

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2023.011D*** |  |
| **Short title:** Establishing 59 new species in the family *Smacoviridae* | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 23 June 2023 |
| Date of this revision (if different to above) | 14 Aug 2023 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| --- |
| 2023.011D.N.v2.Smacoviridae\_59nsp.xlsx |

**Abstract**

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| There are 12 genera in the family *Smacoviridae.* Here we propose to establish 59 new species in the genera *Porprismacovirus* (n=25), *Inpeasmacovirus* (n=1), *Felismacovirus* (n=22), *Drosmacovirus* (n=4), *Dragsmacovirus* (n=2), *Bovismacovirus* (n=4) and *Bonzesmacovirus* (n=1). |

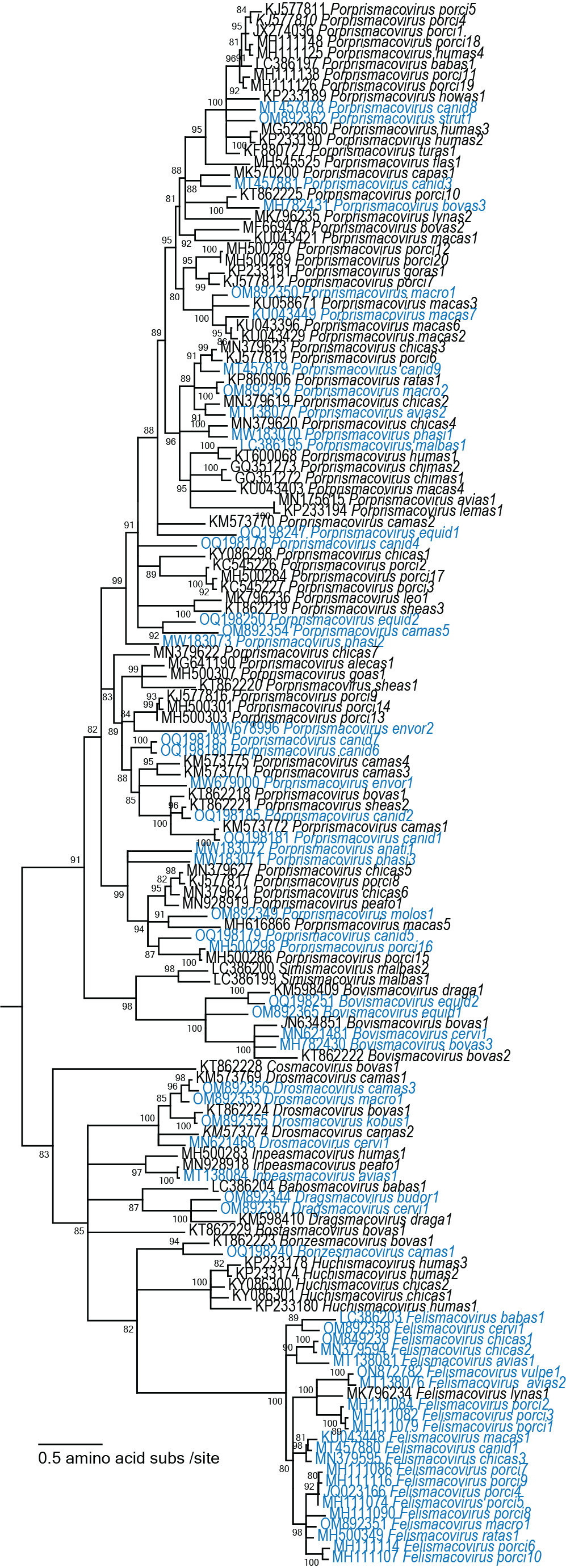
**Text of proposal**

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| |  | | --- | | Smacoviruses have small circular single stranded DNA genomes that encode for a rolling-circle replication initiation protein (Rep) and unique capsid protein (Cp). There are 12 established genera in the family *Smacoviridae* [1]. The single member of the genus *Felismacovirus* which is classified in the species *Felismacovirus lynas1* encodes the Rep and Cp in a unidirectional orientation, whereas members of the other 11 genera in an ambience orientation.  In the last couple of years, a large number of smacoviruses (n=176) have been identified and many display considerable sequence divergence to be considered as representatives of new species. We assembled a dataset of the complete genomes (with annotations available in GenBank) of smacoviruses that have not yet been classified since the last report by Krupovic and Varsani [1]. These were analysed with previously classified viruses to first determine their genus and species level classification. We identified 144 smacoviruses that could not be classified into existing species and for these we propose 59 new species based on the species demarcation criteria (77% pairwise identity threshold) outlined in Varsani and Krupovic [2]. These 59 new species are distributed across the genera *Porprismacovirus* (n=25), *Inpeasmacovirus* (n=1), *Felismacovirus* (n=22), *Drosmacoviru*s (n=4), *Dragsmacovirus* (n=2), *Bovismacovirus* (n=4) and *Bonzesmacovirus* (n=1).  Similar to the sole member of *Felismacovirus* (*Felismacovirus lynas1*; MK796234) all the members of the 22 new proposed species of *Felismacovirus* also have genomes with Rep and Cp organized in a unidirectional orientation.  The species epithets are derived from the first 5 letters of the host or source family name or generic name followed by a number in sequence. | |

