**Figure 4 – Source data 4**

*Genes of central carbon metabolism, amino acid biosynthesis and fatty acid metabolism, that showed strain-specific expression change to starvation.* Genes were selected with the help of the KEGG Mapper tool. Numbering of genes in Figure 4 – Figure supplement 4-6 can be found in the last column. Genes, that are direct targets of WCC are marked with bold typesetting.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | ***wt*** | ***∆wc-1*** |  |
| **gene ID** | **protein** | **fold change to starvation** | **adjusted p** | **fold change to starvation** | **adjusted p** | **#** |
| **Central carbon metabolism** |  |  |  |  |  |  |  |
| ***wt* specific** | NCU04400 | triose/dihydroxyacetone kinase / FAD-AMP lyase | 70.57 | 1.42312E-07 | 25.91 | 0.001830917 | 1a |
|
| NCU10107 | ribose 5-phosphate isomerase | 45.11 | 7.76669E-06 | 5.62 | ns | 2a |
| NCU09873 | acu-6; acetate utilization-6 | 39.04 | 1.60306E-59 | 11.60 | 3.71073E-21 | 3a |
| NCU02366 | tca-3; tricarboxylic acid-3 | 2.98 | 5.33757E-24 | 1.39 | 0.002131163 | 4a |
| NCU06836 | acu-5; acetate utilization-5 | 0.50 | 2.60354E-10 | ns | ns | 5a |
| NCU07608 | ppm-3; pentose phosphate metabolism-3 | 0.44 | 4.48606E-11 | ns | ns | 6a |
| NCU02004 | phosphoserine phosphatase | 0.43 | 2.44333E-15 | ns | ns | 7a |
| NCU02505 | suc; succinate | 0.37 | 5.69527E-33 | ns | ns | 8a |
| NCU07281 | gpi-1; glucose-6-phosphate isomerase | 0.35 | 3.47405E-10 | ns | ns | 9a |
| NCU09810 | succinyl-CoA synthetase subunit alpha | 0.27 | 3.97874E-06 | ns | ns | 10a |
| NCU02274 | for; formate | 0.17 | 1.43926E-26 | ns | ns | 11a |
| NCU01439 | D-3-phosphoglycerate dehydrogenase 1 | 0.10 | 2.5872E-28 | 0.21 | 2.98019E-09 | 12a |
|  | NCU04797 | fbp-1; fructose-bisphosphatase-1 | 6.05 | 1.09682E-45 | 14.35 | 4.00722E-17 | 1b |
| ***∆wc-1* specific** | NCU09732 | acetyl-CoA acetyltransferase | 4.78 | 3.85062E-53 | 13.23 | 1.80206E-83 | 2b |
| NCU03761 | L-serine/L-threonine ammonia-lyase | 3.04 | 2.03651E-21 | 9.41 | 3.88952E-67 | 3b |
| NCU05169 | cat-4; catalase-4 | 3.87 | 1.87553E-39 | 8.73 | 9.9475E-21 | 4b |
| NCU08827 | D-glycerate 3-kinase | 2.38 | 9.0648E-10 | 6.14 | 1.59766E-26 | 5b |
| **NCU08791** | **cat-1; catalase-1** | **ns** | **Ns** | **5.63** | **5.7231E-25** | **6b** |
| NCU01866 | lactonohydrolase | ns | ns | 5.19 | 4.62773E-06 | 7b |
| NCU01870 | Eno3 protein | ns | ns | 3.43 | 6.01917E-06 | 8b |
| NCU02482 | tca-2; tricarboxylic acid-2 | 0.59 | 8.36369E-07 | 2.89 | 1.30995E-09 | 9b |
| **NCU00575** | **Glucokinase** | **ns** | **ns** | **2.78** | **8.4829E-07** | **10b** |
| NCU09266 | methylmalonate-semialdehyde dehydrogenase | 1.30 | 0.002723935 | 2.75 | 1.35703E-25 | 11b |
| **NCU02712** | **acetate kinase** | **ns** | **ns** | **2.48** | **5.0573E-08** | **12b** |
| NCU04230 | acu-3; acetate utilization-3 | ns | ns | 2.43 | 0.003354321 | 13b |
