**Table S1.** Relative expression of genes affected during acclimation to WLM, grouped by Clusters of Orthologous Groups (COGs). Time samples with over- or under-expression are highlighted (green and yellow, respectively).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **COGs** | **Old locus tag** | **Gene symbol** | **Gene annotation** | **Relative expression in function of time (h)** | | | | | |
|  |  |  |  | **0.5** | **1** | **2** | **4** | **6** | **8** |
| **C: Energy production and conversion** |  |  |  |  |  |  |  |  |  |
| C | OEOE\_0238 | OEOE\_RS01135 | carbonic anhydrase | -1.37 | -1.39 | -1.80 | -2.07 | -2.15 | -2.08 |
| C | OEOE\_0419 | OEOE\_RS02015 | malate permease | 2.25 | 2.45 | 2.08 | 1.74 | 1.71 | 1.67 |
| C | OEOE\_0423 | OEOE\_RS02035 | citrate lyase subunit alpha | 0.73 | 1.13 | 0.93 | 0.59 | 0.54 | 0.64 |
| C | OEOE\_0441 | OEOE\_RS02125 | phosphosulfolactate synthase | 1.01 | 1.62 | 2.22 | 1.99 | 1.73 | 1.66 |
| C | OEOE\_0516 | OEOE\_RS02455 | NADH-dependent flavin oxidoreductase | -0.71 | -0.61 | -0.83 | -1.10 | -1.05 | -1.07 |
| C | OEOE\_0550 | OEOE\_RS02615 | ABC transporter permease | 1.57 | 1.86 | 2.17 | 2.27 | 2.08 | 2.00 |
| C | OEOE\_0551 | OEOE\_RS02620 | sulfonate ABC transporter ATP-binding protein | 1.70 | 1.70 | 1.71 | 1.82 | 1.78 | 1.62 |
| C | OEOE\_0659 | OEOE\_RS03155 | F0F1 ATP synthase subunit A | -1.03 | -1.08 | -0.42 | -0.31 | -0.35 | -0.37 |
| C | OEOE\_0662 | OEOE\_RS03170 | ATP synthase subunit delta | -0.92 | -1.16 | -0.92 | -0.90 | -0.91 | -0.91 |
| C | OEOE\_0664 | OEOE\_RS03180 | ATP synthase subunit gamma | -1.28 | -1.25 | -0.97 | -0.93 | -0.84 | -0.83 |
| C | OEOE\_0666 | OEOE\_RS03190 | F0F1 ATP synthase subunit epsilon | -1.35 | -1.26 | -1.45 | -1.49 | -1.56 | -1.69 |
| C | OEOE\_0749 | OEOE\_RS03585 | NADH-flavin reductase | -0.71 | -0.73 | -0.98 | -1.01 | -0.97 | -0.84 |
| C | OEOE\_0829 | OEOE\_RS03985 | energy-coupling factor transporter ATP-binding protein EcfA2 | -0.23 | -0.34 | -0.78 | -0.93 | -1.01 | -0.97 |
| C | OEOE\_1046 | OEOE\_RS05025 | NADH:flavin oxidoreductase | -1.09 | -1.54 | -1.76 | -1.70 | -1.70 | -1.51 |
| C | OEOE\_1047 | OEOE\_RS05030 | NADH:flavin oxidoreductase | -1.13 | -1.44 | -1.67 | -1.78 | -1.93 | -1.76 |
| C | OEOE\_1087 | OEOE\_RS05225 | energy-coupling factor transporter ATP-binding protein EcfA3 | -0.79 | -1.02 | -1.16 | -0.87 | -0.87 | -0.82 |
| C | OEOE\_1110 | OEOE\_RS05335 | Fe-S cluster formation protein, NifU | -0.37 | -0.25 | -0.76 | -0.95 | -1.04 | -1.01 |
| C | OEOE\_1187 | OEOE\_RS05720 | ABC transporter ATPase | -1.24 | -1.04 | -1.29 | -1.32 | -1.29 | -1.24 |
| C | OEOE\_1290 | OEOE\_RS06215 | NADPH:quinone reductase | -0.98 | -0.96 | -0.95 | -1.12 | -0.98 | -1.16 |
| C | OEOE\_1446 | OEOE\_RS06985 | malate transporter | 3.28 | 4.03 | 4.19 | 3.84 | 3.68 | 3.69 |
| C | OEOE\_1838 | OEOE\_RS08875 | pyridine nucleotide-disulfide oxidoreductase | -1.11 | -1.37 | -1.39 | -1.34 | -1.29 | -1.29 |
| **D: Cell cycle control, cell division, chromosome partitioning** |  |  |  |  |  |  |  |  |  |
| D | OEOE\_0247 | OEOE\_RS01180 | GTP-binding protein | -1.20 | -1.11 | -1.17 | -1.35 | -1.34 | -1.43 |
| D | OEOE\_1150 | OEOE\_RS05535 | cell division protein FtsL | -1.07 | -0.87 | -0.76 | -0.66 | -0.48 | -0.42 |
| D | OEOE\_1261 | OEOE\_RS06080 | cell division protein | 0.42 | 0.58 | 0.79 | 1.03 | 1.06 | 1.10 |
| **E: Amino acid transport and metabolism** |  |  |  |  |  |  |  |  |  |
| E | OEOE\_0017 | OEOE\_RS00080 | peptidase | -1.00 | -1.23 | -0.78 | -0.63 | -0.68 | -0.67 |
| E | OEOE\_0149 | OEOE\_RS00695 | chorismate mutase | 2.34 | 2.33 | 2.16 | 1.91 | 2.16 | 2.29 |
| E | OEOE\_0239 | OEOE\_RS01140 | O-acetylhomoserine aminocarboxypropyltransferase | -0.74 | -1.13 | -1.04 | -1.08 | -1.34 | -1.25 |
| E | OEOE\_0267 | OEOE\_RS01280 | peptide ABC transporter substrate-binding protein | 0.85 | 1.71 | 1.39 | 1.04 | 1.21 | 1.94 |
| E | OEOE\_0268 | OEOE\_RS01285 | branched-chain amino acid ABC transporter permease | 0.91 | 2.11 | 1.86 | 1.48 | 1.79 | 2.64 |
| E | OEOE\_0269 | OEOE\_RS01290 | phosphonate ABC transporter ATP-binding protein | 0.47 | 1.89 | 1.67 | 1.43 | 1.74 | 2.65 |
| E | OEOE\_0270 | OEOE\_RS01295 | peptide ABC transporter ATPase | 0.54 | 0.56 | 0.38 | 0.37 | 0.75 | 1.23 |
| E | OEOE\_0287 | OEOE\_RS01375 | D-alanine--poly(phosphoribitol) ligase | -2.24 | -2.07 | -2.01 | -1.87 | -1.93 | -1.95 |
| E | OEOE\_0388 | OEOE\_RS01865 | amino acid permease | 2.81 | 3.11 | 3.12 | 3.08 | 3.01 | 3.05 |
| E | OEOE\_0438 | OEOE\_RS02110 | peptide ABC transporter permease | 4.02 | 4.40 | 4.48 | 4.19 | 4.00 | 4.07 |
| E | OEOE\_0443 | OEOE\_RS02135 | branched-chain amino acid transporter II carrier protein | 1.11 | 1.39 | 1.64 | 1.64 | 1.78 | 1.95 |
| E | OEOE\_0508 | OEOE\_RS02415 | peptide methionine sulfoxide reductase | -1.26 | -1.25 | -0.81 | -0.56 | -0.55 | -0.54 |
| E | OEOE\_0559 | OEOE\_RS02660 | phosphate ABC transporter ATP-binding protein | 0.80 | 0.78 | 0.64 | 0.98 | 1.09 | 1.04 |
| E | OEOE\_0570 | OEOE\_RS02715 | ATP-dependent Clp protease proteolytic subunit | 0.14 | 0.41 | 0.47 | 0.05 | 0.10 | 0.02 |
| E | OEOE\_0630 | OEOE\_RS03010 | spermidine/putrescine import ATP-binding protein PotA | 0.69 | 0.61 | 0.99 | 1.27 | 1.21 | 1.20 |
| E | OEOE\_0631 | OEOE\_RS03015 | spermidine/putrescine ABC transporter permease | 0.53 | 0.65 | 0.84 | 1.14 | 1.08 | 1.03 |
| E | OEOE\_0632 | OEOE\_RS03020 | spermidine/purescine ABC transporter permease | 0.68 | 0.78 | 0.97 | 1.32 | 1.28 | 1.31 |
| E | OEOE\_0751 | OEOE\_RS03595 | amino acid ABC transporter substrate-binding protein | 1.06 | 1.25 | 0.58 | 0.41 | 0.58 | 0.58 |
| E | OEOE\_0840 | OEOE\_RS04040 | peptide ABC transporter substrate-binding protein | -0.57 | -0.91 | -1.16 | -1.22 | -1.15 | -1.15 |
| E | OEOE\_0841 | OEOE\_RS04045 | peptide ABC transporter substrate-binding protein | -1.51 | -1.62 | -1.98 | -2.12 | -2.10 | -2.04 |
| E | OEOE\_0951 | OEOE\_RS04560 | glutamine synthetase | 1.73 | 2.21 | 2.47 | 2.23 | 1.97 | 1.78 |
| E | OEOE\_0959 | OEOE\_RS04600 | Xaa-Pro aminopeptidase | 0.58 | 0.47 | 1.16 | 1.75 | 1.90 | 1.93 |
| E | OEOE\_1055 | OEOE\_RS05065 | ABC transporter permease | 1.25 | 0.86 | 0.62 | 0.62 | 0.58 | 0.56 |
| E | OEOE\_1056 | OEOE\_RS05070 | methionine import ATP-binding protein MetN 1 | 1.11 | 0.73 | 0.64 | 0.64 | 0.64 | 0.64 |
| E | OEOE\_1092 | OEOE\_RS05245 | oligoendopeptidase F | 0.56 | 0.66 | 0.83 | 1.17 | 1.59 | 1.90 |
| E | OEOE\_1191 | OEOE\_RS05740 | glutathione reductase | -0.63 | -0.78 | -0.83 | -0.96 | -1.00 | -0.98 |
| E | OEOE\_1299 | OEOE\_RS06260 | succinate-semialdehyde dehydrogenase | -1.07 | -1.14 | -1.40 | -1.39 | -1.24 | -1.20 |
| E | OEOE\_1427 | OEOE\_RS06890 | ABC transporter ATP-binding protein | -0.95 | -0.81 | -0.91 | -1.00 | -0.91 | -1.03 |
| E | OEOE\_1464 | OEOE\_RS07070 | spermidine/putrescine ABC transporter ATP-binding protein | 1.69 | 1.40 | 1.21 | 1.06 | 0.97 | 0.99 |
| E | OEOE\_1465 | OEOE\_RS07075 | spermidine/putrescine ABC transporter ATP-binding protein | 1.66 | 1.16 | 1.01 | 0.92 | 0.91 | 0.86 |
| E | OEOE\_1466 | OEOE\_RS07080 | spermidine/putrescine ABC transporter permease | 1.27 | 0.75 | 0.71 | 0.51 | 0.41 | 0.49 |
| E | OEOE\_1538 | OEOE\_RS07415 | peptide methionine sulfoxide reductase | -0.51 | -0.63 | -1.00 | -1.07 | -0.95 | -1.12 |
| E | OEOE\_1562 | OEOE\_RS07535 | S-ribosylhomocysteine lyase | -1.21 | -1.39 | -1.32 | -1.47 | -1.55 | -1.62 |
