## Additional file 3: Genes differentially expressed grouped by function *

| ORF # | Common | Organism | 2h fold change | 6h fold change | Protein name | GO | Class | Annotation |
|---|---|---|---|---|---|---|---|---|
| **SA0162** | *aldA* | N315 | 3.70 | | aldehyde dehydrogenase homologue | COG1012 | **C** | Energy production and conversion |
| **SA1907** | *atpA* | N315 | 0.08 | 0.25 | ATP synthase alpha chain | COG0056 | **C** | Energy production and conversion |
| **SA1911** | *atpB* | N315 | 0.01 | 0.03 | ATP synthase A chain | | **C** | Energy production and conversion |
| **SA1904** | *atpC* | N315 | 0.19 | 0.24 | FoF1ATP synthase epsilon subunit | | **C** | Energy production and conversion |
| **SA1905** | *atpD* | N315 | 0.02 | 0.09 | ATP synthase beta chain | COG0055 | **C** | Energy production and conversion |
| **SA1910** | *atpE* | N315 | 0.01 | 0.10 | ATP synthase C chain | COG0636 | **C** | Energy production and conversion |
| **SA1909** | *atpF* | N315 | 0.01 | 0.12 | ATP synthase B chain | COG0711 | **C** | Energy production and conversion |
| **SA1906** | *atpG* | N315 | 0.05 | 0.15 | ATP synthase gamma chain | COG0224 | **C** | Energy production and conversion |
| **SA1908** | *atpH* | N315 | 0.08 | 0.20 | ATP synthase delta chain | COG0712 | **C** | Energy production and conversion |
| **SA1347** | *bfmBAB* | N315 | 0.23 | 0.28 | branched-chain alphaketo acid dehydrogenase E1 | COG0022 | **C** | Energy production and conversion |
| **SA1346** | *bmfBB* | N315 | 0.31 | | branched-chain alphaketo acid dehydrogenase E2 | COG0508 | **C** | Energy production and conversion |
| **SA1184** | *citB* | N315 | 0.01 | 0.01 | aconitate hydratase | COG1048 | **C** | Energy production and conversion |
| **SA1517** | *citC* | N315 | 0.16 | 0.19 | isocitrate dehyrogenase | COG0538 | **C** | Energy production and conversion |
| **SA1518** | *citZ* | N315 | 0.18 | 0.17 | citrate synthase II | COG0372 | **C** | Energy production and conversion |
| **SA0820** | *glpQ* | N315 | 3.16 | | glycerophosphoryl diester phosphodiesterase | COG0584 | **C** | Energy production and conversion |
| **SA1306** | *gpsA* | N315 | 0.05 | 0.08 | glycerol-3-phosphate dehydrogenase | COG0240 | **C** | Energy production and conversion |
| **SA0232** | *lctE* | N315 | 0.29 | 0.20 | L-lactate dehydrogenase | COG0039 | **C** | Energy production and conversion |
| **SA0813** | *mnhA* | N315 | 0.32 | | Na+/H+ antiporter subunit | COG2111,COG1009 | **C** | Energy production and conversion |
| **SA0810** | *mnhD* | N315 | 0.05 | 0.07 | Na+/H+antiporter subunit | COG0651 | **C** | Energy production and conversion |
| **MW0820** | *MW0820* | MW2 | 0.20 | | NADH dehydrogenase | COG1252 | **C** | Energy production and conversion |
| **MW1173** | *MW1173* | MW2 | | 0.25 | 2-oxoacid ferredoxin oxidoreductase, beta subunit | COG1013 | **C** | Energy production and conversion |
| **MW2317** | *MW2317* | MW2 | 0.10 | 0.09 | nitrate reductase delta chain | COG2180 | **C** | Energy production and conversion |
| **SA2182** | *narI* | N315 | 0.33 | 0.33 | nitrate reductase gamma chain | COG2181 | **C** | Energy production and conversion |
| **SA2188** | *nasD* | N315 | | 0.33 | nitrite reductase | COG1251 | **C** | Energy production and conversion |
| **MW1303** | *odhA* | MW2 | 0.30 | | oxoglutarate dehydrogenase | COG0567 | **C** | Energy production and conversion |
| **SA1245** | *odhA* | N315 | 0.02 | 0.31 | 2-oxoglutarate dehydrogenase E1 | COG0567 | **C** | Energy production and conversion |
| **SA1244** | *odhB* | N315 | 0.05 | 0.09 | dihydrolipoamide succinyltransferase | COG0508 | **C** | Energy production and conversion |
| **SA09431** | *pdhA* | N315 | 0.09 | 0.09 | pyruvate dehydrogenase E1 component alpha subunit | COG1071 | **C** | Energy production and conversion |
| **SA0944** | *pdhB* | N315 | 0.01 | 0.04 | pyruvate dehydrogenase E1 component beta subunit | COG0022 | **C** | Energy production and conversion |
| **SA0945** | *pdhC* | N315 | 0.01 | 0.03 | dihydrolipoamide S Ac transferase of pyruvate dehydrogenase complex | COG0508 | **C** | Energy production and conversion |
| **SA0946** | *pdhD* | N315 | 0.04 | 0.12 | dihydrolipoamide dehydrogenase of pyruvate dehydrogenase E3 | COG1249 | **C** | Energy production and conversion |
| **SA0218** | *pflB* | N315 | 0.23 | 0.29 | formate acetyltransferase | COG1882 | **C** | Energy production and conversion |
| **SA0963** | *pycA* | N315 | 0.27 | 0.22 | pyruvate carboxylase | COG1038 | **C** | Energy production and conversion |
| **SA0912** | *qoxB* | N315 | 0.02 | 0.06 | Quinol oxidase polypeptide I QoxB | COG0843 | **C** | Energy production and conversion |
| **SA0911** | *qoxC* | N315 | 0.06 | 0.09 | Quinol oxidase polypeptide III QoxC | COG1845 | **C** | Energy production and conversion |
| **SA0036** | *SA0036* | N315 | | 3.05 | glycerophosphoryldiester phosphodiesterase homologue | COG0584 | **C** | Energy production and conversion |
| **SA0220** | *SA0220* | N315 | 3.47 | 3.11 | glycerophosphodiester phosphodiesterase | COG0584,COG4781 | **C** | Energy production and conversion |
| **SA0231** | *SA0231* | N315 | 0.33 | | flavo-hemoprotein | COG1017,COG1018 | **C** | Energy production and conversion |
| **SA0312** | *SA0312* | N315 | 0.33 | | alkanal monooxygenase alpha chain | COG2141 | **C** | Energy production and conversion |
| **SA0557** | *SA0557* | N315 | | 0.24 | oxidoreductase, ion channel | COG0667 | **C** | Energy production and conversion |
| **SA0640** | *SA0640* | N315 | 0.33 | 0.21 | ABC transporter required for expression of cytochrome bd | COG4987COG | **C** | Energy production and conversion |
| **SA0777** | *SA0777* | N315 | 0.10 | 0.19 | nitrogen fixation protein NifU | COG0822 | **C** | Energy production and conversion |
| **SA0910** | *SA0910* | N315 | 0.05 | 0.13 | quinol oxidase polypeptide IV QoxD | COG3125 | **C** | Energy production and conversion |
| **SA0913** | *SA0913* | N315 | 0.05 | 0.10 | quinol oxidase polypeptide II QoxA | COG1622 | **C** | Energy production and conversion |
| **SA0969** | *SA0969* | N315 | | 3.31 | glycerophosphoryl diester phosphodiesterase | COG0584 | **C** | Energy production and conversion |
| **SA1131** | *SA1131* | N315 | 0.07 | 0.25 | 2-oxoacid ferredoxin oxidoreductase, alpha subunit | COG1014,COG0674 | **C** | Energy production and conversion |
| **SA1132** | *SA1132* | N315 | 0.12 | 0.18 | 2-oxoacid ferredoxin oxidoreductase, beta subunit | COG1013 | **C** | Energy production and conversion |
| **SA1349** | *SA1349* | N315 | 0.18 | 0.21 | dihydrolipoamide dehydrogenase | COG1249 | **C** | Energy production and conversion |
| **SA1524** | *SA1524* | N315 | 0.24 | 0.32 | malate dehydrogenase homolog | COG0281 | **C** | Energy production and conversion |
| **SA1735** | *SA1735* | N315 | 0.12 | 0.14 | manganesedependent inorganic pyrophosphatase | COG1227 | **C** | Energy production and conversion |
| **SA2311** | *SA2311* | N315 | 3.36 | | NAD(P)Hflavin oxidoreductase | COG0778 | **C** | Energy production and conversion |
| **SA0995** | *sdhA* | N315 | 0.04 | 0.12 | succinate dehydrogenase flavoprotein subunit | COG1053 | **C** | Energy production and conversion |
| **SA0996** | *sdhB* | N315 | 0.13 | 0.16 | succinate dehydrogenase ironsulfur protein subunit | COG0479 | **C** | Energy production and conversion |
| **SA0994** | *sdhC* | N315 | 0.19 | 0.24 | succinate dehydrogenase cytochrome b558 | COG2009 | **C** | Energy production and conversion |
| **SA1089** | *sucD* | N315 | 0.18 | 0.13 | succinylCoA synthetase | COG0074 | **C** | Energy production and conversion |
