# Genomic and metagenomic signatures of giant viruses are ubiquitous in water samples from sewage, inland lake, waste water treatment plant, and municipal water supply in Mumbai, India

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*Key words*: giant virus; metagenomics; WWTP; municipal water supply

*Running Title*: giant viruses in Mumbai

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**Supplementary Table 1: List of viruses with genome length > 300,000 bp used to generated blast databse for querying the metagenomes**

| NCBI Accession Number | Taxonomic ID | Genome Length (in bps) |
|---|---|---:|
| AFYC0100000 | Acanthamoeba polyphaga lentillevirus isolate lvs contig00005 | 788571 |
| JF801956.1 | Acanthamoeba castellanii mamavirus strain Hal-V | 1191693 |
| AP017645.1 | Acanthamoeba castellanii mimivirus DNA | 1182849 |
| AP017644.1 | Acanthamoeba castellanii mimivirus DNA | 1182801 |
| NC_014649.1 | Acanthamoeba polyphaga mimivirus | 1181549 |
| HQ336222.2 | Acanthamoeba polyphaga mimivirus | 1181549 |
| AY653733.1 | Acanthamoeba polyphaga mimivirus | 1181404 |
| JN036606.1 | Acanthamoeba polyphaga mimivirus isolate M4 | 981813 |
| MF405918.1 | Acanthamoeba polyphaga mimivirus isolate Tupan deep ocean | 1516267 |
| KY523104.1 | Acanthamoeba polyphaga mimivirus isolate Tupanvirus | 1439508 |
| JX962719.1 | Acanthamoeba polyphaga moumouvirus | 1021348 |
| NC_020104.1 | Acanthamoeba polyphaga moumouvirus | 1021348 |
| JX997156.1 | Acanthocystis turfacea Chlorella virus Can0610SP | 306752 |
| JX997168.1 | Acanthocystis turfacea Chlorella virus GM0701.1 | 315239 |
| JX997174.1 | Acanthocystis turfacea Chlorella virus MN0810.1 | 327406 |
| JX997177.1 | Acanthocystis turfacea Chlorella virus NE-JV-2 | 319583 |
| JX997180.1 | Acanthocystis turfacea Chlorella virus NTS-1 | 323517 |
| JX997185.1 | Acanthocystis turfacea Chlorella virus OR0704.3 | 311647 |
| JX997186.1 | Acanthocystis turfacea Chlorella virus TN603.4.2 | 320880 |
| MF403008.1 | Agrobacterium phage Atu_ph07 | 490380 |
| KR819915.1 | Apis mellifera filamentous virus isolate CH-CO5 | 496396 |
| NC_027925.1 | Apis mellifera filamentous virus isolate CH-CO5 | 496396 |
| KJ645900.1 | Aureococcus anophagefferens virus isolate BtV-01 | 370920 |
| NC_024697.1 | Aureococcus anophagefferens virus isolate BtV-01 | 370920 |
| JN638751.1 | Bacillus phage G | 497513 |
| NC_023719.1 | Bacillus phage G | 497513 |
| MF782455.1 | Bodo saltans virus strain NG1 | 1385869 |
| NC_029692.1 | Brazilian marseillevirus strain BH2014 | 362276 |
| KT752522.1 | Brazilian marseillevirus strain BH2014 | 362276 |
| NC_014637.1 | Cafeteria roenbergensis virus BV-PW1 | 617453 |
| GU244497.1 | Cafeteria roenbergensis virus BV-PW1 | 617453 |
| NC_005309.1 | Canarypox virus | 359853 |
| AY318871.1 | Canarypox virus strain ATCC VR-111 | 359853 |
| KF261120.1 | Cannes 8 virus | 374041 |
| KY684083.1 | Catovirus CTV1 Catovirus_1 genomic sequence | 1152313 |
| KY684084.1 | Catovirus CTV1 Catovirus_2 genomic sequence | 379946 |
| NC_032108.1 | Cedratvirus A11 genome assembly | 589068 |
| LT671577.1 | Cedratvirus A11 genome assembly | 589068 |
| LT907979.1 | Cedratvirus lausannensis genome assembly | 575161 |
| HF679132.1 | Choristoneura biennis entomopoxvirus 'L' | 307691 |

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|---|---|---|
| NC_021248.1 | Choristoneura biennis entomopoxvirus 'L' | 307691 |
| KT820662.1 | Chrysochromulina ericina virus isolate CeV-01B | 473558 |
| NC_028094.1 | Chrysochromulina ericina virus isolate CeV-01B | 473558 |
| HF586473.1 | Cotesia congregata sequence containing Cotesia congregata bracovirus proviral locus 2 (PL2) | 522749 |
| JN882285.1 | Cronobacter phage vB_CsaM_GAP32 | 358663 |
| NC_019401.1 | Cronobacter phage vB_CsaM_GAP32 | 358663 |
| AF204951.2 | Ectocarpus siliculosus virus | 335593 |
| NC_002687.1 | Ectocarpus siliculosus virus 1 | 335593 |
| KF481686.1 | Emiliania huxleyi virus 145 partial genome sequence | 399873 |
| KF481687.1 | Emiliania huxleyi virus 156 partial genome sequence | 400341 |
| KF481688.1 | Emiliania huxleyi virus 164 partial genome sequence | 401558 |
| KF481685.1 | Emiliania huxleyi virus 18 partial genome sequence | 400762 |
| JF974311.1 | Emiliania huxleyi virus 201 | 407301 |
| HQ634145.1 | Emiliania huxleyi virus 202 | 407516 |
| JF974291.1 | Emiliania huxleyi virus 203 | 400520 |
| JF974317.1 | Emiliania huxleyi virus 207 | 421891 |
| JF974318.1 | Emiliania huxleyi virus 208 | 411003 |
| JF974290.1 | Emiliania huxleyi virus 84 | 396620 |
| NC_007346.1 | Emiliania huxleyi virus 86 | 407339 |
| AJ890364.1 | Emiliania huxleyi virus 86 isolate EhV86 | 407339 |
| JF974310.1 | Emiliania huxleyi virus 88 | 397298 |
| FN429076.1 | Emiliania huxleyi virus 99B1 draft genome sequence | 376759 |
| HQ634146.1 | Emiliania huxleyi virus PS401 | 301520 |
| NC_019526.1 | Enterobacteria phage vB_KleM-RaK2 | 345809 |
| JQ513383.1 | Enterobacteria phage vB_KleM-RaK2 | 345809 |
| NC_025447.1 | Escherichia phage 121Q | 348532 |
| KM507819.1 | Escherichia phage 121Q | 348532 |
| NC_027364.1 | Escherichia phage PBECO 4 | 348113 |
| KC295538.1 | Escherichia phage PBECO 4 | 348113 |
| LT603033.1 | Escherichia phage vB_Eco_slurp01 genome assembly | 348043 |
| LT839607.1 | Faustovirus ST1 genome assembly | 470659 |
| KU556803.1 | Faustovirus strain D3 | 455803 |
| KU702950.1 | Faustovirus strain D5a | 466051 |
| KU702949.1 | Faustovirus strain D5b | 464523 |
| KU702951.1 | Faustovirus strain D6 | 462011 |
| KJ614390.1 | Faustovirus strain E12 | 466265 |
| KU702952.1 | Faustovirus strain E23 | 465956 |
| KU702948.1 | Faustovirus strain E24 | 466012 |
| KT835053.1 | Golden Marseillevirus | 360610 |
| NC_031465.1 | Golden Marseillevirus | 360610 |
| KF493731.1 | Hirudovirus strain Sangsue | 1181042 |
| KY684103.1 | Hokovirus HKV1 Hokovirus_1 genomic sequence | 450695 |
| KY684104.1 | Hokovirus HKV1 Hokovirus_2 genomic sequence | 317278 |