| E | OEOE\_1615 | OEOE\_RS07790 | peptide ABC transporter substrate-binding protein | -0.94 | -1.16 | -1.38 | -1.29 | -1.13 | -1.06 |
| E | OEOE\_1616 | OEOE\_RS07795 | peptide ABC transporter permease | -1.22 | -1.57 | -1.41 | -1.00 | -0.67 | -0.47 |
| E | OEOE\_1638 | OEOE\_RS07900 | amino acid permease | 2.93 | 3.16 | 3.18 | 2.98 | 2.90 | 2.81 |
| E | OEOE\_1665 | OEOE\_RS08035 | amino acid ABC transporter substrate-binding protein | 1.44 | 1.58 | 1.58 | 1.58 | 1.75 | 1.93 |
| E | OEOE\_1667 | OEOE\_RS08045 | amino acid ABC transporter permease | 1.28 | 1.24 | 1.19 | 1.28 | 1.53 | 1.51 |
| E | OEOE\_1705 | OEOE\_RS08230 | glyoxalase | -0.49 | -0.75 | -0.93 | -1.00 | -0.93 | -1.03 |
| E | OEOE\_1717 | OEOE\_RS08285 | ABC transporter substrate-binding protein | 0.83 | 0.85 | 0.93 | 1.34 | 1.56 | 1.56 |
| E | OEOE\_1719 | OEOE\_RS08295 | peptidase M20 | 0.89 | 1.14 | 1.08 | 1.35 | 1.49 | 1.53 |
| E | OEOE\_1806 | OEOE\_RS08705 | glutamine ABC transporter substrate-binding protein | 1.92 | 2.14 | 2.22 | 2.20 | 2.12 | 2.09 |
| **F. Nucleotide transport and metabolism** |  |  |  |  |  |  |  |  |  |
| F | OEOE\_0259 | OEOE\_RS01240 | dihydroorotase | -1.13 | -1.26 | -1.67 | -2.01 | -2.16 | -2.06 |
| F | OEOE\_0262 | OEOE\_RS01255 | orotidine 5'-phosphate decarboxylase | -0.62 | -0.82 | -1.07 | -1.44 | -1.63 | -1.64 |
| F | OEOE\_0263 | OEOE\_RS01260 | orotate phosphoribosyltransferase | -0.57 | -0.77 | -1.04 | -1.53 | -1.62 | -1.61 |
| F | OEOE\_0264 | OEOE\_RS01265 | dihydroorotate dehydrogenase | -0.63 | -0.70 | -1.05 | -1.42 | -1.54 | -1.51 |
| F | OEOE\_0316 | OEOE\_RS01510 | deoxyuridine 5'-triphosphate nucleotidohydrolase | -1.15 | -1.28 | -1.15 | -1.26 | -1.42 | -1.31 |
| F | OEOE\_0320 | OEOE\_RS01530 | nucleoside-triphosphate diphosphatase | 0.83 | 1.21 | 1.09 | 0.82 | 0.83 | 0.82 |
| F | OEOE\_0376 | OEOE\_RS01805 | uracil transporter | -0.90 | -1.09 | -0.64 | -0.21 | -0.30 | -0.45 |
| F | OEOE\_0849 | OEOE\_RS04085 | deoxyadenosine kinase | -1.23 | -1.25 | -1.08 | -1.07 | -1.13 | -1.24 |
| F | OEOE\_0880 | OEOE\_RS04215 | ribonucleoside-diphosphate reductase | -1.00 | -0.91 | -1.00 | -1.00 | -1.01 | -1.30 |
| F | OEOE\_0969 | OEOE\_RS04650 | nucleoside 2-deoxyribosyltransferase | 1.14 | 1.04 | 1.01 | 0.94 | 0.93 | 1.00 |
| F | OEOE\_0981 | OEOE\_RS04710 | nucleoside 2-deoxyribosyltransferase | 0.76 | 0.69 | 0.83 | 1.15 | 1.14 | 1.01 |
| F | OEOE\_1033 | OEOE\_RS04965 | uridine/cytidine kinase | -1.17 | -1.34 | -1.46 | -1.32 | -1.36 | -1.41 |
| F | OEOE\_1069 | OEOE\_RS05140 | adenine phosphoribosyltransferase | -1.32 | -1.32 | -1.41 | -1.42 | -1.51 | -1.43 |
| F | OEOE\_1123 | OEOE\_RS05400 | GMP synthase | -0.32 | -0.58 | -1.01 | -1.08 | -1.08 | -1.02 |
| F | OEOE\_1413 | OEOE\_RS06810 | deaminase | 1.11 | 1.55 | 1.80 | 2.09 | 1.76 | 1.56 |
| F | OEOE\_1543 | OEOE\_RS07440 | purine operon repressor | -1.10 | -1.30 | -1.42 | -1.55 | -1.62 | -1.50 |
| F | OEOE\_1579 | OEOE\_RS07615 | uracil phosphoribosyltransferase | -1.81 | -2.02 | -1.91 | -1.82 | -1.82 | -1.88 |
| **G: Carbohydrate transport and metabolism** |  |  |  |  |  |  |  |  |  |
| G | OEOE\_0026 | OEOE\_RS00125 | mannose-6-phosphate isomerase | -2.56 | -2.56 | -2.56 | -2.56 | -2.58 | -2.81 |
| G | OEOE\_0077 | OEOE\_RS00350 | diacetyl reductase [(S)-acetoin forming] | -1.31 | -1.59 | -1.80 | -1.93 | -1.90 | -1.81 |
| G | OEOE\_0128 | OEOE\_RS00595 | sugar phosphate isomerase | -1.71 | -1.98 | -2.05 | -1.72 | -1.58 | -1.71 |
| G | OEOE\_0221 | OEOE\_RS01045 | PTS sugar transporter subunit IIA | -0.63 | -0.61 | -0.79 | -0.90 | -0.96 | -1.01 |
| G | OEOE\_0222 | OEOE\_RS01050 | PTS cellobiose transporter subunit IIA | -0.39 | -0.70 | -0.86 | -0.97 | -1.06 | -0.86 |
| G | OEOE\_0224 | OEOE\_RS01060 | 6-phospho-β-glucosidase | -1.04 | -1.23 | -1.58 | -1.81 | -2.02 | -1.94 |
| G | OEOE\_0233 | OEOE\_RS01110 | PTS fructose transporter subunit IIA | -1.85 | -2.20 | -2.60 | -2.90 | -2.69 | -2.79 |
| G | OEOE\_0234 | OEOE\_RS01115 | PTS sugar transporter subunit IIA | -1.05 | -1.35 | -1.74 | -1.81 | -1.68 | -1.89 |
| G | OEOE\_0235 | OEOE\_RS01120 | PTS galactitol transporter subunit IIC | -0.44 | -0.23 | -0.70 | -1.05 | -1.13 | -1.02 |
| G | OEOE\_0236 | OEOE\_RS01125 | PTS galactitol transporter subunit IIB | -0.40 | -0.12 | -0.62 | -0.98 | -1.08 | -1.24 |
| G | OEOE\_0253 | OEOE\_RS01210 | sugar ABC transporter substrate-binding protein | 1.11 | 0.93 | 0.75 | 0.71 | 0.67 | 0.75 |
| G | OEOE\_0254 | OEOE\_RS01215 | sugar ABC transporter permease | 1.51 | 1.38 | 1.11 | 1.10 | 1.10 | 1.11 |
| G | OEOE\_0255 | OEOE\_RS01220 | sugar ABC transporter permease | 1.33 | 1.23 | 1.06 | 1.08 | 1.25 | 1.43 |
| G | OEOE\_0303 | OEOE\_RS01445 | peptidase S24 | -0.68 | -0.78 | -0.88 | -0.98 | -1.01 | -1.08 |
| G | OEOE\_0324 | OEOE\_RS01550 | aldehyde dehydrogenase | -0.48 | -0.72 | -1.13 | -1.35 | -1.39 | -1.43 |
| G | OEOE\_0379 | OEOE\_RS01820 | PTS mannose transporter subunit IID | 2.10 | 2.31 | 2.69 | 2.38 | 2.18 | 1.90 |
| G | OEOE\_0380 | OEOE\_RS01825 | PTS fructose transporter subunit IIC | 2.15 | 2.34 | 2.31 | 2.15 | 2.06 | 2.07 |
| G | OEOE\_0381 | OEOE\_RS01830 | PTS fructose transporter subunit IID | 1.84 | 2.20 | 2.22 | 1.97 | 1.79 | 1.70 |
| G | OEOE\_0382 | OEOE\_RS01835 | PTS sugar transporter subunit IIA | 1.38 | 1.90 | 1.90 | 1.61 | 1.49 | 1.44 |
| G | OEOE\_0413 | OEOE\_RS01985 | lactate dehydrogenase | -1.18 | -1.41 | -1.65 | -1.95 | -1.90 | -1.75 |
| G | OEOE\_0464 | OEOE\_RS02230 | PTS mannose transporter subunit IIAB | -0.73 | -1.02 | -1.31 | -1.38 | -1.06 | -1.00 |
| G | OEOE\_0465 | OEOE\_RS02235 | PTS alpha-glucoside transporter subunit IIBC | -0.48 | -0.83 | -0.97 | -1.12 | -0.85 | -0.81 |
| G | OEOE\_0466 | OEOE\_RS02240 | PTS mannose transporter subunit IID | -0.76 | -1.08 | -1.43 | -1.43 | -1.23 | -0.97 |
| G | OEOE\_0643 | OEOE\_RS03075 | phosphocarrier protein HPr | -2.19 | -2.16 | -2.20 | -2.33 | -2.25 | -2.32 |
| G | OEOE\_0644 | OEOE\_RS03080 | glucosamine-6-phosphate deaminase | -1.27 | -1.16 | -1.51 | -1.86 | -1.95 | -1.79 |
| G | OEOE\_1182 | OEOE\_RS05695 | lactate dehydrogenase | -1.20 | -0.93 | -1.10 | -1.22 | -1.14 | -1.37 |
| G | OEOE\_1204 | OEOE\_RS05805 | PTS sugar transporter | -2.37 | -2.45 | -2.68 | -2.86 | -2.87 | -2.90 |
| G | OEOE\_1341 | OEOE\_RS06450 | PTS β-glucoside transporter subunit IIABC | -0.94 | -1.26 | -1.40 | -1.23 | -0.89 | -0.56 |
| G | OEOE\_1342 | OEOE\_RS06455 | PTS sugar transporter subunit IIA | -1.31 | -1.61 | -1.41 | -0.92 | -0.50 | -0.39 |
| G | OEOE\_1456 | OEOE\_RS07030 | glycerol-3-phosphate ABC transporter ATP-binding protein | -1.42 | -1.92 | -2.10 | -2.34 | -2.51 | -2.54 |
| G | OEOE\_1457 | OEOE\_RS07035 | glycerol-3-phosphate ABC transporter permease | -0.90 | -1.36 | -1.53 | -1.65 | -1.72 | -1.76 |
| G | OEOE\_1458 | OEOE\_RS07040 | glycerol-3-phosphate ABC transporter permease | -1.03 | -1.54 | -1.64 | -1.81 | -2.01 | -1.93 |
| G | OEOE\_1459 | OEOE\_RS07045 | glycerol-3-phosphate ABC transporter substrate-binding protein | -1.16 | -1.47 | -1.86 | -2.13 | -2.20 | -2.22 |
| G | OEOE\_1504 | OEOE\_RS07255 | UDP-phosphate galactose phosphotransferase | -1.98 | -1.96 | -1.96 | -2.01 | -1.94 | -1.96 |
| G | OEOE\_1532 | OEOE\_RS07385 | fructosamine kinase | 0.31 | 0.11 | 0.48 | 0.87 | 0.83 | 1.05 |
| G | OEOE\_1602 | OEOE\_RS07730 | diacetyl reductase | -0.63 | -1.01 | -1.25 | -1.35 | -1.37 | -1.43 |
| G | OEOE\_1609 | OEOE\_RS07760 | sugar ABC transporter permease | -0.38 | -0.52 | -1.03 | -1.23 | -1.22 | -1.21 |