| **SA0846** | *SA0846* | N315 | 0.01 | 0.01 | oligopeptide transport system permease protein OppC | COG1173 | **E** | Amino acid transport and metabolism |
| **SA0848** | *oppF* | N315 | 0.01 | 0.02 | oligopeptide transport system ATPbinding protein OppF homologue | COG4608 | **E** | Amino acid transport and metabolism |
| **SA0849** | *SA0849* | N315 | 0.02 | 0.02 | peptide binding protein OppA | COG4166 | **E** | Amino acid transport and metabolism |
| **SA1424** | *aroE* | N315 | 0.03 | 0.04 | shikimate dehydrogenease | COG0169 | **E** | Amino acid transport and metabolism |
| **SA1045** | *pyrAA* | N315 | 0.03 | 0.20 | carbamoylphosphate synthase small chain | COG0505 | **E** | Amino acid transport and metabolism |
| **SA1915** | *glyA* | N315 | 0.03 | 0.06 | serine hydroxymethyl transferase | COG0112 | **E** | Amino acid transport and metabolism |
| **SA1572** | *SA1572* | N315 | 0.03 | 0.03 | XaaHis dipeptidase homolog | COG0624 | **E** | Amino acid transport and metabolism |
| **SA0242** | *SA0242* | N315 | 0.04 | 0.04 | xylitol dehydrogenase | COG1063 | **E** | Amino acid transport and metabolism |
| **SA0847** | *oppD* | N315 | 0.05 | 0.05 | oligopeptide transport system ATPbinding protein OppD homologue | COG0444 | **E** | Amino acid transport and metabolism |
| **SA1365** | *SA1365* | N315 | 0.06 | 0.08 | glycine dehydrogenase (decarboxylating) subunit 2 homolog | COG1003 | **E** | Amino acid transport and metabolism |
| **MW1267** | *opp2F* | MW2 | 0.06 | 0.09 | oligopeptide transporter putative ATPase domain | COG4608 | **E** | Amino acid transport and metabolism |
| **SA1232** | *lysA* | N315 | 0.07 | 0.12 | diaminopimelate decarboxylase | COG0019 | **E** | Amino acid transport and metabolism |
| **SA1227** | *dapA* | N315 | 0.08 | 0.14 | dihydrodipicolinate synthase | COG0329 | **E** | Amino acid transport and metabolism |
| **SA1297** | *aroA* | N315 | 0.08 | 0.17 | 3 phosphoshikimate 1-carboxyvinyl-transferase | COG0128 | **E** | Amino acid transport and metabolism |
| **SA1165** | *thrC* | N315 | 0.08 | 0.22 | threonine synthase | COG0498 | **E** | Amino acid transport and metabolism |
| **SA0246** | *SA0246* | N315 | 0.08 | 0.18 | hypotheticl protein, similar to D-xylulose reductase | COG1063 | **E** | Amino acid transport and metabolism |
| **SA1859** | *ilvB* | N315 | 0.08 | 0.08 | acetolactate synthase large subunit | COG0028 | **E** | Amino acid transport and metabolism |
| **SA1046** | *pyrAB* | N315 | 0.09 | 0.21 | carbamoylphosphate synthase large chain | COG0458 | **E** | Amino acid transport and metabolism |
| **SA1225** | *lysC* | N315 | 0.09 | 0.11 | aspartokinase II | COG0527 | **E** | Amino acid transport and metabolism |
| **SA1367** | *SA1367* | N315 | 0.09 | 0.12 | aminomethyltransferase | COG0404 | **E** | Amino acid transport and metabolism |
| **SA1366** | *SA1366* | N315 | 0.10 | 0.12 | glycine dehydrogenase subunit 1 | COG0403 | **E** | Amino acid transport and metabolism |
| **SA0670** | *SA0670* | N315 | 0.10 | 0.29 | paraaminobenzoate synthase component I | COG0115 | **E** | Amino acid transport and metabolism |
| **SA2125** | *SA2125* | N315 | 0.13 | 0.14 | formiminoglutamase | COG0010 | **E** | Amino acid transport and metabolism |
| **SA1226** | *asd* | N315 | 0.13 | 0.23 | aspartate semialdehyde dehydrogenase | COG0136 | **E** | Amino acid transport and metabolism |
| **SA0845** | *oppB* | N315 | 0.16 | 0.14 | oligopeptide transport system permease protein | COG0601 | **E** | Amino acid transport and metabolism |
| **SA1519** | *aapA* | N315 | 0.17 | 0.17 | D serine/Dalanine/glycine transporter | COG1113 | **E** | Amino acid transport and metabolism |
| **SA1695** | *ampS* | N315 | 0.17 | 0.18 | aminopeptidase ampS | COG2309 | **E** | Amino acid transport and metabolism |
| **SA1190** | *alsT* | N315 | 0.18 | | amino acid carrier protein | COG1115 | **E** | Amino acid transport and metabolism |
| **SA0010** | *SA0010* | N315 | 0.19 | 0.17 | amino acid permease | COG1296 | **E** | Amino acid transport and metabolism |
| **SA0471** | *cysK* | N315 | 0.19 | 0.12 | cysteine synthase (oacetylserine sulfhydrylase) homologue | COG0031 | **E** | Amino acid transport and metabolism |
| **SA0953** | *potD* | N315 | 0.20 | 0.29 | spermidine/putrescinebinding protein precursor homolog | COG0687 | **E** | Amino acid transport and metabolism |
| **SA2201** | *SA2201* | N315 | 0.20 | 0.24 | ABC transporter, permease protein | COG0765 | **E** | Amino acid transport and metabolism |
| **SA0951** | *potB* | N315 | 0.20 | 0.22 | potB | COG1176 | **E** | Amino acid transport and metabolism |
| **SA0678** | *SA0678* | N315 | 0.22 | 0.25 | choline transporter | COG1174,COG1732 | **E** | Amino acid transport and metabolism |
| **MW0539** | *MW0539* | MW2 | 0.23 | 0.26 | cationic amino acid transporter | COG0531 | **E** | Amino acid transport and metabolism |
| **SA2405** | *betA* | N315 | 0.24 | 0.30 | choline dehydrogenase | COG2303 | **E** | Amino acid transport and metabolism |
| **SA1538** | *SA1538* | N315 | 0.24 | 0.23 | ironsulfur cofactor synthesis protein nifZ | COG1104 | **E** | Amino acid transport and metabolism |
| **SA1169** | *SA1169* | N315 | 0.24 | 0.21 | gammaaminobutyrate permease | COG0833 | **E** | Amino acid transport and metabolism |
| **SA0990** | *SA0990* | N315 | 0.25 | | DNAdependent DNA polymerase beta chain | COG1796L,COG138 | **E** | Amino acid transport and metabolism |
| **SA0682** | *SA0682* | N315 | 0.25 | 0.14 | ditripepride ABC transporter | COG3104 | **E** | Amino acid transport and metabolism |
| **SA0679** | *SA0679* | N315 | 0.25 | 0.17 | histidinol-phosphate aminotransferase | COG0079 | **E** | Amino acid transport and metabolism |
| **SA1545** | *serA* | N315 | 0.25 | 0.32 | D3phosphoglycerate dehydrogenase | COG0111 | **E** | Amino acid transport and metabolism |
| **SA1571** | *SA1571* | N315 | 0.26 | 0.24 | Dalanine aminotransferase | COG0115 | **E** | Amino acid transport and metabolism |

| ORF # | Common | Organism | 2h fold change | 6h fold change | Protein name | GO | Class | Annotation |
|---|---|---|---|---|---|---|---|---|
| **SA0776** | *SA0776* | N315 | 0.26 |  | aminotransferase NifS homologue | COG0520 | **E** | Amino acid transport and metabolism |
| **SA1298** | *aroB* | N315 | 0.27 |  | 3 dehydroquinate synthase | COG0337 | **E** | Amino acid transport and metabolism |
| **SA0818** | *rocD* | N315 | 0.27 | 0.16 | ornithine aminotransferase | COG4992 | **E** | Amino acid transport and metabolism |
| **SA0950** | *potA* | N315 | 0.27 |  | spermidine/putrescine ABC transporter, ATPbinding protein homolog | COG3842 | **E** | Amino acid transport and metabolism |
| **SA0859** | *SA0859* | N315 | 0.28 | 0.22 | thimet oligopeptidase homologue | COG1164 | **E** | Amino acid transport and metabolism |
| **SA1164** | *dhoM* | N315 | 0.28 |  | homoserine dehydrogenase | COG0460 | **E** | Amino acid transport and metabolism |
| **SA0482** | *SA0482* | N315 | 0.29 |  | creatine kinase | COG3869 | **E** | Amino acid transport and metabolism |
| **SA0313** | *SA0313* | N315 | 0.29 | 0.20 | glycine cleavage system H protein | COG0509 | **E** | Amino acid transport and metabolism |
| **SA0822** | *argG* | N315 | 0.30 |  | argininosuccinate synthase | COG0137 | **E** | Amino acid transport and metabolism |
| **MW1284** | *dapB* | MW2 | 0.31 | 0.29 | dihydrodipicolinate reductase | COG0289 | **E** | Amino acid transport and metabolism |
| **SA0677** | *SA0677* | N315 | 0.31 |  | choline transport ATPbinding protein | COG1125 | **E** | Amino acid transport and metabolism |
