## Key to deletion results

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|---|---|
| ORF | ORF name |
| Name | Gene name |
| Annotation | Gene annotation (from SGD) |
| Ess sim | Essential (YPD) simulation |
| Ess call | Essential call (FP/TN) |
| Slow sim | Slow growth simulation |
| Slow exp | Slow growth experimental [Giaever02] |
| Slow call | Slow growth call (FP/TN) |
| MMD sim | Glucose minimal media simulation |
| MMD exp | MMD experimental (1=normal growth, 0=retarded growth) |
| MMD ave | MMD average of experimental scores |
| MMD call | MMD call (FP/FN/TP/TN) |
| YPGal sim | YP galactose simulation |
| YPGal exp | YPGal experimental (1=normal growth, 0=retarded growth) |
| YPGal ave | YPGal average of experimental scores |
| YPGal call | YPGal call (FP/FN/TP/TN) |
| YPD sim | YPD simulation |
| YPD exp | YPD experimental |
| YPD call | YPD call (FP/FN/TP/TN) |
| YPDGE sim | YPDGE simulation |
| YPDGE exp | YPDGE experimental |
| YPDGE call | YPDGE call (FP/FN/TP/TN) |
| YPG sim | YPG simulation |
| YPG exp | YPG experimental |
| YPG call | YPG call (FP/FN/TP/TN) |
| YPE sim | YPE simulation |
| YPE exp | YPE experimental |
| YPE call | YPE call (FP/FN/TP/TN) |
| YPL sim | YPL simulation |
| YPL exp | YPL experimental |
| YPL call | YPL call (FP/FN/TP/TN) |
| Class | Primary source for false prediction(s) |
| Explanation | Detailed explanation for false prediction(s) |
| Forster et al | Result in Forster et al. study - only false predictions are listed |

## Abbreviations for sources for false predictions

| | |
|---|---|
| Acc | Accumulation of a toxic intermediate |
| Bio | Problems with in silico biomass constitution |
| Den | Dead end in the in silico model |
| Dis | Discrepancy in experimental data |
| Iso | Problems with in silico gene-protein-reaction associations |
| Med | Problems with in silico media composition |
| Mod | Problems with in silico model structure |
| Oth | Involvement of the gene in non-metabolic processes |
| Reg | Missing transcriptional regulation |
| Unk | Unknown source for false prediction |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YMR056C | AAC1 | ADP/ATP translocator | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNL141W | AAH1 | Adenine aminohydrolase (adenine deaminase) | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YKL106W | AAT1 | Aspartate aminotransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.05 | TP | 1.08 | 0.98 | TP | 1.1 | 0.97 | TP | 1.09 | 0.87 | TP | 1.11 | 0.82 | TP | 1.1 | 0.84 | TP | NA | NA | NA |
| YLR027C | AAT2 | Aspartate aminotransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.96 | TP | 1 | 1 | 0 | TP | 1.08 | 0.93 | TP | 1.1 | 0.83 | FP | 1.08 | 0.74 | FP | 1.11 | 0.65 | FP | 1.1 | 0.87 | TP | Unk | The model correctly predicts that the effect of the deletion is larger on non-fermentable carbon sources, but the predicted change in growth rate is too small for the slow growth criterion. The model does not predict higher growth of lactate than on other non-fermentable carbon sources though. | NA |
| YNR033W | ABZ1 | Aminodeoxychorismate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YGR037C | ACB1 | Acyl-CoA-binding protein (ACBP)/diazepam binding inhibitor (DBI)/endozepine (EP) | NA | NA | NA | NA | NA | 0 | 1 | 0.23 | FN | 0 | 1 | -0.04 | FN | 0 | 0.93 | FN | 0 | 0.97 | FN | 0 | 0.94 | FN | 0 | 0.95 | FN | 0 | 0.94 | FN | Unk | Product of ACB1 is part of FAS complex; involved in termination of fatty acid synthesis and transport of newly synthesized acyl-CoA esters from the fatty acid synthetase to acyl-CoA-consuming processes, may also transport medium- and long-chain acyl CoA esters [MIPS]; since enzymatic mechanism is unknown and transport function is not well defined, may want to remove from FAS complex. | NA |
| YNR016C | ACC1 | Acetyl CoA carboxylase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YBL015W | ACH1 | Acetyl CoA hydrolase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 0.99 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.05 | TP | 1.1 | 1.04 | TP | 0.96 | 1.06 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YLR304C | ACO1 | Aconitase | NA | NA | 1 | 3.6 | FP | 1 | 1 | 0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.86 | FP | 1.1 | 0.75 | FP | 1.11 | 0.59 | FP | 1.12 | 0.52 | FP | 1.11 | 0.6 | FP | Iso | YJL200C codes for an isozyme for Aco1p, but Aco1p is probably the major isoform. | NA |
| YKL192C | ACP1 | Acyl carrier protein | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Acp1p used in synthesis of fatty-acyl ACPs, which are not required in the model. | NA |
| YAL054C | ACS1 | Acetyl CoA synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 0.98 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR153C | ACS2 | Acetyl CoA synthetase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | FP |
| YAR015W | ADE1 | Phosphoribosyl amino imidazolesuccinocarbozamide synthetase | NA | NA | NA | NA | NA | 0 | 1 | 0.02 | FN | 1 | 1 | 0 | TP | 1.08 | 0.97 | TP | 1.1 | 0.93 | TP | 1.11 | 0.99 | TP | 1.12 | 0.97 | TP | 1.11 | 0.95 | TP | Med | Should be an adenine auxotroph [SGD] - should not grow normally on minimal media. | NA |
| YNL220W | ADE12 | Adenylosuccinate synthetase | NA | NA | 1 | 4.5 | FP | 0 | 1 | -0.01 | TN | 1 | 1 | 0 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Med | FP for rich media - TN for MMD. There appears to be an extra component in the in silico rich medium. | NA |
| YLR359W | ADE13 | Adenylosuccinate lyase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Med | Null mutant is an adenine auxotroph [MIPS]. The deletion is lethal if adenine is removed from the rich media. | NA |
| YLR028C | ADE16 | 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.05 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YMR120C | ADE17 | 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGR204W | ADE3 | C1-tetrahydrofolate synthase | NA | NA | NA | NA | NA | 0 | 1 | 2.08 | TN | 0.99 | 1 | 0 | TP | 1.07 | 1.01 | TP | 1.09 | 0.99 | TP | 1.06 | 0.99 | TP | 1.12 | 1 | TP | 1.06 | 1 | TP | NA | Weak false negative | FN |
| YMR300C | ADE4 | Phosphoribosylpyrophosphate amidotransferase | NA | NA | NA | NA | NA | 0 | 0 | 4.2 | TN | 1 | 1 | -0.06 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YGL234W | ADE5, | Aminoimidazole ribotide synthetase\|glycinamide ribotide synthetase | NA | NA | NA | NA | NA | 0 | 1 | 0.95 | FN | 1 | 1 | -0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 0.99 | TP | Med | Should be an adenine auxotroph [SGD] - should not grow normally on minimal media. | NA |
| YGR061C | ADE6 | 5'-phosphoribosylformyl glycinamidine synthetase | NA | NA | NA | NA | NA | 0 | 0 | 5.08 | TN | 1 | 1 | -0.02 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YDR408C | ADE8 | Glycinamide ribotide transformylase | NA | NA | NA | NA | NA | 0 | 1 | 1.1 | TN | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | Weak false negative | NA |
| YOL086C | ADH1 | Alcohol dehydrogenase | NA | NA | 1 | 10.1 | FP | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 0.76 | FP | 1.1 | 0.87 | TP | 1.11 | 1.12 | TP | 1.12 | 1.09 | TP | 1.11 | 1.15 | TP | Reg | Most likely a regulatory effect as this may be the only isozyme (out of five) active under severely glucose repressed conditions. | NA |
| YMR303C | ADH2 | Alcohol dehydrogenase II | NA | NA | NA | NA | NA | 1 | 1 | 0.13 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YMR083W | ADH3 | Alcohol dehydrogenase isoenzyme III | NA | NA | NA | NA | NA | 1 | 1 | 1.2 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.98 | TP | 1.1 | 0.97 | TP | 1.11 | 0.97 | TP | 1.12 | 0.93 | TP | 1.11 | 0.95 | TP | NA | NA | NA |
| YGL256W | ADH4 | Alcohol dehydrogenase isoenzyme IV | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YBR145W | ADH5 | Alcohol dehydrogenase isoenzyme V | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YDR226W | ADK1 | Adenylate kinase | NA | NA | 0 | 9.7 | TN | 0 | 1 | 0 | TN | 0 | 1 | -0.03 | TN | 0 | 0.7 | TN | 0 | 0.75 | TN | 0 | 0.74 | TN | 0 | 0.72 | TN | 0 | 0.76 | TN | NA | NA | FN |
| YER170W | ADK2 | Adenylate kinase\|mitochondrial GTP:AMP phosphotransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YJR105W | ADO1 | Adenosine kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.73 | TP | 1 | 1 | 0 | TP | 1.08 | 0.79 | FP | 1.1 | 0.8 | FP | 1.11 | 0.94 | TP | 1.12 | 0.92 | TP | 1.11 | 0.94 | TP | Unk | There is an alternative pathway involving Pnp1p that can substitute for the function of this adenosine kinase. This activity of Pnp1p does not seem to have been established conclusively in the literature. | NA |
| YCL025C | AGP1 | Amino acid permease | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YFL055W | AGP3 | The acronym may be misleading. AGP3 has not been shown to be a general amino acid permease with broad substrate specificity | NA | NA | NA | NA | NA | 1 | 1 | 0.12 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 0.99 | TP | 1.12 | 1.03 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YOR335C | ALA1 | Cytoplasmic alanyl-tRNA synthetase gene | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model. | NA |
| YMR170C | ALD2 | Aldeyhde dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.08 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.99 | TP | 1.1 | 1 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YMR169C | ALD3 | Aldehyde dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YOR374W | ALD4 | Aldehyde dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YER073W | ALD5 | Aldehyde dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.07 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YPL061W | ALD6 | Aldehyde dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.1 | TP | 1 | 1 | -0.04 | TP | 1.07 | 0.86 | FP | 1.08 | 0.91 | TP | 1.11 | 1 | TP | 1.06 | 0.93 | TP | 1.11 | 0.98 | TP | Unk | The model uses a mitochondrial acetaldehyde dehydrogenase in the deletion strain. In vivo this activity cannot fully compensate for the cytoplasmic activity. | NA |
| YNL270C | ALP1 | Basic amino acid permease | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 1.01 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YML035C | AMD1 | AMP deaminase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 1.02 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YDR242W | AMD2 | Amidase (putative) | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1.03 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPR128C | ANT1 | Adenine nucleotide transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.99 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YCL050C | APA1 | Diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase I | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.06 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YDR530C | APA2 | 5',5'''-P-1,P-4-tetraphosphate phosphorylase II | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YML022W | APT1 | Adenine phosphoribosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | 1.41 | TP | 1 | 1 | 0 | TP | 1.08 | 0.96 | TP | 1.1 | 0.95 | TP | 1.11 | 0.96 | TP | 1.12 | 0.96 | TP | 1.11 | 0.96 | TP | NA | NA | NA |
| YDR441C | APT2 | Similar to adenine phosphoribosyltransferase; appears to be a nonfunctional pseudogene | NA | NA | NA | NA | NA | 1 | 1 | 0.11 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.99 | TP | 1.1 | 1 | TP | 1.11 | 0.97 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YBR149W | ARA1 | D-arabinose dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 1 | TP | 1.12 | 0.98 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YOL058W | ARG1 | Arginosuccinate synthetase | NA | NA | NA | NA | NA | 0 | 1 | 5.51 | TN | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.1 | 1.02 | TP | NA | Weak false negative | NA |
| YJL071W | ARG2 | Acetylglutamate synthase | NA | NA | NA | NA | NA | 1 | 1 | 3.27 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1 | TP | 1.1 | 1.04 | TP | 1.11 | 1.05 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YJL088W | ARG3 | Ornithine carbamoyltransferase | NA | NA | NA | NA | NA | 0 | 1 | 2.1 | TN | 1 | 1 | -0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.05 | TP | 1.12 | 1.04 | TP | 1.1 | 1.04 | TP | NA | Weak false negative | NA |
| YHR018C | ARG4 | Argininosuccinate lyase | NA | NA | NA | NA | NA | 0 | 1 | 6.58 | TN | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.1 | 1.03 | TP | NA | Weak false negative | NA |
| YER069W | ARG5, | N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase | NA | NA | NA | NA | NA | 0 | 1 | 2.36 | TN | 1 | 1 | -0.06 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | Weak false negative | NA |
| YDR127W | ARO1 | 3-dehydroquinate dehydratase (3-dehydroquinase)\|3-dehydroquinate synthase\|epsp synthase\|pentafunctional arom polypeptide\|shikimate 5-dehydrogenase\|shikimate kinase | NA | NA | 1 | 10.5 | FP | 0 | 1 | -0.03 | TN | 1 | 1 | -0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.02 | TP | Med | FP for rich media - TN for MMD. There appears to be an extra component in the in silico rich medium. | NA |
| YDR380W | ARO10 | NA | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.04 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.09 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YGL148W | ARO2 | Chorismate synthase | NA | NA | NA | NA | NA | 0 | 1 | 5.13 | TN | 1 | 1 | -0.03 | TP | 1.08 | 0.98 | TP | 1.1 | 1 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.05 | TP | NA | Weak false negative | NA |
| YDR035W | ARO3 | DAHP synthase; a.k.a. phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited; phospho-2-keto-3-deoxyheptonate aldolase; 2-dehydro-3-deoxyphosphoheptonate aldolase; 3-deoxy-D-arabine-heptulosonate-7-phosphate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YBR249C | ARO4 | 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase isoenzyme | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YPR060C | ARO7 | Chorismate mutase | NA | NA | NA | NA | NA | 0 | 0 | 3.64 | TN | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YGL202W | ARO8 | Aromatic amino acid aminotransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 1.02 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YHR137W | ARO9 | Aromatic amino acid aminotransferase II | NA | NA | NA | NA | NA | 0 | 1 | 0.18 | FN | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | Iso | ARO8 should be able to complement ARO9 deletion on minimal media, but the gpr association might be wrong [Urrestarazu98]. | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YDL100C | ARR4 | Provides low levels of resistance to arsenicals | NA | NA | NA | NA | NA | 1 | 1 | 0.4 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.97 | TP | 1.1 | 0.96 | TP | 1.11 | 0.93 | TP | 1.12 | 0.91 | TP | 1.11 | 0.92 | TP | NA | NA | NA |
| YPR145W | ASN1 | Asparagine synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGR124W | ASN2 | Asparagine synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0.07 | TP | 1 | 1 | 0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YDR321W | ASP1 | Asparaginase I\|intracellular isozyme | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YPR026W | ATH1 | Acid trehalase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YBL099W | ATP1 | F1F0-ATPase alpha subunit | NA | NA | 0.91 | 4 | TN | 0.91 | 1 | 0 | TP | 0.82 | 1 | -0.03 | TP | 0.98 | 0.91 | TP | 0.24 | 0.81 | TN | 0.14 | 0.56 | TN | 0.16 | 0.49 | TN | 0.05 | 0.54 | TN | NA | NA | NA |
| YLR295C | ATP14 | ATP synthase subunit h | NA | NA | 0.91 | 4.7 | TN | 0.91 | 1 | 0 | TP | 0.82 | 1 | -0.01 | TP | 0.98 | 0.73 | FP | 0.24 | 0.59 | TN | 0.14 | 0.56 | TN | 0.16 | 0.52 | TN | 0.05 | 0.5 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YPL271W | ATP15 | ATP synthase epsilon subunit\|nuclear encoded | NA | NA | 0.91 | 9.5 | TN | 0.91 | 1 | -0.03 | TP | 0.82 | 1 | -0.03 | TP | 0.98 | 0.72 | FP | 0.24 | 0.69 | TN | 0.14 | 0.58 | TN | 0.16 | 0.54 | TN | 0.05 | 0.57 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YDL004W | ATP16 | ATP synthase delta subunit | 0.91 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | NA |
| YDR377W | ATP17 | ATP synthase subunit f | NA | NA | 0.91 | 3.3 | TN | 0.91 | 1 | -0.03 | TP | 0.82 | 1 | -0.04 | TP | 0.98 | 0.83 | FP | 0.24 | 0.78 | TN | 0.14 | 0.66 | TN | 0.16 | 0.66 | TN | 0.05 | 0.69 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YML081CA | ATP18 | ATP synthase associated protein | NA | NA | NA | NA | NA | 0.91 | 1 | -0.02 | TP | 0.82 | 1 | 0.15 | TP | 0.98 | 1.03 | TP | 0.24 | 0.96 | FN | 0.14 | 0.65 | TN | 0.16 | 0.63 | TN | 0.05 | 0.65 | TN | Med | This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. | NA |
| YJR121W | ATP2 | F(1)F(0)-ATPase complex beta subunit | NA | NA | NA | NA | NA | 0.91 | 1 | 0 | TP | 0.82 | 1 | -0.02 | TP | 0.98 | 0.86 | FP | 0.24 | 0.82 | TN | 0.14 | 0.51 | TN | 0.16 | 0.55 | TN | 0.05 | 0.53 | TN | Med | This is close enough to count as a correct prediction. With small changes in uptake rates this would be true negative. | NA |
| YPR020W | ATP20 | ATP synthase subunit g homolog | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 0.98 | TP | 1.11 | 0.94 | TP | 1.12 | 0.95 | TP | 1.11 | 0.94 | TP | NA | NA | NA |
