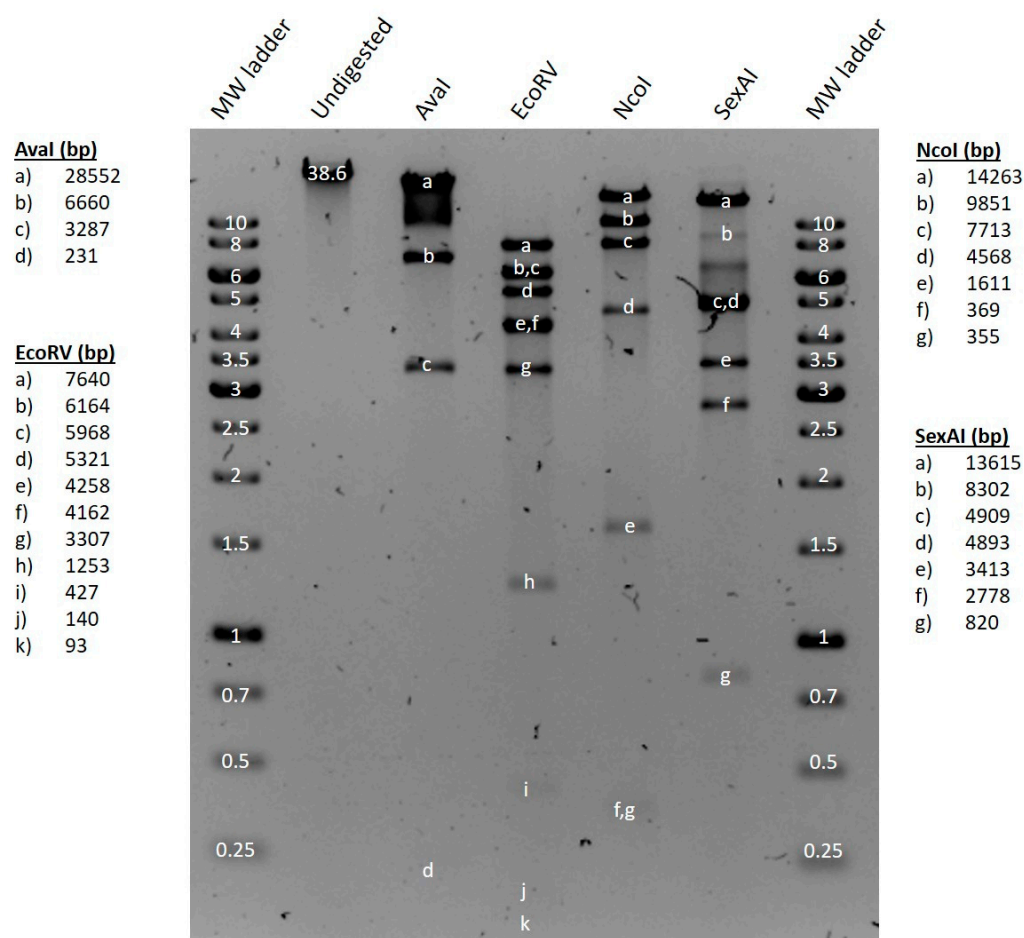


# Bacteriophages fEV-1 and fD1 infect *Yersinia pestis*

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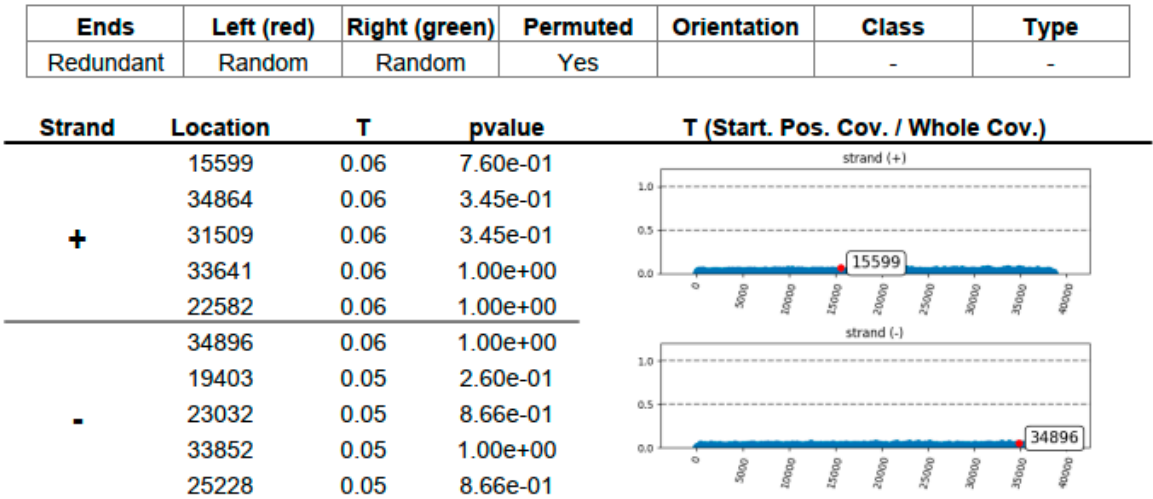


**Figure S1.** The restriction digestion analysis of the fEV-1 genomic DNA with Aval, EcoRV, NcoI, and SexAI. The predicted sizes of the restriction fragments based on a circular genome are indicated on both sides of the gel. Notice the presence of partially digested DNA in the Aval and SexAI lanes.

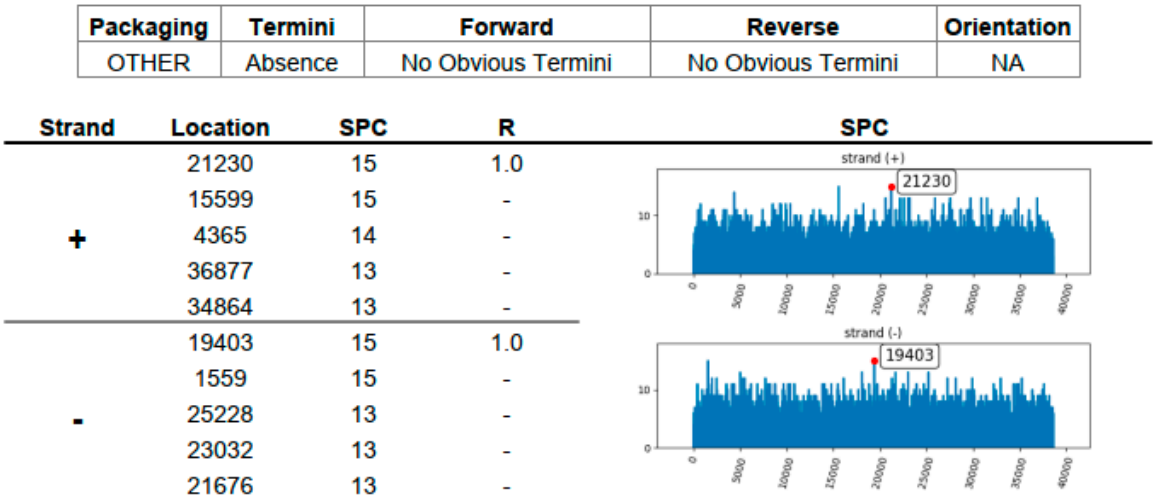
# fEV1 PhageTerm Analysis



## PhageTerm Method



## Li's Method



**Figure S2.** Determination of the physical termini of the phage fEV-1 genome. Failure of the PhageTerm to identify the genome termini.

**Table S1.** The predicted sigma-70 promoters of phage fEV-1.

| Prom | Next gene | Sequence upstream of the start codon of the gene   | LDF  | -35 box score | -10 box score |
|------|-----------|--|------|---------------|---------------|
| P1   | g55       | TGCGCGTTCTGTATCTGAAACCTGCCCCCGCTGAAAAATGCTTTGACTATTGATGATTTGAGTACATA<br>CAATGCACAAAGGTATCAGGAGGGTTATTTA    | 3.40 | 61            | 47            |
| P2   | g33       | TCGAACGCGGCGTGCCGCCTGGGGTGTATTACTATCAACTTGAAAACAATTGACGGTGTGACTGCAACAG<br>GTGTTCTGTCAGCATACTGGGAGGAACGACC  | 2.09 | 60            | 27            |
| P3   | g42       | ATCACCACCAATGACCTGGAAGTGAACCTTTTTTAAAGCGGTTGCCTTTTGTGGTACGTTGTGCAACAA<br>TACGCATACATTCAACAAACGGGAACTGAA    | 3.35 | 56            | 36            |
| P4   | g47       | TAGACATATGAAACCTAATAAAATTCCTCAAAGGTCGATCTGGAAATATACGGCATTTCGCAACTTGGTCAA<br>CGATAAAATATACATCGGTAAACTAAGTGC | 2.00 | 4             | 71            |
| P5   | g52       | GCCGTTGATAATCATTGACA CAACAAATCCATGCTTGACAGCATACCAGAATTGTTAACAATGTGCCA<br>CGTAGTACAACAAACCAGCGAGGAATAAACC   | 3.27 | 66            | 21            |
| P6   | g53       | GCACATTGTAAACAATTCTGGTATGCTGTCAAGCATGGATTGTGTGTGTCAATGATTATCAACGGCTA<br>TCATCCGCTATCAACGGCTAAGGAGCGTCCA    | 3.02 | 39            | 67            |

**Table S2.** Annotation of the genome of *Yersinia* phage fEV-1.

| fEV-1      |  |                   |           |        |          |             | PSI-BLAST search results <sup>2</sup> |  |                                      |       |                      |
|------------|--|-------------------|-----------|--------|----------|-------------|---------------------------------------|--|--------------------------------------|-------|----------------------|
| Gene       | Putative Function                      | PPAP <sup>1</sup> | Range     | Strand | MW (kDa) | Length (aa) | Acc. ID                               | Annotation                             | Organism                             | Score | E-value              |
| <b>g01</b> | Pentapeptide repeat-containing protein | PPAP              | 38297:514 | +      | 30.0     | 279         | ECC5451575.1                          | Pentapeptide repeat-containing protein | <i>Salmonella enterica</i>           | 122   | $4 \times 10^{-33}$  |
| <b>g02</b> | Hypothetical protein                   |                   | 504:794   | +      | 10.0     | 96          | -                                     | -                                      | -                                    | -     | -                    |
| <b>g03</b> | Phage terminase, small subunit         | PPAP              | 796:1371  | +      | 21.0     | 191         | WP_206047523.1                        | Terminase small subunit                | <i>Halomonas venusta</i>             | 268   | $2 \times 10^{-88}$  |
| <b>g04</b> | Phage terminase, large subunit         |                   | 1368:2756 | +      | 51.7     | 462         | CAB4157474.1                          | Putative large terminase               | Archaeophage PsiM2                   | 637   | 0.0                  |
| <b>g05</b> | Portal protein                         | PPAP              | 2753:3922 | +      | 43.8     | 389         | AUR91016.1                            | Portal protein                         | Vibrio phage 1.154.O._10N.222.52.B12 | 382   | $4 \times 10^{-127}$ |
| <b>g06</b> | Head morphogenesis protein             | PPAP              | 3915:4715 | +      | 30.2     | 266         | AUR84233.1                            | Head morphogenesis domain protein      | Vibrio phage 1.052.A._10N.286.46.C3  | 283   | $2 \times 10^{-92}$  |
| <b>g07</b> | Hypothetical protein                   | PPAP              | 4772:5884 | +      | 40.5     | 370         | YP_007674345.1                        | Hypothetical protein VPGG_00036        | Vibrio phage VBM1                    | 294   | $1 \times 10^{-92}$  |
| <b>g08</b> | Hypothetical protein                   | PPAP              | 5887:6348 | +      | 15.7     | 153         | AUR84235.1                            | Hypothetical protein NVP1052A_06       | Vibrio phage 1.052.A._10N.286.46.C3  | 109   | $3 \times 10^{-27}$  |
| <b>g09</b> | Major capsid protein                   | PPAP              | 6360:7319 | +      | 34.4     | 319         | AUR84236.1                            | Major capsid protein                   | Vibrio phage 1.052.A._10N.286.46.C3  | 349   | $1 \times 10^{-116}$ |
| <b>g10</b> | Hypothetical protein                   | PPAP              | 7371:7664 | +      | 10.9     | 97          | -                                     | -                                      | -                                    | -     | -                    |
| <b>g11</b> | Hypothetical protein                   | PPAP              | 7666:8010 | +      | 12.9     | 114         | YP_007674341.1                        | Hypothetical protein VPGG_00032        | Vibrio phage VBM1                    | 92.4  | $2 \times 10^{-21}$  |
| <b>g12</b> | Hypothetical protein                   | PPAP              | 8060:8533 | +      | 17.2     | 157         | WP_085071357.1                        | Hypothetical protein                   | <i>Pantoea alhagi</i>                | 141   | $3 \times 10^{-40}$  |
| <b>g13</b> | Hypothetical protein                   | PPAP              | 8530:8874 | +      | 12.8     | 114         | MAB53531.1                            | Hypothetical protein                   | Marinobacter sp.                     | 115   | $8 \times 10^{-31}$  |
| <b>g14</b> | Hypothetical protein                   | PPAP              | 8871:9356 | +      | 17.7     | 161         | MBL1319590.1                          | Hypothetical protein                   | Methylophaga sp.                     | 140   | $3 \times 10^{-39}$  |

