This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2012.002a-fV***	(to be completed by ICTV officers)

Short title: Create 1 species and 1 genus, *Sprivivirus* in the family *Rhabdoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

David Stone
Centre for Environment, Fisheries and Aquaculture Sciences
Weymouth Laboratory
Barrack Road
The Nothe
Weymouth
Dorset DT4 8UB
UK
email: david.stone@cefas.co.uk

Gael Kurath
Western Fisheries Research Center
6505 NE 65th St.
Seattle, WA 98115
USA
email: gkurath@usgs.gov

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	*Rhabdoviridae* study group

ICTV-EC or Study Group comments and response of the proposer:

1. Remove descriptions (text and phylogenetic trees) of GrCRV and TenRV (neither recognized nor proposed as species). - The text has been revised to include GrCRV and TenRV as viruses within the new species *Pike fry rhabdovirus* and therefore, they remain in the proposal. Genbank numbers for the TenRV and GrCRV have been added to the text.

2. Clarify species demarcation criteria for new genus - Done. The relationship between SVCV and PFRV is more clearly defined as is the relationship between other viruses within the species *Pike fry rhabdovirus.*

Date first submitted to ICTV: May 12, 2012
Date of this revision (if different to above): March 15, 2013

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2012.002aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Sprivivirus* (new)**
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Pike fry rhabdovirus	
Viruses in the species:	
Pike fry rhabdovirus (PFRV)	FJ872827
Tench rhabdovirus (TenRV)	KC113517
Grass carp rhabdovirus (GrCRV)	KC113518

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

We propose to create 1 new species for PFRV, TenRV and GrCRV and include it together with *Spring viraemia of carp virus* (currently recognized species in the genus *Vesiculovirus*) into a new genus *Sprivivirus*, proposed below.

The complete genome sequence of spring viraemia of carp virus (SVCV, Hoffman et al, 2002, GenBank AJ318079; Ahne et al., 2002, GenBank NC_002803) and pike fry rhabdovirus (PFRV, Chen et al., 2009, GenBank FJ872827) have been deposited with Genbank and described in published literature. The N, P, M, G and L gene sequences are also available for closely related viruses grass carp rhabdovirus (GrCRV) isolate V76 (GenBank KC113518) and Tench rhabdovirus (TenRV) isolate S64 (GenBank KC113517).

Phylogenetic analysis assigns PFRV, TenRV and GrCRV to same lineage as SVCV (module 9), and separate from members of the genera *Novirhabdovirus and Perhabdovirus*, the two other genera for fish rhabdoviruses.

Similar to other fish rhabdoviruses the replication temperature range of the

sprivivirus es is lower than that of mammalian rhabdoviruses, reflecting the aquatic poikilothermic nature of the host. Fish viruses are typically isolated on cultured fish cell lines at 15-25ºC.

Other serologically related rhabdoviruses have been isolated from a wide variety of cyprinid fish, pike, and trout. Phylogenetic analysis of partial (401nt) G gene sequences identified four lineages which included spring viraemia of carp virus (SVCV) pike fry rhabdovirus (PFRV), grass carp rhabdovirus (GrCRV) and tench rhabdovirus (TenRV). The virus names were then given based on the fish from which the viruses were first isolated (Rowley *et al* 2001, Stone *et al* 2003, Sheppard *et al* 2007).

Although SVCV and PFRV cross-react in some serological assays they can be distinguished serologically based on the lack of cross-neutralisation with polyclonal antisera and are considered distinct viruses belonging to separate species (Jorgensen et al., 1989; Ahne et al. 1998). SVCV isolate share 65-66% nucleotide identity with the PFRV isolate F4 based on partial G gene sequences. Similarly, SVCV isolates share <67% nucleotide identity with isolates of GrCRV and TenRV. Multiple variants of SVCV and PFRV have also been clearly distinguished by RNase protection assay (Ahne et al., 1998).

Discrimination between PFRV, TenRV and GrCRV using serum neutralisation and ELISA is more difficult and is heavily dependent on the quality of the antiserum available. Discrimination between PFRV, TenRV and GrCRV can be achieved by gene sequence comparison (figure1). Based on partial (410 nt) G gene sequences, the TenRV isolates show a high degree of nucleotide sequence identity to each other (>93.7%). Similarly, isolates within the GrCRV lineage share >98.5% nucleotide identity. However, when compared to PFRV, isolates of TenRV and GrCRV share 82.0-83.5% and 75-75.5% nucleotide identity, respectively, based on partial G gene sequences, and the GrCRV and TenRV strains share between 71.5-72.5% nucleotide identity. By phylogenetic analysis PFRV, GrCRV and TenRV isolates are assigned to different lineages supported by bootstrap values of 99%.