| **SA2200** | *SA2200* | N315 | 0.31 |  | ABC transporter, ATP binding subunit | COG1126 | **E** | Amino acid transport and metabolism |
| **SA0487** | *cysE* | N315 | 0.32 |  | Serine acetyltransferase homologue | COG1045 | **E** | Amino acid transport and metabolism |
| **SA0458** | *prs* | N315 | 0.32 | 0.26 | ribosephosphate pyrophosphokinase | COG0462 | **E** | Amino acid transport and metabolism |
| **MW1625** | *lysP* | MW2 | 0.32 |  | lysine-specific permease | COG0833 | **E** | Amino acid transport and metabolism |
| **SA2081** | *SA2081* | N315 | 3.02 | 4.18 | urea transporter | COG4413 | **E** | Amino acid transport and metabolism |
| **SA0112** | *SA0112* | N315 | 3.06 | 3.47 | cysteine synthase | COG0031 | **E** | Amino acid transport and metabolism |
| **SA1531** | *ald* | N315 | 3.07 |  | alanine dehydrogenase | COG0686 | **E** | Amino acid transport and metabolism |
| **SA0303** | *SA0303* | N315 | 3.08 |  | sodiumcoupled permease | COG0591 | **E** | Amino acid transport and metabolism |
| **SA2293** | *gntP* | N315 | 3.13 |  | gluconate permease | COG2610 | **E** | Amino acid transport and metabolism |
| **SA1749** | *SA1749* | N315 | 3.22 |  | aspartate transaminase protein | COG0436 | **E** | Amino acid transport and metabolism |
| **SA0304** | *nanA* | N315 | 3.30 |  | N acetylneuraminate lyase subunit | COG0329 | **E** | Amino acid transport and metabolism |
| **MW1680** | *MW1680* | MW2 | 3.37 | 4.67 | chorismate mutase homolog | COG2876,COG1605 | **E** | Amino acid transport and metabolism |
| **SA0418** | *cysM* | N315 | 3.39 | 3.69 | cysteine synthase homologue | COG0031 | **E** | Amino acid transport and metabolism |
| **SA2227** | *truncatedSA* | N315 | 3.40 |  | truncatedSA | COG1113 | **E** | Amino acid transport and metabolism |
| **SA1204** | *trpB* | N315 | 3.42 | 3.15 | tryptophan synthase beta chain | COG0133 | **E** | Amino acid transport and metabolism |
| **SA0698** | *pepT* | N315 | 3.46 |  | aminotripeptidase | COG2195 | **E** | Amino acid transport and metabolism |
| **SA1814** | *SA1814* | N315 | 3.57 |  | succinyldiaminopimelate desuccinylase | COG0624 | **E** | Amino acid transport and metabolism |
| **SA2318** | *SA2318* | N315 | 3.65 | 3.02 | Lserine dehydratase | COG1760 | **E** | Amino acid transport and metabolism |
| **SA1270** | *SA1270* | N315 | 3.70 | 3.64 | amino acid pearmease | COG0531 | **E** | Amino acid transport and metabolism |
| **SA0201** | *rlp* | N315 | 3.83 | 3.52 | RGDcontaining lipoprotein | COG0747 | **E** | Amino acid transport and metabolism |
| **SA1203** | *trpF* | N315 | 3.86 | 3.23 | phosphoriborylanthranilate isomerase | COG0135 | **E** | Amino acid transport and metabolism |
| **SA2430** | *aur* | N315 | 3.91 |  | zinc metallo-proteinase aureolysin | COG3227 | **E** | Amino acid transport and metabolism |
| **SA2319** | *SA2319* | N315 | 4.10 | 3.40 | betasubunit of Lserine dehydratas | COG1760 | **E** | Amino acid transport and metabolism |
| **SA0476** | *SA0476* | N315 | 4.69 | 3.13 | transcription regulator GntR family | COG1167 | **E** | Amino acid transport and metabolism |
| **SA0851** | *SA0851* | N315 | 5.26 | 4.72 | oligopeptide ABC transporter ATPbinding protein homologue | COG0444 | **E** | Amino acid transport and metabolism |
| **SA0113** | *SA0113* | N315 | 24.10 | 27.78 | ornithine cyclodeaminase | COG2423 | **E** | Amino acid transport and metabolism |
| **SA0119** | *SA0119* | N315 |  | 3.13 | diaminopimelate decarboxylase | COG0019 | **E** | Amino acid transport and metabolism |
| **SA0180** | *SA0180* | N315 |  | 0.30 | branched-chain amino acid transport system carrier protein | COG1114 | **E** | Amino acid transport and metabolism |
| **SA0819** | *gudB* | N315 |  | 0.33 | NADspecific glutamate dehydrogenase | COG0334 | **E** | Amino acid transport and metabolism |
| **SA1216** | *SA1216* | N315 |  | 0.24 | oligoendopeptidase | COG1164 | **E** | Amino acid transport and metabolism |
| **SA1730** | *SA1730* | N315 |  | 0.28 | nitricoxide synthase homolog | COG4362 | **E** | Amino acid transport and metabolism |
| **SA2124** | *fosB* | N315 |  | 3.45 | fosfomycin resistance protein fofB | COG0346 | **E** | Amino acid transport and metabolism |
| **SA2234** | *opuCD* | N315 |  | 3.10 | probable glycine betaine/carnitine/choline ABC transporter opuCD | COG1174 | **E** | Amino acid transport and metabolism |
| **SA0917** | *purK* | N315 | 0.00 | 0.02 | P-ribosylaminoimidazole carboxylase carbon dioxidefixation chain | COG0026 | **F** | Nucleotide transport and metabolism |
| **SA0920** | *purQ* | N315 | 0.01 | 0.02 | phosphoribosylformylglycinamidine synthase I PurQ | COG0047 | **F** | Nucleotide transport and metabolism |
| **SA2027** | *adk* | N315 | 0.01 | 0.15 | adenylate kinase | COG0563 | **F** | Nucleotide transport and metabolism |
| **SA0926** | *purD* | N315 | 0.01 | 0.01 | phosphoribosylamineglycine ligase PurD | COG0151 | **F** | Nucleotide transport and metabolism |
| **SA0921** | *purL* | N315 | 0.01 | 0.02 | phosphoribosylformylglycinamidine synthetase | COG0046 | **F** | Nucleotide transport and metabolism |
| **SA1048** | *pyrE* | N315 | 0.01 | 0.03 | orotate phosphoribosyltransferase | COG0461 | **F** | Nucleotide transport and metabolism |
| **SA0923** | *purM* | N315 | 0.02 | 0.03 | phosphoribosylformylglycinamidine cycloligase PurM | COG0150 | **F** | Nucleotide transport and metabolism |
| **SA1914** | *upp* | N315 | 0.02 | 0.06 | uracil phosphoribosyl transferase | COG0035 | **F** | Nucleotide transport and metabolism |
| **SA1044** | *pyrC* | N315 | 0.03 | 0.10 | dihydroorotase | COG0044 | **F** | Nucleotide transport and metabolism |
| **SA0374** | *pbuX* | N315 | 0.03 | 0.05 | xanthine permease | COG2233 | **F** | Nucleotide transport and metabolism |
| **SA1043** | *pyrB* | N315 | 0.03 | 0.08 | aspartate transcarbamoylase chain A | COG0540 | **F** | Nucleotide transport and metabolism |
| **SA0922** | *purF* | N315 | 0.04 | 0.06 | phosphoribosylpyrophosphate amidotransferase PurF | COG0034 | **F** | Nucleotide transport and metabolism |
| **SA0454** | *purR* | N315 | 0.05 | 0.11 | pur operon repressor homologue | COG0503 | **F** | Nucleotide transport and metabolism |
| **SA1047** | *pyrF* | N315 | 0.05 | 0.07 | orotidine5phosphate decarboxylase | COG0284 | **F** | Nucleotide transport and metabolism |
| **SA1042** | *pyrP* | N315 | 0.08 | 0.24 | uracil permease | COG2233 | **F** | Nucleotide transport and metabolism |
| **SA0468** | *SA0468* | N315 | 0.09 | 0.17 | hypoxanthineguanine phosphoribosyltransferase homologue | COG0634 | **F** | Nucleotide transport and metabolism |
| **SA0916** | *SA0916* | N315 | 0.10 | 0.10 | phosphoribosylaminoimidazole carboxylase PurE | COG0041 | **F** | Nucleotide transport and metabolism |
| **SA1929** | *ctrA* | N315 | 0.10 | 0.11 | CTP synthase | COG0504 | **F** | Nucleotide transport and metabolism |
| **SA1439** | *udk* | N315 | 0.11 | 0.27 | uridine kinase | COG0572 | **F** | Nucleotide transport and metabolism |
| **SA0376** | *guaA* | N315 | 0.11 | 0.12 | GMP synthase | COG0518,COG0519 | **F** | Nucleotide transport and metabolism |
| **SA0373** | *xprT* | N315 | 0.11 | 0.11 | xanthine phosphoribosyltransferase | COG0503 | **F** | Nucleotide transport and metabolism |
| **SA1553** | *fhs* | N315 | 0.14 | 0.19 | formyltetrahydrofolate synthetase | COG2759 | **F** | Nucleotide transport and metabolism |
| **SA1397** | *cdd* | N315 | 0.15 | 0.19 | cytidine deaminase | COG0295 | **F** | Nucleotide transport and metabolism |