|            |                             |      |             |   |      |     |                |                                   |                                |      |                      |
|------------|-----------------------------|------|-------------|---|------|-----|----------------|-----------------------------------|--------------------------------|------|----------------------|
| <b>g15</b> | Hypothetical protein        | PPAP | 9367:10863  | + | 53.8 | 498 | WP_145558960.1 | DUF3383 domain-containing protein | <i>Yersinia mollaretii</i>     | 601  | 0.0                  |
| <b>g16</b> | Hypothetical protein        | PPAP | 10874:11302 | + | 15.4 | 142 | MBL1319593.1   | Hypothetical protein              | <i>Methylophaga</i> sp         | 161  | $6 \times 10^{-48}$  |
| <b>g17</b> | Hypothetical protein        | PPAP | 11313:11729 | + | 15.9 | 138 | MBA0943622.1   | Hypothetical protein              | <i>Escherichia coli</i>        | 123  | $5 \times 10^{-33}$  |
| <b>g18</b> | Hypothetical protein        |      | 11738:11896 | + | 6.0  | 52  | WP_180272578.1 | Uncharacterised protein           | <i>Yersinia mollaretii</i>     | 76.3 | $5 \times 10^{-17}$  |
| <b>g19</b> | Hypothetical protein        | PPAP | 11883:13598 | + | 60.9 | 571 | EEM3686798.1   | Hypothetical protein              | <i>Salmonella enterica</i>     | 389  | $1 \times 10^{-124}$ |
| <b>g20</b> | Hypothetical protein        | PPAP | 13595:14374 | + | 27.8 | 259 | WP_085071364.1 | Hypothetical protein              | <i>Pantoea alhagi</i>          | 222  | $3 \times 10^{-68}$  |
| <b>g21</b> | Hypothetical protein        | PPAP | 14376:14714 | + | 13.1 | 112 | WP_145558952.1 | Hypothetical protein              | <i>Yersinia mollaretii</i>     | 124  | $3 \times 10^{-34}$  |
| <b>g22</b> | Hypothetical protein        | PPAP | 14711:15553 | + | 30.8 | 280 | WP_145527456.1 | Hypothetical protein              | <i>Yersinia frederiksenii</i>  | 303  | $6 \times 10^{-99}$  |
| <b>g23</b> | Hypothetical protein        |      | 15546:16178 | + | 22.5 | 210 | HAT2746464.1   | Hypothetical protein              | <i>Citrobacter farmeri</i>     | 256  | $1 \times 10^{-83}$  |
| <b>g24</b> | Hypothetical protein        | PPAP | 16192:16551 | + | 13.8 | 119 | MBE0469603.1   | Hypothetical protein              | <i>Methyloprofundus</i> sp     | 115  | $2 \times 10^{-30}$  |
| <b>g25</b> | Hypothetical protein        | PPAP | 16548:17729 | + | 42.9 | 393 | MAB53542.1     | Hypothetical protein              | <i>Marinobacter</i> sp         | 388  | $1 \times 10^{-129}$ |
| <b>g26</b> | Hypothetical protein        | PPAP | 17726:18451 | + | 27.7 | 241 | HAH8787749.1   | DUF2612 domain-containing protein | <i>Escherichia coli</i>        | 273  | $3 \times 10^{-89}$  |
| <b>g27</b> | Putative tail fiber protein | PPAP | 18444:20246 | + | 64.8 | 600 | QMP83030.1     | Hypothetical protein              | <i>Myoviridae</i> sp           | 263  | $5 \times 10^{-76}$  |
| <b>g28</b> | Hypothetical protein        |      | 20298:20414 | + | 4.1  | 38  | -              |                                   |                                |      |                      |
| <b>g29</b> | Reverse transcriptase       |      | 20532:21491 | + | 38.0 | 319 | NCB03306.1     | RNA-directed DNA polymerase       | <i>Spirochaetia bacterium</i>  | 300  | $3 \times 10^{-97}$  |
| <b>g30</b> | Hypothetical protein        |      | 21476:22081 | + | 22.6 | 201 | MBE0435221.1   | Hypothetical protein              | <i>Methylochromium</i> sp      | 83.2 | $2 \times 10^{-16}$  |
| <b>g31</b> | Phage holin                 |      | 22078:22356 | + | 10.2 | 92  | WP_141128063.1 | Phage holin, lambda family        | <i>Pseudomonas fluorescens</i> | 71.6 | $7 \times 10^{-14}$  |
| <b>g32</b> | Hypothetical protein        |      | 22353:22568 | + | 7.8  | 71  | NGR07855.1     | Hypothetical protein              | <i>Bacterium</i> SGD-2         | 109  | $2 \times 10^{-29}$  |

|             |   |      |             |   |      |     |                |   |                                    |      |                      |
|-------------|---|------|-------------|---|------|-----|----------------|---|------------------------------------|------|----------------------|
| <b>g33</b>  | N-acetylmuramoyl-L-alanine amidase, putative                    | PPAP | 22680:23309 | + | 22.3 | 209 | WP_119020686.1 | N-acetylmuramoyl-L-alanine amidase                  | Halomonas sp. JS92-SW72            | 245  | $3 \times 10^{-79}$  |
| <b>g34</b>  | Hypothetical protein  |      | 23299:23562 | + | 9.9  | 87  | WP_092567721.1 | Hypothetical protein                                | <i>Aidingimonas halophila</i>      | 84.7 | $3 \times 10^{-19}$  |
| <b>g35</b>  | Hypothetical protein  |      | 23516:23764 | + | 8.9  | 82  | WP_153016708.1 | Hypothetical protein                                | <i>Halomonas axialensis</i>        | 97.1 | $3 \times 10^{-24}$  |
| <b>g36c</b> | Hypothetical protein  |      | 23739:23936 | - | 7.6  | 65  | WP_150556912.1 | Hypothetical protein                                | <i>Pandoraea nosoerga</i>          | 64.7 | $6 \times 10^{-12}$  |
| <b>g37c</b> | Deoxycytidine triphosphate deaminase (EC3.5.4.30)(dUMP-forming) |      | 23933:24469 | - | 20.2 | 178 | WP_141391763.1 | dCTP deaminase                                      | <i>Cobetia marina</i>              | 157  | $2 \times 10^{-45}$  |
| <b>g38c</b> | Hypothetical protein  |      | 24460:24711 | - | 9.2  | 83  | NYT81399.1     | Hypothetical protein                                | <i>Alcaligenaceae bacterium</i>    | 50.4 | $6 \times 10^{-6}$   |
| <b>g39c</b> | Hypothetical protein  |      | 24704:24823 | - | 4.5  | 39  | ERS04819.1     | Hypothetical protein Q673_06280                     | Marinobacter sp. EN3               | 42.7 | $5 \times 10^{-04}$  |
| <b>g40c</b> | Hypothetical protein  |      | 24820:25194 | - | 14.2 | 124 | -              |   |                                    |      |                      |
| <b>g41c</b> | Predicted transcriptional regulator                             | PPAP | 25197:26060 | - | 32.6 | 287 | WP_035234726.1 | Chromosome partitioning protein ParB                | <i>Alcanivorax nanhaiticus</i>     | 310  | $4 \times 10^{-102}$ |
| <b>g42c</b> | Hypothetical protein  |      | 26064:26363 | - | 10.8 | 99  | WP_134021476.1 | Hypothetical protein                                | <i>Halomonas xianhensis</i>        | 121  | $3 \times 10^{-33}$  |
| <b>g43c</b> | DNA helicase, phage-associated                                  | PPAP | 26428:27912 | - | 56.6 | 494 | AUR93211.1     | Helicase superfamily 1/2 ATP-binding domain protein | Vibrio phage 1.185.O_10N.286.49.C2 | 845  | 0.0                  |
| <b>g44c</b> | Hypothetical protein  |      | 27912:28541 | - | 23.9 | 209 | CAB4141357.1   | Hypothetical protein UFOVP414_10                    | Uncultured Caudovirales phage      | 269  | $1 \times 10^{-88}$  |
| <b>g45c</b> | Hypothetical protein  |      | 28529:28822 | - | 10.7 | 97  | AUR93213.1     | VRR-NUC domain protein                              | Vibrio phage 1.185.O_10N.286.49.C2 | 121  | $3 \times 10^{-33}$  |
| <b>g46c</b> | Hypothetical protein  | PPAP | 28828:29364 | - | 20.3 | 178 | QGT52244.1     | Ribonuclease H-like domain protein                  | Vibrio phage MZH0603               | 216  | $6 \times 10^{-63}$  |
| <b>g47c</b> | Hypothetical protein  |      | 29354:29929 | - | 22.8 | 191 | NCD06171.1     | Hypothetical protein                                | <i>Spirochaetia bacterium</i>      | 147  | $2 \times 10^{-40}$  |

|             |                         |      |             |   |      |     |                |   |                                      |      |                      |
|-------------|-------------------------|------|-------------|---|------|-----|----------------|---|--------------------------------------|------|----------------------|
| <b>g48c</b> | DNA polymerase B region | PPAP | 30041:31480 | - | 55.7 | 479 | CAB4146555.1   | Hypothetical protein UFOVP503_34              | Uncultured <i>Caudovirales</i> phage | 583  | 0.0                  |
| <b>g49c</b> | Hypothetical protein    | PPAP | 31534:32253 | - | 25.0 | 239 | AUR82098.1     | Protein of unknown function DUF2815           | Vibrio phage 1.021.A._10N.222.51.F 9 | 177  | $2 \times 10^{-32}$  |
| <b>g50c</b> | Hypothetical protein    | PPAP | 32278:33582 | - | 48.2 | 434 | AUR82099.1     | Coil containing protein                       | Vibrio phage 1.021.A._10N.222.51.F 9 | 403  | $4 \times 10^{-134}$ |
| <b>g51c</b> | Hypothetical protein    | PPAP | 33579:34031 | - | 17.6 | 150 | -              |   |                                      |      |                      |
| <b>g52c</b> | Hypothetical protein    | PPAP | 34028:34204 | - | 6.8  | 58  | XP_010444284.1 | Pyruvate kinase, cytosolic isozyme isoform X3 | <i>Camelina sativa</i>               | 35.0 | 2.7                  |
| <b>g53</b>  | Hypothetical protein    |      | 34338:34511 | + | 6.6  | 57  | SDT10036.1     | Hypothetical protein SAMN05216271_3587        | <i>Pseudomonas sabulinigri</i>       | 68.2 | $6 \times 10^{-14}$  |
| <b>g54</b>  | Putative primase        | PPAP | 34501:37023 | + | 93.9 | 840 | WP_112054867.1 | Bifunctional DNA primase/polymerase           | <i>Halomonas taeanensis</i>          | 1092 | 0.0                  |
| <b>g55</b>  | Hypothetical protein    |      | 37462:37716 | + | 9.5  | 84  | MAD98753.1     | Hypothetical protein                          | Flavobacteriaceae bacterium          | 56.6 | $2 \times 10^{-08}$  |
| <b>g56</b>  | Hypothetical protein    |      | 37713:38087 | + | 14.3 | 124 | TDX21640.1     | Hypothetical protein DFO67_1348               | <i>Halomonas xianhensis</i>          | 131  | $2 \times 10^{-36}$  |
| <b>g57</b>  | Hypothetical protein    |      | 38143:38307 | + | 6.1  | 54  | MBL4781756.1   | Hypothetical protein                          | <i>Porticoccaceae bacterium</i>      | 62.0 | $1 \times 10^{-10}$  |

<sup>1</sup> PPAP: phage-associated protein identified by LC-MS/MS; <sup>2</sup> PSI-BLAST at <https://blast.ncbi.nlm.nih.gov> using default setting against the non-redundant protein sequence database release of 2021/05.

**Table S3.** Annotation of the genome of *Yersinia* phage fD1.

| fD1      |   |                   |       |      |            |             |                 | PSI-BLAST search results <sup>3</sup> |   |                             |       |             |                 |  |
|----------|---|-------------------|-------|------|------------|-------------|-----------------|---------------------------------------|---|-----------------------------|-------|-------------|-----------------|--|
| Gen<br>e | Putative<br>function <sup>1</sup>                     | PPAP <sup>2</sup> | Start | End  | Stran<br>d | MW<br>(kDa) | Lengt<br>h (aa) | Acc. ID                               | Annotation                                  | Organism                    | Score | E-<br>value | T4 <sup>4</sup> |  |
| g001     | Protector from<br>prophage-<br>induced early<br>lysis | PPAP              | 12    | 2189 | -          | 82.6        | 725             | QHR63679.1                            | Protector from prophage-induced early lysis | Escherichia<br>phage teqhal | 1484  | 0.0         | Yes             |  |