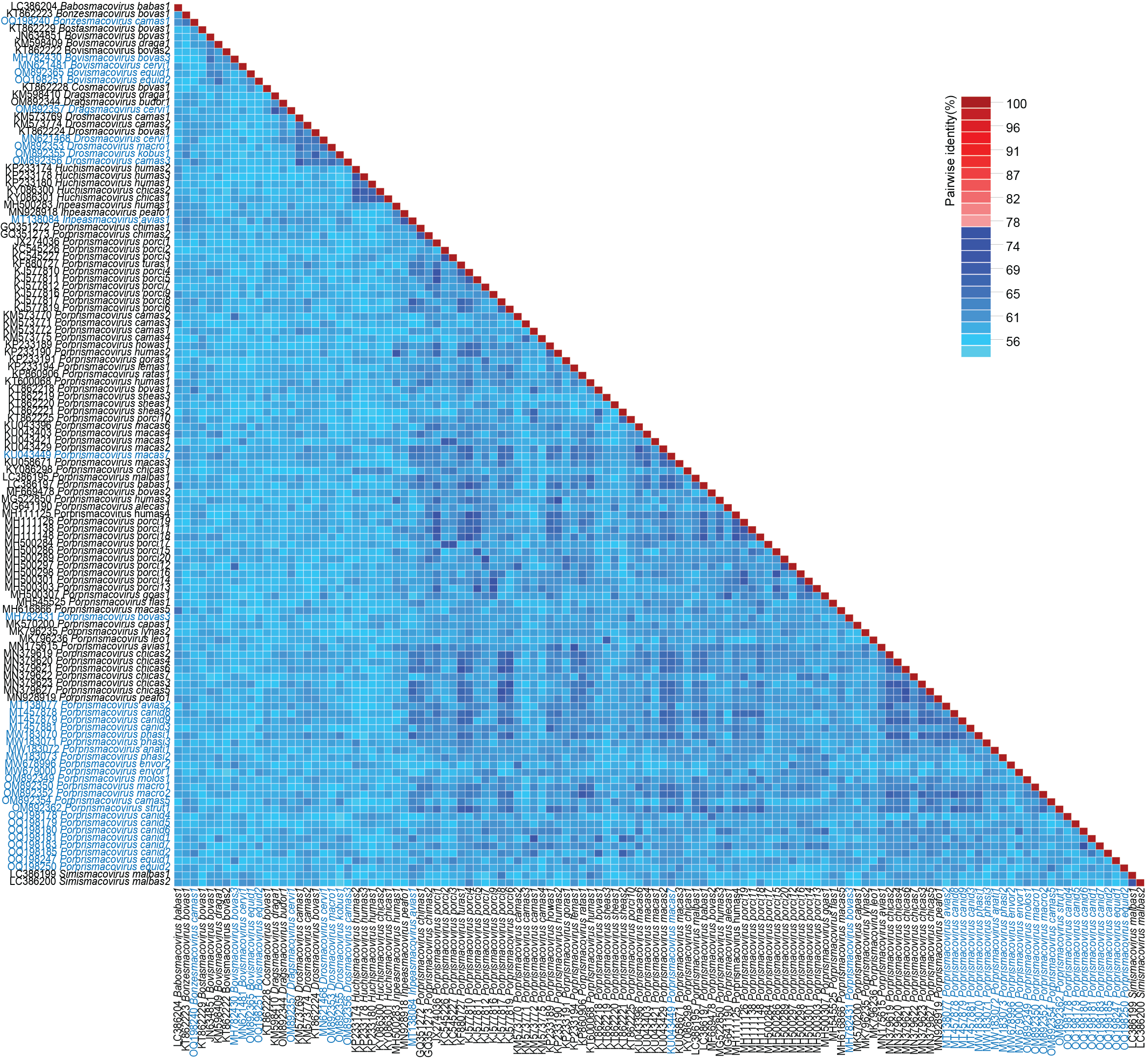
**Supporting evidence**

**Table 1: Summary of the 59 new species and the exemplar sequences.**

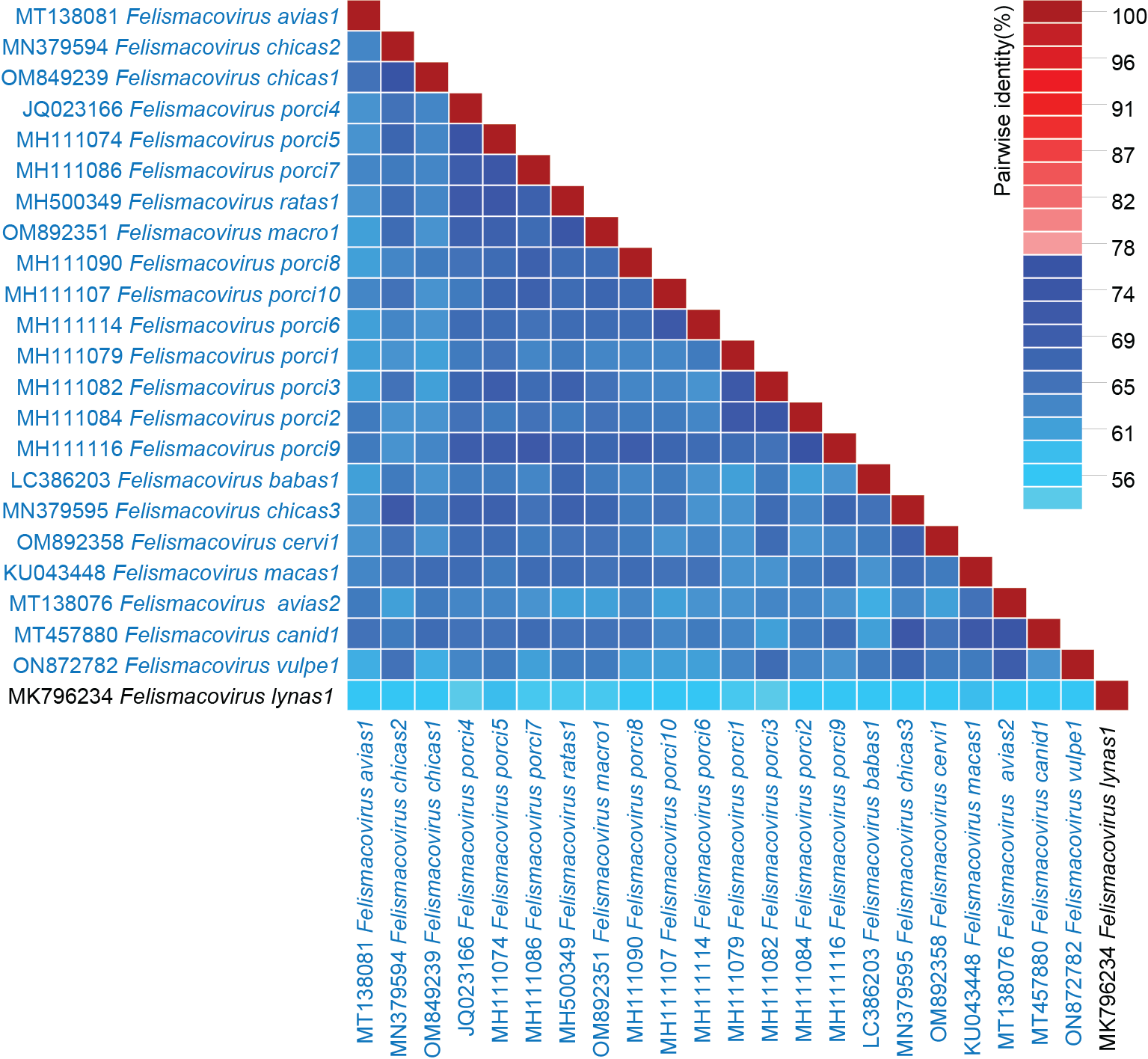
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| **Species** | **Accession #** | **Description** | **host** | **isolate** |
| *Bonzesmacovirus camas1* | OQ198240 | MAG: Smacoviridae CM13\_Smaco | camel | CM13\_Smaco |
| *Bovismacovirus bovas3* | MH782430 | Genomoviridae sp. C021765 | dairy cow | C021765 |
| *Bovismacovirus cervi1* | MN621481 | CRESS virus sp. UJSL004 | forest musk deer | UJSL004 |
| *Bovismacovirus equid1* | OM892365 | MAG: Smacoviridae sp. 215Smaco-1 | wild horse | 215Smaco-1 |
| *Bovismacovirus equid2* | OQ198251 | MAG: Smacoviridae D33\_Smaco\_3 | donkey | D33\_Smaco\_3 |
| *Dragsmacovirus budor1* | OM892344 | MAG: Smacoviridae sp. 132Smaco-3 | takin | 132Smaco-3 |
| *Dragsmacovirus cervi1* | OM892357 | MAG: Smacoviridae sp. 195Smaco | deer | 195Smaco |
| *Drosmacovirus camas3* | OM892356 | MAG: Smacoviridae sp. 190Smaco | camel | 190Smaco |
| *Drosmacovirus cervi1* | MN621468 | CRESS virus sp. UJSL002 | forest musk deer | UJSL002 |
| *Drosmacovirus kobus1* | OM892355 | MAG: Smacoviridae sp. 180Smaco | waterbuck | 180Smaco |
| *Drosmacovirus macro1* | OM892353 | MAG: Smacoviridae sp. 172Smaco | white kangaroo | 172Smaco |
| *Felismacovirus avias2* | MT138076 | Smacoviridae sp. w3chi090cir1 | Avian | w3chi090cir1 |
| *Felismacovirus avias1* | MT138081 | Smacoviridae sp. w3chi091cir5 | Avian | w3chi091cir5 |
| *Felismacovirus babas1* | LC386203 | Papio kindae associated smacovirus 1/ZM09-64 | *Papio kindae* | 1/ZM09-64 |
