

**Table S6. Taxonomic and functional analysis of the protein-coding genes with assigned function identified in the *T. phenacola* PPER genome.**

When two different gene copies exist, only the first one appears on the table, highlighted in yellow in column B (Locust tag). The results of the two methods used for taxonomic assignment, as well as the final taxonomic class finally assigned are indicated on the left (columns D, E and F, respectively). Highlighted in blue: betaproteobacteria; highlighted in orange, gammaproteobacteria. In the "gene name" column (C) genes that could not be assigned to either category are highlighted in green, while genes that gave an inconsistent result by both methods are highlighted in yellow.

On the right (columns J to N), gene products and functional classification, based on the categories described by Gil et al. (2004) for the core of their proposed minimal genome. The corresponding *T. phenacola* PAVE orthologous classes are also indicated (column I).

| Contig         | Locust tag  | Gene name   | MEGAN               | phylozjmer          | Taxonomic class     | PPER       | PAVE       | product   | Functional category                           |  |  |   |
|----------------|-------------|-------------|---------------------|---------------------|---------------------|------------|------------|---|---|--|--|---|
| TPPER_contig1  | TPPER_0001  | rpsU_A      | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpsU_A     | TPPAVE_010 | 30S ribosomal protein S21                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_0002  | leuC        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | leuC       | TPPAVE_001 | 3-isopropylmalate dehydratase large subunit 1                   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_0003  | leuD        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | leuD       | TPPAVE_002 | 3-isopropylmalate dehydratase small subunit 1                   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_0004  | leuB        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | leuB       | TPPAVE_003 | 3-isopropylmalate dehydrogenase                                 | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_0005  | asd         | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | asd        | TPPAVE_004 | Aspartate-semialdehyde dehydrogenase                            | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.2. Aspartate family                  |   |
|                | TPPER_0006  | dnaE        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | dnaE       | TPPAVE_058 | DNA polymerase III subunit alpha                                | 1. INFORMATION STORAGE AND PROCESSING         | 1.1. DNA metabolism                          | 1.1.2. DNA replication                   |   |
|                | TPPER_0007  | rfsS        | Bacteria            | Unknown             | Unknown             | rfsS       | TPPAVE_059 | Ribosomal silencing factor RfsS                                 | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.4. Ribosome function, maturation and modification |
|                | TPPER_0008  | cysS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | cysS       | TPPAVE_087 | Cysteine-lyase  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_0010  | ompB        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | ompB       | TPPAVE_098 | SrA-binding protein   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_0011  | lepB        | Vibrionaceae        | Betaproteobacteria  | Unknown             | lepB       | TPPAVE_099 | Signal peptidase 1  | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.1. Protein post-translational modification |  |   |
| TPPER_contig2  | TPPER_00012 | leuS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | leuS       | TPPAVE_209 | Leucine-tRNA ligase   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00015 | rpmH        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpmH       | TPPAVE_088 | 50S ribosomal protein L34                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00016 | dnaN        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | dnaN       | TPPAVE_006 | DNA polymerase III subunit beta                                 | 1. INFORMATION STORAGE AND PROCESSING         | 1.1. DNA metabolism                          | 1.1.2. DNA replication                   |   |
|                | TPPER_00017 | rpoD        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpoD       | TPPAVE_009 | RNA polymerase sigma factor RpoD                                | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.1. Transcription                     |   |
|                | TPPER_00019 | tIS         | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | tIS        | TPPAVE_088 | tRNA(Ile)-lysidine synthase                                     | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.2. tRNA maturation and modification               |
|                | TPPER_00022 | trpA        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | trpA       | TPPAVE_007 | Tryptophan synthase alpha chain                                 | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00023 | trpB        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | trpB       | TPPAVE_008 | Tryptophan synthase beta chain                                  | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00024 | trpC        | Proteobacteria      | Unknown             | Betaproteobacteria  | trpC       | TPPAVE_080 | Tryptophan biosynthesis protein TrpCF                           | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00025 | trpD        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | trpD       | TPPAVE_081 | Bifunctional protein TrpGD                                      | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00028 | fmt         | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | fmt        | TPPAVE_196 | Methionyl-tRNA formyltransferase                                | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
