**Complete genome analysis of a novel *Shewanella* phage vB\_Sb\_QDWS**

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Fig. 1 Phage vB\_Sb\_QDWS is a DNA genome verified by digestion of phage nucleic acids. The phage nucleic acids were treated with DNase A (0.2 mg/mL) and RNase A (0.2 mg/mL) at 37°C for 1 h before they were loaded on the agarose gel. M, Marker; lane1, phage nucleic acids; lane 2, DNase A-treated phage nucleic acids; lane 3, RNase A-treated phage nucleic acids.

**Table 1 ORF analysis of the *Shewanella* phage vB\_Sb\_QDWS genome.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ORF** | **Size (aa)** | **Strand** | **Blast P top hit**  **name** | **Description**  **[homolog]** | **Similarity (%)** | **E-value** |
| 1 | 225 | + | QDP58333.1 | hypothetical protein  [Prokaryotic dsDNA virus sp.] | 35.42 | 1e-25 |
| 2 | 241 | + | ABY40551.1 | hypothetical protein  [*Burkholderia* phage Bups phi1] | 59.26 | 6e-17 |
| 3 | 118 | **+** | - | hypothetical protein **-** | - | - |
| 4 | 156 | **+** | - | hypothetical protein | - | - |
| 5 | 118 | **+** | - | hypothetical protein | - | - |
| 6 | 343 | + | AJA42431.1 | retron-type RNA-directed DNA polymerase  [*Bacillus* phage BalMu-1] | 34.27 | 5e-57 |
| 7 | 349 | + | ABY40517.1 | DNA cytosine methylase  [*Burkholderia* phage Bups phi1] | 66.5 | 9e-165 |
| 8 | 133 | + | AGC34619.1 | host nuclease inhibitor protein  [*Pseudomonas* virus H66] | 55.6 | 2e-15 |
| 9 | 102 | **+** | - | hypothetical protein | - | - |
| 10 | 171 | **+** | - | hypothetical protein | - | - |
| 11 | 101 | **+** | - | hypothetical protein | - | - |
| 12 | 117 | **+** | - | hypothetical protein | - | - |
| 13 | 322 | + | WP\_062910840.1 | site-specific integrase  [Phage NGI136] | 42.9 | 0.0 |
| 14 | 198 | **-** | DAG73188.1 | Lipase  [*Podoviridae* sp.] | 91.67 | 1e-104 |
| 15 | 154 | **-** | - | hypothetical protein | - | - |
| 16 | 69 | **-** | - | hypothetical protein | - | - |
| 17 | 204 | **-** | - | hypothetical protein | - | - |
| 18 | 357 | - | QDK02787.1 | minor tail protein  [*Mesorhizobium* phage vB\_MloP\_Lo5R7ANS] | 37.4 | 1e-15 |
| 19 | 136 | **-** | - | hypothetical protein | - | - |
| 20 | 216 | - | QGF22045.1 | endolysin  [*Erwinia* phage Midgardsormr38] | 48.4 | 5e-55 |
| 21 | 67 | **-** | - | hypothetical protein | - | - |
| 22 | 350 | **+** | DAG76218.1 | putative O-acyltransferase  [*Myoviridae* sp.] | 36.39 | 3e-44 |
| 23 | 418 | **-** | - | hypothetical protein | - | - |
| 24 | 194 | **+** | - | hypothetical protein | - | - |
| 25 | 237 | **-** | DAG81839.1 | tail fiber protein  **[***Siphoviridae* sp.**]** | 48.39 | 3e-04 |
| 26 | 299 | **-** | - | hypothetical protein | - | - |
| 27 | 471 | - | DAP43852.1 | Baseplate J like protein [*Siphoviridae* sp.] | 47.1 | 2e-106 |
| 28 | 115 | - | - | hypothetical protein | - | - |
| 29 | 218 | - | ALP46885.1 | baseplate protein [*Escherichia* phage Rac-SA53] | 43.45 | 5e-29 |
| 30 | 323 | - | DAG81874.1 | hypothetical protein  [*Siphoviridae* sp.] | 31.9 | 3e-62 |