| *Felismacovirus canid1* | MT457880 | Raccoon dog stool-associated smacovirus 3 CJY6 | raccoon dog | 3 CJY6 |
| *Felismacovirus cervi1* | OM892358 | MAG: Smacoviridae sp. 198Smaco | white-lipped deer | 198Smaco |
| *Felismacovirus chicas1* | OM849239 | Cressdnaviricota sp. Y02-smal-02 | *Gallus gallus* | Y02-smal-02 |
| *Felismacovirus chicas2* | MN379594 | Chicken virus mg5\_1345 | *Gallus gallus* | mg5\_1345 |
| *Felismacovirus chicas3* | MN379595 | Chicken virus mg6\_1197 | *Gallus gallus* | mg6\_1197 |
| *Felismacovirus macas1* | KU043448 | Unidentified circular ssDNA virus cg5862 | *Macaca mulatta* | cg5862 |
| *Felismacovirus macro1* | OM892351 | MAG: Smacoviridae sp. 167Smaco-2 | macropusrufus | 167Smaco-2 |
| *Felismacovirus porci1* | MH111079 | CRESS virus sp. 17489x95\_4644 | *Sus scrofa domesticus* | 17489x95\_4644 |
| *Felismacovirus porci10* | MH111107 | CRESS virus sp. 17668x34\_1256 | *Sus scrofa domesticus* | 17668x34\_1256 |
| *Felismacovirus porci2* | MH111084 | CRESS virus sp. 17668x41\_1812 | *Sus scrofa domesticus* | 17668x41\_1812 |
| *Felismacovirus porci3* | MH111082 | CRESS virus sp. 17499x9\_1430 | *Sus scrofa domesticus* | 17499x9\_1430 |
| *Felismacovirus porci4* | JQ023166 | Pig stool associated circular ssDNA virus GER2011 | *Sus scrofa domesticus* | GER2011 |
| *Felismacovirus porci5* | MH111074 | CRESS virus sp. 17489x12\_563 | *Sus scrofa domesticus* | 17489x12\_563 |
| *Felismacovirus porci6* | MH111114 | CRESS virus sp. 17489x27\_1313 | *Sus scrofa domesticus* | 17489x27\_1313 |
| *Felismacovirus porci7* | MH111086 | CRESS virus sp. 17668x7\_933 | *Sus scrofa domesticus* | 17668x7\_933 |