| YPL078C | ATP4 | F(1)F(0)-ATPase complex subunit b | NA | NA | 0.91 | 4.1 | TN | 0.91 | 1 | 0.19 | TP | 0.82 | 1 | 0.15 | TP | 0.98 | 0.83 | FP | 0.24 | 0.77 | TN | 0.14 | 0.52 | TN | 0.16 | 0.51 | TN | 0.05 | 0.54 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YDR298C | ATP5 | ATP synthase subunit 5\|oligomycin sensitivity-conferring protein | NA | NA | 0.91 | 7.7 | TN | 0.91 | 1 | -0.03 | TP | 0.82 | 1 | -0.02 | TP | 0.98 | 0.75 | FP | 0.24 | 0.66 | TN | 0.14 | 0.53 | TN | 0.16 | 0.53 | TN | 0.05 | 0.57 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YKL016C | ATP7 | ATP synthase d subunit | NA | NA | 0.91 | 3.7 | TN | 0.91 | 1 | -0.03 | TP | 0.82 | 1 | 0.02 | TP | 0.98 | 0.76 | FP | 0.24 | 0.64 | TN | 0.14 | 0.48 | TN | 0.16 | 0.44 | TN | 0.05 | 0.59 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YKL004W | AUR1 | Involved in phospolipid metabolism | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Sphingolipid synthesis not required in the model | FP |
| YOR011W | AUS1 | ATP-binding cassette (ABC) family | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YBR068C | BAP2 | Amino acid permease for leucine, valine, and isoleucine (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.81 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YDR046C | BAP3 | Valine transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YJR148W | BAT2 | Branched-chain amino acid transaminase | NA | NA | NA | NA | NA | 0 | 1 | -0.04 | FN | 1 | 1 | -0.01 | TP | 0.69 | 1.03 | FN | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | Iso | BAT2 single deletion should not be lethal as there is a mitochondrial isozyme (BAT1) - double deletion should be lethal. Bat1p currently does not catalyze valine transamination so this functionality should probably be added [Kispal96]. | NA |
| YPR176C | BET2 | Geranylgeranyltransferase type II beta subunit | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Quinone biosynthesis is not required in the model. | FP |
| YJL031C | BET4 | Geranylgeranyltransferase type II alpha subunit (PGGTase-II, alpha subunit) | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Quinone biosynthesis is not required in the model. | NA |
| YGR282C | BGL2 | Cell wall endo-beta-1,3-glucanase | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | 0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YGR286C | BIO2 | Biotin synthase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YNR058W | BIO3 | 7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.04 | TP | 1.1 | 1.04 | TP | 1.11 | 1.02 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YNR057C | BIO4 | Dethiobiotin synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.01 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNR056C | BIO5 | Transmembrane regulator of KAPA/DAPA transport | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0.08 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YJR025C | BNA1 | 3-hydroxyanthranilic acid dioxygenase | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YJR078W | BNA2 | Tryptophan 2,3-dioxygenase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.05 | TP | 1.11 | 1.05 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YBL098W | BNA4 | Kynurenine 3-mono oxygenase | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YLR231C | BNA5 | Kynureninase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YFR047C | BNA6 | Quinolinate phosphoribosyl transferase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YCR032W | BPH1 | Beige protein homologue 1 | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.05 | 1.06 | TP | 1.11 | 1.05 | TP | 1.1 | 1.07 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YEL063C | CAN1 | Arginine permease | NA | NA | NA | NA | NA | 1 | 1 | 0.1 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YPL111W | CAR1 | Arginase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 0.99 | 1 | TP | 1.11 | 0.98 | TP | 1.03 | 0.97 | TP | NA | NA | NA |
| YLR438W | CAR2 | Ornithine aminotransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.11 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.01 | 0.98 | TP | 1.11 | 1 | TP | 1.05 | 0.98 | TP | NA | NA | NA |
| YML042W | CAT2 | Carnitine O-acetyltransferase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YLR307W | CDA1 | Chitin deacetylase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.03 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YLR308W | CDA2 | Chitin deacetylase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | 0.23 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.98 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YAL038W | CDC19 | Pyruvate kinase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Reg | Model has Pyk2p as an isozyme. Pyk2p may only be expressed under conditions of very low glycolytic flux [MIPS] | FP |
| YOR074C | CDC21 | Thymidylate synthase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Essential for nuclear and mitochondrial biosynthesis, which are not required in our model. | NA |
| YGL155W | CDC43 | Protein geranylgeranyltransferase type 1 polypeptide subunit | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Quinone biosynthesis is not required in the model. | NA |
| YPL160W | CDC60 | Leucine--tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YJR057W | CDC8 | Thymidylate kinase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Essential for DNA synthesis, which is not required in our model. | FP |
| YBR029C | CDS1 | Phosphatidate cytidylyltransferase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YER061C | CEM1 | Beta-keto-acyl synthase homolog | NA | NA | NA | NA | NA | 1 | 1 | 0.55 | TP | 1 | 1 | 0.05 | TP | 1.08 | 0.81 | FP | 1.1 | 0.77 | FP | 1.11 | 0.57 | FP | 1.12 | 0.54 | FP | 1.11 | 0.54 | FP | Oth | Cem1p is involved in the synthesis of a specialized molecule related to fatty acids, which is essential for mitochondrial function. | NA |
| YCL064C | CHA1 | Catabolic serine (threonine) dehydratase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YGR157W | CHO2 | Phosphatidyl-ethanolamine N-methyltransferase | NA | NA | NA | NA | NA | 0 | 1 | -0.03 | FN | 0 | 1 | -0.01 | FN | 0 | 1.01 | FN | 0 | 1 | FN | 0 | 0.97 | FN | 0 | 0.98 | FN | 0 | 0.99 | FN | Bio | Catalyzes 1st step in pathway from PE to PC. Opi3p can also catalyze this step, but it is very inefficient; mutant cells are viable and not auxotrophic for choline or other phospholipid intermediates; membranes of mutants contain 10% PC and 40-50% PE (WT is 40-45% PC and 15-20% PE); this deletion is lethal in silico since we require fixed amounts of these specific phospholipids in our biomass (in vivo there is flexibility as to which phospholipids are used). | FN |
| YNL192W | CHS1 | Chitin synthase 1 | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YBR038W | CHS2 | Chitin synthase 2 | 1 | FP | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.03 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Dis | Gene is listed as essential, but there is data for MMD and YPGal. In any case chitin synthesis is not required in the model. | NA |
| YBR023C | CHS3 | Chitin synthase 3 | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YNR001C | CIT1 | Citrate synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.19 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.99 | TP | 1.1 | 0.96 | TP | 1.11 | 0.79 | TP | 1.12 | 0.92 | TP | 1.11 | 0.81 | TP | NA | NA | NA |
| YCR005C | CIT2 | Citrate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YPR001W | CIT3 | Citrate synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.21 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YLR133W | CKI1 | Choline kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 1.01 | TP | 1.11 | 1.04 | TP | 1.12 | 1.08 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YBR003W | COQ1 | Hexaprenyl pyrophosphate synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0.09 | TP | 1.08 | 0.95 | TP | 1.1 | 0.83 | FP | 1.11 | 0.48 | FP | 1.12 | 0.45 | FP | 1.11 | 0.58 | FP | Bio | Quinone biosynthesis is not required in the model. | NA |
| YNR041C | COQ2 | Para hydroxybenzoate: polyprenyl transferase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0.11 | TP | 1.08 | 0.95 | TP | 1.1 | 0.91 | TP | 1.11 | 0.56 | FP | 1.12 | 0.54 | FP | 1.11 | 0.52 | FP | Bio | Quinone biosynthesis is not required in the model. | NA |
| YOL096C | COQ3 | 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase | NA | NA | 1 | 4.3 | FP | 1 | 1 | 0.21 | TP | 1 | 1 | 0.06 | TP | 1.08 | 0.85 | FP | 1.1 | 0.78 | FP | 1.11 | 0.51 | FP | 1.12 | 0.49 | FP | 1.11 | 0.57 | FP | Bio | Quinone biosynthesis is not required in the model. | NA |
| YML110C | COQ5 | C-methyltransferase (putative) | NA | NA | 1 | 4.7 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.77 | FP | 1.1 | 0.64 | FP | 1.11 | 0.53 | FP | 1.12 | 0.52 | FP | 1.11 | 0.49 | FP | Bio | Quinone biosynthesis is not required in the model | NA |
| YGR255C | COQ6 | Monooxygenase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0.11 | TP | 1.08 | 0.87 | FP | 1.1 | 0.8 | FP | 1.11 | 0.5 | FP | 1.12 | 0.52 | FP | 1.11 | 0.58 | FP | Bio | Quinone biosynthesis is not required in the model | NA |
| YBL045C | COR1 | Coenzyme QH2 cytochrome c reductase 44 kDa core protein subunit | NA | NA | 0.9 | 4 | TN | 0.89 | 1 | -0.03 | TP | 0.82 | 1 | -0.03 | TP | 0.98 | 0.82 | FP | 0.24 | 0.77 | TN | 0.14 | 0.5 | TN | 0.08 | 0.47 | TN | 0.17 | 0.54 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YPL172C | COX10 | Farnesyl transferase (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0.4 | TP | 1.08 | 0.97 | TP | 1.1 | 0.94 | TP | 1.11 | 0.59 | FP | 1.12 | 0.54 | FP | 1.11 | 0.61 | FP | Bio | Quinone biosynthesis is not required in the model | NA |
| YLR038C | COX12 | Cytochrome c oxidase subunit VIb | NA | NA | NA | NA | NA | 0.89 | 1 | 0.31 | TP | 0.82 | 1 | 0.02 | TP | 0.98 | 0.98 | TP | 0.24 | 0.91 | FN | 0.14 | 0.55 | TN | 0.08 | 0.5 | TN | 0.05 | 0.57 | TN | Med | This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. | NA |
| YNL052W | COX5A | Cytochrome c oxidase chain Va | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.17 | TP | 1.08 | 1.02 | TP | 1.1 | 0.94 | TP | 1.11 | 0.65 | FP | 1.12 | 0.61 | FP | 1.11 | 0.68 | FP | Iso | COX5A is the dominant isoform - COX5B cannot fully compensate [SGD]. | NA |
| YIL111W | COX5B | Cytochrome c oxidase chain Vb | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YHR051W | COX6 | Cytochrome c oxidase subunit | NA | NA | NA | NA | NA | 0.89 | 1 | -0.04 | TP | 0.82 | 1 | -0.01 | TP | 0.98 | 0.82 | FP | 0.24 | 0.73 | TN | 0.14 | 0.62 | TN | 0.08 | 0.61 | TN | 0.05 | 0.63 | TN | Med | Higher oxygen uptake rate or lower glucose uptake rate will make this deleterious in the model. | NA |
| YMR256C | COX7 | Cytochrome c oxidase subunit VII | NA | NA | 0.9 | 3.6 | TN | 0.89 | 1 | -0.03 | TP | 0.82 | 1 | 0 | TP | 0.98 | 0.8 | FP | 0.24 | 0.74 | TN | 0.14 | 0.71 | TN | 0.08 | 0.69 | TN | 0.05 | 0.69 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YLR395C | COX8 | Cytochrome c oxidase chain VIII | NA | NA | NA | NA | NA | 0.89 | 1 | -0.04 | TP | 0.82 | 1 | -0.03 | TP | 0.98 | 1.01 | TP | 0.24 | 0.99 | FN | 0.14 | 0.91 | FN | 0.08 | 0.91 | FN | 0.05 | 0.94 | FN | Dis | Null mutant is viable, but should be deficient in cellular respiration and cytochrome C oxidase activity [SGD] so there should be a growth defect on non-fermentable carbon sources. | NA |
| YDL067C | COX9 | Cytochrome c oxidase subunit VIIa | NA | NA | NA | NA | NA | 0.89 | 1 | 0.14 | TP | 0.82 | 1 | 0.05 | TP | 0.98 | 0.82 | FP | 0.24 | 0.75 | TN | 0.14 | 0.53 | TN | 0.08 | 0.5 | TN | 0.05 | 0.52 | TN | Med | Higher oxygen uptake rate or lower glucose uptake rate will make this deleterious in the model. | NA |
| YOR303W | CPA1 | Arginine specific\|carbamoyl phosphate synthetase | NA | NA | NA | NA | NA | 0 | 1 | 6.82 | TN | 1 | 1 | -0.1 | TP | 1.08 | 1.02 | TP | 1.1 | 0.98 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.1 | 0.98 | TP | NA | Weak false negative | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YJR109C | CPA2 | Carbamyl phosphate synthetase | NA | NA | NA | NA | NA | 0 | 1 | 8.21 | TN | 1 | 1 | 0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.1 | 1.04 | TP | NA | Weak false negative | NA |
| YNL130C | CPT1 | Sn-1,2-diacylglycerol cholinephosphotransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YOR100C | CRC1 | Carnitine transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDL142C | CRD1 | Cardiolipin synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.98 | TP | 1.1 | 0.99 | TP | 1.11 | 0.93 | TP | 1.12 | 0.85 | TP | 1.11 | 0.93 | TP | NA | NA | NA |
| YBR036C | CSG2 | Required for mannosylation of inositolphosphorylceramide (IPC) | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 0.98 | TP | 1.12 | 0.99 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR256C | CTA1 | Catalase A | NA | NA | NA | NA | NA | 1 | 1 | 0.28 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YBR291C | CTP1 | Citrate tranporter | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | 0.21 | TP | 1.08 | 0.99 | TP | 1.1 | 0.98 | TP | 1.11 | 0.96 | TP | 0.79 | 0.93 | FN | 1.08 | 0.93 | TP | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YGR088W | CTT1 | Catalase T | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YEL027W | CUP5 | 17 kDa\|VO sector subunit\|dicyclohexylcarbodiimide binding subunit\|proteolipid\|vacuolar ATP synthase proteolipid C\|vacuolar ATPase V0 domain subunit c (dicyclohexylcarbodiimide binding subunit) (17 kDa) | NA | NA | 1 | 17.9 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.72 | FP | 1.1 | 0.62 | FP | 1.11 | 0.53 | FP | 1.12 | 0.58 | FP | 1.11 | 0.58 | FP | Oth | The cup5 null mutant is viable but lacks vacuolar (H )-ATPase activity, and is defective in vacuolar acidification, vacuole biogenesis, vacuolar protein targeting, and endocytosis [SGD]. The slow growth phenotype could be due to problems in pH balancing. | NA |
| YML054C | CYB2 | L-lactate cytochrome c oxidoreductase\|cytochrome b2 | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.06 | TP | 1.12 | 1.08 | TP | 0.64 | 1.07 | FN | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YJL005W | CYR1 | Adenylate cyclase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | cAMP synthesis not required in model as its primarily used as a signaling molecule. | FP |
| YAL012W | CYS3 | Cystathionine gamma-lyase | NA | NA | NA | NA | NA | 1 | 1 | 0.29 | TP | 1 | 1 | 0.63 | TP | 1.08 | 0.94 | TP | 1.1 | 0.9 | TP | 1.11 | 0.67 | FP | 1.12 | 0.77 | FP | 1.11 | 0.88 | TP | Med | This reaction is not used in complete media, because cysteine is available. Should only be a cysteine auxotroph [SGD]. | NA |
| YGR155W | CYS4 | Cystathionine beta-synthase | NA | NA | 1 | 3.7 | FP | 1 | 1 | 0.11 | TP | 1 | 1 | 0.17 | TP | 1.08 | 0.91 | TP | 1.1 | 0.9 | TP | 1.11 | 0.71 | FP | 1.12 | 0.72 | FP | 1.11 | 0.83 | TP | Oth | CYS4 null mutant is deficient in vacuolar ATPase activity and vacuolar acidification [MIPS]. The false positives could be due to pH balancing, which is not accounted for in the model. | NA |
| YOR065W | CYT1 | Cytochrome c1 | NA | NA | NA | NA | NA | 0.89 | 1 | 0.02 | TP | 0.82 | 1 | 0.23 | TP | 0.98 | 0.96 | TP | 0.24 | 0.92 | FN | 0.14 | 0.62 | TN | 0.08 | 0.57 | TN | 0.17 | 0.61 | TN | Med | This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. | NA |
| YML070W | DAK1 | Dihydroxyacetone kinase (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YFL053W | DAK2 | Dihydroxyacetone kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YIR027C | DAL1 | Allantoinase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YIR029W | DAL2 | Allantoicase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YIR032C | DAL3 | Ureidoglycolate hydrolase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YIR028W | DAL4 | Allantoin permease | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | 0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YJR152W | DAL5 | Allantoate permease | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YIR031C | DAL7 | Malate synthase 2 | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 0.98 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YHR019C | DED81 | Asparaginyl-tRNA synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | FP |
| YFL001W | DEG1 | Similar to rRNA methyltransferase (Caenorhabditis elegans) and hypothetical 28K protein (alkaline endoglucanase gene 5' region) from Bacillus sp. | NA | NA | 1 | 3.5 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.86 | FP | 1.1 | 0.79 | FP | 1.11 | 0.8 | TP | 1.12 | 0.8 | TP | 1.11 | 0.81 | TP | Oth | Pseudouridine biosynthesis not required in the model. | NA |
| YOR236W | DFR1 | Dihydrofolate reductase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Acc | Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02]. | FP |
| YHR011W | DIA4 | Protein similar to bacterial seryl-tRNA synthases | NA | NA | 1 | 6.5 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | 0.19 | TP | 1.08 | 0.74 | FP | 1.1 | 0.65 | FP | 1.11 | 0.54 | FP | 1.12 | 0.44 | FP | 1.11 | 0.49 | FP | Oth | Protein synthesis not included in the model. | NA |
| YLR348C | DIC1 | Dicarboxylate transport protein | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YPL266W | DIM1 | Dimethyladenosine transferase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Quinone biosynthesis is not required in the model | FP |
| YPL265W | DIP5 | Dicarboxylic amino acid permease | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 0.96 | TP | 1.11 | 0.87 | TP | 1.12 | 0.81 | TP | 1.11 | 0.88 | TP | NA | NA | NA |
