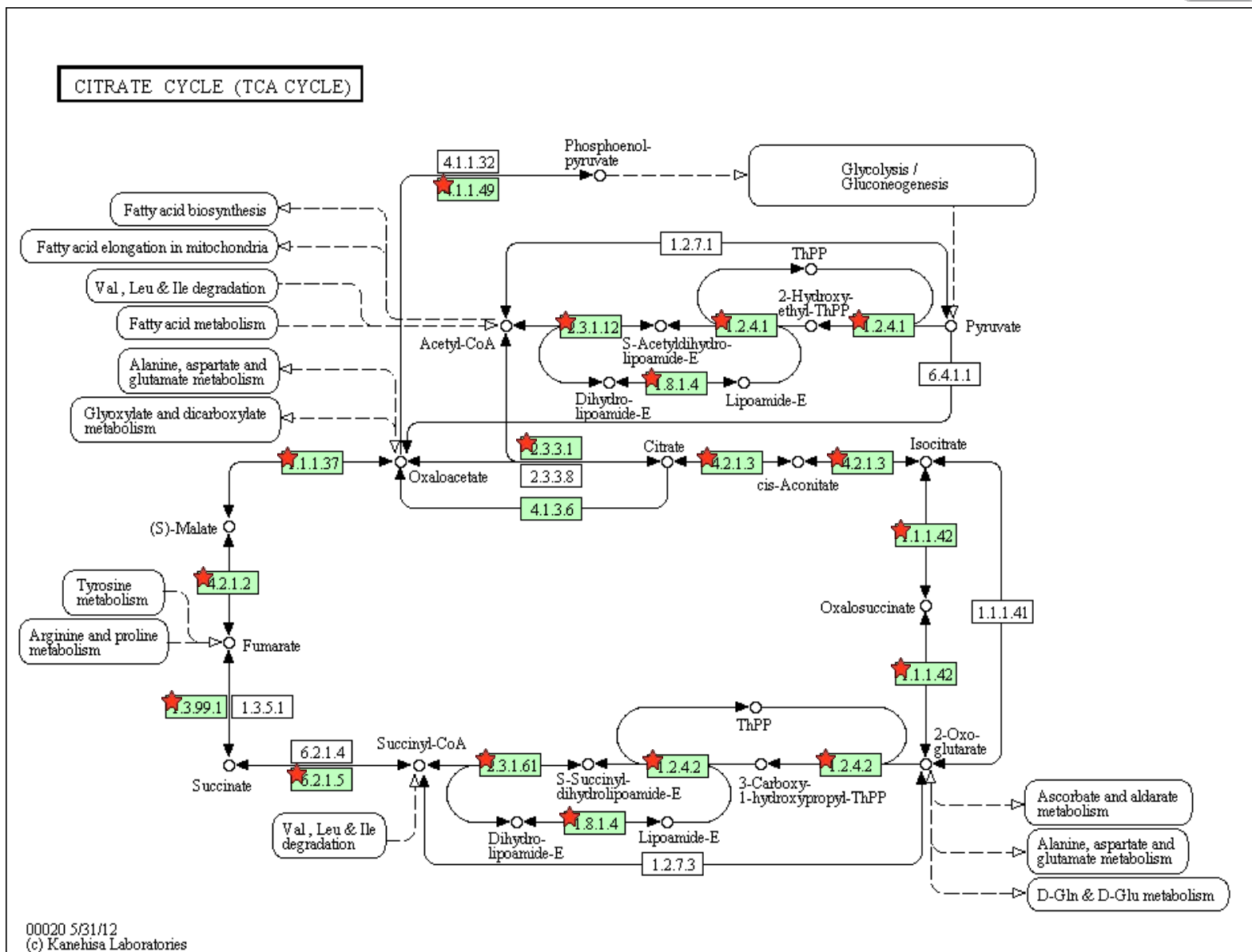
Supplemental Figure S2 H

Pathway: Citrate cycle (TCA cycle)

Pathway information generated by [KEGG](http://www.kegg.jp/).

