

Table S7. Differences in protein-coding genes between *T. phenacola* PPER and PAVE.
The beta or gamma origin of the PPER genes is indicated by background color (blue and orange, respectively).

| Function | gene name | PPER | PAVE | Product | COG | Presence in <i>T. princeps</i> (TP) genomes (Husnik et al., 2016) |
|--|-------------------|---------------------|---------------------------------------|---|-----|---|
| DNA metabolism | ligA | PROKKA_00108 | | DNA ligase | L | 0 |
| | dnaN | PROKKA_00085 | | DNA polymerase III subunit beta | L | All |
| | dnaX | | TPPAVE_135 | DNA polymerase III subunit tau | L | All |
| | ssb | | TPPAVE_136 | Single-stranded DNA-binding protein | L | present in most TP, pseudogenized in TPPLON and TPPCIT |
| Translation | alaS | PROKKA_00212 | | Alanine--tRNA ligase | J | 0 |
| | glyS | PROKKA_00009 | | Glycine--tRNA ligase beta subunit | J | 0 |
| | lysS | PROKKA_00022 | | Lysine--tRNA ligase | J | 0 |
| | map | PROKKA_00002 | | Methionine aminopeptidase | J | 0 |
| | mnmE | PROKKA_00077 | | tRNA modification GTPase MnmE | J | absent (TPMAR) or pseudogenized |
| | obg | PROKKA_00044 | | GTPase Obg | J | 0 |
| | pnp | PROKKA_00150 | | Polyribonucleotide nucleotidyltransferase | J | 0 |
| | rluD | PROKKA_00056 | | Ribosomal large subunit pseudouridine synthase D | J | 0 |
| | rplI | PROKKA_00147 | | 50S ribosomal protein L9 | J | All |
| | rpmH | PROKKA_00084.1 | | 50S ribosomal protein L34 | J | All |
| | trpS | PROKKA_00082 | | Tryptophan--tRNA ligase | J | 0 |
| | tsaB | PROKKA_00154 | | tRNA threonylcarbamoyladenosine biosynthesis protein TsaB | J | only in PCVAL (that does not have tsaD) |
| | tyrS | PROKKA_00067 | | Tyrosine--tRNA ligase | J | 0 |
| | ybeY | PROKKA_00046 | | Endoribonuclease YbeY | J | 0 |
| | gatA | | TPPAVE_193 | glutamyl-tRNA(Gln) amidotransferase, A subunit | J | All |
| | gatB | | TPPAVE_192 | glutamyl-tRNA(Gln) amidotransferase, B subunit | J | All |
| | miaA | | TPPAVE_025 | tRNA dimethylallyltransferase | J | 0 |
| | mnmA | | TPPAVE_030 | tRNA-specific 2-thiouridylase MnmA | J | absent or pseudogenized (TPFVIR, TPPLON, TPPCIT, TPTPER) |
| | rsmA | | TPPAVE_205 | Ribosomal RNA small subunit methyltransferase A | J | 0 |
| thrS | | TPPAVE_103 | Threonine--tRNA ligase | J | 0 | |
| Protein processing, folding, and secretion | lepB | PROKKA_00197 | | Signal peptidase I | N | 0 |
| | lon | PROKKA_00049 | | Lon protease | O | 0 |
| | secA | PROKKA_00034 | | Protein translocase subunit SecA | N | 0 |
| | secY | PROKKA_00163 | | Protein translocase subunit SecY | N | 0 |
| Carbohydrate metabolism | acnA | PROKKA_00106 | | Aconitate hydratase A | C | 0 |
| | lpdA | PROKKA_00051 | | Dihydrolipoyl dehydrogenase | C | All pseudogenized |
| | pykF ¹ | PROKKA_00070 | | Pyruvate kinase I | G | 0 |
| Biosynthesis of nucleotides | cmk | | TPPAVE_049 | Cytidylate kinase | F | 0 |
| | ndk ¹ | | TPPAVE_134 | Nucleoside diphosphate kinase | F | present in most TP, pseudogenized in TPPCIT, absent in TPMHIR |
| | prs | | TPPAVE_199 | Ribose-phosphate pyrophosphokinase | F | All |
| Biosynthesis of amino acids | cysE | PROKKA_00023 | | Serine acetyltransferase | E | 0 |
| | cysH | PROKKA_00027 | | Phosphoadenosine phosphosulfate reductase | E | 0 |
| | cysK | PROKKA_00112 | | Cysteine synthase A | E | 0 |
| | hom ² | PROKKA_00148 | | Homoserine dehydrogenase | E | 0 |
| | ilvI ³ | PROKKA_00006 | | Acetolactate synthase isozyme 3 large subunit | E | 0 |
| | aroE | | TPPAVE_125 | Shikimate dehydrogenase (NADP(+)) | E | 0 |
| | ilvB ³ | | TPPAVE_060 | Acetolactate synthase isozyme 1 large subunit | E | All |
| | thrA ² | | TPPAVE_113 | Bifunctional aspartokinase/homoserine dehydrogenase 1 | E | All |
| trpF | | TPPAVE_005 | Tryptophan biosynthesis protein TrpCF | E | 0 | |
| Sulfure metabolism | cysI | PROKKA_00028 | | Sulfite reductase [NADPH] hemoprotein beta-component | P | 0 |
| | cysJ | PROKKA_00029 | | Sulfite reductase [NADPH] flavoprotein alpha-component | P | 0 |
| Coenzyme metabolism | cysG | PROKKA_00073 and 74 | | Siroheme synthase | H | 0 |
| | lipA | PROKKA_00137 | | Lipoyl synthase | H | 0 |
| | panB | PROKKA_00213 | | 3-methyl-2-oxobutanoate hydroxymethyltransferase | H | 0 |
| Energy metabolism | trxA | PROKKA_00080 | | Thioredoxin-1 | O | 0 |
| | ahpC | | TPPAVE_124 | Alkyl hydroperoxide reductase subunit C | O | 0 |