| YDL174C | DLD1 | D-lactate ferricytochrome c oxidoreductase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YLR172C | DPH5 | Diphthamide biosynthesis | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 1 | TP | 1.12 | 1.02 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YDR294C | DPL1 | Dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase) | NA | NA | NA | NA | NA | 1 | 1 | 0.06 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YPR183W | DPM1 | Dolichol phosphate mannose synthase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YDR284C | DPP1 | Diacylglycerol pyrophosphate phosphatase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | FN |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YLL018C | DPS1 | Aspartyl-tRNA synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YBR208C | DUR1, | Urea amidolyase (contains urea carboxylase and allophanate hydrolase) | NA | NA | NA | NA | NA | 1 | 1 | 0.11 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1 | TP | 1.1 | 0.98 | TP | 1.11 | 0.96 | TP | 1.12 | 0.97 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YHL016C | DUR3 | Urea active transport protein | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.07 | 1.03 | TP | 1.11 | 1.04 | TP | 1.07 | 1.02 | TP | NA | NA | NA |
| YBR252W | DUT1 | DUTP pyrophosphatase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Converts dUTP to dUMP preventing uracil incorporation into DNA [MIPS]. Since we do not include DNA replication in our model, this function is unnecessary. | FP |
| YHR068W | DYS1 | Deoxyhypusine synthase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Dys1p catalyzes first two steps in hypusine biosynthesis. Hypusine is required in our model. | FP |
| YJR137C | ECM17 | Sulfite reductase (putative) | NA | NA | NA | NA | NA | 1 | 1 | 2.28 | TP | 1 | 1 | 0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YBR176W | ECM31 | ExtraCellular Mutant | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YLR299W | ECM38 | Gamma-glutamyltransferase homolog | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YMR062C | ECM40 | Acetylornithine acetyltransferase | NA | NA | NA | NA | NA | 0 | 1 | 2.04 | TN | 1 | 1 | -0.01 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | Weak false negative | NA |
| YDR147W | EKI1 | Ethanolamine kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.98 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YGR254W | ENO1 | Enolase I | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YHR123W | EPT1 | Sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGR175C | ERG1 | Squalene monooxygenase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YPL028W | ERG10 | Acetoacetyl CoA thiolase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | FP |
| YHR007C | ERG11 | Cytochrome P450 lanosterol 14a-demethylase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YMR208W | ERG12 | Mevalonate kinase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YML126C | ERG13 | 3-hydroxy-3-methylglutaryl coenzyme A synthase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0 | 0.96 | FN | 0 | 0.91 | FN | 0 | 0.92 | FN | 0 | 0.9 | FN | 0 | 0.9 | FN | Dis | Deletion of ERG13 is lethal [Daum98]. Discrepancy between the two experimental studies. | FP |
| YMR202W | ERG2 | C-8 sterol isomerase | NA | NA | 1 | 3.2 | FP | 1 | 1 | 0.54 | TP | 1 | 1 | 0.16 | TP | 1.08 | 0.92 | TP | 1.1 | 0.76 | FP | 1.11 | 0.86 | TP | 1.12 | 0.75 | FP | 1.11 | 0.73 | FP | Mod | Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG2 gene product. This bypass is probably incorrect. | NA |
| YJL167W | ERG20 | Farnesyl diphosphate synthetase (FPP synthetase) | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YNL280C | ERG24 | Sterol C-14 reductase | NA | NA | 0 | 7 | TN | 0 | 1 | 0.11 | TN | 0 | 1 | 0 | TN | 0 | 0.79 | TN | 0 | 0.62 | TN | 0 | 0.7 | TN | 0 | 0.55 | TN | 0 | 0.68 | TN | NA | NA | NA |
| YGR060W | ERG25 | C-4 sterol methyl oxidase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YGL001C | ERG26 | C-3 sterol dehydrogenase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YLR100W | ERG27 | 3-keto sterol reductase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YLR056W | ERG3 | C-5 sterol desaturase | NA | NA | 1 | 5.5 | FP | 1 | 1 | 0.06 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.92 | TP | 1.1 | 0.9 | TP | 1.11 | 0.82 | TP | 1.12 | 0.84 | TP | 1.11 | 0.92 | TP | Mod | Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG3 gene product. This bypass is probably incorrect. | FN |
| YGL012W | ERG4 | Sterol C-24 reductase | NA | NA | NA | NA | NA | 0 | 1 | 0.03 | FN | 0 | 1 | 0 | FN | 0 | 0.96 | FN | 0 | 0.96 | FN | 0 | 0.93 | FN | 0 | 1.01 | FN | 0 | 0.95 | FN | Bio | Erg4p catalyzes the last step in the synthesis of ergosterol. when it is deleted, the precursor accounts for 90% of the cell's sterol composition, suggesting that Erg4p is the only enzyme that can catalyze this reaction; ergosterol is completely replaced by its precursor in the plasma membrane of erg4 mutants; the mutant is viable, but there are distinct defects relating to drug sensitivity [Zweytick00]; thus, this FN is a result of our biomass function, which requires ergosterol. | FN |
| YMR015C | ERG5 | Cytochrome P450\|involved in C-22 denaturation of the ergosterol side-chain | NA | NA | NA | NA | NA | 1 | 1 | 0.14 | TP | 1 | 1 | -0.1 | TP | 1.08 | 1 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.03 | TP | 1.11 | 1.04 | TP | NA | NA | FN |
| YML008C | ERG6 | Ergosterol synthesis | NA | NA | 1 | 3.2 | FP | 1 | 1 | 0.36 | TP | 1 | 1 | 0.02 | TP | 1.08 | 0.84 | FP | 1.1 | 0.81 | FP | 1.11 | 0.82 | TP | 1.12 | 0.78 | TP | 1.11 | 0.72 | FP | Mod | Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG6 gene product. This bypass is probably incorrect. | FN |
| YHR072W | ERG7 | 2,3-oxidosqualene-lanosterol cyclase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YMR220W | ERG8 | 48 kDa phosphomevalonate kinase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YHR190W | ERG9 | Squalene synthetase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YLR300W | EXG1 | Exo-1,3-beta-glucanase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR261C | EXG2 | Exo-1,3-beta-glucanase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YOR317W | FAA1 | Long chain fatty acyl:CoA synthetase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YIL009W | FAA3 | Acyl-CoA synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YMR246W | FAA4 | Long chain fatty acyl:CoA synthetase\|long-chain fatty acid:CoA ligase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YFR019W | FAB1 | 1-phosphatidylinositol-3-phosphate 5-kinase | NA | NA | 1 | 8.3 | FP | 1 | 1 | 0 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.63 | FP | 1.1 | 0.73 | FP | 1.11 | 0.55 | FP | 1.12 | 0.5 | FP | 1.11 | 0.54 | FP | Oth | Mutation causes pleiotropic effects on nuclear migration and orientation, and separation of mitotic chromosomes (forms aploid and binucleate cells).Mutant has defects in vacuolar function and morphology [SGD]. | NA |
| YDL045C | FAD1 | FAD synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Riboflavin biosynthesis is not required in the model | FP |
| YKL182W | FAS1 | Acetyl transferase\|dehydratase\|enoyl reductase\|malonyl/palmityl transferase\|pentafunctional enzyme | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YPL231W | FAS2 | Fatty acid synthase alpha subuni | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YBR041W | FAT1 | Fatty acid transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YER183C | FAU1 | 5,10-methenyltetrahydrofolate synthetase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YKL060C | FBA1 | Aldolase | 0.19 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | NA |
| YLR377C | FBP1 | Fructose-1,6-bisphosphatase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 0.85 | TP | 0.41 | 0.84 | FN | 0.89 | 0.88 | TP | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YJL155C | FBP26 | Fructose-2,6-bisphosphatase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 0.96 | TP | 1.12 | 0.91 | TP | 1.11 | 0.92 | TP | NA | NA | NA |
| YPR062W | FCY1 | Cytosine deaminase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YER056C | FCY2 | Purine-cytosine permease | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.97 | TP | 1.1 | 1 | TP | 1.11 | 1.04 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YER060W | FCY21 | Purine-cytosine permease | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YER060WA | FCY22 | Purine-cytosine permease | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YCR034W | FEN1 | 1,3-beta-glucan synthase subunit (putative)\|ELO1 homolog | NA | NA | NA | NA | NA | 0 | 1 | 0.36 | FN | 0 | 1 | -0.05 | FN | 0 | 0.93 | FN | 0 | 0.94 | FN | 0 | 0.92 | FN | 0 | 0.81 | FN | 0 | 0.94 | FN | Bio | Involved in synthesis of 1,3-beta-glucan, probable beta-1,3-glucan synthase subunit - unknown whether it is a catalytic subunit or GTP-binding subunit. Membranes of mutant cells have 90% less beta-1,3-glucan synthase activity - could an alternate subunit exist? This is lethal in silico because beta-1,3-glucan is required in biomass. | NA |
| YCR028C | FEN2 | Plasma Membrane H+-Pantothenate Symporter | NA | NA | 1 | 3.1 | FP | 1 | 1 | 0.11 | TP | 1 | 1 | 0 | TP | 1.08 | 0.8 | FP | 1.1 | 0.8 | FP | 1.11 | 0.83 | TP | 1.12 | 0.77 | FP | 1.11 | 0.72 | FP | Oth | Pantothenate is necessary for CoA biosynthesis, which is not required by the model. | NA |
| YLR342W | FKS1 | 1,3-beta-D-glucan synthase | NA | NA | 1 | 4.5 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.62 | FP | 1.1 | 0.74 | FP | 1.11 | 0.84 | TP | 1.12 | 0.84 | TP | 1.11 | 0.87 | TP | Iso | There are three alternate isozymes in the model, but FKS1 deletion experimentally disrupts the enzymatic function significantly. | NA |
| YMR306W | FKS3 | Protein with similarity to Gls1p and Gls2p (GB:Z49212) | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YIL134W | FLX1 | FAD carrier protein | NA | NA | 1 | 3.4 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.99 | TP | 1.1 | 1.03 | TP | 1.11 | 1.07 | TP | 1.12 | 1.03 | TP | 1.11 | 0.99 | TP | Dis | There is no evidence of significant deleterious phenotype. Experimentally flx1 strain has low FMN/FAD ratio [MIPS]. The two studies also show conflicting results. | NA |
| YDR236C | FMN1 | Riboflavin kinase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Riboflavin biosynthesis is not required in the model | FP |
| YBL013W | FMT1 | Methionyl-tRNA transformylase | NA | NA | NA | NA | NA | 1 | 1 | 0.42 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 0.95 | TP | 1.12 | 0.97 | TP | 1.11 | 0.94 | TP | NA | NA | NA |
| YNL256W | FOL1 | Dihydro-6-hydroxymethylpterin pyrophosphokinase\|dihydroneopterin aldolase\|dihydropteroate synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Acc | Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02]. | FP |
| YGR267C | FOL2 | GTP-cyclohydrolase I | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Acc | Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02]. | FP |
| YMR113W | FOL3 | Dihydrofolate synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Acc | Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02]. | FP |
| YKR009C | FOX2 | Multifunctional beta-oxidation protein | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.03 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YLL043W | FPS1 | Glycerol channel protein | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.99 | TP | 1.08 | 1.02 | TP | 0.9 | 1.05 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YLR060W | FRS1 | Phenylalanine-tRNA ligase subuni | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YFL022C | FRS2 | Phenylalanine-tRNA ligase subuni | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YBL042C | FUI1 | Uridine permease | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.94 | TP | 1.1 | 0.89 | TP | 1.11 | 0.88 | TP | 1.12 | 0.82 | TP | 1.11 | 0.94 | TP | NA | NA | NA |
| YPL262W | FUM1 | Fumarase (fumarate hydralase) | NA | NA | NA | NA | NA | 1 | 1 | 0.7 | TP | 1 | 1 | 0.04 | TP | 1.08 | 0.97 | TP | 1.08 | 0.96 | TP | 0.96 | 0.73 | FP | 0.59 | 0.82 | FN | 0.95 | 0.71 | FP | Unk | The model predicts a reduced growth rate, but the drop is not that large. | NA |
| YMR250W | GAD1 | Glutamate decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.08 | TP | 1.12 | 1.08 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YBR020W | GAL1 | Galactokinase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 0.18 | 1 | 2.08 | TN | 1.08 | 0.99 | TP | 1.1 | 0.97 | TP | 1.11 | 0.99 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YBR019C | GAL10 | UDP-glucose 4-epimerase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 0.18 | 0 | 3.14 | TN | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YLR081W | GAL2 | Galactose permease | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 0 | 1.52 | FP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | Iso | Gal2p is the high-affinity galactose transporter, which is known to be a major player in gal transport. Deletion of GAL2 drastically reduces growth on galactose [Douglas64]. Model includes other isozymes (HXT genes) that are not nearly as efficient for gal transport so disabling their gal transport ability should result correct prediction. | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YBR018C | GAL7 | Galactose-1-phosphate uridyl transferase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 0.18 | 0 | 5.37 | TN | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKR039W | GAP1 | General amino acid permease | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR019C | GCV1 | Glycine decarboxylase complex T subunit | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 0.99 | 1 | -0.03 | TP | 1.07 | 1.03 | TP | 1.09 | 1.05 | TP | 1.03 | 1.05 | TP | 0.87 | 1.08 | TP | 1.04 | 1.06 | TP | NA | NA | NA |
| YMR189W | GCV2 | Glycine cleavage system P subunit\|glycine decarboxylase complex P subunit\|glycine synthase P subunit | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 0.99 | 1 | -0.04 | TP | 1.07 | 0.99 | TP | 1.09 | 1.01 | TP | 1.03 | 1.03 | TP | 0.87 | 1.02 | TP | 1.04 | 1.02 | TP | NA | NA | NA |
| YAL044C | GCV3 | Glycine cleavage system H-protein subunit | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 0.99 | 1 | -0.01 | TP | 1.07 | 0.76 | FP | 1.09 | 0.77 | FP | 1.03 | 0.6 | FP | 0.87 | 0.58 | FP | 1.04 | 0.55 | FP | Dis | Should not be deleterious except when glycine is the only nitrogen source [Nagarajan97]. Could also be due to complicated gene-protein-reaction associations. | NA |
| YEL042W | GDA1 | Guanosine diphosphatase of Golgi membrane | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.06 | TP | 1.08 | 0.97 | TP | 1.1 | 0.97 | TP | 1.11 | 1.02 | TP | 1.12 | 0.99 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YOR375C | GDH1 | NADP-specific glutamate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.39 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YDL215C | GDH2 | NAD-dependent glutamate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YAL062W | GDH3 | NADP-linked glutamate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.05 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YKL104C | GFA1 | Glucoseamine-6-phosphate synthase\|glutamine_fructose-6-phosphate amidotransferase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Essential for synthesis of cell wall precursors (leading to chitin biosynthesis), which are not required in the model. | FP |
| YCR098C | GIT1 | Permease involved in the uptake of glycerophosphoinositol (GroPIns) | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.97 | TP | 1.1 | 0.94 | TP | 1.11 | 0.97 | TP | 1.12 | 0.94 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YEL011W | GLC3 | 1,4-glucan-6-(1,4-glucano)-transferase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YCL040W | GLK1 | Glucokinase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YPR035W | GLN1 | Glutamine synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Med | Null mutants are glutamine auxotrophs [MIPS]. The deletion is lethal if glutamine is removed from the media. | NA |
| YOR168W | GLN4 | Glutamine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.03 | TP | Oth | Protein synthesis not required in the model | NA |
| YML004C | GLO1 | Lactoylglutathione lyase (glyoxalase I) | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.03 | TP | 1.1 | 1.06 | TP | 1.11 | 1.07 | TP | 1.12 | 1.07 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YDR272W | GLO2 | Glyoxylase-II | NA | NA | NA | NA | NA | 1 | 1 | 0.07 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YOR040W | GLO4 | Glyoxylase-II | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPL091W | GLR1 | Glutathione oxidoreductase\|EC 1.6.4.2 | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YDL171C | GLT1 | Glutamate synthase (NADH) | NA | NA | NA | NA | NA | 1 | 1 | 0.29 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YEL046C | GLY1 | Threonine aldolase | NA | NA | 1 | 5.5 | FP | 1 | 1 | 0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 0.71 | FP | 1.1 | 0.7 | FP | 1.11 | 0.83 | TP | 1.12 | 0.77 | FP | 1.11 | 0.85 | TP | Dis | Should be a glycine auxotroph when grown on glucose so that the deletion strain should grow normally in complex media [Monschau97]. | NA |