|  | NCU09553 | 3-hydroxybutyryl CoA dehydrogenase | ns | ns | 2.05 | 2.24894E-08 | 14b |

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | ***wt*** | ***∆wc-1*** |  |
| **gene ID** | **protein** | **fold change to starvation** | **adjusted p** | **fold change to starvation** | **adjusted p** | **#** |
| **Amino acid biosynthesis** |  |  |  |  |  |  |  |
| ***wt* specific** | NCU10107 | ribose 5-phosphate isomerase | 45.11 | 7.76669E-06 | ns | 0.000123509 | 1a |
| NCU02366 | tricarboxylic acid-3 | 2.98 | 5.33757E-24 | 1.39 | ns | 2a |
| NCU05526 | lysine-5 | 0.48 | 1.11532E-14 | ns | 0.038773183 | 3a |
| **NCU06724** | **glutamine-1** | **0.48** | **6.72569E-18** | **ns** | **0.000618487** | **4a** |
| NCU04292 | branched-chain-amino-acid aminotransferase | 0.44 | 2.85537E-08 | ns | 2.98019E-09 | 5a |
| NCU07608 | pentose phosphate metabolism-3 | 0.44 | 4.48606E-11 | ns | ns | 6a |
| NCU02004 | phosphoserine phosphatase | 0.43 | 2.44333E-15 | ns | ns | 7a |
| NCU07725 | chorismate mutase | 0.41 | 1.21477E-10 | ns | ns | 8a |
| NCU08216 | cystathionine beta-synthase | 0.39 | 4.64984E-13 | ns | 0.002131163 | 9a |
| NCU02505 | succinate | 0.37 | 5.69527E-33 | 1.16 | ns | 10a |
| NCU02479 | glutamine synthetase | 0.26 | 1.84704E-33 | 0.82 | ns | 11a |
| NCU02785 | aromatic-8 | 0.20 | 4.50433E-24 | 0.42 | ns | 12a |
| **NCU00554** | **homoserine-1** | **0.19** | **9.32897E-23** | **0.42** | **ns** | **13a** |
| NCU02274 | formate | 0.17 | 1.43926E-26 | 1.56 | ns | 14a |
| NCU01439 | D-3-phosphoglycerate dehydrogenase 1 | 0.10 | 2.5872E-28 | 0.21 | ns | 15a |
| ***∆wc-1* specific** | NCU05093 | cystathionine gamma-synthase | ns | ns | 28.37 | 3.03124E-09 | 1b |
| NCU03761 | hypothetical protein | 3.04 | 2.03651E-21 | 9.41 | 3.88952E-67 | 2b |
| NCU01870 | Eno3 protein | ns | ns | 3.43 | 6.01917E-06 | 3b |
| NCU02482 | tricarboxylic acid-2 | 0.59 | 8.36369E-07 | 2.89 | 1.30995E-09 | 4b |
| **NCU02333** | **arginase-1** | **ns** | **ns** | **2.24** | **1.06577E-12** | **5b** |
|  | NCU04280 | aconitate hydratase | 0.55 | 9.00499E-11 | 0.25 | 1.17999E-18 | 6b |
| **Fatty acid metabolism** |  |  |  |  |  |  |  |
| ***wt* specific** | *NCU06905* | *tetrahydroxynaphthalene reductase-2* | 64.91 | 6.22898E-29 | ns | ns | 1a |
| ***∆wc-1* specific** | *NCU09732* | *acetyl-CoA acetyltransferase* | 4.78 | 3.85062E-53 | 13.22 | 1.80206E-83 | 1b |
| *NCU04796* | *3-ketoacyl-CoA thiolase* | 2.56 | 4.87813E-29 | 6.11 | 9.49553E-48 | 2b |
| *NCU04462* | *3-ketoacyl-CoA reductase* | ns | ns | 0.48 | 2.29782E-05 | 3b |
| *NCU08535* | *acetyl-CoA carboxylase* | 0.66 | 0.015656731 | 0.15 | 2.75695E-14 | 4b |
| *NCU02209* | *delta-12 fatty acid desaturase* | 0.34 | 1.50063E-31 | 0.12 | 4.11109E-26 | 5b |
| *NCU07307* | *cel-2; chain elongation-2* | 0.42 | 3.57317E-12 | 0.10 | 5.72319E-25 | 6b |
| *NCU07308* | *cel-1; chain elongation-1* | 0.32 | 1.8954E-24 | 0.09 | 4.39545E-22 | 7b |