| G | OEOE\_1612 | OEOE\_RS07775 | ribokinase | -1.53 | -1.87 | -2.32 | -2.18 | -1.64 | -1.57 |
| G | OEOE\_1613 | OEOE\_RS07780 | D-ribose pyranase | -1.27 | -1.82 | -2.09 | -2.08 | -1.59 | -1.33 |
| G | OEOE\_1614 | OEOE\_RS07785 | sugar:proton symporter | -1.28 | -1.75 | -2.22 | -2.19 | -1.73 | -1.56 |
| G | OEOE\_1651 | OEOE\_RS07965 | sugar ABC transporter ATP-binding protein | -0.89 | -0.80 | -0.88 | -1.06 | -1.06 | -1.04 |
| G | OEOE\_1669 | OEOE\_RS08055 | sugar phosphate isomerase | -1.35 | -1.33 | -1.79 | -2.11 | -2.02 | -2.24 |
| G | OEOE\_1708 | OEOE\_RS08245 | fructokinase | -1.42 | -2.08 | -2.15 | -2.28 | -2.40 | -2.46 |
| G | OEOE\_1714 | OEOE\_RS08275 | glucose transporter | 0.62 | 0.81 | 0.82 | 1.17 | 1.31 | 1.30 |
| **H: Coenzyme Metabolism** |  |  |  |  |  |  |  |  |  |
| H | OEOE\_0327 | OEOE\_RS01565 | lipoate-protein ligase A | -1.07 | -1.21 | -1.27 | -1.53 | -1.43 | -1.24 |
| H | OEOE\_0676 | OEOE\_RS03240 | dephospho-CoA kinase | -0.88 | -1.23 | -1.38 | -1.43 | -1.26 | -1.23 |
| H | OEOE\_0779 | OEOE\_RS03730 | 5-formyltetrahydrofolate cyclo-ligase | 0.66 | 1.13 | 1.35 | 1.08 | 0.88 | 0.90 |
| H | OEOE\_0791 | OEOE\_RS03790 | thiamine pyrophosphokinase | -0.93 | -1.07 | -1.05 | -0.96 | -0.93 | -0.84 |
| H | OEOE\_1036 | OEOE\_RS04980 | pyridoxal biosynthesis protein | -0.89 | -1.10 | -1.22 | -1.19 | -1.23 | -1.15 |
| H | OEOE\_1473 | OEOE\_RS07110 | 6-pyruvoyl-tetrahydropterin synthase | 1.22 | 1.00 | 0.59 | 0.57 | 0.60 | 0.59 |
| H | OEOE\_1597 | OEOE\_RS07705 | biotin transporter | 0.41 | 0.93 | 0.94 | 1.04 | 0.94 | 0.85 |
| H | OEOE\_1642 | OEOE\_RS07920 | holo-ACP synthase | 2.36 | 2.55 | 2.69 | 2.94 | 2.85 | 2.58 |
| H | OEOE\_1834 | OEOE\_RS08855 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase | 1.03 | 1.04 | 0.97 | 0.99 | 0.97 | 0.85 |
| **I: Lipid transport and metabolism** |  |  |  |  |  |  |  |  |  |
| I | OEOE\_0145 | OEOE\_RS00675 | phospholipid phosphatase | -1.52 | -1.50 | -1.25 | -1.04 | -1.13 | -1.27 |
| I | OEOE\_0485 | OEOE\_RS02315 | phospholipid phosphatase | -1.35 | -1.88 | -1.76 | -1.75 | -1.75 | -1.79 |
| I | OEOE\_1015 | OEOE\_RS04875 | lysophospholipase | 0.78 | 0.87 | 1.10 | 1.14 | 1.06 | 1.16 |
| I | OEOE\_1049 | OEOE\_RS05040 | tannase | 1.88 | 2.26 | 2.72 | 2.22 | 1.89 | 1.90 |
| I | OEOE\_1176 | OEOE\_RS05660 | cyclopropane-fatty-acyl-phospholipid synthase | -0.90 | -1.11 | -0.98 | -0.90 | -0.86 | -0.83 |
| I | OEOE\_1292 | OEOE\_RS06225 | esterase | -1.02 | -0.96 | -0.96 | -1.12 | -0.99 | -0.82 |
| I | OEOE\_1343 | OEOE\_RS06460 | lysophospholipase | -0.32 | -0.43 | -0.93 | -1.22 | -1.18 | -1.14 |
| I | OEOE\_1366 | OEOE\_RS06570 | acyl-CoA synthetase | -1.33 | -1.62 | -2.00 | -1.78 | -1.70 | -1.61 |
| I | OEOE\_1460 | OEOE\_RS07050 | glycerophosphoryl diester phosphodiesterase | -1.49 | -1.64 | -2.08 | -2.51 | -2.57 | -2.56 |
| I | OEOE\_1675 | OEOE\_RS08085 | lipid kinase | 1.42 | 1.44 | 1.51 | 1.38 | 1.29 | 1.37 |
| **J: Translation, ribosomal structure and biogenesis** |  |  |  |  |  |  |  |  |  |
| J | OEOE\_0014 | OEOE\_RS00065 | 50S ribosomal protein L9 | 0.01 | 0.53 | 1.04 | 1.12 | 0.79 | 0.52 |
| J | OEOE\_0019 | OEOE\_RS00090 | D-aminoacyl-tRNA deacylase | -1.33 | -1.53 | -1.57 | -1.47 | -1.41 | -1.26 |
| J | OEOE\_0176 | OEOE\_RS00835 | pseudouridylate synthase | 1.06 | 1.19 | 1.00 | 0.89 | 0.94 | 0.88 |
| J | OEOE\_0321 | OEOE\_RS01535 | glutamate--tRNA ligase | 0.82 | 1.33 | 1.26 | 1.06 | 1.06 | 1.10 |
| J | OEOE\_0429 | OEOE\_RS02065 | ribosome maturation factor RimP | 0.93 | 1.00 | 1.41 | 1.79 | 1.83 | 1.74 |
| J | OEOE\_0432 | OEOE\_RS02080 | 50S ribosomal protein L7ae | 1.06 | 0.95 | 1.06 | 1.18 | 1.23 | 1.28 |
| J | OEOE\_0433 | OEOE\_RS02085 | translation initiation factor IF-2 | 0.68 | 0.63 | 0.81 | 1.02 | 1.08 | 1.01 |
| J | OEOE\_0434 | OEOE\_RS02090 | ribosome-binding factor A | 0.48 | 0.54 | 0.83 | 1.07 | 1.14 | 1.02 |
| J | OEOE\_0440 | OEOE\_RS02120 | serine--tRNA ligase | 1.44 | 1.93 | 2.07 | 1.93 | 1.77 | 1.72 |
| J | OEOE\_0517 | OEOE\_RS02460 | elongation factor 3 | 1.48 | 1.97 | 2.28 | 1.95 | 1.83 | 1.82 |
| J | OEOE\_0581 | OEOE\_RS02770 | elongation factor 4 | 0.80 | 1.09 | 0.89 | 0.74 | 0.60 | 0.69 |
| J | OEOE\_0589 | OEOE\_RS02810 | histidyl-tRNA synthetase | 0.69 | 0.65 | 0.84 | 0.94 | 0.93 | 1.08 |
| J | OEOE\_0594 | OEOE\_RS02840 | 30S ribosomal protein S10 | 1.88 | 1.82 | 1.88 | 1.92 | 1.93 | 1.90 |
| J | OEOE\_0595 | OEOE\_RS02845 | 50S ribosomal protein L3 | 1.73 | 1.63 | 1.68 | 1.70 | 1.66 | 1.66 |
| J | OEOE\_0596 | OEOE\_RS02850 | 50S ribosomal protein L4 | 1.20 | 1.18 | 1.19 | 1.16 | 1.18 | 1.16 |
| J | OEOE\_0598 | OEOE\_RS02860 | 50S ribosomal protein L2 | 1.38 | 1.39 | 1.29 | 1.29 | 1.29 | 1.29 |
| J | OEOE\_0599 | OEOE\_RS02865 | 30S ribosomal protein S19 | 1.50 | 1.47 | 1.61 | 1.52 | 1.53 | 1.48 |
| J | OEOE\_0600 | OEOE\_RS02870 | 50S ribosomal protein L22 | 1.44 | 1.40 | 1.40 | 1.41 | 1.40 | 1.37 |
| J | OEOE\_0601 | OEOE\_RS02875 | 30S ribosomal protein S3 | 1.66 | 1.66 | 1.74 | 1.73 | 1.66 | 1.66 |
| J | OEOE\_0602 | OEOE\_RS02880 | 50S ribosomal protein L16 | 1.44 | 1.41 | 1.41 | 1.46 | 1.49 | 1.36 |
| J | OEOE\_0603 | OEOE\_RS02885 | 50S ribosomal protein L29 | 1.66 | 1.69 | 1.69 | 1.75 | 1.79 | 1.70 |
| J | OEOE\_0604 | OEOE\_RS02890 | 30S ribosomal protein S17 | 1.52 | 1.43 | 1.53 | 1.61 | 1.56 | 1.64 |
| J | OEOE\_0605 | OEOE\_RS02895 | 50S ribosomal protein L14 | 1.00 | 1.00 | 1.03 | 1.05 | 1.13 | 1.06 |
| J | OEOE\_0606 | OEOE\_RS02900 | 50S ribosomal protein L24 | 1.40 | 1.39 | 1.44 | 1.51 | 1.55 | 1.42 |
| J | OEOE\_0607 | OEOE\_RS02905 | 50S ribosomal protein L5 | 1.50 | 1.50 | 1.66 | 1.79 | 1.74 | 1.62 |
| J | OEOE\_0608 | OEOE\_RS02910 | 30S ribosomal protein S8 | 2.07 | 2.04 | 2.35 | 2.57 | 2.45 | 2.42 |
| J | OEOE\_0609 | OEOE\_RS02915 | 50S ribosomal protein L6 | 1.27 | 1.29 | 1.41 | 1.43 | 1.46 | 1.32 |
| J | OEOE\_0610 | OEOE\_RS02920 | 50S ribosomal protein L18 | 1.53 | 1.56 | 1.76 | 1.91 | 1.90 | 1.77 |
| J | OEOE\_0611 | OEOE\_RS02925 | 30S ribosomal protein S5 | 0.98 | 0.97 | 1.05 | 1.11 | 1.04 | 1.05 |
| J | OEOE\_0612 | OEOE\_RS02930 | 50S ribosomal protein L30 | 0.99 | 0.98 | 1.04 | 1.17 | 1.19 | 1.20 |
| J | OEOE\_0613 | OEOE\_RS02935 | 50S ribosomal protein L15 | 1.00 | 1.18 | 1.41 | 1.70 | 1.64 | 1.63 |
| J | OEOE\_0619 | OEOE\_RS02960 | 30S ribosomal protein S11 | 0.64 | 0.82 | 0.95 | 1.09 | 1.13 | 1.10 |
| J | OEOE\_0621 | OEOE\_RS02970 | 50S ribosomal protein L17 | 0.56 | 0.93 | 1.41 | 1.75 | 1.83 | 1.75 |
| J | OEOE\_0629 | OEOE\_RS03005 | 30S ribosomal protein S9 | 0.48 | 0.45 | 0.91 | 1.28 | 1.24 | 1.02 |
| J | OEOE\_0739 | OEOE\_RS03530 | 2'-5' RNA ligase | -1.26 | -1.35 | -1.35 | -1.47 | -1.39 | -1.69 |
| J | OEOE\_0770 | OEOE\_RS03680 | 50S ribosomal protein L32 | -0.14 | 0.59 | 0.78 | 0.87 | 0.88 | 1.07 |
| J | OEOE\_0798 | OEOE\_RS03825 | 30S ribosomal protein S16 | -1.55 | -1.20 | -1.26 | -1.24 | -1.26 | -1.37 |
| J | OEOE\_0800 | OEOE\_RS03835 | ribosome maturation factor RimM | -0.93 | -1.10 | -0.86 | -0.94 | -0.94 | -0.93 |
| J | OEOE\_0834 | OEOE\_RS04010 | acetyltransferase | 2.37 | 2.70 | 2.99 | 3.18 | 3.07 | 2.77 |
| J | OEOE\_0899 | OEOE\_RS04310 | arginine--tRNA ligase | 1.78 | 2.04 | 1.78 | 1.78 | 1.76 | 1.79 |
| J | OEOE\_0917 | OEOE\_RS04400 | phenylalanine--tRNA ligase subunit alpha | -1.23 | -1.31 | -1.03 | -0.78 | -0.70 | -0.45 |
| J | OEOE\_0957 | OEOE\_RS04590 | 50S ribosomal protein L21 | 0.52 | 0.76 | 1.06 | 1.20 | 1.20 | 1.18 |