| **SA1939** | *SA1939* | N315 | 0.15 | 0.25 | deoxyribosephosphate aldolase | COG0274 | **F** | Nucleotide transport and metabolism |
| **SA1172** | *SA1172* | N315 | 0.16 | 0.27 | GMP reductase | COG0516 | **F** | Nucleotide transport and metabolism |
| **SA1724** | *purB* | N315 | 0.21 | 0.21 | adenylosuccinate lyase | COG0015 | **F** | Nucleotide transport and metabolism |
| **SA1101** | *smbA* | N315 | 0.23 | 0.17 | uridylate kinase | COG0528 | **F** | Nucleotide transport and metabolism |
| **SA1938** | *pdp* | N315 | 0.24 | 0.25 | pyrimidine nucleoside phosphorylase | COG0213 | **F** | Nucleotide transport and metabolism |
| **SA0686** | *nrdE* | N315 | 0.28 | 0.29 | ribonuceloside diphosphate reductase major subunit | COG0209 | **F** | Nucleotide transport and metabolism |
| **SA0234** | *SA0234* | N315 | 3.76 | 3.55 | inosineuridine preferring nucleoside hydrolase | COG1957 | **F** | Nucleotide transport and metabolism |
| **SA0881** | *SA0881* | N315 | 3.76 | 3.57 | nucleotidase | COG0737 | **F** | Nucleotide transport and metabolism |
| **MW1034** | *MW1034* | MW2 |  | 0.13 | hypothetical protein | COG0127 | **F** | Nucleotide transport and metabolism |
| **SA0131** | *pnp* | N315 |  | 3.05 | purine nucleoside phosphorylase | COG0813 | **F** | Nucleotide transport and metabolism |
| **SA0729** | *tpi* | N315 | 0.02 | 0.10 | triosephosphate isomerase | COG0149 | **G** | Carbohydrate transport and metabolism |
| **SA0823** | *pgi* | N315 | 0.02 | 0.04 | glucose6phosphate isomerase A | COG0166 | **G** | Carbohydrate transport and metabolism |
| **SA0731** | *eno* | N315 | 0.04 | 0.13 | enolase | COG0148 | **G** | Carbohydrate transport and metabolism |
| **SA0905** | *atl* | N315 | 0.04 | 0.20 | autolysin | COG4193,COG5632 | **G** | Carbohydrate transport and metabolism |
| **SA2129** | *SA2129* | N315 | 0.06 | 0.04 | aldose 1epimerase | COG2017 | **G** | Carbohydrate transport and metabolism |
| **SA0935** | *ptsI* | N315 | 0.07 | 0.07 | phosphoenolpyruvateprotein phosphatase | COG1080 | **G** | Carbohydrate transport and metabolism |
| **SA0528** | *SA0528* | N315 | 0.07 | 0.06 | hexulose-6-phosphate synthase | COG0269 | **G** | Carbohydrate transport and metabolism |
| **SA0730** | *pgm* | N315 | 0.08 | 0.22 | 2, 3diphosphoglycerateindependentphosphoglycer ate mutase | COG0696 | **G** | Carbohydrate transport and metabolism |
| **SA0934** | *ptsH* | N315 | 0.09 | 0.13 | phophocarrier protein HPR | COG1925 | **G** | Carbohydrate transport and metabolism |
| **SA1342** | *gnd* | N315 | 0.09 | 0.09 | phosphogluconate dehydrogenase | COG0362 | **G** | Carbohydrate transport and metabolism |
| **SA0727** | *gap* | N315 | 0.10 | 0.27 | glyceraldehyde3phosphate dehydrogenase | COG0057 | **G** | Carbohydrate transport and metabolism |
| **SA0790** | *SA0790* | N315 | 0.12 | 0.17 | Nacetylglucosamine catabolism homologue | COG0647 | **G** | Carbohydrate transport and metabolism |
| **SA2326** | *ptsG* | N315 | 0.13 | 0.17 | PTS system, glucosespecific IIABC component | COG1263 | **G** | Carbohydrate transport and metabolism |
| **SA1927** | *fbaA* | N315 | 0.14 | 0.15 | fructosebisphosphate aldolase | COG0191 | **G** | Carbohydrate transport and metabolism |
| **SA0183** | *glcA* | N315 | 0.15 | 0.14 | PTS enzyme II (EC 2.7.1.69), glucosespecific, factor IIA homologue | COG1263 | **G** | Carbohydrate transport and metabolism |
| **SA1177** | *tkt* | N315 | 0.17 | 0.16 | transketolase | COG0021 | **G** | Carbohydrate transport and metabolism |
| **SA1688** | *SA1688* | N315 | 0.17 | 0.33 | teichoic acid translocation ATPbinding protein tagH | COG1134 | **G** | Carbohydrate transport and metabolism |
| **SA0157** | *capN* | N315 | 0.18 | 0.32 | capsular polysaccharide synthesis enzyme Cap5N | COG0451 | **G** | Carbohydrate transport and metabolism |
| **SA1377** | *glcK* | N315 | 0.19 | 0.16 | glucokinase | COG1940 | **G** | Carbohydrate transport and metabolism |
| **SA1547** | *ptaA* | N315 | 0.19 | 0.23 | PTS system, Nacetylglucosaminespecific IIABC component | COG1263 | **G** | Carbohydrate transport and metabolism |
| **SA1521** | *pfk* | N315 | 0.23 | 0.32 | 6phosphofructokinase | COG0205 | **G** | Carbohydrate transport and metabolism |
| **SA0149** | *capF* | N315 | 0.23 | 0.25 | capsular polysaccharide synthesis enzyme Cap5F | COG1898,COG0451 | **G** | Carbohydrate transport and metabolism |

| ORF # | Common | Organism | 2h fold change | 6h fold change | Protein name | GO | Class | Annotation |
|---|---|---|---|---|---|---|---|---|
| **SA0605** | *SA0605* | N315 | 0.24 | 0.27 | dihydroxyacetone kinase | COG2376 | **G** | Carbohydrate transport and metabolism |
| **SA0259** | *rbsD* | N315 | 0.27 | 0.22 | ribose permease | COG1869 | **G** | Carbohydrate transport and metabolism |
| **SA1065** | *cfxE* | N315 | 0.28 | 0.31 | ribulose5phosphate 3epimerase homolog | COG0036 | **G** | Carbohydrate transport and metabolism |
| **SA1965** | *glmM(femD)* | N315 | 0.32 | 0.28 | phospho glucosamine mutase | COG1109 | **G** | Carbohydrate transport and metabolism |
| **SA0134** | *drm* | N315 | 0.32 |  | phosphopentomutase | COG1015 | **G** | Carbohydrate transport and metabolism |
| **SA2434** | *SA2434* | N315 | 3.09 |  | fructose phosphotransferase system enzyme fruA homolog | COG1762,COG1299 | **G** | Carbohydrate transport and metabolism |
| **SA2127** | *SA2127* | N315 | 3.13 | 4.10 | ribose 5phosphate isomerase (rpi) | COG0120 | **G** | Carbohydrate transport and metabolism |
| **SA1995** | *lacC* | N315 | 3.22 | 3.14 | tagatose-6-phosphate kinase | COG1105 | **G** | Carbohydrate transport and metabolism |
| **SA2480** | *drp35* | N315 | 3.25 | 3.47 | Drp35 | COG3386 | **G** | Carbohydrate transport and metabolism |
| **SA1994** | *lacD* | N315 | 3.30 | 3.82 | tagatose 1,6-diphosphate aldolase | COG3684 | **G** | Carbohydrate transport and metabolism |
| **SA1997** | *lacA* | N315 | 3.37 |  | galactose-6-phosphate isomerase LacA subunit | COG0698 | **G** | Carbohydrate transport and metabolism |
| **SA0655** | *fruA* | N315 | 3.47 | 3.65 | fructose specific permease | COG1762,COG1299 | **G** | Carbohydrate transport and metabolism |
| **SA2294** | *gntK* | N315 | 3.51 |  | gluconokinase | COG1070 | **G** | Carbohydrate transport and metabolism |
| **SA0299** | *SA0299* | N315 | 3.53 | 3.60 | carbohydrate kinase, PfkB family | COG0524 | **G** | Carbohydrate transport and metabolism |
| **SA0432** | *treP* | N315 | 3.60 |  | PTS enzyme II, phosphoenolpyruvatedependent, trehalosespecific | COG1263 | **G** | Carbohydrate transport and metabolism |
| **SA0041** | *xylR* | N315 | 3.75 | 4.72 | xylose repressor homologue | COG1940 | **G** | Carbohydrate transport and metabolism |
| **SA2462** | *icaC* | N315 | 3.91 | 5.18 | intercellular adhesion protein C | COG3936 | **G** | Carbohydrate transport and metabolism |
| **SA0214** | *uhpT* | N315 | 4.05 | 4.29 | hexose phosphate transport protein | COG2271 | **G** | Carbohydrate transport and metabolism |
| **SA0361** | *SA0361* | N315 | 4.22 | 5.26 | truncated phosphoglycerate mutase; Gpm3p | COG0406 | **G** | Carbohydrate transport and metabolism |
| **SA0207** | *SA0207* | N315 | 4.42 |  | maltose/maltodextrinbinding protein | COG2182 | **G** | Carbohydrate transport and metabolism |
| **SAS020** | *SAS020* | N315 | 4.46 | 4.61 | phosphoglycerate mutase | COG0406 | **G** | Carbohydrate transport and metabolism |
| **SA0325** | *glpT* | N315 | 4.74 | 4.10 | glycerol3phosphate transporter | COG2271 | **G** | Carbohydrate transport and metabolism |
