Table S1. Bacteria strains used in the isolation and the testing of host range of *Pectobacterium* phages CB5

|  |  |  |
| --- | --- | --- |
| **Bacteria** | **Strain** | **Isolation source** |
| *Pectobacterium atrosepticum* | DSM 18077 (type strain) | Potato (*Solanum tuberosum*) |
| DSM 30184 | Potato (*Solanum tuberosum* cv. Bodenkraft) |
| DSM 30185 | Potato (*Solanum tuberosum*) |
| DSM 30186 | Potato (*Solanum tuberosum* cv. Maritta) |
| CB BL1-1 | *Solanum tuberosum* cv. British Queen |
| CB BL2-1 | Solanum tuberosum cv. British Queen |
| CB BL3-1 | *Solanum tuberosum* cv. British Queen |
| CB BL4-1 | *Solanum tuberosum* cv. British Queen |
| CB BL5-1 | Solanum tuberosum cv. British Queen |
| CB BL7-1 | Solanum tuberosum cv. Golden wonder |
| CB BL9-1 | Solanum tuberosum cv. Golden wonder |
| CB BL11-1 | *Solanum tuberosum cv.* Rooster |
| CB BL12-2 | *Solanum tuberosum* cv. Golden wonder |
| CB BL13-1 | *Solanum tuberosum* cv. Golden wonder |
| CB BL14-1 | *Solanum tuberosum* cv. Golden wonder |
| CB BL15-1 | *Solanum tuberosum* cv. Golden wonder |
| CB BL16-1 | *Solanum tuberosum* cv. Golden wonder |
| CB BL18-1 | *Solanum tuberosum* cv. Golden wonder |
| CB BL19-1 | *Solanum tuberosum* cv. Golden wonder |
| *Pectobacterium carotovorum subsp. carotovorum* | DSMZ 30168 (type strain) | Potato (*Solanum tuberosum*) |
| DSMZ 30169 | *Brassica oleracea* var.*capitata* |
| DSMZ 30170 | Potato (*Solanum tuberosum* "Maritta") |
| CB BL19-1-37 | *Solanum tuberosum* cv. Golden wonder |
| *Dickeya chrysanthemi bv chrysanthemi* | LMG 2804 (type strain) | *Chrysanthemum* |
| *Dickeya dianthicola* | PD 482 | *Solanum tuberosum* cv. Ostara |
| PD 2174 | - |
| GBBC 1538 | - |
| *Dickeya solani* | sp. PRI 2222 | - |
| LMG 25865 | *Solanum tuberosum* cv. Première |
| GBBC 1502 | - |
| GBBC 1586 | - |

Table S2 – Details of proteins used in the phylogenetic analysis of 52 phages from the subfamily *Autographivirinae* and *Pectobacterium* phage CB5