| TPPER_contig3  | TPPER_00029 | def         | Proteobacteria      | Gammaproteobacteria | Gammaproteobacteria | def        | TPPAVE_197 | Peptide deformylase   | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.1. Protein post-translational modification |  |   |
|                | TPPER_00032 | mmmG        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | mmmG       | TPPAVE_033 | RNA uridine 5-carboxymethylaminomethyl modification enzyme MmmG | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.2. tRNA maturation and modification               |
|                | TPPER_00033 | rImE_1      | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | rImE_1     | TPPAVE_065 | Ribosomal RNA large subunit methyltransferase E                 | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.4. Ribosome function, maturation and modification |
|                | TPPER_00036 | rsmH        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | rsmH       | TPPAVE_065 | Ribosomal RNA small subunit methyltransferase H                 | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.4. Ribosome function, maturation and modification |
|                | TPPER_00037 | lon         | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | lon        | TPPAVE_006 | Lon protease  | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.4. Protein turnover                        |  |   |
|                | TPPER_00038 | clpX        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | clpX       | TPPAVE_013 | ATP-dependent Clp protease ATP-binding subunit ClpX             | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.2. Chaperones                              |  |   |
|                | TPPER_00041 | trxA        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | trxA       | TPPAVE_013 | Thioredoxin-1   | 4. METABOLISM                                 | 4.3. Energy metabolism                       | 4.3.1. Electron transport                |   |
|                | TPPER_00042 | argG        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | argG       | TPPAVE_015 | Argininosuccinate synthase                                      | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.4. Glutamate family                  |   |
|                | TPPER_00043 | trpS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | trpS       | TPPAVE_108 | Tryptophan-tRNA ligase  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00044 | pheT        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | pheT       | TPPAVE_108 | Phenylalanine-tRNA ligase beta subunit                          | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
| TPPER_contig5  | TPPER_00045 | pheS        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | pheS       | TPPAVE_107 | Phenylalanine-tRNA ligase alpha subunit                         | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00046 | clpP        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | clpP       | TPPAVE_014 | ATP-dependent Clp protease proteolytic subunit precursor        | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.2. Chaperones                              |  |   |
|                | TPPER_00047 | serS        | Burkholderia        | Gammaproteobacteria | Unknown             | serS       | TPPAVE_017 | Serine-tRNA ligase  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00048 | glyS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | glyS       | TPPAVE_209 | Glycine-tRNA ligase beta subunit                                | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00049 | glyQ        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | glyQ       | TPPAVE_209 | Glycine-tRNA ligase alpha subunit                               | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00051 | lpdA        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | lpdA       | TPPAVE_154 | Dihydrolipoyl dehydrogenase                                     | 4. METABOLISM                                 | 4.2. Pyruvate and TCA metabolism             |  |   |
|                | TPPER_00052 | infA_1      | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | infA_1     | TPPAVE_018 | Translation initiation factor IF-1                              | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_00053 | trxB        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | trxB       | TPPAVE_018 | Thioredoxin reductase   | 4. METABOLISM                                 | 4.3. Energy metabolism                       | 4.3.1. Electron transport                |   |
|                | TPPER_00055 | aroQ        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | aroQ       | TPPAVE_132 | 3-dehydroquinate dehydratase                                    | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00056 | der         | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | der        | TPPAVE_132 | GPase Der   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.4. Ribosome function, maturation and modification |
| TPPER_contig7  | TPPER_00057 | ybeY        | Burkholderiales     | Unknown             | Betaproteobacteria  | ybeY       | TPPAVE_019 | Endonuclease YbeY   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.4. Ribosome function, maturation and modification |
|                | TPPER_00058 | rbeE        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | rbeE       | TPPAVE_019 | 67-dimethyl-8-ribityllumazine synthase                          | 4. METABOLISM                                 | 4.8. Metabolism of cofactors and vitamins    | 4.8.10. Riboflavin metabolism            |   |
|                | TPPER_00059 | obp         | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | obp        | TPPAVE_139 | Stringent starvation protein B                                  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00060 | pspB        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | pspB       | TPPAVE_041 | Dihydroxy-acid dehydratase                                      | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.4. Protein turnover                        |  |   |