| *Felismacovirus porci8* | MH111090 | CRESS virus sp. 17489x57\_911 | *Sus scrofa domesticus* | 17489x57\_911 |
| *Felismacovirus porci9* | MH111116 | CRESS virus sp. 17489x90\_2227 | *Sus scrofa domesticus* | 17489x90\_2227 |
| *Felismacovirus ratas1* | MH500349 | Rat associated smacovirus 22084x8\_1043 | *Rattus argentiventer* | 22084x8\_1043 |
| *Felismacovirus vulpe1* | ON872782 | MAG: Vulpes vulpes-associated smacovirus SMCO22 | *Vulpes vulpes* | SMCO22 |
| *Inpeasmacovirus avias1* | MT138084 | MAG: Smacoviridae sp. wbp226sma1 | Avian | wbp226sma1 |
| *Porprismacovirus anati1* | MW183072 | MAG: Cygnus columbianus Smacoviridae sp. swn66sma1 | *Cygnus columbianus* | swn66sma1 |
| *Porprismacovirus avias2* | MT138077 | MAG: Smacoviridae sp. w3chi091cir1 | Avian | w3chi091cir1 |
| *Porprismacovirus bovas3* | MH782431 | Genomoviridae sp. C025899 | dairy cow | C025899 |
| *Porprismacovirus camas5* | OM892354 | MAG: Smacoviridae sp. 173Smaco | alpaca | 173Smaco |
| *Porprismacovirus canid1* | OQ198181 | MAG: Canine associated porprismacovirus SmacoviridaeDogfe369C1 | canine | SmacoviridaeDogfe369C1 |
| *Porprismacovirus canid2* | OQ198185 | MAG: Canine associated porprismacovirus SmacoviridaeDogfe322C1 | canine | SmacoviridaeDogfe322C1 |
| *Porprismacovirus canid3* | MT457881 | Raccoon dog stool-associated smacovirus 4 CJY7 | raccoon dog | 4 CJY7 |
| *Porprismacovirus canid4* | OQ198178 | MAG: Canine associated porprismacovirus SmacoviridaeDogfe433C1 | canine | SmacoviridaeDogfe433C1 |
| *Porprismacovirus canid5* | OQ198179 | MAG: Canine associated porprismacovirus SmacoviridaeDogfe401C1 | canine | SmacoviridaeDogfe401C1 |
