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| **SNP** | **Chromosome** |  **Index**  | **Ref** | **Var** | **Effect** | **Codon Change** | **Gene** | **Gene ID** | **Gene Name** |
| 1 | NC\_016445.1 |  91,519  | C | T | NON-SYNONYMOUS CODING | aCc/aTc | Vch1786\_I0077 | ID: 11462798 | transposase Tn3 |
| 2 | NC\_016445.1 |  125,712  | T | C | SYNONYMOUS CODING | ggT/ggC | Vch1786\_I0103 | ID: 11462824 | conjugal transfer pilus assembly protein TraI |
| 3 | NC\_016445.1 |  125,757  | G | T | SYNONYMOUS CODING | gcG/gcT | Vch1786\_I0103 | ID: 11462824 | conjugal transfer pilus assembly protein TraI |
| 4 | NC\_016445.1 |  125,766  | A | T | SYNONYMOUS CODING | gcA/gcT | Vch1786\_I0103 | ID: 11462824 | conjugal transfer pilus assembly protein TraI |
| 5 | NC\_016445.1 |  133,215  | C | T | SYNONYMOUS CODING | agC/agT | Vch1786\_I0111 | ID: 11462832 | conjugal transfer pilus assembly protein TraK |
| 6 | NC\_016445.1 |  264,678  | A | G | NON-SYNONYMOUS CODING | Ttt/Ctt | Vch1786\_I0238 | ID: 11462959 | peroxiredoxin (alkyl hydroperoxide reductase subunit C) |
| 7 | NC\_016445.1 |  272,397  | T | G | SYNONYMOUS CODING | ggT/ggG | tgt | ID: 11462968 | queuine tRNA-ribosyltransferase |
| 8 | NC\_016445.1 |  351,281  | G | T | NON-SYNONYMOUS CODING | Gat/Tat | Vch1786\_I0323 | ID: 11460142 | hypothetical protein |
| 9 | NC\_016445.1 |  415,957  | C | A | NON-SYNONYMOUS CODING | Ggt/Tgt | Vch1786\_I0381 | ID: 11460200 | prolyl-tRNA synthetase  |
| 10 | NC\_016445.1 |  498,051  | A | T | NON-SYNONYMOUS CODING | cTa/cAa | leuS | ID: 11460279 | leucyl-tRNA synthetase |
| 11 | NC\_016445.1 |  504,895  | G | A | SYNONYMOUS CODING | ggG/ggA | Vch1786\_I0467 | ID: 11460286 | 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase |
| 12 | NC\_016445.1 |  567,468  | C | G | NON-SYNONYMOUS CODING | aCc/aGc | Vch1786\_I0525 | ID: 11460344 | two-component system, repressor protein LuxO |
| 13 | NC\_016445.1 |  567,531  | T | G | NON-SYNONYMOUS CODING | aTc/aGc | Vch1786\_I0525 | ID: 11460344 | two-component system, repressor protein LuxO |
| 14 | NC\_016445.1 |  568,200  | G | A | NON-SYNONYMOUS CODING | gGc/gAc | Vch1786\_I0525 | ID: 11460344 | two-component system, repressor protein LuxO |
| 15 | NC\_016445.1 |  688,901  | C | G | NON-CODING | - | - | - | - |
| 16 | NC\_016445.1 |  754,407  | C | T | NON-SYNONYMOUS CODING | Ggc/Agc | hutH | ID: 11460525 | hutH histidine ammonia-lyase |
| 17 | NC\_016445.1 |  824,155  | C | T | NON-SYNONYMOUS CODING | gCt/gTt | Vch1786\_I0776 | ID: 11460525 | hutH histidine ammonia-lyase |
| 18 | NC\_016445.1 |  883,838  | C | T | SYNONYMOUS CODING | Cta/Tta | Vch1786\_I0823 | ID: 11460642 | membrane carboxypeptidase |
| 19 | NC\_016445.1 |  884,385  | C | A | NON-SYNONYMOUS CODING | aCg/aAg | Vch1786\_I0823 | ID: 11460642 | membrane carboxypeptidase |
| 20 | NC\_016445.1 |  956,950  | G | T | SYNONYMOUS CODING | gtG/gtT | lplA | ID: 11460707 | lipoate-protein ligase A |