|                | TPPER_00061 | livD        | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  | livD       | TPPAVE_041 | Dihydroxy-acid dehydratase                                      | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_00062 | erpA        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | erpA       | TPPAVE_067 | Iron-sulfur cluster insertion protein ErpA                      | 4. METABOLISM                                 | 4.8. Metabolism of cofactors and vitamins    | 4.8.2. Fe/S biosynthesis                 |   |
|                | TPPER_00063 | rpsI        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpsI       | TPPAVE_039 | 30S ribosomal protein S9  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00064 | tal         | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | tal        | TPPAVE_207 | Transaldolase   | 4. METABOLISM                                 | 4.1. Carbohydrate metabolism                 | 4.1.2. Pentose phosphate pathway         |   |
|                | TPPER_00065 | frr         | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | frr        | TPPAVE_097 | Ribosome-recycling factor                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_00066 | dnaB        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | dnaB       | TPPAVE_112 | Replicative DNA helicase  | 1. INFORMATION STORAGE AND PROCESSING         | 1.1. DNA metabolism                          | 1.1.2. DNA replication                   |   |
| TPPER_contig8  | TPPER_00067 | rpmA        | cellular organisms  | Betaproteobacteria  | Betaproteobacteria  | rpmA       | TPPAVE_011 | 50S ribosomal protein L27                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00068 | rplU        | Bacteria            | Betaproteobacteria  | Betaproteobacteria  | rplU       | TPPAVE_021 | 50S ribosomal protein L21                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00069 | secA        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | secA       | TPPAVE_079 | Protein translocase subunit SecA                                | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.3. Protein translocation and secretion     |  |   |
|                | TPPER_00071 | TPPER_00071 | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | PPER_00181 | TPPAVE_047 | Hypothetical protein  | 5. POORLY CHARACTERIZED                       |  |  |   |
|                | TPPER_00072 | pheA        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | pheA       | TPPAVE_047 | P-protein   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00073 | aroA        | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  | aroA       | TPPAVE_048 | 3-phosphoshikimate 1-carboxyvinyltransferase                    | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00074 | rpsA        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | rpsA       | TPPAVE_050 | 30S ribosomal protein S1  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00075 | rpsP        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpsP       | TPPAVE_051 | 30S ribosomal protein S16                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00076 | rplS        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rplS       | TPPAVE_052 | 50S ribosomal subunit protein L19                               | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00077 | metF        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | metF       | TPPAVE_053 | 5,10-methylenetetrahydrofolate reductase                        | 4. METABOLISM                                 | 4.8. Metabolism of cofactors and vitamins    | 4.8.5. One-carbon pool by folate         |   |
| TPPER_contig9  | TPPER_00078 | vggX        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | vggX       | TPPAVE_054 | Probable Fe(2+)-trafficking protein                             | 5. POORLY CHARACTERIZED                       |  |  |   |
|                | TPPER_00079 | aroC        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | aroC       | TPPAVE_101 | Chorismate synthase   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.1. Aromatic amino acids              |   |
|                | TPPER_00080 | infC        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | infC       | TPPAVE_104 | Translation initiation factor IF-3                              | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_00250 | rmpI        | Unknown             | Betaproteobacteria  | Betaproteobacteria  | rmpI       | TPPAVE_105 | 50S ribosomal protein L35                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00081 | rplT        | cellular organisms  | Betaproteobacteria  | Betaproteobacteria  | rplT       | TPPAVE_106 | 50S ribosomal protein L20                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00083 | prfA_A      | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | prfA_A     | TPPAVE_079 | Peptide chain release factor 1                                  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_00084 | panB        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | panB       | TPPAVE_079 | 3-methyl-2-oxobutanoate hydroxymethyltransferase                | 4. METABOLISM                                 | 4.8. Metabolism of cofactors and vitamins    | 4.8.9. Pantothenate and CoA biosynthesis |   |
|                | TPPER_00085 | alaS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | alaS       | TPPAVE_145 | Alanine-tRNA ligase   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
|                | TPPER_00087 | rpsE        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | rpsE       | TPPAVE_056 | 50 kDa chaperone  | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.2. Chaperones                              |  |   |
