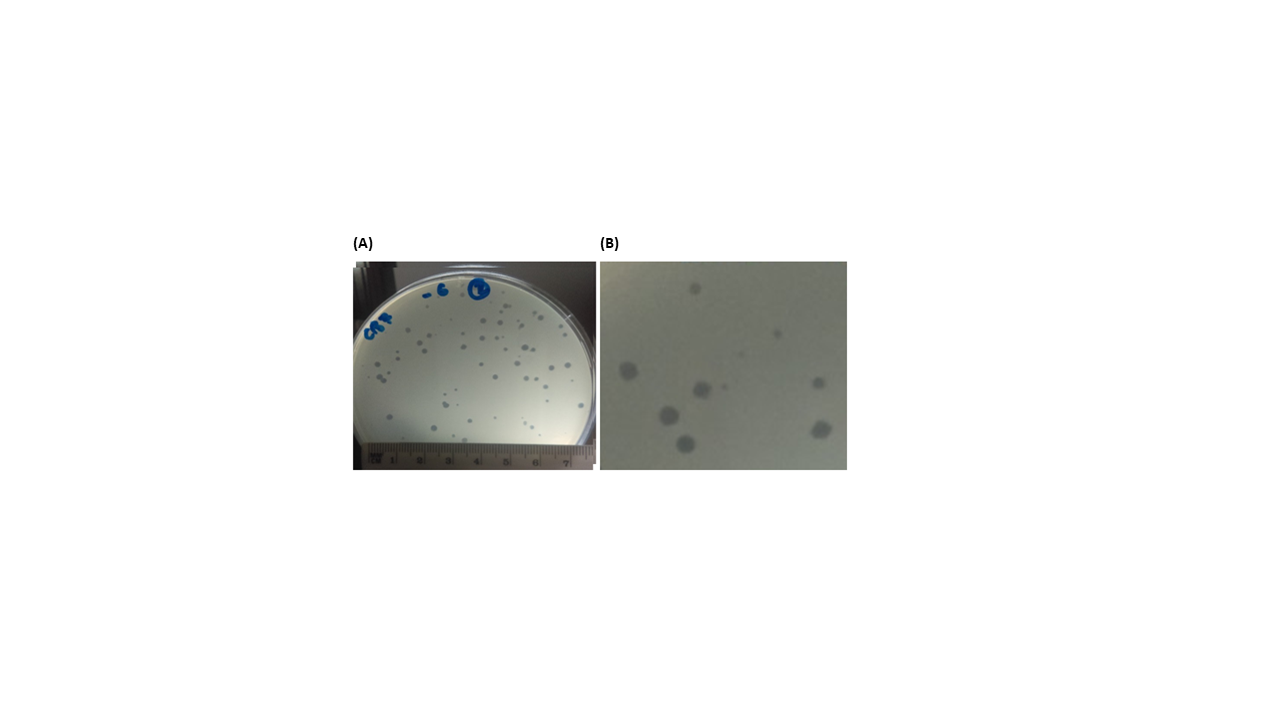


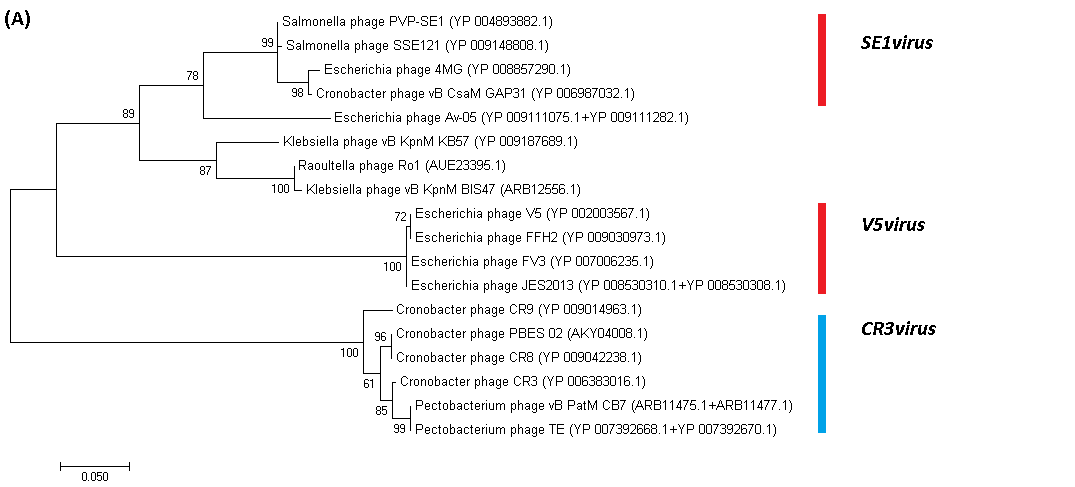
**Figure S1.** Genomic DNA of *Pectobacterium* phage CB7 digested with restriction enzyme BglII (A) and SspI (B). Lane 1; DNA marker (Hyperladder 1kb, Bioline), Lane 2; undigested CB7 genomic DNA, Lanes 3 and 4; digestion of CB7 genomic DNA with BglII and SspI respectively. The gel concentration was 0.8 % (w/v).