|  |  |  |
| --- | --- | --- |
| **Phage** | **Genome accession no.** | **Major capsid accession no.** |
| Acinetobacter phage Abp1 | NC\_021316.1 | YP\_008058231.1 |
| Acinetobacter phage Fri1 | NC\_028848.1 | YP\_009203047.1 |
| Acinetobacter phage Petty | NC\_023570.1 | YP\_009006529.1 |
| Acinetobacter phage phiAB1 | NC\_028675.1 | YP\_009189372.1 |
| Acinetobacter phage vB\_ApiP\_P2 | MF033351.1 | ASN73550.1 |
| Aeromonas phage phiAS7 | NC\_019528.1 | YP\_007007808.1 |
| Cronobacter phage vB\_CskP\_GAP227 | NC\_020078.1 | YP\_007348355.1 |
| Dickeya phage BF25/12 | KT240186.1 | ALA46504.1 |
| Enterobacteria phage J8-65 | NC\_025445.1 | YP\_009101383.1 |
| Enterobacteria phage K30 | NC\_015719.1 | YP\_004678755.1 |
| Enterobacteria phage T7 | NC\_001604.1 | NP\_041997.1 |
| Erwinia amylovora phage Era103 | NC\_009014.1 | YP\_001039668.1 |
| Escherichia phage phiKT | NC\_019520.1 | YP\_007006600.1 |
| Escherichia virus K1-5 | NC\_008152.1 | YP\_654132.1 31 |
| Escherichia virus K1E | NC\_007637.1 | YP\_425009.1 |
| Klebsiella phage F19 | NC\_023567.2 | YP\_009006057.1 |
| Klebsiella phage K11 | NC\_011043.1 | YP\_002003823.1 |
| Klebsiella phage KP32 | NC\_013647.1 | YP\_003347548.1 |
| Klebsiella phage KP34 | NC\_013649.2 | YP\_003347636.1 |
| Klebsiella phage NTUH-K2044-K1-1 | NC\_025418.1 | YP\_009098373.1 |
| Klebsiella phage vB\_KpnP\_SU503 | NC\_028816.1 | YP\_009199922.1 |
| Klebsiella phage vB\_KpnP\_SU552A | NC\_028870.1 | YP\_009204828.1 |
| Kluyvera phage Kvp1 | FJ194439.1 | ACJ14590.1 |
| Pantoea phage LIMElight | NC\_019454.1 | YP\_007002894.1 |
| Pantoea phage LIMEzero | NC\_015585.1 | YP\_004539113.1 |
| Pectobacterium phage PhiM1 | JX290549.1 | AFQ22523.1 |
| Pectobacterium phage PP16 | NC\_031068.1 | YP\_009286812.1 |
| Pectobacterium phage PP90 | NC\_031096.1 | YP\_009289647.1 |
| Pectobacterium phage PPWS1 | LC063634.2 | BAS69556.1 |
| Pectobacterium\_phage\_Peat1 | NC\_029081.1 | YP\_009224669.1+YP\_009224670.1 |
| Pseudomonad phage gh-1 | AF493143.1 | AAO73167.1 |
| Pseudomonas phage Bf7 | NC\_016764.1 | YP\_005098192.1 |
| Pseudomonas phage LKA1 | NC\_009936.1 | YP\_001522884.1 |
| Pseudomonas phage LKD16 | NC\_009935.1 | YP\_001522824.1 |
| Pseudomonas phage LUZ19 | NC\_010326.1 | YP\_001671977.1 |
| Pseudomonas phage MPK6 | NC\_022746.1 | YP\_008766800.1 |
| Pseudomonas phage MPK7 | NC\_022091.1 | YP\_008431345.1 |
| Pseudomonas phage phi-2 | NC\_013638.1 | YP\_003345495.1 |
| Pseudomonas phage phikF77 | NC\_012418.1 | YP\_002727855.1 |
| Pseudomonas phage phiKMV | NC\_005045 | NP\_877471.1 |
| Pseudomonas phage PT2 | NC\_011107.1 | YP\_002117817.1 |
| Pseudomonas phage PT5 | EU056923.1 | ABW23115.1 |
| Ralstonia phage RSB1 | NC\_011201.1 | YP\_002213721.1 |
| Ralstonia phage RSB3 | NC\_022917.1 | YP\_008853924.1 |
| Ralstonia virus phiAp1 | KY117485.1 | APU03181.1 |
| Salmonella phage SP6 | NC\_004831.2 | NP\_853592.1 |
| Vibrio phage VP93 | NC\_012662 | YP\_002875653.1 |
| Xanthomonas phage f20-Xaj | KU595432.1 | AMM44667.1 |
| Xanthomonas phage f30-Xaj | KU595433.1 | AMM44714.1 |
| Xylella phage Prado | NC\_022987.1 | YP\_008859419.1 |
| Yersinia phage phi80-18 | HE956710.2 | CCI88880.2 |
| Yersinia phage phiR8-01 | HE956707.2 | CCI88417.2 |
| Pectobacterium phage vB\_Pat\_CB5 | KY953156 | ARW59018 |

Table S4.Taxonomy output from VICTOR analysis of 52 phages from the subfamily *Autographivirinae* and *Pectobacterium* phage CB5, OPTSIL clustering of taxon boundaries based on the D4 formula at genus and subfamily level. Numbers represent the genus and subfamily which phages have been allocated.