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DAVID Gene Name
2-oxoglutarate dehydrogenase E1 component.
Aconitate hydratase 1.
Aconitate hydratase 2.
Citrate lyase acyl carrier protein.
Citrate lyase alpha chain.
Citrate lyase subunit beta.
Citrate synthase.
Dihydrolipoyl dehydrogenase.
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex.
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex.
Fumarate hydratase class I, aerobic.
Fumarate hydratase class I, anaerobic.
Fumarate hydratase class II.
Fumarate reductase flavoprotein subunit.
Fumarate reductase subunit C.
Fumarate reductase subunit D.
Isocitrate dehydrogenase [NADP].
Malate dehydrogenase.
Phosphoenolpyruvate carboxykinase [ATP].
Pyruvate dehydrogenase E1 component.
Succinate dehydrogenase cytochrome b556 subunit.
Succinate dehydrogenase flavoprotein subunit.
Succinate dehydrogenase hydrophobic membrane anchor subunit.

Succinate dehydrogenase iron-sulfur subunit
Succinyl-CoA ligase [ADP-forming] subunit alpha
Succinyl-CoA ligase [ADP-forming] subunit beta
Uncharacterized oxidoreductase ybiC
Uncharacterized protein ybh

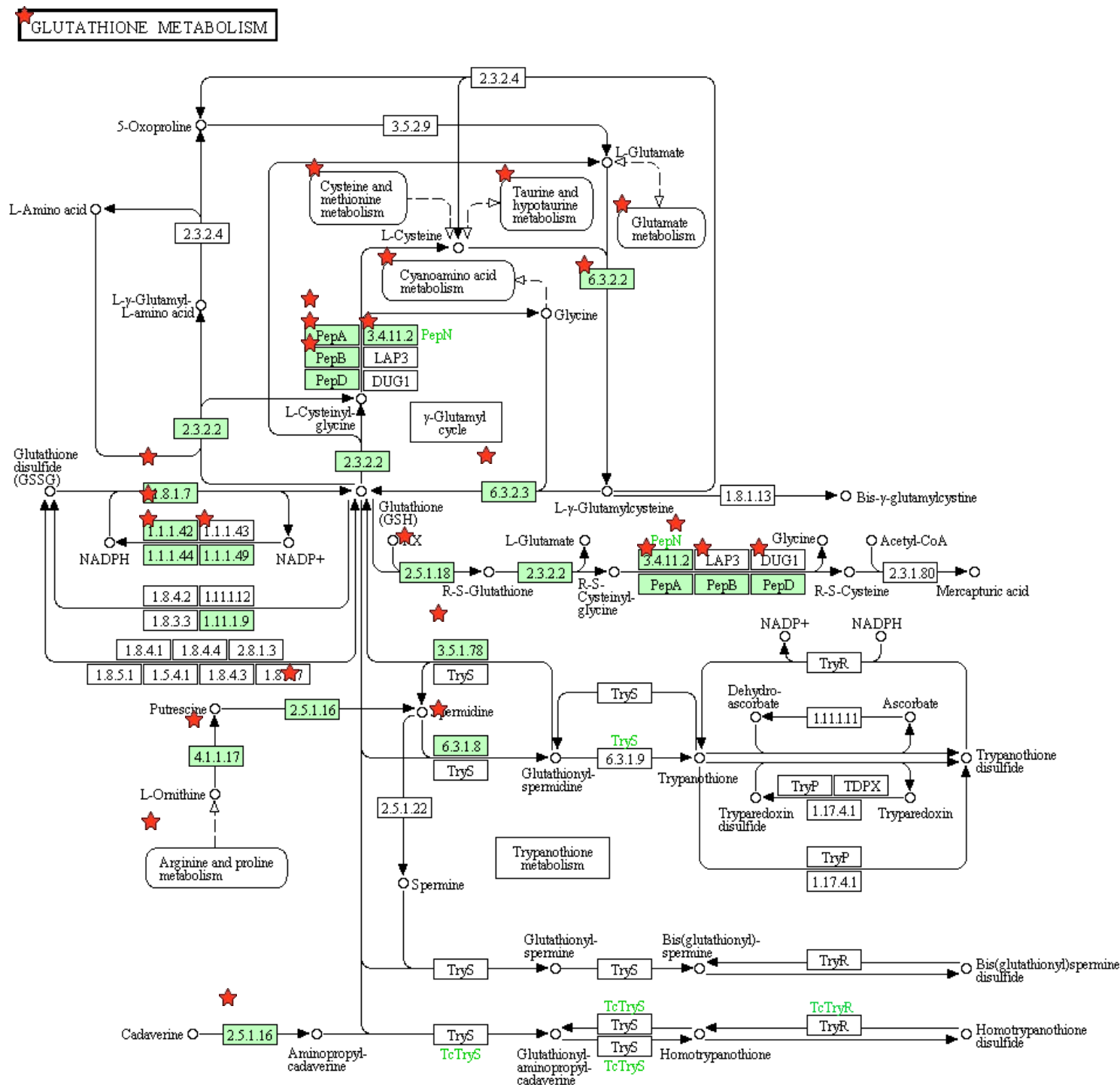
Supplemental Figure S2 I

Pathway: Glutathione metabolism

Pathway information generated by [KEGG](#).

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List genes are shown in red

DAVID Gene Name
6-phosphogluconate dehydrogenase, decarboxylating
Aminoacyl-histidine dipeptidase
Aminopeptidase N
EC1A139 3484: EC1A1 3137: EC55989 3404: ECUMN 3472: ECS88 3370: ECDH10B 3165: ECED1 3638
Gamma-glutamyltranspeptidase
Glucose-6-phosphate 1-dehydrogenase
Glutamate--cysteine ligase
Glutathione S-transferase
Glutathione reductase
Glutathione synthetase

Isocitrate dehydrogenase [NADP]
Ornithine decarboxylase, constitutive
Ornithine decarboxylase, inducible
Peptidase B
Probable cytosol aminopeptidase: Cytosol aminopeptidase
Spermidine synthase
Vitamin B12 transport periplasmic protein btuE: Glutathione peroxidase

