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:	***2014.017a-dV***	(to be completed by ICTV officers)

Short title: Creation of a new species (*Sakobuvirus A*) in a new genus (*Sakobuvirus*)
(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:

Nick Knowles (nick.knowles@pirbright.ac.uk) on behalf of the *Picornaviridae* Study Group

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)	*Picornaviridae* Study Group

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

Date first submitted to ICTV:	07/07/2014
Date of this revision (if different to above):	06/11/2014

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	***2014.017aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Sakobuvirus*** (new)
Subfamily:	-
Family:	***Picornaviridae***
Order:	***Picornavirales***

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.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Sakobuvirus A	feline sakobuvirus 1 FFUP1/Portugal/2012	KF387721

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

A novel picornavirus has been found in cats in Portugal (Ng *et al*., 2014). Amino acid pairwise comparison over the entire polyprotein show that feline sakobuvirus A (SakoV-A) is slightly more related to members of the *Kobuvirus* genus (41%) than to members of the *Salivirus* genus (40%) or the *Passerivirus* genus (33%). Specifically, the SakoV-A genome shared 37%, 38%, and 45% identities to the human Aichi virus 1 (genus *Kobuvirus*) over the P1–P3 regions, respectively, and lower identities to all other picornaviruses including *SalivirusA* and *Passerivirus A*. When the 3D region only was analyzed the highest identity was to *Passerivirus A* (60%) followed closely by *Aichivirus B* (*Kobuvirus* genus) (59%). Current SG criteria states that members of the same picornavirus genus share greater than 40%, 40%, and 50% amino acid identities for the P1–P3 regions, respectively. Thus the feline sakobuvirus A represents the prototype species for a novel picornavirus genus.

Genome organisation:

VPg+5'UTR$^{\text{IRES-IV}}$[L/1AB-1C-1D/2A$^{\text{H-Box/NC}}$-2B-2C/3A-3B$^{\text{VPg}}$-3C$^{\text{pro}}$-3D$^{\text{pol}}$]3'UTR-poly(A)

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2014.017bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	-
Family:	***Picornaviridae***
Order:	***Picornavirales***

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	***2014.017cV***	(assigned by ICTV officers)

To name the new genus: *Sakobuvirus*

Assigning the type species and other species to a new genus

Code	***2014.017dV***	(assigned by ICTV officers)

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

Sakobuvirus A	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:**

one

Reasons to justify the creation of a new genus:

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

Feline sakobuvirus clusters phylogenetically with members of the *Kobuvirus* and *Salivirus* genera, lying between the two (Figures 1 and 2). Features in common (presence of a Leader polypeptide, an uncleaved VP0 capsid polypeptide and general genome layout) are also shared with feline sakobuvirus. The 2A polypeptide of kobuviruses and feline sakobuvirus possess H-box and NC motifs, which are also present in the class II tumor suppressor H-rev107. Parechoviruses, avian encephalomyelitis virus and the calicivirus Norwalk virus also share these motifs, however, they are absent in the salivirus 2A (which may be a trypsin-like protease). The Internal Ribosome Entry Site (IRES) of feline sakobuvirus is predicted to be type IV (hepatitis C virus-like) in common with members of the *Aichivirus C* species (genus Kobuvirus), however, the IRES of the other kobuvirues (*Aichivirus A* and *Aichivirus B*) and *Salivirus A* is of type V. Phylogenetic relationships with other picornaviruses are shown in Appendix Figures 1 and 2.

Despite similarities with members of the *Kobuvirus* and *Salivirus* genera, the low amino acid identities shared with “Sakobuvirus A” (e.g. 37%, 38%, and 45% with the kobuvirus Aichi virus) are below those which we use for the designation of new genera (i.e. P1 <40%, P2 <40% and P3 <50%).

Origin of the new genus name:

Sakobuvirus (***Sa****livirus*- and ***Kobu****virus*-related virus).

Reasons to justify the choice of type species:

Only a single species.

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.

Only a single species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Ng, T.F.F., Mesquita, J.R., Nascimento, M.S., Kondov, N.O., Wong, W., Reuter, G., Knowles, N.J., Vega, E.M., Esona, M.D., Deng, X., Vinje, J. and Delwart, E. (2014). Feline fecal virome reveals novel and prevalent enteric viruses. Vet. Microbiol. 171: 102-111.