|  |  |  |
| --- | --- | --- |
| **Phage** | **genus** | **subfamily** |
| Enterobacteria phage SP6 (NC\_004831) | 1 | 1 |
| Escherichia virus K1E (NC\_007637) | 1 | 1 |
| Escherichia virus K1-5 (NC\_008152) | 1 | 1 |
| Erwinia amylovora phage Era103 (NC\_009014) | 1 | 1 |
| Pseudomonad phage gh-1 (AF493143) | 3 | 2 |
| Kluyvera phage Kvp1 (FJ194439) | 3 | 2 |
| Enterobacteria phage T7 (NC\_001604) | 3 | 2 |
| Klebsiella phage K11 (NC\_011043) | 3 | 2 |
| Klebsiella phage KP32 (NC\_013647) | 3 | 2 |
| Escherichia phage K30 (NC\_015719) | 3 | 2 |
| Ralstonia phage RSB1 (NC\_011201) | 2 | 3 |
| Pseudomonas phage Bf7 (NC\_016764) | 4 | 3 |
| Escherichia phage phiKT (NC\_019520) | 5 | 3 |
| Yersinia phage phiR8-01 (HE956707) | 6 | 3 |
| Yersinia phage phi80-18 (HE956710) | 6 | 3 |
| Aeromonas phage phiAS7 (NC\_019528) | 6 | 3 |
| Cronobacter phage vB\_CskP\_GAP227 (NC\_020078) | 6 | 3 |
| Xanthomonas phage f20-Xaj (KU595432) | 9 | 3 |
| Xanthomonas phage f30-Xaj (KU595433) | 9 | 3 |
| Xylella phage Prado (NC\_022987) | 9 | 3 |
| Pseudomonas phage PT5 (EU056923) | 7 | 4 |
| Pseudomonas phage phiKMV (NC\_005045) | 7 | 4 |
| Pseudomonas phage LKD16 (NC\_009935) | 7 | 4 |
| Pseudomonas phage LKA1 (NC\_009936) | 7 | 4 |
| Pseudomonas phage LUZ19 (NC\_010326) | 7 | 4 |
| Pseudomonas phage PT2 (NC\_011107) | 7 | 4 |
| Pseudomonas phage phikF77 (NC\_012418) | 7 | 4 |
| Pseudomonas phage phi-2 (NC\_013638) | 7 | 4 |
| Pseudomonas phage MPK7 (NC\_022091) | 7 | 4 |
| Pseudomonas phage MPK6 (NC\_022746) | 7 | 4 |
| Ralstonia virus phiAp1 (KY117485) | 8 | 4 |
| Ralstonia phage RSB3 (NC\_022917) | 8 | 4 |
| Pantoea phage LIMEzero (NC\_015585) | 10 | 4 |
| Enterobacteria phage J8-65 (NC\_025445) | 10 | 4 |
| Acinetobacter phage vB\_ApiP\_P2 (MF033351) | 11 | 4 |
| Acinetobacter phage Abp1 (NC\_021316) | 11 | 4 |
| Acinetobacter phage Petty (NC\_023570) | 11 | 4 |
| Acinetobacter phage phiAB1 (NC\_028675) | 11 | 4 |
| Acinetobacter phage Fri1 (NC\_028848) | 11 | 4 |
| Vibrio phage VP93 (NC\_012662) | 12 | 4 |
| Klebsiella phage KP34 (NC\_013649) | 12 | 4 |
| Pantoea phage LIMElight (NC\_019454) | 12 | 4 |
| Klebsiella phage F19 (NC\_023567) | 12 | 4 |
| Klebsiella phage NTUH-K2044-K1-1 (NC\_025418) | 12 | 4 |
| Klebsiella phage vB\_KpnP\_SU503 (NC\_028816) | 12 | 4 |
| Klebsiella phage vB\_KpnP\_SU552A (NC\_028870) | 12 | 4 |
| Pectobacterium phage PhiM1 (JX290549) | 13 | 4 |
| Dickeya phage BF25/12 (KT240186) | 13 | 4 |
| Pectobacterium phage PPWS1 (LC063634) | 13 | 4 |
| Pectobacterium phage Peat1 (NC\_029081) | 13 | 4 |
| Pectobacterium phage PP16 (NC\_031068) | 13 | 4 |
| Pectobacterium phage PP90 (NC\_031096) | 13 | 4 |
| Pectobacterium phage CB5 (KY953156) | 13 | 4 |