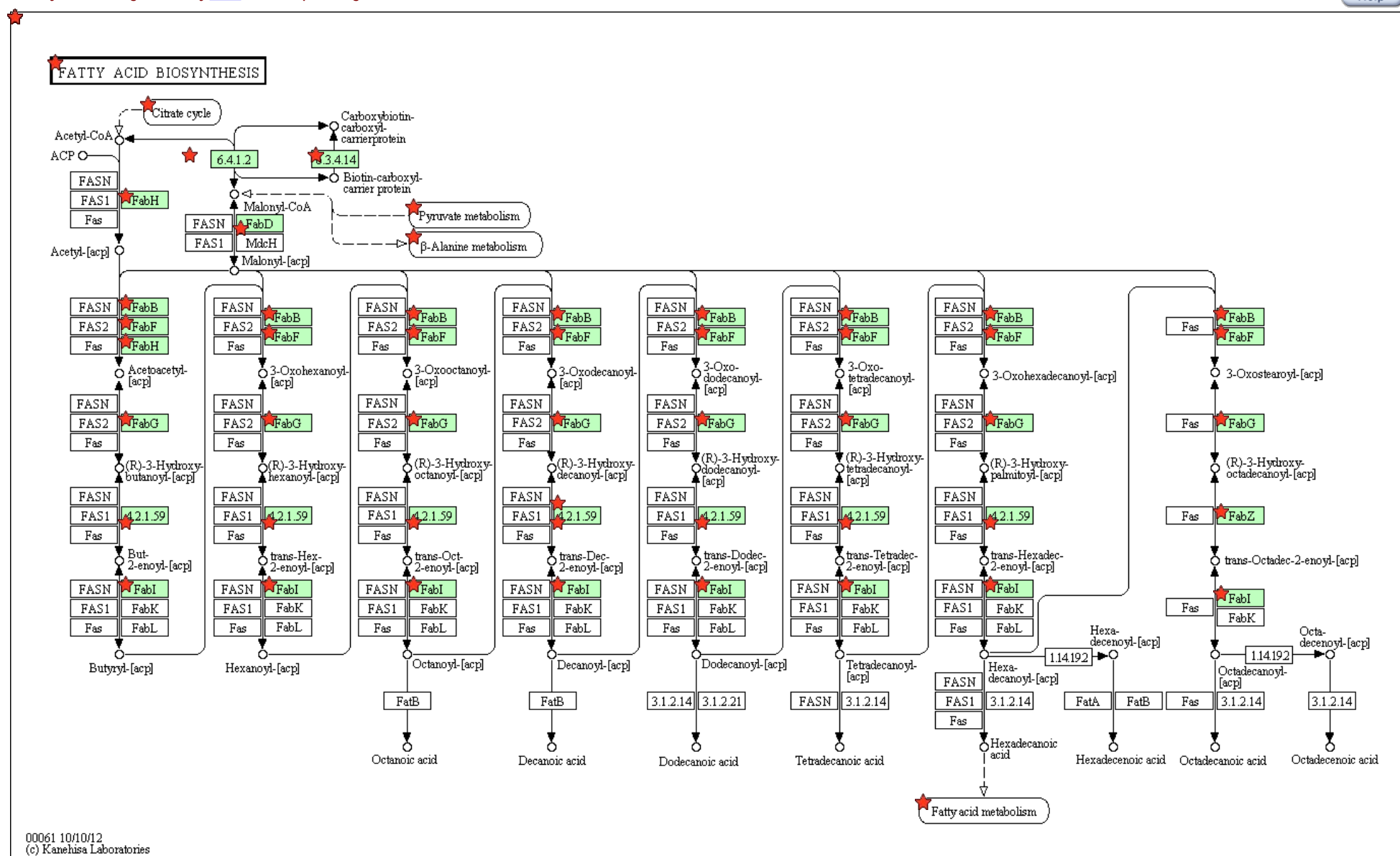
Supplemental Figure S2 J

Pathway: Fatty acid biosynthesis

Pathway information generated by [KEGG](#).