| J | OEOE\_0994 | OEOE\_RS04775 | glycine--tRNA ligase subunit β | -1.04 | -0.79 | -0.40 | -0.16 | 0.08 | 0.05 |
| J | OEOE\_1079 | OEOE\_RS05185 | RNA pseudouridine synthase | 0.73 | 0.82 | 0.87 | 0.87 | 0.90 | 1.02 |
| J | OEOE\_1151 | OEOE\_RS05540 | ribosomal RNA small subunit methyltransferase H | -1.32 | -1.30 | -0.82 | -0.61 | -0.52 | -0.24 |
| J | OEOE\_1158 | OEOE\_RS05575 | pseudouridine synthase | 0.70 | 1.02 | 0.98 | 0.87 | 0.88 | 0.95 |
| J | OEOE\_1228 | OEOE\_RS05915 | RNA-binding protein | -1.73 | -1.31 | -1.73 | -1.81 | -1.93 | -1.98 |
| J | OEOE\_1267 | OEOE\_RS06100 | peptide chain release factor 3 | 1.07 | 0.84 | 0.75 | 0.75 | 0.73 | 0.71 |
| J | OEOE\_1278 | OEOE\_RS06155 | 50S ribosomal protein L20 | 0.73 | 0.82 | 0.92 | 1.06 | 1.18 | 1.11 |
| J | OEOE\_1279 | OEOE\_RS06160 | 50S ribosomal protein L35 | 0.92 | 0.97 | 1.37 | 1.65 | 1.73 | 1.62 |
| J | OEOE\_1283 | OEOE\_RS06180 | 30S ribosomal protein S15 | 0.32 | 1.02 | 1.14 | 1.33 | 1.28 | 1.00 |
| J | OEOE\_1284 | OEOE\_RS06185 | 30S ribosomal protein S20 | 0.29 | 0.84 | 1.07 | 1.29 | 1.32 | 0.83 |
| J | OEOE\_1289 | OEOE\_RS06210 | queuine tRNA-ribosyltransferase | 1.50 | 1.74 | 1.92 | 1.86 | 1.84 | 1.83 |
| J | OEOE\_1360 | OEOE\_RS06545 | raiA ribosome-associated inhibitor A | -1.35 | -1.40 | -1.06 | -1.11 | -1.27 | -1.47 |
| J | OEOE\_1414 | OEOE\_RS06815 | 16S RNA G1207 methylase RsmC | 0.61 | 1.05 | 1.24 | 1.40 | 1.16 | 1.05 |
| J | OEOE\_1416 | OEOE\_RS06825 | 50S ribosomal protein L7/L12 | 0.63 | 1.16 | 1.71 | 2.00 | 1.74 | 1.46 |
| J | OEOE\_1417 | OEOE\_RS06830 | 50S ribosomal protein L10 | 0.87 | 1.20 | 1.27 | 1.56 | 1.48 | 1.30 |
| J | OEOE\_1418 | OEOE\_RS06835 | 50S ribosomal protein L1 | 0.58 | 1.23 | 1.31 | 1.52 | 1.37 | 1.23 |
| J | OEOE\_1419 | OEOE\_RS06840 | 50S ribosomal protein L11 | 0.59 | 0.98 | 1.05 | 1.14 | 1.14 | 0.94 |
| J | OEOE\_1549 | OEOE\_RS07470 | ribosomal RNA small subunit methyltransferase A | 0.11 | 0.57 | 0.97 | 1.00 | 1.07 | 1.14 |
| J | OEOE\_1559 | OEOE\_RS07520 | cysteine--tRNA ligase | -0.32 | -0.54 | -0.81 | -0.98 | -1.03 | -1.04 |
| J | OEOE\_1674 | OEOE\_RS08080 | RNA methyltransferase | 0.99 | 1.09 | 1.02 | 0.95 | 0.88 | 0.90 |
| J | OEOE\_1813 | OEOE\_RS08745 | prolyl-tRNA synthetase | -1.03 | -1.03 | -1.08 | -1.03 | -1.07 | -1.11 |
| J | OEOE\_1863 | OEOE\_RS08995 | ribonuclease P protein component | 0.38 | 0.90 | 1.14 | 0.85 | 0.82 | 0.64 |
| **K: Transcription** |  |  |  |  |  |  |  |  |  |
| K | OEOE\_0047 | OEOE\_RS00215 | XRE family transcriptional regulator | 1.15 | 1.12 | 1.21 | 1.04 | 0.95 | 0.95 |
| K | OEOE\_0099 | OEOE\_RS00455 | XRE family transcriptional regulator | -1.17 | -1.24 | -1.42 | -1.38 | -1.39 | -1.55 |
| K | OEOE\_0179 | OEOE\_RS00850 | TetR family transcriptional regulator | 0.80 | 1.16 | 1.30 | 0.90 | 0.69 | 0.70 |
| K | OEOE\_0195 | OEOE\_RS00930 | XRE family transcriptional regulator | -2.45 | -2.43 | -2.04 | -2.05 | -2.24 | -2.05 |
| K | OEOE\_0209 | OEOE\_RS00995 | AraC family transcriptional regulator | -1.87 | -2.17 | -1.91 | -1.87 | -1.86 | -1.85 |
| K | OEOE\_0215 | OEOE\_RS01020 | TetR family transcriptional regulator | -1.50 | -1.49 | -1.45 | -1.49 | -1.57 | -1.63 |
| K | OEOE\_0225 | OEOE\_RS01065 | transcriptional regulator | -2.34 | -2.52 | -2.45 | -2.34 | -2.47 | -2.28 |
| K | OEOE\_0232 | OEOE\_RS01105 | transcriptional antiterminator | -2.81 | -3.13 | -2.90 | -2.68 | -2.43 | -2.84 |
| K | OEOE\_0245 | OEOE\_RS01170 | TetR family transcriptional regulator | -2.55 | -2.84 | -2.68 | -2.59 | -2.50 | -2.55 |
| K | OEOE\_0302 | OEOE\_RS01440 | LacI family transcriptional regulator | -0.82 | -0.72 | -0.86 | -0.89 | -1.03 | -0.97 |
| K | OEOE\_0417 | OEOE\_RS02005 | citrate lyase | 0.82 | 1.01 | 0.76 | 0.63 | 0.55 | 0.49 |
| K | OEOE\_0430 | OEOE\_RS02070 | transcription termination factor NusA | 1.27 | 1.20 | 1.41 | 1.59 | 1.59 | 1.69 |
| K | OEOE\_0435 | OEOE\_RS02095 | transcriptional regulator | 1.13 | 1.40 | 1.36 | 1.35 | 1.36 | 1.41 |
| K | OEOE\_0540 | OEOE\_RS02565 | MarR family transcriptional regulator | -0.28 | -0.45 | -1.01 | -1.02 | -0.84 | -1.19 |
| K | OEOE\_0569 | OEOE\_RS02710 | sporulation protein | 0.89 | 1.23 | 1.15 | 0.97 | 0.97 | 0.97 |
| K | OEOE\_0704 | OEOE\_RS03375 | ArsR family transcriptional regulator | 0.97 | 1.32 | 1.91 | 1.76 | 1.47 | 1.35 |
| K | OEOE\_0718 | OEOE\_RS03430 | transcriptional regulator | 2.09 | 2.68 | 2.49 | 2.01 | 1.78 | 1.61 |
| K | OEOE\_0724 | OEOE\_RS03455 | transcriptional regulator | 0.66 | 0.70 | 0.94 | 1.08 | 0.89 | 0.89 |
| K | OEOE\_0728 | OEOE\_RS03475 | MarR family transcriptional regulator | 1.07 | 0.37 | 0.58 | 0.57 | 0.60 | 0.61 |
| K | OEOE\_0733 | OEOE\_RS03500 | TetR family transcriptional regulator | -1.12 | -0.68 | -0.17 | -0.41 | -0.47 | -0.65 |
| K | OEOE\_0793 | OEOE\_RS03800 | XRE family transcriptional regulator | 1.87 | 2.01 | 2.13 | 2.04 | 2.09 | 2.13 |
| K | OEOE\_0808 | OEOE\_RS03880 | LacI family transcriptional regulator | -0.76 | -1.12 | -0.96 | -0.93 | -0.93 | -1.08 |
| K | OEOE\_0926 | OEOE\_RS04440 | ArsR family transcriptional regulator | 0.64 | 0.66 | 1.34 | 1.62 | 1.42 | 1.55 |
| K | OEOE\_0996 | OEOE\_RS04785 | RNA polymerase sigma factor RpoD | 0.58 | 0.83 | 1.03 | 1.23 | 1.18 | 0.98 |
| K | OEOE\_1010 | OEOE\_RS04850 | transcriptional regulator | -0.96 | -1.03 | -1.12 | -1.17 | -1.17 | -1.27 |
| K | OEOE\_1045 | OEOE\_RS05020 | LysR family transcriptional regulator | -1.19 | -1.51 | -1.85 | -1.75 | -1.52 | -1.50 |
| K | OEOE\_1152 | OEOE\_RS05545 | transcriptional regulator MraZ | -1.71 | -1.57 | -1.27 | -1.00 | -0.88 | -0.66 |
| K | OEOE\_1238 | OEOE\_RS05965 | transcription termination factor NusB | -1.18 | -1.18 | -0.56 | -0.43 | -0.53 | -0.11 |
| K | OEOE\_1297 | OEOE\_RS06250 | MarR family transcriptional regulator | -0.48 | -0.38 | -0.31 | -0.70 | -0.52 | -1.04 |
| K | OEOE\_1346 | OEOE\_RS06470 | ArsR family transcriptional regulator | -1.04 | -1.52 | -1.52 | -1.82 | -1.56 | -1.89 |
| K | OEOE\_1376 | OEOE\_RS06620 | cold-shock protein | -1.75 | -1.14 | -1.30 | -1.49 | -1.73 | -1.81 |
| K | OEOE\_1450 | OEOE\_RS07005 | cell filamentation protein Fic | -0.52 | -0.86 | -1.03 | -1.07 | -0.88 | -0.94 |
| K | OEOE\_1455 | OEOE\_RS07025 | AraC family transcriptional regulator | -1.48 | -1.52 | -1.59 | -1.62 | -1.71 | -1.60 |
| K | OEOE\_1467 | OEOE\_RS07085 | GntR family transcriptional regulator | -1.01 | -1.11 | -1.16 | -1.21 | -0.92 | -0.89 |
| K | OEOE\_1572 | OEOE\_RS07585 | AraC family transcriptional regulator | -1.53 | -1.68 | -1.79 | -1.69 | -1.60 | -1.60 |
| K | OEOE\_1575 | OEOE\_RS07600 | AraC family transcriptional regulator | -1.12 | -1.31 | -1.50 | -1.40 | -1.30 | -1.28 |
| K | OEOE\_1685 | OEOE\_RS08130 | TetR family transcriptional regulator | 0.77 | 0.96 | 1.18 | 1.32 | 1.25 | 1.21 |
| K | OEOE\_1733 | OEOE\_RS08360 | RNA polymerase I and III, subunit | 0.35 | 0.22 | 0.30 | 0.65 | 0.98 | 1.00 |
| K | OEOE\_1765 | OEOE\_RS08510 | MarR family transcriptional regulator | -2.63 | -2.44 | -2.26 | -2.39 | -2.46 | -2.36 |
| **L: Replication, recombination and repair** |  |  |  |  |  |  |  |  |  |
| L | OEOE\_0308 | OEOE\_RS01470 | ATP-dependent helicase/deoxyribonuclease subunit B | 0.35 | 0.95 | 1.02 | 0.52 | 0.37 | 0.35 |
| L | OEOE\_0309 | OEOE\_RS01475 | ATP-dependent helicase/nuclease subunit A | 0.43 | 0.75 | 1.23 | 1.07 | 0.87 | 0.77 |
| L | OEOE\_0318 | OEOE\_RS01520 | DNA repair protein RadA | 1.02 | 1.38 | 1.19 | 1.01 | 0.87 | 0.93 |
| L | OEOE\_0795 | OEOE\_RS03810 | DNA polymerase III subunit alpha | 0.44 | 0.73 | 0.89 | 1.03 | 1.09 | 1.25 |
