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:	***2016.007a,bD***	(to be completed by ICTV officers)

Short title: 5 new species in the genus *Circovirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☒ **10** ☐

Author(s):

Arvind Varsani, Karyna Rosario and Mya Breitbart on behalf of study group

Corresponding author with e-mail address:

avarsani@gmail.com; mya@usf.edu

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)	Circoviridae Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:	July 18, 2016
Date of this revision (if different to above):	27 November 2016

ICTV-EC comments and response of the proposer:

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	***2016.007aD***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Circovirus***
Subfamily:	***Unassigned***
Family:	***Circoviridae***
Order:	***Unassigned***

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: (only 1 per species please)**	**GenBank sequence accession number(s)**
Bat associated circovirus 4	bat circovirus 4 Tadarida brasiliensis circovirus 1	KT783484
Bat associated circovirus 5	bat circovirus 5 isolate BtPa-CV-1/NX2013	KJ641727
Bat associated circovirus 6	bat circovirus 6 isolate BtRa-CV/JS2013	KJ641724
Bat associated circovirus 7	bat circovirus 7 isolate BtRs-CV/HuB2013	KJ641723
Bat associated circovirus 8	bat circovirus 8 isolate BtMr-CV/GD2012	KJ641711

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 11

The current species demarcation for members of the genus Circovirus is 80%, i.e. circovirus sequences that share <80% genome-wide pairwise identity are classified as new species. We have analyzed new full genomes of circoviruses available in public databases using SDT v1.2 (Muhire et al., 2014). Our analysis reveals that five new virus genomes (see Table 1 for details) recovered from bats should be classified as new species based on genome-wide pairwise identities (Figure 1) coupled with phylogenetic support for species status for these taxa.

MODULE 9: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

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Renaming one or more taxa

Code	***2016.007bD***	(assigned by ICTV officers)

To rename the following taxon (or taxa):

Current name	**Proposed name**
Bat circovirus 1	*Bat associated circovirus 1*
Bat circovirus 2	*Bat associated circovirus 2*
Bat circovirus 3	*Bat associated circovirus 3*
Chimpanzee faeces associated circovirus	*Chimpanzee associated circovirus 1*
Human faeces associated circovirus	*Human associated circovirus 1*

Reasons to justify the renaming:

Explain why the taxon (or taxa) should be renamed

Studies that describe circoviruses detected in bats have used metagenomic approaches and have not confirmed bats as a definitive host for these viruses. In addition, there is no data regarding the detection of a given circovirus species in various tissues from bats (other than pooled pharyngeal and rectal samples as well as guts). Since the detection of a given circovirus in bats does not grant its infectivity to this potential host, it is important to make this distinction in bat circovirus species names. We propose adding the word ‘associated’ as a modifier to bat circovirus species, thus reflecting that replication within bats has not been reported. In addition, it is important to make species names similar and uniform across all members of the family *Circoviridae.* We propose removing any specific tissues used for virus isolation, such as faeces, from species names representing members of the *Circoviridae* (i.e., circovirus and cyclovirus species).

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Lima, F. E., Cibulski, S. P., Dall Bello, A. G., Mayer, F. Q., Witt, A. A., Roehe, P. M. & d'Azevedo, P. A. (2015). A Novel Chiropteran Circovirus Genome Recovered from a Brazilian Insectivorous Bat Species. Genome announcements 3.

Muhire, B. M., Varsani, A. & Martin, D. P. (2014). SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PloS one 9, e108277.

Wu, Z., Yang, L., Ren, X., He, G., Zhang, J., Yang, J., Qian, Z., Dong, J., Sun, L., Zhu, Y., Du, J., Yang, F., Zhang, S. & Jin, Q. (2016). Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. The ISME journal 10, 609-620.

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.

Table 1: Details of new viruses in the genus *Circovirus*

Accession #	**Name**	**Acronym**	**Isolate**	**Isolation source**	**Country**	
KT783484	bat associated circovirus 4	BatCV-4	Tadarida brasiliensis circovirus 1	*Tadarida brasiliensis*	Brazil	Lima et al., 2015
KJ641727	bat associated circovirus 5	BatCV-5	BtPa-CV-1/NX2013	*Plecotus auritus*	China	Wu et al, 2016
KJ641724	bat associated circovirus 6	BatCV-6	BtRa-CV/JS2013	*Rhinolophus affinis*	China	Wu et al, 2016
KJ641723	bat associated circovirus 7	BatCV-7	BtRs-CV/HuB2013	*Rhinolophus sinicus*	China	Wu et al, 2016
KJ641711	bat associated circovirus 8	BatCV-8	BtMr-CV/GD2012	*Myotis ricketti*	China	Wu et al, 2016

Table 2: Acronyms for taxa in phylogenetic trees and pairwise identity matrices.