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|---|---|---|
| KY684105.1 | Hokovirus HKV1 Hokovirus_3 genomic sequence | 407933 |
| KF527888.1 | Insectomime virus strain V478 | 386631 |
| HG428764.1 | Insectomime virus V478 genomic scaffold | 382785 |
| KX552040.1 | Kaumoebavirus isolate Sc | 350731 |
| NC_034249.1 | Kaumoebavirus isolate Sc | 350731 |
| AB897757.1 | Klebsiella phage K64-1 DNA | 346602 |
| NC_027399.1 | Klebsiella phage K64-1 DNA | 346602 |
| KY684108.1 | Klosneuvirus KNV1 Klosneuvirus_1 genomic sequence | 451653 |
| KY684109.1 | Klosneuvirus KNV1 Klosneuvirus_2 genomic sequence | 333228 |
| KY073338.1 | Kurlavirus BKC-1 | 361368 |
| NC_015326.1 | Lausannevirus | 346754 |
| HQ113105.1 | Lausannevirus isolate 7715 | 346754 |
| NC_013756.1 | Marseillevirus marseillevirus strain T19 | 368454 |
| GU071086.1 | Marseillevirus marseillevirus strain T19 | 368454 |
| LN867403.1 | Megavirus avenue9 genome assembly Megavirus avenue9 | 1214278 |
| LN868256.1 | Megavirus battle43 genome assembly Megavirus battle43 | 1226044 |
| LN868539.1 | Megavirus bus genome assembly Megavirus bus | 1229128 |
| NC_016072.1 | Megavirus chiliensis | 1259197 |
| JN258408.1 | Megavirus chiliensis | 1259197 |
| JX975216.1 | Megavirus courdo11 | 1246126 |
| LN868540.1 | Megavirus courdo5 genome assembly Megavirus courdo5 | 921986 |
| JN885991.1 | Megavirus courdo7 isolate Mv13-c7 | 529672 |
| JX885207.1 | Megavirus lba isolate LBA111 | 1230522 |
| LN868518.1 | Megavirus montpellier3 genome assembly Megavirus montpellier3 | 1242698 |
| LN868520.1 | Megavirus shan genome assembly Megavirus shan scaffold scaffold00002 | 1258603 |
| LN868526.1 | Megavirus T1 genome assembly Megavirus T1 | 1216769 |
| LN869537.1 | Megavirus T4 genome assembly Megavirus T4 | 970404 |
| KF527229.1 | Megavirus terra1 genome | 1244621 |
| KM275475.1 | Melbournevirus isolate 1 | 369360 |
| NC_025412.1 | Melbournevirus isolate 1 | 369360 |
| LN867402.1 | Mimivirus amazonia genome assembly Mimivirus amazonia | 1179120 |
| KU761889.1 | Mimivirus Bombay isolate 1 genomic sequence | 1182200 |
| LN871163.1 | Mimivirus fauteuil genome assembly Mimivirus fauteuil | 1180980 |
| LN871173.1 | Mimivirus longchamps genome assembly Mimivirus longchamps | 1104869 |
| LN871174.1 | Mimivirus pointerouge1 genome assembly Mimivirus pointerouge1 | 1150884 |
| LN871172.1 | Mimivirus pointerouge2 genome assembly Mimivirus pointerouge2 | 1162847 |
| KF527228.1 | Mimivirus terra2 genome | 1168989 |
| NC_023639.1 | Mimivirus terra2 genome | 1168989 |
| KR921745.1 | Mollivirus sibericum isolate P1084-T | 651523 |
| NC_027867.1 | Mollivirus sibericum isolate P1084-T | 651523 |
| LN871171.1 | Moumouvirus battle49 genome assembly Moumouvirus battle49 | 844927 |

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| JN885998.1 | Moumouvirus Monve isolate Mv13-mv | 345413 |
| KT599914.1 | Niemeyer virus | 1299140 |
| KX066233.1 | Noumeavirus isolate NMV1 | 376207 |
| NC_033775.1 | Noumeavirus isolate NMV1 | 376207 |
| KX857749.1 | Only Syngen Nebraska virus 5 | 327147 |
| NC_032001.1 | Only Syngen Nebraska virus 5 | 327147 |
| HQ704802.1 | Organic Lake phycodnavirus 1 genomic sequence | 344723 |
| NC_036594.1 | Orpheovirus IHUMI-LCC2 genome assembly | 1473573 |
| LT906555.1 | Orpheovirus IHUMI-LCC2 genome assembly | 1473573 |
| LT706986.1 | Pacmanvirus A23 genome assembly | 395405 |
| NC_034383.1 | Pacmanvirus A23 genome assembly | 395405 |
| KC977570.1 | Pandoravirus dulcis | 1908524 |
| NC_021858.1 | Pandoravirus dulcis | 1908524 |
| KP136319.1 | Pandoravirus inopinatum isolate KlaHel | 2243109 |
| NC_026440.1 | Pandoravirus inopinatum isolate KlaHel | 2243109 |
| NC_022098.1 | Pandoravirus salinus | 2473870 |
| KC977571.1 | Pandoravirus salinus | 2473870 |
| NC_000852.5 | Paramecium bursaria Chlorella virus 1 | 330611 |
| JF411744.1 | Paramecium bursaria Chlorella virus 1 (PBCV-1) | 330611 |
| JX997153.1 | Paramecium bursaria Chlorella virus AN69C | 332309 |
| JX997154.1 | Paramecium bursaria Chlorella virus AP110A | 327349 |
| NC_009899.1 | Paramecium bursaria Chlorella virus AR158 | 344691 |
| DQ491003.2 | Paramecium bursaria Chlorella virus AR158 genomic sequence | 344691 |
| JX997157.1 | Paramecium bursaria Chlorella virus Can18-4 | 329890 |
| JX997159.1 | Paramecium bursaria Chlorella virus CVA-1 | 326592 |
| JX997160.1 | Paramecium bursaria Chlorella virus CVB-1 | 319457 |
| JX997161.1 | Paramecium bursaria Chlorella virus CVG-1 | 318742 |
| JX997162.1 | Paramecium bursaria Chlorella virus CviKI | 309195 |
| JX997163.1 | Paramecium bursaria Chlorella virus CVM-1 | 327107 |
| JX997164.1 | Paramecium bursaria Chlorella virus CVR-1 | 330002 |
| JX997165.1 | Paramecium bursaria Chlorella virus CvsA1 | 311223 |
| JX997166.1 | Paramecium bursaria Chlorella virus CZ-2 | 305715 |
| NC_008603.1 | Paramecium bursaria Chlorella virus FR483 | 321240 |
| DQ890022.1 | Paramecium bursaria Chlorella virus FR483 | 321240 |
| JX997167.1 | Paramecium bursaria Chlorella virus Fr5L | 303810 |
| JX997169.1 | Paramecium bursaria Chlorella virus IL-3A | 323497 |
| JX997170.1 | Paramecium bursaria Chlorella virus IL-5-2s1 | 345255 |
| JX997172.1 | Paramecium bursaria Chlorella virus MA-1D | 339653 |
| JX997173.1 | Paramecium bursaria Chlorella virus MA-1E | 339391 |
| DQ491001.1 | Paramecium bursaria chlorella virus MT325 genomic sequence | 314335 |
| JX997176.1 | Paramecium bursaria Chlorella virus NE-JV-1 | 326559 |
| JX997179.1 | Paramecium bursaria Chlorella virus NE-JV-4 | 328315 |
| JX997181.1 | Paramecium bursaria Chlorella virus NW665.2 | 325996 |
| NC_009898.1 | Paramecium bursaria Chlorella virus NY2A | 368683 |