| L | OEOE\_0799 | OEOE\_RS03830 | methylated DNA-protein cysteine methyltransferase | -1.29 | -1.54 | -0.92 | -1.16 | -1.23 | -1.11 |
| L | OEOE\_0990 | OEOE\_RS04755 | DNA repair protein RecO | -1.40 | -1.40 | -1.31 | -1.18 | -1.31 | -1.44 |
| L | OEOE\_0995 | OEOE\_RS04780 | DNA primase | 0.82 | 1.17 | 1.31 | 1.63 | 1.53 | 1.47 |
| L | OEOE\_1020 | OEOE\_RS04900 | DNA-binding protein | 0.83 | 1.01 | 1.00 | 0.96 | 0.99 | 1.05 |
| L | OEOE\_1021 | OEOE\_RS04905 | DNA topoisomerase I | 0.97 | 0.88 | 0.77 | 1.35 | 1.58 | 1.64 |
| L | OEOE\_1023 | OEOE\_RS04915 | tyrosine recombinase XerC | -1.19 | -1.26 | -1.03 | -0.68 | -0.51 | -0.40 |
| L | OEOE\_1094 | OEOE\_RS05255 | Holliday junction DNA helicase RecU | -1.09 | -1.22 | -0.91 | -0.77 | -0.55 | -0.68 |
| L | OEOE\_1096 | OEOE\_RS05265 | DNA replication protein DnaD | -1.10 | -1.20 | -1.20 | -1.12 | -1.11 | -1.12 |
| L | OEOE\_1099 | OEOE\_RS05280 | DNA helicase | -0.92 | -1.12 | -0.97 | -0.81 | -0.88 | -0.78 |
| L | OEOE\_1106 | OEOE\_RS05315 | ATPase AAA | 0.84 | 0.56 | 0.90 | 1.03 | 0.99 | 0.98 |
| L | OEOE\_1382 | OEOE\_RS06650 | protein RecA | 0.92 | 0.84 | 0.95 | 1.18 | 1.21 | 1.28 |
| L | OEOE\_1440 | OEOE\_RS06955 | ATP-dependent DNA helicase | 1.22 | 1.52 | 1.52 | 1.63 | 1.47 | 1.31 |
| L | OEOE\_1525 | OEOE\_RS07355 | DNA replication initiation protein | 0.65 | 0.81 | 1.18 | 1.05 | 0.81 | 0.88 |
| **M: Cell wall/membrane/envelope biogenesis** |  |  |  |  |  |  |  |  |  |
| M | OEOE\_0121 | OEOE\_RS00560 | D-alanyl-D-alanine carboxypeptidase | -1.41 | -1.41 | -1.53 | -1.41 | -1.41 | -1.45 |
| M | OEOE\_0197 | OEOE\_RS00940 | hemolysin D | 2.23 | 1.79 | 1.60 | 1.55 | 1.53 | 1.47 |
| M | OEOE\_0218 | OEOE\_RS01030 | glycosyltransferase | -1.17 | -1.38 | -1.31 | -1.39 | -1.49 | -1.51 |
| M | OEOE\_0284 | OEOE\_RS01360 | D-Ala-teichoic acid biosynthesis protein | -1.03 | -1.36 | -1.30 | -1.30 | -1.40 | -1.59 |
| M | OEOE\_0286 | OEOE\_RS01370 | D-alanyl-lipoteichoic acid biosynthesis protein DltB | -1.93 | -1.81 | -1.81 | -1.81 | -1.92 | -1.82 |
| M | OEOE\_0288 | OEOE\_RS01380 | D-alanyl-lipoteichoic acid biosynthesis protein DltD | -1.60 | -1.55 | -1.61 | -1.66 | -1.66 | -1.71 |
| M | OEOE\_0696 | OEOE\_RS03340 | aggregation promoting factor surface protein | -2.57 | -2.92 | -2.81 | -2.61 | -2.48 | -2.29 |
| M | OEOE\_0719 | OEOE\_RS03435 | D-alanyl-D-alanine carboxypeptidase | 5.53 | 5.83 | 6.01 | 5.82 | 5.61 | 5.64 |
| M | OEOE\_0850 | OEOE\_RS04090 | large-conductance mechanosensitive channel | -1.73 | -1.73 | -1.79 | -1.78 | -1.69 | -1.99 |
| M | OEOE\_0882 | OEOE\_RS04225 | peptidoglycan interpeptide bridge formation protein | -1.09 | -1.22 | -1.09 | -1.09 | -1.12 | -1.09 |
| M | OEOE\_0988 | OEOE\_RS04745 | diacylglycerol kinase | -0.87 | -1.05 | -0.08 | 0.46 | 0.22 | 0.22 |
| M | OEOE\_1199 | OEOE\_RS05780 | peptidoglycan-binding protein | -1.16 | -1.56 | -1.79 | -1.80 | -1.59 | -1.43 |
| M | OEOE\_1332 | OEOE\_RS06410 | 2-dehydro-3-deoxyphosphooctonate aldolase | 0.39 | 0.82 | 1.05 | 0.53 | 0.30 | 0.23 |
| M | OEOE\_1430 | OEOE\_RS06905 | peptidoglycan-binding protein | -0.67 | -1.02 | -1.31 | -1.42 | -1.27 | -1.31 |
| M | OEOE\_1442 | OEOE\_RS06965 | peptidoglycan interpeptide bridge formation protein | 0.95 | 1.87 | 2.52 | 2.39 | 1.85 | 1.70 |
| M | OEOE\_1443 | OEOE\_RS06970 | sortase | 1.46 | 2.00 | 2.48 | 2.27 | 1.94 | 1.91 |
| M | OEOE\_1444 | OEOE\_RS06975 | peptidoglycan interpeptide bridge formation protein | 1.55 | 2.27 | 2.77 | 2.52 | 2.24 | 2.19 |
| M | OEOE\_1451 | OEOE\_RS07010 | glycosyl transferase | -2.14 | -2.39 | -2.08 | -2.03 | -2.02 | -1.73 |
| M | OEOE\_1452 | OEOE\_RS07015 | glycosyl transferase | -0.98 | -1.08 | -1.07 | -0.84 | -0.69 | -0.47 |
| M | OEOE\_1502 | OEOE\_RS07245 | glycosyl transferase family 1 | -1.15 | -1.24 | -1.25 | -1.26 | -1.38 | -1.36 |
| M | OEOE\_1503 | OEOE\_RS07250 | glycosyl transferase | -1.78 | -1.78 | -1.78 | -1.83 | -1.80 | -1.83 |
| M | OEOE\_1506 | OEOE\_RS07265 | capsular polysaccharide biosynthesis protein | -2.39 | -2.18 | -1.99 | -1.88 | -1.89 | -1.71 |
| M | OEOE\_1561 | OEOE\_RS07530 | D-alanyl-D-alanine carboxypeptidase | -0.96 | -1.45 | -1.49 | -1.60 | -1.75 | -1.70 |
| M | OEOE\_1568 | OEOE\_RS07565 | capsular polysaccharide biosynthesis protein | -1.35 | -1.37 | -1.42 | -1.35 | -1.38 | -1.35 |
| M | OEOE\_1621 | OEOE\_RS07820 | glycosyl transferase | 1.78 | 1.90 | 2.86 | 3.39 | 3.35 | 3.08 |
| M | OEOE\_1666 | OEOE\_RS08040 | polar amino acid ABC transporter ATPase | 1.04 | 1.07 | 1.02 | 1.07 | 1.31 | 1.45 |
| M | OEOE\_1689 | OEOE\_RS08150 | macrolide ABC transporter ATP-binding protein | 1.11 | 1.45 | 1.84 | 1.80 | 1.47 | 1.35 |
| M | OEOE\_1839 | OEOE\_RS08880 | peptidoglycan-binding protein | -1.45 | -1.48 | -1.90 | -1.66 | -1.11 | -0.85 |
| **O: Post-translational modification, protein turnover, and chaperones** |  |  |  |  |  |  |  |  |  |
| O | OEOE\_0139 | OEOE\_RS00645 | glutaredoxin | -1.04 | -0.44 | -0.27 | -0.64 | -0.82 | -0.86 |
| O | OEOE\_0189 | OEOE\_RS00900 | disulfide bond formation protein | 0.34 | 0.64 | 0.80 | 0.94 | 0.98 | 1.00 |
| O | OEOE\_0289 | OEOE\_RS01385 | heat-shock protein Hsp20 | -0.92 | -0.43 | -0.55 | -0.89 | -0.88 | -1.13 |
| O | OEOE\_1115 | OEOE\_RS05360 | anaerobic ribonucleoside-triphosphate reductase activating protein | -0.42 | -0.83 | -0.84 | -0.91 | -1.03 | -1.02 |
| O | OEOE\_1308 | OEOE\_RS06305 | molecular chaperone DnaJ | 1.56 | 1.76 | 1.61 | 1.36 | 1.32 | 1.10 |
| O | OEOE\_1309 | OEOE\_RS06310 | molecular chaperone DnaK | 1.03 | 1.35 | 1.38 | 1.04 | 1.03 | 0.95 |
| O | OEOE\_1310 | OEOE\_RS06315 | protein GrpE | 0.93 | 1.41 | 1.59 | 1.11 | 1.02 | 0.94 |
| O | OEOE\_1431 | OEOE\_RS06910 | trypsin | 0.95 | 1.32 | 1.45 | 1.06 | 0.79 | 0.74 |
| O | OEOE\_1554 | OEOE\_RS07495 | methionine sulfoxide reductase B | 1.01 | 0.96 | 0.98 | 0.90 | 0.89 | 0.83 |
| O | OEOE\_1625 | OEOE\_RS07835 | thiol-disulfide isomerase | -1.17 | -1.32 | -1.18 | -1.03 | -1.01 | -1.07 |
| O | OEOE\_1630 | OEOE\_RS07860 | peptidase M13 | -0.66 | -0.88 | -1.04 | -1.06 | -1.09 | -0.93 |
| O | OEOE\_1639 | OEOE\_RS07905 | peptidylprolyl isomerase | 2.23 | 2.74 | 2.62 | 2.30 | 2.10 | 1.97 |
| O | OEOE\_1702 | OEOE\_RS08215 | thioredoxin | -1.10 | -0.71 | -0.71 | -0.70 | -0.68 | -0.81 |
| O | OEOE\_1852 | OEOE\_RS08940 | osmotically inducible protein C | 1.27 | 0.95 | 0.89 | 0.90 | 0.94 | 1.03 |
| **P: Inorganic ion transport and metabolism** |  |  |  |  |  |  |  |  |  |
| P | OEOE\_0172 | OEOE\_RS00815 | cobalt ABC transporter permease | 1.03 | 0.95 | 0.66 | 0.76 | 0.76 | 0.74 |
| P | OEOE\_0173 | OEOE\_RS00820 | cobalt ABC transporter | 1.21 | 1.14 | 0.84 | 0.89 | 0.89 | 0.93 |
| P | OEOE\_0246 | OEOE\_RS01175 | manganese transporter | -0.61 | -1.12 | -1.29 | -1.37 | -1.37 | -1.30 |
| P | OEOE\_0305 | OEOE\_RS01455 | sodium:solute symporter | -1.27 | -1.33 | -1.21 | -1.41 | -1.41 | -1.51 |
| P | OEOE\_0462 | OEOE\_RS02225 | potassium transporter Kef | -2.19 | -2.17 | -1.29 | -0.77 | -0.67 | -0.71 |
| P | OEOE\_0623 | OEOE\_RS02975 | cobalt ABC transporter | 0.27 | 0.26 | 0.56 | 1.08 | 1.16 | 1.16 |
| P | OEOE\_0624 | OEOE\_RS02980 | cobalt ABC transporter | 0.35 | 0.42 | 0.64 | 1.10 | 1.23 | 1.24 |
| P | OEOE\_0625 | OEOE\_RS02985 | cobalt ABC transporter permease | 0.75 | 0.84 | 1.03 | 1.30 | 1.52 | 1.51 |
| P | OEOE\_0706 | OEOE\_RS03385 | chloride channel protein | 0.64 | 0.56 | 0.88 | 1.07 | 0.93 | 0.97 |