To date, no intermediate virus genotypes have been identified to suggest a sequence continuum between TenRV, GrCRV and PFRV. Thus, each of these three lineages may be most logically considered to represent a separate virus (PFRV, GcCRV, TenRV) belonging to the same species, *Pike fry rhabdovirus*. V76, Hecht and 14241/6 are considered isolates of GrCRV, and S64, 84-4 and 9695589 are considered isolates of TenRV (Figure 1).

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2012.002bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2012.002cV***	(assigned by ICTV officers)

To name the new genus: ***Sprivivirus***

Assigning the type species and other species to a new genus

Code	***2012.002dV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Spring viraemia of carp virus

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

2

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Viruses in the genus *Sprivivirus* (new) have five major structural proteins designated L, G, N, P and M. The genome is approximately 11.1kb in length with a short leader sequence that precedes the N gene and a short non translated region following the L gene. The absence of an NV gene at the G-L gene junction is similar to vesiculoviruses and perhabdoviruses, but different from the fish viruses belonging to the *Novirhabdovirus* genus.

The transcriptional start and termination/polyadenylation signal for all genes are 3'-UUGUC and 3'-AU(A/G)C$(U)_{6-7}$ which is which is consistent with viruses assigned to the genus *Vesiculovirus.* The intergenic region is a conserved dinucleotide 3'-GA, with the exception of the G-L intergenic region which is 3'GAUA.

The primary host for viruses in the genus are freshwater fish belonging to the order Cypriniformes. Similar to fish viruses assigned to the genus *Novirhabdovirus* and the genus *Perhabdovirus*, the replication temperature range of spriviviruses is lower than that of mammalian rhabdoviruses, reflecting the aquatic poikilothermic nature of the hosts. Fish viruses are typically isolated on cultured fish cell lines at 15-25ºC.

Phylogenetic analysis based on the N protein sequence consistently places SVCV, PFRV, TenRV and GrCRV in a lineage that is distinct from the viral lineages assigned to the genera *Novirhabdovirus*, *Vesiculovirus,* and *Perhabdovirus* (Figure 2). A similar phylogentic separation of viruses in the proposed genus *Sprivivirus* and the genus *Perhabdovirus*, is also observed for the P, M G and L proteins (Figure 3).

Origin of the new genus name:

Sigil derived from the name of the type species *Spring viraemia of carp virus*, *Sprivivirus*

Reasons to justify the choice of type species:

The complete SVCV genome was the first available of the viruses belonging to the new genus. SVCV is also best characterized, and has the greatest economic impact of any of the viruses in the genus, with a long history of a serious disease burden on carp farms in Europe

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Common with many fish viruses there is a broad and overlapping host range for viruses belonging to the genus *Sprivivirus*. Although the natural host range for SVCV is somewhat limited to carp, including the common carp, (*Cyprininus carpio*), crucian carp (*Carassius carassius*) and goldfish (Carassius auratis), tench (*Tinca tinca*), sheatfish (*Siluris glanis*), and grass carp (*Ctenopharyngodon idella*) are also susceptible. SVCV has been isolated from a range of non-cyprinid fish, including rainbow trout (*Oncorhynchus mykiss*), and has been detected in pike (*Esox lucius*). Similarly, tench rhabdovirus has been isolated from bream (*Abramis brama*), grass carp and tench, and grass carp rhabdovirus has been isolated from grass carp, sheatfish and pike (Stone *et al* 2003, Sheppard *et al* 2007). PFRV infections appear to be restricted to pike.

SVCV and PFRV are distinguished serologically based on the lack of cross- neutralisation with polyclonal antisera and virus strains within the SVCV species are neutralised by a single polyclonal antiserum (Jorgensen et al., 1989; Ahne et al., 1998). Discrimination between PFRV, TenRV and GrCRV variants using serum neutralisation is more difficult and is heavily dependent on the quality of the antiserum. Therefore, distinction between viruses within the genus is more likely to be based on nucleotide sequence divergence and phylogenetic separation based on partial G gene sequences (figure 1).

Phylogenetic analysis based on partial G-gene sequences has identified four subtypes of SVCV that are separated based on geographical origins (Stone *et al.* 2003). These viruses share 82.7%-100% nucleotide sequence identity. Similar subgroups of SVCV can be differentiated via partial L or complete P gene sequence analysis (Miller et al. 2007, Sheppard et al. 2007).

PFRV isolate F4 shares between 65-66% nucleotide identity with SVCV based on partial G gene sequences. The TenRV isolates (e.g S64, 84-4 and 9695589) share >93.7% nucleotide identity, based on partial G gene sequences and GrCRV isolates (e.g V76, Hecht and 14241/6) share >98.5% nucleotide identity in the same region. When compared with each other they share only 71.5-72.5% nucleotide sequence identity. When compared to PFRV F4, isolates of TenRV and GrCRV share a higher degree of

nucleotide sequence identity in the G gene, between 82.0-83.5% and 75-75.5%, and therefore all three viruses are considered to belong to the same species, Pike *fry rhabdovirus*.