| 31 | 92 | **-** | - | hypothetical protein | - | - |
| 32 | 244 | **-** | - | hypothetical protein | - | - |
| 33 | 574 | - | QCW21970.1 | lysis protein  [[*Caulobacter* phage Jess A]](https://blast.ncbi.nlm.nih.gov/Blast.cgi) | 46.03% | 2e-16 |
| 34 | 207 | **-** | - | hypothetical protein | - | - |
| 35 | 148 | **-** | - | hypothetical protein | - | - |
| 36 | 440 | - | DAD90980.1 | hypothetical protein [*Siphoviridae* sp. ctpLW14] | 38.1 | 6e-37 |
| 37 | 102 | **-** | - | hypothetical protein | - | - |
| 38 | 319 | **-** | - | hypothetical protein | - | - |
| 39 | 144 | **-** | - | hypothetical protein | - | - |
| 40 | 152 | **-** | - | hypothetical protein | - | - |
| 41 | 172 | **-** | - | hypothetical protein | - | - |
| 42 | 341 | **-** | - | hypothetical protein | - | - |
| 43 | 198 | **-** | - | hypothetical protein | - | - |
| 44 | 615 | - | AAR89308.1 | hypothetical protein  [*Burkholderia* virus Bcep43] | 36.17 | 5e-18 |
| 45 | 278 | - | ALP46880.1 | hypothetical protein  [*Escherichia* phage Rac-SA53] | 43.94 | 2e-82 |
| 46 | 485 | **-** | DAG28286.1 | portal protein [*Siphoviridae* sp.] | 43.07 | 6e-128 |
| 47 | 424 | - | DAR57718.1 | large subunit terminase [*Siphoviridae* sp.] | 39.5 | 2e-149 |
| 48 | 156 | - | DAE18041.1 | terminase small subunit [*Siphoviridae* sp. ctF6o6] | 54.3 | 1e-43 |
| 49 | 196 | - | ABY40524.1 | hypothetical protein  [*Burkholderia* phage Bups phi1] | 72.63 | 2e-105 |
| 50 | 161 | - | QGF21347.1 | RusA family crossover junction endodeoxyribonuclease  [*Pseudomonas* phage AUS531phi] | 47.06 | 2e-41 |
| 51 | 56 | **-** | - | hypothetical protein | - | - |
| 52 | 57 | **-** | - | hypothetical protein | - | - |
| 53 | 153 | - | ALJ98741.1 | hypothetical protein  [*Burkholderia* phage PE067] | 33.1 | 2e-21 |
| 54 | 324 | - | QBI77607.1 | hypothetical protein  [*Pseudomonas* phage vB\_Pae\_CF67a] | 35.63 | 2e-15 |
| 55 | 95 | **-** | - | hypothetical protein | - | - |
| 56 | 135 | **-** | - | hypothetical protein | - | - |
| 57 | 104 | **-** | DAO68906.1 | antitoxin of bacterial toxin-antitox [*Myoviridae* sp.] | 52.11 | 7e-14 |
| 58 | 265 | + | YP\_009800704.1 | repressor protein C [*Burkholderia*phage vB\_BmuP\_KL4] | 51.4 | 6e-73 |
| 59 | 110 | **+** | - | hypothetical protein | - | - |
| 60 | 147 | **+** | - | hypothetical protein | - | - |
| 61 | 107 | + | AWD90826.1 | hypothetical protein  [Burkholderia phage vB\_BmuP\_KL4] | 65.31 | 3e-18 |
| 62 | 73 | **+** | - | hypothetical protein | - | - |
| 63 | 75 | **+** | - | hypothetical protein | - | - |
| 64 | 52 | **+** | - | hypothetical protein | - | - |
| 65 | 145 | **+** | - | hypothetical protein | - | - |
| 66 | 94 | **+** | - | hypothetical protein | - | - |
| 67 | 346 | + | DAT61729.1 | RecT protein-like protein[*Myoviridae* sp.] | 59.24 | 3e-87 |
| 68 | 206 | **+** | DAN72140.1 | exonuclease  [*Myoviridae* sp.] | 42.79 | 4e-27 |
| 69 | 268 | **+** | - | hypothetical protein | - | - |