| P | OEOE\_0819 | OEOE\_RS03935 | MFS transporter | 1.44 | 1.67 | 2.02 | 2.34 | 2.27 | 2.13 |
| P | OEOE\_1188 | OEOE\_RS05725 | metal ABC transporter substrate-binding protein | -1.11 | -1.33 | -1.48 | -1.72 | -1.64 | -1.70 |
| P | OEOE\_1363 | OEOE\_RS06560 | ATPase | 1.66 | 1.66 | 1.92 | 1.98 | 2.02 | 2.05 |
| P | OEOE\_1533 | OEOE\_RS07390 | sodium ABC transporter permease | 1.28 | 1.06 | 0.93 | 1.08 | 1.14 | 1.23 |
| P | OEOE\_1534 | OEOE\_RS07395 | sodium ABC transporter ATP-binding protein | 1.22 | 0.85 | 0.99 | 1.10 | 1.20 | 1.30 |
| P | OEOE\_1540 | OEOE\_RS07425 | cobalt ABC transporter ATPase | -0.28 | -0.35 | -0.84 | -1.10 | -1.12 | -1.12 |
| P | OEOE\_1679 | OEOE\_RS08100 | ammonia permease | 1.28 | 1.61 | 1.57 | 1.46 | 1.35 | 1.33 |
| **Q: Secondary metabolites biosynthesis, transport, and catabolism** |  |  |  |  |  |  |  |  |  |
| Q | OEOE\_0064 | OEOE\_RS00295 | phytoene synthase | 1.25 | 0.82 | 0.84 | 0.98 | 0.84 | 0.83 |
| Q | OEOE\_0804 | OEOE\_RS03860 | 4-oxalocrotonate tautomerase | 1.56 | 1.14 | 1.38 | 2.01 | 2.16 | 2.19 |
| **R: General function prediction only** |  |  |  |  |  |  |  |  |  |
| R | OEOE\_0025 | OEOE\_RS00120 | 2-hydroxyacid dehydrogenase | -0.55 | -0.85 | -1.07 | -1.12 | -1.24 | -1.20 |
| R | OEOE\_0036 | OEOE\_RS00165 | oxidoreductase ion channel protein IolS | -1.10 | -1.36 | -1.56 | -1.65 | -1.65 | -1.72 |
| R | OEOE\_0043 | OEOE\_RS00200 | ketosteroid isomerase | -1.05 | -0.92 | -1.13 | -1.21 | -1.05 | -1.10 |
| R | OEOE\_0044 | OEOE\_RS00205 | oxidoreductase | -0.99 | -0.58 | -0.99 | -1.08 | -1.15 | -1.09 |
| R | OEOE\_0070 | OEOE\_RS00320 | 2,5-diketo-D-gluconic acid reductase | -0.94 | -1.09 | -1.09 | -1.20 | -1.14 | -1.16 |
| R | OEOE\_0071 | OEOE\_RS00325 | general stress protein | -2.18 | -2.10 | -2.46 | -2.54 | -2.60 | -2.58 |
| R | OEOE\_0076 | OEOE\_RS00345 | MFS transporter | 1.04 | 0.72 | 0.67 | 0.69 | 0.69 | 0.50 |
| R | OEOE\_0097 | OEOE\_RS00445 | MFS transporter | 1.10 | 1.03 | 0.75 | 0.71 | 0.70 | 0.75 |
| R | OEOE\_0103 | OEOE\_RS00475 | phosphoesterase | 1.56 | 1.30 | 1.15 | 1.28 | 1.26 | 1.30 |
| R | OEOE\_0129 | OEOE\_RS00600 | gluconate:proton symporter | -1.16 | -1.09 | -1.43 | -1.59 | -1.64 | -1.35 |
| R | OEOE\_0137 | OEOE\_RS00635 | hemolysin | 1.40 | 1.55 | 1.63 | 1.33 | 1.27 | 1.17 |
| R | OEOE\_0148 | OEOE\_RS00690 | MFS transporter | 1.91 | 1.98 | 2.18 | 1.96 | 2.00 | 1.96 |
| R | OEOE\_0168 | OEOE\_RS00795 | acylphosphatase | -1.31 | -1.18 | -1.04 | -0.90 | -0.88 | -0.97 |
| R | OEOE\_0174 | OEOE\_RS00825 | transporter | 1.01 | 0.79 | 0.70 | 0.75 | 0.76 | 0.81 |
| R | OEOE\_0175 | OEOE\_RS00830 | transporter | 1.44 | 1.28 | 1.27 | 1.17 | 1.09 | 1.03 |
| R | OEOE\_0196 | OEOE\_RS00935 | transporter | 1.54 | 1.05 | 1.05 | 1.05 | 1.05 | 1.05 |
| R | OEOE\_0241 | OEOE\_RS01150 | alpha/β hydrolase | -0.72 | -0.53 | -0.76 | -0.93 | -1.07 | -1.10 |
| R | OEOE\_0242 | OEOE\_RS01155 | 3-β-hydroxysteroid dehydrogenase | -0.84 | -1.07 | -1.38 | -1.48 | -1.50 | -1.52 |
| R | OEOE\_0243 | OEOE\_RS01160 | oxidoreductase ion channel protein IolS | -1.16 | -1.03 | -1.07 | -1.21 | -1.07 | -1.09 |
| R | OEOE\_0244 | OEOE\_RS01165 | DNA-binding protein | -1.71 | -1.67 | -1.96 | -2.01 | -1.99 | -2.00 |
| R | OEOE\_0265 | OEOE\_RS01270 | MFS transporter | -0.83 | -1.11 | -1.17 | -1.28 | -1.49 | -1.41 |
| R | OEOE\_0290 | OEOE\_RS01390 | MFS transporter permease | 1.56 | 1.51 | 1.53 | 1.59 | 1.53 | 1.79 |
| R | OEOE\_0345 | OEOE\_RS01655 | acetyltransferase | -1.27 | -1.02 | -1.29 | -1.40 | -1.27 | -1.27 |
| R | OEOE\_0384 | OEOE\_RS01845 | MFS transporter permease | 0.76 | 1.11 | 1.24 | 1.33 | 1.27 | 1.34 |
| R | OEOE\_0396 | OEOE\_RS01905 | carbonyl reductase | 0.72 | 0.86 | 0.75 | 0.89 | 1.05 | 1.20 |
| R | OEOE\_0408 | OEOE\_RS01960 | oxidoreductase | -1.05 | -1.06 | -1.21 | -1.25 | -1.14 | -1.18 |
| R | OEOE\_0416 | OEOE\_RS02000 | glucosaminidase | 1.09 | 1.07 | 0.90 | 0.79 | 0.70 | 0.80 |
| R | OEOE\_0490 | OEOE\_RS02340 | FMN-binding protein | -0.74 | -0.67 | -0.66 | -0.90 | -0.91 | -1.02 |
| R | OEOE\_0503 | OEOE\_RS02400 | MFS transporter | 1.46 | 1.20 | 1.06 | 1.22 | 1.21 | 1.23 |
| R | OEOE\_0693 | OEOE\_RS03325 | acetoin reductase | -0.96 | -1.32 | -1.53 | -1.80 | -1.82 | -2.01 |
| R | OEOE\_0705 | OEOE\_RS03380 | MFS transporter | 1.30 | 1.42 | 1.76 | 1.73 | 1.63 | 1.63 |
| R | OEOE\_0757 | OEOE\_RS03625 | short-chain dehydrogenase | -0.57 | -0.67 | -0.95 | -1.12 | -1.11 | -1.16 |
| R | OEOE\_0784 | OEOE\_RS03755 | metallophosphatase | -1.07 | -1.14 | -1.18 | -1.16 | -1.13 | -1.13 |
| R | OEOE\_0863 | OEOE\_RS04145 | acyltransferase | 1.03 | 1.90 | 2.28 | 1.87 | 1.73 | 1.70 |
| R | OEOE\_0868 | OEOE\_RS04165 | acetyltransferase | 1.32 | 1.29 | 1.57 | 1.48 | 1.43 | 1.37 |
| R | OEOE\_0869 | OEOE\_RS04170 | MFS transporter | 1.24 | 1.14 | 1.24 | 1.47 | 1.31 | 1.39 |
| R | OEOE\_0881 | OEOE\_RS04220 | ACP phosphodiesterase | 0.58 | 1.35 | 1.51 | 0.58 | 0.31 | 0.01 |
| R | OEOE\_0886 | OEOE\_RS04245 | oxalate:formate antiporter | -1.39 | -1.93 | -2.06 | -2.23 | -2.27 | -2.33 |
| R | OEOE\_0896 | OEOE\_RS04295 | adenylyltransferase | -0.44 | -0.66 | -0.81 | -1.06 | -0.94 | -0.90 |
| R | OEOE\_0927 | OEOE\_RS04445 | acetyltransferase | 1.20 | 1.07 | 1.56 | 1.88 | 1.77 | 1.83 |
| R | OEOE\_0938 | OEOE\_RS04495 | short-chain dehydrogenase | -0.99 | -1.48 | -1.51 | -1.38 | -1.40 | -1.45 |
| R | OEOE\_0989 | OEOE\_RS04750 | GTPase Era | -1.23 | -1.50 | -1.19 | -0.95 | -1.10 | -1.11 |
| R | OEOE\_0997 | OEOE\_RS04790 | SAM-dependent methyltransferase | 0.99 | 1.05 | 1.31 | 1.56 | 1.73 | 1.55 |
| R | OEOE\_1018 | OEOE\_RS04890 | GTPase | 0.50 | 0.84 | 1.07 | 0.95 | 0.90 | 0.88 |
| R | OEOE\_1080 | OEOE\_RS05190 | pore-forming protein | 0.77 | 0.95 | 1.13 | 1.21 | 1.39 | 1.45 |
| R | OEOE\_1202 | OEOE\_RS05795 | general stress protein | -0.74 | -1.00 | -1.03 | -0.91 | -0.82 | -0.86 |
| R | OEOE\_1260 | OEOE\_RS06075 | SAM-dependent methyltransferase | 0.88 | 1.05 | 1.16 | 1.29 | 1.40 | 1.37 |
| R | OEOE\_1322 | OEOE\_RS06370 | amidophosphoribosyltransferase | 1.14 | 0.71 | 0.78 | 0.84 | 0.96 | 0.81 |
| R | OEOE\_1347 | OEOE\_RS06475 | acetyltransferase | -1.08 | -1.22 | -1.14 | -1.23 | -1.19 | -1.12 |
| R | OEOE\_1364 | OEOE\_RS06565 | acyltransferase | -1.53 | -1.90 | -1.91 | -1.57 | -1.42 | -1.18 |
| R | OEOE\_1412 | OEOE\_RS06805 | haloacid dehalogenase | -0.89 | -0.91 | -1.03 | -1.00 | -1.20 | -1.35 |
| R | OEOE\_1424 | OEOE\_RS06865 | competence protein ComX | 1.67 | 1.81 | 1.76 | 1.62 | 1.64 | 1.52 |
| R | OEOE\_1474 | OEOE\_RS07115 | glycosyl transferase | 1.19 | 0.77 | 0.60 | 0.62 | 0.62 | 0.59 |
| R | OEOE\_1514 | OEOE\_RS07295 | glycosyl transferase | 0.99 | 0.87 | 0.77 | 0.94 | 1.01 | 1.13 |
| R | OEOE\_1536 | OEOE\_RS07405 | MFS transporter | 0.76 | 0.62 | 0.74 | 1.12 | 1.31 | 1.44 |
| R | OEOE\_1560 | OEOE\_RS07525 | 17-β-hydroxysteroid dehydrogenase | -0.45 | -0.85 | -1.01 | -1.12 | -1.21 | -1.13 |
| R | OEOE\_1607 | OEOE\_RS07750 | heme ABC transporter ATP-binding protein | -0.42 | -0.85 | -1.14 | -1.36 | -1.37 | -1.37 |
| R | OEOE\_1608 | OEOE\_RS07755 | ABC transporter permease | -0.29 | -0.52 | -1.00 | -1.25 | -1.23 | -1.24 |
| R | OEOE\_1748 | OEOE\_RS08435 | HD family phosphohydrolase | -1.22 | -0.86 | -1.05 | -0.90 | -0.78 | -0.88 |
| R | OEOE\_1782 | OEOE\_RS08590 | aldo/keto reductase | -1.16 | -1.31 | -1.60 | -1.87 | -1.89 | -1.88 |
| R | OEOE\_1820 | OEOE\_RS08780 | acetyltransferase | 0.87 | 0.81 | 0.89 | 0.98 | 1.12 | 1.03 |