| **SA1996** | *lacB* | N315 | 62.50 | 65.36 | galactose6phosphate isomerase LacB subunit | COG0698 | **G** | Carbohydrate transport and metabolism |
| **MW0113** | *drm* | MW2 |  | 0.18 | phosphopentomutase | COG1015 | **G** | Carbohydrate transport and metabolism |
| **MW0381** | *MW0381* | MW2 |  | 4.63 | hypothetical protein | COG0702 | **G** | Carbohydrate transport and metabolism |
| **MW0778** | *MW0778* | MW2 |  | 3.75 | phosphoglycerate mutase | COG0406 | **G** | Carbohydrate transport and metabolism |
| **SA1729** | *SA1729* | N315 | 0.01 | 0.04 | nicotinate phosphoribosyltransferase homolog | COG1488 | **H** | Coenzyme transport and metabolism |
| **SA1537** | *SA1537* | N315 | 0.01 | 0.12 | thiamine biosynthesis protein ThiI | COG0301 | **H** | Coenzyme transport and metabolism |
| **SA1491** | *hemL* | N315 | 0.03 | 0.03 | glutamate1semialdehyde 2,1aminomutase | COG0001 | **H** | Coenzyme transport and metabolism |
| **SA1259** | *dfrA* | N315 | 0.03 | 0.20 | dihydrofolate reductase | COG0262 | **H** | Coenzyme transport and metabolism |
| **SA2212** | *SA2212* | N315 | 0.05 | 0.28 | 8-amino 7-oxononanoate synthase | COG0156 | **H** | Coenzyme transport and metabolism |
| **SA0915** | *folD* | N315 | 0.05 | 0.08 | FolD bifunctional protein | COG0190 | **H** | Coenzyme transport and metabolism |
| **SA2067** | *mobB* | N315 | 0.06 | 0.14 | probable molybdopteringuanine dinucleotide biosynthesis mobB | COG1763 | **H** | Coenzyme transport and metabolism |
| **SA2213** | *bioB* | N315 | 0.08 | 0.14 | biotin synthase | COG0502 | **H** | Coenzyme transport and metabolism |
| **SA1728** | *nadE* | N315 | 0.08 | 0.08 | NAD synthetase, prefers NH3 over glutamine | COG0171 | **H** | Coenzyme transport and metabolism |
| **MW1853** | *nadE* | MW2 | 0.12 | 0.08 | NAD synthetase | COG0171 | **H** | Coenzyme transport and metabolism |
| **SA1487** | *folC* | N315 | 0.12 | 0.33 | folylpolyglutamate synthase | COG0285 | **H** | Coenzyme transport and metabolism |
| **SA1652** | *hemE* | N315 | 0.14 |  | uroporphyrinogen decarboxylase | COG0407 | **H** | Coenzyme transport and metabolism |
| **SA2392** | *panB* | N315 | 0.14 | 0.21 | 3methyl2oxobutanoate hydroxymethyltransferase | COG0413 | **H** | Coenzyme transport and metabolism |
| **SA1650** | *hemY* | N315 | 0.15 | 0.23 | protoporphyrinogen oxidase | COG1232 | **H** | Coenzyme transport and metabolism |
| **SA1496** | *hemA* | N315 | 0.15 | 0.28 | glutamyltRNA reductase | COG0373 | **H** | Coenzyme transport and metabolism |
| **SA2064** | *mobA* | N315 | 0.15 | 0.24 | molybdopteringuanine dinucleotide biosynthesis mobA | COG0746 | **H** | Coenzyme transport and metabolism |
| **SA2071** | *moeB* | N315 | 0.16 | 0.24 | molybdopterin biosynthesis protein moeB | COG0476 | **H** | Coenzyme transport and metabolism |
| **SA2068** | *moeA* | N315 | 0.16 | 0.28 | molybdopterin biosynthesis protein moeA | COG0303 | **H** | Coenzyme transport and metabolism |
| **SA0896** | *menD* | N315 | 0.23 | 0.26 | menaquinone biosynthesis protein | COG1165 | **H** | Coenzyme transport and metabolism |
| **SA1493** | *hemD* | N315 | 0.24 |  | uroporphyrinogen III synthase | COG1587 | **H** | Coenzyme transport and metabolism |
| **SA0791** | *SA0791* | N315 | 0.25 | 0.20 | glycerate dehydrogenase | COG1052 | **H** | Coenzyme transport and metabolism |
| **SA0602** | *fhuA* | N315 | 0.28 |  | ferrichrome transport ATPbinding protein | COG1120 | **H** | Coenzyme transport and metabolism |
| **SA2065** | *moaD* | N315 | 0.31 | 0.28 | probable molybdopterin synthase small subunit | COG1977 | **H** | Coenzyme transport and metabolism |
| **SA1302** | *gerCC* | N315 | 0.32 | 0.22 | heptaprenyl diphosphate syntase component II | COG0142 | **H** | Coenzyme transport and metabolism |
| **SA1289** | *SA1289* | N315 | 0.32 | 0.33 | bifunctional biotin ligase/biotin operon repressor | COG0340,COG1654 | **H** | Coenzyme transport and metabolism |
| **SA2063** | *moaA* | N315 | 0.32 |  | molybdenum cofactor biosynthesis protein A | COG2896 | **H** | Coenzyme transport and metabolism |
| **SA0316** | *SA0316* | N315 | 0.33 |  | lipoateprotein ligase | COG0095 | **H** | Coenzyme transport and metabolism |
| **SA0895** | *SA0895* | N315 | 3.40 | 4.07 | menaquinonespecific isochorismate synthase | COG1169Q | **H** | Coenzyme transport and metabolism |
| **SA1587** | *ribA* | N315 | 3.44 |  | riboflavin biosynthesis protein | COG0807 | **H** | Coenzyme transport and metabolism |
| **SA0472** | *folP* | N315 | 3.52 |  | dihydropteroate synthase chain A synthetase | COG0294 | **H** | Coenzyme transport and metabolism |
| **SA2412** | *SA2412* | N315 | 4.18 |  | uroporphyrinIII Cmethyltransferase | COG1648 | **H** | Coenzyme transport and metabolism |
| **MW0812** | *MW0812* | MW2 |  | 0.26 | glycerate dehydrogenase | COG1052 | **H** | Coenzyme transport and metabolism |
| **SA2025** | *rpsM* | N315 | 0.01 | 0.12 | 30S Protein synthesis S13 | COG0099 | **J** | Translation, ribosomal structure and biogenesis |
| **SAS078** | *rpmJ* | N315 | 0.01 | 0.17 | 50S Protein synthesis L36 | COG0257 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2026** | *infA* | N315 | 0.01 | 0.16 | translation initiation factor IF1 | COG0361 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1112** | *infB* | N315 | 0.02 | 0.14 | translation initiation factor IF2 | COG0532 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2039** | *rpmC* | N315 | 0.03 | 0.26 | 50S Protein synthesis L29 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA2035** | *rplE* | N315 | 0.03 | 0.26 | 50S Protein synthesis L5 | COG0094 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2038** | *rpsQ* | N315 | 0.03 | 0.19 | 30S Protein synthesis S17 | COG0186 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2041** | *rpsC* | N315 | 0.03 | 0.21 | 30S Protein synthesis S3 | COG0092 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2034** | *rpsH* | N315 | 0.03 | 0.25 | 30S Protein synthesis S8 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA1094** | *gid* | N315 | 0.04 | 0.07 | glucoseinhibited division protein gid | COG1206 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2029** | *rplO* | N315 | 0.04 | 0.32 | 50S Protein synthesis L15 | COG0200 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2036** | *rplX* | N315 | 0.04 | 0.22 | 50S Protein synthesis L24 | COG0198 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0504** | *rpsG* | N315 | 0.04 | 0.23 | 30S Protein synthesis S7 | COG0049 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2033** | *rplF* | N315 | 0.04 |  | 50S Protein synthesis L6 | COG0097 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2030** | *rpmD* | N315 | 0.05 |  | 50S Protein synthesis L30 | COG1841 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1579** | *leuS* | N315 | 0.05 | 0.15 | leucyltRNA synthetase | COG0495 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0475** | *lysS* | N315 | 0.05 | 0.13 | lysyl-tRNA synthetase | COG1190 | **J** | Translation, ribosomal structure and biogenesis |