|                | TPPER_00089 | groL        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | groL       | TPPAVE_055 | 60 kDa chaperonin   | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.2. Chaperones                              |  |   |
| TPPER_contig10 | TPPER_00090 | livI        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | livI       | TPPAVE_061 | Acetolactate synthase isozyme 3 large subunit                   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_00091 | livC        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | livC       | TPPAVE_061 | Ketol-acid reductoisomerase                                     | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_00092 | leuA        | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  | leuA       | TPPAVE_062 | 2-isopropylmalate synthase                                      | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.3. Branched-chain family             |   |
|                | TPPER_00093 | rpsO        | Bacteria            | Unknown             | Unknown             | rpsO       | TPPAVE_063 | 30S ribosomal protein S15                                       | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00094 | map         | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | map        | TPPAVE_210 | Methionine aminopeptidase                                       | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.1. Protein post-translational modification |  |   |
|                | TPPER_00095 | dapB        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | dapB       | TPPAVE_210 | 4-hydroxy-tetrahydrodipicolinate reductase                      | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.2. Aspartate family                  |   |
|                | TPPER_00097 | hisC_A      | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisC_A     | TPPAVE_145 | ATP phosphoribosyltransferase                                   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids             | 4.4.2. Aspartate family                  |   |
|                | TPPER_00098 | prnC_A      | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | prnC_A     | TPPAVE_078 | Release factor glutamine methyltransferase                      | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_0100  | prfB_A      | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | prfB_A     | TPPAVE_069 | Peptide chain release factor 2                                  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                          | 1.2.2. Translation                       | 1.2.2.5. Translation factors                            |
|                | TPPER_01005 | rpmB        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpm        |            |   |   |  |  |   |

|                |                |             |                     |                     |                     |                     |              |  |   |   |   |   |
|----------------|----------------|-------------|---------------------|---------------------|---------------------|---------------------|--------------|--|---|---|---|---|
| TPPER_contig12 | TPPER_00110    | dapD        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | dapD                | TPPAVE_095   | 2 3 4 5-tetrahydropyridine-2 6-dicarboxylate N-succinyltransferase                               | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.2. Aspartate family                   |   |
|                | TPPER_00111    | thrB        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | thrB                | TPPAVE_012   | Homoserine kinase  | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.2. Aspartate family                   |   |
|                | TPPER_00112    | trpE        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | trpE                | TPPAVE_083   | Anthraniolate synthase component 1   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.1. Aromatic amino acids               |   |
|                | TPPER_00113    | trpS        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | trpS                | TPPAVE_082   | Anthraniolate synthase component 2   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.1. Aromatic amino acids               |   |
|                | TPPER_00114    | trcA        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | trcA                | TPPAVE_081   | Aconitate hydratase 1  | 4. METABOLISM                                   | 4.2. Pyruvate and TCA metabolism          |   |   |
|                | TPPER_00115    | rpmF        | Betaproteobacteria  | Unknown             | Betaproteobacteria  | rpmF                | TPPAVE_022   | 50S ribosomal protein L32  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00116    | TPPER_00116 | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | TPPER_00116         | TPPAVE_023   | pseudouridine synthase, RluA family protein  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.4. Ribosome function, maturation and modification |
|                | TPPER_00118    | ligA        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | ligA                | TPPAVE_024   | DNA ligase   | 1. INFORMATION STORAGE AND PROCESSING           | 1.1. DNA metabolism                       | 1.1.2. DNA replication                    |   |
|                | TPPER_00119    | grpE        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | grpE                | TPPAVE_028   | Protein GrpE   | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION   | 2.2. Chaperones                           |   |   |
|                | TPPER_00120    | argF        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | argF                | TPPAVE_035   | Ornithine carbamoyltransferase chain F   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.4. Glutamate family                   |   |
|                | TPPER_00121    | cysK        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | cysK                | TPPAVE_034   | Cysteine synthase A  | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.6. Serine family                      |   |