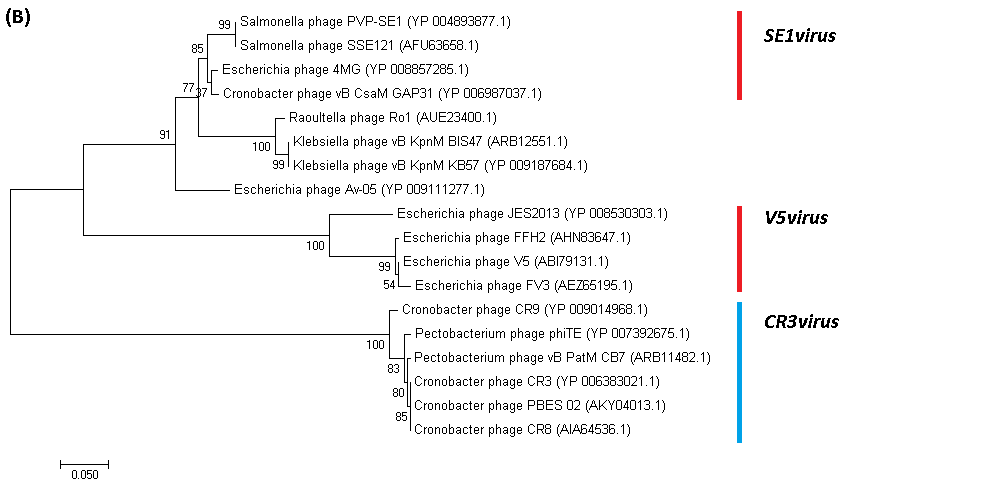


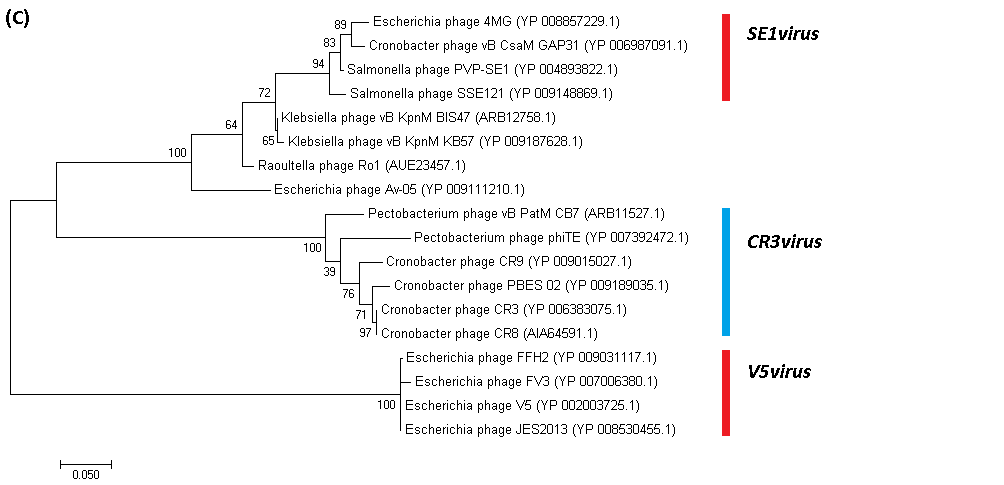
**Figure S2.**(A) Plaque assay with *Pectobacterium* phage CB7 against host strain *P. atrosepticum* DSM 30186 after 12-hours of incubation on 0.4% w/v LB overlay and (B) typical plaque morphology.

C:\Users\Colin\Desktop\fix 2.tif

**Figure S3.** Treatment of *Pectobacterium* phage CB7 genomic DNA with BAL-31 for 60 minutes (Lane 1), 80 minutes (Lane 2), 100 minutes (lane 3), 120 minutes (Lane 4), 140 minutes (Lane 4), 160 minutes (Lane 5), 180 minutes (Lane 6) and (Lane 7) 200 minutes followed with restriction digestion with BglII Molecular weight marker (Hyperladder 1kb, Bioline) (lane 8). Gel concentration 1% (w/v) agarose.

****





**Figure S4.** Phylograms constructed using the large terminase (A), major head (B) and DNA polymerase (C) of *Pectobacterium* phage CB7 and homologs of 17 phages of the *Vequintavirinae* subfamily, analysed using maximum likelihood (Whelan and Goldman substitution model), with 1000 bootstrap replicates, using MEGA7.

**Table S2.** Putative sigma70–like promoter sequences detected in the genome of *Pectobacterium* phage CB7.

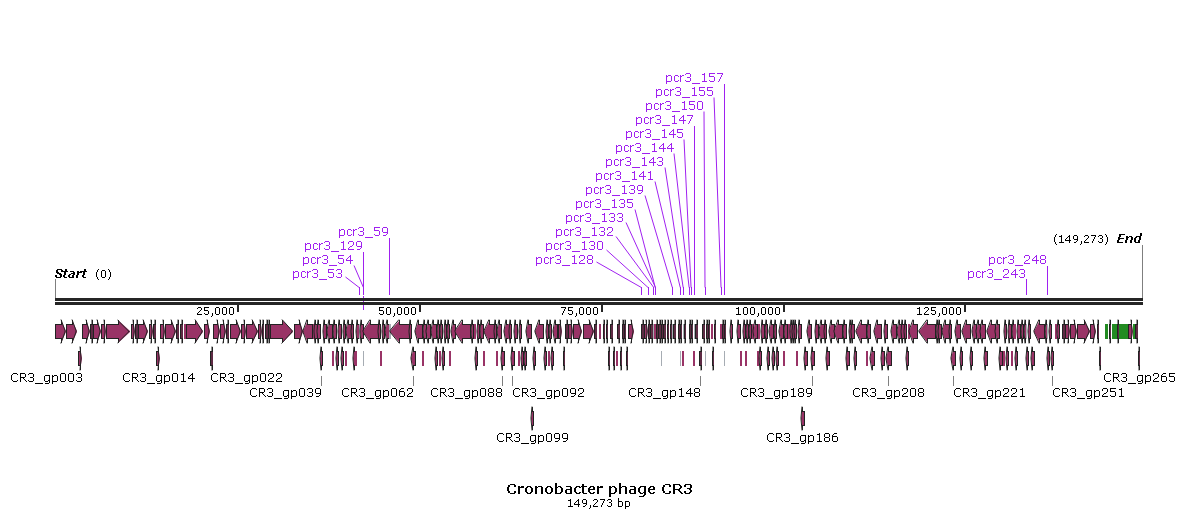


|  |  |  |  |
| --- | --- | --- | --- |
| **Promoter** | **Start** | **Stop** | **Sequence** |
| Porf56 | 45103 | 45065 | TACAACATTGTTGTCGCCAAAGGCGGGGACCGCAATAAC |
| Porf79 | 54853 | 54815 | GACATTATTGTTGACCAAGGTGTCCGTAAGTTCTATCAT |
| Porf97 | 62188 | 62188 | TAAAATTCGGTTGACAGTAGAGATCGGGGCCTGTAATAT |
| Porf125 | 76101 | 76139 | AAATCATTTGTTGACAACCTGGCCGGGCCGGGCCACAAT |
| Porf126 | 76489 | 76527 | TAAATAGTTGTTGACACCGGGGCCACGTGGCCCCATACT |
| Porf128 | 77200 | 77238 | GTTTTAGGGGTTGACGCCCGGCGGCGTTACCCCCATAAT |
| Porf129 | 77,776 | 77814 | AAAATAATTGTTGACGCCGGGCACCGTCCCGGCATACAA |
| Porf131 | 78811 | 78849 | AAAATAGTTGTTGACTCTTGCCCCGTCCCGCTGGCATAA |
| Porf135 | 80067 | 80105 | AAAAAGGGGCTTGACGTTGTGAAACGTTAGGCCCTATAA |
| Porf136 | 80590 | 80628 | AAAATAAAAGTTGACACCGGGGCCACCTGGCCCCATAAT |
| Porf138 | 81288 | 81326 | GAAAATAAACTTGACGCCGGGACGGTTCCCGGCTTATAA |
| Porf139 | 81536 | 81574 | AAAATAAATGTTGACGCCGGGCACCGTCCCGGCTATACT |
| Porf140 | 82045 | 82083 | AAAAATTAGTTTGACACCCGGCCCGGAGGGGCCGATAAT |

**Table S3.** Putative sigma70-like promoters detected in the genome of *Cronobacter* phage CR3 (accession no. JQ691612).



