## Additional file 7 – Sequence analysis of prophage 04 of *P. fluorescens* Pf-5

| CDS | Gene name | Position | Protein length (residues) | Protein mol weight (kDa) | Putative ribosome binding site | Closest protein of phage or plasmid origin (accession no.), blastp E-value [a] | Other similar proteins (accession no.), blastP E-value [a] | Predicted function (functional domains) |
|---|---|---|---|---|---|---|---|---|
| PFL_2119 | tRNA-Pro *(attL)* | 2338296..2338372 | CGGGGCGTAGCGCAGTCCGGTAGCGCACTAGCATGGGGTGCTAGGGGTCGAGTGTTCGAATCACTCCGTCCCGACCA | | | | | |
| 1[b] | *int3* | 2338455..2339156 (-) | 233 | 26.312 | GTGG | Phage integrase from *Shigella flexneri* phage SfX (AAD10295); $2e^{-06}$ | Putative integrase PputGB1_3473 from *Pseudomonas putida* GB-1 (ABY99364), $8e^{-99}$ | Phage integrase |
| 2[b] | *orf2* | 2339231..2339893 | 220 | 24.660 | GGCG | Putative replication protein SfVp39 from *Shigella flexneri* bacteriophage V (NP_599071); $4e^{-05}$ | None detected | Putative phage related conserved protein |
| PFL_2120 | PFL_2120 | 2339491..2339670 | 59 | 6.438 | GTGAA | None detected | Hypothetical protein PFL_3776 from *Pseudomonas fluorescens* Pf-5 (AAY93041), 7e-22 | Conserved hypothetical protein |
| PFL_2121 | PFL_2121 | 2339919..2340170 | 83 | 9.154 | GTGAG | Phage protein Orf84 from *Pseudomonas aeruginosa* phage D3 (NP_061580); $1e^{-09}$ | Hypothetical protein PFL_3772 from *Pseudomonas fluorescens* Pf-5 (AAY93037), 6e-36 | Conserved phage related protein |
| 3[bc] | *orf3* | 2341690..2342074 | 77 | 8.460 | GAGG | L-shaped tail fiber protein of *E.coli* bacteriophage T5 (P13390), $7e^{-12}$ | None detected | Tail fiber protein |
| 4[b] | *orf4* | 2342156..2343202 | 348 | 38.797 | AGGA | None detected | Putative acyltransferase PTD2_11199 from *Pseudoalteromonas tunicata* D2 (EAR29378); $6e^{-19}$ | Putative acyltransferase (COG1835) |
| PFL_2122[d] | PFL_2122 | 2342156..2344091 | 283 | 31.778 | TAAG | Putative minor phage tail protein L from *Burkholderia pseudomallei* phage | Hypothetical protein PFL_3749 from *Pseudomonas fluorescens* Pf-5 (AAY93014), 2e-48 | Putative minor tail protein similar to lambda protein L |

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|---|---|---|---|---|---|---|---|---|
| | | | | | | phi1026b (NP_945047); $5e^{-29}$ | | (COG4672) |
| PFL_2123 | PFL_2123 | 2344115..2344513 | 132 | 15.082 | CAAG | Tail component protein gp19 of *Burkholderia thailandensis* phage phiE125 (NP_536375), $5e^{-19}$ | Hypothetical protein PFL_3749 from *Pseudomonas fluorescens* Pf-5 (AAY93014), 4e-57 | Conserved phage related protein |
| 5[b] | *orf5* | 2344589..2345038 | 149 | 16.397 | AGGAA | None detected | None detected | Hypothetical protein |
| 6[b] | *orf6* | 2345493..2346008 | 171 | 18.287 | GGGCG | Putative protein gp80 from *Burkholderia* phage Bcep22 (AAQ55012); 6e-06 | Hypothetical protein PFL_2019 from *Pseudomonas fluorescens* Pf-5 (AAY91305), 3e-31 | Putative phage protein |
| 7[b] | *orf7* | 2346162..2346701 (-) | 179 | 18.591 | GAGG | None detected | Conserved hypothetical protein XCC3128 from *Xanthomonas campestris* pv. *campestris* ATCC 33913 (NP_638475), $1e^{-26}$ | Conserved hypothetical protein |
| PFL_2124 | PFL_2124 | 2347171..2347848 (-) | 225 | 25.124 | AGGGG | None detected | Hypothetical protein PFL_3740 from *Pseudomonas fluorescens* Pf-5 (AAY93005), 5e-108 | Conserved hypothetical protein (COG2135) |
| 8[b] | *orf8* | 2347920..2348480 (-) | 186 | 21.430 | GAGG | None detected | Putative ATP-dependent DNA ligase PflO1_2097 from *Pseudomonas fluorescens* PfO-1 (ABA73840); $3e^{-61}$ | Putative ATP-dependent DNA ligase |
| 9[bc] | *orf9* | 2348722..2348895 | 57 | 6.244 | na | None detected | Hypothetical protein PFL_2878 from *Pseudomonas fluorescens* Pf-5 (AAY92150), 4e-06 | Putative cell wall glycosyltransferase (COG0463) |
| PFL_2125 | PFL_2125 | 2349053..2349262 (-) | 69 | 7.647 | GAGG | None detected | Hypothetical protein | Hypothetical protein |
| PFL_2126 | PFL_2126 | 2349714..2350442 (-) | 242 | 27.075 | CTGG | Pyocin regulator PrtR from *Pseudomonas aeruginosa* (Q06553); $3e^{-50}$ | Hypothetical protein PFL_3780 from *Pseudomonas fluorescens* Pf-5 (AAY93045), 3e-80 | Cro/C1-type repressor protein (COG2932) |

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|---|---|---|---|---|---|---|---|---|
| 10[b] | *orf10* | 2350540..2350722 | 60 | 6.480 | GGCAG | None detected | Hypothetical protein PFL_3780 from *Pseudomonas fluorescens* Pf-5 (AAY93045), 3e-80 | Conserved hypothetical protein |
| PFL_2127 | *llpA1* | 2350955..2351797 | 280 | 31.104 | AGGT | None detected | Putidacin PFL_1229 from *Pseudomonas fluorescens* Pf-5 (AAY90516), 2e-155 | Bacteriocin putidacin L1 |

[a] Only expectation values of 1e$^{-05}$ and below were considered as significant matches during BLAST database searches; [b] open reading frame(s) not present in the original genome annotation; [c] part of a longer open reading frame with internal frameshifts; [d] open reading frame has an alternative start site.