| *Porprismacovirus canid6* | OQ198180 | MAG: Canine associated porprismacovirus SmacoviridaeDogfe373C1 | canine | SmacoviridaeDogfe373C1 |
| *Porprismacovirus canid7* | OQ198183 | MAG: Canine associated porprismacovirus SmacoviridaeDogfe342C1 | canine | SmacoviridaeDogfe342C1 |
| *Porprismacovirus canid8* | MT457878 | Raccoon dog stool-associated smacovirus 1 CJY4 | raccoon dog | CJY4 |
| *Porprismacovirus canid9* | MT457879 | Raccoon dog stool-associated smacovirus 2 CJY5 | raccoon dog | CJY5 |
| *Porprismacovirus envor1* | MW679000 | Virus sp. D3\_464 | Dust | D3\_464 |
| *Porprismacovirus envor2* | MW678996 | Virus sp. D3\_567 | Dust | D3\_567 |
| *Porprismacovirus equid1* | OQ198247 | MAG: Smacoviridae D23\_Smaco | donkey | D23\_Smaco |
| *Porprismacovirus equid2* | OQ198250 | MAG: Smacoviridae D33\_Smaco\_2 | donkey | D33\_Smaco\_2 |
| *Porprismacovirus macas7* | KU043449 | Macaca mulatta feces associated virus 1 cg6982 | *Macaca mulatta* (Rhesus macaque) | cg6982 |
| *Porprismacovirus macro1* | OM892350 | MAG: Smacoviridae sp. 167Smaco-1 | macropusrufus | 167Smaco-1 |
| *Porprismacovirus macro2* | OM892352 | MAG: Smacoviridae sp. 171Smaco | red-necked wallaby | 171Smaco |
| *Porprismacovirus molos1* | OM892349 | MAG: Smacoviridae sp. 164Smaco-1 | monkey | 164Smaco-1 |
| *Porprismacovirus phasi1* | MW183070 | MAG: Chrysolophus pictus Smacoviridae sp. gps222sma2 | *Chrysolophus pictus* | gps222sma2 |
| *Porprismacovirus phasi2* | MW183073 | MAG: Pavo cristatus Smacoviridae sp. blp211sma3 | *Pavo cristatus* | blp211sma3 |