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|---|---|---|
| DQ491002.1 | Paramecium bursaria Chlorella virus NY2A Chlorella virus NY2A ctg_13 genomic sequence | 368683 |
| JX997182.1 | Paramecium bursaria Chlorella virus NY-2B | 344863 |
| JX997183.1 | Paramecium bursaria Chlorella virus NYs1 | 348463 |
| JX997184.1 | Paramecium bursaria Chlorella virus OR0704.2.2 | 313584 |
| KU574722.1 | Pectobacterium phage CBB | 378379 |
| KJ859677.1 | Penguinpox virus isolate PSan92 | 306862 |
| NC_024446.1 | Penguinpox virus isolate PSan92 | 306862 |
| HQ634147.1 | Phaeocystis globosa virus 12T | 460002 |
| HQ634144.1 | Phaeocystis globosa virus 14T | 452892 |
| NC_021312.1 | Phaeocystis globosa virus strain 16T | 459984 |
| KC662249.1 | Phaeocystis globosa virus strain 16T | 459984 |
| NC_023423.1 | Pithovirus sibericum isolate P1084-T | 610033 |
| KF740664.1 | Pithovirus sibericum isolate P1084-T | 610033 |
| LT598836.1 | Pithovirus sp. LC8 genome assembly | 683254 |
| KT428292.1 | Port-miou virus | 349275 |
| KU877344.1 | Powai lake megavirus isolate 1 | 1208707 |
| EU197055.1 | Pseudomonas phage 201phi2-1 | 316674 |
| NC_010821.1 | Pseudomonas phage 201phi2-1 | 316674 |
| MF042360.1 | Pseudomonas phage Phabio | 309157 |
| NC_028999.1 | Pseudomonas phage PhiPA3 | 309208 |
| HQ630627.1 | Pseudomonas phage PhiPA3 | 309208 |
| MF360958.1 | Salicola phage SCTP-2 | 440001 |
| KF959826.2 | Samba virus | 1181380 |
| KY110734.1 | Saudi moumouvirus | 1030056 |
| AX151396.1 | Sequence 1 from Patent WO0138351 | 305107 |
| KY630187.1 | Serratia phage BF | 357154 |
| KX857216.1 | Shearwaterpox virus strain SWPV-1 | 326929 |
| KX857215.1 | Shearwaterpox virus strain SWPV-2 | 351108 |
| AF440570.1 | Shrimp white spot syndrome virus | 307287 |
| NC_030230.1 | Tokyovirus A1 DNA | 372707 |
| AP017398.1 | Tokyovirus A1 DNA | 372707 |
| KF483846.1 | Tunisvirus fontaine2 strain U484 | 380011 |
| KM982403.1 | UNVERIFIED: Acanthamoeba polyphaga mimivirus strain Amazonia | 1179119 |
| KM982402.1 | UNVERIFIED: Acanthamoeba polyphaga mimivirus strain Kroon | 1221932 |
| KM982401.1 | UNVERIFIED: Acanthamoeba polyphaga mimivirus strain Oyster | 1200220 |
| KC008572.1 | UNVERIFIED: Moumouvirus goulette | 1016844 |
| MG592671.1 | Vibrio phage 2.275.O._10N.286.54.E11 | 348911 |
| AF332093.3 | White spot syndrome virus | 305119 |
| KR083866.1 | White spot syndrome virus isolate EG3 | 305119 |
| KT995472.1 | White spot syndrome virus strain CN01 | 309286 |
| NC_003225.3 | White spot syndrome virus strain CN01 | 309286 |
| AP018399.1 | Xanthomonas phage XacN1 DNA | 384670 |
| LT960552.1 | Yersinia phage fHe-Yen9-03 genome assembly | 352596 |

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| LT960551.1 | Yersinia phage fHe-Yen9-04 genome assembly | 354378 |

**Supplementary Table 2: Top hits of giant viruses in pre-filter**

| NCBI Accession Number | Taxonomic name | Blast Score | E-Value |
|---|---|---:|---:|
| HF679132.1 | Choristoneura biennis entomopoxvirus 'L' | 55.4 | 0.0006 |
| JQ360576.1 | Chimpanzee alpha-1 herpesvirus strain 105640 | 57.2 | 0.0002 |
| KU893109.1 | Human herpesvirus 2 isolate 2012-9333, partial genome | 57.2 | 0.0002 |
| DQ517337.1 | Trichoplusia ni ascovirus 2c, complete genome | 59 | 0.00005 |
| HG425349.2 | Spodoptera exigua multiple nucleopolyhedrovirus | 60.8 | 0.00001 |
| AY386371.1 | Yaba monkey tumor virus, complete genome | 60.8 | 0.00001 |
| KR921745.1 | Mollivirus sibericum isolate P1084-T, complete genome | 62.6 | 0.000004 |
| DQ123841.1 | Agrotis segetum nucleopolyhedrovirus, complete genome | 68 | 1E-07 |
| AF033815.1 | Mason-Pfizer monkey virus, complete genome | 66.2 | 2E-08 |
| M12349.1 | Simian Mason-Pfizer D-type retrovirus (MPMV/6A) | 66.2 | 2E-08 |
| AB107976.1 | Chlorella virus k2-gfat gene for glutamine:fructose-6 | 71.6 | 8E-09 |
| KP296186.1 | Diatraea saccharalis granulovirus, complete genome | 71.6 | 8E-09 |
| KF158713.1 | Hemileuca sp. nucleopolyhedrovirus, complete genome | 71.6 | 8E-09 |
| DQ453159.1 | Geobacillus virus E2, complete genome | 73.4 | 2E-09 |
| EF524222.1 | Shrimp white spot syndrome virus unknown gene | 73.4 | 2E-09 |
| AP013055.1 | Anomala cuprea entomopoxvirus DNA, complete genome | 75.2 | 7E-10 |
| AF246223.1 | Mycoplasma virus P1, complete genome | 75.2 | 7E-10 |
| KC662249.1 | Phaeocystis globosa virus strain 16T, complete genome | 77 | 1E-10 |
| HF920633.1 | Invertebrate iridovirus 22 complete genome | 78.8 | 6E-11 |
| JF411744.1 | Paramecium bursaria Chlorella virus 1 (PBCV-1) | 78.8 | 1E-11 |
| HQ632826.1 | Micromonas pusilla virus 12T genomic sequence | 82.4 | 5E-12 |
| KT835053.1 | Golden Marseillevirus, complete genome | 82.4 | 4E-12 |
| KR083866.1 | White spot syndrome virus isolate EG3, complete genome | 82.4 | 4E-12 |
| AY009089.1 | Camelpox virus CMS, complete genome | 84.2 | 1E-12 |
| HF920634.1 | Invertebrate iridescent virus 22 isolate IIV22 | 84.2 | 1E-12 |
| L22579.1 | Variola major virus (strain Bangladesh-1975) | 84.2 | 1E-12 |
| KR819915.1 | Apis mellifera filamentous virus isolate CH-CO5 | 86 | 4E-13 |
| AY225133.1 | Feldmannia irregularis virus a strain FirrV-1 contig | 86 | 4E-13 |
| KM009991.1 | Peridroma alphabaculovirus isolate GR_167 | 86 | 2E-13 |
| KC540776.1 | Uncultured virus isolate P4 ribonucleotide reductase | 86 | 2E-13 |
| KU199244.1 | Crucian carp herpesvirus isolate 1301, complete genome | 87.8 | 1E-13 |
| AY689437.1 | Deerpox virus W-1170-84, complete genome | 87.8 | 1E-13 |
| DQ437594.1 | Taterapox virus strain Dahomey 1968, complete genome | 87.8 | 1E-13 |
| GU244497.1 | Cafeteria roenbergensis virus BV-PW1, complete genome | 89.7 | 3E-14 |
| AY318871.1 | Canarypox virus strain ATCC VR-111, complete genome | 89.7 | 3E-14 |
| EU522111.1 | Musca domestica salivary gland hypertrophy virus | 89.7 | 2E-14 |
| KX857749.1 | Only Syngen Nebraska virus 5, complete genome | 89.7 | 2E-14 |
| KP874736.1 | Ostreococcus lucimarinus virus 2 isolate Olv2 | 89.7 | 2E-14 |
| AJ920288.1 | Euproctis pseudoconspersa nucleopolyhedrovirus p24 | 91.5 | 9E-15 |