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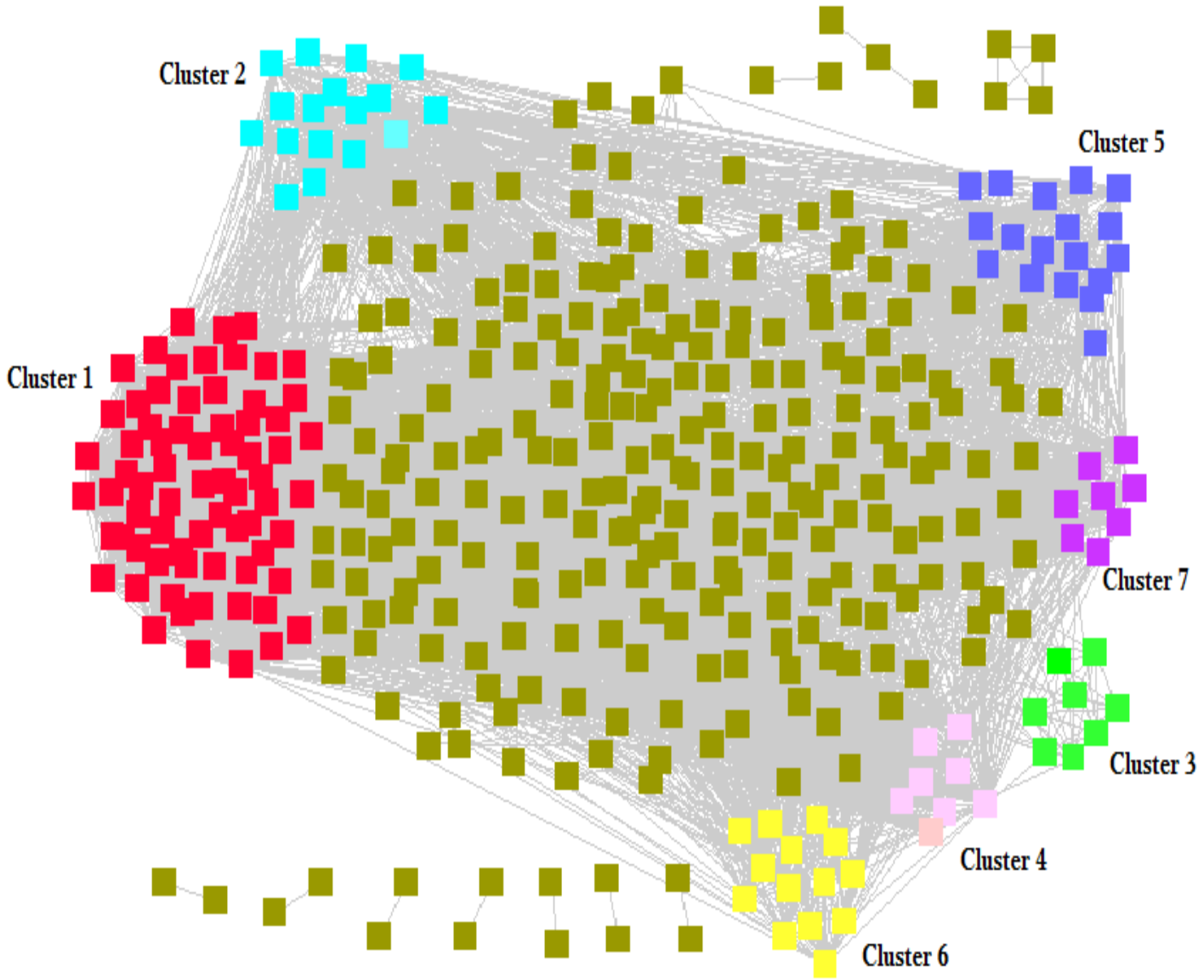
List genes are shown in red

DAVID Gene Name
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase
3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
3-oxoacyl-[acyl-carrier-protein] reductase
3-oxoacyl-[acyl-carrier-protein] synthase 1
3-oxoacyl-[acyl-carrier-protein] synthase 2
3-oxoacyl-[acyl-carrier-protein] synthase 3
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
Biotin carboxyl carrier protein of acetyl-CoA carboxylase
Biotin carboxylase

[Enoyl-\[acyl-carrier-protein\] reductase \[NADH\]](#)

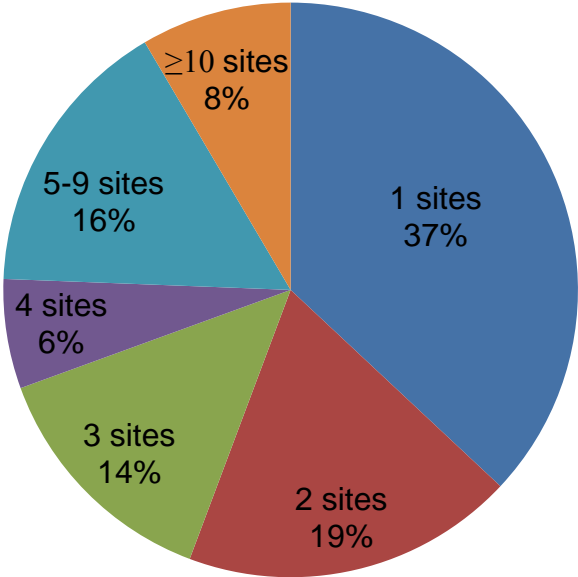
[Malonyl CoA-acyl carrier protein transacylase](#)