|             |   |      |      |       |   |      |     |                |  |   |      |                      |     |
|-------------|---|------|------|-------|---|------|-----|----------------|--|---|------|----------------------|-----|
| <b>g002</b> | Hypothetical protein DNA topoisomerase              |      | 2200 | 2403  | - | 8.1  | 67  | WP_015983553.1 | Hypothetical protein                           | <i>Escherichia coli</i>                   | 135  | $6 \times 10^{-40}$  | Yes |
| <b>g003</b> | subunit DNA-dependent ATPase                        | PPAP | 2458 | 4275  | - | 68.3 | 605 | WP_015983554.1 | DNA topoisomerase subunit DNA-dependent ATPase | <i>Escherichia coli</i>                   | 1255 | 0.0                  | Yes |
| <b>g004</b> | Hypothetical protein                                |      | 4345 | 4605  | - | 9.3  | 86  | QEG05043.1     | Hypothetical protein JK23_00004                | <i>Shigella</i> phage JK23                | 179  | $1 \times 10^{-56}$  | Yes |
| <b>g005</b> | Hypothetical protein                                |      | 4611 | 4982  | - | 14.0 | 123 | QIN97406.1     | Hypothetical protein PhiZZ23_005               | <i>Citrobacter</i> phage PhiZZ23          | 144  | $1 \times 10^{-42}$  | No  |
| <b>g006</b> | Hypothetical protein mRNA                           |      | 4985 | 5161  | - | 6.8  | 58  | WP_015995878.1 | Zinc ribbon domain-containing protein          | <i>Escherichia coli</i>                   | 123  | $1 \times 10^{-35}$  | Yes |
| <b>g007</b> | metabolism modulator                                | PPAP | 5164 | 5589  | - | 16.7 | 141 | QIN97408.1     | mRNA metabolism moderator                      | <i>Citrobacter</i> phage PhiZZ23          | 289  | $1 \times 10^{-98}$  | Yes |
| <b>g008</b> | Modifier of suppressor tRNAs                        | PPAP | 5589 | 5804  | - | 8.5  | 71  | AUV61145.1     | Modifier of suppressor tRNAs                   | <i>Escherichia</i> phage vB_EcoM-fHoEco02 | 147  | $2 \times 10^{-44}$  | No  |
| <b>g009</b> | Hypothetical protein                                | ppap | 5818 | 6087  | - | 10.2 | 89  | WP_016059243.1 | Hypothetical protein                           | <i>Escherichia coli</i>                   | 185  | $6 \times 10^{-59}$  | No  |
| <b>g010</b> | Modifier of transcription                           | PPAP | 6185 | 6676  | - | 18.3 | 163 | YP_009288377.1 | Transcriptional regulator                      | <i>Shigella</i> phage SHBML-50-1          | 329  | $9 \times 10^{-114}$ | Yes |
| <b>g011</b> | Hypothetical protein                                |      | 6750 | 7250  | - | 19.0 | 166 | WP_016059245.1 | Hypothetical protein                           | <i>Escherichia coli</i>                   | 341  | $3 \times 10^{-118}$ | Yes |
| <b>g012</b> | Hypothetical protein                                |      | 7261 | 7764  | - | 19.9 | 167 | WP_016059245.1 | Hypothetical protein AS348_gp127               | <i>Escherichia</i> phage slur14           | 345  | $5 \times 10^{-120}$ | Yes |
| <b>g013</b> | Exonuclease   | PPAP | 7828 | 8511  | - | 26.0 | 227 | YP_009180784.1 | 3'-5' exoribonuclease                          | <i>Escherichia coli</i>                   | 470  | $2 \times 10^{-167}$ | Yes |
| <b>g014</b> | Hypothetical protein                                | PPAP | 8511 | 8753  | - | 9.3  | 80  | WP_015969175.1 | Hypothetical protein                           | <i>Salmonella enterica</i>                | 160  | $1 \times 10^{-49}$  | Yes |
| <b>g015</b> | Hypothetical protein                                |      | 8746 | 8991  | - | 9.4  | 81  | WP_080181614.1 | Exonuclease                                    | <i>Yersinia</i> phage PYPS2T              | 160  | $2 \times 10^{-49}$  | Yes |
| <b>g016</b> | Hypothetical protein DNA helicase, phage-associated |      | 8978 | 9238  | - | 10.0 | 86  | AYJ74532.1     | Hypothetical protein RB51ORF017                | Enterobacteria phage RB51                 | 172  | $3 \times 10^{-54}$  | No  |
| <b>g017</b> |   | PPAP | 9245 | 10564 | - | 50.0 | 439 | YP_002853972.1 | AAA family ATPase                              | Enterobacteriaceae                        | 903  | 0                    | Yes |



|             |                                       |      |       |       |   |      |     |                 |  |                                      |     |                      |     |
|-------------|---------------------------------------|------|-------|-------|---|------|-----|-----------------|--|--------------------------------------|-----|----------------------|-----|
| <b>g018</b> | Hypothetical protein                  |      | 10561 | 10872 | - | 12.1 | 103 | WP_01605925.0.1 | Hypothetical protein                     | Enterobacteria phage RB51            | 210 | $2 \times 10^{-68}$  | Yes |
| <b>g019</b> | Anti-sigma factor, putative RNA       |      | 10874 | 11620 | - | 29.1 | 248 | YP_002853974.1  | Hypothetical protein                     | <i>Shigella flexneri</i>             | 496 | $5 \times 10^{-177}$ | Yes |
| <b>g020</b> | polymerase ADP-ribosylase NAD-protein |      | 11742 | 12344 | - | 23.4 | 200 | EFW4204073.1    | RNA polymerase ADP-ribosylase            | Enterobacteria phage RB27            | 417 | $2 \times 10^{-147}$ | Yes |
| <b>g021</b> | ADP-ribosyltransferase                |      | 12341 | 12964 | - | 24.3 | 207 | YP_009102226.1  | NAD-protein ADP-ribosyltransferase       | <i>Serratia</i> phage PhiZZ30        | 427 | $7 \times 10^{-151}$ | Yes |
| <b>g022</b> | Hypothetical protein                  |      | 13032 | 13214 | - | 7.0  | 60  | QIN97692.1      | Hypothetical protein T4p022              | <i>Escherichia</i> virus T4          | 125 | $4 \times 10^{-36}$  | Yes |
| <b>g023</b> | Hypothetical protein                  | PPAP | 13223 | 13693 | - | 18.4 | 156 | NP_049637.1     | Hypothetical protein F412_gp251          | <i>Escherichia</i> phage wV7         | 319 | $6 \times 10^{-110}$ | Yes |
| <b>g024</b> | Hypothetical protein                  |      | 13686 | 13850 | - | 6.1  | 54  | YP_007004765.1  | Hypothetical protein ECML134_023         | <i>Escherichia</i> phage ECML-134    | 108 | $1 \times 10^{-29}$  | Yes |
| <b>g025</b> | Transcription modulator               |      | 13847 | 14050 | - | 8.1  | 67  | YP_009102498.1  | Hypothetical protein                     | <i>Escherichia coli</i>              | 134 | $2 \times 10^{-39}$  | Yes |
| <b>g026</b> | Transcription modulator               | PPAP | 14025 | 14510 | - | 18.4 | 161 | WP_01596918.6.1 | Transcription modulator under heat shock | Enterobacteria phage Apg8            | 324 | $1 \times 10^{-111}$ | Yes |
| <b>g027</b> | Hypothetical protein                  |      | 14519 | 14851 | - | 12.3 | 110 | YP_010066079.1  | Hypothetical protein RB3_028             | <i>Escherichia</i> phage RB3         | 224 | $8 \times 10^{-74}$  | Yes |
| <b>g028</b> | Hypothetical protein                  | ppap | 14851 | 15057 | - | 8.2  | 68  | YP_009098414.1  | Hypothetical protein                     | <i>Escherichia</i> virus RB14        | 143 | $3 \times 10^{-43}$  | Yes |
| <b>g029</b> | Capsid protein                        | PPAP | 15154 | 15399 | - | 9.2  | 81  | YP_002854363.1  | Hypothetical protein                     | Enterobacteriaceae                   | 169 | $5 \times 10^{-53}$  | Yes |
| <b>g030</b> | Hypothetical protein dCTP             |      | 15416 | 15625 | - | 7.9  | 69  | WP_07414636.1.1 | Hypothetical protein KMB99_gp030         | Enterobacteria phage T6              | 142 | $9 \times 10^{-43}$  | No  |
| <b>g031</b> | pyrophosphatase                       | PPAP | 15825 | 16343 | - | 20.2 | 172 | YP_010067184.1  | dCTP pyrophosphatase                     | <i>Escherichia</i> phage vB_EcoM_112 | 361 | $4 \times 10^{-126}$ | Yes |
| <b>g032</b> | Hypothetical protein                  |      | 16430 | 16615 | + | 6.5  | 61  | YP_009030637.1  | Hypothetical protein                     | Enterobacteriaceae                   | 117 | $4 \times 10^{-33}$  | No  |
| <b>g033</b> | DNA primase                           |      | 16612 | 17640 | - | 39.8 | 342 | WP_01599589.8.1 | Hypothetical protein AVU02_gp166         | <i>Escherichia</i> phage slur07      | 704 | 0.0                  | Yes |
| <b>g034</b> | Hypothetical protein                  | ppap | 17643 | 17807 | - | 5.9  | 54  | YP_009197418.1  | Hypothetical protein                     | Bacteria                             | 105 | $1 \times 10^{-28}$  | Yes |

|             |  |      |       |       |   |      |     |                |  |                                   |      |                      |     |
|-------------|--|------|-------|-------|---|------|-----|----------------|--|-----------------------------------|------|----------------------|-----|
| <b>g035</b> | Hypothetical protein                     |      | 17809 | 18165 | - | 13.8 | 118 | YP_009102240.1 | Hypothetical protein RB27_035              | Enterobacteria phage RB27         | 240  | $5 \times 10^{-80}$  | Yes |
| <b>g036</b> | Hypothetical protein                     |      | 18167 | 18268 | - | 3.3  | 33  | EEV9360713.1   | Hypothetical protein                       | <i>Escherichia coli</i>           | 60.8 | $7 \times 10^{-11}$  | Yes |
| <b>g037</b> | Hypothetical protein                     |      | 18361 | 18717 | - | 13.6 | 118 | YP_009102240.1 | Hypothetical protein RB27_035              | Enterobacteria phage RB27         | 238  | $6 \times 10^{-79}$  | Yes |
| <b>g038</b> | Hypothetical protein                     | ppap | 18719 | 19345 | - | 24.5 | 208 | EEV9360713.1   | Hypothetical protein AS348_gp100           | <i>Escherichia</i> phage slur14   | 429  | $9 \times 10^{-152}$ | Yes |
| <b>g039</b> | Hypothetical protein                     | ppap | 19345 | 19638 | - | 11.0 | 97  | YP_009102240.1 | Hypothetical protein ACQ54_gp033           | <i>Escherichia</i> phage HY01     | 202  | $2 \times 10^{-65}$  | Yes |
| <b>g040</b> | Hypothetical protein                     | ppap | 19699 | 19956 | - | 10.2 | 85  | YP_009180811.1 | Hypothetical protein ECML134_037           | <i>Escherichia</i> phage ECML-134 | 174  | $6 \times 10^{-55}$  | Yes |
| <b>g041</b> | Discriminator of mRNA degradation DNA    |      | 19958 | 20140 | - | 6.9  | 60  | YP_009148484.1 | Hypothetical protein                       | <i>Bacillus cereus</i>            | 120  | $2 \times 10^{-34}$  | Yes |
| <b>g042</b> | primase/helicase                         |      | 20199 | 21626 | - | 53.6 | 475 | YP_009102512.1 | Helicase                                   | <i>Escherichia</i> virus T4       | 987  | 0.0                  | Yes |
| <b>g043</b> | Head vertex assembly chaperone RecA-like |      | 21775 | 21978 | - | 6.1  | 67  | WP_01596919.1  | Hypothetical protein                       | <i>Shigella sonnei</i>            | 92   | $4 \times 10^{-22}$  | Yes |
| <b>g044</b> | recombination protein                    | PPAP | 21971 | 23152 | - | 44.1 | 393 | NP_049654.1    | RecA-like recombination protein            | Enterobacteria phage RB18         | 810  | 0.0                  | Yes |
| <b>g045</b> | Glucosyl transferase dCMP                | PPAP | 23230 | 24072 | - | 32.4 | 280 | EFW0223305.1   | RB32ORF041c hypothetical protein           | <i>Escherichia</i> virus RB14     | 592  | 0.0                  | No  |
| <b>g046</b> | hydroxymethylase                         | PPAP | 24069 | 24809 | - | 28.6 | 246 | YP_010066924.1 | Deoxycytidylate 5-hydroxymethyltransferase | <i>Escherichia coli</i>           | 512  | 0.0                  | Yes |
| <b>g047</b> | Hypothetical protein                     |      | 24817 | 24966 | - | 5.5  | 49  | YP_002854377.1 | Hypothetical protein RB27_045              | Enterobacteria phage RB27         | 91.3 | $6 \times 10^{-23}$  | Yes |
| <b>g048</b> | Immunity to superinfection protein       |      | 24963 | 25214 | - | 9.1  | 83  | WP_01605926.1  | Superinfection immunity protein            | Bacteria                          | 158  | $2 \times 10^{-48}$  | Yes |
| <b>g049</b> | Hypothetical protein                     |      | 25222 | 25602 | - | 14.2 | 126 | YP_009102250.1 | Hypothetical protein                       | <i>Escherichia coli</i>           | 260  | $1 \times 10^{-87}$  | Yes |