| YFL017C | GNA1 | Glucosamine-phosphate N-acetyltransferase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | N-Acetylglucosamine synthesis is not required in the model. | NA |
| YHR183W | GND1 | 6-phosphogluconate dehydrogenase, decarboxylating; converts 6-phosphogluconate + NADP to ribulose-5-phosphate + NADPH + CO2 | NA | NA | 1 | 5 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.65 | FP | 1.1 | 0.82 | FP | 1.11 | 0.83 | TP | 1.12 | 0.99 | TP | 1.11 | 0.95 | TP | Iso | This is the major isozyme (80% of activity) [MIPS]. | NA |
| YGR256W | GND2 | 6-phosphogluconate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YDR508C | GNP1 | High affinity glutamine permease | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.08 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YDL022W | GPD1 | Glycerol-3-phosphate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.06 | TP | 1.11 | 1.05 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YOL059W | GPD2 | Glycerol-3-phosphate dehydrogenase (NAD+) | NA | NA | NA | NA | NA | 1 | 1 | 0.24 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPR160W | GPH1 | Glycogen phosphorylase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.03 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKL152C | GPM1 | Phosphoglycerate mutase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Essential for sporulation, which is not required in our model. | FP |
| YDL021W | GPM2 | Similar to GPM1 (phosphoglycerate mutase); converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.06 | TP | 1.12 | 1.07 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YOL056W | GPM3 | Phosphoglycerate mutase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YKL026C | GPX1 | Glutathione peroxidase paralogue | NA | NA | NA | NA | NA | 1 | 1 | 0.13 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YBR244W | GPX2 | Glutathione peroxidase paralogue | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0.05 | TP | 1.08 | 0.98 | TP | 1.1 | 0.94 | TP | 1.11 | 0.96 | TP | 1.12 | 0.98 | TP | 1.11 | 1.01 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YHR104W | GRE3 | Aldose reductase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.99 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YBR121C | GRS1 | Glycine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YGR032W | GSC2 | 1,3-beta-D-glucan synthase catalytic component | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YJL101C | GSH1 | Gamma-glutamylcysteine synthetase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0.2 | TP | 1.08 | 0.99 | TP | 1.1 | 1 | TP | 1.11 | 0.93 | TP | 1.12 | 0.94 | TP | 1.11 | 0.94 | TP | NA | NA | NA |
| YOL049W | GSH2 | Glutathione synthetase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YFR015C | GSY1 | Glycogen synthase (UDP-glucose-starch glucosyltransferase) | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.07 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YLR258W | GSY2 | Glycogen synthase (UDP-glucose-starch glucosyltransferase) | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YDR454C | GUK1 | Guanylate kinase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YHL032C | GUT1 | Converts glycerol to glycerol-3-phosphate\|glyerol kinase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1 | TP | 1.08 | 1.02 | TP | 0.9 | 0.98 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YIL155C | GUT2 | Glycerol-3-phosphate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.08 | 0.99 | TP | 0.9 | 0.93 | TP | 1.12 | 0.96 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YDR232W | HEM1 | 5-aminolevulinate synthase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Heme biosynthesis not required in the model | FP |
| YDR047W | HEM12 | Uroporphyrinogen decarboxylase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Heme biosynthesis not required in the model | FP |
| YDR044W | HEM13 | Coproporphyrinogen III oxidase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Heme biosynthesis not required in the model | FP |
| YER014W | HEM14 | Protoporphyrinogen oxidase | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 0.82 | FP | 1.1 | 0.84 | FP | 1.11 | 0.85 | TP | 1.12 | 0.68 | FP | 1.11 | 0.74 | FP | Acc | Heme is not required in the model. May also result in heme precursor accumulation in vivo [SGD]. | NA |
| YOR176W | HEM15 | Ferrochelatase (protoheme ferrolyase) | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 1.04 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.03 | TP | 1.11 | 1.04 | TP | Dis | Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates. | FP |
| YGL040C | HEM2 | Delta-aminolevulinate dehydratase (porphobilinogen synthase) | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Heme biosynthesis not required in the model. | FP |
| YDL205C | HEM3 | Phorphobilinogen deaminase (uroporphyrinogen synthase) | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 1.04 | TP | 1.1 | 1.04 | TP | 1.11 | 1.05 | TP | 1.12 | 1.06 | TP | 1.11 | 1.03 | TP | Dis | Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates. | FP |
| YOR278W | HEM4 | Uroporphyrinogen III synthase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Heme biosynthesis not required in the model | FP |
| YGR191W | HIP1 | Histidine permease | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Used as a histidine transporter in our model, but there are isozymes for this function. Lethality may be due to the role of Hip1p in Mg2+ transport. | FP |
| YER055C | HIS1 | ATP phosphoribosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.29 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YFR025C | HIS2 | Histidinolphosphatase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YOR202W | HIS3 | Imidazoleglycerol-phosphate dehydratase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YCL030C | HIS4 | Histidinol dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YIL116W | HIS5 | Histidinol-phosphate aminotransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.02 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YIL020C | HIS6 | Phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase | NA | NA | NA | NA | NA | 1 | 1 | 0.09 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YBR248C | HIS7 | Glutamine amidotransferase:cyclase\|imidazole glycerol phosphate synthase (synonym) | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | 0.13 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YML075C | HMG1 | 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme | NA | NA | NA | NA | NA | 1 | 1 | 0.06 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YLR450W | HMG2 | 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YBR034C | HMT1 | Arginine methyltransferase\|mono-and asymmetrically dimethylating enzyme | NA | NA | NA | NA | NA | 1 | 1 | 0.06 | TP | 1 | 1 | 0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGL077C | HNM1 | Transporter (permease) for choline and nitrogen mustard; share homology with UGA4 | NA | NA | NA | NA | NA | 1 | 1 | 0.31 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR305C | HNT2 | Fhit homolog, member of the histidine triad superfamily of nucleotide binding-proteins | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.97 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YDR158W | HOM2 | Aspartic beta semi-aldehyde dehydrogenase | NA | NA | NA | NA | NA | 1 | 0 | 10.74 | FP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.06 | TP | 1.11 | 1.06 | TP | Unk | Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model. | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YER052C | HOM3 | Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4) | NA | NA | NA | NA | NA | 1 | 0 | 4.46 | FP | 1 | 1 | 0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.05 | TP | Unk | Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model. | NA |
| YJR139C | HOM6 | L-homoserine:NADP oxidoreductase\|homoserine dehydrogenase | NA | NA | NA | NA | NA | 1 | 0 | 9.11 | FP | 1 | 1 | -0.03 | TP | 1.08 | 0.98 | TP | 1.1 | 0.98 | TP | 1.11 | 0.96 | TP | 1.12 | 0.91 | TP | 1.11 | 0.97 | TP | Unk | Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model. | NA |
| YER062C | HOR2 | DL-glycerol-3-phosphatase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR399W | HPT1 | Hypoxanthine guanine phosphoribosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPR033C | HTS1 | Histidine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | FP |
| YFR053C | HXK1 | Hexokinase I (PI) (also called hexokinase A) | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YGL253W | HXK2 | Hexokinase II (PII) (also called hexokinase B) | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | 0 | TP | 1.08 | 0.95 | TP | 1.1 | 1.02 | TP | 1.11 | 1.07 | TP | 1.12 | 1.07 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YHR094C | HXT1 | Hexose transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YFL011W | HXT10 | High affinity hexose transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 0.97 | TP | 1.11 | 0.98 | TP | 1.12 | 0.97 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YNL318C | HXT14 | Hexose transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.1 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YNR072W | HXT17 | Hexose transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.08 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YMR011W | HXT2 | High affinity hexose transporter-2 | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.06 | TP | 1.11 | 1.07 | TP | 1.12 | 1.07 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YDR345C | HXT3 | Low affinity glucose transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YHR092C | HXT4 | High affinity glucose transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.06 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YHR096C | HXT5 | Hexose transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.85 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YJL214W | HXT8 | Hexose permease | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YIR037W | HYR1 | Glutathione-peroxidase (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 0.97 | TP | 1.11 | 0.98 | TP | 1.12 | 0.96 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YER065C | ICL1 | Isocitrate lyase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.02 | TP | 0.79 | 0.99 | FN | 1.08 | 1 | TP | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YPR006C | ICL2 | 2-methylisocitrate lyase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNL037C | IDH1 | Isocitrate dehydrogenase 1 alpha-4-beta-4 subunit | NA | NA | 1 | 4.7 | FP | 1 | 1 | -0.06 | TP | 1 | 1 | 0.02 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Unk | The model does not utilize this part of the TCA cycle. | NA |
| YOR136W | IDH2 | NAD-dependent isocitrate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.96 | TP | 1 | 1 | 0.17 | TP | 1.08 | 0.99 | TP | 1.1 | 0.88 | TP | 1.11 | 0.68 | FP | 1.12 | 0.78 | TP | 1.11 | 0.6 | FP | Unk | The model does not use the corresponding reaction when grown on glycerol or lactate. In vivo there is a NAD/NADH balancing issue. | NA |
| YPL117C | IDI1 | Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase) | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YDL066W | IDP1 | NADP-dependent isocitrate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.12 | TP | 1 | 1 | 0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.07 | TP | 1.12 | 1.05 | TP | 1.11 | 1.09 | TP | NA | NA | NA |
| YLR174W | IDP2 | NADP-dependent isocitrate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YNL009W | IDP3 | NADP-dependent isocitrate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.04 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YBL076C | ILS1 | Isoleucine-tRNA synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YER086W | ILV1 | Threonine deaminase | NA | NA | NA | NA | NA | 0 | 0 | 10.66 | TN | 1 | 1 | -0.01 | TP | 0.95 | 0.99 | TP | 1.1 | 0.98 | TP | 1.11 | 1.01 | TP | 1.12 | 0.96 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YJR016C | ILV3 | Dihydroxyacid dehydratase | 0.64 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | FP |
| YLR355C | ILV5 | Acetohydroxyacid reductoisomerase | 0.64 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | FP |
| YCL009C | ILV6 | Acetolactate synthase regulatory subunit | NA | NA | NA | NA | NA | 0 | 1 | -0.01 | FN | 1 | 1 | 0 | TP | 0.69 | 1.01 | FN | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | Iso | Ilv6p is the regulatory subunit of phenylalanine transaminase [SGD]. Null mutant has defective retroinhibition by valine [Cullin96], but apparently this subunit is otherwise non-essential for the enzymatic function. | FP |
| YLR432W | IMD3 | IMP dehydrogenase homolog | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YML056C | IMD4 | IMP dehydrogenase homolog | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.06 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YHR046C | INM1 | Inositol monophosphatase | NA | NA | NA | NA | NA | 0 | 1 | 0 | FN | 0 | 1 | -0.01 | FN | 0 | 1.01 | FN | 0 | 1.04 | FN | 0 | 1.08 | FN | 0 | 1.1 | FN | 0 | 1.08 | FN | Iso | YDR287W may code for an isozyme for Inm1p. May not be lethal if inositol is in media. | FN |
| YJL153C | INO1 | L-myo-inositol-1-phosphate synthase | NA | NA | NA | NA | NA | 0 | 1 | 0.11 | FN | 0 | 1 | -0.04 | FN | 0 | 1.04 | FN | 0 | 1.07 | FN | 0 | 1.07 | FN | 0 | 1.06 | FN | 0 | 1.05 | FN | Med | Null mutant is viable, but an inositol auxotroph [SGD]. This is consistent with in silico results. Thus, experiments may have some inositol in media. | NA |
| YBR011C | IPP1 | Inorganic pyrophosphatase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YDR072C | IPT1 | Inositolphosphotransferase 1 | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPL040C | ISM1 | Isoleucine-tRNA ligase | NA | NA | 1 | 5.2 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.69 | FP | 1.1 | 0.66 | FP | 1.11 | 0.48 | FP | 1.12 | 0.45 | FP | 1.11 | 0.56 | FP | Oth | Protein synthesis not required in the model | NA |
| YDR497C | ITR1 | Myo-inositol transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.09 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YOL103W | ITR2 | Myo-inositol transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.01 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YKL217W | JEN1 | Carboxylic acid transporter protein homolog | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1 | TP | 0.64 | 1.01 | FN | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YIL125W | KGD1 | Alpha-ketoglutarate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0.03 | TP | 1.08 | 0.96 | TP | 1.1 | 0.92 | TP | 1.09 | 0.6 | FP | 1.11 | 0.66 | FP | 1.1 | 0.66 | FP | Unk | Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate. | NA |
| YDR148C | KGD2 | Alpha-ketoglutarate dehydrogenase complex dihydrolipoyl transsuccinylase component | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0.06 | TP | 1.08 | 1 | TP | 1.1 | 0.95 | TP | 1.09 | 0.64 | FP | 1.11 | 0.71 | FP | 1.1 | 0.6 | FP | Unk | Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate. | NA |
| YDR483W | KRE2 | Alpha-1,2-mannosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 1.03 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YDR037W | KRS1 | Lysine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | FP |
| YOR099W | KTR1 | Type II transmembrane protein | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YKR061W | KTR2 | Mannosyltransferase (putative)\|type 2 membrane protein | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YBR205W | KTR3 | Alpha-1,2-mannosyltransferase (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.13 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YBR199W | KTR4 | Alpha-1,2-mannosyltransferase (putative) | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | 0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNL029C | KTR5 | Mannosyltransferase (putative) | NA | NA | 1 | 4.2 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Affects cell wall composition, but should not necessarily have a slow growth phenotype [MIPS]. | NA |
| YPL053C | KTR6 | Mannosylphosphate transferase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNL071W | LAT1 | Pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component (E2) | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 0.99 | TP | 1.11 | 0.78 | FP | 1.12 | 0.89 | TP | 1.11 | 0.89 | TP | Unk | The model can bypass the PDH complex if necessary. | NA |
| YMR296C | LCB1 | Serine palmitoyltransferase component | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Sphingolipid synthesis not required in the model. | FP |
| YDR062W | LCB2 | Serine palmitoyltransferase component | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Sphingolipid synthesis not required in the model. | FP |
| YJL134W | LCB3 | Dihydrosphingosine-1-phosphate phophatase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.05 | TP | 1.11 | 1.06 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YOR171C | LCB4 | Sphingoid long chain base (LCB) kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.23 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YLR260W | LCB5 | Sphingoid long chain base (LCB) kinase | NA | NA | 1 | 4.2 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.7 | FP | 1.1 | 0.61 | FP | 1.11 | 0.55 | FP | 1.12 | 0.48 | FP | 1.11 | 0.57 | FP | Bio | Sphingolipid synthesis not required in the model. | NA |