Supplemental Figure S3

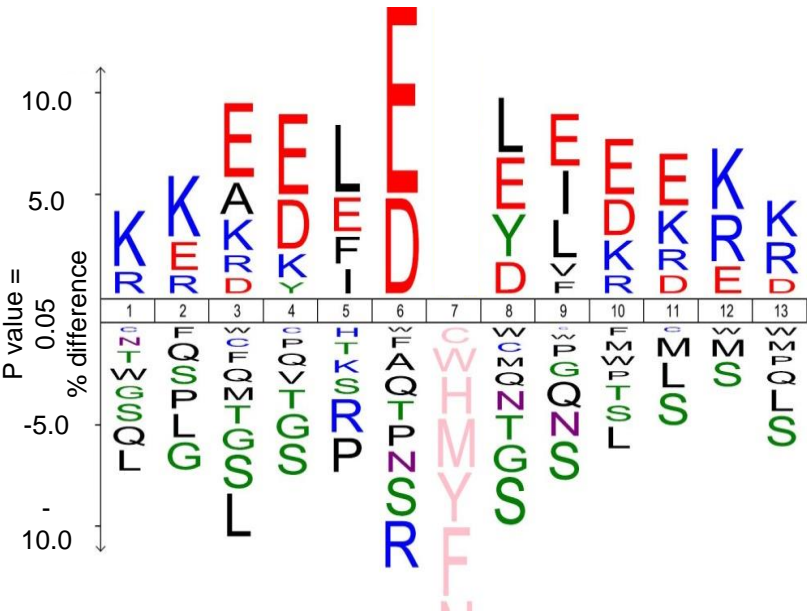


Supplemental Figure S4

A

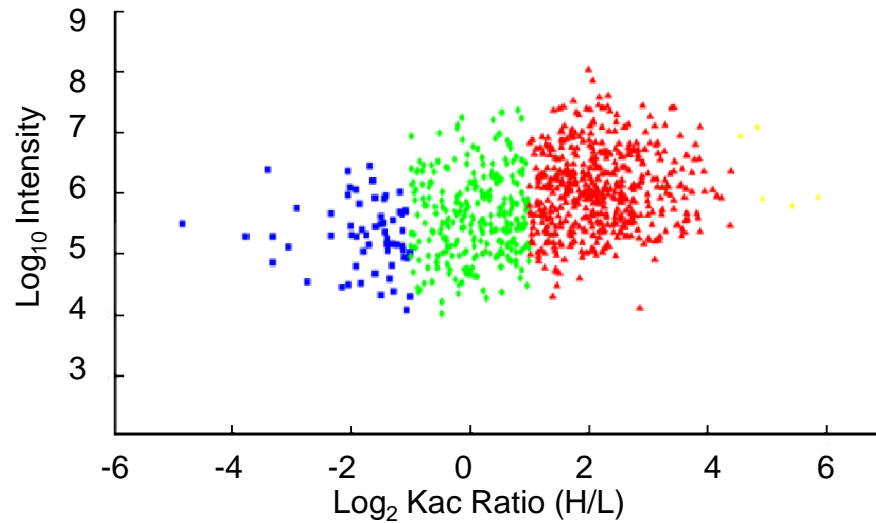


B