|                | TPPER_00122    | rpsT        | Enterobacteriaceae  | Unknown             | Gammaproteobacteria | rpsT                | TPPAVE_036   | 30S ribosomal protein S20  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00123    | his         | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisC                | TPPAVE_074   | Hisicase-1 RNA ligase  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.1. Aminocyl-1RNA synthetases                      |
|                | TPPER_contig14 | TPPER_00127 | glx_B               | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | glx          | TPPAVE_091   | Glutamate-1RNA ligase                           | 1. INFORMATION STORAGE AND PROCESSING     | 1.2. RNA metabolism                       | 1.2.2. Translation                                      |
| TPPER_00129    |                | hisS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisS                | TPPAVE_133   | Histidine-1RNA ligase  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.1. Aminocyl-1RNA synthetases                      |
| TPPER_00130    |                | rluD        | Enterobacteriaceae  | Gammaproteobacteria | Betaproteobacteria  | rluD                | TPPAVE_092   | Ribosomal large subunit pseudouridine synthase D   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.4. Ribosome function, maturation and modification |
| TPPER_00132    |                | lysC        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | lysC                | TPPAVE_089   | Lysine-sensitive aspartokinase 3   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.2. Aspartate family                   |   |
| TPPER_00133    |                | proS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | proS                | TPPAVE_127   | Proline-1RNA ligase  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.1. Aminocyl-1RNA synthetases                      |
| TPPER_00134    |                | rplM        | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria | rplM                | TPPAVE_038   | 50S ribosomal protein L13  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
| TPPER_00135    |                | gluS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | gluS                | TPPAVE_129   | Glutamine-1RNA ligase  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.1. Aminocyl-1RNA synthetases                      |
| TPPER_00136    |                | valS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | valS                | TPPAVE_099   | Valine-1RNA ligase   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.1. Aminocyl-1RNA synthetases                      |
| TPPER_00140    |                | rpmE        | Bacteria            | Gammaproteobacteria | Gammaproteobacteria | rpmE                | TPPAVE_115   | 50S ribosomal protein L31  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
| TPPER_00141    |                | tsaD        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | tsaD                | TPPAVE_011   | RNA N6-adenosine threonylcarbamoyltransferase  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.2. tRNA maturation and modification               |
| TPPER_00142    |                | tyrS        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | tyrS                | TPPAVE_100   | Tyrosine-1RNA ligase   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.1. Aminocyl-1RNA synthetases                      |
| TPPER_00143    |                | tadA        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | tadA                | TPPAVE_100   | RNA-specific adenosine deaminase   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2.2. tRNA maturation and modification |   |
| TPPER_00145    |                | pykF        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | pykF                | TPPAVE_041   | Pyruvate kinase I  | 4. METABOLISM                                   | 4.1. Carbohydrate metabolism              | 4.1.1. Glycolysis                         |   |
| TPPER_00148    |                | cysG_B      | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | cysG_B              | TPPAVE_042   | Siroheme synthase, N-terminal domain   | 4. METABOLISM                                   | 4.8. Metabolism of cofactors and vitamins | 4.8.7. Heme and porphirin metabolism      |   |
| TPPER_contig15 | TPPER_00149    | cysG_C      | Enterobacteriaceae  | Unknown             | Gammaproteobacteria | cysG_C              | TPPAVE_043   | Siroheme synthase, C-terminal domain   | 4. METABOLISM                                   | 4.8. Metabolism of cofactors and vitamins | 4.8.7. Heme and porphirin metabolism      |   |
|                | TPPER_00150    | iscA        | Bacteria            | Unknown             | Unknown             | iscA                | TPPAVE_040   | Iron-sulfur cluster insertion protein IscA   | 4. METABOLISM                                   | 4.8. Metabolism of cofactors and vitamins | 4.8.2. FeS biosynthesis                   |   |
|                | TPPER_00151    | iscU        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | iscU                | TPPAVE_066.1 | NiU-like protein   | 4. METABOLISM                                   | 4.8. Metabolism of cofactors and vitamins | 4.8.2. FeS biosynthesis                   |   |
|                | TPPER_00152    | iscS        | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  | iscS                | TPPAVE_066   | Cysteine desulfurase   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.2. tRNA maturation and modification               |
|                | TPPER_00153    | infB        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | infB                | TPPAVE_109   | Translation initiation factor IF-2   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.5. Translation factors                            |
|                | TPPER_00154    | rbfA        | Unknown             | Unknown             | Unknown             | rbfA                | TPPAVE_075   | Ribosome-binding factor A  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.4. Ribosome function, maturation and modification |