|             |                                   |      |       |       |   |       |     |                    |                                       |   |      |                      |     |
|-------------|-----------------------------------|------|-------|-------|---|-------|-----|--------------------|---------------------------------------|---|------|----------------------|-----|
| <b>g050</b> | Hypothetical protein              |      | 25613 | 25849 | - | 8.1   | 78  | WP_01598359<br>2.1 | Hypothetical protein D862_gp227       | <i>Escherichia</i> phage<br>vB_EcoM_ACG-<br>C40     | 154  | $5 \times 10^{-47}$  | No  |
| <b>g051</b> | DNA polymerase                    | PPAP | 26030 | 28726 | - | 103.6 | 898 | WP_01605926<br>7.1 | DNA polymerase                        | <i>Escherichia coli</i>                             | 1865 | 0.0                  | Yes |
| <b>g052</b> | Translational repressor RegA      | PPAP | 28805 | 29173 | - | 14.6  | 122 | YP_006986599<br>.1 | Translational repressor RegA          | Bacteria  | 253  | $7 \times 10^{-85}$  | Yes |
| <b>g053</b> | Phage DNA polymerase clamp loader |      | 29175 | 29738 | - | 21.4  | 187 | WP_01599570<br>0.1 | DNA polymerase clamp loader subunit A | <i>Escherichia coli</i>                             | 383  | $2 \times 10^{-134}$ | Yes |
| <b>g054</b> | AAA family ATPase                 | PPAP | 29740 | 30699 | - | 35.8  | 319 | WP_01596920<br>9.1 | AAA family ATPase                     | Enterobacteriaceae                                  | 665  | 0.0                  | Yes |
| <b>g055</b> | Sliding clamp                     | PPAP | 30751 | 31437 | - | 24.9  | 228 | WP_01599570<br>2.1 | Sliding clamp DNA polymerase          | <i>Escherichia coli</i>                             | 464  | $4 \times 10^{-165}$ | Yes |
| <b>g056</b> | RNA polymerase binding protein    | PPAP | 31493 | 31882 | - | 14.7  | 129 | WP_01596921<br>1.1 | RNA polymerase binding protein        | <i>Escherichia</i> virus<br>T4                      | 270  | $3 \times 10^{-91}$  | Yes |
| <b>g057</b> | Hypothetical protein              |      | 31892 | 32080 | - | 7.5   | 62  | WP_01598359<br>8.1 | Hypothetical protein                  | <i>Escherichia coli</i>                             | 130  | $4 \times 10^{-38}$  | Yes |
| <b>g058</b> | AAA family ATPase                 | PPAP | 32136 | 33818 | - | 63.7  | 560 | NP_049667.1        | AAA family ATPase                     | <i>Escherichia coli</i>                             | 1145 | 0.0                  | Yes |
| <b>g059</b> | Hypothetical protein              |      | 33815 | 34021 | - | 8.1   | 68  | WP_01596921<br>4.1 | Hypothetical protein                  | <i>Escherichia</i> virus<br>RB14                    | 139  | $2 \times 10^{-41}$  | Yes |
| <b>g060</b> | Hypothetical protein              |      | 34002 | 34265 | - | 10.2  | 87  | WP_17192154<br>3.1 | Hypothetical protein                  | <i>Escherichia coli</i>                             | 178  | $2 \times 10^{-56}$  | Yes |
| <b>g061</b> | Endonuclease subunit              | ppap | 34262 | 35281 | - | 39.2  | 339 | YP_002854391<br>.1 | Recombination endonuclease subunit    | <i>Yersinia</i> phage<br>PST                        | 706  | 0.0                  | Yes |
| <b>g062</b> | Hypothetical protein              |      | 35382 | 35468 | + | 3.3   | 28  | WP_01605901<br>7.1 | No significant hits                   |   |      |                      | No  |
| <b>g063</b> | Glucosyl transferase              | PPAP | 35458 | 36660 | - | 46.9  | 400 | YP_009153659<br>.1 | Alpha-glucosyl-transferase            | <i>Escherichia</i> virus<br>RB14                    | 836  | 0.0                  | Yes |
| <b>g064</b> | Hypothetical protein              |      | 36727 | 36900 | - | 6.7   | 57  | YP_010071539<br>.1 | Hypothetical protein KMC15_gp063      | <i>Escherichia</i> phage<br>KIT03                   | 118  | $1 \times 10^{-33}$  | Yes |
| <b>g065</b> | Hypothetical protein              | PPAP | 36904 | 37107 | - | 7.9   | 67  | YP_002854395<br>.1 | Hypothetical protein KMC13_gp173      | <u><i>Escherichia</i></u><br>phage<br>vB_EcoM_IME53 | 141  | $2 \times 10^{-42}$  | Yes |

|             |   |      |       |       |   |      |     |                 |   |  |      |                      |     |
|-------------|---|------|-------|-------|---|------|-----|-----------------|---|--|------|----------------------|-----|
| <b>g066</b> | Hypothetical protein                              |      | 37076 | 37393 | - | 12.4 | 105 | YP_010071539    | DUF2654 domain-containing protein                                     | <i>Salmonella enterica</i>               | 208  | $1 \times 10^{-67}$  | Yes |
| <b>g067</b> | Hypothetical protein RNA                          |      | 37395 | 37613 | - | 8.5  | 72  | YP_010071101.1  | Hypothetical protein  | Bacteria                                 | 144  | $1 \times 10^{-43}$  | Yes |
| <b>g068</b> | polymerase sigma factor                           |      | 37597 | 38154 | - | 21.5 | 185 | EBK7480135.1    | Sigma factor  | <i>Escherichia</i> phage vB_EcoM_112     | 386  | $1 \times 10^{-135}$ | Yes |
| <b>g069</b> | Hypothetical protein                              | PPAP | 38233 | 38502 | - | 10.8 | 89  | WP_01596922.5.1 | Hypothetical protein  | Bacteria                                 | 185  | $5 \times 10^{-59}$  | Yes |
| <b>g070</b> | Hypothetical protein                              |      | 38499 | 38714 | - | 8.1  | 71  | YP_009030673.1  | Hypothetical protein AS348_gp070                                      | <i>Escherichia</i> phage slur14          | 144  | $6 \times 10^{-42}$  | Yes |
| <b>g071</b> | Hypothetical protein                              | PPAP | 38717 | 39043 | - | 12.8 | 108 | WP_01599591.6.1 | Hypothetical protein FDJ02_gp066                                      | <i>Shigella</i> phage Sf2                | 218  | $3 \times 10^{-71}$  | Yes |
| <b>g072</b> | Hypothetical protein                              |      | 39097 | 39297 | - | 7.7  | 66  | YP_009180841.1  | Hypothetical protein  | <i>Salmonella enterica</i>               | 139  | $2 \times 10^{-41}$  | Yes |
| <b>g073</b> | Hypothetical protein                              |      | 39298 | 39429 | - | 5.1  | 43  | YP_009618880.1  | Hypothetical protein KMC13_gp181                                      | <i>Escherichia</i> phage vB_EcoM_IME53_7 | 91.7 | $5 \times 10^{-23}$  | Yes |
| <b>g074</b> | Hypothetical protein                              |      | 39437 | 39730 | - | 11.8 | 97  | WP_01598361.1.1 | Hypothetical protein  | <i>Escherichia coli</i>                  | 193  | $5 \times 10^{-62}$  | Yes |
| <b>g075</b> | Hypothetical protein                              |      | 39723 | 39905 | - | 6.9  | 60  | YP_010071109.1  | Hypothetical protein  | Bacteria                                 | 122  | $7 \times 10^{-35}$  | Yes |
| <b>g076</b> | Hypothetical protein                              |      | 39930 | 40016 | + | 3.1  | 28  | WP_01596923.1.1 | Hypothetical protein RB14ORF72  | <i>Escherichia</i> virus RB14            | 55.1 | $4 \times 10^{-09}$  | No  |
| <b>g077</b> | NrdH glutaredoxin                                 |      | 40064 | 40372 | - | 11.7 | 102 | WP_10077131.3.1 | NrdH glutaredoxin   | Bacteria                                 | 211  | $1 \times 10^{-68}$  | Yes |
| <b>g078</b> | Hypothetical protein                              |      | 40375 | 40587 | - | 7.9  | 70  | YP_002854408.1  | Hypothetical protein  | Bacteria                                 | 137  | $1 \times 10^{-40}$  | Yes |
| <b>g079</b> | Hypothetical protein                              |      | 40597 | 40710 | - | 4.5  | 37  | WP_01596923.3.1 | Putative ribonucleotide reductase of class III activating protein     | <i>Salmonella</i> phage pSe_SNUABM_0_1   | 78.6 | $8 \times 10^{-18}$  | No  |
| <b>g080</b> | Ribonucleotide reductase of class III (anaerobic) |      | 40703 | 41173 | - | 18.1 | 156 | WP_01596923.4.1 | Ribonucleotide reductase of class III (anaerobic), activating protein | <i>Escherichia</i> phage ECML-134        | 323  | $1 \times 10^{-111}$ | Yes |
| <b>g081</b> | Anaerobic NTP reductase, large subunit            | PPAP | 41170 | 42987 | - | 67.4 | 605 | YP_010075342.1  | Anaerobic NTP reductase large subunit                                 | <i>Escherichia</i> phage wV7             | 1256 | 0.0                  | Yes |

|      |                                |      |       |       |   |      |     |                 |                                       |  |     |                      |     |
|------|--------------------------------|------|-------|-------|---|------|-----|-----------------|---------------------------------------|--|-----|----------------------|-----|
| g082 | Recombination endonuclease VII | PPAP | 42984 | 43457 | - | 18.2 | 157 | YP_009102550.1  | Recombination endonuclease VII        | Bacteria                               | 322 | $4 \times 10^{-111}$ | Yes |
|      | Pin protease inhibitor         |      | 43499 | 43984 | - | 18.8 | 161 | YP_007004820.1  | Hypothetical protein KMC04_gp083      | <i>Escherichia</i> phage vB_EcoM_F1    | 329 | $9 \times 10^{-114}$ | Yes |
| g084 | Hypothetical protein           |      | 43968 | 44123 | - | 6.2  | 51  | WP_01596923.9.1 | Conserved protein of unknown function | <i>Escherichia</i> virus T4            | 105 | $2 \times 10^{-28}$  | Yes |
| g085 | Hypothetical protein           | PPAP | 44108 | 44428 | - | 12.7 | 106 | YP_010068568.1  | Hypothetical protein KMC11_gp082      | <i>Escherichia</i> phage vB_EcoM_G4507 | 214 | $5 \times 10^{-70}$  | Yes |
| g086 | Hypothetical protein           |      | 44440 | 44610 | - | 6.6  | 56  | NP_049695.1     | Hypothetical protein KMC34_gp078      | <i>Shigella</i> phage SH7              | 114 | $4 \times 10^{-31}$  | Yes |
| g087 | Hypothetical protein           | ppap | 44613 | 44828 | - | 8.1  | 71  | YP_010070460.1  | Hypothetical protein KMC34_gp078      | <i>Shigella</i> phage SH7              | 146 | $2 \times 10^{-43}$  | No  |
| g088 | NrdC thioredoxin               |      | 44825 | 45088 | - | 10.0 | 87  | YP_010076700.1  | NrdC thioredoxin                      | Enterobacteriaceae                     | 182 | $4 \times 10^{-58}$  | Yes |
| g089 | Hypothetical protein           | PPAP | 45090 | 45311 | - | 8.5  | 73  | YP_010076700.1  | Hypothetical protein                  | Enterobacteria phage RB51              | 150 | $7 \times 10^{-46}$  | Yes |
| g090 | Hypothetical protein           |      | 45335 | 45724 | - | 14.9 | 129 | WP_01596924.5.1 | Hypothetical protein                  | <i>Escherichia</i> virus RB14          | 268 | $8 \times 10^{-91}$  | Yes |
| g091 | Thioredoxin, phage-associated  | PPAP | 45721 | 46650 | - | 36.0 | 309 | YP_002854044.1  | Thioredoxin                           | Enterobacteria phage GiZh              | 635 | 0.0                  | Yes |
| g092 | Thioredoxin, phage-associated  | PPAP | 46703 | 47704 | - | 38.9 | 333 | YP_002854422.1  | Thioredoxin                           | <i>Escherichia</i> phage PE37          | 672 | 0.0                  | Yes |
| g093 | Thioredoxin, phage-associated  | PPAP | 47762 | 48781 | - | 39.7 | 339 | ANZ51524.1      | Thioredoxin                           | <i>Citrobacter</i> phage PhiZZ23       | 703 | 0.0                  | Yes |
| g094 | Thioredoxin, phage-associated  |      | 48790 | 49677 | - | 33.8 | 295 | YP_010073276.1  | Hypothetical protein                  | <i>Escherichia coli</i>                | 596 | 0.0                  | Yes |
| g095 | Thioredoxin, phage-associated  |      | 49685 | 50092 | - | 15.5 | 135 | YP_010065734.1  | Thioredoxin                           | Enterobacteria phage Kha5h             | 274 | $7 \times 10^{-93}$  | Yes |
| g096 | Hypothetical protein           |      | 50148 | 50675 | - | 20.8 | 175 | EGI3119413.1    | Hypothetical protein                  | Enterobacteriaceae                     | 352 | $2 \times 10^{-122}$ | Yes |
| g097 | Hypothetical protein           |      | 50736 | 51038 | - | 11.9 | 100 | YP_010066760.1  | Hypothetical protein KMC34_gp088      | <i>Shigella</i> phage SH7              | 209 | $4 \times 10^{-68}$  | Yes |