|  |  |  |  |
| --- | --- | --- | --- |
| **Promoter** | **Start** | **Stop** | **Sequence** |
| pcr3\_53 | 41845 | 41810 | AAAATTGTTGACTTCCTTCCTGATTTCCCGCATAAT |
| pcr3\_54 | 42349 | 42314 | TTTTTAATTGACAGCGGGGCCGAAAGGCCCCATAAT |
| pcr3\_59 | 45981 | 45946 | AAAATTCTTGTATTCCGGGGGCTTCGGCCCCTTTTC |
| pcr3\_128 | 80533 | 80568 | ATTTTTCTTGACCTGCCAGGCAAGCCGGGCCACAAT |
| pcr3\_129 | 80932 | 80967 | ATAATGCTTGACGGGGCCAGCGATAGGCCCCATAAT |
| pcr3\_130 | 81471 | 81506 | AAGAGTATTGACACCGGGGCCACCTGGCCCCATACT |
| pcr3\_132 | 82181 | 82216 | TTTGGGGTTGACGCCCGGCCAGGATGGGTCCATAAT |
| pcr3\_133 | 82513 | 82548 | ATAATTGTTGACCGGGGCCGGGTTAGGCCCCATAAT |
| pcr3\_135 | 91606 | 91571 | TCTTTTGTTGACACCGGGGCCGATAGGCCCCATAAT |
| pcr3\_135 | 83275 | 83310 | ATTTTGGTTGACACGGGGCCGGGTTAGGCCCCATAA |
| pcr3\_139 | 84806 | 84841 | AAGGGGCTTGACGTCGTGAAACGTTAGGCCCTATAA |
| pcr3\_141 | 85882 | 85917 | AAAGCGCTTGACGCCGGGACGGTTCCCGGCTTATAA |
| pcr3\_143 | 86335 | 86370 | ATAATTCTTGACGCCGGGCACCGTCCCGGCTTACAA |
| pcr3\_144 | 87078 | 87113 | TAAATGATTGACATCCGGCCCGAAAGGGCCGATAAT |
| pcr3\_145 | 87356 | 87391 | AAAGTAGTTGACGGCGGGGCCGATAGGCCCCATAAT |
| pcr3\_147 | 87898 | 87933 | ACTATTGTTGACGCCGGGCACCGTCCCGGCCTATAA |
| pcr3\_150 | 89365 | 89400 | TCCGGGGTTGACACCCGGCGCAATAGGGCCGATAAT |
| pcr3\_157 | 91952 | 91987 | AATAATATTGACTCAGGGGCCGAAAGGCCCCATAAT |
| pcr3\_242 | 133519 | 133484 | AAAGTTGTTGACACACTGAGTTAAAACGAGCATAAT |
| pcr3\_243 | 133519 | 133484 | AAACCGCTTGACGTTGGTTTCTGCCGGGTCCATAAT |
| pcr3\_248 | 136375 | 136340 | AAGTGGCTTGACGCCGGGATCGATAAGTGCCTTAAT |

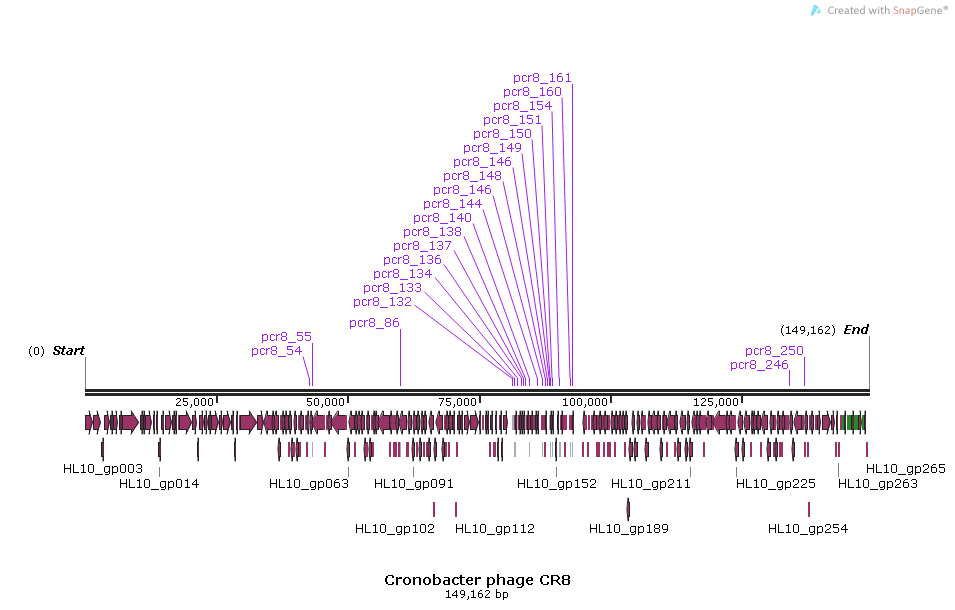


**Figure S5.** Genome map of *Cronobacter* phage CR3 (accession no. JQ691612), showing locations of a putative sigma70-like promoter. Arrows on the map indicate ORF positions and promoters are highlighted in purple. Genome map created with SnapGene 2.3.2.

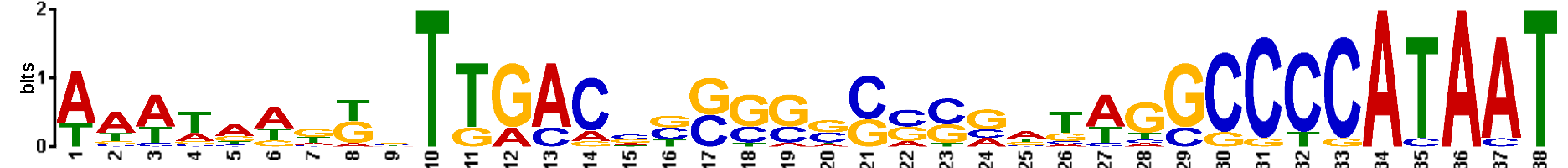
**Table S4.** Putative sigma70-like promoters detected in the genome of *Cronobacter* phage CR8 (accession no. KC954774).