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|---|---|---|---|
| HM004429.1 | Micromonas sp. RCC1109 virus MpV1, complete genome | 93.3 | 3E-15 |
| AF170722.1 | Rabbit fibroma virus, complete genome | 93.3 | 2E-15 |
| AY484669.1 | Rabbitpox virus, complete genome | 96.9 | 2E-16 |
| AF095689.1 | Vaccinia virus (strain Tian Tan) complete genome | 96.9 | 2E-16 |
| EF101928.1 | Acanthocystis turfacea Chlorella virus 1 | 96.9 | 1E-16 |
| LC015647.1 | Yellowstone lake phycodnavirus 1 DNA | 98.7 | 6E-17 |
| JQ410350.1 | Ectromelia virus ERPV culture-collection ATCC:VR-1431 | 102 | 5E-18 |
| DQ792504.1 | Horsepox virus isolate MNR-76, complete genome | 102 | 5E-18 |
| LN864566.1 | Cowpox virus complete genome, strain FM2292 | 105 | 4E-19 |
| KP849469.1 | Monkeypox virus isolate Boende_DRC_2008, complete genome | 105 | 4E-19 |
| KU877344.1 | Powai lake megavirus isolate 1, complete genome | 107 | 1E-19 |
| AP006270.1 | Adoxophyes honmai nucleopolyhedrovirus DNA, complete | 109 | 3E-20 |
| HM004432.1 | Bathycoccus sp. RCC1105 virus BpV1, complete genome | 109 | 3E-20 |
| KX027736.1 | Anguillid herpesvirus 1 isolate HVA980811 | 114 | 8E-22 |
| KU556803.1 | Faustovirus strain D3, complete genome | 114 | 8E-22 |
| KJ645900.1 | Aureococcus anophagefferens virus isolate BtV-01 | 116 | 2E-22 |
| HF679134.1 | Mythimna separata entomopoxvirus 'L', complete genome | 116 | 2E-22 |
| KY094066.1 | BeAn 58058 virus, complete genome | 118 | 6E-23 |
| LT671577.1 | Cedratvirus A11 genome assembly | 118 | 6E-23 |
| KF481686.1 | Emiliania huxleyi virus 145 partial genome sequence | 118 | 6E-23 |
| JX975216.1 | Megavirus courdo11, complete genome | 118 | 3E-23 |
| JN258408.1 | Megavirus chiliensis, complete genome | 122 | 2E-24 |
| JN885991.1 | Megavirus courdo7 isolate Mv13-c7, partial genome | 122 | 2E-24 |
| JX885207.1 | Megavirus lba isolate LBA111, complete genome | 122 | 2E-24 |
| KF527229.1 | Megavirus terra1 genome | 122 | 2E-24 |
| AY208990.1 | Carp nephritis and gill necrosis virus genomic fragment | 123 | 1E-24 |
| EU001284.1 | Glyptapanteles flavicoxis bracovirus segment 29 | 122 | 1E-24 |
| JQ815363.1 | Cyprinid herpesvirus 1 strain NG-J1, complete genome | 125 | 2E-25 |
| AY786308.2 | Koi herpesvirus ribonucleotide reductase gene | 127 | 1E-25 |
| JX962719.1 | Acanthamoeba polyphaga moumouvirus, complete genome | 127 | 6E-26 |
| JN885998.1 | Moumouvirus Monve isolate Mv13-mv, partial genome | 127 | 6E-26 |
| HQ113105.1 | Lausannevirus isolate 7715, complete genome | 132 | 3E-27 |
| KT428292.1 | Port-miou virus, complete genome | 132 | 3E-27 |
| KX618634.1 | Lymantria dispar multiple nucleopolyhedrovirus | 132 | 2E-27 |
| AP017398.1 | Tokyovirus A1 DNA, nearly complete genome | 140 | 7E-30 |
| AP017645.1 | Acanthamoeba castellanii mimivirus DNA | 141 | 6E-30 |
| KU761889.1 | Mimivirus Bombay isolate 1 genomic sequence | 141 | 6E-30 |
| KT599914.1 | Niemeyer virus, partial genome | 141 | 6E-30 |
| KF959826.2 | Samba virus, complete genome | 141 | 6E-30 |
| EU552531.1 | Recombinant virus 6918VP60-T2, complete sequence | 141 | 5E-30 |
| KC951854.1 | Goatpox virus FZ, complete genome | 143 | 2E-30 |
| JX565584.1 | Myxoma virus isolate BD23, complete genome | 143 | 2E-30 |
| KU749310.1 | Skunkpox virus strain WA, complete genome | 143 | 2E-30 |
| KJ859677.1 | Penguinpox virus isolate PSan92, complete genome | 145 | 2E-31 |
| JF801956.1 | Acanthamoeba castellanii mamavirus strain Hal-V | 147 | 1E-31 |
| KF493731.1 | Hirudovirus strain Sangsue, complete genome | 147 | 1E-31 |

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|---|---|---|---|
| KF527228.1 | Mimivirus terra2 genome | 147 | 1E-31 |
| KC977570.1 | Pandoravirus dulcis, complete genome | 147 | 1E-31 |
| KP136319.1 | Pandoravirus inopinatum isolate KlaHel, complete genome | 149 | 4E-32 |
| KT820662.1 | Chrysochromulina ericina virus isolate CeV-01B | 152 | 3E-33 |
| KU749309.1 | Raccoonpox virus strain 85A, complete genome | 152 | 3E-33 |
| AF063866.1 | Melanoplus sanguinipes entomopoxvirus, complete genome | 154 | 9E-34 |
| HQ704802.1 | Organic Lake phycodnavirus 1 genomic sequence | 168 | 4E-38 |
| KC977571.1 | Pandoravirus salinus, complete genome | 168 | 4E-38 |
| AF065756.1 | Stealth virus 1 clone 3B43 T7 | 291 | 5E-75 |