|             |  |      |       |       |   |      |     |                    |   |   |      |                      |     |
|-------------|--|------|-------|-------|---|------|-----|--------------------|---|---|------|----------------------|-----|
| <b>g098</b> | Hypothetical protein                         |      | 51140 | 52108 | - | 35.8 | 322 | WP_01599593<br>9.1 | Hypothetical protein                                    | <i>Salmonella enterica</i>                        | 636  | 0.0                  | Yes |
| <b>g099</b> | Hypothetical protein                         |      | 52166 | 52366 | - | 7.7  | 66  | YP_010076710<br>.1 | Hypothetical protein                                    | <i>Shigella flexneri</i>                          | 137  | $8 \times 10^{-41}$  | No  |
| <b>g100</b> | Hypothetical protein                         | PPAP | 52486 | 53496 | - | 38.9 | 336 | WP_01605928<br>8.1 | Hypothetical protein ACQ28_gp094                        | <i>Yersinia</i> phage PST                         | 701  | 0.0                  | Yes |
| <b>g101</b> | Hypothetical protein                         |      | 53496 | 53957 | - | 17.9 | 153 | EFW3029406.1       | Hypothetical protein                                    | <i>Shigella sonnei</i>                            | 308  | $9 \times 10^{-10}$  | No  |
| <b>g102</b> | Hypothetical protein                         | PPAP | 53960 | 54481 | - | 19.2 | 173 | YP_009153697<br>.1 | Hypothetical protein                                    | <i>Salmonella enterica</i> subsp. <i>enterica</i> | 353  | $8 \times 10^{-123}$ | No  |
| <b>g103</b> | Hypothetical protein                         |      | 54488 | 55021 | - | 20.7 | 177 | EFX0167658.1       | Hypothetical protein KMB91_gp052                        | <i>Citrobacter</i> phage vB_CroM_CrRp1<br>0       | 357  | $3 \times 10^{-124}$ | Yes |
| <b>g104</b> | Hypothetical protein                         | ppap | 55023 | 55289 | - | 10.2 | 88  | EDU9380925.1       | Hypothetical protein KMC13_gp215                        | <i>Escherichia</i> phage vB_EcoM_IME53<br>7       | 182  | $7 \times 10^{-58}$  | No  |
| <b>g105</b> | Hypothetical protein                         |      | 55291 | 55476 | - | 6.9  | 61  | YP_010065158<br>.1 | Hypothetical protein RB3_102                            | <i>Escherichia</i> phage RB3                      | 123  | $2 \times 10^{-35}$  | No  |
| <b>g106</b> | Hypothetical protein                         |      | 55476 | 55580 | - | 4.2  | 34  | YP_010071143<br>.1 | Hypothetical protein RB3_103                            | <i>Escherichia</i> phage RB3                      | 65.9 | $3 \times 10^{-13}$  | Yes |
| <b>g107</b> | Hypothetical protein                         |      | 55641 | 55814 | - | 6.7  | 57  | YP_009098488<br>.1 | Hypothetical protein                                    | <i>Escherichia coli</i>                           | 118  | $2 \times 10^{-33}$  | Yes |
| <b>g108</b> | Hypothetical protein                         |      | 55804 | 55998 | - | 7.6  | 64  | YP_009098489<br>.1 | Hypothetical protein                                    | Bacteria  | 131  | $1 \times 10^{-38}$  | Yes |
| <b>g109</b> | Hypothetical protein                         |      | 56001 | 56204 | - | 7.7  | 67  | WP_01599594<br>9.1 | Hypothetical protein ACQ28_gp103                        | <i>Yersinia</i> phage PST                         | 129  | $1 \times 10^{-37}$  | Yes |
| <b>g110</b> | Hypothetical protein                         |      | 56204 | 56392 | - | 7.2  | 62  | WP_01599574<br>0.1 | Molybdopterin-guanine dinucleotide biosynthesis protein | <i>Escherichia coli</i>                           | 127  | $7 \times 10^{-37}$  | Yes |
| <b>g111</b> | Hypothetical protein                         | ppap | 56488 | 56874 | - | 14.6 | 128 | YP_009153706<br>.1 | Hypothetical protein                                    | Bacteria  | 259  | $3 \times 10^{-87}$  | Yes |
| <b>g112</b> | Lysis inhibition regulator, membrane protein |      | 56871 | 57164 | - | 11.1 | 97  | YP_002854065<br>.1 | rI membrane protein                                     | Enterobacteria phage RB51                         | 203  | $7 \times 10^{-66}$  | Yes |
| <b>g113</b> | Hypothetical protein                         | PPAP | 57177 | 57389 | - | 8.3  | 79  | WP_07414647<br>8.1 | Hypothetical protein                                    | Bacteria  | 141  | $2 \times 10^{-42}$  | Yes |

|             |   |      |       |       |   |      |     |                    |  |  |     |                      |     |
|-------------|---|------|-------|-------|---|------|-----|--------------------|--|--|-----|----------------------|-----|
| <b>g114</b> | Thymidine kinase                                      | ppap | 57432 | 58013 | - | 21.6 | 193 | WP_01596926<br>4.1 | Thymidine kinase                               | <i>Escherichia coli</i>                | 402 | $2 \times 10^{-141}$ | Yes |
| <b>g115</b> | Hypothetical protein                                  |      | 58023 | 58178 | - | 6.1  | 51  | YP_002854065<br>.1 | Hypothetical protein                           | <i>Escherichia coli</i>                | 100 | $2 \times 10^{-26}$  | Yes |
| <b>g116</b> | Hypothetical protein                                  |      | 58206 | 58382 | - | 6.5  | 58  | WP_01596926<br>6.1 | Hypothetical protein                           | <i>Escherichia coli</i>                | 112 | $4 \times 10^{-31}$  | No  |
| <b>g117</b> | Hypothetical protein                                  | ppap | 58379 | 58585 | - | 7.9  | 68  | WP_01598364<br>4.1 | Hypothetical protein RB3_114                   | <i>Escherichia</i> phage<br>RB         | 114 | $2 \times 10^{-43}$  | No  |
| <b>g118</b> | Hypothetical protein                                  |      | 58582 | 58794 | - | 8.5  | 70  | WP_17922678<br>7.1 | Hypothetical protein                           | Enterobacteria<br>phage RB51           | 148 | $6 \times 10^{-45}$  | Yes |
| <b>g119</b> | Macro domain-<br>containing<br>protein                | ppap | 58766 | 59245 | - | 17.5 | 159 | WP_17922678<br>6.1 | Hypothetical protein Sf25_gp241                | <i>Shigella</i> phage<br>Sf25          | 327 | $6 \times 10^{-113}$ | Yes |
| <b>g120</b> | Valyl-tRNA<br>synthetase<br>modifier                  | PPAP | 59242 | 59583 | - | 12.9 | 113 | YP_009098500<br>.1 | Hypothetical protein                           | <i>Escherichia coli</i>                | 231 | $1 \times 10^{-76}$  | Yes |
| <b>g121</b> | Transglycosyla<br>se domain-<br>containing<br>protein |      | 59576 | 60121 | - | 20.7 | 181 | YP_002854071<br>.1 | Transglycosylase SLT domain-containing protein | Enterobacteriace<br>ae                 | 371 | $8 \times 10^{-130}$ | Yes |
| <b>g122</b> | Site-specific<br>RNA<br>endonuclease                  |      | 60129 | 60590 | - | 18.0 | 153 | AUV63521.1         | Site-specific RNA endonuclease                 | Enterobacteriace<br>ae                 | 318 | $9 \times 10^{-11}$  | Yes |
| <b>g123</b> | Hypothetical<br>protein                               | PPAP | 60650 | 60928 | - | 10.9 | 92  | WP_01599574<br>8.1 | Hypothetical protein                           | <i>Escherichia coli</i>                | 187 | $6 \times 10^{-60}$  | Yes |
| <b>g124</b> | Hypothetical<br>protein                               |      | 60928 | 61194 | - | 10.1 | 88  | WP_01596927<br>3.1 | Hypothetical protein                           | <i>Escherichia</i> virus<br>RB14       | 180 | $4 \times 10^{-57}$  | Yes |
| <b>g125</b> | Hypothetical<br>protein                               |      | 61187 | 61408 | - | 8.3  | 73  | WP_01605415<br>0.1 | Hypothetical protein                           | <i>Escherichia coli</i>                | 152 | $1 \times 10^{-46}$  | Yes |
| <b>g126</b> | Hypothetical<br>protein                               |      | 61408 | 61770 | - | 13.8 | 120 | WP_01599595<br>5.1 | Autonomous glycyl radical cofactor GrcA        | <i>Bacillus cereus</i>                 | 246 | $3 \times 10^{-8}$   | Yes |
| <b>g127</b> | Hypothetical<br>protein                               |      | 61778 | 62107 | - | 12.8 | 109 | YP_002854457<br>.1 | Hypothetical protein F412_gp150                | <i>Escherichia</i> phage<br>wV7        | 226 | $1 \times 10^{-74}$  | Yes |
| <b>g128</b> | Hypothetical<br>protein                               |      | 62104 | 62643 | - | 20.3 | 179 | WP_01598365<br>4.1 | Hypothetical protein e112_126                  | <i>Escherichia</i> phage<br>vB_EcoM_11 | 372 | $2 \times 10^{-130}$ | Yes |
| <b>g129</b> | Head protein  | PPAP | 62785 | 63258 | - | 17.8 | 157 | WP_01598365<br>5.1 | Hypothetical protein                           | Enterobacteriace<br>a                  | 320 | $2 \times 10^{-11}$  | Yes |

|             |   |      |       |       |   |      |     |                |  |  |     |                      |     |
|-------------|---|------|-------|-------|---|------|-----|----------------|--|--|-----|----------------------|-----|
| <b>g130</b> | DenV endonuclease V, N-glycosylase UV repair enzyme T4-like phage baseplate hub and tail lysozyme | PPAP | 63268 | 63684 | - | 16.3 | 138 | YP_007004866.1 | Pyrimidine dimer DNA glycosylase/endonuclease V    | <i>Escherichia coli</i>                  | 286 | $2 \times 10^{-97}$  | Yes |
| <b>g131</b> | NudE nudix hydrolase  | PPAP | 63744 | 64238 | - | 18.1 | 164 | YP_009030731.1 | Glycoside hydrolase family protein                 | <i>Escherichia coli</i>                  | 331 | $2 \times 10^{-114}$ | Yes |
| <b>g132</b> | Hypothetical protein  | PPAP | 64276 | 64716 | - | 17.0 | 146 | WP_015983658.1 | Nudix hydrolase                                    | <i>Escherichia phage vB_EcoM_ACG-C40</i> | 308 | $4 \times 10^{-106}$ | Yes |
| <b>g133</b> | Hypothetical protein  |      | 64713 | 65201 | - | 18.9 | 162 | WP_171921338.1 | Hypothetical protein                               | <i>Escherichia coli</i>                  | 327 | $5 \times 10^{-113}$ | Yes |
| <b>g134</b> | Hypothetical protein  |      | 65198 | 65560 | - | 14.1 | 120 | EFD8442378.1   | Hypothetical protein KMC04_gp133                   | <i>Escherichia phage vB_EcoM_F1</i>      | 241 | $2 \times 10^{-80}$  | Yes |
| <b>g135</b> | Hypothetical protein  |      | 65542 | 65934 | - | 14.6 | 130 | YP_006986679.1 | Conserved hypothetical, predicted membrane protein | <i>Escherichia virus T4</i>              | 243 | $7 \times 10^{-81}$  | Yes |
| <b>g136</b> | Hypothetical protein  | PPAP | 65903 | 66511 | - | 23.9 | 202 | EFD7933955.1   | Hypothetical protein JB75_0139                     | <i>Escherichia phage vB_EcoM_JB75</i>    | 412 | $4 \times 10^{-145}$ | Yes |
| <b>g137</b> | Hypothetical protein  | PPAP | 66553 | 67146 | - | 22.1 | 197 | YP_010068618.1 | Hypothetical protein                               | <i>Escherichia coli</i>                  | 384 | $2 \times 10^{-134}$ | Yes |
| <b>g138</b> | Hypothetical protein  |      | 67190 | 67366 | - | 6.5  | 58  | NP_049740.1    | Hypothetical protein RB14ORF134                    | <i>Escherichia virus RB14</i>            | 119 | $9 \times 10^{-34}$  | No  |
| <b>g139</b> | Hypothetical protein  |      | 67435 | 67698 | - | 10.2 | 87  | AXC34057.1     | Phage protein                                      | <i>Escherichia phage ime09</i>           | 183 | $6 \times 10^{-58}$  | Yes |
| <b>g140</b> | Hypothetical protein  | PPAP | 67942 | 68415 | - | 17.3 | 157 | WP_015969290.1 | Hypothetical protein e112_137                      | <i>Escherichia phage vB_EcoM_112</i>     | 317 | $5 \times 10^{-109}$ | No  |
| <b>g141</b> | Hypothetical protein  | PPAP | 69572 | 70180 | - | 22.9 | 202 | VUF55460.1     | Hypothetical protein                               | <i>Escherichia phage T4_ev151</i>        | 404 | $4 \times 10^{-14}$  | No  |
| <b>g142</b> | Hypothetical protein  | PPAP | 70280 | 70795 | - | 20.0 | 171 | YP_002854470.1 | Hypothetical protein KMC31_gp267                   | <i>Shigella phage CM8</i>                | 343 | $6 \times 10^{-119}$ | No  |
| <b>g143</b> | Hypothetical protein  |      | 70798 | 71088 | - | 10.8 | 96  | YP_009197316.1 | Hypothetical protein AVU02_gp120                   | <i>Escherichia phage slur07</i>          | 187 | $7 \times 10^{-60}$  | Yes |
| <b>g144</b> | Hypothetical protein  | PPAP | 71091 | 71471 | - | 14.3 | 126 | YP_007004513.1 | Hypothetical protein                               | <i>Shigella flexneri</i>                 | 261 | $4 \times 10^{-88}$  | Yes |



