**Supplementary Table S2 General features of EspM4VN and related phages’ genomes**

|  |  |
| --- | --- |
| **Features** | **Bacteriophages** |
| **EspM4VN** | **SboM-AG3** | **SKML-39** | **SH19** | **Coodle** | **PP35** | **JA15** | **LIMEstone1** | **phiDP23.1** | **D3** | **D5** | **XF4** |
| **Genome size (bp)** | 160,766 | 158,006 | 159,624 | 157,785 | 152,515 | 152,048 | 153,757 | 152,427 | 188,540 | 152 308 | 155,346 | 151519 |
| **% of coding regions in the genome** | 90.6 | 92.7 | 88.6 | - | 94.4 | 92.7 | 90.7 | - | 83.2 | 91.2 | 89.9 | 91 |
| **Number of predicted ORFs (PEGs)** | 219 | 216 | 209 | 339 | 202 | 198 | 199 | 201 | 223 | 191 | 196 | 196 |
| **% of PEGs with assigned fuctions** | 30% with assigned 9% with hypthetical functions 61% with unknown function | 33% with assigned functions 67% with hypothetical functions | 9% with assigned functions 91% with hypothetical functions | 31% with assigned functions 17% with hypothetical functions52% with unknown function | 42% with assigned functions 58% with hypothetical functions | 54% with assigned functions 46% with hypothetical functions | 45% with assigned 48% with hypthetical functions7% with unknown function | 46% with assigned 54% with unknown function | 39.5% with assigned 22.4% with cal functions8% with unknown function | 54.9% with assigned 45.1% with hypthetical functions | 25.5% with assigned 49% with hypthetical functions25.5% with unknown function | 　 |
| **Average gene length (bp)** | 653 | 731 | 677 | - | 709 | 712 | 693 | - | 538-804 | 730 | 711 | 703 |
| **Number of PEGs in functional groups** |  Phage replication (8) Phage tail proteins 2 (1) Phage lysis modules (1)Nucleosides and Nucleotides (2) | - |  Phage tail proteins 2 (1) Phage tail fiber proteins (1) Phage lysis modules (1)RNA Metabolism (1)Nucleosides and Nucleotides (2) DNA Metabolism (1) |  Phage replication (10) Phage tail proteins 2 (1) Phage lysis modules (1)Nucleosides and Nucleotides (2) |  Phage replication (9) Phage tail proteins 2 (1) Phage lysis modules (1)RNA Metabolism (1)Nucleosides and Nucleotides (2)DNA Metabolism (1) |  Phage replication (14) Phage tail proteins 2 (1) Phage tail fiber proteins (1) Phage lysis modules (1)RNA processing and modification (1)Nucleosides and Nucleotides (2)DNA Metabolism (1) |  Phage replication (14) Phage tail proteins 2 (1) Phage tail fiber proteins (1) Phage lysis modules (1) RNA Metabolism (1)Nucleosides and Nucleotides (2)DNA Metabolism (1) |  Phage replication (10) Phage tail proteins 2 (1) Phage lysis modules (1)RNA Metabolism (1)Nucleosides and Nucleotides (2)DNA Metabolism (1) | - |  Phage replication (10) Phage tail proteins 2 (1) Phage lysis modules (1)RNA Metabolism (1) Nucleosides and Nucleotides (2)DNA Metabolism (1) | - |  Phage replication (14) Phage tail proteins 2 (1) Phage tail fiber proteins (1) Phage lysis modules (1)RNA metablolism (1)Nucleosides and Nucleotides (2)DNA Metabolism (1) |
| **Transcription start codon (% of genes of this start codon)** | - | ATG (95.4%)GTG (3.2%)CTG (0.9%)TTG (0.5%) | - | - | - | - | - | - | ATG (85.3%)GTG (13.6%)TTG (1.1%) | - | ATG (94.4%)GTG (4.1%)TTG (1.5%) | - |