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.

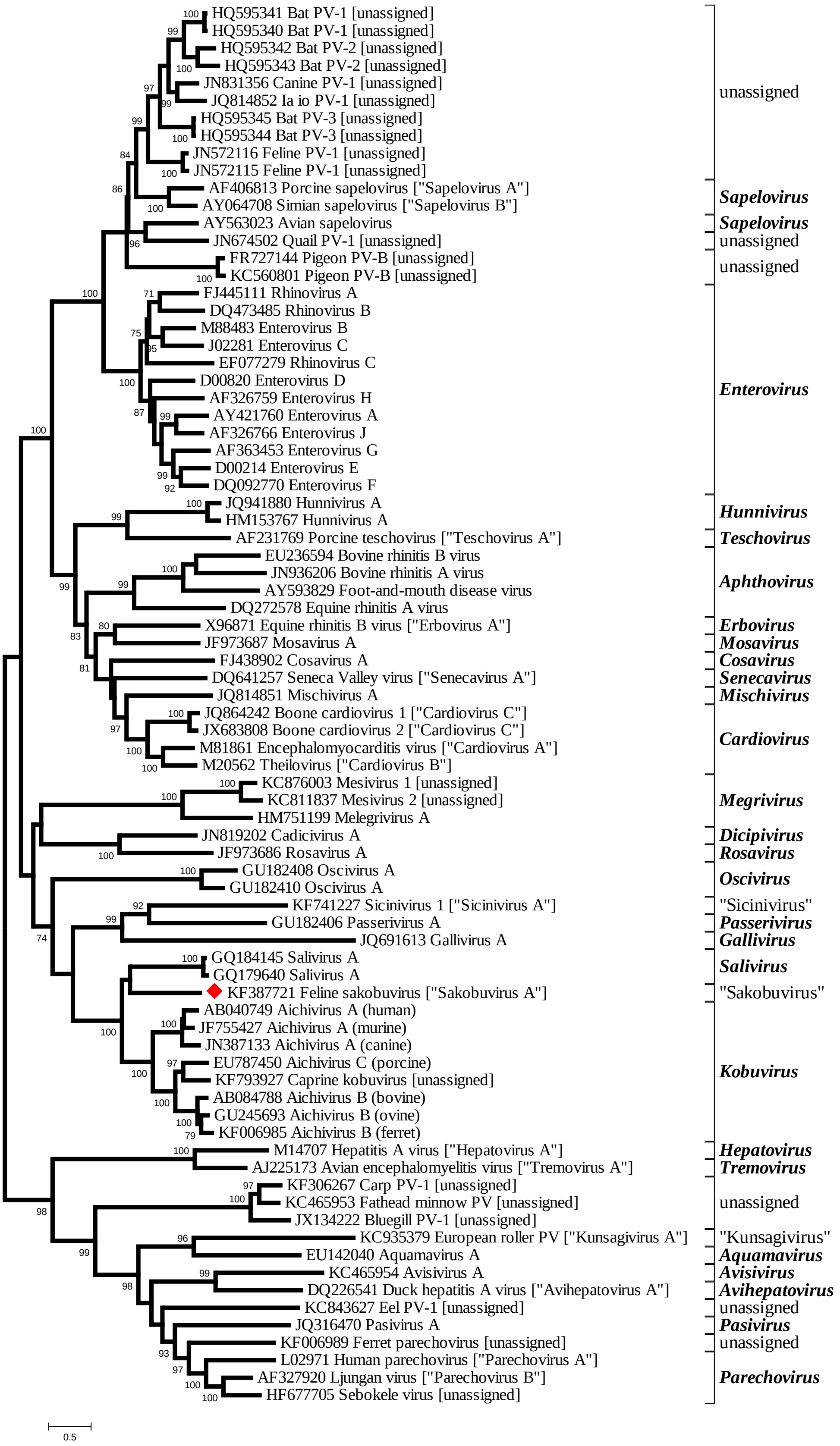

Fig. 1. Phylogenetic tree showing the relationships (amino acid) between picornaviruses in the P1 capsid. Maximum likelihood mtREV with Freqs. (+F) model, Gamma distributed with Invariant sites (G+I), with 1000 bootstrap replicates. Proposed new genus and species names are shown in quotes (species names are also within square brackets []). The subject(s) of this proposal are indicated by a red diamond (♦).

