**Supplementary file 1.** Viral species included in the final multiple sequence alignments (54 taxa) with their accession numbers and source reference.

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **ID** | **GenBank/metagenomic accessions** | **Source** |
| *Maverick* (*Danio rerio*) | Proteo5 | NC\_007136.7: 27671708-27687993 | (Barreat and Katzourakis, 2021) |
| *Maverick* (*Xenopus tropicalis*) | Proteo18 | NC\_030686.1: 6013889-6026611 | (Barreat and Katzourakis, 2021) |
| *Maverick* (*Anolis carolinensis*) | Proteo2 | NC\_014778.1: 129158247-129172346 | (Barreat and Katzourakis, 2021) |
| *Maverick* (*Xiphophorus hellerii*) | Proteo19 | QPIH01000028.1: 6019497-6036410 | (Barreat and Katzourakis, 2021) |
| *Maverick* (*Oreochromis niloticus*) | Proteo15 | NW\_020327416.1: 45576-61017 | (Barreat and Katzourakis, 2021) |
| *Maverick* (*Oxygymnocypris stewartii*) | Proteo11 | QVTF01001200.1: 1425766-1443135 | (Barreat and Katzourakis, 2021) |
| *Maverick* (*Plutella xylostella*) | Group2\_9 | NW\_011952032.1: 283307-321039 | This work |
| *Maverick* (*Ostrinia furnacalis*) | Group2\_10 | NW\_021132744.1: 18414-41178 | This work |
| *Maverick* (*Diachasma alloeum*) | Group2\_5 | NW\_021681489.1: 105940-131438 | This work |
| *Maverick* (*Diachasma alloeum*) | Group2\_6 | NW\_021680987.1: 30857-54497 | This work |
| *Maverick* (*Photinus pyralis*) | Group2\_7 | NW\_022171288.1: 44859-60568 | This work |
| *Maverick* (*Sitophilus oryzae*) | Group2\_8 | NW\_022147237.1: 411147-463473 | This work |
| Metagenomic NCLDV | NCLDV\_Roux3157 | Trout\_Epilimnion\_TBL\_comb48\_EPIDRAFT\_1006965 | (Roux et al., 2017) |
| Metagenomic NCLDV | NCLDV\_Mo545 | SRX331950.48.dc.fa\_4042 | (Moniruzzaman et al., 2020) |
| Metagenomic NCLDV | NCLDV\_Mo338 | SRX330942.38.dc.fa\_3117 | (Moniruzzaman et al., 2020) |
| Metagenomic NCLDV | NCLDV\_Mo338 | SRX330942.38.dc.fa\_13478 | (Moniruzzaman et al., 2020) |
| Metagenomic NCLDV | NCLDV\_Roux1456 | Mendota\_contig-68000307\_4926\_nucleotides | (Roux et al., 2017) |
| Metagenomic NCLDV | NCLDV\_Sch668 | MN740268.1 | (Schulz et al., 2020) |
| *Shrimp hemocyte iridescent virus* | — | NC\_055165.1 | NCBI |
| *Infectious spleen and kidney necrosis virus* | — | NC\_003494.1 | NCBI |
| *Heterosigma akashiwo virus 01* | — | NC\_038553.1 | NCBI |
| *Akhmeta virus* | — | NC\_055230.1 | NCBI |
| *Tupanvirus soda lake* | — | KY523104.2 | NCBI |
| *Diadromus pulchellus ascovirus 4a* | — | NC\_011335.1 | NCBI |
| Metagenomic PLV | PLV\_BS940 | 3300009435\_\_\_\_\_Ga0115546\_1002426 | (Bellas and Sommaruga, 2021) |
| Metagenomic PLV | PLV\_BS718 | Ga0115028\_10000066 | (Bellas and Sommaruga, 2021) |
| Metagenomic PLV | PLV\_BS13 | V563K\_contig\_8723\_len\_16581\_bp | (Bellas and Sommaruga, 2021) |
| Metagenomic PLV | PLV\_BS395 | ERR1823950\_NODE\_975\_length\_11499\_cov\_287.344855 | (Bellas and Sommaruga, 2021) |
| Metagenomic PLV | PLV\_BS539 | ERX2821583\_NODE\_576\_length\_19830\_cov\_33.560977 | (Bellas and Sommaruga, 2021) |
| Metagenomic PLV | PLV\_BS262 | HanCross\_NODE\_1742\_length\_13974\_cov\_48.888145 | (Bellas and Sommaruga, 2021) |
| Metagenomic PLV | Plike\_4 | SAF4 | (Yutin et al., 2015) |
| Metagenomic PLV | Plike\_7 | INO1 | (Yutin et al., 2015) |
| Metagenomic PLV | Plike\_17 | RED1 | (Yutin et al., 2015) |
| Metagenomic PLV | Plike\_1 | SAF1 | (Yutin et al., 2015) |
| Metagenomic PLV | Plike\_19 | YSL1 | (Yutin et al., 2015) |
| Metagenomic PLV | Plike\_25 | ACE1 | (Yutin et al., 2015) |
| Metagenomic virophage | Virophage\_PE125 | 3300009070\_\_\_\_\_Ga0066256\_1001637 | (Paez-Espino et al., 2019) |
| Metagenomic virophage | Virophage\_PE85 | 3300009781\_\_\_\_\_Ga0116178\_10003357 | (Paez-Espino et al., 2019) |
| Metagenomic virophage | Virophage\_PE47 | 3300012984\_\_\_\_\_Ga0164309\_10000286 | (Paez-Espino et al., 2019) |
| Metagenomic virophage | Virophage\_PE169 | 3300009154\_\_\_\_\_Ga0114963\_10000678 | (Paez-Espino et al., 2019) |
| Metagenomic virophage | Virophage\_PE184 | 3300007609\_\_\_\_\_Ga0102945\_1000484 | (Paez-Espino et al., 2019) |
| Metagenomic virophage | Virophage\_Roux27 | TBH\_10005622 | (Roux et al., 2017) |
| *Maverick*-related virus strain Spezl | — | NC\_015230.1 | NCBI |
| Yellowstone Lake virophage 7 | — | KM502591.1 | NCBI |
| Zamilon virus | — | NC\_022990.1 | NCBI |
| Yellowstone Lake virophage 5 | — | NC\_028269.1 | NCBI |
| Dishui Lake virophage 6 | — | MN940573.1 | NCBI |
| Dishui Lake virophage 2 | — | MN940570.1 | NCBI |
| *Bat mastadenovirus WIV17* | — | NC\_034626.1 | NCBI |
| *Murine mastadenovirus A* | — | AC\_000012.1 | NCBI |
| *Murine adenovirus 2* | — | NC\_014899.1 | NCBI |
| *Fowl aviadenovirus 5* | — | NC\_021221.1 | NCBI |
| *Frog adenovirus 1* | — | NC\_002501.1 | NCBI |
| *Snake adenovirus 1* | — | NC\_009989.1 | NCBI |