**Supplementary Table 3: Top hits of giant viruses in WWTP Dry Bed**

| NCBI Accession Number | Taxonomic name | Blast Score | E-Value |
|---|---|---|---|
| HM004432.1 | Bathycoccus sp. RCC1105 virus BpV1, complete genome | 57.2 | 2.00E-04 |
| AF198100.1 | Fowlpox virus, complete genome | 57.2 | 2.00E-04 |
| KT159937.1 | Salmon gill poxvirus, complete genome | 57.2 | 2.00E-04 |
| AF410153.1 | Swinepox virus isolate 17077-99, complete genome | 59 | 5.00E-05 |
| KR921745.1 | Mollivirus sibericum isolate P1084-T, complete genome | 60.8 | 1.00E-05 |
| AY386371.1 | Yaba monkey tumor virus, complete genome | 62.6 | 4.00E-06 |
| AP009046.1 | Hyphantria cunea nucleopolyhedrovirus genomic DNA | 64.4 | 1.00E-06 |
| JX997183.1 | Paramecium bursaria Chlorella virus NYs1, partial genome | 64.4 | 1.00E-06 |
| FR719956.1 | Roseovarius Plymouth Podovirus 1 partial sequence | 64.4 | 1.00E-06 |
| JX997187.1 | Acanthocystis turfacea Chlorella virus WI0606 | 66.2 | 3.00E-07 |
| KJ859677.1 | Penguinpox virus isolate PSan92, complete genome | 66.2 | 3.00E-07 |
| KJ801920.1 | Pigeonpox virus isolate FeP2, complete genome | 66.2 | 3.00E-07 |
| AF170722.1 | Rabbit fibroma virus, complete genome | 69.8 | 3.00E-08 |
| DQ643392.1 | Aedes taeniorhynchus iridescent virus, complete genome | 71.6 | 8.00E-09 |
| KX857749.1 | Only Syngen Nebraska virus 5, complete genome | 71.6 | 8.00E-09 |
| GU244497.1 | Cafeteria roenbergensis virus BV-PW1, complete genome | 71.6 | 6.00E-09 |
| AY208990.1 | Carp nephritis and gill necrosis virus genomic fragment | 73.4 | 2.00E-09 |
| KP747440.1 | Dasychira pudibunda nucleopolyhedrovirus isolate ML1 | 73.4 | 2.00E-09 |
| AF325155.1 | Spodoptera litura nucleopolyhedrovirus strain G2 | 73.4 | 2.00E-09 |
| AF012825.2 | Ectromelia virus strain Moscow, complete genome | 75.2 | 7.00E-10 |
| AF380138.1 | Monkeypox virus strain Zaire-96-I-16, complete genome | 75.2 | 7.00E-10 |
| KC662249.1 | Phaeocystis globosa virus strain 16T, complete genome | 77 | 2.00E-10 |
| AF440570.1 | Shrimp white spot syndrome virus, complete genome | 77 | 2.00E-10 |
| AF332093.3 | White spot syndrome virus, complete genome | 77 | 2.00E-10 |
| HQ420900.1 | Cowpox virus strain UK2000_K2984, complete genome | 80.6 | 2.00E-11 |
| DQ792504.1 | Horsepox virus isolate MNR-76, complete genome | 80.6 | 2.00E-11 |
| AY484669.1 | Rabbitpox virus, complete genome | 80.6 | 2.00E-11 |
| KF179385.1 | Vaccinia virus, complete genome | 80.6 | 2.00E-11 |
| HQ632826.1 | Micromonas pusilla virus 12T genomic sequence | 82.4 | 4.00E-12 |
| DQ657948.1 | Cyprinid herpesvirus 3 strain KHV-U, complete genome | 82.4 | 3.00E-12 |
| KT835053.1 | Golden Marseillevirus, complete genome | 84.2 | 1.00E-12 |
| JF801956.1 | Acanthamoeba castellanii mamavirus strain Hal-V | 86 | 4.00E-13 |
| KU702951.1 | Faustovirus strain D6, complete genome | 87.8 | 1.00E-13 |
| KP768318.1 | Camelpox virus strain 0408151v, complete genome | 89.7 | 3.00E-14 |
| HQ336222.2 | Acanthamoeba polyphaga mimivirus, complete genome | 91.5 | 9.00E-15 |
| KT820662.1 | Chrysochromulina ericina virus isolate CeV-01B | 91.5 | 9.00E-15 |
| KF493731.1 | Hirudovirus strain Sangsue, complete genome | 91.5 | 9.00E-15 |
| KU761889.1 | Mimivirus Bombay isolate 1 genomic sequence | 91.5 | 9.00E-15 |
| KF527228.1 | Mimivirus terra2 genome | 91.5 | 9.00E-15 |
| KT599914.1 | Niemeyer virus, partial genome | 91.5 | 9.00E-15 |
| KF959826.2 | Samba virus, complete genome | 91.5 | 9.00E-15 |
| DQ437594.1 | Taterapox virus strain Dahomey 1968, complete genome | 93.3 | 3.00E-15 |

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|---|---|---|---|
| DQ441448.1 | Variola virus strain Yugoslavia 1972 V72-164 | 93.3 | 3.00E-15 |
| JX975216.1 | Megavirus courdo11, complete genome | 100 | 2.00E-17 |
| JN885991.1 | Megavirus courdo7 isolate Mv13-c7, partial genome | 100 | 2.00E-17 |
| KF527229.1 | Megavirus terra1 genome | 100 | 2.00E-17 |
| KU877344.1 | Powai lake megavirus isolate 1, complete genome | 105 | 4.00E-19 |
| AJ890364.1 | Emiliania huxleyi virus 86 isolate EhV86 | 109 | 3.00E-20 |
| KT752522.1 | Brazilian marseillevirus strain BH2014, complete genome | 113 | 3.00E-21 |
| KJ645900.1 | Aureococcus anophagefferens virus isolate BtV-01 | 118 | 6.00E-23 |
| JX885207.1 | Megavirus lba isolate LBA111, complete genome | 118 | 6.00E-23 |
| KP136319.1 | Pandoravirus inopinatum isolate KlaHel, complete genome | 122 | 5.00E-24 |
| JN258408.1 | Megavirus chiliensis, complete genome | 127 | 1.00E-25 |
| KR029585.1 | Uncultured marine virus isolate Anoxic2_1 | 127 | 1.00E-25 |
| KC977570.1 | Pandoravirus dulcis, complete genome | 141 | 6.00E-30 |
| KC977571.1 | Pandoravirus salinus, complete genome | 161 | 6.00E-36 |
| JX962719.1 | Acanthamoeba polyphaga moumouvirus | 187 | 1.00E-43 |
| JN885999.1 | Moumouvirus Monve isolate Mv13-mv, partial genome | 187 | 1.00E-43 |
| AF191073.1 | Stealth virus 1 clone 3B43, genomic sequence | 291 | 5.00E-75 |