| YGL009C | LEU1 | Isopropylmalate isomerase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YNL104C | LEU4 | Alpha-isopropylmalate synthase (2-isopropylmalate synthase) | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YOR108W | LEU9 | Alpha-isopropylmalate synthase (2-isopropylmalate synthase) | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YFL018C | LPD1 | Dihydrolipoamide dehydrogenase precursor (mature protein is the E3 component of alpha-ketoacid dehydrogenase complexes) | NA | NA | 1 | 3.7 | FP | 1 | 1 | 0.18 | TP | 0.97 | 1 | -0.04 | TP | 1.06 | 0.76 | FP | 0.98 | 0.75 | FP | 0.94 | 0.55 | FP | 0.84 | 0.53 | FP | 0.93 | 0.55 | FP | Unk | Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate. | NA |
| YDR503C | LPP1 | Lipid phosphate phosphatase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YOR142W | LSC1 | Alpha subunit of succinyl-CoA ligase (synthetase; ATP-forming), a mitochondrial enzyme of the TCA cycle | NA | NA | NA | NA | NA | 1 | 1 | 0.08 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.09 | 0.96 | TP | 1.11 | 1 | TP | 1.1 | 0.98 | TP | NA | NA | NA |
| YGR244C | LSC2 | Beta subunit of succinyl-CoA ligase (synthetase; ATP-forming), a mitochondrial enzyme of the TCA cycle | NA | NA | NA | NA | NA | 1 | 1 | 0.38 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.09 | 0.98 | TP | 1.11 | 1.05 | TP | 1.1 | 1.01 | TP | NA | NA | NA |
| YNL268W | LYP1 | Lysine permease | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YIR034C | LYS1 | Saccharopine dehydrogenase | NA | NA | NA | NA | NA | 0 | 0 | 2.88 | TN | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 0.98 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YIL094C | LYS12 | Homo-isocitrate dehydrogenase | NA | NA | NA | NA | NA | 0 | 0 | 5.15 | TN | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YDL182W | LYS20 | YDL131W (LYS21) homolog\|homocitrate synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.3 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YDL131W | LYS21 | YDL182W (LYS20) homolog\|homocitrate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YDR234W | LYS4 | Homoaconitase | NA | NA | NA | NA | NA | 0 | 0 | 1.55 | TN | 1 | 1 | -0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGL154C | LYS5 | Alpha aminoadipate reductase phosphopantetheinyl transferase | NA | NA | NA | NA | NA | 0 | 0 | 8.33 | TN | 1 | 1 | 0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNR050C | LYS9 | Seventh step in lysine biosynthesis pathway | NA | NA | NA | NA | NA | 0 | 1 | 1.27 | TN | 1 | 1 | -0.02 | TP | 1.08 | 0.9 | TP | 1.1 | 0.97 | TP | 1.11 | 0.97 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YKL029C | MAE1 | Malic enzyme | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.05 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YGR289C | MAL11 | Alpha-glucoside transporter\|hexose transporter\|maltose permease | NA | NA | NA | NA | NA | 1 | 1 | 0.09 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGR292W | MAL12 | Maltase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YBR298C | MAL31 | Maltose permease | NA | NA | NA | NA | NA | 1 | 1 | 0.14 | TP | 1 | 1 | 0.16 | TP | 1.08 | 0.97 | TP | 1.1 | 0.99 | TP | 1.11 | 0.96 | TP | 1.12 | 0.92 | TP | 1.11 | 0.93 | TP | NA | NA | NA |
| YBR299W | MAL32 | Maltase | NA | NA | NA | NA | NA | 1 | 1 | 0.18 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YOR221C | MCT1 | Malonyl-CoA:ACP transferase | NA | NA | NA | NA | NA | 1 | 1 | 0.08 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.8 | FP | 1.1 | 0.76 | FP | 1.11 | 0.49 | FP | 1.12 | 0.45 | FP | 1.11 | 0.57 | FP | Oth | Component of the mitochondrial FAS that supplies phopholipids to the mitochondrial membrane. The model does not account for the formation of the mitochondrial membrane. | NA |
| YKL085W | MDH1 | Malate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.83 | TP | 1.12 | 0.97 | TP | 1.11 | 0.86 | TP | NA | NA | NA |
| YOL126C | MDH2 | Malate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.04 | TP | 1.1 | 1.06 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YDL078C | MDH3 | Malate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGR121C | MEP1 | Ammonia permease | NA | NA | NA | NA | NA | 1 | 1 | 0.25 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YNL142W | MEP2 | Ammonia transport protein | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YPR138C | MEP3 | NH4+ transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0.08 | TP | 1.08 | 1.01 | TP | 1.1 | 0.98 | TP | 1.11 | 0.98 | TP | 1.12 | 0.97 | TP | 1.11 | 0.96 | TP | NA | NA | NA |
| YGR264C | MES1 | Methionine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YKR069W | MET1 | Methionine metabolism | NA | NA | NA | NA | NA | 1 | 1 | 1.55 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.04 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YFR030W | MET10 | Assimilatory sulfite reductase subunit | NA | NA | NA | NA | NA | 1 | 1 | 0.29 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YPL023C | MET12 | Methylenetetrahydrofolate reductase (mthfr) (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.33 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGL125W | MET13 | Methylenetetrahydrofolate reductase (mthfr) (putative) | NA | NA | NA | NA | NA | 1 | 0 | 3.97 | FP | 1 | 1 | -0.01 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 1 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | Iso | Met13p is the dominant isozyme, but the model contains an additional isozyme (Met12p). | NA |
| YKL001C | MET14 | Adenylylsulfate kinase | NA | NA | NA | NA | NA | 0 | 1 | 0.18 | FN | 1 | 1 | -0.08 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | Med | Should not grow as sulfate as only sulfur source [Thomas97]. Maybe minimal media in experimental study has some other sulfur sources. | NA |
| YPR167C | MET16 | 3'phosphoadenylylsulfate reductase | NA | NA | NA | NA | NA | 0 | 1 | 0.64 | FN | 1 | 1 | -0.04 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | Med | Should not grow as sulfate as only sulfur source [Thomas97]. Maybe minimal media in experimental study has some other sulfur sources. | NA |
| YLR303W | MET17 | O-acetylhomoserine (thiol)-lyase | NA | NA | NA | NA | NA | 1 | 0 | 2.78 | FP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | Unk | Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model. | NA |
| YOL064C | MET22 | 3'(2')5'-bisphosphate nucleotidase | NA | NA | NA | NA | NA | 0.99 | 1 | 1.33 | TP | 1 | 1 | 0 | TP | 1.08 | 0.84 | FP | 1.1 | 0.84 | FP | 1.11 | 0.81 | TP | 1.12 | 0.81 | TP | 1.11 | 0.85 | TP | Acc | Mutant probably accumulates phosphoadenylyl sulfate (PAPS), which is toxic [Thomas90]. | NA |
| YJR010W | MET3 | ATP sulfurylase | NA | NA | NA | NA | NA | 1 | 1 | 0.96 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YER091C | MET6 | Vitamin B12-(cobalamin)-independent isozyme of methionine synthase (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase) | NA | NA | NA | NA | NA | 0 | 0 | 3.2 | TN | 0 | 1 | 0 | FN | 0 | 1 | FN | 0 | 1 | FN | 0 | 1.01 | FN | 0 | 1 | FN | 0 | 1 | FN | Unk | The in silico met6 strain is incapable of balancing homocysteine, which is a byproduct of phospholipid biosynthesis. For some reason this does not happen in vivo at least not in rich media. There may be another way to drain off excess homocysteine. | FN |
| YOR241W | MET7 | Folylpolyglutamate synthetase | NA | NA | 1 | 7.1 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.74 | FP | 1.1 | 0.73 | FP | 1.11 | 0.58 | FP | 1.12 | 0.48 | FP | 1.11 | 0.51 | FP | Den | This is a dead end in the model, but it should be part of the one carbon metabolic conversions. Also the gene product is present in both cytoplam and mitochondia and its deletion causes a petite phenotype as the production of mitochondrial f-Met-tRNA (necessary for mitochondrial translation) is disrupted [DeSouza00]. | NA |
| YLL062C | MHT1 | S-Methylmethionine Homocysteine methylTransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YJR077C | MIR1 | Product of gene unknown | NA | NA | NA | NA | NA | 0.96 | 1 | 0.24 | TP | 0.96 | 1 | 0.1 | TP | 1.05 | 0.98 | TP | 0.91 | 0.92 | TP | 0.92 | 0.64 | FP | 0.94 | 0.61 | FP | 0.93 | 0.66 | FP | Oth | Mutant implicated in blocking mitochondrial protein import and disrupts mitochondrial function [MIPS]. Model has other ways to transport phosphate into mitochondria. | NA |
| YBR084W | MIS1 | C1-tetrahydrofolate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.9 | TP | 1.12 | 0.92 | TP | 1.11 | 0.91 | TP | NA | NA | NA |
| YNL117W | MLS1 | Carbon-catabolite sensitive malate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | 0.14 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.93 | TP | 1.12 | 0.88 | TP | 1.11 | 0.91 | TP | NA | NA | NA |
| YLL061W | MMP1 | High affinity S-methylmethionine permease | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YPL104W | MSD1 | Aspartyl-tRNA synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0.03 | TP | 1.08 | 0.88 | FP | 1.1 | 0.77 | FP | 1.11 | 0.59 | FP | 1.12 | 0.54 | FP | 1.11 | 0.57 | FP | Oth | Protein synthesis not required in the model | NA |
| YOL033W | MSE1 | Glutamine-tRNA ligase | NA | NA | 1 | 6.3 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.71 | FP | 1.1 | 0.67 | FP | 1.11 | 0.55 | FP | 1.12 | 0.59 | FP | 1.11 | 0.59 | FP | Oth | Protein synthesis not required in the model | NA |
| YPR047W | MSF1 | Phenylalanyl-tRNA synthetase alpha subunit | NA | NA | 1 | 3.7 | FP | 1 | 1 | 0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.79 | FP | 1.1 | 0.69 | FP | 1.11 | 0.49 | FP | 1.12 | 0.45 | FP | 1.11 | 0.53 | FP | Oth | Protein synthesis not required in the model. | NA |
| YNL073W | MSK1 | Lysine-tRNA ligase | NA | NA | 1 | 4.9 | FP | 1 | 1 | 0 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.74 | FP | 1.1 | 0.7 | FP | 1.11 | 0.51 | FP | 1.12 | 0.52 | FP | 1.11 | 0.58 | FP | Oth | Protein synthesis not required in the model | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YGR171C | MSM1 | Methionine-tRNA ligase | NA | NA | 1 | 5.9 | FP | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.72 | FP | 1.1 | 0.65 | FP | 1.11 | 0.43 | FP | 1.12 | 0.5 | FP | 1.11 | 0.56 | FP | Oth | Protein synthesis not required in the model | NA |
| YHR091C | MSR1 | Arginyl-tRNA synthetase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.71 | FP | 1.1 | 0.67 | FP | 1.11 | 0.53 | FP | 1.12 | 0.52 | FP | 1.11 | 0.54 | FP | Oth | Protein synthesis not required in the model | NA |
| YDR208W | MSS4 | Phosphatidylinositol 4-phosphate kinase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Phospholipid produced by this reaction leads to a dead end (1D-myo-Inositol 1,4,5-trisphosphate = IP3). This metabolite is used in other cellular processes such as signaling. | FP |
| YDR268W | MSW1 | Tryptophan-tRNA ligase | NA | NA | 1 | 4.3 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | 0.04 | TP | 1.08 | 0.76 | FP | 1.1 | 0.65 | FP | 1.11 | 0.47 | FP | 1.12 | 0.43 | FP | 1.11 | 0.53 | FP | Oth | Protein synthesis not required in the model | NA |
| YPL097W | MSY1 | Tyrosine-tRNA ligase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.74 | FP | 1.1 | 0.69 | FP | 1.11 | 0.55 | FP | 1.12 | 0.48 | FP | 1.11 | 0.55 | FP | Oth | Protein synthesis not required in the model | NA |
| YKR080W | MTD1 | NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGR055W | MUP1 | High affinity methionine permease | NA | NA | NA | NA | NA | 1 | 1 | 0.29 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YHL036W | MUP3 | Very low affinity methionine permease | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YGR007W | MUQ1 | Choline phosphate cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphocholine cytidylyltransferase) | NA | NA | NA | NA | NA | 1 | 1 | 0.3 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.01 | TP | 1.11 | 0.99 | TP | 1.12 | 1.02 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YNR043W | MVD1 | Mevalonate pyrophosphate decarboxylase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YLR382C | NAM2 | Leucine-tRNA ligase | NA | NA | 1 | 11.2 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.69 | FP | 1.1 | 0.68 | FP | 1.11 | 0.51 | FP | 1.12 | 0.56 | FP | 1.11 | 0.56 | FP | Oth | Protein synthesis not required in the model | NA |
| YDL040C | NAT1 | N-terminal acetyltransferase | NA | NA | 1 | 3.8 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.89 | TP | 1.1 | 0.87 | TP | 1.11 | 0.88 | TP | 1.12 | 0.8 | TP | 1.11 | 0.89 | TP | Oth | Protein N-terminal acetylation not required in the model | NA |
| YGR147C | NAT2 | N alpha-acetyltransferase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 0.9 | TP | 1.1 | 0.89 | TP | 1.11 | 0.96 | TP | 1.12 | 0.96 | TP | 1.11 | 0.96 | TP | Dis | Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates. | FP |
| YMR145C | NDE1 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.05 | TP | 1.12 | 1.05 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YDL085W | NDE2 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.26 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YML120C | NDI1 | NADH dehydrogenase (ubiquinone) | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.98 | TP | 1.1 | 0.97 | TP | 1.11 | 0.65 | FP | 1.12 | 0.93 | TP | 1.11 | 0.61 | FP | Unk | The model will ferment glycerol or lactate in a ndi1 strain, but the yields are much lower than the wild type strain yield. | NA |
| YLR138W | NHA1 | Putative Na+/H+ antiporter | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YJL126W | NIT2 | Nit protein, nitrilase superfamily member | NA | NA | NA | NA | NA | 1 | 1 | 0.72 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR351C | NIT3 | Nit protein, nitrilase superfamily member | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YLR328W | NMA1 | Nicotinamide/nicotinic acid mononucleotide adenylyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.05 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YGR010W | NMA2 | Nicotinamide/nicotinic acid mononucleotide adenylyltransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.38 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.03 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR195C | NMT1 | N-myristoyl transferase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Den | Metabolite produced by this reaction is a dead-end (N-Tetradecanoylglycylpeptide). | FP |
| YOR209C | NPT1 | Nicotinate phosphoribosyltransferase | NA | NA | 1 | 4.8 | FP | 1 | 1 | 0 | TP | 1 | 1 | 0.06 | TP | 1.08 | 0.89 | TP | 1.1 | 0.9 | TP | 1.11 | 0.97 | TP | 1.12 | 0.92 | TP | 1.11 | 0.95 | TP | Oth | Also potentially involved in cromatin silencing through adjusting the NAD/NADH balance. | NA |
| YGL067W | NPY1 | NADH pyrophosphatase 1 | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR001C | NTH1 | Neutral trehalase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YBR001C | NTH2 | Neutral trehalase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKL120W | OAC1 | Oxaloacetate transport protein | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YKL055C | OAR1 | 3-oxoacyl-[acyl-carrier-protein] reductase | NA | NA | 1 | 5.7 | FP | 1 | 1 | 0.09 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.75 | FP | 1.1 | 0.73 | FP | 1.11 | 0.47 | FP | 1.12 | 0.45 | FP | 1.11 | 0.56 | FP | Oth | It has been proposed that the role of the mitochondrial fatty acid synthase is to provide phospholipids for the mitochondrial inner membrane and that the disruption of genes in the FAS (including OAR1) would lead into inability to properly synthesize the inner membrane [Schneider97]. | NA |
| YPL134C | ODC1 | Mitochondrial 2-oxodicarboxylate transport protein | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YOR222W | ODC2 | Mitochondrial 2-oxodicarboxylate transport protein | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YGL055W | OLE1 | Delta-9-fatty acid desaturase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YJR073C | OPI3 | Unsaturated phospholipid N-methyltransferase | NA | NA | NA | NA | NA | 0 | 1 | 1.04 | TN | 0 | 1 | 0.16 | FN | 0 | 1.01 | FN | 0 | 1.01 | FN | 0 | 0.97 | FN | 0 | 1.03 | FN | 0 | 1.03 | FN | Unk | The activities catalyzed by this gene are totally lost when it is disrupted, but mutants are viable. The cells accumulate mmPE and membrane is devoid of PC [MIPS]. Surpsingly, mutant were not strict choline auxotrophs (choline req'd for an alternate route to produce PC). Reason why cells are viable is unknown; it has been speculated that a mutation in CHO2 may alter its substrate specificity (CHO2 catalyzes 1st of 3 steps in pathway from PE to PC, OPI3 primarily catalyzes 2nd and 3rd steps, can also catalyze 1st step but is very inefficient). | FN |
| YOR130C | ORT1 | Mitochondrial integral membrane protein, ornithine transporter | NA | NA | NA | NA | NA | 0 | 1 | 4.31 | TN | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | Weak false negative | NA |
| YJR051W | OSM1 | Osmotic growth protein | NA | NA | NA | NA | NA | 1 | 1 | 0.27 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YDR538W | PAD1 | Phenylacrylic acid decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YIL145C | PAN6 | Pantothenate synthase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YKR097W | PCK1 | Phosphoenolpyruvate carboxylkinase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 0.43 | 0.93 | FN | 0.93 | 1.04 | TP | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YEL058W | PCM1 | Phosphoacetylglucosamine mutase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | N-Acetylglucosamine synthesis is not required in the model. | FP |
