

**Table S4.** List of metabolic pathway modules based on KEGG databases

| Module | Description                                                                          |
|--------|--------------------------------------------------------------------------------------|
| M00001 | Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate                            |
| M00002 | Glycolysis, core module involving three-carbon compounds                             |
| M00003 | Gluconeogenesis, oxaloacetate => fructose-6P                                         |
| M00004 | Pentose phosphate pathway (Pentose phosphate cycle)                                  |
| M00005 | PRPP biosynthesis, ribose 5P => PRPP                                                 |
| M00006 | Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P                |
| M00007 | Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P             |
| M00008 | Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate                 |
| M00009 | Citrate cycle (TCA cycle, Krebs cycle)                                               |
| M00010 | Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate                |
| M00011 | Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate               |
| M00015 | Proline biosynthesis, glutamate => proline                                           |
| M00016 | Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine                       |
| M00017 | Methionine biosynthesis, aspartate => homoserine => methionine                       |
| M00018 | Threonine biosynthesis, aspartate => homoserine => threonine                         |
| M00019 | Valine/isoleucine biosynthesis,<br>pyruvate => valine / 2-oxobutanoate => isoleucine |
| M00023 | Tryptophan biosynthesis, chorismate => tryptophan                                    |
| M00026 | Histidine biosynthesis, PRPP => histidine                                            |
| M00035 | Methionine degradation                                                               |
| M00045 | Histidine degradation, histidine => N-formiminoglutamate => glutamate                |
| M00048 | De novo purine biosynthesis, PRPP + glutamine => IMP                                 |

| Module | Description                                                                |
|--------|----------------------------------------------------------------------------|
| M00049 | Adenine ribonucleotide biosynthesis, IMP => ADP,ATP                        |
| M00050 | Guanine ribonucleotide biosynthesis, IMP => GDP,GTP                        |
| M00052 | Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP             |
| M00053 | Deoxyribonucleotide biosynthesis, ADP/GDP/CDP/UDP => dATP/dGTP/dCTP/dUTP   |
| M00060 | KDO2-lipid A biosynthesis, Raetz pathway, LpxL-LpxM type                   |
| M00061 | D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde 3P |
| M00063 | CMP-KDO biosynthesis                                                       |
| M00064 | ADP-L-glycero-D-manno-heptose biosynthesis                                 |
| M00082 | Fatty acid biosynthesis, initiation                                        |
| M00083 | Fatty acid biosynthesis, elongation                                        |
| M00086 | beta-Oxidation, acyl-CoA synthesis                                         |
| M00091 | Phosphatidylcholine (PC) biosynthesis, PE => PC                            |
| M00093 | Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE                 |
| M00096 | C5 isoprenoid biosynthesis, non-mevalonate pathway                         |
| M00115 | NAD biosynthesis, aspartate => quinolinate => NAD                          |
| M00119 | Pantothenate biosynthesis, valine/L-aspartate => pantothenate              |
| M00120 | Coenzyme A biosynthesis, pantothenate => CoA                               |
| M00121 | Heme biosynthesis, plants and bacteria, glutamate => heme                  |
| M00125 | Riboflavin biosynthesis, plants and bacteria, GTP => riboflavin/FMN/FAD    |
| M00126 | Tetrahydrofolate biosynthesis, GTP => THF                                  |
| M00156 | Cytochrome c oxidase, cbb3-type                                            |
| M00168 | CAM (Crassulacean acid metabolism), dark                                   |
| M00173 | Reductive citrate cycle (Arnon-Buchanan cycle)                             |

| Module | Description                                                                               |
|--------|-------------------------------------------------------------------------------------------|
| M00307 | Pyruvate oxidation, pyruvate => acetyl-CoA                                                |
| M00308 | Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P                  |
| M00338 | Cysteine biosynthesis, homocysteine + serine => cysteine                                  |
| M00358 | Coenzyme M biosynthesis                                                                   |
| M00432 | Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate                                |
| M00526 | Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine                       |
| M00527 | Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine                    |
| M00531 | Assimilatory nitrate reduction, nitrate => ammonia                                        |
| M00535 | Isoleucine biosynthesis, pyruvate => 2-oxobutanoate                                       |
| M00552 | D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => glycerate-3P        |
| M00570 | Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine                        |
| M00579 | Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate                 |
| M00621 | Glycine cleavage system                                                                   |
| M00627 | beta-Lactam resistance, Bla system                                                        |
| M00631 | D-Galacturonate degradation (bacteria), D-galacturonate => pyruvate + D-glyceraldehyde 3P |
| M00632 | Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P                    |
| M00793 | dTDP-L-rhamnose biosynthesis                                                              |
| M00846 | Siroheme biosynthesis, glutamyl-tRNA => siroheme                                          |
| M00854 | Glycogen biosynthesis, glucose-1P => glycogen/starch                                      |
| M00866 | KDO2-lipid A biosynthesis, Raetz pathway, non-LpxL-LpxM type                              |
| M00868 | Heme biosynthesis, animals and fungi, glycine => heme                                     |
| M00881 | Lipoic acid biosynthesis, plants and bacteria, octanoyl-ACP => dihydrolipoyl-E2/H         |
| M00913 | Pantothenate biosynthesis, 2-oxoisovalerate/spermine => pantothenate                      |

| Module | Description                                                              |
|--------|--------------------------------------------------------------------------|
| M00923 | UDP-L-FucNAc biosynthesis                                                |
| M00926 | Heme biosynthesis, bacteria, glutamyl-tRNA => coproporphyrin III => heme |
| M00930 | Menaquinone biosynthesis, futasine pathway                               |
| M00931 | Menaquinone biosynthesis, modified futasine pathway                      |
| M00938 | Pyrimidine deoxyribonucleotide biosynthesis, UDP => dTTP                 |
| M00948 | Hydroxyproline degradation, trans-4-hydroxy-L-proline => 2-oxoglutarate  |
| M00959 | Guanine ribonucleotide degradation, GMP => Urate                         |
| M00970 | Proline degradation, proline => glutamate                                |
| M00972 | Proline metabolism                                                       |