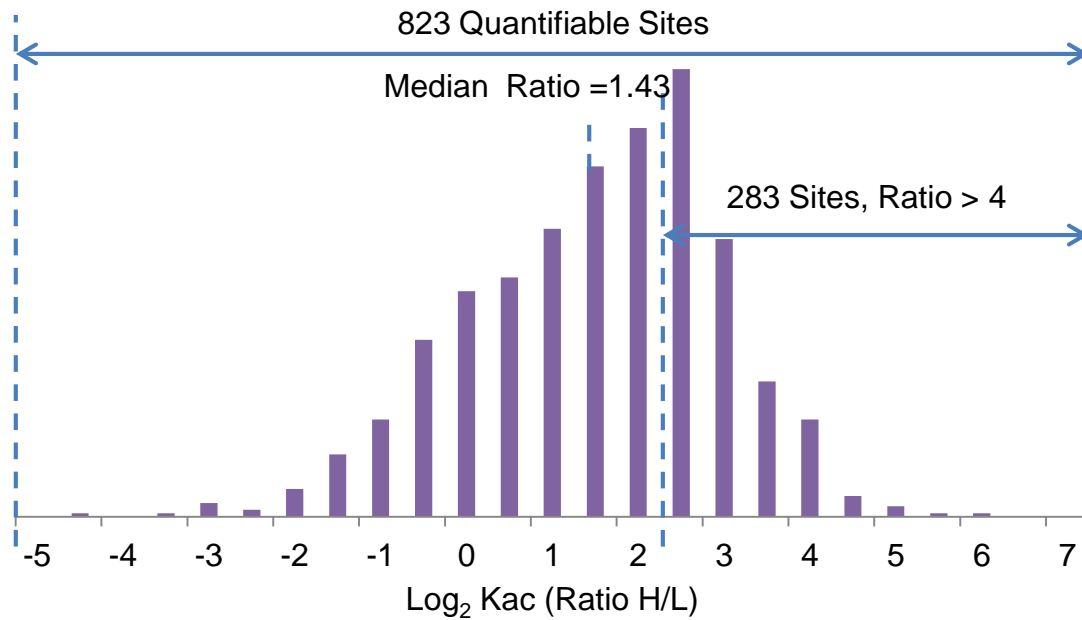


Supplemental Figure S5

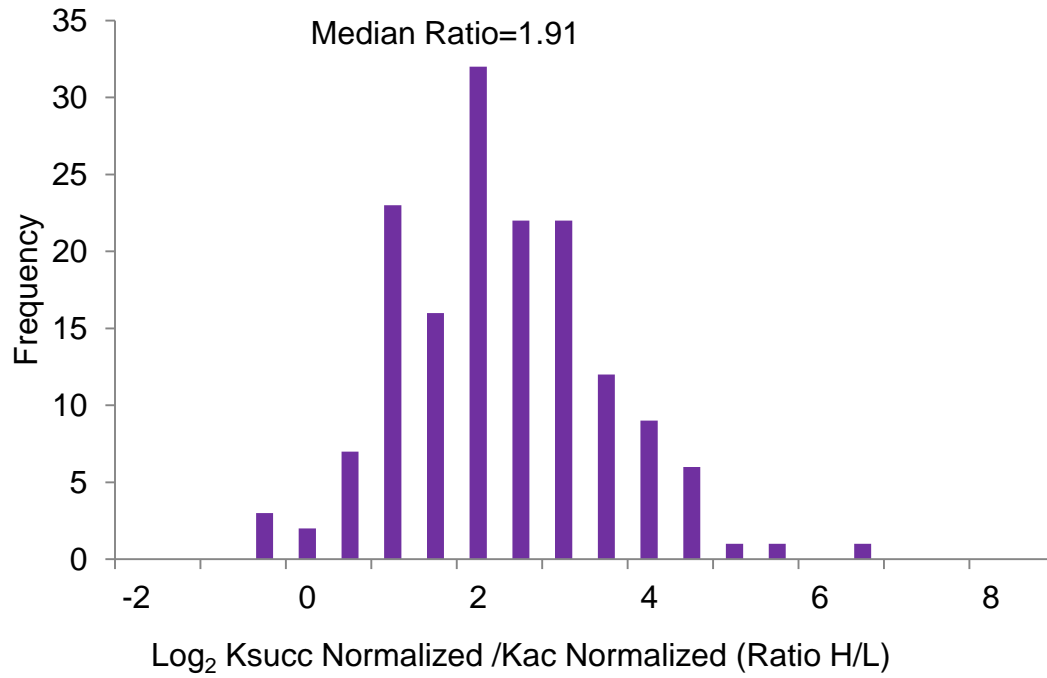
A



B



Supplemental Figure S6



Supplemental Figure S7