| YGR202C | PCT1 | Cholinephosphate cytidylyltransferase\|phosphorylcholine transferase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | 0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 0.98 | TP | 1.12 | 1.01 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YER178W | PDA1 | Pyruvate dehydrogenase alpha subunit (E1 alpha) | NA | NA | NA | NA | NA | 1 | 1 | 0.35 | TP | 1 | 1 | 0.28 | TP | 1.08 | 1 | TP | 1.1 | 0.96 | TP | 1.11 | 0.78 | FP | 1.12 | 0.79 | TP | 1.11 | 0.9 | TP | Unk | Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol. | NA |
| YBR221C | PDB1 | Pyruvate dehydrogenase beta subunit (E1 beta) | NA | NA | NA | NA | NA | 1 | 1 | 0.09 | TP | 1 | 1 | 0 | TP | 1.08 | 0.93 | TP | 1.1 | 0.91 | TP | 1.11 | 0.66 | FP | 1.12 | 0.71 | FP | 1.11 | 0.8 | TP | Unk | Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol or ethanol. | NA |
| YLR044C | PDC1 | Pyruvate decarboxylase | NA | NA | 1 | 3.8 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.97 | TP | 1.11 | 0.99 | TP | Iso | There are three alternate isozymes in the model , but PDC1 deletion alone is sufficient to reduce PDC activity significantly enough to result in a slow growth phenotype. | NA |
| YLR134W | PDC5 | Pyruvate decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YGR087C | PDC6 | Pyruvate decarboxylase isozyme | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGL248W | PDE1 | 3',5'-cyclic-nucleotide phosphodiesterase, low affinity | NA | NA | NA | NA | NA | 1 | 1 | 2.85 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.97 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YOR360C | PDE2 | High affinity cAMP phosphodiesterase | NA | NA | NA | NA | NA | 1 | 1 | 0.24 | TP | 1 | 1 | 0.05 | TP | 1.08 | 1.06 | TP | 1.1 | 1.03 | TP | 1.11 | 1 | TP | 1.12 | 0.81 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YBR035C | PDX3 | Pyridoxine (pyridoxiamine) phosphate oxidase | NA | NA | NA | NA | NA | 1 | 1 | 0.71 | TP | 1 | 1 | -0.05 | TP | 1.08 | 0.86 | FP | 1.1 | 0.85 | FP | 1.11 | 0.74 | FP | 1.12 | 0.55 | FP | 1.11 | 0.61 | FP | Den | The whole pyridoxine metabolism is a dead end in the model. | NA |
| YBL030C | PET9 | ADP/ATP translocator | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | Dis | Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates. | FP |
| YGR240C | PFK1 | Phosphofructokinase alpha subunit | NA | NA | 0.19 | 4.8 | TN | 0.18 | 1 | -0.01 | TN | 0.19 | 1 | 0 | TN | 0.2 | 0.89 | FN | 1.06 | 0.95 | TP | 1.1 | 1.05 | TP | 1.12 | 1.08 | TP | 1.11 | 1.05 | TP | Dis | Slow growth in [Giaever02], but apparently normal growth in [Steinmetz02]. | NA |
| YMR205C | PFK2 | Phosphofructokinase beta subunit | NA | NA | 0.19 | 16.7 | TN | 0.18 | 1 | -0.01 | TN | 0.19 | 1 | -0.03 | TN | 0.2 | 0.7 | TN | 1.06 | 0.76 | FP | 1.1 | 0.95 | TP | 1.12 | 1.01 | TP | 1.11 | 0.97 | TP | Med | In YPDGE media the max glc uptake in the simulation is too low to cause pfk2 to have a growth defect. | NA |
| YIL107C | PFK26 | 6-phosphofructose-2-kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0.1 | TP | 1.08 | 1 | TP | 1.1 | 0.98 | TP | 1.11 | 0.99 | TP | 1.12 | 0.96 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YOL136C | PFK27 | 6-phosphofructo-2-kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YBR196C | PGI1 | Glucose-6-phosphate isomerase | 0.54 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | NA |
| YCR012W | PGK1 | 3-phosphoglycerate kinase | 0.1 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | NA |
| YKL127W | PGM1 | Phosphoglucomutase minor isoform | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YMR105C | PGM2 | Phosphoglucomutase | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 0 | 7.28 | FP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | Iso | Pgm2p is major isomform of phosphoglucomutase. Maybe the minor isoform (Pgm1p) can't fully compensate for loss of Pgm2p. | NA |
| YCL004W | PGS1 | 17 kDa phosphatidylglycerolphosphate synthase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Dis | Should not be absolutely essential [SGD]. Disrupts mitochondrial function somewhat. | FP |
| YNL316C | PHA2 | Prephenate dehydratase | NA | NA | NA | NA | NA | 0 | 0 | 9.87 | TN | 1 | 1 | -0.08 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YBR092C | PHO3 | Acid phosphatase | NA | NA | NA | NA | NA | 1 | 1 | -0.07 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YDR481C | PHO8 | Repressible alkaline phosphatase | NA | NA | NA | NA | NA | 1 | 1 | 0.19 | TP | 1 | 1 | 0 | TP | 1.08 | 1.03 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YML123C | PHO84 | Inorganic phosphate transporter | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.96 | TP | 1.1 | 0.83 | FP | 1.11 | 0.85 | TP | 1.12 | 0.82 | TP | 1.11 | 0.99 | TP | Iso | There are multiple alternative isozymes for the phosphate transporters, but Pho84p may be the dominant one under some conditions. | NA |
| YCR037C | PHO87 | Phosphate permease | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YBR296C | PHO89 | Na+/Pi symporter (putative) | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YJL198W | PHO90 | Low-affinity phosphate transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YNR013C | PHO91 | Low-affinity phosphate transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YNL267W | PIK1 | Phosphatidylinositol 4-kinase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Den | Phospholipid produced by this reaction leads to a dead-end (1D-myo-Inositol 1,4,5-trisphosphate). Also Stt4p is an isozyme. | FP |
| YPR113W | PIS1 | Phosphatidylinositol synthase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YPL268W | PLC1 | Phosphoinositide-specific phospholipase C | NA | NA | 1 | 14.8 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.72 | FP | 1.1 | 0.7 | FP | 1.11 | 0.88 | TP | 1.12 | 0.81 | TP | 1.11 | 0.89 | TP | Oth | Also involved in kinetochore function. | NA |
| YGL008C | PMA1 | Plasma membrane H+-ATPase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Iso | This is the major isoform of the cytosolic ATPase, but in the model a minor isoform can compensate for the function. Deletion of the minor isoform (which contains Pma2p instead of Pma1p) is not lethal experimentally. | FP |
| YPL036W | PMA2 | Plasma membrane ATPase | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YER003C | PMI40 | Mannose-6-phosphate isomerase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YCR024CA | PMP1 | Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p) | NA | NA | NA | NA | NA | 0.85 | 1 | 0.04 | TP | 0.23 | 1 | 0.01 | FN | 0.99 | 1.03 | TP | 1.03 | 1.03 | TP | 1.07 | 1.02 | TP | 1.03 | 1 | TP | 1.04 | 1 | TP | Med | If oxygen uptake rate on YPGal is increased the pmp1 growth rate increases to that of the wild type. | NA |
| YEL017CA | PMP2 | Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p) | NA | NA | NA | NA | NA | 0.85 | 1 | 0.33 | TP | 0.23 | 1 | 0 | FN | 0.99 | 1.02 | TP | 1.03 | 1.03 | TP | 1.07 | 1.03 | TP | 1.03 | 1.04 | TP | 1.04 | 1.03 | TP | Med | If oxygen uptake rate on YPGal is increased the pmp2 growth rate increases to that of the wild type. | NA |
| YDL095W | PMT1 | Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.04 | TP | 1.08 | 0.99 | TP | 1.1 | 1.02 | TP | 1.11 | 0.98 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YAL023C | PMT2 | Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase | NA | NA | 1 | 6.3 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.94 | TP | 1.1 | 0.94 | TP | 1.11 | 0.94 | TP | 1.12 | 0.96 | TP | 1.11 | 0.96 | TP | Oth | Mannosyntransferase activity not required in the model. | NA |
| YOR321W | PMT3 | Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YDL093W | PMT5 | Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGR199W | PMT6 | Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | 0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YGL037C | PNC1 | Nicotinamidase\|pyrazinamidase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.04 | TP | 1.1 | 1.06 | TP | 1.11 | 1.05 | TP | 1.12 | 1.09 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YLR209C | PNP1 | Purine nucleoside phosphorylase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.05 | 1 | TP | 1.1 | 1.02 | TP | 1.07 | 1.01 | TP | NA | NA | NA |
| YPL188W | POS5 | Involved in oxidative stress | NA | NA | 1 | 8.3 | FP | 1 | 1 | 0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.7 | FP | 1.1 | 0.82 | FP | 1.11 | 0.58 | FP | 1.12 | 0.54 | FP | 1.11 | 0.6 | FP | Mod | Does not grow well under aerobic conditions, because Pos5p is the primary source of NADPH in mitochondria [Outten03]. May need to change the model so that only Pos5p can provide NADPH in mitochondria. | NA |
| YIL160C | POT1 | 3-oxoacyl CoA thiolase | NA | NA | NA | NA | NA | 1 | 1 | 0.69 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 0.95 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YGL205W | POX1 | Fatty-acyl coenzyme A oxidase | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.97 | TP | 1.12 | 1 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YHR026W | PPA1 | Proteolipid\|vacuolar ATPase V0 domain subunit c" | NA | NA | 1 | 5.6 | FP | 1 | 1 | 0.03 | TP | 1 | 1 | 0.01 | TP | 1.08 | 0.8 | FP | 1.1 | 0.65 | FP | 1.11 | 0.61 | FP | 1.12 | 0.6 | FP | 1.11 | 0.68 | FP | Oth | See other vacuolar ATPase components. | NA |
| YMR267W | PPA2 | Inorganic pyrophosphatase | NA | NA | 1 | 3.4 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.74 | FP | 1.1 | 0.67 | FP | 1.11 | 0.54 | FP | 1.12 | 0.49 | FP | 1.11 | 0.54 | FP | Mod | PPA2 deletion strain has lost mitochondrial DNA apparently because pyrophosphate produced during replication cannot be converted into phosphate [Lundin91]. The model does not run any of the reactions producing ppi[m] in the ppa2 and utilizes the cytoplasmic forms of the reactions instead. | NA |
| YPL148C | PPT2 | Phosphopantetheine:protein transferase (PPTase) | NA | NA | 1 | 7 | FP | 1 | 1 | 0.04 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.64 | FP | 1.1 | 0.65 | FP | 1.11 | 0.52 | FP | 1.12 | 0.53 | FP | 1.11 | 0.51 | FP | Oth | CoA biosynthesis not required in the model. | FN |
| YDR300C | PRO1 | Gamma-glutamyl kinase | NA | NA | 1 | 12.6 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.64 | FP | 1.1 | 0.69 | FP | 1.11 | 0.95 | TP | 1.12 | 0.97 | TP | 1.11 | 1.06 | TP | Unk | Should be a proline auxotroph, but should grow fine on rich media. Model synthesizes proline from glutamate using ornithine as an intermediate. | NA |
| YOR323C | PRO2 | Gamma-glutamyl phosphate reductase | NA | NA | NA | NA | NA | 1 | 0 | 5.16 | FP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | Unk | Should be a proline auxotroph. Model synthesizes proline from glutamate using ornithine as an intermediate. | NA |
| YER023W | PRO3 | Delta 1-pyrroline-5-carboxylate reductase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 1.06 | TP | 1.1 | 1.05 | TP | 1.01 | 1.04 | TP | 1.11 | 1.11 | TP | 1.05 | 1.06 | TP | Dis | Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates. | FP |
| YHL011C | PRS3 | Ribose-phosphate pyrophosphokinase | NA | NA | 1 | 7.6 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 0.66 | FP | 1.1 | 0.73 | FP | 1.11 | 1 | TP | 1.12 | 0.91 | TP | 1.11 | 0.92 | TP | Oth | Prs3p has an unknown role in controlling cell growth. Its deletion causes a wide variety of phenotypes including small cell size. | NA |
| YBL068W | PRS4 | Ribose-phosphate pyrophosphokinase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YOL061W | PRS5 | Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase) | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.99 | TP | 1.1 | 1.01 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YDL055C | PSA1 | GDP-mannose pyrophosphorylase\|mannose-1-phosphate guanylyltransferase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YNL169C | PSD1 | Phosphatidylserine decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.02 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YGR170W | PSD2 | Phosphatidylserine decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | 0.06 | TP | 1 | 1 | 0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKR093W | PTR2 | Peptide transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YPL212C | PUS1 | TRNA pseudouridine synthase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.03 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YGL063W | PUS2 | Pseudouridine synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.35 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YNL292W | PUS4 | Pseudouridine synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR142W | PUT1 | Proline oxidase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.09 | 1 | TP | 0.91 | 1 | TP | 1.1 | 1 | TP | 0.99 | 1.01 | TP | NA | NA | NA |
| YHR037W | PUT2 | Delta-1-pyrroline-5-carboxylate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 0.97 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YOR348C | PUT4 | Proline specific permease | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPL147W | PXA1 | ABC transporter of long-chain fatty acids | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1.02 | TP | 1.1 | 1.05 | TP | 1.11 | 1.05 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YKL188C | PXA2 | ABC transporter 2 | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YGL062W | PYC1 | Pyruvate carboxylase | NA | NA | NA | NA | NA | 1 | 1 | 0.13 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YBR218C | PYC2 | Pyruvate carboxylase | NA | NA | NA | NA | NA | 1 | 1 | 0.16 | TP | 1 | 1 | 0.1 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YOR347C | PYK2 | Pyruvate kinase, glucose-repressed isoform | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.04 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YHR001WA | QCR1 | Ubiqunol-cytochrome c oxidoreductase complex 8.5 kDa subunit | NA | NA | NA | NA | NA | 0.89 | 1 | -0.03 | TP | 0.82 | 1 | 0 | TP | 0.98 | 1.01 | TP | 0.24 | 1.02 | FN | 0.14 | 1.02 | FN | 0.08 | 1.01 | FN | 0.17 | 1.03 | FN | Iso | Deletion of QCR10 does not impair growth on non-fermentable carbon source [MIPS]. QCR10 is not essential to formation of cytochrome bc1 complex [Cruciat00]. Thus, the false prediction is due to way we have modeled the complex. This subunit should be made a non-essential part of the complex since it only plays structural role. | NA |
| YPR191W | QCR2 | 40 kDa ubiquinol cytochrome-c reductase core protein 2 | NA | NA | 0.9 | 4.4 | TN | 0.89 | 1 | -0.01 | TP | 0.82 | 1 | -0.05 | TP | 0.98 | 0.92 | TP | 0.24 | 0.87 | FN | 0.14 | 0.49 | TN | 0.08 | 0.39 | TN | 0.17 | 0.6 | TN | Med | This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. | NA |
| YFR033C | QCR6 | Ubiquinol cytochrome C oxidoreductase subunit 6 (17 kDa) | NA | NA | NA | NA | NA | 0.89 | 1 | -0.02 | TP | 0.82 | 1 | 0.1 | TP | 0.98 | 1.02 | TP | 0.24 | 0.98 | FN | 0.14 | 0.87 | FN | 0.08 | 0.82 | FN | 0.17 | 0.92 | FN | Iso | Deletion of QCR6 does not have significant effect on the formation or stability of cytochrome bc complex so that it should not play an essential role in complex formation as indicated by the gene-protein-reaction associations currently. | NA |
| YDR529C | QCR7 | Ubiquinol cytochrome C oxidoreductase subunit 7 (14 kDa) | NA | NA | 0.9 | 5.3 | TN | 0.89 | 1 | -0.02 | TP | 0.82 | 1 | -0.02 | TP | 0.98 | 0.67 | FP | 0.24 | 0.65 | TN | 0.14 | 0.53 | TN | 0.08 | 0.51 | TN | 0.17 | 0.59 | TN | Oth | Mitochondrial maintenance not required in the model in primarily fermentative conditions. | NA |
| YJL166W | QCR8 | Ubiquinol cytochrome C reductase subunit 8 (11 kDa) | NA | NA | 0.9 | 6.3 | TN | 0.89 | 1 | 0.05 | TP | 0.82 | 1 | 0.15 | TP | 0.98 | 0.93 | TP | 0.24 | 0.86 | FN | 0.14 | 0.6 | TN | 0.08 | 0.52 | TN | 0.17 | 0.54 | TN | Med | This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. | NA |
| YGR183C | QCR9 | Ubiquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9 | NA | NA | NA | NA | NA | 0.89 | 1 | 0.13 | TP | 0.82 | 1 | 0.21 | TP | 0.98 | 0.96 | TP | 0.24 | 0.85 | TN | 0.14 | 0.6 | TN | 0.08 | 0.58 | TN | 0.17 | 0.63 | TN | NA | NA | NA |
| YHR074W | QNS1 | Glutamine-dependent NAD synthetase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | NAD biosynthesis not required in the model. | FP |
| YDL103C | QRI1 | UDP-N-acetylglucosamine pyrophosphorylase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | UDP-N-Acetylglucosamine synthesis is not required in the model. | FP |
| YDL090C | RAM1 | Farnesyltransferase beta subunit | NA | NA | 1 | 7 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.79 | FP | 1.1 | 0.82 | FP | 1.11 | 0.97 | TP | 1.12 | 0.79 | TP | 1.11 | 0.88 | TP | Oth | Farnesyltransferases not required in the model | NA |
| YKL019W | RAM2 | CAAX farnesyltransferase alpha subunit | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Quinone biosynthesis is not required in the model. | NA |
| YCR036W | RBK1 | Ribokinase | NA | NA | NA | NA | NA | 1 | 1 | 0.27 | TP | 1 | 1 | 0.24 | TP | 1.08 | 0.98 | TP | 1.1 | 0.99 | TP | 1.11 | 0.97 | TP | 1.12 | 0.94 | TP | 1.11 | 0.93 | TP | NA | NA | NA |
| YBR002C | RER2 | Cis-prenyltransferase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Quinone biosynthesis is not required in the model | FP |