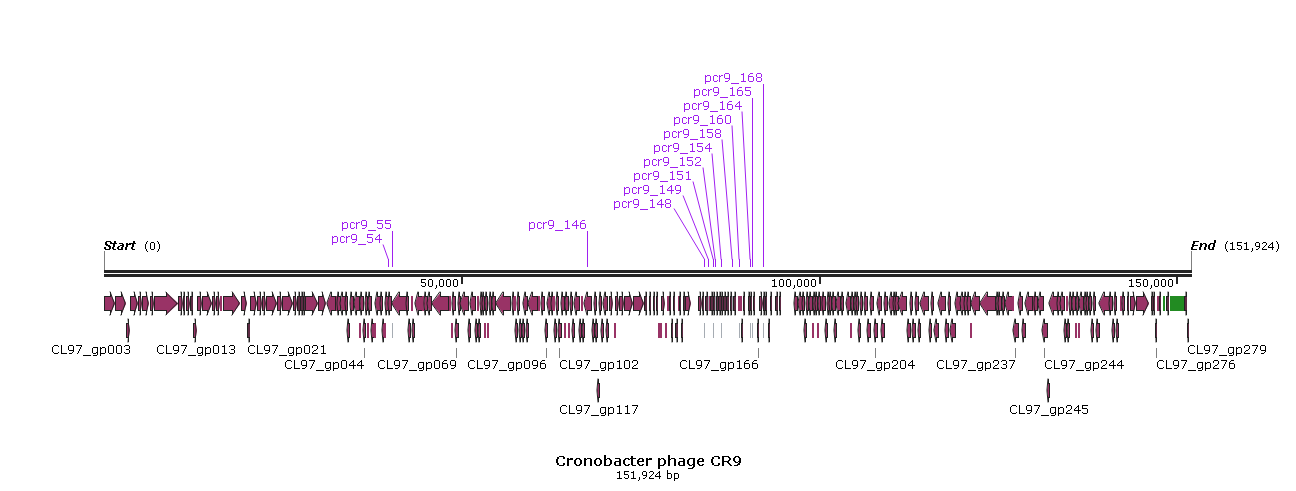
|  |  |  |  |
| --- | --- | --- | --- |
| **Promoter** | **Start** | **Stop** | **Sequence** |
| pcr8\_54 | 42743 | 42706 | ACAAAATTGTTGACTTCCTTCCTGATTTCCCGCATAAT |
| pcr8\_55 | 43247 | 43210 | ATTTTTTAATTGACAGCGGGGCCGAAAGGCCCCATAAT |
| pcr8\_86 | 59955 | 59918 | ACATTATTGTTGACCAAGGTGTCCGTAAGTTCTATCAT |
| pcr8\_132 | 81405 | 81442 | AAATTTTTCTTGACCTGCCAGGCAAGCCGGGCCACAAT |
| pcr8\_133 | 81,804 | 81841 | AAATAGTGCTTGACGGGGCCGATGATAGGCCCCATAAT |
| pcr8\_134 | 82342 | 82379 | AAAAGACTATTGACATCGGGGCCACCTGGCCCCATACT |
| pcr8\_136 | 83054 | 83091 | TTTTAGGGGTTGACGCCCGGCGGCGTTACCCTCATAAT |
| pcr8\_137 | 83414 | 83451 | AAATAATTGTTGACGCCGGGAACCGTCCCGGCTTATAA |
| pcr8\_138 | 83740 | 83777 | AAATAATTGTTGACCGGGGCCGGGTTAGGCCCCATAAT |
| pcr8\_140 | 84503 | 84540 | TAATTTTGGTTGACACGGGGCCGGGTTAGGCCCCATAA |
| pcr8\_144 | 86044 | 86081 | TCCCGGGGCTTGACGTCCGGCCCCGGTTCCTCCATAAT |
| pcr8\_146 | 87117 | 87154 | TAAAAGCGCTTGACGCCGGGACGGTTCCCGGCTTATAA |
| pcr8\_148 | 87570 | 87607 | AAATAATTGTTGACGCCGGGCACCGTCCCGGCTTACAA |
| pcr8\_149 | 88313 | 88350 | TTTAAATGATTGACATCCGGCCCAAAAGGGCCGATAAT |
| pcr8\_150 | 88587 | 88624 | AAAAAGTAGTTGACGGCGGGGCCGATAGGCCCCATAAT |
| pcr8\_151 | 88906 | 88943 | AAATAATGCTTGACGGGGCCAACGTTAGGCCCCATAAT |
| pcr8\_154 | 90372 | 90409 | GATCCGGGGTTGACACCCGGCGCAATAGGGCCGATAAT |
| pcr8\_160 | 92418 | 92455 | AATCTTTTGTTGACACCGGGGCCGATAGGCCCCATAAT |
| pcr8\_161 | 92798 | 92835 | AAAATAATATTGACTCAGGGGCCGAAAGGCCCCATAAT |
| pcr8\_246 | 134079 | 134042 | AAAAAGTTGTTGACACACTGAGTTAAAACGAGCATAAT |
| pcr8\_250 | 136935 | 136898 | AAAAGTGGCTTGACGCCGGGATCGGTAAGTGCCTTAAT |

**Figure S6.** Genome map of *Cronobacter* phage CR8 (accession no. KC954774) showing locations of a putative sigma70-like promoter. Arrows on the map indicate ORF positions and promoters are highlighted in purple. Genome map created with SnapGene 2.3.2.

**Table S5.** Putative sigma70-like promoters detected in the genome of *Cronobacter* phage CR9 (accession no. JQ691611).



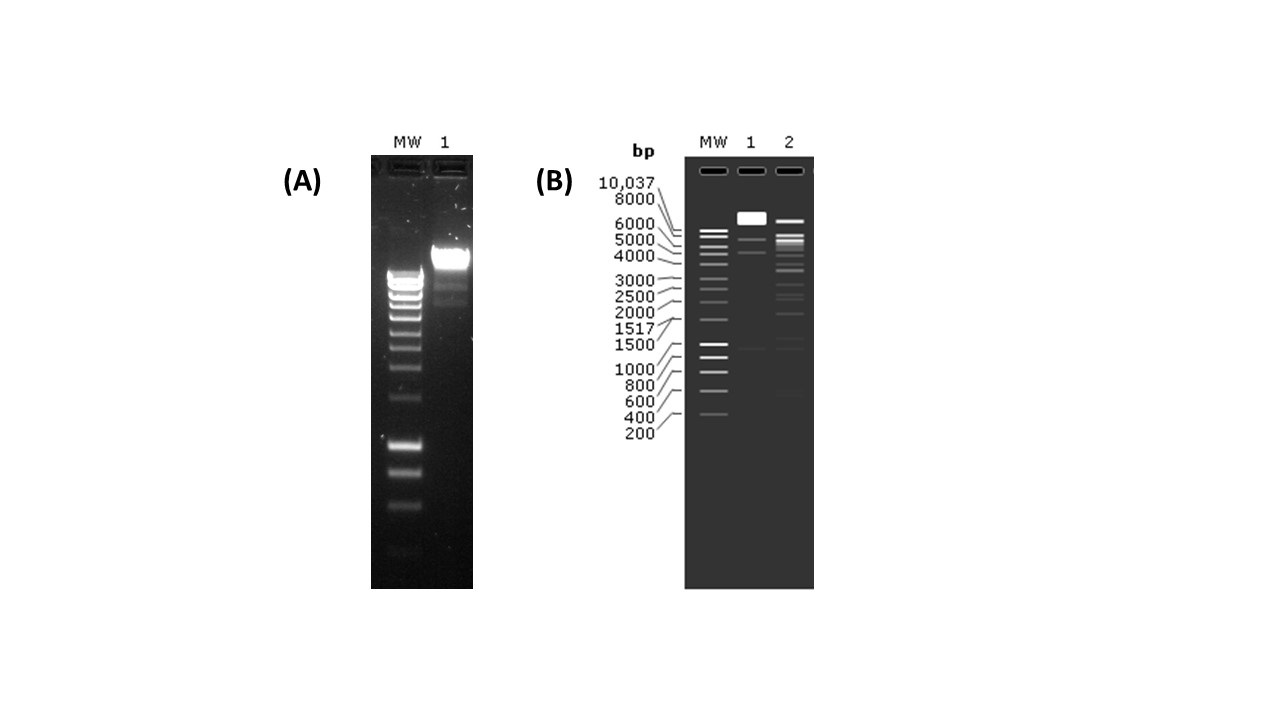
|  |  |  |  |
| --- | --- | --- | --- |
| **Promoter** | **Start** | **Stop** | **Sequence** |
| 54 | 39759 | 39722 | ACAAAAGTATTGACTTCCCTCCCAAGTTCCCTCATAAT |
| 55 | 40262 | 40225 | TTTTCTGATTGACAACCGGGGCCGGAAGGCCCCATAAT |
| 146 | 83055 | 83092 | AAATTTTTCTTGACCTGCCAGGCAAGCCGGGCCACAAT |
| 148 | 83952 | 83989 | AAATATTGCTTGACGGGGCCGATGATAGGCCCCATAAT |
| 149 | 84490 | 84527 | AAAAGACTATTGACATCGGGGCCACCTGGCCCCATACT |
| 151 | 85201 | 85238 | TTTTAGGGGTTGACGCCCAGCGGCGTTACCCTCATAAT |
| 152 | 85532 | 85569 | AAATAATTGTTGACCGGGGGCCGGATAGGCCCCATAAT |
| 155 | 86296 | 86333 | AATTTAGGTTGACACGGGGCCGGGTTAGGCCCCATAAT |
| 158 | 87840 | 87877 | TTCCGGGGCTTGACGCCCGGCCCCGGTTCCCCCATAAT |
| 160 | 88865 | 88902 | AAATAATTGTTGACCGGGGCCGGGTTAGGCCCCATAAT |
| 164 | 90355 | 90392 | AAAAGTAGTTGACGCCGGGGCCGCTTAGGCCCCATAAT |
| 165 | 90676 | 90713 | AAATAAATCTTGACGGGGCCGACGATAGGCCCCATAAT |
| 168 | 92144 | 92181 | TGTGAAGGGTTGACACCTGCCGCGATAGGGCCGATAAT |