|             |   |      |       |       |   |      |     |                 |   |  |      |                      |     |
|-------------|---|------|-------|-------|---|------|-----|-----------------|---|--|------|----------------------|-----|
| <b>g145</b> | Hypothetical protein                          |      | 71473 | 71658 | - | 6.6  | 61  | EEX1215785.1    | Hypothetical protein  | <i>Escherichia coli</i>                  | 117  | $6 \times 10^{-33}$  | Yes |
| <b>g146</b> | Head protein                                  | PPAP | 71727 | 72011 | - | 10.1 | 94  | YP_009030742.1  | Hypothetical protein KMC01_gp262                              | <i>Escherichia</i> phage EC121           | 188  | $4 \times 10^{-60}$  | Yes |
| <b>g147</b> | Hypothetical protein                          | ppap | 72084 | 72539 | - | 17.1 | 151 | WP_01598367.5.1 | Hypothetical protein  | Bacteria                                 | 312  | $2 \times 10^{-107}$ | Yes |
| <b>g148</b> | Chaperone for tail fiber formation            | PPAP | 72539 | 72781 | - | 8.7  | 80  | VUF55460.1      | Putative chaperone long and short tail fiber assembly protein | <i>Shigella</i> phage Shfl2              | 151  | $7 \times 10^{-46}$  | Yes |
| <b>g149</b> | Deoxynucleoside monophosphate kinase          | PPAP | 72781 | 73506 | - | 27.3 | 241 | QEG04817.1      | Putative deoxynucleotide monophosphate kinase                 | <i>Shigella</i> phage Shfl2              | 499  | $1 \times 10^{-17}$  | Yes |
| <b>g150</b> | Tail completion and sheath stabilizer protein | PPAP | 73556 | 74086 | - | 19.7 | 176 | YP_009197316.1  | Tail completion and sheath stabilizer protein                 | <i>Escherichia</i> phage vB_EcoM_ACG-C40 | 362  | $2 \times 10^{-126}$ | Yes |
| <b>g151</b> | DNA end protector protein                     | PPAP | 74193 | 75017 | - | 31.5 | 274 | EFW3029441.1    | DNA end protector protein                                     | Enterobacteria phage RB18                | 561  | 0.0                  | Yes |
| <b>g152</b> | Head completion protein                       |      | 75017 | 75469 | - | 17.6 | 150 | EEX1215785.1    | Head completion   | Bacteria                                 | 309  | $3 \times 10^{-10}$  | Yes |
| <b>g153</b> | Baseplate wedge protein                       | PPAP | 75517 | 76107 | + | 22.7 | 196 | YP_010067823.1  | Baseplate wedge protein                                       | <i>Escherichia coli</i>                  | 399  | $4 \times 10^{-140}$ | Yes |
| <b>g154</b> | Baseplate hub subunit and tail lysozyme       |      | 76091 | 76222 | + | 4.5  | 43  | WP_01598367.5.1 | Phage tail protein  | <i>Shigella flexneri</i>                 | 77.4 | $1 \times 10^{-17}$  | Yes |
| <b>g155</b> | Baseplate hub subunit and tail lysozyme       | PPAP | 76222 | 77817 | + | 58.1 | 531 | YP_004415038.1  | Baseplate hub subunit and tail lysozyme                       | Enterobacteria phage RB51                | 1084 | 0.0                  | Yes |
| <b>g156</b> | Hypothetical protein                          |      | 77810 | 78346 | + | 20.0 | 178 | YP_004415039.1  | Hypothetical protein ECML134_147                              | <i>Escherichia</i> phage ECML-134        | 359  | $4 \times 10^{-125}$ | Yes |
| <b>g157</b> | PAAR domain-containing protein                |      | 78347 | 78640 | + | 10.2 | 97  | YP_006986698.1  | PAAR domain-containing protein                                | Bacteria                                 | 199  | $3 \times 10^{-64}$  | Yes |
| <b>g158</b> | Baseplate wedge subunit                       | PPAP | 78649 | 80631 | + | 74.4 | 660 | YP_010067029.1  | Baseplate wedge subunit                                       | Enterobacteria phage GiZh                | 1346 | 0.0                  | Yes |

|             |   |      |        |        |   |      |      |                |   |   |      |                      |     |
|-------------|---|------|--------|--------|---|------|------|----------------|---|---|------|----------------------|-----|
| <b>g159</b> | Baseplate wedge initiator                     | PPAP | 80628  | 83726  | + | 11.9 | 1032 | WP_015983680.1 | Baseplate wedge subunit                       | <i>Escherichia coli</i>                 | 2138 | 0.0                  | Yes |
| <b>g160</b> | Baseplate wedge subunit                       | PPAP | 83719  | 84723  | + | 37.5 | 334  | WP_016039570.1 | Baseplate wedge subunit                       | Enterobacteria phage GiZh               | 684  | 0.0                  | Yes |
| <b>g161</b> | Baseplate wedge tail fiber connector          | PPAP | 84787  | 85653  | + | 31.0 | 288  | EFW4640011.1   | Putative baseplate wedge tail fiber connector | <i>Shigella</i> phage Shfl2             | 587  | 0.0                  | Yes |
| <b>g162</b> | Baseplate wedge subunit and tail pin          | PPAP | 85653  | 87461  | + | 65.6 | 602  | YP_002854107.1 | Baseplate wedge subunit and tail pin          | <i>Citrobacter</i> phage vB_CroM_CrRp10 | 1220 | 0.0                  | Yes |
| <b>g163</b> | Baseplate wedge subunit and tail pin          | PPAP | 87461  | 88120  | + | 23.7 | 219  | YP_009102622.1 | Phage baseplate wedge                         | <i>Escherichia</i> phage ime09          | 447  | $2 \times 10^{-158}$ | Yes |
| <b>g164</b> | Short tail fibers                             | PPAP | 88117  | 89700  | + | 55.8 | 527  | WP_015969311.1 | Putative short tail fiber protein             | <i>Shigella</i> phage Shfl2             | 1079 | 0.0                  | Yes |
| <b>g165</b> | Fibritin                                      | PPAP | 89697  | 91160  | + | 51.8 | 487  | YP_010066350.1 | Hypothetical protein SAJKIND_2                | <i>Staphylococcus</i> phage SAJK-IND    | 95   | 0.0                  | Yes |
| <b>g166</b> | Neck protein                                  | ppap | 91193  | 92122  | + | 34.7 | 309  | EFR8158913.1   | Putative neck protein                         | <i>Bacillus cereus</i>                  | 640  | 0.0                  | Yes |
| <b>g167</b> | Neck protein                                  | ppap | 92124  | 92894  | + | 29.6 | 256  | YP_010066352.1 | Neck protein                                  | <i>Escherichia</i> phage vB_EcoM_112    | 523  | 0.0                  | Yes |
| <b>g168</b> | Tail sheath stabilizer and completion protein | PPAP |        | +      |   | 29.6 | 256  | YP_004415050.1 | Tail sheath stabilizer and completion protein | <i>Escherichia coli</i>                 | 529  | 0.0                  | Yes |
| <b>g169</b> | Small terminase protein                       | ppap | 93763  | 94257  | + | 18.4 | 164  | YP_010065217.1 | Small terminase protein                       | Bacteria                                | 338  | $4 \times 10^{-117}$ | Yes |
| <b>g170</b> | Large terminase protein                       |      | 94241  | 96073  | + | 69.7 | 610  | YP_007004536.1 | Terminase large subunit                       | <i>Escherichia</i> phage ECML-134       | 1273 | 0.0                  | Yes |
| <b>g171</b> | Tail sheath protein                           | PPAP | 96105  | 98084  | + | 71.3 | 659  | YP_004415053.1 | Putative tail sheath protein                  | <i>Escherichia</i> phage vB_EcoM_G8     | 1342 | 0.0                  | Yes |
| <b>g172</b> | Tail protein                                  | PPAP | 98201  | 98692  | + | 18.4 | 163  | ATN93928.1     | Phage tail protein                            | Bacteria                                | 336  | $2 \times 10^{-116}$ | Yes |
| <b>g173</b> | Portal protein                                | PPAP | 98776  | 100350 | + | 61.0 | 524  | WP_016039581.1 | Putative portal vertex of the head            | <i>Shigella</i> phage Shfl2             | 1095 | 0.0                  | Yes |
| <b>g174</b> | Prohead core protein                          |      | 100350 | 100589 | + | 8.9  | 79   | YP_009030770.1 | Prohead core protein                          | Bacteria                                | 143  | $9 \times 10^{-43}$  | Yes |

|             |   |      |            |            |   |      |     |                    |   |  |      |                      |     |
|-------------|---|------|------------|------------|---|------|-----|--------------------|---|--|------|----------------------|-----|
| <b>g175</b> | Prohead core protein                          | PPAP | 10072<br>1 | 10101<br>4 | + | 11.0 | 97  | WP_01605418<br>5.1 | Prohead core                                    | <i>Escherichia virus</i><br>RB3                | 192  | $3 \times 10^{-61}$  | Yes |
| <b>g176</b> | Prohead core scaffolding protein and protease | PPAP | 10101<br>4 | 10165<br>2 | + | 23.3 | 212 | WP_01596932<br>3.1 | Prohead core scaffolding protein and protease   | Bacteria                                       | 431  | $1 \times 10^{-152}$ | Yes |
| <b>g177</b> | Prohead core protein                          | PPAP | 10168<br>3 | 10249<br>2 | + | 29.9 | 269 | YP_009102636<br>.1 | Prohead core scaffold protein                   | <i>Escherichia</i> phage<br>vB_EcoM_ACG-C40    | 525  | 0.0                  | Yes |
| <b>g178</b> | Major capsid protein                          | PPAP | 10251<br>1 | 10407<br>6 | + | 56.3 | 521 | YP_010069460<br>.1 | Major capsid protein                            | <i>Shigella</i> phage<br>SHFML-11              | 1065 | 0.0                  | Yes |
| <b>g179</b> | Capsid vertex protein                         | PPAP | 10416<br>0 | 10544<br>3 | + | 47.0 | 427 | WP_01596932<br>9.1 | Capsid vertex protein                           | <i>Escherichia coli</i>                        | 872  | 0.0                  | Yes |
| <b>g180</b> | RNA ligase                                    | PPAP | 10547<br>3 | 10647<br>7 | - | 37.5 | 334 | YP_004415062<br>.1 | RNA ligase                                      | <i>Escherichia</i> phage<br>slur14             | 681  | 0.0                  | Yes |
| <b>g181</b> | Hypothetical protein                          |      | 10648<br>7 | 10676<br>5 | - | 11.0 | 92  | WP_01605418<br>8.1 | Hypothetical protein                            | Enterobacteriaceae                             | 188  | $5 \times 10^{-60}$  | Yes |
| <b>g182</b> | Hypothetical protein                          |      | 10675<br>2 | 10695<br>5 | - | 7.8  | 67  | YP_803112.1        | Hypothetical protein e112_188                   | <i>Escherichia</i> phage<br>vB_EcoM_112        | 134  | $2 \times 10^{-39}$  | Yes |
| <b>g183</b> | Capsid protein                                | PPAP | 10705<br>7 | 10847<br>5 | - | 50.6 | 472 | WP_01599578<br>7.1 | PKD domain protein                              | <i>Escherichia</i> phage<br>vB_EcoM_G1040<br>0 | 916  | 0.0                  | Yes |
| <b>g184</b> | Inhibitor of prohead protease                 | PPAP | 10848<br>5 | 10916<br>5 | - | 25.5 | 226 | YP_006986725<br>.1 | Inhibitor of prohead protease                   | <i>Escherichia</i> phage<br>vB_EcoM_ACG-C40    | 454  | $3 \times 10^{-161}$ | Yes |
| <b>g185</b> | ATP-dependent DNA helicase                    | PPAP | 10921<br>6 | 11072<br>7 | + | 57.9 | 503 | YP_009277546<br>.1 | Helicase  | <i>Shigella</i> phage<br>Sf23                  | 1042 | 0.0                  | Yes |
| <b>g186</b> | ATP-dependent DNA helicase                    | PPAP | 11075<br>3 | 11098<br>3 | + | 8.8  | 76  | WP_01599579<br>0.1 | RNA-DNA and DNA-DNA helicase ATPase             | <i>Escherichia</i> phage<br>vB_EcoM_112        | 148  | $7 \times 10^{-45}$  | Yes |
| <b>g187</b> | Hypothetical protein                          | PPAP | 11103<br>9 | 11120<br>6 | - | 6.1  | 55  | YP_009180676<br>.1 | DUF2685 domain-containing protein               | Bacteria                                       | 112  | $3 \times 10^{-31}$  | Yes |
| <b>g188</b> | Hypothetical protein                          |      | 11123<br>5 | 11145<br>9 | - | 9.0  | 74  | WP_01599579<br>2.1 | Hypothetical protein RB3_183                    | <i>Escherichia</i> phage<br>RB3                | 154  | $4 \times 10^{-47}$  | Yes |
| <b>g189</b> | Recombination, repair and                     | PPAP | 11145<br>9 | 11187<br>2 | - | 15.8 | 137 | YP_009030785<br>.1 | Recombination, repair and ssDNA-binding protein | <i>Escherichia</i> phage<br>ime09              | 276  | $9 \times 10^{-94}$  | Yes |