As a general rule, nucleotide sequence identities in the G gene of >70% indicate that viruses belong the same species, whereas virus isolates with nucleotide identities of <66% belong to a different species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2012.002eV***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Spring viraemia of carp virus

The present taxonomic position of these taxon/taxa:

Genus:	***Vesiculovirus***
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

It is proposed to include this species in the newly proposed genus, *Sprivivirus* (See modules 1-3)

Part (b) re-assign to a higher taxon

Code	***2012.002fV***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Sprivivirus*** **(new)**
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

The primary host for SVCV and other viruses in the new genus are freshwater fish within the order Cypriniformes. Similar to fish viruses assigned to the genera

Novirhabdovirus and *Perhabdovirus*, the replication temperature range of viruses in the genus *Sprivivirus*, including SVCV, is lower than those of the mammalian rhabdoviruses (including vesiculoviruses) reflecting the aquatic poikilothermic nature of the host species. Fish viruses are typically isolated on cultured fish cell lines at 15-25ºC.

The ecologic separation is supported by phylogenetic analysis. Phylogenetic analysis based on N protein sequence consistently places SVCV and three related viruses PFRV, TenRV and GrCRV in a lineage that is distinct from novirhabdoviruses, vesiculoviruses and perhabdoviruses (Figure 2), and is supported by bootstrap values of 100%. A similar phylogentic separation of viruses belonging to the genera, *Sprivivirus* (newly proposed) and *Perhabdovirus* from each other, and from viruses belonging to the established *Vesiculovirus* genus, is also observed for the P, M G and L proteins (Figure 3).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Ahne W, Bjorklund HV, Essbauer S, Fijan N, Kurath G, Winton JR. 2002. Spring viremia of carp. Review, Dis. Aquat. Org., 52:261-272.

Ahne W, Kurath G, Winton JR. 1998. A ribonuclease protection assay can distinguish spring viremia of carp virus from pike fry rhabdovirus. Bull. Eur. Ass. Fish Pathol. 18:220-224.

Chen HL, Liu H, Liu ZX, He JQ, Gao LY, Shi XJ, Jiang YL. 2009. Characterization of the complete genome sequence of pike fry rhabdovirus. Arch. Virol. 1489-1494.

Hoffman B, Schutze H, Mettenleiter TC. 2002. Determination of the complete genomic sequence and analysis of the gene products of the virus of Spring Viremia of Carp, a fish rhabdovirus. Virus Res. 84:89-100.

Jorgensen PEV, Olesen NJ, Ahne W, and Lorenzen N. 1989. SVCV and PFR viruses: serological examination of 22 isolates indicates close relationship between the two fish rhabdoviruses. In: Viruses of Lower Vertebrates, Springer Verlag. Heidelberg, pp. 349-366.

Miller O, Fuller FJ, Gebreyes WA, Lewbart GA, Shchelkunov IS, Shivappa RB, Joiner C, Wollford G, Stone DM, Dixon PF, Raley ME, Levine JF. 2007. Phylogenetic analysis of spring viremia of carp virus reveals distinct subgroups with common origins for recent isolates in North America and the UK. Diseases of Aquatic Organisms 76:193-204.

Rowley H, Graham DA, Campbell S, Way K, Stone DM, Curran WL, Bryson DG. 2001. Isolation and characterization of rhabdovirus from wild common bream Abramis brama, roach Ritilus rutilus, farmed brown trout Salmo trutta and rainbow trout Oncorhynchus mykiss in Northern Ireland. Diseases of Aquatic Organisms 48:7-15.

Sheppard AM, Le Deuff RM, Martin PD, Woolford G, Way K, Stone DM. 2007. Genotyping spring viraemia of carp virus and other piscine vesiculo-like viruses using reverse hybridisation. Diseases of Aquatic Organisms 76:163-168.

Stone DM, Ahne W, Denham KL, Dixon PF, Liu CTY, Sheppard AM, Taylor GR, Way K. 2003. Nucleotide sequence analysis of the glycoprotein gene of putatuve spring viraemia of carp virus and pike fry rhabdovirus isolates reveals four genogroups. Diseases of Aquatic Organisms 53:203-210.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Figure 1
Phylogenetic relationships between sprivivirus based on partial (401nt) G gene sequences. The tree was generated using neighbor-joining methods and bootstrap values >70% are shown. The scale bar represents 10% nucleotide substitutions.