**Figure S7.** Genome map of *Cronobacter* phage CR9(accession no. JQ691611) showing locations of a putative sigma70-like promoter. The map comprises of arrows indicating the location of ORFs. Genome map created with SnapGene 2.3.2.

**Table S6.** High ΔG rho-independent terminators predicted in the genome *Pectobacterium* phage CB7, identified using ARNold and QuikFold.



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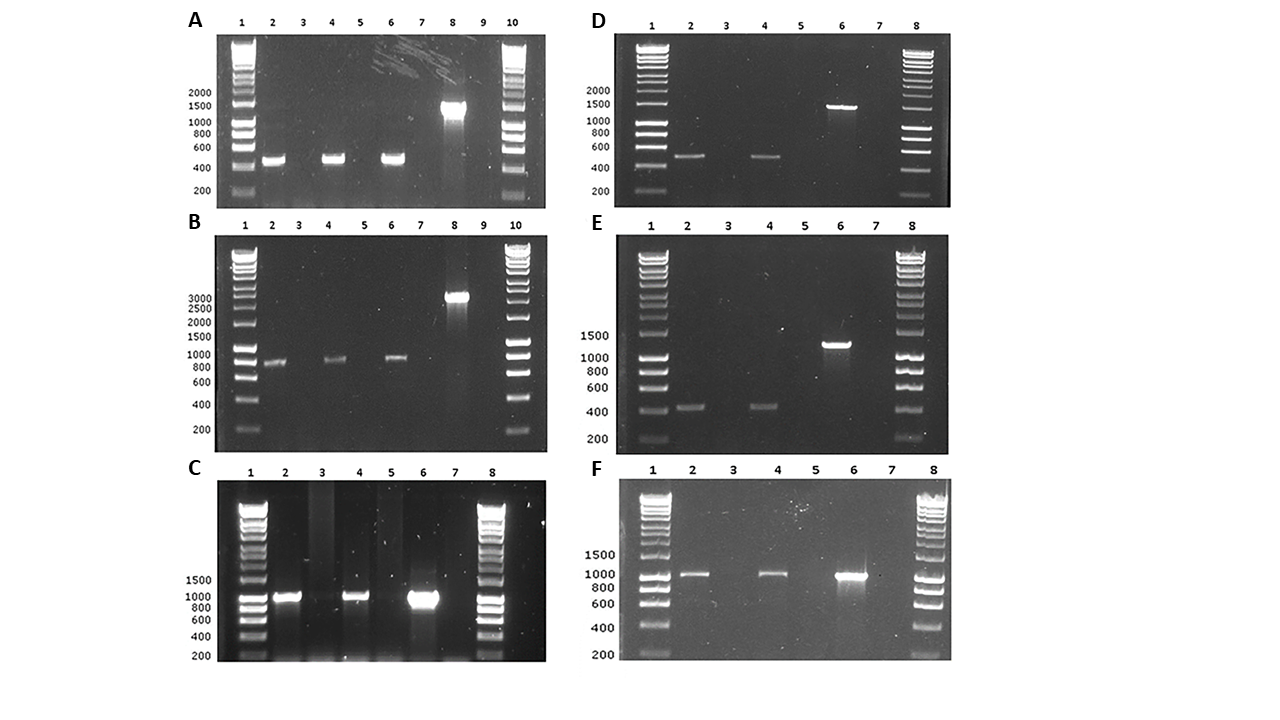
**Figure S8.** (A) Genomic DNA of *Pectobacterium* phage vB\_PatM\_CB7, digested with restriction enzyme ClaI (Lane 1), with DNA marker (Hyperladder 1kb, Bioline) (Lane MW). (B) *In silico* digest of CB7 genomic DNA with ClaI with DAM methylation (Lane 2); without DAM methylation (Lane 3); DNA marker (HyperLadder 1kb, Bioline) (Lane MW). Gel concentration 1% (w/v) agarose. Image B was generated using SnapGene 2.3.2.