| **SAS079** | *rpsN* | N315 | 0.06 | 0.20 | 30S Protein synthesis S14 | COG0199 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2032** | *rplR* | N315 | 0.06 | 0.33 | 50S Protein synthesis L18 | COG0256 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2040** | *rplP* | N315 | 0.06 | 0.21 | 50S Protein synthesis L16 | COG0197 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0503** | *rpsL* | N315 | 0.06 | 0.20 | 30S Protein synthesis S12 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA0505** | *fus* | N315 | 0.07 | 0.25 | translational elongation factor G | COG0480 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2042** | *rplV* | N315 | 0.07 | 0.23 | 50S Protein synthesis L22 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA2037** | *rplN* | N315 | 0.08 | 0.23 | 50S Protein synthesis L14 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA2043** | *rpsS* | N315 | 0.08 |  | 30S Protein synthesis S19 | COG0185 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0488** | *cysS* | N315 | 0.09 | 0.13 | cysteinyltRNA synthetase | COG0215 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1456** | *aspS* | N315 | 0.10 | 0.06 | aspartyltRNA synthetase | COG0173 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2047** | *rplC* | N315 | 0.10 | 0.20 | 50S Protein synthesis L3 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA0877** | *prfC* | N315 | 0.11 | 0.27 | peptide chain release factor 3 | COG4108 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1099** | *rpsB* | N315 | 0.11 | 0.26 | 30S Protein synthesis S2 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SAS042** | *rpmG* | N315 | 0.11 | 0.30 | 50S Protein synthesis L33 | COG0267 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2022** | *rplQ* | N315 | 0.12 |  | 50S Protein synthesis L17 | COG0203 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0985** | *pheS* | N315 | 0.13 | 0.19 | PhetRNA synthetase alpha chain | COG0016 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2044** | *rplB* | N315 | 0.13 |  | 50S Protein synthesis L2 | COG0090 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2017** | *rplM* | N315 | 0.14 | 0.22 | 50S Protein synthesis L13 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA2031** | *rpsE* | N315 | 0.14 | 0.30 | 30S Protein synthesis S5 | COG0098 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1117** | *pnpA* | N315 | 0.15 | 0.18 | polyribonucleotide nucleotidyltransferase | COG1185 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2045** | *rplW* | N315 | 0.15 | 0.23 | 50S Protein synthesis L23 | COG0089 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1473** | *rplU* | N315 | 0.16 | 0.24 | 50S Protein synthesis L21 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA0498** | *rplL* | N315 | 0.16 |  | 50S Protein synthesis L7/L12 | COG0222 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1324** | *rluB* | N315 | 0.16 | 0.31 | ribosomal large subunit pseudouridine synthase B | COG1187 | **J** | Translation, ribosomal structure and biogenesis |

| ORF # | Common | Organism | 2h fold change | 6h fold change | Protein name | GO | Class | Annotation |
|---|---|---|---|---|---|---|---|---|
| **SA0014** | *rplI* | N315 | 0.18 | 0.16 | 50S Protein synthesis L9 | COG0359 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0486** | *gltX* | N315 | 0.18 | 0.18 | glutamyltRNA synthetase | COG0008 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0564** | *argS* | N315 | 0.19 | 0.17 | arginyltRNA synthetase | COG0018 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2046** | *rplD* | N315 | 0.20 | 0.20 | 50S Protein synthesis L4 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA2048** | *rpsJ* | N315 | 0.20 | 0.28 | 30S Protein synthesis S10 | COG0051 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2024** | *rpsK* | N315 | 0.21 | 0.26 | 30S Protein synthesis S11 | COG0100 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1106** | *proS* | N315 | 0.22 | 0.29 | prolinetRNA ligase | COG0442 | **J** | Translation, ribosomal structure and biogenesis |
| **SA0352** | *rpsF* | N315 | 0.24 | 0.28 | 30S Protein synthesis S6 | COG0360 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1920** | *prfA* | N315 | 0.25 |  | peptide chain release factor 1 | COG0216 | **J** | Translation, ribosomal structure and biogenesis |
| **MW1076** | *ileS* | MW2 | 0.26 | 0.18 | Ile tRNA synthetase | COG0060 | **J** | Translation, ribosomal structure and biogenesis |
| **SA2016** | *rpsI* | N315 | 0.26 | 0.16 | 30S Protein synthesis S9 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA1471** | *rpmA* | N315 | 0.29 |  | 50S Protein synthesis L27 |  | **J** | Translation, ribosomal structure and biogenesis |
| **SA1504** | *infC* | N315 | 0.33 |  | translation initiation factor IF3 | COG0290 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1082** | *rimM* | N315 | 0.33 |  | probable 16S rRNA processing protein | COG0806 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1113** | *rbfA* | N315 | 0.33 |  | ribosomebinding factor A | COG0858 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1414** | *rpsT* | N315 | 3.12 |  | 30S Protein synthesis S20 | COG0268 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1922** | *rpmE* | N315 | 3.75 |  | 50S Protein synthesis L31 | COG0254 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1704** | *map* | N315 | 3.98 | 3.72 | methionyl aminopeptidase map | COG0024 | **J** | Translation, ribosomal structure and biogenesis |
| **MW0318** | *MW0318* | MW2 |  | 3.30 | ribosomalproteinserine Nacetyltransferase | COG1670 | **J** | Translation, ribosomal structure and biogenesis |
| **MW1696** | *MW1696* | MW2 |  | 0.11 | 16S pseudouridylate synthase | COG1187 | **J** | Translation, ribosomal structure and biogenesis |
| **SA1557** | *ccpA* | N315 | 0.29 | 0.29 | catabolite control protein A | COG1609 | **K** | Transcription |
| **SA0726** | *gapR* | N315 | 0.31 |  | glycolytic operon regulator | COG2390 | **K** | Transcription |
| **SA1139** | *glpP* | N315 | 0.15 | 0.12 | glycerol uptake operon antiterminator regulatory protein | COG1954 | **K** | Transcription |
| **SA1925** | *HP* | N315 | 0.23 | 0.22 | Hypothetical protein | COG1733 | **K** | Transcription |
| **SA1868** | *HP* | N315 | 0.28 | 0.21 | Hypothetical protein | COG2183 | **K** | Transcription |
| **SA1109** | *nusA* | N315 | 0.05 | 0.20 | transcription terminationantitermination factor | COG0195 | **K** | Transcription |
| **SA0494** | *nusG* | N315 | 0.23 | 0.26 | transcription antitermination protein | COG0250 | **K** | Transcription |
| **SA1923** | *rho* | N315 | 0.23 | 0.14 | transcription termination factor Rho | COG1158 | **K** | Transcription |
| **SA0735** | *rnr* | N315 | 0.17 | 0.23 | ribonuclease R | COG0557 | **K** | Transcription |
| **SA2023** | *rpoA* | N315 | 0.10 |  | DNA directed RNA polymerase alpha chain | COG0202 | **K** | Transcription |
| **SA0500** | *rpoB* | N315 | 0.07 | 0.32 | RNA polymerase beta chain | COG0085 | **K** | Transcription |
| **SA0501** | *rpoC* | N315 | 0.16 | 0.27 | RNA polymerase betaprime chain | COG0086 | **K** | Transcription |
| **SA0337** | *SA0337* | N315 | 3.91 |  | transcriptional repressor | COG1476 | **K** | Transcription |
| **SA0492** | *SA0492* | N315 | 0.07 |  | HP | COG1595 | **K** | Transcription |
| **SA0590** | *SA0590* | N315 | 4.50 | 3.47 | iron dependent repressor | COG1321 | **K** | Transcription |
| **SA1355** | *SA1355* | N315 | 0.08 | 0.14 | transcription termination factor | COG0781 | **K** | Transcription |
| **SA1748** | *SA1748* | N315 | 0.12 |  | transcription regulator, GntR family | COG1725 | **K** | Transcription |
| **SA2002** | *SA2002* | N315 | 3.16 | 4.33 | transcription regulator MerR family | COG0789 | **K** | Transcription |
| **SA2108** | *SA2108* | N315 | 0.28 |  | transcription regulator, RpiR family | COG1737 | **K** | Transcription |
| **SA2165** | *SA2165* | N315 | 0.15 | 0.18 | transcriptional regulator tetR family | COG1309 | **K** | Transcription |
| **SA2174** | *SA2174* | N315 | 3.34 | 4.29 | transcriptional regulator | COG1846 | **K** | Transcription |