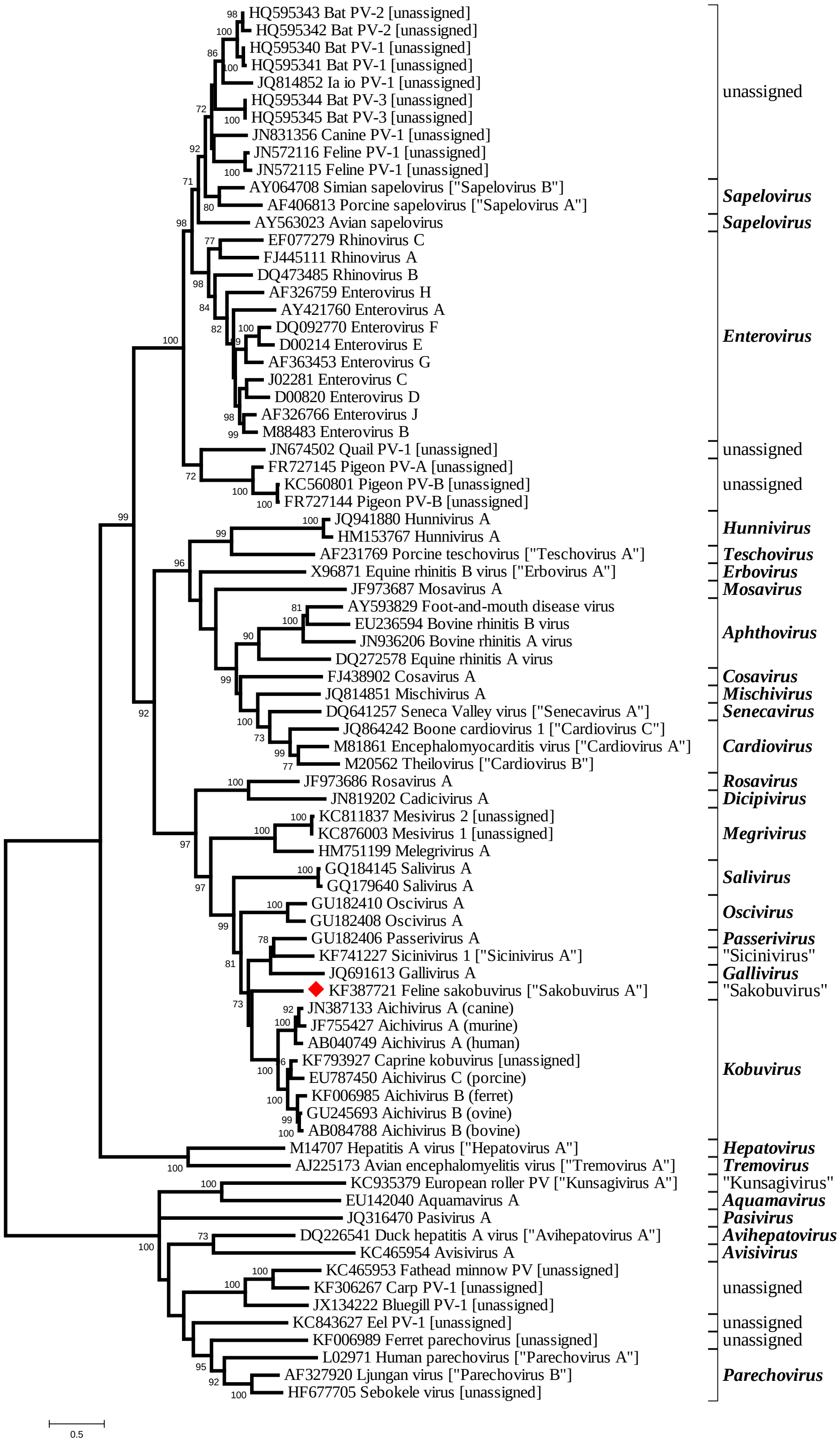

Fig. 2. Phylogenetic tree showing the relationships (amino acid) between picornaviruses in the 3D polymerase. Maximum likelihood mtREV with Freqs. (+F) model, Gamma distributed with Invariant sites (G+I), with 1000 bootstap replicates. Proposed new genus and species names are shown in quotes (species names are also within square brackets []).The subject(s) of this proposal are indicated by a red diamond (♦).