**Additional File 2.** Gene loci under positive selection inferred based on the overall test (Test 1)

| Gene Locus_tag | Locus | Annotation | LRT -p-value | FDR-p-value |
|---|---|---|---|---|
| CT681 | *ompA* | major outer membrane protein | 0.000116125 | 0.002606405 |
| CT694 | - | hypothetical protein | 0.005119211 | 0.06248935 |
| CT711 | - | hypothetical protein | 0.008126101 | 0.09119444 |
| CT745 | *hemG* | protoporphyrinogen oxidase | 0.001364036 | 0.02109071 |
| CT774 | *cysQ* | 3'(2'),5'-bisphosphate nucleotidase | 0.003787879 | 0.04972767 |
| CT809 | - | hypothetical protein | 0.00467214 | 0.06020048 |
| CT823 | *htrA* | serine protease | 4.17E-06 | 0.000145072 |
| CT824 | - | insulinase family zinc metalloprotease | 2.68E-06 | 9.81E-05 |
| CT826 | *pssA* | CDP-diacylglycerol--serine O-phosphatidyltransferase | 0.00148357 | 0.02244027 |
| CT840 | *mesJ* | tRNA(Ile)-lysidine synthase/ PP-loop superfamily ATPase | 0.002079681 | 0.0291408 |
| CT841 | *ftsH* | ATP-dependent zinc protease/Cell division protein | 0.004771383 | 0.06036142 |
| CT847 | - | hypothetical protein | 0.002321161 | 0.03166744 |
| CT859 | *ispH* | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | 0.001348244 | 0.02109071 |
| CT860 | - | hypothetical protein | 0.004925704 | 0.06120095 |
| CT866 | *glgB* | glycogen branching enzyme | 1.25E-06 | 4.83E-05 |
| CT867 | - | hypothetical protein | 1.82E-07 | 8.44E-06 |
| CT868 | - | hypothetical protein | 4.48E-07 | 1.89E-05 |
| CT869 | *pmpE* | polymorphic outer membrane protein | 4.45E-35 | 1.55E-32 |
| CT870 | *pmpF* | polymorphic outer membrane protein | 3.05E-35 | 1.55E-32 |
| CT875 | - | hypothetical protein | 3.37E-09 | 2.93E-07 |
| CT011 | - | hypothetical protein | 0.000466488 | 0.008772363 |
| CT012 | - | Hypothetical protein/putative integral membrane protein | 1.84E-14 | 2.56E-12 |
| CT013 | *cydA* | cytochrome D ubiquinol oxidase subunit I | 0.003609565 | 0.04829803 |
| CT015 | *phoH* | ATPase/hypothetical protein | 8.84E-05 | 0.002113776 |
| CT017 | - | hypothetical protein | 0.007273621 | 0.08434848 |
| CT018 | - | hypothetical protein | 0.000540329 | 0.009639878 |
| CT040 | *ruvB* | Holliday junction DNA helicase RuvB | 0.000172746 | 0.003642268 |
| CT042 | *gigX* | glycogen hydrolase | 0.000479851 | 0.008786191 |
| CT049 | - | hypothetical protein | 1.20E-07 | 6.42E-06 |
| CT056 | - | hypothetical protein | 0.007953859 | 0.09072478 |
| CT064 | *lepA* | GTP-binding protein LepA | 0.000171077 | 0.003642268 |
| CT082 | - | hypothetical protein | 4.61E-07 | 1.89E-05 |
| CT089 | *icrE* | low calcium response protein E (TTSS effector protein) | 3.80E-05 | 0.001100994 |
| CT099 | *trxB* | thioredoxin reductase | 0.001601461 | 0.02370808 |

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|---|---|---|---|---|
| CT107 | *mutY* | A/G-specific adenine DNA glycosylase | 2.10E-12 | 2.44E-10 |
| CT109 | - | hypothetical protein | 6.07E-05 | 0.001632857 |
| CT115 | - | inclusion membrane protein D | 1.36E-05 | 0.000451064 |
| CT139 | *oppA_1* | oligopeptide transport system binding protein | 0.000878121 | 0.01490213 |
| CT140 | - | Hypothetical protein/exported protein | 0.001781622 | 0.0258257 |
| CT144 | - | hypothetical protein | 3.32E-15 | 5.78E-13 |
| CT147 | - | Hypothetical protein/putative integral membrane protein | 2.72E-16 | 6.31E-14 |
| CT198 | *oppA_3* | oligopeptide transport system binding protein | 0.002094082 | 0.0291408 |
| CT205 | *pfkA_1* | diphosphate--fructose-6-phosphate 1-phosphotransferase | 1.19E-08 | 9.20E-07 |
| CT209 | *leuS* | leucyl-tRNA synthetase | 1.48E-07 | 7.36E-06 |
| CT211 | - | hypothetical protein | 6.10E-05 | 0.001632857 |
| CT212 | - | hypothetical protein | 8.48E-05 | 0.002106175 |
| CT213 | *rpiA* | ribose-5-phosphate isomerase A | 0.000598795 | 0.01041588 |
| CT216 | *xasA* | glutamate/gamma-aminobutyrate antiporter | 0.006532079 | 0.07703308 |
| CT223 | - | hypothetical protein | 4.90E-08 | 2.95E-06 |
| CT227 | - | hypothetical protein | 6.59E-05 | 0.00169819 |
| CT229 | - | hypothetical protein | 2.86E-05 | 0.000864391 |
| CT244 | - | hypothetical protein | 4.55E-08 | 2.95E-06 |
| CT249 | - | hypothetical protein | 0.000193596 | 0.00384863 |
| CT286 | *clpC* | ATP-dependent Clp protease | 0.001214478 | 0.01965165 |
| CT288 | - | Hypothetical protein/candidate inclusion membrane protein | 5.09E-08 | 2.95E-06 |
| CT362 | *lysC* | aspartate kinase | 0.005246584 | 0.06293996 |
| CT455 | *murA* | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | 1.95E-05 | 0.000615701 |
| CT456 | - | hypothetical protein/translocated actin-recruiting protein (tarp) | 9.11E-05 | 0.002113776 |
| CT470 | *recO* | DNA repair protein RecO | 0.000180022 | 0.003684042 |
| CT529 | - | hypothetical protein | 0.001031138 | 0.01708226 |
| CT580 | - | hypothetical protein/putative integral membrane protein | 1.47E-11 | 1.46E-09 |
| CT604 | *groEL_2* | 60 kDa chaperonin GroEL2 | 0.000333033 | 0.00643669 |