|                       |  |      |            |            |   |      |     |                    |  |                                      |      |                      |     |
|-----------------------|--|------|------------|------------|---|------|-----|--------------------|--|--------------------------------------|------|----------------------|-----|
| ssDNA-binding protein |  |      |            |            |   |      |     |                    |  |                                      |      |                      |     |
| <b>g190</b>           | Baseplate wedge subunit                        | PPAP | 11193<br>9 | 11233<br>7 | - | 15.1 | 132 | QBO63695.1         | GPW/gp25 family protein                      | Bacteria                             | 267  | $3 \times 10^{-90}$  | Yes |
| <b>g191</b>           | Baseplate hub subunit                          | ppap | 11233<br>7 | 11296<br>3 | - | 23.6 | 208 | YP_006986734<br>.1 | gp26 family baseplate hub assembly chaperone | <i>Escherichia coli</i>              | 422  | $4 \times 10^{-149}$ | Yes |
| <b>g192</b>           | Baseplate hub assembly protein                 | PPAP | 11301<br>4 | 11376<br>3 | + | 28.9 | 249 | YP_010076380<br>.1 | Hypothetical protein e112_19                 | <i>Escherichia</i> phage vB_EcoM_112 | 496  | $7 \times 10^{-177}$ | Yes |
| <b>g193</b>           | Baseplate hub subunit                          | PPAP | 11376<br>3 | 11493<br>8 | + | 44.4 | 391 | YP_009030789<br>.1 | Baseplate hub subunit                        | <i>Escherichia</i> virus RB14        | 81   | 0.0                  | Yes |
| <b>g194</b>           | Baseplate hub distal subunit                   | PPAP | 11488<br>3 | 11541<br>6 | + | 20.1 | 177 | WP_01596934<br>6.1 | Base plate distal hub subunit                | Bacteria                             | 357  | $2 \times 10^{-124}$ | Yes |
| <b>g195</b>           | Baseplate hub subunit, tail length determinant | PPAP | 11541<br>3 | 11598<br>8 | + | 19.9 | 191 | YP_009098569<br>.1 | Hypothetical protein                         | <i>Shigella sonnei</i>               | 278  | $5 \times 10^{-90}$  | Yes |
| <b>g196</b>           | Baseplate hub subunit, tail length determinant | PPAP | 11607<br>5 | 11718<br>4 | + | 40.7 | 369 | YP_007004562<br>.1 | Hypothetical protein                         | <i>Shigella flexneri</i>             | 759  | 0.0                  | Yes |
| <b>g197</b>           | Baseplate tail tube cap                        | PPAP | 11719<br>3 | 11828<br>7 | + | 39.6 | 364 | WP_01603959<br>9.1 | Baseplate subunit                            | <i>Escherichia</i> virus RB14        | 740  | 0.0                  | Yes |
| <b>g198</b>           | Baseplate tail tube initiator                  | PPAP | 11828<br>7 | 11925<br>2 | + | 34.9 | 321 | WP_01605932<br>9.1 | Hypothetical protein ECML134_192             | <i>Escherichia</i> phage ECML-134    | 656  | 0.0                  | Yes |
| <b>g199</b>           | Hypothetical protein                           | ppap | 11928<br>1 | 11957<br>1 | - | 10.7 | 96  | YP_009030796<br>.1 | Hypothetical protein                         | <i>Salmonella enterica</i>           | 189  | $3 \times 10^{-60}$  | Yes |
| <b>g200</b>           | RNA polymerase ADP-ribosylase                  | PPAP | 11963<br>2 | 12168<br>9 | - | 75.6 | 685 | YP_002854524<br>.1 | RNA polymerase-ADP-ribosyltransferase        | <i>Citrobacter</i> phage PhiZZ23     | 140  | 0.0                  | No  |
| <b>g201</b>           | RNA polymerase-ADP-ribosyltransferase          | PPAP | 12169<br>3 | 12378<br>6 | - | 77.6 | 697 | WP_01598371<br>7.1 | NAD-protein ADP-ribosyltransferase           | <i>Escherichia</i> phage ime09       | 1422 | 0.0                  | No  |
| <b>g202</b>           | Hypothetical protein                           | ppap | 12383<br>9 | 12402<br>7 | - | 7.1  | 62  | EFX0168239.1       | Hypothetical protein                         | Bacteria                             | 125  | $2 \times 10^{-36}$  | Yes |

|             |                                    |      |       |       |   |      |     |                 |
|-------------|------------------------------------|------|-------|-------|---|------|-----|-----------------|
| <b>g203</b> | DNA ligase                         | PPAP | 12402 | 12548 | - | 55.3 | 487 | EFW3029236.1    |
|             |                                    |      | 4     | 7     |   |      |     |                 |
| <b>g204</b> | Hypothetical protein               |      | 12548 | 12575 | - | 10.8 | 89  | YP_002854527.1  |
|             |                                    |      | 4     | 3     |   |      |     |                 |
| <b>g205</b> | Hypothetical protein               | PPAP | 12575 | 12658 | - | 32.3 | 278 | YP_009102667.1  |
|             |                                    |      | 3     | 9     |   |      |     |                 |
| <b>g206</b> | Hypothetical protein               |      | 12658 | 12704 | - | 17.1 | 152 | WP_01605420.8.1 |
|             |                                    |      | 6     | 4     |   |      |     |                 |
| <b>g207</b> | Hypothetical protein               |      | 12703 | 12724 | - | 8.1  | 68  | YP_010065838.1  |
|             |                                    |      | 7     | 3     |   |      |     |                 |
| <b>g208</b> | Hypothetical protein               |      | 12724 | 12743 | - | 7.2  | 65  | YP_007004573.1  |
|             |                                    |      | 0     | 7     |   |      |     |                 |
| <b>g209</b> | Hypothetical protein               |      | 12743 | 12772 | - | 10.8 | 95  | WP_01603960.9.1 |
|             |                                    |      | 7     | 4     |   |      |     |                 |
| <b>g210</b> | Hypothetical protein               |      | 12776 | 12813 | - | 14.2 | 121 | YP_009180698.1  |
|             |                                    |      | 5     | 0     |   |      |     |                 |
| <b>g211</b> | Hypothetical protein               |      | 12819 | 12853 | - | 12.9 | 110 | WP_01598372.4.1 |
|             |                                    |      | 9     | 1     |   |      |     |                 |
| <b>g212</b> | Hypothetical protein               | PPAP | 12864 | 12881 | - | 6.5  | 58  | YP_009288565.1  |
|             |                                    |      | 2     | 8     |   |      |     |                 |
| <b>g213</b> | Lysis inhibition accessory protein | PPAP | 12906 | 12931 | - | 9.3  | 82  | QEG06046.1      |
|             |                                    |      | 4     | 2     |   |      |     |                 |
| <b>g214</b> | Co-chaperone GroES                 | PPAP | 12946 | 12979 | - | 12.1 | 111 | WP_01599581.3.1 |
|             |                                    |      | 0     | 5     |   |      |     |                 |
| <b>g215</b> | Hypothetical protein               | ppap | 12985 | 13016 | - | 11.5 | 102 | YP_002854159.1  |
|             |                                    |      | 2     | 0     |   |      |     |                 |
| <b>g216</b> | Hypothetical protein               |      | 13016 | 13039 | - | 9.4  | 78  | YP_009098589.   |
|             |                                    |      | 1     | 7     |   |      |     |                 |
| <b>g217</b> | Deoxycytidylate deaminase          | PPAP | 13039 | 13097 | - | 21.3 | 193 | YP_010071953.1  |
|             |                                    |      | 7     | 8     |   |      |     |                 |
| <b>g218</b> | Hypothetical protein               |      | 13097 | 13131 | - | 12.8 | 112 | NP_049822.1     |
|             |                                    |      | 5     | 3     |   |      |     |                 |
| <b>g219</b> | Hypothetical protein               |      | 13131 | 13154 | - | 8.8  | 78  | YP_009153807.1  |
|             |                                    |      | 0     | 6     |   |      |     |                 |
| <b>g220</b> | Hypothetical protein               |      | 13154 | 13206 | - | 20.2 | 175 | WP_01596937.4.1 |
|             |                                    |      | 0     | 7     |   |      |     |                 |

|                                    |   |     |                      |     |
|------------------------------------|---|-----|----------------------|-----|
| DNA ligase                         | <i>Escherichia</i> phage slur14         | 993 | 0.0                  | Yes |
| DUF3045 domain-containing protein  | <i>Escherichia coli</i>                 | 188 | $2 \times 10^{-60}$  | Yes |
| Hypothetical protein BI058_gp203   | <i>Shigella</i> phage SHBML-50-1        | 578 | 0.0                  | Yes |
| Hypothetical protein JK38_00196    | <i>Shigella</i> phage JK38              | 313 | $8 \times 10^{-108}$ | Yes |
| Hypothetical protein               | <i>Escherichia coli</i>                 | 140 | $6 \times 10^{-42}$  | Yes |
| Hypothetical protein               | Enterobacteria phage RB51               | 130 | $7 \times 10^{-38}$  | Yes |
| Hypothetical protein RB3_203       | <i>Escherichia</i> phage RB3            | 199 | $1 \times 10^{-64}$  | Yes |
| Hypothetical protein KMC16_gp211   | <i>Escherichia</i> phage vB_EcoM_Lutter | 149 | $2 \times 10^{-44}$  | Yes |
| Conserved hypothetical protein     | <i>Escherichia</i> virus T4             | 225 | $3 \times 10^{-74}$  | Yes |
| Hypothetical protein ACQ28_gp199   | <i>Yersinia</i> phage PST               | 112 | $5 \times 10^{-31}$  | Yes |
| Hypothetical protei                | Bacteria                                | 166 | $8 \times 10^{-52}$  | Yes |
| co-chaperone GroES family protein  | Bacteria                                | 222 | $5 \times 10^{-73}$  | Yes |
| DUF2693 domain-containing protein  | <i>Salmonella enterica</i>              | 206 | $6 \times 10^{-67}$  | Yes |
| Tail fiber protein                 | <i>Shigella</i> phage CM8               | 159 | $4 \times 10^{-49}$  | Yes |
| Putative deoxycytidylate deaminase | <i>Shigella</i> phage ShfI2             | 400 | $6 \times 10^{-141}$ | Yes |
| Hypothetical protein ShfI2p216     | <i>Shigella</i> phage ShfI2             | 229 | $1 \times 10^{-75}$  | Yes |
| Hypothetical protein               | Enterobacteriaceae                      | 156 | $4 \times 10^{-48}$  | Yes |
| Hypothetical protein KMC13_gp056   | <i>Escherichia</i> phage vB_EcoM_IME53  | 349 | $2 \times 10^{-121}$ | No  |

|             |  |      |       |       |   |      |     |                    |   |  |      |                      |     |
|-------------|--|------|-------|-------|---|------|-----|--------------------|---|--|------|----------------------|-----|
| <b>g221</b> | Hypothetical protein                               |      | 13213 | 13240 | - | 10.1 | 91  | WP_01596937<br>5.1 | Conserved hypothetical protein                      | <i>Escherichia</i> virus T4              | 185  | $5 \times 10^{-59}$  | Yes |
| <b>g222</b> | Hypothetical protein                               |      | 13240 | 13260 | - | 7.9  | 66  | WP_01596937<br>6.1 | Hypothetical protein KNU25_gp032                    | <i>Escherichia</i> phage MLF4            | 132  | $6 \times 10^{-39}$  | Yes |
| <b>g223</b> | Hypothetical protein                               |      | 13260 | 13279 | - | 7.6  | 65  | YP_010076017<br>.1 | Hypothetical protein F413_gp048                     | <i>Escherichia</i> phage ime09           | 136  | $3 \times 10^{-40}$  | Yes |
| <b>g224</b> | AAA family ATPase                                  | PPAP | 13279 | 13370 | - | 34.9 | 302 | YP_004415106<br>.1 | Polynucleotide 5'-kinase and 3'-phosphatase         | <i>Escherichia</i> phage vB_EcoM_ACG-C40 | 623  | 0.0                  | Yes |
| <b>g225</b> | Hypothetical protein                               |      | 13370 | 13402 | - | 12.1 | 106 | YP_004415107<br>.1 | Hypothetical protein D862_gp055                     | <i>Escherichia</i> phage vB_EcoM_ACG-C40 | 218  | $1 \times 10^{-71}$  | No  |
| <b>g226</b> | Hypothetical protein                               |      | 13402 | 13425 | - | 8.7  | 74  | WP_01598373<br>6.1 | Hypothetical protein FDJ03_gp07                     | <i>Shigella</i> phage Sf24               | 155  | $1 \times 10^{-47}$  | Yes |
| <b>g227</b> | Hypothetical protein                               |      | 13424 | 13454 | - | 11.6 | 99  | YP_010070984<br>.1 | Hypothetical protein                                | Bacteria                                 | 205  | $1 \times 10^{-66}$  | Yes |
| <b>g228</b> | Hypothetical protein                               |      | 13454 | 13489 | - | 13.1 | 117 | NP_049831.1        | Hypothetical protein                                | <i>Salmonella enterica</i>               | 229  | $9 \times 10^{-76}$  | Yes |
| <b>g229</b> | Inhibitor of host transcription                    |      | 13488 | 13539 | - | 19.0 | 167 | YP_010099699<br>.1 | Hypothetical protein pSs1_00233                     | <i>Shigella</i> phage pSs-1              | 347  | $8 \times 10^{-121}$ | Yes |
| <b>g230</b> | RNA ligase A                                       | PPAP | 13545 | 13658 | - | 43.5 | 374 | YP_007004594<br>.1 | Putative RNA ligase A                               | <i>Escherichia</i> phage vB_EcoM-G28     | 775  | 0.0                  | Yes |
| <b>g231</b> | Endonuclease II                                    |      | 13663 | 13704 | - | 15.8 | 136 | YP_006986775<br>.1 | GIY-YIG nuclease family protein                     | Bacteria                                 | 280  | $5 \times 10^{-95}$  | Yes |
| <b>g232</b> | NrdB aerobic NDP reductase, small subunit          | PPAP | 13707 | 13754 | - | 18.1 | 156 | YP_006986776<br>.  | Ribonucleoside-diphosphate reductase 1 subunit beta | <i>Escherichia</i> phage vB_EcoM_G8      | 327  | $5 \times 10^{-113}$ | Yes |
| <b>g233</b> | Homing endonuclease                                |      | 13771 | 13851 | - | 30.8 | 269 | YP_009619152<br>.1 | HNH endonuclease                                    | <i>Salmonella enterica</i>               | 563  | 0.0                  | Yes |
| <b>g234</b> | NrdB aerobic NDP reductase, small subunit          | PPAP | 13866 | 13934 | - | 26.2 | 225 | WP_01598374<br>2.1 | Ribonucleoside-diphosphate reductase                | <i>Escherichia coli</i>                  | 466  | $5 \times 10^{-166}$ | Yes |
| <b>g235</b> | Ribonucleoside-diphosphate reductase subunit alpha |      | 13939 | 14165 | - | 86.0 | 754 | WP_01605911<br>8.1 | Ribonucleoside-diphosphate reductase subunit alpha  | <i>Escherichia coli</i>                  | 1576 | 0.0                  | Yes |

