**Table S2.** Putative functions assigned to PANV2 ORF products.

| ORF | Start, nt | Stop, nt | Directiona | Gene product (gp) | Protein size, aa | TMHs b | Putative function | Best Blastx match (thresholds: E-value 1e-5, query cover 30%, identity 30%, search dated 18.02.2021) |
|-----|-----------|----------|-------------|------------------|-----------------|--------|------------------|-----------------------------------------------------------------------------------|
| ORF1 | 1 | 585 | F | gp1 | 194 | 0 | Terminase small subunit | TPA: terminase small subunit [Methylococcaceae bacterium], HHZ70429.1, 75/72, 6e-72 |
| ORF2 | 572 | 1 828 | F | gp2 | 418 | 0 | Terminase large subunit | TPA: terminase [Glacieola sp.], HAQ49901.1, 97/72, 0 |
| ORF3 | 1 839 | 3 281 | F | gp3 | 480 | 0 | Portal protein | Putative prophage PSSB64-02 [uncultured Mediterranean phage uvMED], BAQ84211.1, 95/50, 7e-157 |
| ORF4 | 3 281 | 4 327 | F | gp4 | 348 | 0 | Head morphogenesis protein | minor capsid protein [Pantoea septica], WP_084885774.1, 97/40, 2e-64 |
| ORF5 | 4 380 | 5 033 | F | gp5 | 217 | 0 | | Putative prophage PSSB64-02 [uncultured Mediterranean phage uvMED], BAQ84212.1, 88/47, 3e-24 |
| ORF6 | 5 047 | 6 204 | F | gp6 | 385 | 2 | Major capsid protein | TPA: P22 coat - protein 5 family protein [Shewanella frigidimarina], HBF47038.1, 99/69, 9e-173 |
| ORF7 | 6 252 | 6 446 | R | gp7 | 64 | 0 | | - |
| ORF8 | 6 443 | 6 934 | R | gp8 | 163 | 0 | hypothetical protein COA78_21100 [Blastopirellula sp.], PHS02420.1, 62/39, 4e-13 |
| ORF9 | 6 927 | 7 112 | R | gp9 | 61 | 0 | | - |
| ORF10 | 7 109 | 7 411 | R | gp10 | 100 | 0 | | - |
| ORF11 | 7 411 | 7 638 | R | gp11 | 75 | 0 | | - |
| ORF12 | 7 626 | 7 865 | R | gp12 | 79 | 0 | | - |
| ORF13 | 7 987 | 8 118 | F | gp13 | 43 | 0 | | - |
| ORF14 | 8 115 | 8 729 | F | gp14 | 204 | 0 | | - |
| ORF15 | 8 722 | 9 114 | F | gp15 | 130 | 0 | | - |
| ORF16 | 9 124 | 9 924 | F | gp16 | 266 | 0 | | TPA: hypothetical protein [Flavobacteriales bacterium], HHZ97169.1, 88/51, 4e-61 |
| ORF17 | 9 924 | 10 289 | F | gp17 | 121 | 0 | | TPA: hypothetical protein [Methylococcaceae bacterium], HHZ69969.1, 99/48, 3e-17 |
| ORF  | Start  | End    | Type   | Description                  | Gene          | Identity   | E-value | Description                  |
|------|--------|--------|--------|--------------------------------|---------------|------------|---------|--------------------------------|
| ORF18| 10 289 | 10 750 | F      | gp18 153 0                     | Tail protein  | TPA: hypothetical protein [Flavobacteriales bacterium], HHZ97787.1 | 99/57, 3e-53 |
| ORF19| 10 750 | 11 169 | F      | gp19 139 0                     | Tail protein  | TPA: hypothetical protein [Flavobacteriales bacterium], HHZ94507.1 | 84/49, 2e-33 |
| ORF20| 11 184 | 11 597 | F      | gp20 137 0                     | Portal/tail protein | - | - |
| ORF21| 11 599 | 12 042 | F      | gp21 147 0                     | hypothetical protein [Alteromonas sp.], MBU35306.1 | 88/38, 1e-23 |
| ORF22| 12 148 | 14 094 | F      | gp22 648 0                     | Tail tape measure protein | TPA: hypothetical protein [Methylococcaceae bacterium], HHZ68955.1 | 40/57, 6e-73 |
| ORF23| 14 091 | 14 819 | F      | gp23 242 1                     | hypothetical protein [Alteromonas sp.], MBU35304.1 | 99/52, 4e-72 |
| ORF24| 14 816 | 17 113 | F      | gp24 765 0                     | Tail fiber protein | hypothetical protein [Alteromonas sp.], MBU35303.1 | 84/58, 0 |
| ORF25| 17 124 | 17 375 | F      | gp25 83 0                      | - | - |
| ORF26| 17 375 | 19 447 | F      | gp26 690 0                     | - | - |
| ORF27| 19 484 | 19 627 | F      | gp27 47 0                      | - | - |
| ORF28| 19 624 | 20 097 | F      | gp28 157 4                     | - | - |
| ORF29| 20 094 | 20 372 | F      | gp29 92 2                      | - | - |
| ORF30| 20 369 | 20 710 | F      | gp30 113 0                     | Transpeptidase | hypothetical protein Tp138OMZ00d2C19078241_28 [Prokaryotic dsDNA virus sp.], QDP55696.1 | 69/51, 3e-17 |
| ORF31| 20 710 | 21 090 | F      | gp31 126 2                     | - | - |
| ORF32| 21 091 | 21 219 | R      | gp32 42 1                      | - | - |
| ORF33| 21 209 | 21 346 | R      | gp33 45 1                      | - | - |
| ORF34| 21 339 | 21 488 | R      | gp34 49 0                      | - | - |
| ORF35| 21 485 | 21 652 | R      | gp35 55 0                      | RNA polymerase sigma factor | - | - |
| ORF36| 21 649 | 21 900 | R      | gp36 83 0                      | Transcriptional regulator | - | - |
| ORF37| 21 884 | 22 165 | R      | gp37 93 0                      | - | - |