|                | TPPER_00155    | sucA        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | sucA                | TPPAVE_076   | 2-oxoglutarate dehydrogenase E1 component  | 4. METABOLISM                                   | 4.2. Pyruvate and TCA metabolism          |   |   |
|                | TPPER_00156    | sucB        | Proteobacteria      | Gammaproteobacteria | Gammaproteobacteria | sucB                | TPPAVE_077   | Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex | 4. METABOLISM                                   | 4.2. Pyruvate and TCA metabolism          |   |   |
|                | TPPER_00157    | rpsF        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | rpsF                | TPPAVE_110   | 30S ribosomal protein S6   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00158    | rpsR        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpsR                | TPPAVE_111   | 30S ribosomal protein S18  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00159    | rplI        | Alphaproteobacteria | Betaproteobacteria  | Unknown             | rplI                | TPPAVE_112   | 50S ribosomal protein L9   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00160    | hom         | Bacteria            | Betaproteobacteria  | Betaproteobacteria  | hom                 | TPPAVE_113   | Homoserine dehydrogenase   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.2. Aspartate family                   |   |
|                | TPPER_00161    | thrC        | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  | thrC                | TPPAVE_114   | Threonine synthase   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.2. Aspartate family                   |   |
|                | TPPER_contig16 | TPPER_00162 | argH_B              | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | argH_B       | TPPAVE_116   | Argininosuccinate lyase                         | 4. METABOLISM                             | 4.4. Biosynthesis of amino acids          | 4.4.4. Glutamate family                                 |
| TPPER_00163    |                | rnpA        | Unknown             | Unknown             | Unknown             | rnpA                | TPPAVE_117   | Ribonuclease P protein component   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.2. tRNA maturation and modification               |
| TPPER_00164    |                | rImE_2      | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rImE_2              | TPPAVE_119   | Ribosomal RNA large subunit methyltransferase E  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.4. Ribosome function, maturation and modification |
| TPPER_00165    |                | carB        | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  | carB                | TPPAVE_120   | Carbamoyl-phosphate synthase large chain   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.4. Glutamate family                   |   |
| TPPER_00166    |                | carA        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | carA                | TPPAVE_121   | Carbamoyl-phosphate synthase small chain   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.4. Glutamate family                   |   |
| TPPER_00167    |                | dnaQ_A      | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | dnaQ_A              | TPPAVE_122   | DNA polymerase III subunit epsilon   | 1. INFORMATION STORAGE AND PROCESSING           | 1.1. DNA metabolism                       | 1.1.2. DNA replication                    |   |
| TPPER_00168    |                | dnaQ_B      | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | dnaQ_B              | TPPAVE_122   | DNA polymerase III subunit epsilon   | 1. INFORMATION STORAGE AND PROCESSING           | 1.1. DNA metabolism                       | 1.1.2. DNA replication                    |   |
| TPPER_00169    |                | TPPER_00169 | Unknown             | Unknown             | Unknown             | TPPER_00169         | TPPAVE_123   | 5. POORLY CHARACTERIZED  | 5. POORLY CHARACTERIZED                         |   |   |   |
| TPPER_00174    |                | hisI_B      | Bacteria            | Gammaproteobacteria | Gammaproteobacteria | hisI_B              | TPPAVE_140   | Histidine biosynthesis bifunctional protein HisI   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.5. Histidine                          |   |
| TPPER_00175    |                | hisF        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisF                | TPPAVE_141   | Imidazole glycerol phosphate synthase subunit HisF   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.5. Histidine                          |   |
| TPPER_00176    |                | hisA        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisA                | TPPAVE_142   | 1-[(5-phosphoribosyl)-5-[(5-phosphorylamino)methylideneamino]imidazole-4-carboxamide isomerase   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.5. Histidine                          |   |
| TPPER_00177    |                | hisH        | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisH                | TPPAVE_143   | Imidazole glycerol phosphate synthase subunit HisH   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.5. Histidine                          |   |
| TPPER_00178    |                | hisB_B      | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria | hisB_B              | TPPAVE_144   | Histidine biosynthesis bifunctional protein HisB   | 4. METABOLISM                                   | 4.4. Biosynthesis of amino acids          | 4.4.5. Histidine                          |   |
| TPPER_contig19 |                | TPPER_00183 | ar08                | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | ar08         | TPPAVE_146   | 3-dehydroquinate synthase                       | 4. METABOLISM                             | 4.4. Biosynthesis of amino acids          | 4.4.1. Aromatic amino acids                             |