| R | OEOE\_1841 | OEOE\_RS08890 | CAAX amino protease | 1.02 | 0.81 | 0.73 | 0.72 | 0.68 | 0.65 |
| R | OEOE\_1843 | OEOE\_RS08900 | permease | 1.57 | 1.39 | 1.39 | 1.48 | 1.44 | 1.63 |
| R | OEOE\_1851 | OEOE\_RS08935 | O-acetyltransferase | 1.04 | 0.81 | 0.73 | 0.81 | 0.84 | 0.81 |
| R | OEOE\_1858 | OEOE\_RS08970 | 2,5-diketo-D-gluconic acid reductase | -0.81 | -0.61 | -0.97 | -1.22 | -1.28 | -1.20 |
| R | OEOE\_1859 | OEOE\_RS08975 | oxidoreductase | 1.15 | 1.47 | 1.37 | 1.14 | 1.15 | 1.04 |
| **S: Function unknown** |  |  |  |  |  |  |  |  |  |
| S | OEOE\_0069 | OEOE\_RS00315 | membrane protein | -1.66 | -1.64 | -1.84 | -1.95 | -2.01 | -2.19 |
| S | OEOE\_0406 | OEOE\_RS01950 | membrane protein | 1.70 | 1.87 | 1.62 | 1.48 | 1.54 | 1.50 |
| S | OEOE\_0483 | OEOE\_RS02305 | membrane protein | -2.20 | -2.54 | -2.49 | -2.61 | -2.59 | -2.99 |
| S | OEOE\_0484 | OEOE\_RS02310 | cytochrome O ubiquinol oxidase | -2.05 | -2.42 | -2.40 | -2.59 | -2.40 | -2.69 |
| S | OEOE\_0547 | OEOE\_RS02595 | amidase | 1.16 | 1.10 | 1.23 | 1.08 | 1.15 | 1.03 |
| S | OEOE\_0634 | OEOE\_RS03030 | membrane protein | 1.44 | 1.24 | 1.37 | 1.84 | 1.75 | 1.83 |
| S | OEOE\_0639 | OEOE\_RS03055 | membrane protein | -1.49 | -1.56 | -1.63 | -1.57 | -1.51 | -1.51 |
| S | OEOE\_0650 | OEOE\_RS03110 | membrane protein | 1.59 | 1.71 | 1.72 | 1.67 | 1.72 | 1.67 |
| S | OEOE\_0713 | OEOE\_RS03410 | membrane protein | 2.72 | 3.21 | 3.72 | 3.61 | 3.47 | 3.40 |
| S | OEOE\_0753 | OEOE\_RS03605 | membrane protein | 1.82 | 2.06 | 2.07 | 2.14 | 2.18 | 2.15 |
| S | OEOE\_0835 | OEOE\_RS04015 | membrane protein | 1.72 | 1.42 | 1.72 | 2.02 | 1.83 | 1.81 |
| S | OEOE\_0930 | OEOE\_RS04465 | membrane protein | 2.28 | 2.77 | 3.32 | 3.10 | 2.70 | 2.56 |
| S | OEOE\_0933 | OEOE\_RS04470 | 5'-3'-deoxyribonucleotidase | 1.24 | 1.52 | 1.81 | 2.38 | 2.94 | 3.25 |
| S | OEOE\_1035 | OEOE\_RS04975 | membrane protein | -1.30 | -1.71 | -1.80 | -1.76 | -1.73 | -1.88 |
| S | OEOE\_1109 | OEOE\_RS05330 | membrane protein | -1.23 | -0.96 | -0.66 | -0.46 | -0.49 | -0.52 |
| S | OEOE\_1229 | OEOE\_RS05920 | cytochrome O ubiquinol oxidase | 0.46 | 0.45 | 0.67 | 0.90 | 0.94 | 1.06 |
| S | OEOE\_1354 | OEOE\_RS06515 | membrane protein | -1.33 | -1.55 | -1.28 | -1.07 | -0.89 | -1.14 |
| S | OEOE\_1367 | OEOE\_RS06575 | membrane protein | -0.40 | -0.92 | -1.20 | -0.99 | -0.92 | -1.08 |
| S | OEOE\_1472 | OEOE\_RS07105 | membrane protein | 0.96 | 1.07 | 0.62 | 0.55 | 0.60 | 0.70 |
| S | OEOE\_1567 | OEOE\_RS07560 | membrane protein | 1.49 | 1.31 | 1.08 | 1.04 | 0.98 | 1.07 |
| S | OEOE\_1606 | OEOE\_RS07745 | membrane protein | -0.98 | -1.08 | -1.46 | -1.74 | -1.69 | -1.74 |
| S | OEOE\_1620 | OEOE\_RS07815 | membrane protein | -0.36 | 0.06 | 0.54 | 0.97 | 1.00 | 0.54 |
| S | OEOE\_1829 | OEOE\_RS08830 | glycosyl transferase | 1.38 | 1.07 | 0.96 | 1.07 | 1.07 | 1.12 |
| **T: Signal transduction mechanisms** |  |  |  |  |  |  |  |  |  |
| T | OEOE\_0120 | OEOE\_RS00555 | histidine kinase | -1.07 | -1.18 | -1.28 | -1.14 | -1.17 | -1.14 |
| T | OEOE\_0143 | OEOE\_RS00665 | histidine kinase | 0.82 | 0.93 | 1.02 | 1.13 | 1.01 | 0.96 |
| T | OEOE\_0420 | OEOE\_RS02020 | [citrate [pro-3S]-lyase] ligase | 1.85 | 2.22 | 1.77 | 1.23 | 1.20 | 1.17 |
| T | OEOE\_0421 | OEOE\_RS02025 | citrate lyase ACP | 1.68 | 1.96 | 1.88 | 1.44 | 1.24 | 1.45 |
| T | OEOE\_0422 | OEOE\_RS02030 | citrate lyase | 1.25 | 1.50 | 1.25 | 0.95 | 0.91 | 1.07 |
| T | OEOE\_0489 | OEOE\_RS02335 | histidine kinase | -0.75 | -0.84 | -1.22 | -1.32 | -1.24 | -1.23 |
| **U: Intracellular trafficking, secretion, and vesicular transport** |  |  |  |  |  |  |  |  |  |
| U | OEOE\_0614 | OEOE\_RS02940 | preprotein translocase subunit SecY | 1.20 | 1.05 | 1.32 | 1.62 | 1.56 | 1.50 |
| U | OEOE\_0794 | OEOE\_RS03805 | type VI secretion protein ImpB | 0.63 | 0.98 | 1.01 | 1.06 | 1.13 | 1.31 |
| U | OEOE\_1254 | OEOE\_RS06045 | type II secretion protein | 1.21 | 0.82 | 0.61 | 0.60 | 0.61 | 0.49 |
| U | OEOE\_1255 | OEOE\_RS06050 | competence protein ComGC | 1.08 | 0.67 | 0.45 | 0.44 | 0.46 | 0.17 |
| U | OEOE\_1256 | OEOE\_RS06055 | type II secretion system protein F | 1.35 | 0.80 | 0.66 | 0.56 | 0.58 | 0.47 |
| U | OEOE\_1862 | OEOE\_RS08990 | membrane protein | 1.18 | 1.52 | 1.70 | 1.68 | 1.59 | 1.53 |
| **V: Defense mechanisms** |  |  |  |  |  |  |  |  |  |
| V | OEOE\_0439 | OEOE\_RS02115 | multidrug ABC transporter ATP-binding protein | 3.69 | 4.43 | 4.75 | 4.45 | 4.26 | 4.08 |
| V | OEOE\_0512 | OEOE\_RS02435 | diguanylate cyclase | 1.23 | 1.22 | 0.99 | 1.08 | 1.04 | 1.15 |
| V | OEOE\_0588 | OEOE\_RS02805 | N-acetylmuramoyl-L-alanine amidase | 1.85 | 2.06 | 2.14 | 2.01 | 1.79 | 1.71 |
| V | OEOE\_0720 | OEOE\_RS03440 | acetyl esterase | 3.23 | 3.72 | 4.21 | 4.03 | 3.69 | 3.61 |
| V | OEOE\_0722 | OEOE\_RS03445 | multidrug ABC transporter ATPase | 1.72 | 1.69 | 2.02 | 2.16 | 1.93 | 2.02 |
| V | OEOE\_0723 | OEOE\_RS03450 | multidrug ABC transporter permease | 2.15 | 2.01 | 2.34 | 2.48 | 2.35 | 2.18 |
| V | OEOE\_0737 | OEOE\_RS03520 | multidrug ABC transporter permease | -0.79 | -0.88 | -0.96 | -0.98 | -1.06 | -1.01 |
| V | OEOE\_0761 | OEOE\_RS03640 | multidrug ABC transporter permease | 0.88 | 1.23 | 1.10 | 1.03 | 1.06 | 1.17 |
| V | OEOE\_0877 | OEOE\_RS04200 | multidrug MFS transporter | 2.39 | 2.77 | 3.14 | 3.51 | 3.73 | 3.75 |
| V | OEOE\_1345 | OEOE\_RS06465 | multidrug ABC transporter permease | -0.50 | -0.52 | -0.99 | -1.21 | -1.29 | -0.94 |
| V | OEOE\_1636 | OEOE\_RS07890 | multidrug ABC transporter ATP-binding protein | 1.07 | 0.93 | 0.72 | 0.69 | 0.59 | 0.65 |
| V | OEOE\_1711 | OEOE\_RS08260 | multidrug ABC transporter ATP-binding protein | 1.48 | 1.54 | 1.68 | 1.80 | 1.47 | 1.05 |
| V | OEOE\_1712 | OEOE\_RS08265 | multidrug ABC transporter ATP-binding protein | 1.01 | 1.04 | 1.25 | 1.40 | 1.10 | 0.76 |
| **Multi COGs** |  |  |  |  |  |  |  |  |  |
| A J K F | OEOE\_1643 | OEOE\_RS07925 | DEAD/DEAH box helicase | 2.15 | 2.46 | 2.37 | 2.47 | 2.47 | 2.37 |
| C H | OEOE\_0769 | OEOE\_RS03675 | formate--tetrahydrofolate ligase | 1.02 | 1.45 | 1.27 | 1.25 | 1.30 | 1.32 |
| C O | OEOE\_0414 | OEOE\_RS01990 | cysteine ABC transporter ATP-binding protein | -0.62 | -0.86 | -1.01 | -1.16 | -1.23 | -1.25 |
| C R | OEOE\_1358 | OEOE\_RS06535 | NADPH:quinone reductase | -0.74 | -1.14 | -1.03 | -0.99 | -0.94 | -0.99 |
| E F | OEOE\_0260 | OEOE\_RS01245 | carbamoyl phosphate synthase small subunit | -1.08 | -1.62 | -1.82 | -2.07 | -2.28 | -2.24 |
| E C G T | OEOE\_0952 | OEOE\_RS04565 | glutamine synthetase | 1.88 | 2.08 | 2.20 | 2.01 | 1.83 | 1.81 |
| E F | OEOE\_0261 | OEOE\_RS01250 | carbamoyl-phosphate synthase large chain | -0.66 | -0.89 | -1.18 | -1.54 | -1.69 | -1.78 |
| E G | OEOE\_0387 | OEOE\_RS01860 | 4-aminobutyrate aminotransferase | 2.98 | 3.30 | 3.27 | 3.20 | 3.21 | 3.30 |
| E G | OEOE\_0638 | OEOE\_RS03050 | phosphoglycerate kinase | -1.12 | -1.25 | -1.39 | -1.29 | -1.22 | -1.22 |
| E G V | OEOE\_0635 | OEOE\_RS03035 | glucosamine--fructose-6-phosphate aminotransferase | 2.94 | 3.14 | 3.65 | 3.92 | 3.99 | 3.97 |
| E H Q V | OEOE\_1296 | OEOE\_RS06245 | branched-chain amino acid aminotransferase | 0.95 | 1.42 | 2.04 | 2.25 | 2.61 | 3.02 |
| E M S | OEOE\_1644 | OEOE\_RS07930 | UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase | 1.30 | 1.50 | 1.29 | 1.29 | 1.29 | 1.29 |
| E Q | OEOE\_0766 | OEOE\_RS03660 | cystathionine β-lyase | 0.82 | 1.15 | 0.81 | 0.69 | 0.74 | 0.77 |
| E Q | OEOE\_0895 | OEOE\_RS04290 | aspartate aminotransferase | 1.42 | 1.89 | 1.99 | 2.06 | 1.85 | 2.02 |