| **SA2296** | *SA2296* | N315 | 3.32 |  | transcriptional regulator, MerR family | COG0789 | **K** | Transcription |
| **SA2330** | *SA2330* | N315 | 4.31 | 3.61 | transcription regulator | COG0583 | **K** | Transcription |
| **SA2358** | *SA2358* | N315 | 4.26 | 3.57 | transcriptional regulator (TetR/AcrR family) | COG1309 | **K** | Transcription |
| **SA2429** | *SA2429* | N315 | 3.95 |  | arginine repressor | COG1438 | **K** | Transcription |
| **SA2498** | *SA2498* | N315 | 0.10 | 0.15 | DNAbinding protein Spo0Jlike homolog | COG1475 | **K** | Transcription |
| **SA0108** | *sarS* | N315 | 4.08 | 4.20 | sarS | COG1846 | **K** | Transcription |
| **SA1869** | *sigB* | N315 | 0.11 | 0.15 | sigma factor B | COG1191 | **K** | Transcription |
| **SA1874** | *alr* | N315 | 0.21 | 0.23 | alanine racemase | COG0787 | **M** | Cell wall/membrane/envelope biogenesis |
| **MW0136** | *cap8M* | MW2 | 0.07 | 0.23 | capsular polysaccharide synthesis enzyme Cap8M | COG2148 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0150** | *capG* | N315 | 0.15 | 0.24 | capsular polysaccharide synthesis enzyme Cap5G | COG0381 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0152** | *capI* | N315 | 3.16 |  | capsular polysaccharide synthesis enzyme Cap5I | COG0438 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1887** | *ddlA* | N315 | 0.33 |  | D-alanine D-alanine ligase | COG1181 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1027** | *div1b* | N315 | 0.05 | 0.11 | cell division protein, FtsQ homolog | COG1589 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0794** | *dltB* | N315 | 0.04 | 0.10 | DltB membrane protein | COG1696 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0796** | *dltD* | N315 | 0.16 | 0.18 | poly Dalanine transfer protein | COG3966 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA2499** | *gidB* | N315 | 0.12 | 0.32 | glucose inhibited division protein B | COG0357 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA2459** | *icaA* | N315 | 3.92 | 3.64 | intercellular adhesion protein A | COG1215 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA2461** | *icaB* | N315 | 3.75 |  | intercellular adhesion protein B |  | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1413** | *lepA* | N315 | 0.26 | 0.27 | GTPbinding protein | COG0481 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0265** | *lytM* | N315 | 14.88 |  | peptidoglycan hydrolase | COG0739 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0038** | *mecA* | N315 | 3.32 | 3.50 | penicillin binding protein 2' | COG0768 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1614** | *menC* | N315 |  | 0.23 | osuccinylbenzoic acid synthetase | COG4948 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1913** | *mnaA* | N315 | 0.01 | 0.07 | UDPGlcNAc 2epimerase | COG0381 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1025** | *mraY* | N315 | 0.22 | 0.26 | phosphoNmuramic acidpentapeptide translocase | COG0472 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1902** | *murA* | N315 | 0.04 | 0.23 | UDPNacetylglucosamine 1carboxyvinyl transferase 1 | COG0766 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1561** | *murC* | N315 | 0.10 | 0.19 | UDPNAacerylmuramatealanine ligase | COG0773 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1026** | *murD* | N315 | 0.04 | 0.08 | UDPNacetylmuramoylalanineDglutamate ligase | COG0771 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1886** | *murF* | N315 | 0.07 | 0.08 | UDP-N-Ac mur-D-glu-diaminopimelate-Dala-ala ligase | COG0770 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1251** | *murG* | N315 | 0.28 | 0.31 | Undecaprenyl PPMurNAc-UDPGlcNAc GlcNAc transferase | COG0707 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0997** | *murI* | N315 | 0.09 | 0.11 | glutamate racemase | COG0796 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1926** | *murZ* | N315 | 0.14 | 0.17 | UDPNacetylglucosamine 1carboxylvinyl transferase 2 | COG0766 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1183** | *opuD* | N315 | 0.30 | 0.32 | glycine betaine transporter | COG1292 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1283** | *pbp2* | N315 | 0.15 | 0.17 | PBP2 | COG0744 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1381** | *pbp3* | N315 | 0.23 | 0.31 | penicillinbinding protein 3 | COG0768 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0125** | *SA0125* | N315 | 3.62 |  | Eps (Exopolysaccharide) G | COG0438 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0243** | *SA0243* | N315 | 0.11 |  | teichoic acid biosynthesis protein B | COG1887 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0247** | *SA0247* | N315 |  | 0.09 | teichoic acid biosynthesis protein B | COG1887 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0248** | *SA0248* | N315 | 0.13 | 0.17 | betaglycosyltransferase | COG0463 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0674** | *SA0674* | N315 | 0.12 | 0.20 | anionbinding protein | COG1368 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0693** | *SA0693* | N315 | 0.33 |  | UDPN acetylenol pyruvoyl glucosamine reductase | COG0812 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1231** | *SA1231* | N315 |  | 0.10 | alanine racemase | COG0787 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1291** | *SA1291* | N315 |  | 0.30 | lipopolysaccharide biosynthesis related pr homolog | COG0438 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1708** | *SA1708* | N315 | 0.24 | 0.20 | UDPNacetylmuramyl tripeptide synthetase homolog | COG0769 | **M** | Cell wall/membrane/envelope biogenesis |
| **SAV0913** | *SAV0913* | Mu50 | 6.29 |  | amidase | COG5632 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA1551** | *sgtA* | N315 | 7.46 | 7.75 | probable transglycosylase | COG0744 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0456** | *spoVG* | N315 | 5.95 |  | stage V sporulation protein G homologue | COG2088 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0595** | *tagB* | N315 |  | 0.15 | teichoic acid biosynthesis protein B | COG1887 | **M** | Cell wall/membrane/envelope biogenesis |
| **SA0880** | *SA0880* | N315 | 0.05 | 0.04 | Na+transporting ATP synthase | COG0168 | **P** | Inorganic ion transport and metabolism |
| **SA0587** | *SA0587* | N315 | 0.08 | 0.10 | lipoprotein, Streptococcal adhesin PsaA homologue | COG0803 | **P** | Inorganic ion transport and metabolism |
| **SA2137** | *SA2137* | N315 | 0.08 | 0.31 | divalent cation transport | COG0598 | **P** | Inorganic ion transport and metabolism |
| **SA1384** | *SA1384* | N315 | 0.12 |  | ABC transporter | COG1108 | **P** | Inorganic ion transport and metabolism |
| **SA0589** | *SA0589* | N315 | 0.15 |  | ABC transporter ATPbinding protein | COG1121 | **P** | Inorganic ion transport and metabolism |
| **SA0603** | *fhuB* | N315 | 0.16 | 0.24 | ferrichrome transport permease | COG0609 | **P** | Inorganic ion transport and metabolism |
| **SA0580** | *SA0580* | N315 | 0.18 |  | Na+/H+ antiporter | COG1006 | **P** | Inorganic ion transport and metabolism |
| **SA2072** | *modC* | N315 | 0.20 |  | molybdenum transport ATPbinding protein ModC | COG4148 | **P** | Inorganic ion transport and metabolism |
| **SA1329** | *SA1329* | N315 | 0.22 | 0.26 | ferric uptake regulator homolog | COG0735 | **P** | Inorganic ion transport and metabolism |
| **SA1238** | *SA1238* | N315 | 0.23 | 0.20 | tellurite resistance protein | COG3853 | **P** | Inorganic ion transport and metabolism |