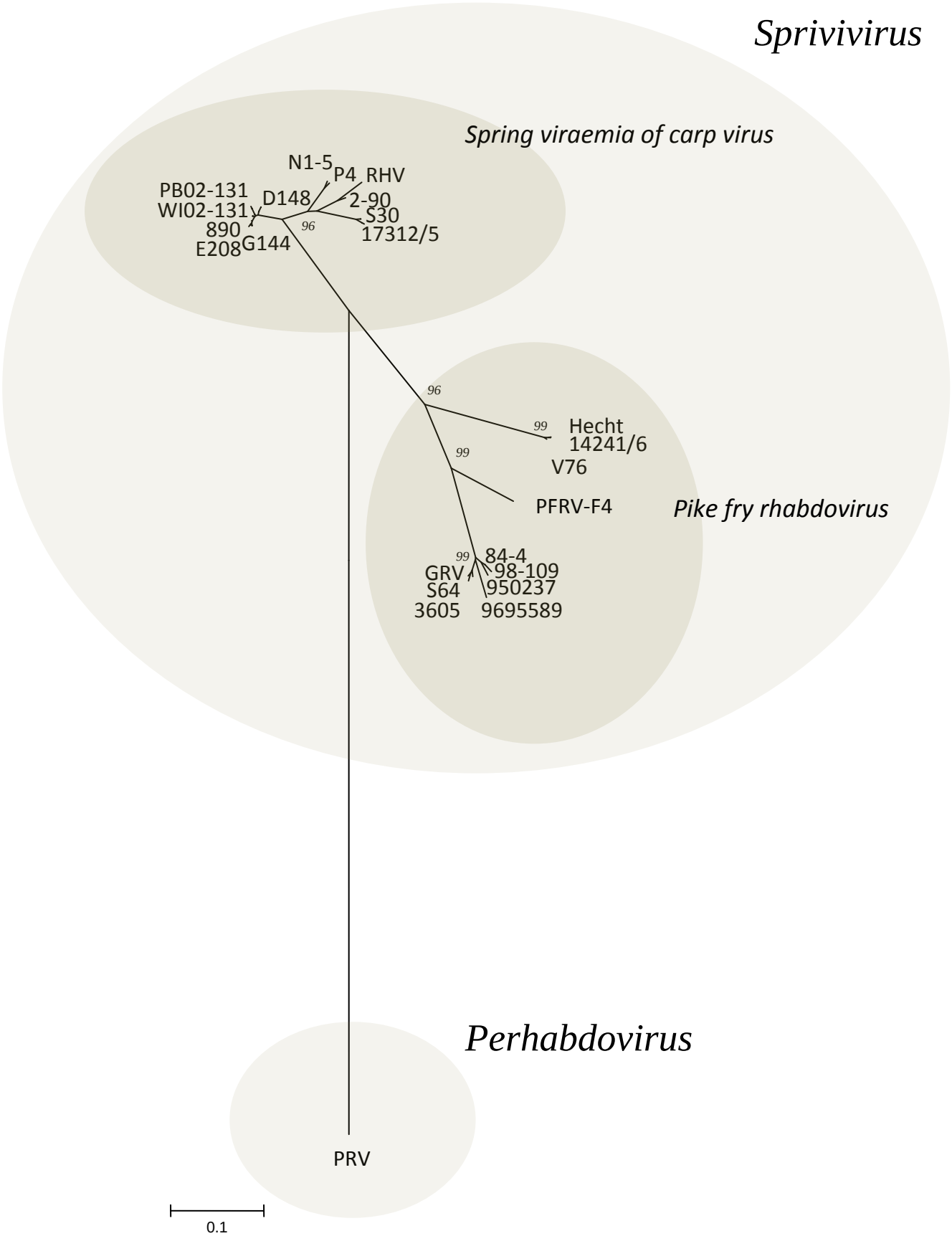
Sprivivirus
Spring viraemia of carp virus
N1-5
P4
RHV
PB02-131
D148
2-90
WI02-131
S30
890
96
17312/5
E208
G144
96
99
Hecht
14241/6
99
V76
PFRV-F4
Pike fry rhabdovirus
99
84-4
GRV
98-109
S64
950237
3605
9695589
Perhabdovirus
PRV
0.1

Figure 2

Phylogenetic relationships between rhabdoviruses based on the complete N protein and using human parainfluenza virus 1 (HPIV-1) as an out group. Rhabdoviruses used in the analysis were vesicular stomatitis Alagoas virus (VSAV), cocal virus (COCV), vesicular stomatitis Indiana virus (VSIV), vesicular stomatitis New Jersey virus (VSNJV), Isfahan virus (ISFV), chandipura virus (CHPV), grass carp rhabdovirus (GrCRV), tench rhabdovirus (TenRV), pike fry rhabdovirus (PFRV), European and Asian spring viraemia of carp virus (SVCV Fijan and SVCV Asian), siniperca chuatsi rhabdovirus (SCRV), eel rhabdovirus European X (EVEX), perch rhabdovirus (PRV), Swedish sea trout virus (SSTV), European lake trout rhabdovirus (LTRV), Adelaide river virus (ARV), bovine ephemeral fever virus (BEFV), Sigma virus (SIGMAV), mokola virus (MOKV), rabies virus (RABV), Australian bat lyssavirus (ABLV), potato yellow dwarf virus (PYDV), sonchus yellow net virus (SYNV), lettuce necrotic yellows virus (LNYV), Northern cereal mosaic virus (NCMV), viral haemorrhagic septicaemia virus (VHSV), snakehead rhabdovirus (SHRV), infectious haematopoietic necrosis virus (IHNV) and hirame rhabdovirus (HIRRV). Trees were generated using (A) maximum parsimony and (B) neighbor-joining methods and bootstrap values >70% are shown on the trees.