| YIL053W | RHR2 | DL-glycerol-3-phosphatase | NA | NA | NA | NA | NA | 1 | 1 | 0.16 | TP | 1 | 1 | -0.07 | TP | 1.08 | 0.97 | TP | 1.1 | 0.99 | TP | 1.11 | 1.06 | TP | 1.12 | 1.01 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YBL033C | RIB1 | GTP cyclohydrolase II | NA | NA | 1 | 10.3 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.75 | FP | 1.1 | 0.73 | FP | 1.11 | 0.67 | FP | 1.12 | 0.65 | FP | 1.11 | 0.67 | FP | Bio | FAD biosynthesis not required in the model | NA |
| YOL143C | RIB4 | 6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) | NA | NA | 1 | 4.5 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Riboflavin biosynthesis is not required in the model. | NA |
| YBR256C | RIB5 | Riboflavin biosynthesis | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Riboflavin biosynthesis is not required in the model | FP |
| YBR153W | RIB7 | Protein involved in the biosynthesis of riboflavin, second step in the riboflavin biosynthesis pathway | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Riboflavin biosynthesis is not required in the model. | NA |
| YEL024W | RIP1 | Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex | NA | NA | NA | NA | NA | 0.89 | 1 | 0.36 | TP | 0.82 | 1 | 0.46 | TP | 0.98 | 0.9 | TP | 0.24 | 0.82 | TN | 0.14 | 0.54 | TN | 0.08 | 0.42 | TN | 0.17 | 0.55 | TN | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YOR095C | RKI1 | Ribose-5-phosphate ketol-isomerase | 0.81 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | In silico slow growth. | NA |
| YER070W | RNR1 | Ribonucleotide reductase, large (R1) subunit | NA | NA | 1 | 22.3 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | -0.04 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | DNA synthesis not required in the model. | NA |
| YJL026W | RNR2 | Ribonucleotide reductase subunit\|ribonucleotide reductase, small (R2) subunit | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | DNA synthesis not required in the model. | NA |
| YIL066C | RNR3 | Ribonucleotide reductase, large (R1) subunit | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGR180C | RNR4 | Ribonucleotide reductase, small (R2) subunit | NA | NA | 1 | 8.5 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.81 | FP | 1.1 | 0.69 | FP | 1.11 | 0.59 | FP | 1.12 | 0.62 | FP | 1.11 | 0.6 | FP | Oth | DNA synthesis not required in the model. | NA |
| YJL121C | RPE1 | D-ribulose-5-Phosphate 3-epimerase | NA | NA | NA | NA | NA | 0.97 | 1 | 0.67 | TP | 1 | 1 | 0.22 | TP | 1.08 | 0.92 | TP | 1.1 | 0.84 | FP | 1.06 | 0.78 | FP | 1.11 | 0.78 | TP | 1.08 | 0.92 | TP | Unk | The PPP is only used at a low level on glycerol. The effect of this deletion is small in vivo anyway. | NA |
| YER043C | SAH1 | S-adenosyl-L-homocysteine hydrolase (putative) | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YLR180W | SAM1 | S-adenosylmethionine synthetase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.05 | TP | 1.08 | 0.98 | TP | 1.1 | 0.96 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YDR502C | SAM2 | Methionine biosynthesis regulation | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YPL274W | SAM3 | High affinity S-adenosylmethionine permease | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.02 | TP | 1.1 | 1.05 | TP | 1.11 | 1.05 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YPL273W | SAM4 | AdoMet-homocysteine methyltransferase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.05 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YMR272C | SCS7 | Desaturase\|hydroxylase | NA | NA | NA | NA | NA | 1 | 1 | 2.17 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 0.99 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YKL148C | SDH1 | Succinate dehydrogenase flavoprotein subunit | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | 0.06 | TP | 1.08 | 1 | TP | 1.1 | 0.97 | TP | 1.11 | 0.69 | FP | 1.12 | 0.79 | TP | 1.11 | 0.61 | FP | Iso | Sdh1p is not considered to be an essential part of the succinate dehydrogenase complex. | NA |
| YLL041C | SDH2 | Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0.07 | TP | 1.08 | 0.97 | TP | 1.01 | 0.97 | TP | 0.8 | 0.67 | TN | 0.58 | 0.75 | TN | 0.93 | 0.59 | FP | Med | With a lower lactate uptake rate the model shows slow growth on lactate. | NA |
| YKL141W | SDH3 | Succinate dehydrogenase cytochrome b | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Unk | The model has an isozyme that includes an alternate subunit with high imilarity to Sdh3p, but even if this is removed the mutation is non-lethal. | NA |
| YDR178W | SDH4 | Succinate dehydrogenase membrane anchor subunit | NA | NA | NA | NA | NA | 1 | 1 | -0.07 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 0.82 | TP | 1.12 | 0.92 | TP | 1.11 | 0.74 | FP | Iso | Sdh4p is not considered to be an essential part of the succinate dehydrogenase complex. | NA |
| YIL168W | SDL1 | NA | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YFL045C | SEC53 | Phosphomannomutase | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YMR013C | SEC59 | Membrane protein\|required for core glycosylation | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Den | Substrate in this reaction is a dead-end (dolichol). | FP |
| YOR184W | SER1 | Phosphoserine transaminase | NA | NA | NA | NA | NA | 1 | 0 | 28.8 | FP | 0.99 | 1 | -0.02 | TP | 1.07 | 1.03 | TP | 1.09 | 1.02 | TP | 1.1 | 1.02 | TP | 1.12 | 0.99 | TP | 1.11 | 1.04 | TP | Unk | Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source. | NA |
| YGR208W | SER2 | Phosphoserine phosphatase | NA | NA | NA | NA | NA | 1 | 0 | 5.08 | FP | 0.99 | 1 | 0.03 | TP | 1.07 | 1.02 | TP | 1.09 | 0.99 | TP | 1.1 | 0.98 | TP | 1.12 | 0.95 | TP | 1.11 | 1 | TP | Unk | Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source. | NA |
| YER081W | SER3 | 3-phosphoglycerate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | 0.33 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YIL074C | SER33 | 3-phosphoglycerate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.05 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YDR023W | SES1 | Serine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YDL168W | SFA1 | Glutathione-dependent formaldehyde dehydrogenase\|long-chain alcohol dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YJR095W | SFC1 | Succinate-fumarate transport protein | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YBR263W | SHM1 | Serine hydroxymethyltransferase, mitochondrial | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.04 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR058C | SHM2 | Serine hydroxymethyltransferase | NA | NA | NA | NA | NA | 1 | 0 | 4.29 | FP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | Unk | Shm2p should not be required for growth in minimal media as even a shm1/shm2 double mutant is a glycine prototroph. | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YDL052C | SLC1 | 1-acyl-sn-gylcerol-3-phosphate acyl transferase (putative) | NA | NA | NA | NA | NA | 0 | 1 | 0.1 | FN | 0 | 1 | 0.02 | FN | 0 | 0.99 | FN | 0 | 1 | FN | 0 | 0.99 | FN | 0 | 1.04 | FN | 0 | 1 | FN | Bio | Two distinct enzymes are necessary for PA synthesis in lipid particles: the second step, acylation of lysophosphatidic acid is catalyzed by Slc1p; a specific point mutant allows cells to grow without making sphingolipids; this deletion is lethal because PA is req'd in our biomass. | NA |
| YNR034W | SOL1 | Multicopy Suppressor Of los1 | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YCR073WA | SOL2 | Multicopy suppressor of los1-1 | NA | NA | NA | NA | NA | 1 | 1 | 0.12 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YHR163W | SOL3 | Weak multicopy suppressor of los1-1 | NA | NA | NA | NA | NA | 1 | 1 | 0.31 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YGR248W | SOL4 | 6-phosphogluconolactonase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YKL184W | SPE1 | Ornithine decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YOL052C | SPE2 | S-adenosylmethionine decarboxylase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0 | TP | 1.08 | 1.03 | TP | 1.1 | 1.06 | TP | 1.11 | 1.05 | TP | 1.12 | 1.08 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YPR069C | SPE3 | Putrescine aminopropyltransferase (spermidine synthase) | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR146C | SPE4 | Spermine synthase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YOR190W | SPR1 | Exo-1,3-beta-glucanase, sporulation-specific | NA | NA | NA | NA | NA | 1 | 1 | 0.23 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.07 | TP | 1.11 | 1.05 | TP | NA | NA | NA |
| YMR101C | SRT1 | Cis-prenyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKL218C | SRY1 | Pyridoxal-5'phosphate-dependent enzyme homologous to mouse glial serine racemase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.04 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YDR536W | STL1 | Sugar transporter-like protein | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.03 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YJR130C | STR2 | Cystathionine gamma-synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.07 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YLR305C | STT4 | Phosphatidylinositol-4-kinase\|similar to VPC34 | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Den | Phospholipid produced by this reaction leads to a dead-end (1D-myo-Inositol 1,4,5-trisphosphate). Also Pik1p is an isozyme. | FP |
| YMR054W | STV1 | 110 kDa subunit; not in vacuole membrane\|vacuolar H-ATPase | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | -0.05 | TP | 1.08 | 0.97 | TP | 1.1 | 0.97 | TP | 1.11 | 0.83 | TP | 1.12 | 0.86 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YIL162W | SUC2 | Invertase (sucrose hydrolyzing enzyme) | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 0.98 | TP | 1.12 | 0.96 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YBR294W | SUL1 | Sulfate uptake is mediated by specific sulfate transporters SUL1 and SUL2, which control the concentration of endogenous activated sulfate intermediates. | NA | NA | NA | NA | NA | 1 | 1 | 0.08 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR092W | SUL2 | High affinity sulfate permease | NA | NA | NA | NA | NA | 1 | 1 | 0.1 | TP | 1 | 1 | 0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPL057C | SUR1 | Integral membrane protein\|similar to YBR161w, Hoc1p, and Och1p | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 0.97 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YDR297W | SUR2 | Sphingosine hydroxylase | NA | NA | NA | NA | NA | 1 | 1 | 0.29 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YLR372W | SUR4 | Elongase | NA | NA | 1 | 3.4 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.75 | FP | 1.1 | 0.79 | FP | 1.11 | 0.89 | TP | 1.12 | 0.91 | TP | 1.11 | 0.92 | TP | Bio | Involved in sphingolipid biosynthesis. These lipids are not currently required for growth by the model. | NA |
| YLR354C | TAL1 | Transaldolase, enzyme in the pentose phosphate pathway | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.99 | TP | 1.1 | 1.02 | TP | 1.11 | 0.92 | TP | 1.12 | 1.09 | TP | 1.11 | 0.95 | TP | NA | NA | NA |
| YBR069C | TAT1 | Amino acid transport protein for valine, leucine, isoleucine, and tyrosine | NA | NA | NA | NA | NA | 1 | 1 | 0.7 | TP | 1 | 1 | 0 | TP | 1.08 | 0.87 | FP | 1.1 | 0.98 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1.01 | TP | Iso | There are multiple alternative isozymes for amino acid transporters. | NA |
| YOL020W | TAT2 | Tryptophan permease, high affinity | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YJL052W | TDH1 | Glyceraldehyde-3-phosphate dehydrogenase 1 | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 1.02 | TP | 1.11 | 1.05 | TP | 1.12 | 1.05 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YJR009C | TDH2 | Glyceraldehyde 3-phosphate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 1.02 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YGR192C | TDH3 | Glyceraldehyde-3-phosphate dehydrogenase 3 | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.97 | TP | 1.1 | 0.94 | TP | 1.11 | 0.98 | TP | 1.12 | 0.95 | TP | 1.11 | 0.98 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YDL185W | TFP1 | Site-specific endonuclease VDE (PI-SceI)\|vacuolar ATPase V1 domain subunit A (69 kDa)\|protein with three regions (ABC) that are spliced to yield the extein AC and the intein B; AC is a 69K vacuolar (H+)-ATPase, and B is a 50K site-specfic endonuclease named VDE (PI-SceI) that is homologous to HO. Cleavage is meiosis-specific and induces ge | NA | NA | 1 | 12.2 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.7 | FP | 1.1 | 0.66 | FP | 1.11 | 0.49 | FP | 1.12 | 0.57 | FP | 1.11 | 0.59 | FP | Oth | The tfp1 null mutant is viable but is calcium-sensitive, lacks vacuolar (H )-ATPase activity, and is defective in vacuolar acidification and assembly of the remaining V1 subunits [SGD]. pH balancing problem. | NA |
| YPL234C | TFP3 | Vacuolar ATPase V0 domain subunit c' (17 kDa)\|vacuolar H(+) ATPase 17 kDa subunit C | NA | NA | 1 | 7.1 | FP | 1 | 1 | 0.03 | TP | 1 | 1 | 0.04 | TP | 1.08 | 0.79 | FP | 1.1 | 0.66 | FP | 1.11 | 0.63 | FP | 1.12 | 0.62 | FP | 1.11 | 0.63 | FP | Oth | See other vacuolar ATPase components. | NA |
| YOL055C | THI20 | THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3. | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YPL258C | THI21 | THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3. | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.1 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YPR121W | THI22 | THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3. | NA | NA | NA | NA | NA | 1 | 1 | 0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 0.99 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YPL214C | THI6 | TMP pyrophosphorylase\|hydroxyethylthiazole kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.07 | TP | 1 | 1 | 0 | TP | 1.08 | 0.94 | TP | 1.1 | 0.98 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR237W | THI7 | Thiamine transporter | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.04 | TP | 1.1 | 1.07 | TP | 1.11 | 1.07 | TP | 1.12 | 1.1 | TP | 1.11 | 1.08 | TP | NA | NA | NA |
| YOR143C | THI80 | Thiamin pyrophosphokinase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Thiamin biosynthesis not required in the model | FP |
| YHR025W | THR1 | Homoserine kinase | NA | NA | NA | NA | NA | 1 | 1 | 6.34 | TP | 1 | 1 | -0.08 | TP | 1.08 | 0.99 | TP | 1.1 | 0.92 | TP | 1.11 | 0.89 | TP | 1.12 | 0.76 | FP | 1.11 | 0.97 | TP | Dis | This should only be a threonine auxotroph [SGD]. May play some other uncharacterized role. | NA |
| YCR053W | THR4 | Threonine synthase | NA | NA | NA | NA | NA | 1 | 0 | 7.67 | FP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 0.99 | TP | 1.11 | 1.03 | TP | Unk | Threonine can be synthesized by the model from glycine using Gly1p. If CYSTL (Cys1p) and AHCi (Sah1p) reactions are removed the false positive prediction is corrected and both of these have putative assignments, but neither can be removed from the model. | NA |
| YIL078W | THS1 | Threonine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 1.08 | 1.2 | TP | 1.1 | 1.23 | TP | 1.11 | 1.38 | TP | 1.12 | 1.24 | TP | 1.11 | 1.25 | TP | Oth | Protein synthesis not required in the model | NA |
| YPR074C | TKL1 | Transketolase 1 | NA | NA | NA | NA | NA | 1 | 1 | 4.11 | TP | 1 | 1 | 0.1 | TP | 1.08 | 0.99 | TP | 1.1 | 0.97 | TP | 1.11 | 0.9 | TP | 1.12 | 1 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YJR066W | TOR1 | Phosphatidylinositol kinase homolog | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YKL203C | TOR2 | Putative protein/phosphatidylinositol kinase involved in signaling activation of translation initiation, distribution of the actin cytoskeleton, and meiosis | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Den | Phospholipid produced by this reaction leads to a dead end (phosphatidyl-1D-myo-inositol 3,4-bisphosphate). | FP |
| YDR050C | TPI1 | Triosephosphate isomerase | 0.2 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0.22 | 0.98 | FN | 1.04 | 0.93 | TP | 1.04 | 0.93 | TP | 0.41 | 0.93 | FN | 0.89 | 0.92 | TP | Dis | Mutant is unable to grow on glucose as sole carbon source. If ethanol or acetate is added to media containing glucose or galactose, cells are viable. Impaired growth probably due to NADH/energy shortage on glucose [Compagno01]. In one study this gene is found to be essential [Giaever02], wheras in the other one it has no phenotype [Steinmetz02]. | FP |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YBR126C | TPS1 | Trehalose-6-phosphate synthase/phosphatase complex 56 kDa synthase subunit | NA | NA | 1 | 6.8 | FP | 0 | 1 | -0.06 | TN | 1 | 1 | -0.02 | TP | 1.08 | 0.81 | FP | 1.1 | 0.83 | FP | 1.11 | 0.91 | TP | 1.12 | 0.86 | TP | 1.11 | 0.89 | TP | Med | Essential for growth on glucose and fructose [MIPS]. Deletion of TPS1 totally abolishes trehalose-6-phosphate synthase activity and measurable trehalose production, but YP media contains trehalose so TPS1 should not be required. | NA |
| YDR074W | TPS2 | Trehalose-6-phosphate phosphatase | NA | NA | 1 | 18 | FP | 0 | 1 | 0 | TN | 1 | 1 | -0.05 | TP | 1.08 | 0.96 | TP | 1.1 | 0.95 | TP | 1.11 | 1.06 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | Med | See TPS1. | NA |