**Table S7.** Comparison of potential gene products of CB7 identified to be involved in DNA replication, methylation and nucleotide metabolism members of *Certrevirus* members, generated using ACT (TBLASTX)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Phages** | **CB7** | **ΦTE** | **DU\_PP\_I** | **DU\_PP\_IV** | **CR3** | **CR8** | **CR9** | **PEB02** |
| Accession no. |  | JQ015307 | MF979569 | MF979563 | JQ691612 | KC954774 | JQ691611 | KT353109 |
| DNA polymerase | CB7\_49,51,53 | phiTE\_6, 8, 10 | P1A145kb\_p52 | P12B145kb\_p52 | CR3\_gp060 | HL10\_gp061 | CL97\_gp063, 65 | ADU18\_174 |
| cytosine methylase | CB7\_63 | \_ | \_ | \_ | CR3\_gp067 | HL10\_gp068 | CL97\_gp073 | ADU18\_183 |
| putative primase/helicase | CB7\_73 | phiTE\_23 | P1A145kb\_p70 | P12B145kb\_p71 | CR3\_gp077 | HL10\_gp078 | CL97\_gp084 | ADU18\_194 |
| putative helicase | CB7\_80 | phiTE\_30 | P1A145kb\_p79 | P12B145kb\_p80 | CR3\_gp084 | HL10\_gp087 | CL97\_gp093 | ADU18\_203 |
| putative nucleotidyl transferase | CB7\_175 | phiTE\_132 | P1A145kb\_p185 | P12B145kb\_p186 | CR3\_gp195 | HL10\_gp198 | CL97\_gp211 | ADU18\_34 |
| tRNA nucleotidyl transferase | CB7\_179 | phiTE\_136 | P1A145kb\_p191 | P12B145kb\_p192 | CR3\_gp201 | HL10\_gp204 | CL97\_gp217 | ADU18\_40 |
| adenine methylase | CB7\_183 | phiTE\_140 | P1A145kb\_p194 | P12B145kb\_p195 | CR3\_gp204 | HL10\_gp207 | CL97\_gp0220 | ADU18\_43 |
| NrdG | CB7\_187 | phiTE\_144 | \_ | \_ | \_ | \_ | \_ | \_ |
| NrdD | CB7\_188 | phiTE\_145 | \_ | \_ | \_ | \_ | \_ | \_ |
| NrdB | CB7\_195, 197 | phiTE\_152 | P1A145kb\_p206 | P12B145kb\_p207 | CR3\_gp215 | HL10\_gp218 | CL97\_gp230 | ADU18\_55 |
| NrdA | CB7\_201, 203 | phiTE\_154 | P1A145kb\_p209 | P12B145kb\_p210 | CR3\_gp216 | HL10\_gp220 | CL97\_gp231 | ADU18\_56 |
| thymidylate synthase | CB7\_206 | phiTE\_159 | P1A145kb\_p212 (poor homology) | P12B145kb\_p213 (poor homology) | CR3\_gp219  (poor homology) | HL10\_gp223(poor homology) | CL97\_gp235 (poor homology) | ADU18\_59 (poor homology) |
| 5'(3') deoxyribonuclease | CB7\_209 | phiTE\_162 | P1A145kb\_p214 | P12B145kb\_p215 | CR3\_gp221 | HL10\_gp225 | CL97\_gp237 | ADU18\_61 |
| DNA polymerase/exonuclease | CB7\_211 | phiTE\_164 | P1A145kb\_p218 | P12B145kb\_p219 | CR3\_gp224 | HL10\_gp228 | CL97\_gp240 | ADU18\_64 |
| EndoVII | CB7\_214 | phiTE\_167 | P1A145kb\_p221 | P12B145kb\_p222 | CR3\_gp226 | HL10\_gp230 | CL97\_gp242 | ADU18\_66 |
| endonuclease | CB7\_218 | phiTE\_171 | P1A145kb\_p225 | P12B145kb\_p226 | CR3\_gp230 | HL10\_gp234 | CL97\_gp246 | ADU18\_70 |
| pyrophophatase | CB7\_232 | phiTE\_185 | P1A145kb\_p242 | P12B145kb\_p243 | CR3\_gp245 | HL10\_gp247 | CL97\_gp262 | ADU18\_84 |
| DNA ligase | CB7\_234 | phiTE\_187 | P1A145kb\_p244 | P12B145kb\_p245 | CR3\_gp247 | HL10\_gp249 | CL97\_gp264 | ADU18\_86 |
| ribose phosphate pyrophosphokinase | CB7\_242 | phiTE\_193 | P1A145kb\_p252 | P12B145kb\_p253 | CR3\_gp256 | HL10\_gp258 | CL97\_gp272 | ADU18\_97 |
| nicotinamide phosphoribosyl transferase | CB7\_244, 246 | phiTE\_195, 197 | P1A145kb\_p254, 256 | P12B145kb\_p255, 257 | CR3\_gp257 | HL10\_gp259 | CL97\_gp273 | ADU18\_98 |

**Table S8.** Comparison of potential gene products of CB7 identified in DNA replication, methylation and nucleotide metabolism with that of *Escherichia* phage rv5 and *Salmonella* phage PVP-SE1, using ACT (TBLASTX).

|  |  |  |  |
| --- | --- | --- | --- |
| **Phages** | **CB7** | **rV5** | **PVP-SE1** |
| Accession no. | KY514263 | DQ832317 | GU070616 |
| DNA polymerase | CB7\_49,51,53 | ORF228 | 16 |
| cytosine methylase | CB7\_63 | ORF231 | 9 |
| putative primase/helicase | CB7\_73 | ORF230 | 13 |
| putative helicase | CB7\_80 | ORF237 | 3 |
| putative nucleotidyl transferase | CB7\_175 | \_ | 166 |
| tRNA nucleotidyl transferase | CB7\_179 | \_ | 159 |
| adenine methylase | CB7\_183 | ORF123 | 152 |
| NrdG | CB7\_187 | ORF117 | 143 |
| NrdD | CB7\_188 | ORF112 | 142 |
| NrdB | CB7\_195, 197 | ORF110 | 139 |
| NrdA | CB7\_201, 203 | ORF109 | 138 |
| thymidylate synthase | CB7\_206 | ORF106  (poor homology) | 134  (poor homology) |
| 5'(3') deoxyribonuclease | CB7\_209 | ORF104 | 131 |
| DNA polymerase/exonuclease | CB7\_211 | ORF99 | 128 |
| EndoVII | CB7\_214 | ORF97 | 126 |
| endonuclease | CB7\_218 | ORF94 | 123 |
| pyrophophatase | CB7\_232 | \_ | \_ |
| DNA ligase | CB7\_234 | \_ | \_ |
| ribose phosphate pyrophosphokinase | CB7\_242 | ORF80 | 97 |
| nicotinamide phosphoribosyl transferase | CB7\_244, 246 | \_ | 96 |



**Figure S9.** Gel images showing PCR products demonstrating splicing of intron-associated homing endonucleases associated with *Pectobacterium* phage CB7 using primers complementary to the 5' and 3' ends of the ORFs. (A) CB7\_2; HNH endonuclease situated between ORFs encoding the large terminase (CB7\_1,3), (B) CB7\_50 and CB7\_52; two HNH endonucleases situated between the ORFs encoding the DNA polymerase (CB7\_49, 51, 53), (C) CB7\_54; HNH endonuclease situated between the ORFs encoding the DNA polymerase (CB7\_53) and a structural protein (CB7\_55), (D) CB7\_196; HNH endonuclease situated between the ORFs encoding the ribonucleotide-diphosphate reductase (CB7\_195, 197), (E) CB7\_202; HNH endonuclease situated between the ORFs encoding the ribonucleoside triphosphate reductase (CB7\_201, 203), (F) CB7\_245; HNH endonuclease situated between the ORFs encoding the nicotinamide phosphoribosyl transferase (CB7\_244, 246). First and last lanes in each gel contain DNA marker (Hyperladder 1kb, Bioline), the molecular mass of bands is illustrated. Images A & B: PCR products using cDNA (Lanes 2, 4 & 6) and genomic DNA of *Pectobacterium* phage CB7 (Lane 8) and negative controls with water (Lanes 3, 5, 7 & 9). Lanes 2, 4 & 6 used cDNA from phage host infections times points of 15, 30 and 45 minutes, respectively. Images C, D, E & F: PCR products using cDNA (Lanes 2 & 4) and genomic DNA of *Pectobacterium* phage CB7 (Lane 6) and negative controls with water (Lanes 3, 5 &7). Lanes 2 & 4 used cDNA derived from RNA from phage host infections times points of 15 and 30 min, respectively.