Table S5. Shared early region ORFs between PhiM1-like phages as determined by CoreGenes

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| no. | Early gene region | Peat1 | CB5 | phiM1 | PP90 |
| 1 | hypothetical protein | AXI77\_gp61 | CB5\_3 | PhiM1\_03 | PP90\_2 |
| 2 | hypothetical protein | AXI77\_gp01 | CB5\_6 | PhiM1\_04 | PP90\_3 |
| 3 | hypothetical protein | AXI77\_gp07 | CB5\_12 | PhiM1\_08 | PP90\_7 |
| 4 | hypothetical protein | AXI77\_gp08 | CB5\_13 | PhiM1\_09 | PP90\_8 |
| 5 | peptidase | AXI77\_gp09 | CB5\_15 | PhiM1\_10 | PP90\_9 |
| 6 | hypothetical protein | AXI77\_gp10 | CB5\_16 | PhiM1\_11 | PP90\_10 |

Table S6. Proteins of PhiM1-like phage involved in DNA replication, repair and related metabolism

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **no.** | **DNA replication & nucleotide metabolism** | **Peat1** | **CB5** | **phiM1** | **PP90** |
| 1 | DNA primase | AXI77\_gp12 + AXI77\_gp13 | CB5\_18 | PhiM1\_12 | PP90\_12 |
| 2 | DNA helicase | AXI77\_gp17 | CB5\_22 | PhiM1\_14 | PP90\_15 |
| 3 | DNA polymerase | AXI77\_gp21 | CB5\_28 | PhiM1\_14 | PP90\_21 |
| 4 | 5' exonuclease | AXI77\_gp23 | CB5\_31 | PhiM1\_22 | PP90\_24 |
| 5 | endonuclease VII | AXI77\_gp25 | CB5\_34 | PhiM1\_25 | PP90\_27 |
| 6 | DNA dependent RNA polymerase | AXI77\_gp30 | CB5\_39 | PhiM1\_31 | PP90\_32 |
| 7 | 5' kinase / 3'phosphatase | \_ | \_ | PhiM1\_28 | PP90\_29 |
| 8 | nucleatidyl transferase | \_ | CB5\_24 | \_ | \_ |

Table S7. Structural proteins of the PhiM1-like phages

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **no.** | **Structural protein** | **Peat1** | **CB5** | **phiM1** | **PP90** |
| 1 | head tail connector | AXI77\_gp34 | CB5\_44 | PhiM1\_35 | PP90\_38 |
| 2 | scaffolding protein | AXI77\_gp37 | CB5\_45 | PhiM1\_36 | PP90\_40 +PP90\_41 |
| 3 | major capsid | AXI77\_gp38+AXI77\_gp39 | CB5\_46 | PhiM1\_38 | PP90\_43 |
| 4 | tubular protein A | AXI77\_gp41+AXI77\_gp42 | CB5\_47 | PhiM1\_39 | PP90\_44 |
| 5 | tubular protein B | AXI77\_gp43 | CB5\_49 | PhiM1\_40 | PP90\_45 |
| 6 | internal virion protein A | AXI77\_gp44 | CB5\_50 | PhiM1\_41 | PP90\_46 |
| 7 | internal virion protein B | AXI77\_gp45 | CB5\_51 | PhiM1\_42 | PP90\_47 |
| 8 | internal virion protein C | AXI77\_gp46+AXI77\_gp47 | CB5\_52 | PhiM1\_43 | PP90\_48 |
| 9 | tail fibre | AXI77\_gp48 | CB5\_53 | PhiM1\_44 | PP90\_49 |
| 10 | large terminase | AXI77\_gp50 | CB5\_54 | PhiM1\_45 | PP90\_50 |
| 11 | small terminase | AXI77\_gp51 | CB5\_55 | PhiM1\_46 | PP90\_51 |
| 12 | tail spike | AXI77\_gp57 | CB5\_60 | PhiM1\_52 | PP90\_56 |