|                | TPPER_00184    | rplQ        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rplQ                | TPPAVE_148   | 50S ribosomal protein L17  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00185    | rpoA        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | rpoA                | TPPAVE_149   | DNA-directed RNA polymerase subunit alpha  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.1. Transcription                      |   |
|                | TPPER_00186    | rpsD        | Gammaproteobacteria | Betaproteobacteria  | Unknown             | rpsD                | TPPAVE_150   | 30S ribosomal protein S4   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00187    | rpsK        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpsK                | TPPAVE_151   | 30S ribosomal protein S11  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00188    | rpsM        | Bacteria            | Betaproteobacteria  | Betaproteobacteria  | rpsM                | TPPAVE_152   | 30S ribosomal protein S13  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00251    | rpmJ        | Unknown             | Betaproteobacteria  | Betaproteobacteria  | rpmJ                | TPPAVE_153   | 50S ribosomal protein L36  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00189    | InfA_2      | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | InfA_2              | TPPAVE_154   | Translation initiation factor IF-1   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.5. Translation factors                            |
|                | TPPER_00190    | secY        | Bacteria            | Betaproteobacteria  | Betaproteobacteria  | secY                | TPPAVE_155   | Protein translocase subunit SecY   | 2.3. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.3. Protein translocation and secretion  |   |   |
|                | TPPER_00191    | rplD        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rplD                | TPPAVE_156   | 50S ribosomal protein L15  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00192    | rpmD        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | rpmD                | TPPAVE_157   | 50S ribosomal protein L30  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00193    | rpsE        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rpsE                | TPPAVE_158   | 30S ribosomal protein S5   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00194    | rplR        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rplR                | TPPAVE_159   | 50S ribosomal protein L18  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00195    | rplF        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rplF                | TPPAVE_160   | 50S ribosomal protein L6   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00196    | rpsH        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rpsH                | TPPAVE_161   | 30S ribosomal protein S8   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00197    | rpsN        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rpsN                | TPPAVE_162   | 30S ribosomal protein S14  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00198    | rplE        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rplE                | TPPAVE_163   | 50S ribosomal protein L5   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00199    | rplN        | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  | rplN                | TPPAVE_164   | 50S ribosomal protein L14  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00200    | rpsQ        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rpsQ                | TPPAVE_165   | 30S ribosomal protein S17  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00201    | rplP        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rplP                | TPPAVE_166   | 50S ribosomal protein L16  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00202    | rpsC        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rpsC                | TPPAVE_167   | 30S ribosomal protein S3   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00203    | rplV        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rplV                | TPPAVE_168   | 50S ribosomal protein L22  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00204    | rpsS        | Bacteria            | Betaproteobacteria  | Betaproteobacteria  | rpsS                | TPPAVE_169   | 30S ribosomal protein S19  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00205    | rplB        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | rplB                | TPPAVE_170   | 50S ribosomal protein L2   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00206    | TPPER_00206 | Unknown             | Unknown             | Unknown             | TPPER_00206         | TPPAVE_171   | 5. POORLY CHARACTERIZED  | 5. POORLY CHARACTERIZED                         |   |   |   |
|                | TPPER_00207    | rplD        | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  | rplD                | TPPAVE_172   | 50S ribosomal protein L4   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00208    | rplC        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | rplC                | TPPAVE_173   | 50S ribosomal protein L3   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00209    | rplU        | Alphaproteobacteria | Betaproteobacteria  | Betaproteobacteria  | rplU                | TPPAVE_174   | 30S ribosomal protein S10  | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.3. Ribosomal proteins                             |
|                | TPPER_00210    | tufA        | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  | tufA                | TPPAVE_175   | Elongation factor Tu   | 1. INFORMATION STORAGE AND PROCESSING           | 1.2. RNA metabolism                       | 1.2.2. Translation                        | 1.2.2.5. Translation factors                            |
|                | TPPER_00211    | tusA</      |                     |                     |                     |                     |              |  |   |   |   |   |