| *Porprismacovirus phasi3* | MW183071 | MAG: Chrysolophus pictus Smacoviridae sp. gps222sma6 | *Chrysolophus pictus* | gps222sma6 |
| *Porprismacovirus strut1* | OM892362 | MAG: Smacoviridae sp. 207Smaco | ostrich | 207Smaco |

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**Figure 1:** Maximum likelihood phylogenetic tree of the Rep amino acid sequences of reprehensive member of each species and rooted with a subset of Reps of nanoviruses. The Rep sequence alignment was constructed with MAFFT [3] and trimmed with TrimAL [4] using the gappyout option. The final alignment contained 199 amino-acid sites and was used to infer a maximum likelihood phylogenetic with PhyML [5] with LG+F+I+G4 substitution model. New species are highlighted in blue font.

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**Figure 2:** Pairwise identity matrix of the genome sequences of a representative member from each species in the genera *Babosmacovirus*, *Bonzesmacovirus*, *Bostasmacovirus*, *Bovismacovirus*, *Cosmacovirus*, *Dragsmacovirus*, *Drosmacovirus*, *Huchismacovirus*, *Inpeasmacovirus*, *Porprismacovirus* and *Simismacovirus* determined using SDT v1.2 [6]. New species are highlighted in blue font.

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**Figure 3:** Pairwise identity matrix of the genome sequences of a representative member from each species in the genus *Felismacovirus* determined using SDT v1.2 [6]. New species are highlighted in blue font. *Felismacovirus* genomes have the Rep and CP organized in a unidirectional orientation.

**References**

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