Table S8. Proteins of lysis cassette of the PhiM1-like phages

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **no.** | **Lysis protein** | **Peat1** | **CB5** | **phiM1** | **PP90** |
| 1 | U-spanin | AXI77\_gp54 | CB5\_57 | PhiM1\_49 | PP90\_53 |
| 2 | Holin | AXI77\_gp55 | CB5\_58 | PhiM1\_50 | PP90\_54 |
| 3 | Endolsyin | AXI77\_gp56 | CB5\_59 | PhiM1\_51 | PP90\_55 |



Figure S1. *Pectobacterium* phage CB5 plaque morphology on 0.4% w/v LB overlay using host strain *P. atrosepticum* DSM 30186 (12 hr incubation).

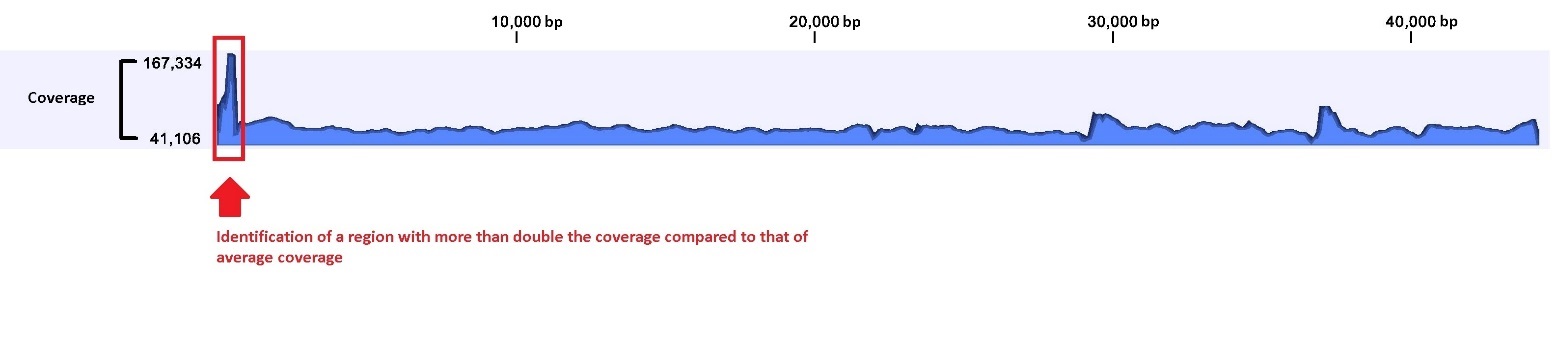
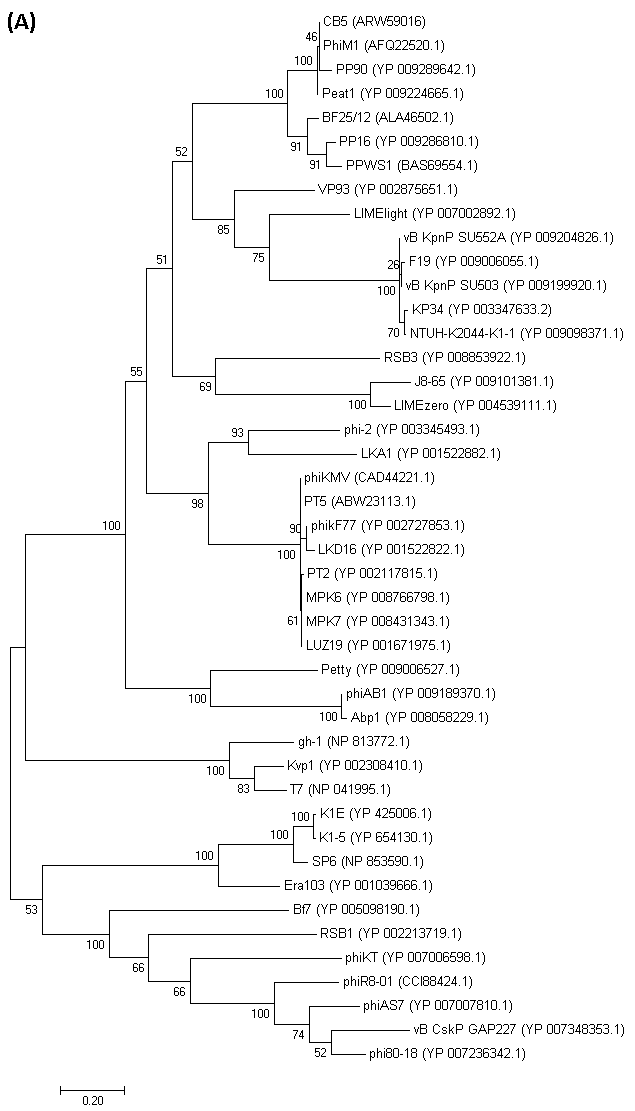
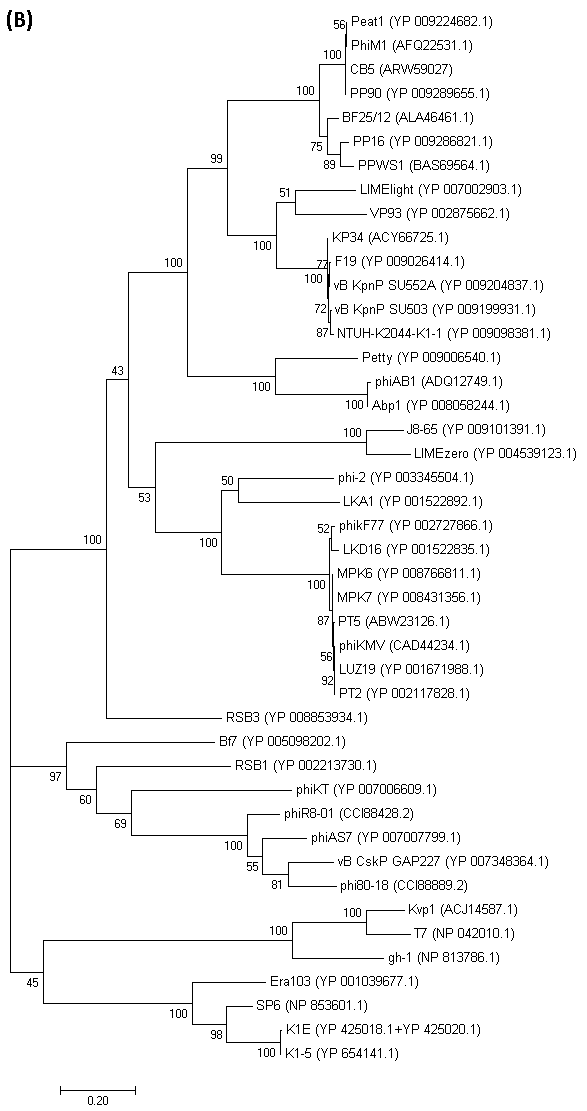
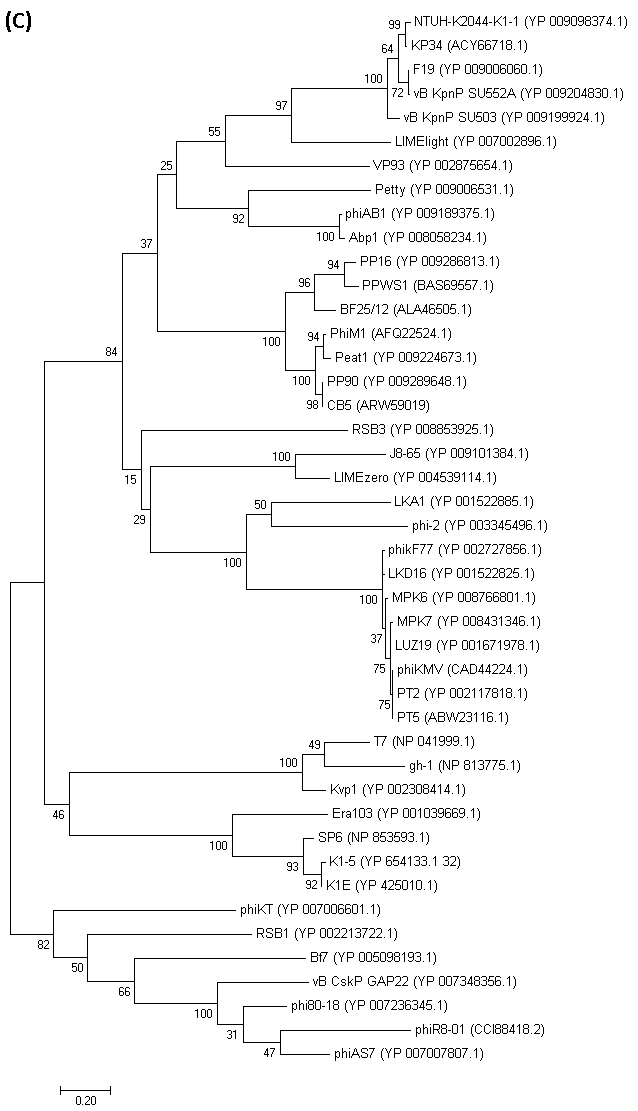