**Table S9.** Shared structural proteins of phages of *Certrevirus* determined using ACT (TBLASTX).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Phages** | **CB7** | **ΦTE** | **DU\_PP\_I** | **DU\_PP\_IV** | **CR3** | **CR8** | **CR9** | **PBES 02** |
| Accession no. | KY514263 | JQ015307 | MF979560 | MF979563 | JQ691612 | KC954774 | JQ691611 | KT353109 |
| putative portal protein | CB7\_4 | phiTE\_209 | P1A145kb\_p2 | P12B145kb\_p2 | CR3\_gp2 | HL10\_gp2 | CL97\_gp2 | ADU18\_109 |
| prohead core protein protease | CB7\_5 | phiTE\_210 | P1A145kb\_p3 | P12B145kb\_p3 | CR3\_gp3 | HL10\_gp3 | CL97\_gp3 | ADU18\_110 |
| unknown structural protein | CB7\_6 | phiTE\_211 | P1A145kb\_p4 | P12B145kb\_p4 | CR3\_gp4 | HL10\_gp4 | CL97\_gp4 | ADU18\_111 |
| head stabilization/decoration protein | CB7\_7 | phiTE\_212 | P1A145kb\_p5 | P12B145kb\_p5 | CR3\_gp5 | HL10\_gp5 | CL97\_gp5 | ADU18\_112 |
| putative major head protein | CB7\_8 | phiTE\_213 | P1A145kb\_p6 | P12B145kb\_p6 | CR3\_gp6 | HL10\_gp6 | CL97\_gp6 | ADU18\_113 |
| putative tail fibre protein | CB7\_10 | phiTE\_215 | P1A145kb\_p8 | P12B145kb\_p8 | CR3\_gp8 | HL10\_gp8 | CL97\_gp8 | ADU18\_115 |
| unknown structural protein | CB7\_11 | phiTE\_210 | P1A145kb\_p9 | P12B145kb\_p9 | CR3\_gp9 | HL10\_gp9 | CL97\_gp9 | ADU18\_116 |
| unknown structural protein | CB7\_12 | phiTE\_217 | P1A145kb\_p10 | P12B145kb\_p10 | CR3\_gp10 | HL10\_gp10 | CL97\_gp10 | ADU18\_117 |
| unknown structural protein | CB7\_13 | phiTE\_218 | P1A145kb\_p11 | P12B145kb\_p11 | CR3\_gp12 | HL10\_gp12 | CL97\_gp11 | ADU18\_119 |
| unknown structural protein | CB7\_15 | phiTE\_220 | P1A145kb\_p13 | P12B145kb\_p13 | CR3\_gp14 | HL10\_gp14 | CL97\_gp13 | ADU18\_121 |
| unknown structural protein | CB7\_16 | phiTE\_211 | P1A145kb\_p14 | P12B145kb\_p14 | CR3\_gp15 | HL10\_gp15 | CL97\_gp14 | ADU18\_122 |
| putative tail sheath protein | CB7\_17 | phiTE\_222 | P1A145kb\_p15 | P12B145kb\_p15 | CR3\_gp16 | HL10\_gp16 | CL97\_gp15 | ADU18\_123 |
| putative tail tube protein | CB7\_18 | phiTE\_223 | P1A145kb\_p16 | P12B145kb\_p16 | CR3\_gp17 | HL10\_gp17 | CL97\_gp16 | ADU18\_124 |
| putative tape measure protein | CB7\_23 | phiTE\_228 | P1A145kb\_p21 | P12B145kb\_p21 | CR3\_gp20 | HL10\_gp20 | CL97\_gp19 | ADU18\_127 |
| unknown structural protein | CB7\_24 | phiTE\_229 | P1A145kb\_p22 | P12B145kb\_p22 | CR3\_gp21 | HL10\_gp21 | CL97\_gp20 | ADU18\_128 |
| unknown structural protein | CB7\_25 | phiTE\_230 | P1A145kb\_p23 | P12B145kb\_p23 | CR3\_gp22 | HL10\_gp22 | CL97\_gp21 | ADU18\_129 |
| putative tail protein | CB7\_26 | phiTE\_231 | P1A145kb\_p24 | P12B145kb\_p24 | CR3\_gp23 | HL10\_gp23 | CL97\_gp22 | ADU18\_130 |
| putative baseplate protein | CB7\_27 | phiTE\_232 | P1A145kb\_p25 | P12B145kb\_p25 | CR3\_gp24 | HL10\_gp24 | CL97\_gp23 | ADU18\_131 |
| putative tail lysozyme | CB7\_28 | phiTE\_233 | P1A145kb\_p26 | P12B145kb\_p26 | CR3\_gp25 | HL10\_gp25 | CL97\_gp24 | ADU18\_132 |
| putative baseplate wedge protein | CB7\_29 | phiTE\_234 | P1A145kb\_p27 | P12B145kb\_p27 | CR3\_gp26 | HL10\_gp26 | CL97\_gp25 | ADU18\_133 |
| putative baseplate protein | CB7\_30 | phiTE\_235 | P1A145kb\_p28 | P12B145kb\_p28 | CR3\_gp27 | HL10\_gp27 | CL97\_gp26 | ADU18\_134 |
| putative tail collar protein | CB7\_31 | phiTE\_236 | P1A145kb\_p29 | P12B145kb\_p29 | CR3\_gp28 | HL10\_gp28 | CL97\_gp27 | ADU18\_135 |
| putative tail fibre protein | CB7\_32 | phiTE\_237 | P1A145kb\_p30 | P12B145kb\_p30 | CR3\_gp29 | HL10\_gp29 | CL97\_gp28 | ADU18\_136 |
| tail chaparone protein | CB7\_36 | phiTE\_241 | P1A145kb\_p34 | P12B145kb\_p34 | CR3\_gp33 | HL10\_gp33 | CL97\_gp32 | ADU18\_140 |
| unknown structural protein | CB7\_37 | phiTE\_237 | P1A145kb\_p35 | P12B145kb\_p35 | CR3\_gp34 | HL10\_gp34 | CL97\_gp33 | ADU18\_141 |
| unknown structural protein | CB7\_55 | - | - | - | - | - | - | - |
| unknown structural protein | CB7\_251 | phiTE\_203 | - | - | - | - | - | - |

**Table S10.** Shared structural proteins (using currently available annotation) of phages of *Vequintavirinae* (*Pectobacterium* phage CB7, *Escherichia* phage rv5 and *Salmonella* phage PVP-SE1) determined using ACT (TBLASTX). Proteins in bold are those that have been determined to be present in the mature virion of the phage in question by ESI-MS/MS. Analysis of rV5 and PVP-SE1 described by Santos *et al*. 2011 and Kropinski *et al*. 2013, respectivitly.