| **SA1592** | *SA1592* | N315 | 0.25 | 0.16 | aesenical pump membrane protein homolog | COG1055 | **P** | Inorganic ion transport and metabolism |
| **SA0136** | *SA0136* | N315 | 0.25 | 0.29 | phosphonates transport permease | COG3639 | **P** | Inorganic ion transport and metabolism |
| **SA1170** | *katA* | N315 | 0.25 | 0.32 | Catalase | COG0753 | **P** | Inorganic ion transport and metabolism |

| ORF # | Common | Organism | 2h fold change | 6h fold change | Protein name | GO | Class | Annotation |
|---|---|---|---|---|---|---|---|---|
| **SA0137** | *SA0137* | N315 | 0.25 | 0.18 | transport system protein | COG3638 | **P** | Inorganic ion transport and metabolism |
| **SA0688** | *SA0688* | N315 | 0.26 | | ferrichrome ABC transporter permease | COG4606 | **P** | Inorganic ion transport and metabolism |
| **SA0956** | *SA0956* | N315 | 0.28 | 0.32 | Mn2+transport protein | COG1914 | **P** | Inorganic ion transport and metabolism |
| **SA0690** | *SA0690* | N315 | 0.28 | 0.24 | ferrichrome ABC transporter ATPbinding protein | COG4604 | **P** | Inorganic ion transport and metabolism |
| **SA1979** | *SA1979* | N315 | 0.30 | 0.26 | HP, similar toferrichrome ABC transporter (binding protein) | COG4594 | **P** | Inorganic ion transport and metabolism |
| **MW1714** | *MW1714* | MW2 | 0.30 | | arsenical pump membrane protein homolog | COG1055 | **P** | Inorganic ion transport and metabolism |
| **SA2073** | *modB* | N315 | 0.31 | | probable molybdenum transport permease | COG4149 | **P** | Inorganic ion transport and metabolism |
| **SA1978** | *SA1978* | N315 | 0.33 | 0.31 | ferrichrome ABC transporter (permease) | COG0609 | **P** | Inorganic ion transport and metabolism |
| **SA1218** | *pstB* | N315 | 3.12 | 4.22 | phosphate ABC transporter, ATPbinding protein | COG1117 | **P** | Inorganic ion transport and metabolism |
| **SA2369** | *SA2369* | N315 | 3.26 | | ferrous iron transporter protein B | COG0370 | **P** | Inorganic ion transport and metabolism |
| **SA0981** | *isdF* | N315 | 3.34 | | ferrichrome ABC transporter | COG0609 | **P** | Inorganic ion transport and metabolism |
| **SA0759** | *SA0759* | N315 | 3.39 | | arsenate reductase | COG1393 | **P** | Inorganic ion transport and metabolism |
| **SA1941** | *dps* | N315 | 3.40 | 3.66 | general stress protein 20U | COG0783 | **P** | Inorganic ion transport and metabolism |
| **SA0168** | *SA0168* | N315 | 3.42 | 3.34 | probable permease of ABC transporter | COG0600 | **P** | Inorganic ion transport and metabolism |
| **SA1678** | *SA1678* | N315 | 3.50 | 3.03 | transcription regulator Fur family homolog | COG0735 | **P** | Inorganic ion transport and metabolism |
| **SA0111** | *sirA* | N315 | 3.53 | | lipoprotein | COG0614 | **P** | Inorganic ion transport and metabolism |
| **SA0422** | *SA0422* | N315 | 3.69 | 3.64 | lactococcal lipoprotein | COG1464 | **P** | Inorganic ion transport and metabolism |
| **SA1382** | *sodA* | N315 | 3.86 | 3.14 | superoxide dismutase SodA | COG0605 | **P** | Inorganic ion transport and metabolism |
| **SA0567** | *SA0567* | N315 | 5.00 | | iron(III) ABC transporter permease protein | COG0609 | **P** | Inorganic ion transport and metabolism |
| **MW0200** | *MW0200* | MW2 | 45.05 | 25.06 | periplasmicironbinding protein BitC | COG1840 | **P** | Inorganic ion transport and metabolism |
| **MW0115** | *MW0115* | MW2 | | 0.28 | phosphonates transport permease | COG3639 | **P** | Inorganic ion transport and metabolism |
| **MW2102** | *MW2102* | MW2 | | 0.09 | ferrichrome ABC transporter (permease) | COG0609 | **P** | Inorganic ion transport and metabolism |
| **SA0583** | *mprF* | N315 | | 0.22 | Na+/H+ antiporter | COG2212 | **P** | Inorganic ion transport and metabolism |
| **SA0808** | *mnhF* | N315 | | 0.21 | Na+/H+ antiporter subunit | COG2212 | **P** | Inorganic ion transport and metabolism |
| **SA1220** | *SA1220* | N315 | | 3.03 | phosphate ABC transporter | COG0573 | **P** | Inorganic ion transport and metabolism |
| **SA1385** | *SA1385* | N315 | | 0.30 | ABC transporter ATPbinding protein | COG1121 | **P** | Inorganic ion transport and metabolism |
| **SA1948** | *czrB* | N315 | | 0.33 | cation efflux system membrane protein homolog | COG1230 | **P** | Inorganic ion transport and metabolism |
| **SA1958** | *SA1958* | N315 | | 3.12 | transposase for IS232 | COG1119 | **P** | Inorganic ion transport and metabolism |
| **SA2228** | *SA2228* | N315 | | 3.13 | NA(+)/H(+) exchanger | COG0025 | **P** | Inorganic ion transport and metabolism |
| **SA1844** | *agrA* | N315 | 0.10 | 0.12 | AgrA | COG3279 | **T** | Signal transduction mechanisms |
| **SA1843** | *agrC* | N315 | 0.01 | 0.02 | AgrC | COG2972 | **T** | Signal transduction mechanisms |
| **SA1246** | *arlS* | N315 | 0.33 | | putative protein histidine kinase ArlS | COG0642 | **T** | Signal transduction mechanisms |
| **SA0715** | *hprK* | N315 | 0.16 | 0.16 | HPr kinase/phosphatase | COG1493 | **T** | Signal transduction mechanisms |
| **SA1882** | *kdpD* | N315 | 0.05 | 0.21 | sensor protein KdpD | COG2205 | **T** | Signal transduction mechanisms |
| **SA0067** | *kdpD* | N315 | 5.81 | 3.91 | kdp operon sensor protein | COG2205 | **T** | Signal transduction mechanisms |
| **SA1400** | *phoH* | N315 | 0.18 | 0.21 | phosphate starvationinduced protein phoH homolog | COG1702 | **T** | Signal transduction mechanisms |
| **SA1872** | *rsbU* | N315 | 0.05 | 0.25 | sigmaB regulation protein RsbU | COG2208 | **T** | Signal transduction mechanisms |
| **SA1871** | *rsbV* | N315 | 0.15 | 0.19 | anti sigmaB factor antagonist | COG1366 | **T** | Signal transduction mechanisms |
| **SA1870** | *rsbW* | N315 | 0.15 | 0.33 | anti sigmaB factor | COG2172 | **T** | Signal transduction mechanisms |
| **SA0215** | *SA0215* | N315 | 3.60 | | two component response regulator | COG4753 | **T** | Signal transduction mechanisms |
| **SA0614** | *SA0614* | N315 | | 0.22 | two component response regulator | COG0745 | **T** | Signal transduction mechanisms |
| **SA1540** | *SA1540* | N315 | | 3.14 | hypothetical protein | COG1956 | **T** | Signal transduction mechanisms |
| **SA1667** | *SA1667* | N315 | 0.11 | 0.23 | two component sensor histidine kinase | COG2203,COG4585 | **T** | Signal transduction mechanisms |
| **SA2179** | *SA2179* | N315 | 0.20 | 0.22 | response regulators of two component regulatory | COG2197 | **T** | Signal transduction mechanisms |
| **SA0661** | *saeR* | N315 | 0.04 | 0.24 | response regulator | COG0745 | **T** | Signal transduction mechanisms |
| **SA0660** | *saeS* | N315 | 0.04 | 0.12 | histidine protein kinase | COG0642 | **T** | Signal transduction mechanisms |
| **SA1323** | *srrA* | N315 | 0.10 | 0.23 | staphylococcal respiratory response protein | COG0745 | **T** | Signal transduction mechanisms |
| **SA1322** | *srrB* | N315 | 0.10 | 0.14 | staphylococcal respiratory response protein | COG0642 | **T** | Signal transduction mechanisms |
| **SA2180** | *SA2180* | N315 | 0.01 | 0.07 | two component sensor histidine kinase | COG4585,COG0642 | **T** | Signal transduction mechanisms |
| **SA1701** | *vraS* | N315 | | 0.19 | two component sensor histidine kinase | COG4585 | **T** | Signal transduction mechanisms |

* Functional categories are colored following COG code, C (Energy production and conversion) appears in grey, J (Translation, ribosomal structure and biogenesis) in pink, K (Transcription) in orange, M ( Cell wall/membrane/envelope biogenesis) in yellow, T (Signal transduction mechanisms) in light bleu. For clarity, all genes involved in transports and metabolism appear in green.