Figure S2. Coverage map showing the distribution of reads when mapped back to the contig representing the genome of *Pectobacterium* phage CB5 obtained from genome assembly. Map created with CLC Genomics Workbench.







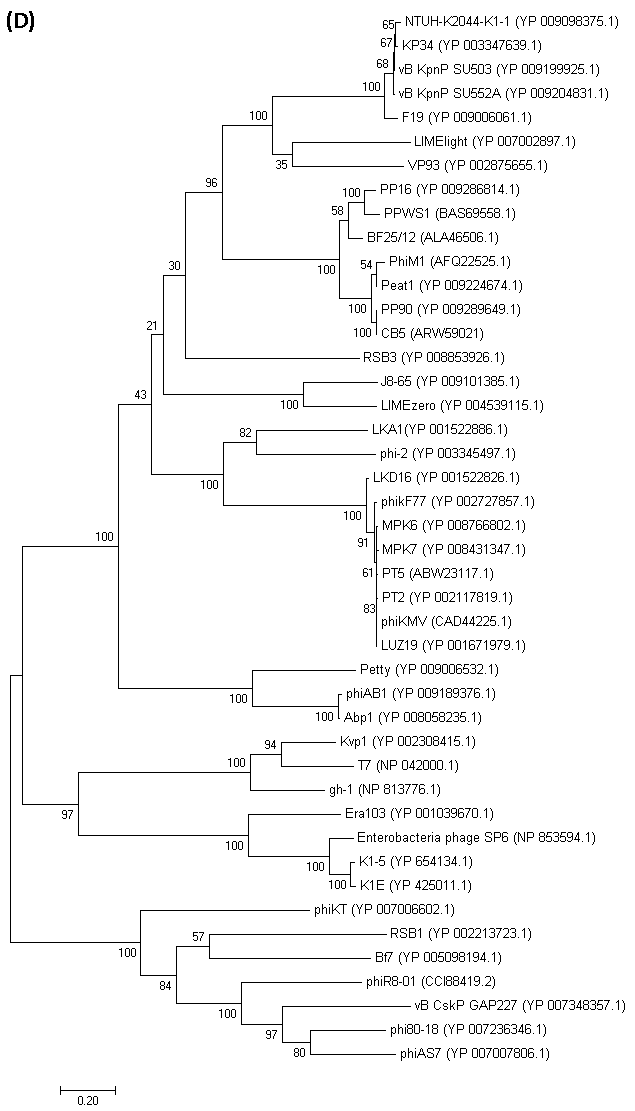


Figure S3. Phylogenetic analyses of amino sequences of the head-tail connecting protein (A), terminase (B), tail tube protein A (C) and tail tube protein B (D) of *Pectobacterium* phage CB5 and 52 members of the *Autographivirinae* subfamily, using maximum likelihood (Whelan and Goldman substitution model), with 100 bootstrap replicates.