**Supplementary Table 4: Top hits of giant viruses in WWTP sludge**

| NCBI Accession Number | Taxonomic name | Blast Score | E-Value |
|---|---|---|---|
| X72087.1 | Aujeszky's disease virus RR1 and RR2 genes | 57.2 | 2.00E-04 |
| KT832477.1 | Elephant endotheliotropic herpesvirus 4 isolate | 57.2 | 2.00E-04 |
| KU552118.1 | Suid alphaherpesvirus 1 isolate LA, complete genome | 57.2 | 2.00E-04 |
| KU360259.1 | Suid herpesvirus 1 isolate DL14/08, complete genome | 57.2 | 2.00E-04 |
| BK001744.1 | TPA: Suid herpesvirus 1, complete genome | 57.2 | 2.00E-04 |
| KT804738.1 | Giant seaperch iridovirus isolate GSIV-K1 | 57.2 | 1.00E-04 |
| AY894343.1 | Orange-spotted grouper iridovirus, complete genome | 57.2 | 1.00E-04 |
| KC244182.1 | Rock bream iridovirus isolate RBIV-C1, complete genome | 57.2 | 1.00E-04 |
| LC015648.1 | Yellowstone lake phycodnavirus 2 DNA | 59 | 5.00E-05 |
| KM609482.1 | Autographa californica multiple nucleopolyhedrovirus | 59 | 4.00E-05 |
| KU697903.1 | Mutant Autographa californica nucleopolyhedrovirus | 59 | 4.00E-05 |
| KP747440.1 | Dasychira pudibunda nucleopolyhedrovirus isolate ML1 | 60.8 | 1.00E-05 |
| AP009046.1 | Hyphantria cunea nucleopolyhedrovirus genomic DNA | 60.8 | 1.00E-05 |
| KF527888.1 | Insectomime virus strain V478, partial genome | 60.8 | 1.00E-05 |
| KP752043.1 | Lambdina fiscellaria nucleopolyhedrovirus isolate GR1 | 60.8 | 1.00E-05 |
| KT428292.1 | Port-miou virus, complete genome | 60.8 | 1.00E-05 |
| AY145471.1 | Rachiplusia ou multiple nucleopolyhedrovirus | 60.8 | 1.00E-05 |
| KF483846.1 | Tunisvirus fontaine2 strain U484, complete genome | 60.8 | 1.00E-05 |
| X98924.1 | Spodoptera littoralis nuclear polyhedrosis virus gene | 62.6 | 2.00E-06 |
| D14469.1 | Chlorella virus CVK1F1 gene, repeat region | 64.4 | 1.00E-06 |
| DQ123841.1 | Agrotis segetum nucleopolyhedrovirus, complete genome | 64.4 | 5.00E-07 |
| KJ003983.1 | IAS virus, complete genome | 66.2 | 3.00E-07 |
| KC117377.1 | Halovirus HVTV-1, complete genome | 68 | 1.00E-07 |
| KR921745.1 | Mollivirus sibericum isolate P1084-T, complete genome | 68 | 1.00E-07 |
| AF204951.2 | Ectocarpus siliculosus virus, complete genome | 69.8 | 2.00E-08 |
| GU244497.1 | Cafeteria roenbergensis virus BV-PW1, complete genome | 73.4 | 2.00E-09 |
| AY689437.1 | Deerpox virus W-1170-84, complete genome | 73.4 | 2.00E-09 |
| KP188543.1 | Dengue virus 1 isolate DENV1 BR/SJRP/484/2012 | 73.4 | 2.00E-09 |
| AB018418.1 | Red sea bream iridovirus genes for largest subunit | 75.2 | 6.00E-10 |
| HF679132.1 | Choristoneura biennis entomopoxvirus 'L' | 77 | 2.00E-10 |
| EU001267.1 | Glyptapanteles flavicoxis bracovirus segment 10 | 77 | 2.00E-10 |
| KU877344.1 | Powai lake megavirus isolate 1, complete genome | 75.2 | 2.00E-10 |
| DQ517337.1 | Trichoplusia ni ascovirus 2c, complete genome | 77 | 2.00E-10 |
| KT781098.1 | Infectious spleen and kidney necrosis virus strain RS | 78.8 | 5.00E-11 |
| KY215944.1 | Bovine alphaherpesvirus 1 isolate 216 II | 80.6 | 2.00E-11 |
| EF101928.1 | Acanthocystis turfacea Chlorella virus 1 | 82.4 | 5.00E-12 |
| KF261120.1 | Cannes 8 virus, complete genome | 84.2 | 1.00E-12 |
| GU071086.1 | Marseillevirus marseillevirus strain T19 | 84.2 | 1.00E-12 |
| KM275475.1 | Melbournevirus isolate 1, complete genome | 84.2 | 1.00E-12 |
| JF909601.1 | Senegalvirus SSV-A contig6 genomic sequence | 84.2 | 1.00E-12 |
| KX853510.1 | Uncultured virus isolate Rctr197k, partial genome | 84.2 | 1.00E-12 |
| EU522111.1 | Musca domestica salivary gland hypertrophy virus | 87.8 | 1.00E-13 |