Fig. 2A. Complete N protein, maximum parsimony

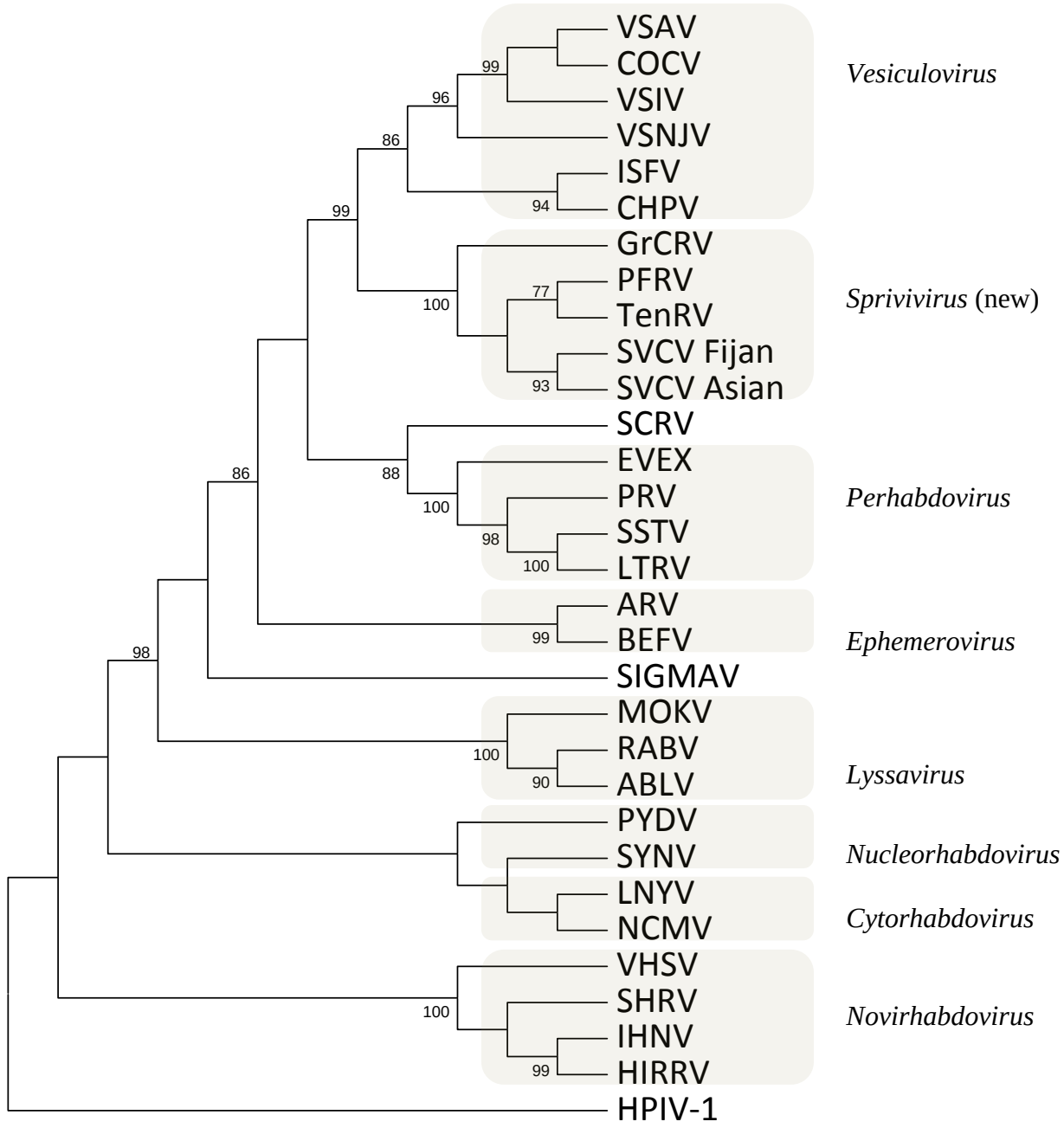

Figure 2B. Complete N protein, neighbor joining

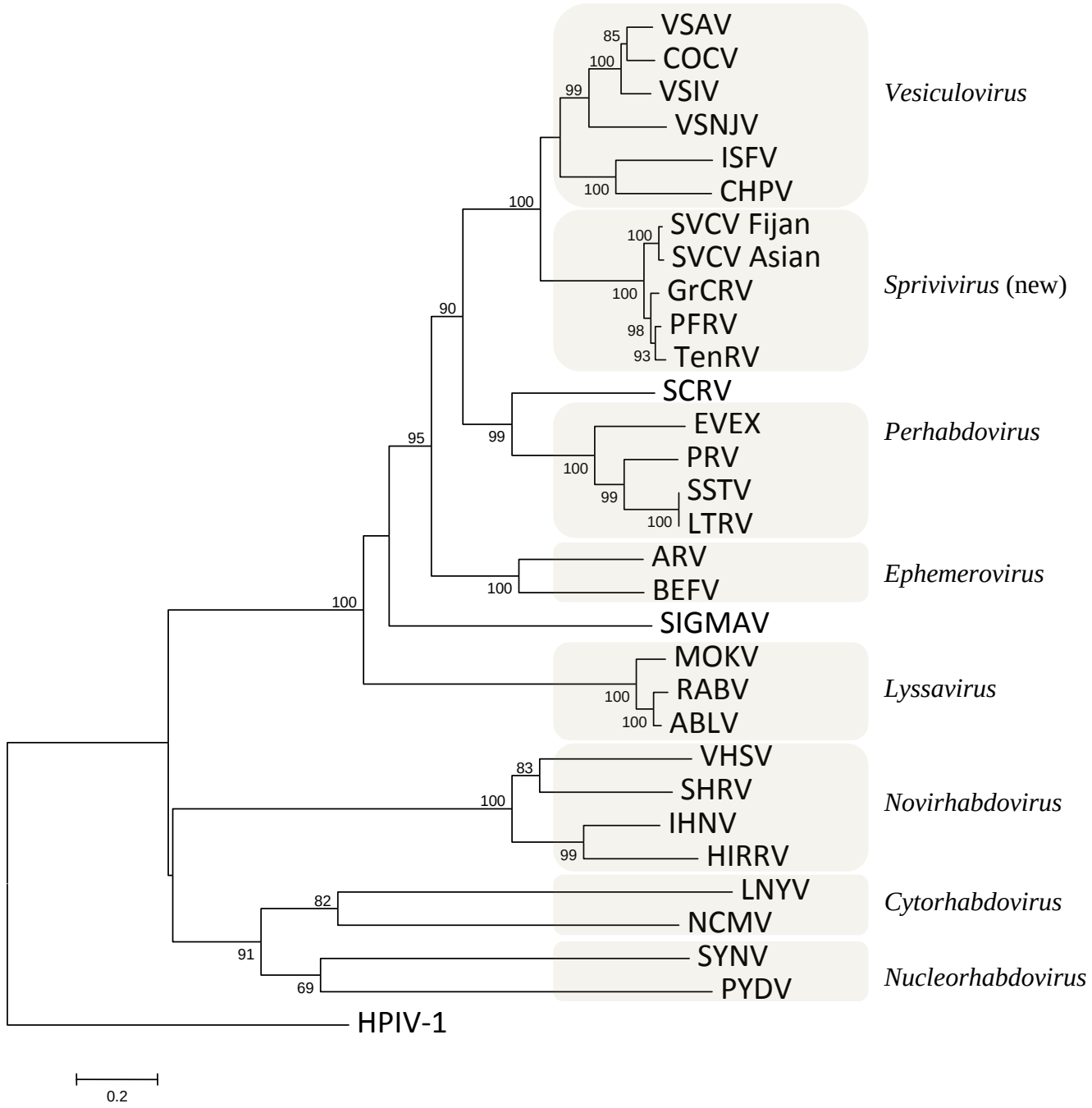

Figure 3 (following 4 pages)

Phylogenetic relationships between rhabdoviruses based on the complete (A) P protein (B) M protein (C) G protein and (D) L protein. Details of the rhabdoviruses used in the analysis are provided in the legend for figure 2. Trees were generated using neighbor-joining methods and bootstrap values >70% are shown on the trees.