|                |             |      |                     |                     |                     |
|----------------|-------------|------|---------------------|---------------------|---------------------|
|                | TPPER_00217 | rplJ | Proteobacteria      | Unknown             | Unknown             |
|                | TPPER_00218 | rplA | Bacteria            | Betaproteobacteria  | Betaproteobacteria  |
|                | TPPER_00219 | rplK | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  |
| TPPER_contig20 | TPPER_00224 | rplY | Proteobacteria      | Betaproteobacteria  | Betaproteobacteria  |
|                | TPPER_00225 | dnaJ | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  |
|                | TPPER_00226 | dnaK | Burkholderia        | Betaproteobacteria  | Betaproteobacteria  |
|                | TPPER_00227 | aroG | Burkholderiaceae    | Betaproteobacteria  | Betaproteobacteria  |
|                | TPPER_00228 | lipA | Betaproteobacteria  | Betaproteobacteria  | Betaproteobacteria  |
|                | TPPER_00229 | metE | Burkholderiales     | Betaproteobacteria  | Betaproteobacteria  |
| TPPER_contig21 | TPPER_00231 | aspS | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00233 | rImB | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00234 | cysJ | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00235 | cysI | Gammaproteobacteria | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00236 | cysH | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00240 | cysE | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00241 | lysS | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00243 | pnp  | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00245 | rsmD | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
|                | TPPER_00246 | aroK | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |
| TPPER_contig23 | TPPER_00247 | tsaB | Gammaproteobacteria | Unknown             | Gammaproteobacteria |
|                | TPPER_00248 | mmE  | Enterobacteriaceae  | Gammaproteobacteria | Gammaproteobacteria |

|      |            |  |   |   |                              |   |
|------|------------|--|---|---|------------------------------|---|
| rplJ | TPPAVE_181 | 50S ribosomal protein L10  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.3. Ribosomal proteins                             |
| rplA | TPPAVE_182 | 50S ribosomal protein L1   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.3. Ribosomal proteins                             |
| rplK | TPPAVE_183 | 50S ribosomal protein L11  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.3. Ribosomal proteins                             |
| rplY | TPPAVE_200 | 50S ribosomal protein L25  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.3. Ribosomal proteins                             |
| dnaJ | TPPAVE_026 | Chaperone protein DnaJ   | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.2. Chaperones                             |                              |   |
| dnaK | TPPAVE_027 | Chaperone protein DnaK   | 2. PROTEIN PROCESSING, FOLDING, AND SECRETION | 2.2. Chaperones                             |                              |   |
| aroG | TPPAVE_029 | Phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive                   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids            | 4.4.1. Aromatic amino acids  |   |
| lipA |            | Lipoyl synthase  | 4. METABOLISM                                 | 4.4. Biosynthesis of cofactors and vitamins | 4.8.3. Lipolate biosynthesis |   |
| metE | TPPAVE_031 | 5-methyltetrahydropteroyltryptolylglutamate-- homocysteine methyltransferase | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids            | 4.4.2. Aspartate family      |   |
| aspS | TPPAVE_206 | Aspartate-tRNA ligase  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
| rImB | TPPAVE_117 | 23S rRNA [guanosine-2'-O-]-methyltransferase RImB                            | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.4. Ribosome function, maturation and modification |
| cysJ |            | Sulfite reductase [NADPH] flavoprotein alpha-component                       | 4. METABOLISM                                 | 4.7. Sulfure metabolism                     |                              |   |
| cysI |            | Sulfite reductase [NADPH] hemoprotein beta-component                         | 4. METABOLISM                                 | 4.7. Sulfure metabolism                     |                              |   |
| cysH |            | Phosphoadenosine phosphosulfate reductase                                    | 4. METABOLISM                                 | 4.7. Sulfure metabolism                     |                              |   |
| cysE |            | Serine acetyltransferase   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids            | 4.4.6. Serine family         |   |
| lysS |            | lysine-tRNA ligase   | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.1. Aminoacyl-tRNA synthetases                     |
| pnp  |            | Polyribonucleotide nucleotidyltransferase                                    | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.3. RNA degradation       |   |
| rsmD | TPPAVE_201 | Ribosomal RNA small subunit methyltransferase D                              | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.4. Ribosome function, maturation and modification |
| aroK | TPPAVE_147 | Shikimate kinase 1   | 4. METABOLISM                                 | 4.4. Biosynthesis of amino acids            | 4.4.1. Aromatic amino acids  |   |
| tsaB |            | tRNA threonylcarbamoyladenosine biosynthesis protein TsaB                    | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.2. tRNA maturation and modification               |
| mmE  |            | tRNA modification GTPase MmmE  | 1. INFORMATION STORAGE AND PROCESSING         | 1.2. RNA metabolism                         | 1.2.2. Translation           | 1.2.2.2. tRNA maturation and modification               |