| E Q | OEOE\_1048 | OEOE\_RS05035 | aspartate racemase | -0.61 | -0.81 | -1.08 | -1.10 | -1.13 | -0.99 |
| E R | OEOE\_0394 | OEOE\_RS01895 | threonine dehydrogenase | -0.99 | -1.29 | -1.15 | -0.99 | -0.96 | -0.87 |
| E R | OEOE\_1707 | OEOE\_RS08240 | alcohol dehydrogenase | -0.41 | -0.77 | -1.02 | -1.14 | -1.27 | -1.30 |
| E R | OEOE\_1780 | OEOE\_RS08580 | alcohol dehydrogenase | -0.66 | -1.31 | -1.40 | -1.50 | -1.64 | -1.68 |
| E V C G | OEOE\_0122 | OEOE\_RS00565 | phosphoglyceromutase | -1.37 | -1.60 | -1.51 | -1.40 | -1.37 | -1.42 |
| E V Q | OEOE\_0152 | OEOE\_RS00715 | 3-phosphoshikimate 1-carboxyvinyltransferase | 1.71 | 1.92 | 1.62 | 1.49 | 1.64 | 1.95 |
| E V Q | OEOE\_0153 | OEOE\_RS00720 | shikimate kinase | 2.12 | 2.16 | 2.08 | 1.92 | 2.08 | 2.26 |
| E V Q | OEOE\_0939 | OEOE\_RS04500 | argininosuccinate synthase | -0.20 | -0.58 | -0.82 | -0.94 | -1.10 | -1.01 |
| E V Q | OEOE\_1546 | OEOE\_RS07455 | homoserine dehydrogenase | 1.40 | 1.52 | 1.58 | 1.65 | 1.59 | 1.74 |
| E V Q C G | OEOE\_0310 | OEOE\_RS01480 | phosphoglycerate mutase | 0.51 | 0.73 | 1.22 | 1.11 | 0.77 | 0.82 |
| E V Q C G | OEOE\_1611 | OEOE\_RS07770 | ribose 5-phosphate isomerase | -0.87 | -0.94 | -1.09 | -1.37 | -1.27 | -1.16 |
| E V Q C G | OEOE\_1652 | OEOE\_RS07970 | triosephosphate isomerase | -1.34 | -1.12 | -1.25 | -1.55 | -1.51 | -1.67 |
| E V Q G C O | OEOE\_1650 | OEOE\_RS07960 | enolase | -0.76 | -0.76 | -0.75 | -1.06 | -1.07 | -1.12 |
| F E | OEOE\_0163 | OEOE\_RS00770 | ferredoxin--NADP reductase | 0.93 | 1.14 | 1.24 | 1.35 | 1.39 | 1.35 |
| F E | OEOE\_0258 | OEOE\_RS01235 | aspartate carbamoyltransferase | -1.14 | -1.75 | -2.00 | -2.27 | -2.56 | -2.50 |
| F E | OEOE\_0566 | OEOE\_RS02695 | thioredoxin reductase | 1.06 | 1.66 | 1.60 | 1.23 | 1.20 | 1.23 |
| F E V Q | OEOE\_1125 | OEOE\_RS05410 | adenylosuccinate lyase | -0.42 | -0.88 | -0.98 | -1.16 | -1.06 | -0.94 |
| F G R | OEOE\_0929 | OEOE\_RS04460 | HIT family hydrolases | 2.67 | 3.22 | 3.98 | 3.81 | 3.44 | 3.28 |
| F H | OEOE\_1469 | OEOE\_RS07095 | allantoin permease | -0.95 | -0.85 | -1.12 | -1.24 | -1.14 | -1.01 |
| F Q | OEOE\_0537 | OEOE\_RS02555 | xanthine phosphoribosyltransferase | -1.08 | -1.09 | -0.82 | -0.28 | -0.07 | -0.03 |
| F V Q | OEOE\_0615 | OEOE\_RS02945 | adenylate kinase | 1.21 | 1.08 | 1.22 | 1.36 | 1.44 | 1.22 |
| G C T | OEOE\_0418 | OEOE\_RS02010 | malate dehydrogenase | 2.20 | 2.51 | 2.25 | 1.77 | 1.68 | 1.61 |
| G I | OEOE\_1781 | OEOE\_RS08585 | alpha-galactosidase | -1.21 | -1.24 | -1.58 | -1.92 | -2.08 | -2.06 |
| G Q | OEOE\_0249 | OEOE\_RS01190 | mannose-6-phosphate isomerase | -1.06 | -1.41 | -1.55 | -1.41 | -1.24 | -1.26 |
| G T | OEOE\_0544 | OEOE\_RS02580 | hydrolase | 1.73 | 1.89 | 1.49 | 1.32 | 1.22 | 1.29 |
| G V | OEOE\_1542 | OEOE\_RS07435 | bifunctional protein GlmU | -0.61 | -1.02 | -1.03 | -1.15 | -1.16 | -1.10 |
| G V Q C | OEOE\_0920 | OEOE\_RS04415 | glucokinase | -0.95 | -1.18 | -1.20 | -0.95 | -0.80 | -0.57 |
| H R | OEOE\_0700 | OEOE\_RS03355 | alpha/β hydrolase | -1.62 | -2.02 | -1.82 | -1.54 | -1.30 | -1.34 |
| H R | OEOE\_0836 | OEOE\_RS04020 | haloacid dehalogenase | 1.37 | 1.20 | 1.27 | 1.42 | 1.43 | 1.34 |
| H R | OEOE\_1196 | OEOE\_RS05765 | haloacid dehalogenase | 0.54 | 0.65 | 0.78 | 0.88 | 0.77 | 1.05 |
| H R | OEOE\_1845 | OEOE\_RS08910 | haloacid dehalogenase | 1.31 | 1.34 | 1.03 | 0.98 | 1.04 | 1.04 |
| I H | OEOE\_1586 | OEOE\_RS07650 | 3-hydroxyacyl-ACP dehydratase | 0.33 | 0.28 | 0.70 | 0.91 | 0.94 | 1.03 |
| J O | OEOE\_0717 | OEOE\_RS03425 | spermidine N1-acetyltransferase | 0.36 | 1.00 | 1.28 | 1.22 | 1.00 | 1.00 |
| L F | OEOE\_1663 | OEOE\_RS08025 | DNA polymerase III subunit alpha | 1.18 | 1.21 | 0.89 | 0.80 | 0.89 | 0.89 |
| L O | OEOE\_1192 | OEOE\_RS05745 | ATPase AAA | -1.08 | -1.15 | -1.21 | -1.20 | -1.20 | -1.08 |
| M G | OEOE\_1649 | OEOE\_RS07955 | saccharopine dehydrogenase | -0.71 | -0.75 | -0.96 | -1.03 | -1.12 | -1.17 |
| M G I | OEOE\_1044 | OEOE\_RS05015 | β-galactosidase | -0.96 | -1.45 | -1.54 | -1.45 | -1.33 | -1.27 |
| M V | OEOE\_0900 | OEOE\_RS04315 | carboxypeptidase | 1.16 | 1.45 | 1.15 | 1.15 | 1.15 | 1.15 |
| Q F | OEOE\_1127 | OEOE\_RS05420 | inosine-5-monophosphate dehydrogenase | -0.74 | -1.14 | -1.14 | -1.27 | -1.27 | -1.31 |
| Q G I V | OEOE\_1248 | OEOE\_RS06015 | alcohol dehydrogenase | -0.51 | -0.76 | -1.09 | -1.46 | -1.61 | -1.58 |
| Q G I V | OEOE\_1330 | OEOE\_RS06400 | alcohol dehydrogenase | -0.64 | -1.02 | -1.06 | -1.10 | -1.24 | -1.30 |
| Q H | OEOE\_0279 | OEOE\_RS01335 | dihydroxynaphthoic acid synthetase | -0.60 | -0.91 | -0.93 | -0.92 | -0.98 | -1.15 |
| Q H | OEOE\_0280 | OEOE\_RS01340 | acyl-CoA synthetase | -0.85 | -0.98 | -1.12 | -1.24 | -1.25 | -1.34 |
| Q V | OEOE\_1100 | OEOE\_RS05285 | kinase | -1.13 | -1.09 | -0.88 | -0.83 | -0.84 | -0.84 |
| Q V | OEOE\_1445 | OEOE\_RS06980 | dTDP-4-dehydrorhamnose reductase | 2.21 | 2.97 | 3.26 | 3.05 | 2.78 | 2.71 |
| Q V | OEOE\_1447 | OEOE\_RS06990 | dTDP-glucose 4,6-dehydratase | -0.72 | -0.89 | -1.06 | -1.35 | -1.38 | -1.23 |
| Q V | OEOE\_1448 | OEOE\_RS06995 | dTDP-4-dehydrorhamnose 3,5-epimerase | -0.55 | -0.72 | -0.88 | -1.09 | -1.18 | -1.12 |
| Q V | OEOE\_1449 | OEOE\_RS07000 | glucose-1-phosphate thymidylyltransferase | -0.62 | -0.95 | -1.09 | -1.36 | -1.32 | -1.25 |
| T K | OEOE\_0142 | OEOE\_RS00660 | transcriptional regulator | 1.18 | 1.67 | 1.99 | 2.17 | 1.93 | 1.67 |
| T K | OEOE\_0488 | OEOE\_RS02330 | PhoB family transcriptional regulator | -0.77 | -1.03 | -1.18 | -1.21 | -1.14 | -1.23 |
| T S | OEOE\_0214 | OEOE\_RS01015 | D-alanyl-D-alanine dipeptidase | -0.75 | -0.46 | -0.81 | -1.02 | -1.33 | -0.99 |
| V Q C E G | OEOE\_0135 | OEOE\_RS00625 | glucose-6-phosphate 1-dehydrogenase | -0.53 | -0.86 | -1.02 | -1.17 | -1.26 | -1.31 |
| V Q C E G | OEOE\_0892 | OEOE\_RS04275 | 6-phosphogluconate dehydrogenase | -0.60 | -0.73 | -1.07 | -1.38 | -1.43 | -1.44 |
| V Q C E G | OEOE\_1523 | OEOE\_RS07345 | 6-phosphogluconate dehydrogenase | -0.79 | -1.25 | -1.35 | -1.57 | -1.76 | -1.73 |
| V Q C G | OEOE\_0328 | OEOE\_RS01570 | pyruvate dehydrogenase E1 subunit alpha | -0.58 | -0.90 | -0.93 | -1.22 | -1.20 | -0.90 |
| V Q C G | OEOE\_0329 | OEOE\_RS01575 | 2-oxoisovalerate dehydrogenase subunit β | -0.41 | -0.59 | -0.70 | -1.08 | -1.03 | -0.75 |
| V Q C G | OEOE\_0330 | OEOE\_RS01580 | dihydrolipoamide acetyltransferase | -0.61 | -0.60 | -0.85 | -1.25 | -1.15 | -0.97 |
| V Q C G E | OEOE\_0331 | OEOE\_RS01585 | dihydrolipoamide dehydrogenase | -0.66 | -0.61 | -0.84 | -1.16 | -1.11 | -0.90 |
| V Q F | OEOE\_1136 | OEOE\_RS05465 | phosphoribosylaminoimidazole-succinocarboxamide synthase | -0.19 | -0.68 | -0.96 | -1.09 | -1.25 | -1.44 |
| V Q F | OEOE\_1137 | OEOE\_RS05470 | phosphoribosylaminoimidazole carboxylase | -0.13 | -0.60 | -0.67 | -0.89 | -1.02 | -0.97 |
| V Q F | OEOE\_1138 | OEOE\_RS05475 | N5-carboxyaminoimidazole ribonucleotide mutase | -1.03 | -1.33 | -1.42 | -1.61 | -1.64 | -1.66 |
| V Q G | OEOE\_0301 | OEOE\_RS01435 | aldose 1-epimerase | -1.52 | -1.02 | -1.55 | -1.77 | -1.76 | -1.85 |
| V Q H F | OEOE\_1129 | OEOE\_RS05430 | bifunctional purine biosynthesis protein PurH | -0.16 | -0.37 | -0.70 | -1.03 | -1.10 | -1.07 |
| V Q H F | OEOE\_1130 | OEOE\_RS05435 | phosphoribosylglycinamide formyltransferase | -0.11 | -0.26 | -0.62 | -0.95 | -1.05 | -1.05 |
| V T | OEOE\_0164 | OEOE\_RS00775 | diguanylate cyclase | 0.96 | 1.20 | 1.44 | 1.51 | 1.60 | 1.56 |