Fig. 3A. P protein

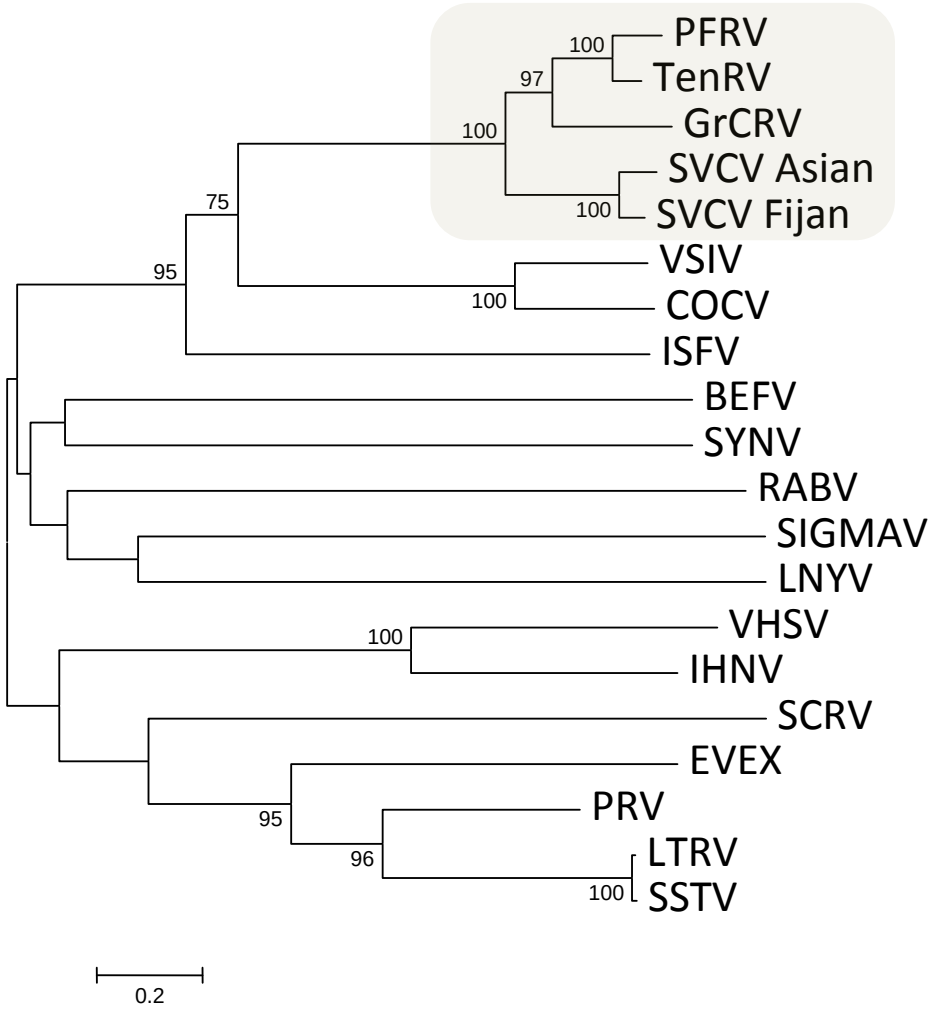

Fig. 3B. M protein