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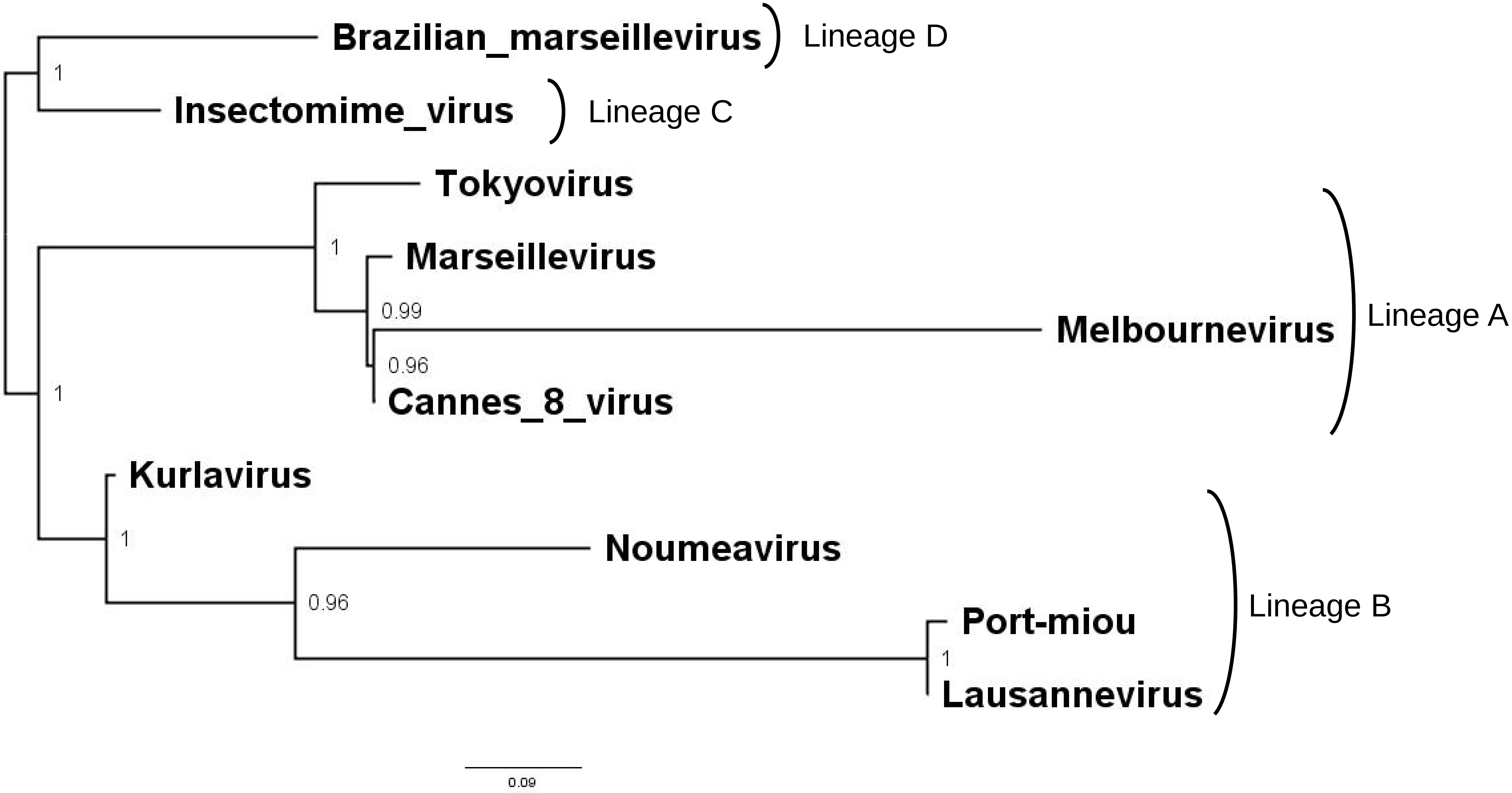
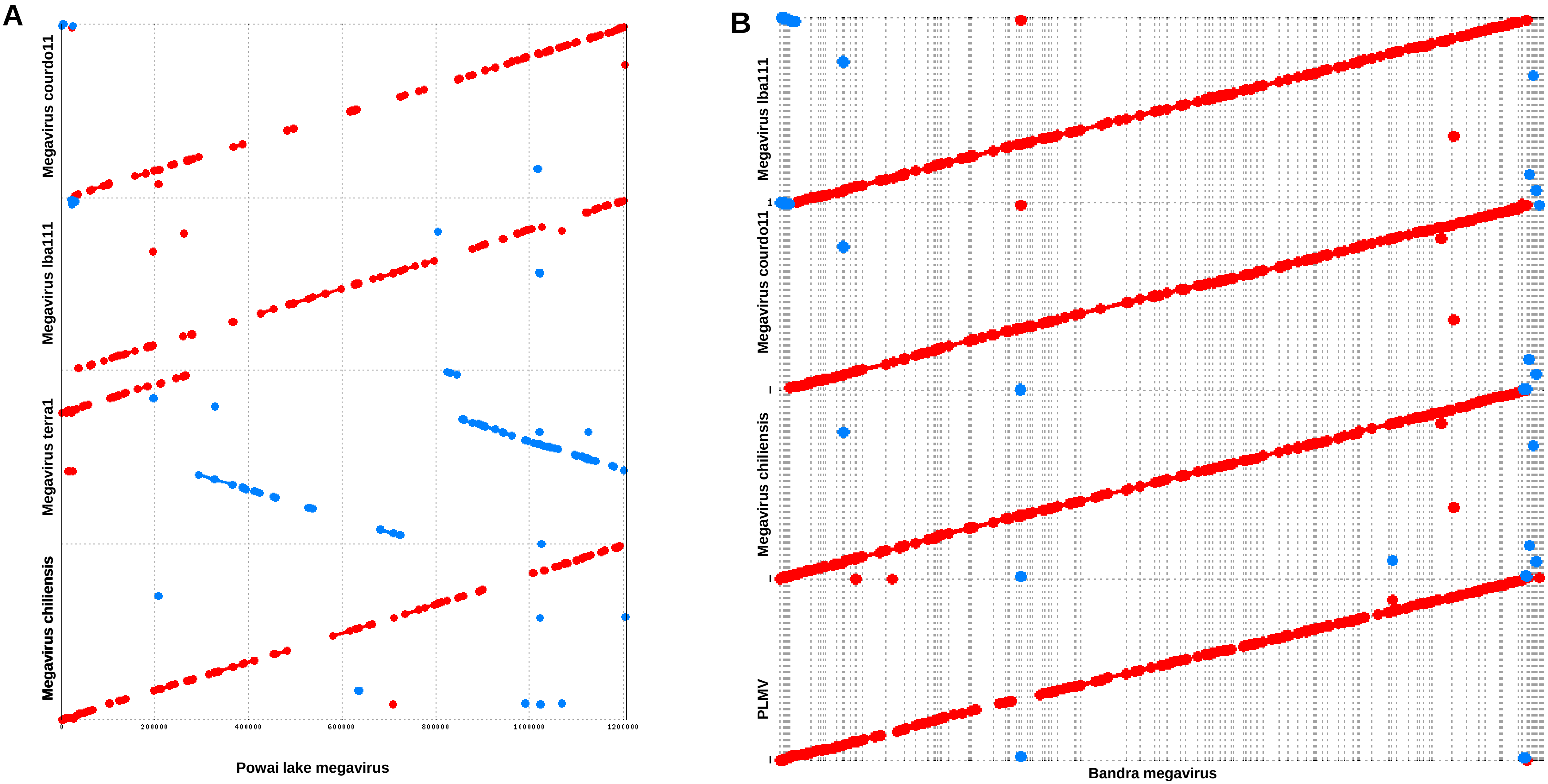
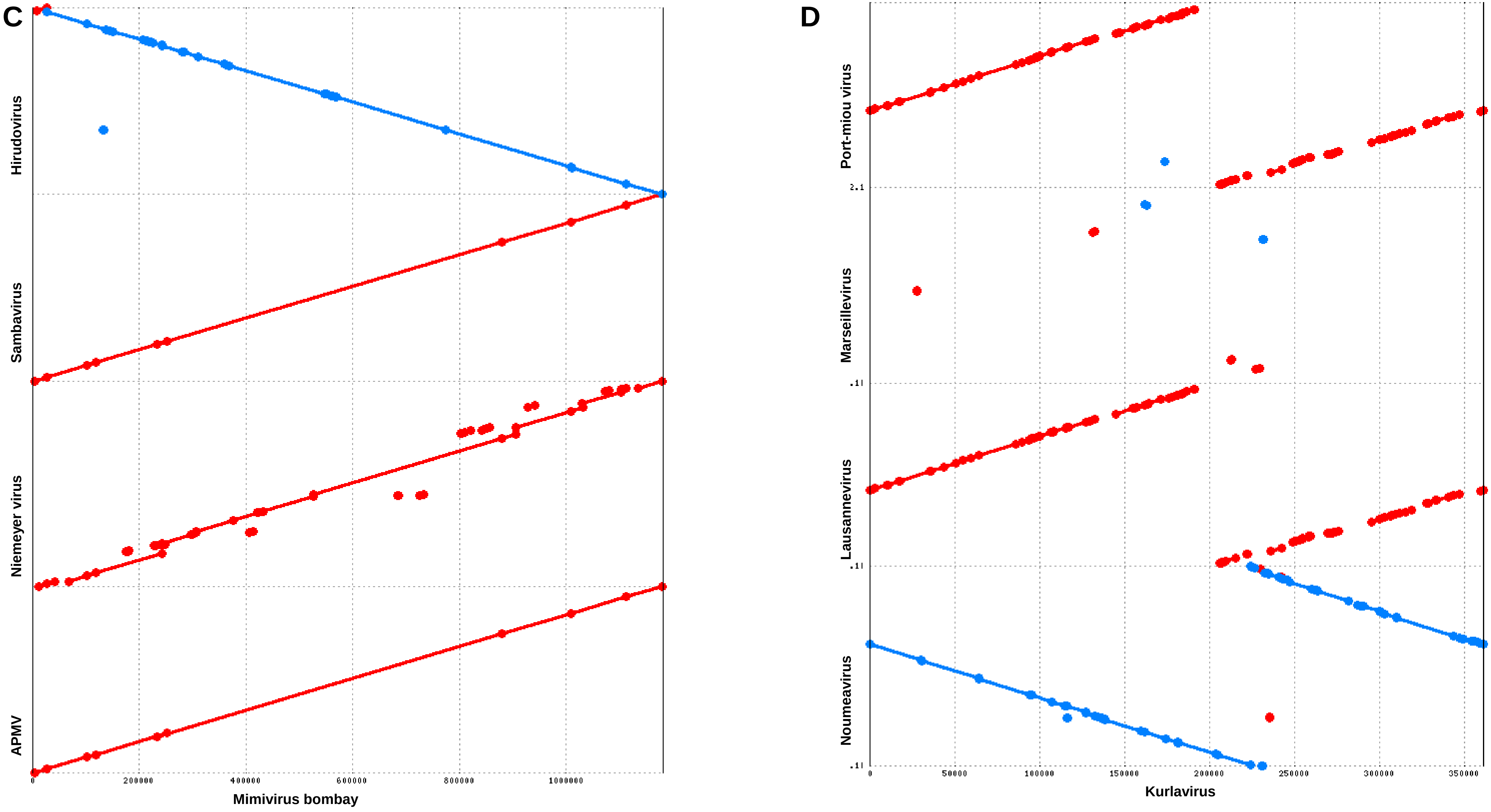
|---|---|---|---|
| JF411744.1 | Paramecium bursaria Chlorella virus 1 (PBCV-1) | 87.8 | 1.00E-13 |
| GQ273492.1 | Turbot reddish body iridovirus, complete genome | 87.8 | 1.00E-13 |
| KF481686.1 | Emiliania huxleyi virus 145 partial genome sequence | 87.8 | 8.00E-14 |
| KR819915.1 | Apis mellifera filamentous virus isolate CH-CO5 | 89.7 | 3.00E-14 |
| KX857749.1 | Only Syngen Nebraska virus 5, complete genome | 89.7 | 3.00E-14 |
| JX962719.1 | Acanthamoeba polyphaga moumouvirus, complete genome | 91.5 | 9.00E-15 |
| KX618634.1 | Lymantria dispar multiple nucleopolyhedrovirus | 93.3 | 3.00E-15 |
| JN885999.1 | Moumouvirus Monve isolate Mv13-mv, partial genome | 95.1 | 7.00E-16 |
| EF420156.1 | Tanapox virus isolate TPV-Kenya, complete genome | 95.1 | 5.00E-16 |
| AJ293568.1 | Yaba-like disease virus (YLDV), complete genome | 95.1 | 5.00E-16 |
| AY208989.1 | Carp nephritis and gill necrosis virus genomic fragment | 96.9 | 2.00E-16 |
| KT820662.1 | Chrysochromulina ericina virus isolate CeV-01B | 96.9 | 2.00E-16 |
| AY786308.2 | Koi herpesvirus ribonucleotide reductase gene | 96.9 | 2.00E-16 |
| LT671577.1 | Cedratvirus A11 genome assembly, complete genome | 100 | 2.00E-17 |
| AP008984.1 | Cyprinid herpesvirus 3 DNA, complete genome | 102 | 5.00E-18 |
| KJ645900.1 | Aureococcus anophagefferens virus isolate BtV-01 | 109 | 3.00E-20 |
| AF410153.1 | Swinepox virus isolate 17077-99, complete genome | 109 | 3.00E-20 |
| KR029585.1 | Uncultured marine virus isolate Anoxic2_1 | 113 | 3.00E-21 |
| KU749309.1 | Raccoonpox virus strain 85A, complete genome | 114 | 7.00E-22 |
| HQ849551.1 | Yoka poxvirus strain DakArB 4268, complete genome | 122 | 5.00E-24 |
| AP017645.1 | Acanthamoeba castellanii mimivirus DNA | 123 | 1.00E-24 |
| HQ336222.2 | Acanthamoeba polyphaga mimivirus, complete genome | 123 | 1.00E-24 |
| KF493731.1 | Hirudovirus strain Sangsue, complete genome | 123 | 1.00E-24 |
| KU761889.1 | Mimivirus Bombay isolate 1 genomic sequence | 123 | 1.00E-24 |
| KF527228.1 | Mimivirus terra2 genome | 123 | 1.00E-24 |