|  |  |  |
| --- | --- | --- |
| ***Pectobacterium* phage CB7**  Accession no. KY514263 | ***Escherichia* phage rV5**  Accession no. DQ832317 | ***Salmonella* phage PVP-SE1**  Accession no. NC\_016071 |
| **CB7\_4, putative portal protein** | **gp64, portal protein** | **PVP-SE1\_gp75, conserved hypothetical protein** |
| **CB7\_5, putative prohead core protein protease** | gp63, conserved hypothetical protein | PVP-SE1\_gp74, hypothetical protein |
| **CB7\_6, unknown structural protein** | gp62, conserved hypothetical protein | **PVP-SE1\_gp73, hypothetical protein** |
| **CB7\_7, putative head stabilization/decoration protein,** | **gp61, putative head stabilization/decoration protein** | **PVP-SE1\_gp72, head stablization/ decorative protein** |
| **CB7\_8, putative major head protein** | **gp60, major capsid protein** | **PVP-SE1\_gp71, putative major head protein** |
| **CB7\_10, putative tail fibre protein** | \_ | **PVP-SE1\_gp69, hypothetical protein** |
| **CB7\_11, unknown structural protein** | \_ | PVP-SE1\_gp68, hypothetical protein |
| **\_** | \_ | **PVP-SE1\_gp67, hypothetical protein** |
| **CB7\_12, unknown structural protein** | \_ | \_ |
| **CB7\_13, unknown structural protein** | gp57, hypothetical protein | **PVP-SE1\_gp65, conserved hypothetical protein** |
| **CB7\_15, unknown structural protein** | gp55, conserved hypothetical protein | **PVP-SE1\_gp63, conserved hypothetical protein** |
| **CB7\_16, unknown structural protein** | gp54, hypothetical protein | **PVP-SE1\_gp62, hypothetical protein** |
| **CB7\_17, putative tail sheath protein** | **gp53, tail sheath protein** | **PVP-SE1\_gp61, structural protein** |
| **CB7\_18, putative tail tube protein** | **gp52, tail tube protein** | **PVP-SE1\_gp60, structural protein** |
| **CB7\_23, putative tape measure protein** | gp49, putative tail protein | **PVP-SE1\_gp57, hypothetical protein** |
| **CB7\_24, unknown structural protein** | gp48, hypothetical protein | **PVP-SE1\_gp56, conserved hypothetical protein** |
| **CB7\_25, unknown structural protein** | gp47, hypothetical protein | **PVP-SE1\_gp55, conserved hypothetical protein** |
| **CB7\_26, putative tail protein** | gp46, conserved hypothetical protein | **PVP-SE1\_gp54, conserved hypothetical protein** |
| **CB7\_27, putative baseplate protein** | gp45, tail baseplate protein | PVP-SE1\_gp53, putative baseplate assembly protein |
| **CB7\_28, putative tail lysozyme** | gp44, conserved hypothetical protein | **PVP-SE1\_gp52, conserved hypothetical protein** |
| **\_** | gp43, tail fibre protein | **PVP-SE1\_gp51, possible tail fibre protein** |
| **\_** | gp42, putative tail protein | **PVP-SE1\_gp50, conserved hypothetical protein** |
| **\_** | \_ | **PVP-SE1\_gp49, conserved hypothetical protein** |
| **\_** | gp41, tail fibre protein | \_ |
| **\_** | gp37, putative tail protein | \_ |
| **CB7\_29, putative baseplate wedge protein** | gp36, tail baseplate protein | **PVP-SE1\_gp48, baseplate component** |
| **CB7\_30, putative baseplate protein** | gp35, hypothetical protein | **PVP-SE1\_gp47, conserved hypothetical protein** |
| **CB7\_31, putative tail collar protein (N-terminus only)** | gp33, putative tail fibre protein | **PVP-SE1\_gp46, putative tail fibre protein** |
| **\_** | gp32, tail fibre protein | PVP-SE1\_gp45, putative tail fibre assembly protein |
| **\_** | gp30, tail fibre protein | **PVP-SE1\_gp46, hypothetical protein** |
| **putative tail fibre protein, CB7\_36** | gp28, putative tail fibre protein (weakening homology towards C terminus) | **PVP-SE1\_gp41, putative tail fibre protein** |
| **unknown structural protein, CB7\_37** | \_ | **PVP-SE1\_gp40, hypothetical with Ig-like domain (weak homology)** |
| **\_** | gp27, hypothetical protein |  |
| **unknown structural protein, CB7\_55** | \_ |  |
| **unknown structural protein, CB7\_251** | \_ |  |
| \_ | **gp133, unknown structural protein** |  |
| \_ | \_ | **PVP-SE1\_gp19, hypothetical protein** |
| \_ | \_ | **PVP-SE1\_gp10, conserved hypothetical protein** |

**Table S11.** Putative cell wall degrading and cell lysis proteins of phages in the subfamily *Vequintavirinae.* Determined using ACT (TBLASTX).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage** | **rV5** | **PVP-SE1** | **CB7** | **ΦTE** | **DU\_PP\_I** | **DU\_PP\_IV** | **CR3** | **CR8** | **CR9** | **PBES 02** |
| Accession no. | DQ832317 | NC\_016071 | KY514263 | NC\_020201 | MF979560 | MF979563 | NC\_017974 | NC\_024354 | NC\_023717 | KT353109 |
| Rz | gp67 | gp78 | CB7\_252 | phiTE\_204 | P1A145kb\_p266 | P12B145kb\_p267 | CR3\_264 | CR8\_268 | CL97\_gp280 | ADU18\_0106 |
| Rz1 | Gp66 | Gp79 | CB7\_253 | phiTE\_205 | P1A145kb\_p267 | P12B145kb\_p268 | CR3\_265 | CR8\_269 | CL97\_gp281 | ADU18\_0107 |
| SleB | Gp2 | Gp243 | CB7\_83 | phiTE\_33 | P1A145kb\_p083 | P12B145kb\_p084 | CR3\_87 | CR8\_90 | CL97\_gp95 | ADU18\_0206 |
| putative class II holin | \_ | \_ | CB7\_82 | phiTE\_032 | P1A145kb\_p081 | P12B145kb\_p082 | CR3\_086 | CR8\_089 | CL97\_gp094 | ADU18\_0205 |
| T4 gp25 - like | Gp44 | Gp52 | CB7\_28 | phiTE\_233 | P1A145kb\_p026 | P12B145kb\_p026 | CR3\_25 | CL97\_gp\_024 | CL97\_gp024 | ADU18\_0132 |
| CB7\_ 190 - like |  |  | CB7\_190 | phiTE\_147 | \_ | \_ | \_ | \_ | \_ | \_ |
| CR3\_ 210 - like |  |  | \_ | \_ | P1A145kb\_p201 | P12B145kb\_p202 | CR3\_210 | CL97\_gp226 | CL97\_gp226 | ADU18\_0050 |

**Table S12.** Bacteria strains used in the isolation and the host range testing of *Pectobacterium* phage CB7.

|  |  |  |
| --- | --- | --- |
| **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 S13.** List of primers used for the creation of PCR products from cDNA and genomic DNA of *Pectobacterium* phage CB7, used for the investigation of HNH endonuclease splicing.

|  |  |  |
| --- | --- | --- |
| **HNHs being examined** | **Primer name** | **Primer sequence 5'-3'** |
| CB7\_2 | CB7\_F | CGTTGCTTCAGTTCTTCC |
| CB7\_R | ATCGTAGACGATCCACG |
| CB7\_50 and CB7\_52 | CB7\_50-52F | ACGACTACGTATTGACG |
| CB7\_50-52R | CCTTCCATGACCATACC |
| CB7\_54 | CB7\_54F | CGACACAGCGACTTATCC |
| CB7\_54R | GACATTGACAGAGTGTCG |
| CB7\_196 | CB7\_196F | CAACATCAACGCACTGG |
| CB7\_196R | TTCAGCCGACATAGAGG |
| CB7\_202 | CB7\_202F | CAAGGTAAGTATGCTGC |
| CB7\_202R | TTCTTCGCCACAGAAGG |
| CB7\_245 | CB7\_245F | CGCAGATGATGTCTTCC |
| CB7\_245R | AACATTGTGAGCATTACC |