| YMR261C | TPS3 | Trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit | NA | NA | NA | NA | NA | 1 | 1 | 0.1 | TP | 1 | 1 | 0 | TP | 1.08 | 0.99 | TP | 1.1 | 0.98 | TP | 1.11 | 0.99 | TP | 1.12 | 0.96 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YDR007W | TRP1 | N-(5'-phosphoribosyl)-anthranilate isomerase | NA | NA | NA | NA | NA | 0 | 0 | 5.83 | TN | 1 | 1 | 0.02 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.05 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YER090W | TRP2 | Anthranilate synthase component | NA | NA | NA | NA | NA | 1 | 1 | 2.88 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.05 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YKL211C | TRP3 | Anthranilate synthase component II\|indole-3-phosphate | NA | NA | NA | NA | NA | 0 | 0 | 7.77 | TN | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.06 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YDR354W | TRP4 | Anthranilate phosphoribosyl transferase | NA | NA | NA | NA | NA | 0 | 1 | 2.64 | TN | 1 | 1 | -0.03 | TP | 1.08 | 0.99 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | Weak false negative | NA |
| YGL026C | TRP5 | Tryptophan synthetase | NA | NA | NA | NA | NA | 0 | 1 | 1.4 | TN | 1 | 1 | 0.06 | TP | 1.08 | 0.97 | TP | 1.1 | 0.99 | TP | 1.11 | 0.95 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | Weak false negative | NA |
| YDR353W | TRR1 | Thioredoxin reductase\|EC 1.6.4.5 | 0 | TN | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| YHR106W | TRR2 | Thioredoxin reductase | NA | NA | NA | NA | NA | 1 | 1 | -0.05 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YBR265W | TSC10 | 3-ketosphinganine reductase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Sphingolipid synthesis not required in the model | FP |
| YML100W | TSL1 | Similar to TPS3 gene product\|trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YBR166C | TYR1 | Prephenate dehydrogenase (NADP+) | NA | NA | 1 | 3.5 | FP | 1 | 1 | 0 | TP | 1 | 1 | -0.01 | TP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Unk | Should be a tyrosine auxotroph, but the media contains tyrosine. Also, the model has an alternative reaction with no gene association. | NA |
| YGR185C | TYS1 | Tyrosine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YGR019W | UGA1 | Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase) | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YBR006W | UGA2 | Succinate semialdehyde dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0.2 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YDL210W | UGA4 | GABA-specific transport protein | NA | NA | NA | NA | NA | 1 | 1 | 0.11 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKL035W | UGP1 | Uridinephosphoglucose pyrophosphorylase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Reaction produces UDPglc, which is not required in our model. | FP |
| YKL216W | URA1 | Dihydroorotate dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 0.98 | TP | 1.11 | 0.98 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YMR271C | URA10 | Orotate phosphoribosyltransferase 2 | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YJL130C | URA2 | Aspartate transcarbamylase\|carbamoyl phosphate synthetase\|glutamine amidotransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.06 | TP | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YLR420W | URA4 | Dihydroorotase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 1.04 | TP | 1.12 | 1.06 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YML106W | URA5 | Orotate phosphoribosyltransferase 1 | NA | NA | NA | NA | NA | 1 | 1 | 0.03 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.03 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YKL024C | URA6 | Uridine-monophosphate kinase (uridylate kinase) | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | RNA and protein synthesis not required in the model. | FP |
| YBL039C | URA7 | CTP synthase | NA | NA | 1 | 3.2 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | 0 | TP | 1.08 | 0.82 | FP | 1.1 | 0.89 | TP | 1.11 | 0.86 | TP | 1.12 | 0.91 | TP | 1.11 | 0.85 | TP | Med | Model does not require ctp to grow on complex media. | NA |
| YJR103W | URA8 | CTP synthase | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 1.01 | TP | 1.12 | 1 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YDR400W | URH1 | Uridine nucleosidase (uridine ribohydrolase); EC 3.2.2.3 | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YNR012W | URK1 | Uridine kinase | NA | NA | NA | NA | NA | 1 | 1 | 0.06 | TP | 1 | 1 | 0 | TP | 1.08 | 0.97 | TP | 1.1 | 0.95 | TP | 1.11 | 0.99 | TP | 1.12 | 1.01 | TP | 1.11 | 1 | TP | NA | NA | NA |
| YJR049C | UTR1 | Associated with ferric reductase | NA | NA | NA | NA | NA | 1 | 1 | 0.14 | TP | 1 | 1 | -0.07 | TP | 1.08 | 0.95 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.95 | TP | 1.11 | 0.97 | TP | NA | NA | NA |
| YGR094W | VAS1 | Valine-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YGR065C | VHT1 | H+-biotin symporter | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | Biotin not required in our model, but bakers' yeast is auxotrophic for biotin (vitamin H) and depends on the efficient uptake of this compound from the environment [Stolz99]. | NA |
| YPR036W | VMA13 | Vacuolar H(+) ATPase V1 sector 54 kDa subunit | NA | NA | 1 | 5.9 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | 0.03 | TP | 1.08 | 0.73 | FP | 1.1 | 0.61 | FP | 1.11 | 0.59 | FP | 1.12 | 0.62 | FP | 1.11 | 0.68 | FP | Oth | See other vacuolar ATPase components. | NA |
| YBR127C | VMA2 | Vacuolar ATPase V1 domain subunit B (60 kDa) | NA | NA | 1 | 10.6 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.86 | FP | 1.1 | 0.7 | FP | 1.11 | 0.75 | FP | 1.12 | 0.7 | FP | 1.11 | 0.73 | FP | Oth | See other vacuolar ATPase components. | NA |
| YOR332W | VMA4 | E subunit of V1 sector\|vacuolar H(+) ATPase 27 kDa subunit | NA | NA | 1 | 5.2 | FP | 1 | 1 | 0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.9 | TP | 1.1 | 0.87 | TP | 1.11 | 0.65 | FP | 1.12 | 0.61 | FP | 1.11 | 0.66 | FP | Oth | See other vacuolar ATPase components. | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YKL080W | VMA5 | V1 sector hydrophilic subunit C\|vacuolar ATPase V1 domain subunit C (42 kDa)\|vacuolar H-ATPase | NA | NA | 1 | 6.1 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.66 | FP | 1.1 | 0.62 | FP | 1.11 | 0.57 | FP | 1.12 | 0.51 | FP | 1.11 | 0.57 | FP | Oth | See other vacuolar ATPase components. | NA |
| YLR447C | VMA6 | Vacuolar ATPase V0 domain subunit d (36 kDa)\|vacuolar H(+) ATPase 36 kDa subunit (D subunit of VO sector) | NA | NA | 1 | 10.9 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.02 | TP | 1.08 | 0.65 | FP | 1.1 | 0.59 | FP | 1.11 | 0.58 | FP | 1.12 | 0.57 | FP | 1.11 | 0.65 | FP | Oth | The vma6 null mutant is viable but shows a growth defect at neutral pH and is sensitive to calcium. pH balancing problem. | NA |
| YGR020C | VMA7 | Vacuolar ATPase V1 domain subunit F (14 kDa) | NA | NA | 1 | 9.9 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | 0 | TP | 1.08 | 0.72 | FP | 1.1 | 0.62 | FP | 1.11 | 0.63 | FP | 1.12 | 0.64 | FP | 1.11 | 0.66 | FP | Oth | See other vacuolar ATPase components. | NA |
| YEL051W | VMA8 | V1 catalytic sector D subunit\|vacuolar H-ATPase | NA | NA | 1 | 14.4 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.75 | FP | 1.1 | 0.65 | FP | 1.11 | 0.57 | FP | 1.12 | 0.58 | FP | 1.11 | 0.63 | FP | Oth | The vma8 null mutant is viable but lacks vacuolar (H )-ATPase activity, cannot grow at neutral pH or on nonfermentable carbon sources, and fails to accumulate quinacrine in the vacuole [SGD]. The slow growth phenotype is probably because of problems with pH balancing. | NA |
| YOR270C | VPH1 | V0 sector subunit\|essential for vacuolar acidification and vacuolar H-ATPase activity\|vacuolar ATPase V0 domain subunit a (100 kDa)\|vacuolar H-ATPase | NA | NA | 1 | 3.4 | FP | 1 | 1 | 0.01 | TP | 1 | 1 | 0.02 | TP | 1.08 | 0.88 | TP | 1.1 | 0.78 | FP | 1.11 | 0.8 | TP | 1.12 | 0.78 | TP | 1.11 | 0.91 | TP | Oth | See other vacuolar ATPase components. | NA |
| YLR240W | VPS34 | Phosphatidylinositol 3-kinase | NA | NA | 1 | 18.9 | FP | 1 | 1 | -0.01 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.58 | FP | 1.1 | 0.56 | FP | 1.11 | 0.61 | FP | 1.12 | 0.55 | FP | 1.11 | 0.56 | FP | Oth | PI3 kinase activity involved in signaling processes - in the model this leads to a dead end. | NA |
| YOL097C | WRS1 | Tryptophan-tRNA ligase | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YGR194C | XKS1 | Xylulokinase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.14 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YJR133W | XPT1 | Xanthine phosphoribosyl transferase | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | 0.04 | TP | 1.08 | 1.03 | TP | 1.1 | 1.05 | TP | 1.11 | 1.04 | TP | 1.12 | 1.08 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YLR070C | XYL2 | Xylitol Dehydrogenase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | 0.01 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.07 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YAR035W | YAT1 | Carnitine acetyltransferase | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.04 | TP | 0.97 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YBR184W | YBR18 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | 0 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.98 | TP | 1.11 | 0.98 | TP | NA | NA | NA |
| YBR284W | YBR28 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | 0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YCR024C | YCR02 | Hypothetical ORF | NA | NA | 1 | 5.2 | FP | 1 | 1 | -0.03 | TP | 1 | 1 | -0.03 | TP | 1.08 | 0.73 | FP | 1.1 | 0.66 | FP | 1.11 | 0.65 | FP | 1.12 | 0.56 | FP | 1.11 | 0.6 | FP | Oth | Protein synthesis not required in the model | NA |
| YDR111C | YDR11 | Hypothetical ORF | NA | NA | NA | NA | NA | 0.95 | 1 | -0.02 | TP | 0.98 | 1 | -0.01 | TP | 1.05 | 1.01 | TP | 1.09 | 1.04 | TP | 1.11 | 1.04 | TP | 0.9 | 1.06 | TP | 1.08 | 1.05 | TP | NA | NA | NA |
| YDR341C | YDR34 | Protein required for cell viability | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | FP |
| YDR531W | YDR53 | Pantothenate kinase (ATP:D-pantothenate 4'-phosphotransferase, EC 2.7.1.33) catalyzes the first committed step in the universal biosynthetic pathway leading to CoA. | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Bio | CoA biosynthesis not required in the model. | NA |
| YEL041W | YEL04 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.11 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.06 | TP | 1.11 | 1.06 | TP | 1.12 | 1.09 | TP | 1.11 | 1.06 | TP | NA | NA | NA |
| YEL047C | YEL04 | Fumurate ReDuctase Soluble | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.02 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YER053C | YER05 | Sequence similarity to mitochondrial phosphate transporters | NA | NA | NA | NA | NA | 1 | 1 | 0.22 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YER087W | YER08 | Hypothetical ORF | NA | NA | 1 | 7.5 | FP | 1 | 1 | -0.02 | TP | 1 | 1 | 0 | TP | 1.08 | 0.97 | TP | 1.1 | 0.89 | TP | 1.11 | 0.78 | FP | 1.12 | 0.72 | FP | 1.11 | 0.78 | FP | Oth | Protein synthesis not required in the model | NA |
| YFL030W | YFL03 | NA | NA | NA | NA | NA | NA | 1 | 1 | 0.08 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.03 | TP | 0.79 | 1.06 | FN | 1.08 | 1.04 | TP | Med | Lower oxygen uptake rate would correct this false negative prediction. | NA |
| YFR055W | YFR05 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGL245W | YGL24 | Protein required for cell viability | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | FP |
| YGR012W | YGR01 | Hypothetical ORF | NA | NA | NA | NA | NA | 0 | 1 | 0 | FN | 1 | 1 | 0 | TP | 1.08 | 1.01 | TP | 1.1 | 0.99 | TP | 1.11 | 0.98 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | Unk | Model can't make cysteine without the rxn catalyzed by this gene. Might be able to bypass this by making cys from pyr using CYS1 [KEGG]. | NA |
| YGR043C | YGR04 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.02 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YGR125W | YGR12 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.1 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YGR287C | YGR28 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.05 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.04 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YHL012W | YHL01 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1 | TP | 1.1 | 1 | TP | 1.11 | 0.96 | TP | 1.12 | 0.97 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YHR020W | YHR02 | Protein required for cell viability | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YJL045W | YJL04 | Similar to SDH1 | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.03 | TP | 1.11 | 1.03 | TP | NA | NA | NA |
| YJL068C | YJL06 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1 | TP | 1.1 | 1.02 | TP | 1.11 | 1.03 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YJL070C | YJL07 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.01 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.04 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YJL200C | YJL20 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 0 | 4.69 | FP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1 | TP | 1.11 | 0.99 | TP | 1.12 | 1 | TP | 1.11 | 0.98 | TP | Unk | Aco1p acts as an isozyme for this reaction. For some reason YJL200C gene product is only required on minimal media. | NA |
| YJL216C | YJL21 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.01 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1.01 | TP | 1.1 | 1.01 | TP | 1.11 | 1.02 | TP | 1.12 | 1.01 | TP | 1.11 | 1.02 | TP | NA | NA | NA |

| ORF | Name | Annotation | Ess sim | Ess call | Slow sim | Slow exp | Slow call | MMD sim | MMD exp | MMD ave | MMD call | YPGal sim | YPGal exp | YPGal ave | YPGal call | YPD sim | YPD exp | YPD call | YPDGE sim | YPDGE exp | YPDGE call | YPG sim | YPG exp | YPG call | YPE sim | YPE exp | YPE call | YPL sim | YPL exp | YPL call | Class | Explanation | Forster et al |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YKL132C | YKL13 | Probable folyl-polyglutamate synthetase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.08 | TP | 1.08 | 1.02 | TP | 1.1 | 1.01 | TP | 1.11 | 1.01 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YLR089C | YLR08 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 1.26 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1 | TP | 1.1 | 1.03 | TP | 1.11 | 0.94 | TP | 1.12 | 0.99 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YLR164W | YLR16 | YLR164Wp is homologous to TIM18p | NA | NA | NA | NA | NA | 1 | 1 | 0.09 | TP | 1 | 1 | -0.03 | TP | 1.08 | 1 | TP | 1.1 | 0.99 | TP | 1.11 | 0.99 | TP | 1.12 | 0.99 | TP | 1.11 | 0.99 | TP | NA | NA | NA |
| YML082W | YML08 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.04 | TP | 1.08 | 1.02 | TP | 1.1 | 1.04 | TP | 1.11 | 1.04 | TP | 1.12 | 1.04 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YML096W | YML09 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.05 | TP | 1.08 | 1.03 | TP | 1.1 | 1.06 | TP | 1.11 | 1.04 | TP | 1.12 | 1.09 | TP | 1.11 | 1.07 | TP | NA | NA | NA |
| YMR084W | YMR08 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YMR085W | YMR08 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | -0.04 | TP | 1 | 1 | -0.06 | TP | 1.08 | 1.03 | TP | 1.1 | 1.03 | TP | 1.11 | 1.02 | TP | 1.12 | 1.05 | TP | 1.11 | 1.04 | TP | NA | NA | NA |
| YMR118C | YMR11 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0 | TP | 1 | 1 | -0.02 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YMR293C | YMR29 | Protein similar to bacterial glutamyl-tRNA amidotransferases | NA | NA | 1 | 3.1 | FP | 1 | 1 | -0.04 | TP | 1 | 1 | -0.01 | TP | 1.08 | 0.74 | FP | 1.1 | 0.7 | FP | 1.11 | 0.63 | FP | 1.12 | 0.59 | FP | 1.11 | 0.63 | FP | Den | This reaction is a dead end. | NA |
| YKL067W | YNK1 | Nucleoside diphosphate kinase | NA | NA | NA | NA | NA | 0 | 1 | -0.04 | FN | 0 | 1 | -0.04 | FN | 0 | 0.99 | FN | 0 | 0.97 | FN | 0 | 0.95 | FN | 0 | 0.9 | FN | 0 | 0.94 | FN | Iso | Null mutant retains 10% of nucleoside diphosphate kinase activity. Sources of remaining enzyme activity are unknown, but possibilities are discussed in [Fukuchi93]. Reaction w/o gene associations could be added to the model to represent these unidentified enzymes. | FN |
| YNL247W | YNL24 | Protein required for cell viability | 1 | FP | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | Oth | Protein synthesis not required in the model | NA |
| YOR071C | YOR07 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.04 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.01 | TP | 1.1 | 1.02 | TP | 1.11 | 1.01 | TP | 1.12 | 1.01 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YOR192C | YOR19 | Hypothetical ORF | NA | NA | NA | NA | NA | 1 | 1 | 0.8 | TP | 1 | 1 | -0.01 | TP | 1.08 | 1.01 | TP | 1.1 | 1.03 | TP | 1.11 | 1.03 | TP | 1.12 | 1.03 | TP | 1.11 | 1.02 | TP | NA | NA | NA |
| YKR053C | YSR3 | DHS-1-P phosphatase | NA | NA | NA | NA | NA | 1 | 1 | -0.03 | TP | 1 | 1 | -0.07 | TP | 1.08 | 1.02 | TP | 1.1 | 1.02 | TP | 1.11 | 1.02 | TP | 1.12 | 1.02 | TP | 1.11 | 1.01 | TP | NA | NA | NA |
| YJL139C | YUR1 | Mannosyltransferase | NA | NA | NA | NA | NA | 1 | 1 | 0.13 | TP | 1 | 1 | 0 | TP | 1.08 | 0.97 | TP | 1.1 | 0.99 | TP | 1.11 | 0.95 | TP | 1.12 | 0.98 | TP | 1.11 | 0.99 | TP | NA | NA | NA |