|             |                                     |             |            |            |   |      |     |                    |  |  |      |                      |     |
|-------------|-------------------------------------|-------------|------------|------------|---|------|-----|--------------------|--|--|------|----------------------|-----|
| <b>g236</b> | Hypothetical protein                | <i>ppap</i> | 14164<br>7 | 14193<br>4 | - | 10.9 | 95  | YP_009111041<br>.  | Hypothetical protein                                     | Enterobacteria phage RB51                | 199  | $1 \times 10^{-64}$  | Yes |
| <b>g237</b> | Hypothetical protein dTMP           |             | 14192<br>7 | 14219<br>0 | - | 10.0 | 87  | YP_010069787<br>.1 | Hypothetical protein BI058_gp175                         | <i>Shigella</i> phage SHBML-50-1         | 178  | $2 \times 10^{-56}$  | Yes |
| <b>g238</b> | (thymidylate) synthase              | <i>ppap</i> | 14218<br>7 | 14269<br>3 | - | 19.7 | 168 | WP_01599583<br>0.1 | Thymidylate synthetase                                   | Enterobacteria phage RB14                | 356  | $2 \times 10^{-122}$ | Yes |
| <b>g239</b> | Thymidylate synthase                |             | 14290<br>5 | 14304<br>8 | - | 4.7  | 47  | YP_010069517<br>.1 | Putative thymidylate synthase 2                          | <i>Escherichia</i> phage vB_EcoM_G2540-3 | 85.9 | $2 \times 10^{-19}$  | Yes |
| <b>g240</b> | Hypothetical protein                |             | 14309<br>4 | 14344<br>1 | - | 13.7 | 115 | WP_08018152<br>7.1 | Hypothetical protein ECML134_232                         | <i>Escherichia</i> phage ECML-134        | 239  | $2 \times 10^{-79}$  | Yes |
| <b>g241</b> | Dihydrofolate reductase             | PPAP        | 14346<br>2 | 14404<br>3 | - | 21.6 | 193 | HAJ1134801.1       | Dihydrofolate reductase                                  | <i>Escherichia coli</i>                  | 401  | $3 \times 10^{-141}$ | No  |
| <b>g242</b> | Hypothetical protein                | PPAP        | 14404<br>3 | 14428<br>8 | - | 9.7  | 81  | WP_01598374<br>7.  | Hypothetical protein pSs1_00243                          | <i>Shigella</i> phage pSs-1              | 165  | $2 \times 10^{-51}$  | No  |
| <b>g243</b> | Hypothetical protein                | <i>ppap</i> | 14429<br>9 | 14454<br>1 | - | 9.3  | 80  | YP_002854184<br>.1 | DUF5417 domain-containing protein                        | <i>Escherichia coli</i>                  | 162  | $2 \times 10^{-50}$  | Yes |
| <b>g244</b> | Hypothetical protein                | PPAP        | 14459<br>7 | 14498<br>3 | - | 14.1 | 128 | YP_009288593<br>.1 | Hypothetical protein e112_254                            | <i>Escherichia</i> phage vB_EcoM_112     | 253  | $7 \times 10^{-85}$  | Yes |
| <b>g245</b> | Hypothetical protein                |             | 14503<br>0 | 14526<br>0 | - | 8.9  | 76  | YP_009210152<br>.1 | Hypothetical protein AR1_249                             | <i>Escherichia</i> phage AR1             | 155  | $1 \times 10^{-47}$  | Yes |
| <b>g246</b> | Single-stranded DNA binding protein | PPAP        | 14540<br>6 | 14631<br>4 | - | 33.5 | 302 | QBO65644.1         | ssDNA binding DNA repair recombination and pre-synthesis | Enterobacteria phage GiZh                | 617  | 0.0                  | Yes |
| <b>g247</b> | Hypothetical protein RNA            |             | 14641<br>4 | 14706<br>7 | - | 26.0 | 217 | YP_009102707<br>.1 | Helicase loading protein                                 | <i>Escherichia coli</i>                  | 436  | $3 \times 10^{-154}$ | Yes |
| <b>g248</b> | polymerase-associated protein       |             | 14706<br>4 | 14740<br>2 | - | 12.8 | 112 | WP_17192148<br>5.1 | Late promoter transcription accessory protein            | Bacteria                                 | 223  | $2 \times 10^{-73}$  | Yes |
| <b>g249</b> | Double-stranded DNA binding protein | PPAP        | 14738<br>0 | 14764<br>9 | - | 9.5  | 89  | YP_009111051<br>.1 | Double-stranded DNA binding protein                      | Bacteria                                 | 162  | $9 \times 10^{-50}$  | Yes |
| <b>g250</b> | RnaseH                              | PPAP        | 14765<br>8 | 14857<br>5 | - | 35.6 | 305 | WP_01596940<br>1.1 | Hypothetical protein                                     | <i>Escherichia coli</i>                  | 627  | 0.0                  | Yes |

|             |  |      |            |            |   |       |      |                    |  |   |      |                      |     |
|-------------|--|------|------------|------------|---|-------|------|--------------------|--|---|------|----------------------|-----|
| <b>g251</b> | Phage long tail fiber proximal subunit   | PPAP | 14868<br>0 | 15254<br>9 | + | 140.0 | 1289 | YP_009030849<br>.1 | Long tail fiber proximal subunit         | <i>Citrobacter</i> phage PhiZZ6           | 2585 | 0.0                  | Yes |
| <b>g252</b> | Phage tail connector protein             | PPAP | 15257<br>0 | 15368<br>5 | + | 40.3  | 371  | YP_009168060<br>.1 | Hypothetical protein FDH37_gp26          | <i>Escherichia</i> phage HP3              | 749  | 0.0                  | Yes |
| <b>g253</b> | Tail fiber protein                       | PPAP | 15374<br>9 | 15441<br>4 | + | 23.6  | 221  | YP_010066187<br>.1 | Putative tail fiber protein              | <i>Escherichia</i> phage vB_EcoM_WFbE 185 | 449  | $4 \times 10^{-159}$ | Yes |
| <b>g254</b> | Long tail fiber, distal subunit          | PPAP | 15442<br>3 | 15753<br>9 | + | 109.8 | 1038 | WP_17192149<br>6.1 | Tail fibers protein                      | <i>Escherichia</i> phage mobillu          | 1947 | 0.0                  | Yes |
| <b>g255</b> | Phage tail fibers                        |      | 15757<br>0 | 15812<br>1 | + | 21.8  | 183  | WP_01596940<br>7.1 | Putative tail fiber assembly protein     | <i>Escherichia</i> phage vB_EcoM_G2469    | 370  | $3 \times 10^{-129}$ | Yes |
| <b>g256</b> | Holin lysis mediator                     |      | 15813<br>1 | 15879<br>0 | + | 24.6  | 219  | WP_01596940<br>8.1 | Holin                                    | <i>Escherichia</i> phage p000v            | 449  | $3 \times 10^{-159}$ | Yes |
| <b>g257</b> | Anti-sigma 70 protein                    |      | 15879<br>1 | 15906<br>3 | - | 10.5  | 90   | WP_01596940<br>9.1 | Hypothetical protein HX01_0196           | <i>Escherichia</i> phage HX01             | 177  | $4 \times 10^{-56}$  | Yes |
| <b>g258</b> | Hypothetical protein                     |      | 15911<br>0 | 15927<br>1 | - | 6.3   | 53   | QIQ68304.1         | Hypothetical protein G2469_00259         | <i>Escherichia</i> phage vB_EcoM_G2469    | 102  | $2 \times 10^{-27}$  | No  |
| <b>g259</b> | Hypothetical protein                     | PPAP | 15926<br>1 | 15956<br>0 | - | 11.6  | 99   | YP_009965878<br>.1 | Hypothetical protein                     | <i>Shigella flexneri</i>                  | 202  | $2 \times 10^{-65}$  | No  |
| <b>g260</b> | Hypothetical protein                     |      | 15963<br>5 | 15985<br>9 | - | 8.7   | 74   | QBQ77759.1         | Hypothetical protein PI26_gp157          | <i>Shigella</i> phage Shf125875           | 153  | $7 \times 10^{-47}$  | Yes |
| <b>g261</b> | Hypothetical protein                     |      | 15984<br>6 | 16012<br>7 | - | 10.9  | 93   | QHR72833.1         | Hypothetical protein JS09_0193           | <i>Escherichia</i> phage vB_EcoM_JS09     | 190  | $5 \times 10^{-61}$  | Yes |
| <b>g262</b> | Phage anti-restriction nuclease          |      | 16012<br>7 | 16058<br>8 | - | 17.9  | 153  | QBO62946.1         | Hypothetical protein JK38_00252          | <i>Shigella</i> phage JK38                | 321  | $6 \times 10^{-111}$ | No  |
| <b>g263</b> | Hypothetical protein                     |      | 16058<br>5 | 16091<br>4 | - | 12.7  | 109  | AYN56434.1         | Hypothetical protein                     | <i>Escherichia coli</i>                   | 227  | $4 \times 10^{-75}$  | Yes |
| <b>g264</b> | Activator of middle period transcription | PPAP | 16092<br>5 | 16156<br>0 | - | 23.6  | 211  | YP_006907273<br>.1 | Activator of middle period transcription | <i>Escherichia</i> phage wV7              | 425  | $5 \times 10^{-150}$ | Yes |
| <b>g265</b> | Hypothetical protein                     |      | 16168<br>8 | 16183<br>7 | - | 4.8   | 49   | QBO62949.1         | Hypothetical protein Shf12p264           | <i>Shigella</i> phage Shf12               | 89.4 | $4 \times 10^{-22}$  | Yes |
| <b>g266</b> | DNA topoisomerase                        | PPAP | 16183<br>4 | 16316<br>2 | - | 49.3  | 442  | EGF3885029.1       | Topoisomerase II medium subunit          | <i>Escherichia</i> phage wV7              | 894  | 0.0                  | No  |



|             |   |      |       |       |   |      |     |                    |  |                                      |      |                      |     |
|-------------|---|------|-------|-------|---|------|-----|--------------------|--|--------------------------------------|------|----------------------|-----|
| <b>g267</b> | Acridine resistance protein                 |      | 16330 | 16345 | - | 5.6  | 52  | YP_009100794<br>.1 | Hypothetical protein                                 | Bacteria                             | 102  | $2 \times 10^{-27}$  | Yes |
| <b>g268</b> | Ndd nucleoid disruption protein             | PPAP | 16354 | 16398 | - | 16.6 | 147 | YP_009037516<br>.1 | Nucleoid disruption protein                          | <i>Serratia</i> phage PhiZZ30        | 308  | $7 \times 10^{-106}$ | Yes |
| <b>g269</b> | Hypothetical protein                        |      | 16405 | 16426 | - | 7.8  | 71  | QEG06102.1         | Hypothetical protein                                 | <i>Escherichia</i> virus RB14        | 141  | $4 \times 10^{-42}$  | Yes |
| <b>g270</b> | Hypothetical protein                        |      | 16427 | 16438 | - | 4.2  | 36  | WP_17922673<br>4.1 | Putative outer membrane protein                      | <i>Yersinia</i> phage PST            | 72.4 | $9 \times 10^{-16}$  | Yes |
| <b>g271</b> | Hypothetical protein                        |      | 16438 | 16457 | - | 7.5  | 65  | YP_007005000<br>.1 | Hypothetical protein                                 | Bacteria                             | 131  | $2 \times 10^{-38}$  | Yes |
| <b>g272</b> | Hypothetical protein                        |      | 16458 | 16469 | - | 4.3  | 37  | YP_004415152<br>.1 | Hypothetical protein e112_284                        | <i>Escherichia</i> phage vB_EcoM_112 | 70.5 | $1 \times 10^{-14}$  | Yes |
| <b>g273</b> | Hypothetical protein                        |      | 16476 | 16486 | - | 3.7  | 32  | YP_007005002<br>.1 | Predicted outer membrane protein                     | <i>Escherichia</i> phage ime09       | 65.1 | $6 \times 10^{-13}$  | Yes |
| <b>g274</b> | Hypothetical protein                        |      | 16494 | 16520 | - | 10.2 | 87  | WP_01599604<br>4.1 | Hypothetical protein                                 | <i>Escherichia coli</i>              | 181  | $1 \times 10^{-57}$  | Yes |
| <b>g275</b> | DenB DNA endonuclease IV                    | PPAP | 16528 | 16583 | - | 21.0 | 185 | YP_010075801<br>.1 | Hypothetical protein FT_0153                         | <i>Escherichia</i> phage vB_EcoM_FT  | 387  | $5 \times 10^{-136}$ | Yes |
| <b>g276</b> | Hypothetical protein                        |      | 16590 | 16609 | - | 7.4  | 64  | YP_002854600<br>.1 | Hypothetical protein F412_gp002                      | <i>Escherichia</i> phage wV7         | 127  | $1 \times 10^{-36}$  | Yes |
| <b>g277</b> | Protector from prophage-induced early lysis | PPAP | 16612 | 16706 | - | 35.5 | 312 | YP_009153867<br>.1 | Putative protector from prophage-induced early lysis | <i>Escherichia</i> phage teqhal      | 646  | 0.0                  | Yes |

<sup>1</sup> By similarity to *Escherichia* phage T4, when applicable; <sup>2</sup> PPAP: phage-associated protein identified by LC-MS/MS; ppap: phage-associated protein identified by 2 or more peptides, but with an average spectral count below 2; *ppap*: phage-associated protein identified by 1 peptide only, with an average spectral count of at least 3 and observed in 3 out of 6 sample replicates. <sup>3</sup> PSI-BLAST at <https://blast.ncbi.nlm.nih.gov> using default setting against the non-redundant protein sequence database release of 2021/06; <sup>4</sup> Similar protein expressed by *Escherichia* phage T4.