| ORF38| 22 190 | 22 507 | R      | gp38 105 0                     | hypothetical protein B1M_00505 [Burkholderia sp. TJ49], EGD06613.1 | 36/58, 6e-6 |
| ORF39| 22 762 | 22 965 | R      | gp39 67 1                      | - | - |
| ORF | Start | Stop  | Type | Function | Accession |
|-----|-------|-------|------|----------|-----------|
| 40  | 22968 | 23177 | R    | gp40     | MAN63724.1 |
| 41  | 23189 | 23473 | R    | gp41     | -         |
| 42  | 23475 | 23765 | R    | gp42     | Nuclease/hydrolase |
|     |       |       |      |          | [Flavobacteriales bacterium], HHZ94256.1 |
| 43  | 23766 | 23989 | R    | gp43     | Single-strand DNA-binding protein |
|     |       |       |      |          | [Paraglaciecola arctica], WP_007618529.1 |
| 44  | 23992 | 24439 | R    | gp44     | hypothetical protein [Chloroflexi bacterium], MBG7617472.1 |
| 45  | 24423 | 24992 | R    | gp45     | Single-strand DNA-binding protein |
|     |       |       |      |          | [Pseudoalteromonas phage Pq0], YP_009226084.1 |
| 46  | 25524 | 25661 | R    | gp46     | -         |
| 47  | 25795 | 26001 | F    | gp47     | -         |
| 48  | 26001 | 26261 | F    | gp48     | -         |
| 49  | 26261 | 26707 | F    | gp49     | Single-strand DNA-binding protein |
|     |       |       |      |          | [Pseudoalteromonas sp.], MAE02312.1 |
| 50  | 26708 | 26905 | F    | gp50     | hypothetical protein [Pseudoalteromonas virus vB_PspS-H6/1], ANJ65543.1 |
| 51  | 26902 | 27297 | F    | gp51     | Nuclease/hydrolase |
|     |       |       |      |          | hypothetical protein [Pseudomonadales bacterium], MBA57003.1 |
| 52  | 27333 | 27624 | F    | gp52     | -         |
| 53  | 27612 | 27821 | F    | gp53     | -         |
| 54  | 27814 | 28005 | F    | gp54     | -         |
| 55  | 28243 | 28710 | F    | gp55     | Phage regulatory protein |
|     |       |       |      |          | Rha, Antirepressor protein [Prokaryotic dsDNA virus sp.], QDP50490.1 |
| 56  | 28721 | 29443 | F    | gp56     | hypothetical protein [Pseudoalteromonas phage Pq0], YP_009226075.1 |
| 57  | 29447 | 30769 | F    | gp57     | Replicative DNA helicase |
|     |       |       |      |          | replicative DNA helicase [Leucothrix sargassi], RVU85441.1 |
| 58  | 30773 | 31030 | F    | gp58     | -         |
| 59  | 31030 | 31263 | F    | gp59     | -         |
| 60  | 31330 | 31488 | F    | gp60     | -         |
| ORF   | Start | Stop  | F/R | Protein ID | Description                                                                 | E-value |
|-------|-------|-------|-----|------------|------------------------------------------------------------------------------|---------|
| ORF61 | 31 680| 31 856|     | gp61       | RNA-binding protein [Vibrio phage 1.023.O._10N.222.51.B4], AUR82377.1       | 96/56, 1e-12 |
| ORF62 | 31 873| 32 016| F   | gp62       | -                                                                            | -       |
| ORF63 | 32 018| 32 161| F   | gp63       | -                                                                            | -       |
| ORF64 | 32 158| 32 391| F   | gp64       | hypothetical protein [Aeromonas salmonicida], WP_04430329.1                | 98/42, 2e-10 |
| ORF65 | 32 388| 32 585| F   | gp65       | -                                                                            | -       |
| ORF66 | 32 585| 32 800| F   | gp66       | hypothetical protein [Parashewanella curva], WP_165904988.1                | 68/63, 6e-10 |
| ORF67 | 32 818| 33 006| F   | gp67       | -                                                                            | -       |
| ORF68 | 33 003| 33 410| F   | gp68       | -                                                                            | -       |
| ORF69 | 33 407| 33 577| F   | gp69       | -                                                                            | -       |
| ORF70 | 33 658| 34 410| F   | gp70       | -                                                                            | -       |
| ORF71 | 34 413| 34 850| F   | gp71       | -                                                                            | -       |
| ORF72 | 34 847| 35 227| F   | gp72       | hypothetical protein [Colwellia sp.], MBL4941164.1                        | 51/57, 2e-12 |
| ORF73 | 35 231| 35 683| F   | gp73       | TPA: hypothetical protein [Glaciecola sp.], HAQ49903.1                     | 99/64, 1e-59 |

- **F**, forward; **R**, reverse.
- **F/R**, transmembrane helices, searched with TMHMM Server v. 2.0.
- **E-value**, no significant similarity found.