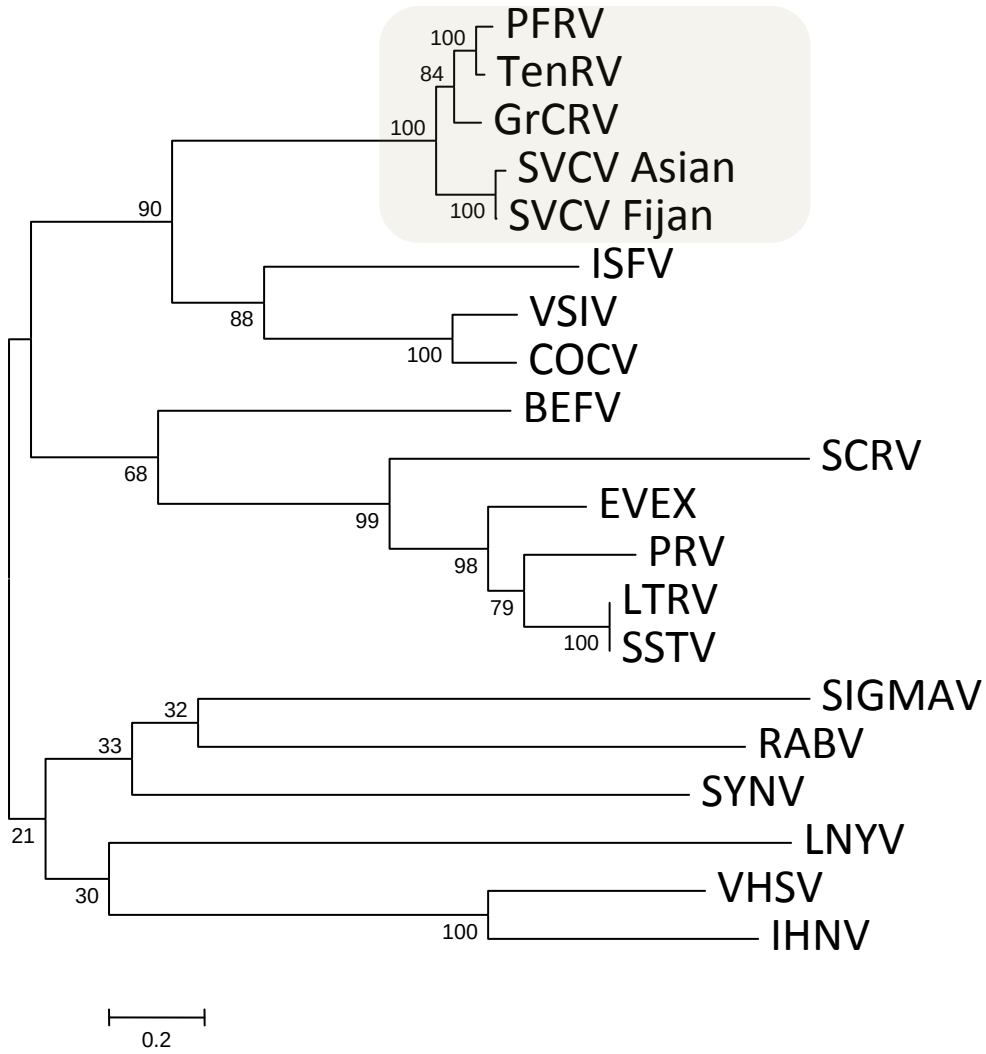

Fig. 3C. G protein

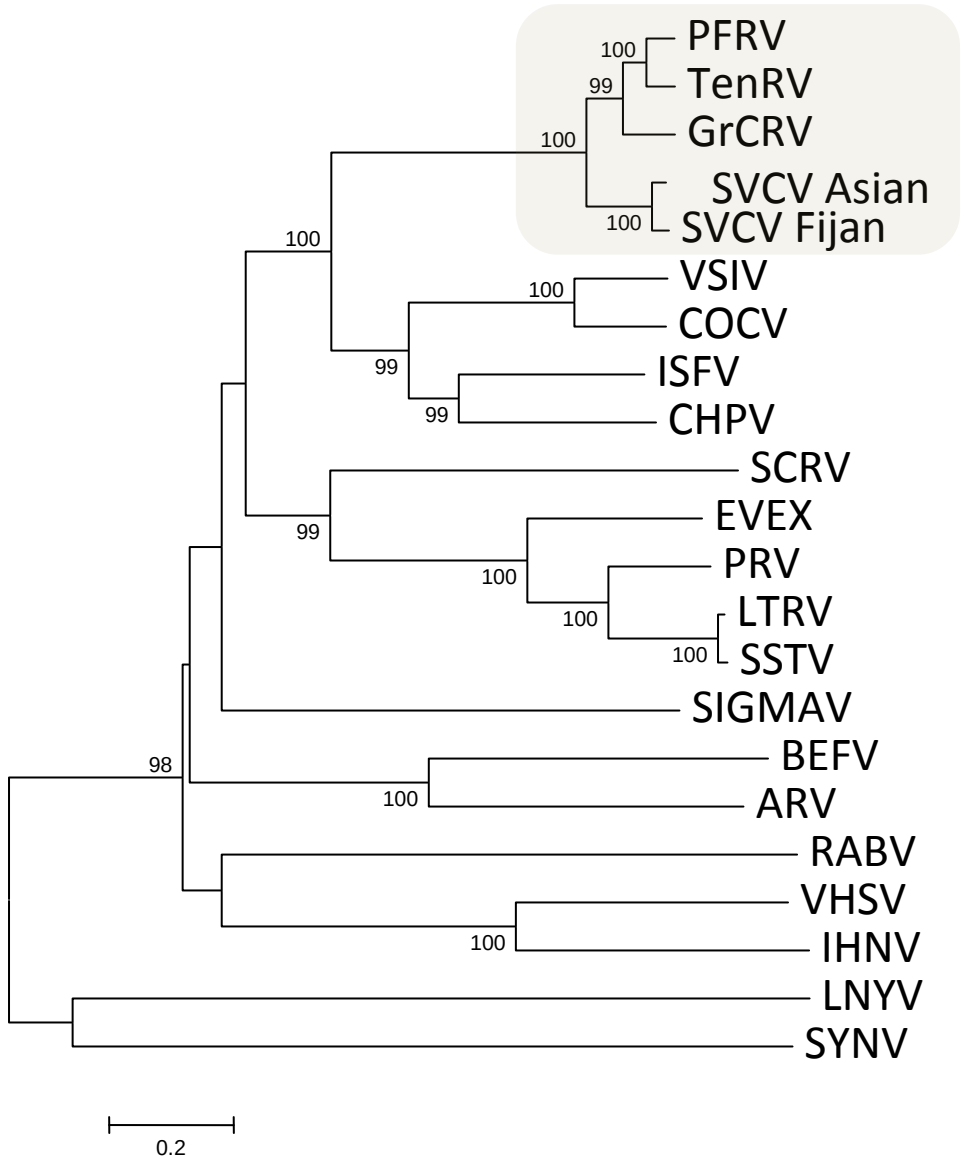

Fig. 3D. L protein