| 21 | NC\_016445.1 |  1,045,847  | C | T | SYNONYMOUS CODING | aaG/aaA | rstB | ID: 11460778 | RstB phage-related integrase |
| 22 | NC\_016445.1 |  1,045,931  | T | C | SYNONYMOUS CODING | gtA/gtG | rstB | ID: 11460778 | RstB phage-related integrase |
| 23 | NC\_016445.1 |  1,045,943  | G | A | SYNONYMOUS CODING | taC/taT | rstB | ID: 11460778 | RstB phage-related integrase |
| 24 | NC\_016445.1 |  1,045,949  | A | T | SYNONYMOUS CODING | gcT/gcA | rstB | ID: 11460778 | RstB phage-related integrase |
| 25 | NC\_016445.1 |  1,067,357  | G | T | NON-SYNONYMOUS CODING | aaC/aaA | rlmL | ID: 11460805 | 23S rRNA methyltransferase |
| 26 | NC\_016445.1 |  1,154,443  | G | A | SYNONYMOUS CODING | gcG/gcA | Vch1786\_I1066 | ID: 11460885 | hypothetical protein |
| 27 | NC\_016445.1 |  1,211,305  | G | A | NON-SYNONYMOUS CODING | aCc/aTc | Vch1786\_I1120 | ID: 11460939 | hypothetical protein |
| 28 | NC\_016445.1 |  1,240,958  | G | A | NON-SYNONYMOUS CODING | Ggg/Agg | Vch1786\_I1142 | ID: 11460961 | methyl-accepting chemotaxis protein |
| 29 | NC\_016445.1 |  1,384,219  | T | C | NON-SYNONYMOUS CODING | Aca/Gca | Vch1786\_I1262 | ID: 11461081 | type I restriction enzyme, S subunit |
| 30 | NC\_016445.1 |  1,464,818  | C | T | NON-SYNONYMOUS CODING | Gct/Act | ompT | ID: 11461165 | OmpT protein |
| 31 | NC\_016445.1 |  1,465,340  | C | T | NON-CODING | - | - | - | - |
| 32 | NC\_016445.1 |  1,465,756  | C | T | SYNONYMOUS CODING | cgC/cgT | dinG | ID: 11461166 | ATP-dependent DNA helicase DinG |
| 33 | NC\_016445.1 |  1,637,831  | C | A | NON-SYNONYMOUS CODING | gCa/gAa | Vch1786\_I1503 | ID: 11461322 | neurotransmitter:Na+ symporter, NSS family |
| 34 | NC\_016445.1 |  1,771,236  | G | A | SYNONYMOUS CODING | acC/acT | flaE | ID: 11461454 | flagellin |
| 35 | NC\_016445.1 |  1,771,457  | G | A | STOP-GAINED | Caa/Taa | flaE | ID: 11461454 | flagellin |
| 36 | NC\_016445.1 |  1,914,688  | G | A | SYNONYMOUS CODING | acC/acT | apbE | ID: 11461601 | thiamin biosynthesis lipoprotein ApbE |
| 37 | NC\_016445.1 |  2,094,531  | T | G | NON-SYNONYMOUS CODING | Aaa/Caa | exeA | ID: 11461756 | general secretion pathway protein A |
| 38 | NC\_016445.1 |  2,124,160  | T | C | NON-CODING | - | - | - | - |
| 39 | NC\_016445.1 |  2,130,106  | G | A | NON-CODING | - | - | - | - |
| 40 | NC\_016445.1 |  2,137,740  | C | T | SYNONYMOUS CODING | gaG/gaA | Vch1786\_I1976 | ID: 11461795 | glycosyltransferase |
| 41 | NC\_016445.1 |  2,140,014  | G | A | NON-CODING | - | - | - | - |
| 42 | NC\_016445.1 |  2,186,814  | C | T | NON-SYNONYMOUS CODING | Ctc/Ttc | Vch1786\_I2030 | ID: 11461849 | magnesium transporter |
| 43 | NC\_016445.1 |  2,204,628  | G | A | SYNONYMOUS CODING | gcG/gcA | Vch1786\_I2046 | ID: 11461865 | hypothetical protein |
| 44 | NC\_016445.1 |  2,257,173  | C | T | NON-SYNONYMOUS CODING | Ggg/Agg | argD | ID: 11461932 | bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein |
| 45 | NC\_016445.1 |  2,371,220  | G | A | SYNONYMOUS CODING | gtC/gtT | epsI | ID: 11462041 | general secretion pathway protein I |
| 46 | NC\_016445.1 |  2,521,466  | G | A | NON-SYNONYMOUS CODING | Gcc/Acc | Vch1786\_I2378 | ID: 11462197 | thiol:disulfide interchange protein DsbA |
| 47 | NC\_016445.1 |  2,532,567  | G | A | NON-CODING | - | - | - | - |
| 48 | NC\_016445.1 |  2,541,675  | A | G | SYNONYMOUS CODING | tgT/tgC | gyrB | ID: 11462216 | DNA gyrase subunit B |
| 49 | NC\_016445.1 |  2,585,616  | T | G | SYNONYMOUS CODING | gcA/gcC | Vch1786\_I2444 | ID: 11462263 | hypothetical protein |
| 50 | NC\_016445.1 |  2,787,072  | A | G | NON-CODING | - | - | - | - |
| 51 | NC\_016445.1 |  2,854,032  | G | A | SYNONYMOUS CODING | ctG/ctA | mshM | ID: 11462532 | MSHA biogenesis protein MshM |
| 52 | NC\_016445.1 |  2,856,505  | G | A | NON-SYNONYMOUS CODING | Ggc/Agc | mshE | ID: 11462534 | MSHA biogenesis protein MshE |
| 53 | NC\_016445.1 |  2,874,265  | T | G | NON-SYNONYMOUS CODING | gTg/gGg | Vch1786\_I2729 | ID: 11462548 | hypothetical protein |
| 54 | NC\_016445.1 |  2,950,920  | C | T | NON-SYNONYMOUS CODING | Gtt/Att | Vch1786\_I2813 | ID: 11462632 | hypothetical protein |
| 55 | NC\_016445.1 |  2,997,670  | C | T | NON-SYNONYMOUS CODING | Ctt/Ttt | Vch1786\_I2865 | ID: 11462684 | NADPH2:quinone reductase |
| 56 | NC\_016445.1 |  3,023,862  | C | T | STOP-GAINED | tgG/tgA | Vch1786\_I2895 | ID: 11462714 | TetR/AcrR family transcriptional regulator, hemagglutinin/protease regulatory protein |
| 57 | NC\_016446.1 |  54,854  | G | A | NON-SYNONYMOUS CODING | Ggt/Agt | Vch1786\_II0067 | ID: 11463101 | hypothetical protein |
| 58 | NC\_016446.2 |  76,133  | T | C | SYNONYMOUS CODING | ggT/ggC | Vch1786\_II0108 | ID: 11463142 | hypothetical protein |
| 59 | NC\_016446.2 |  84,113  | C | T | NON-SYNONYMOUS CODING | Cac/Tac | Vch1786\_II0121 | ID: 11463155 | hypothetical protein |
| 60 | NC\_016446.2 |  214,940  | T | C | NON-SYNONYMOUS CODING | aAt/aGt | Vch1786\_II0263 | ID: 11463297 | LysR family transcriptional regulator |
| 61 | NC\_016446.2 |  312,369  | G | A | NON-SYNONYMOUS CODING | cGc/cAc | napF | ID: 11463392 | iron-sulfur cluster-binding protein NapF |
| 62 | NC\_016446.2 |  315,133  | C | T | NON-SYNONYMOUS CODING | gCc/gTc | Vch1786\_II0360 | ID: 11463394 | periplasmic nitrate reductase NapA |
| 63 | NC\_016446.2 |  409,036  | A | G | NON-CODING | - | - | - | - |
| 64 | NC\_016446.2 |  457,762  | T | C | NON-CODING | - | - | - | - |
| 65 | NC\_016446.2 |  496,854  | C | T | NON-SYNONYMOUS CODING | cGc/cAc | Vch1786\_II0538 | ID: 11463572 | hypothetical protein |
| 66 | NC\_016446.2 |  600,249  | G | A | NON-SYNONYMOUS CODING | aGa/aAa | speG | ID: 11463668 | spermidine N1-acetyltransferase |
| 67 | NC\_016446.2 |  663,294  | C | T | SYNONYMOUS CODING | gcG/gcA | Vch1786\_II0701 | ID: 11463735 | hypothetical protein |
| 68 | NC\_016446.2 |  856,231  | G | T | NON-SYNONYMOUS CODING | cCc/cAc | Vch1786\_II0868 | ID: 11463902 | transcriptional regulator CdgA |