| KT599914.1 | Niemeyer virus, partial genome | 123 | 1.00E-24 |
| KF959826.2 | Samba virus, complete genome | 123 | 1.00E-24 |
| JF801956.1 | Acanthamoeba castellanii mamavirus strain Hal-V | 129 | 3.00E-26 |
| JN258408.1 | Megavirus chiliensis, complete genome | 131 | 8.00E-27 |
| JX975216.1 | Megavirus courdo11, complete genome | 131 | 8.00E-27 |
| JN885991.1 | Megavirus courdo7 isolate Mv13-c7, partial genome | 131 | 8.00E-27 |
| JX885207.1 | Megavirus lba isolate LBA111, complete genome | 131 | 8.00E-27 |
| KF527229.1 | Megavirus terra1 genome | 131 | 8.00E-27 |
| JQ410350.1 | Ectromelia virus ERPV culture-collection ATCC:VR-1431 | 134 | 8.00E-28 |
| KU749310.1 | Skunkpox virus strain WA, complete genome | 134 | 8.00E-28 |
| KC977571.1 | Pandoravirus salinus, complete genome | 136 | 2.00E-28 |
| KX027736.1 | Anguillid herpesvirus 1 isolate HVA980811 | 138 | 7.00E-29 |
| KU749311.1 | Volepox virus strain CA, complete genome | 138 | 7.00E-29 |
| KP136319.1 | Pandoravirus inopinatum isolate KlaHel, complete genome | 161 | 6.00E-36 |
| KC977570.1 | Pandoravirus dulcis, complete genome | 187 | 1.00E-43 |
| AF065756.1 | Stealth virus 1 clone 3B43 T7 | 417 | ####### |

Supplementary Figure 1. Maximum likelihood based phylogeny of 4 Histone-like proteins (concatenated Fastas) in KUV. The phylogeny indicates a lineage specific sequence similarity, wherein KUV shares maximum homology with histone-like proteins in *Noumeavirus* belonging to *Marseilleviridae* Lineage B.



Supplementary Figure 2. Maximum unique matches (MUMs) matches among A) PLMV and other megaviruses, B) BAV and other megaviruses, C) MVB and other mimiviruses, and D) KUV  and other marseilleviruses
MUMs were calculated using Nucmer, with a sliding window size of 100 nulceotides. Forward matches are shown in Red, reverse matches are shown in Blue.




C
Hirudovirus
Sambavirus
Niemeyer virus
APMV
0
200000
400000
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Mimivirus bombay
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Port-miou virus
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Lausannevirus
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Kurlavirus