Species	**Acronym**
Barbel Circovirus	BarCV
Bat associated circovirus 1	BatACV-1
Bat associated circovirus 2	BatACV-2
Bat associated circovirus 3	BatACV-3
Bat associated circovirus 4	BatACV-4
Bat associated circovirus 5	BatACV-5
Bat associated circovirus 6	BatACV-6
Bat associated circovirus 7	BatACV-7
Bat associated circovirus 8	BatACV-8
Beak and feather disease virus	BFDV
Canary circovirus	CaCV
Canine circovirus	CanineCV
Chimpanzee associated circovirus	ChimpACV
Duck circovirus	DuCV
European catfish circovirus	EcatfishCV
Finch circovirus	FiCV
Goose circovirus	GoCV
Gull circovirus	GuCV
Human associated circovirus	HuACV
Mink circovirus	MiCV
Porcine circovirus 1	PCV-1
Porcine circovirus 2	PCV-2
Pigeon circovirus	PiCV
Raven circovirus	RaCV
Starling circovirus	StCV
Swan circovirus	SwCV
Zebra finch circovirus	ZfiCV

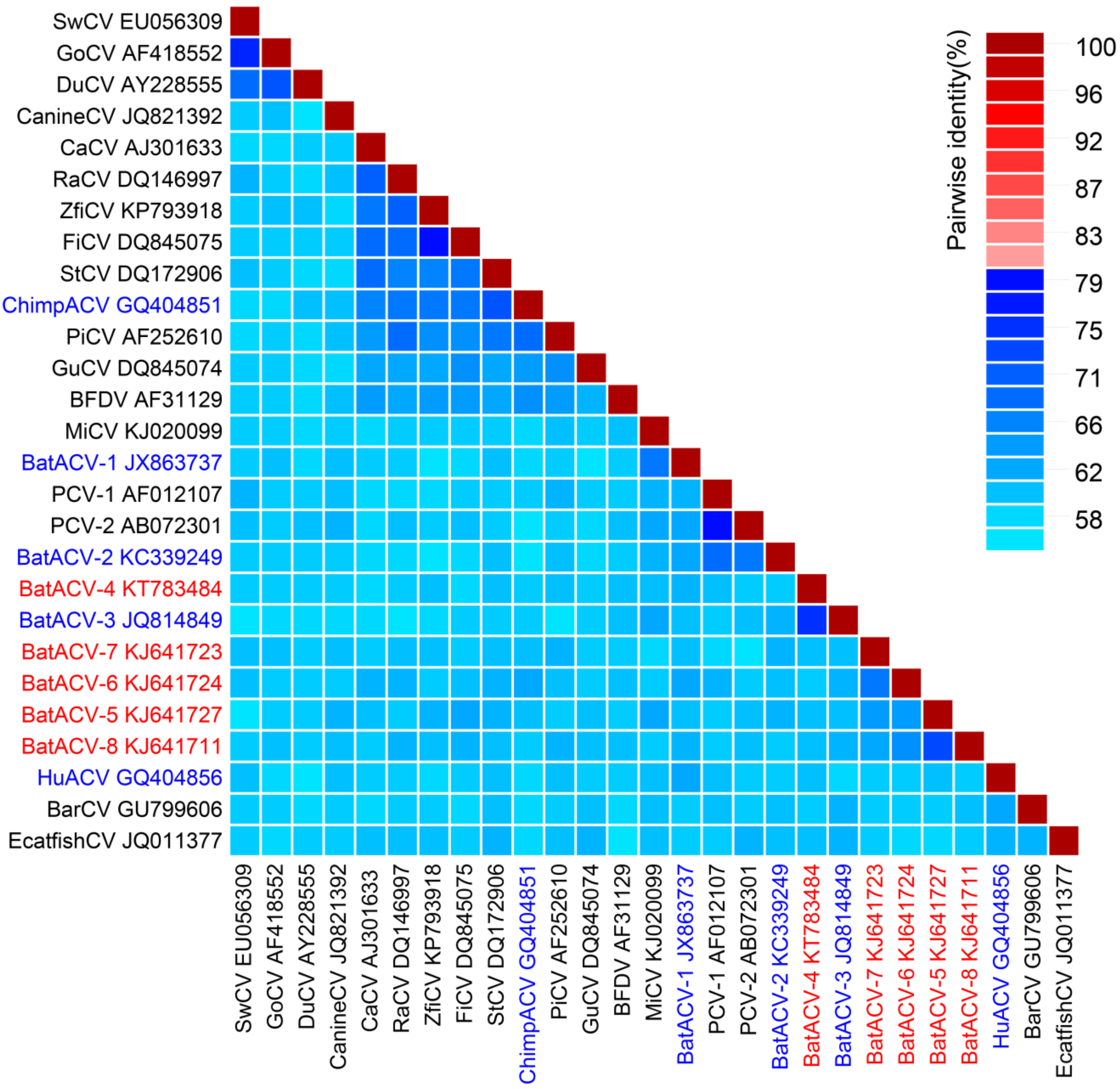

Figure 1: Genome-wide pairwise identities determined using SDT v1.2 (Muhire et al., 2014) with a ‘three colour’ profile highlighting that the 80% species demarcation threshold is valid for the 5 new taxa which are highlighted in red. Taxa for which we are proposing a new species name are highlighted in blue font.

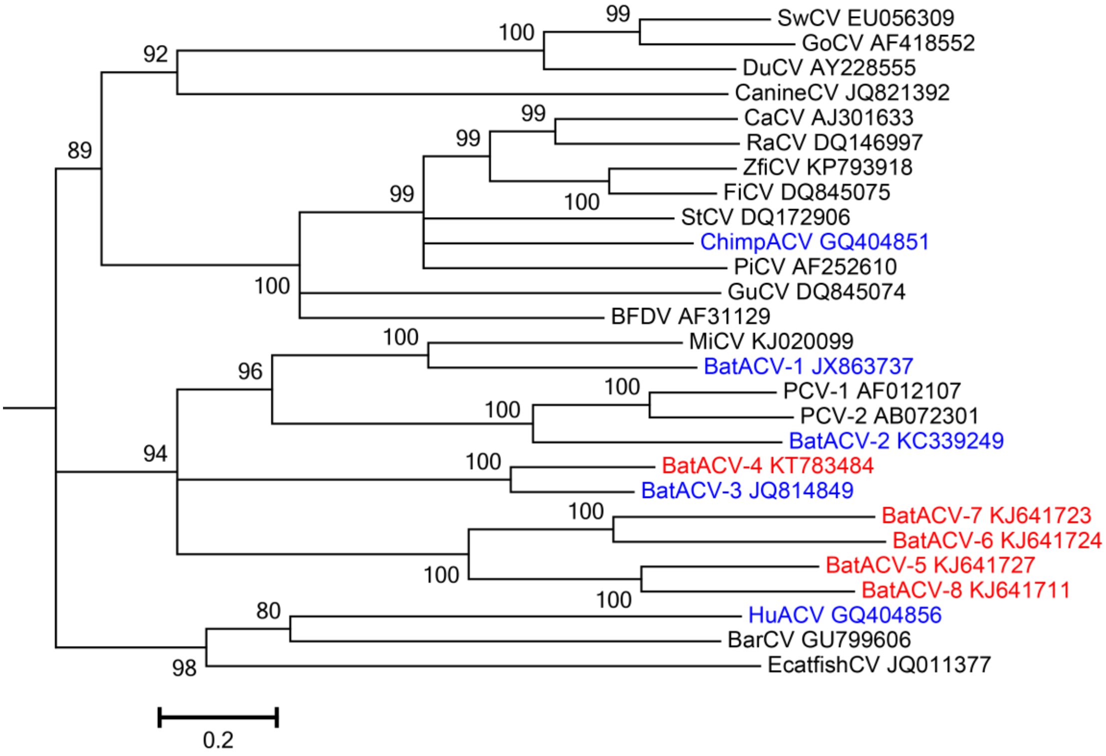

Figure 2: Maximum likelihood phylogenetic tree of the representative circovirus species based on complete genome sequences. The ML tree was inferred using PHYML with the GTR+G model of substitution (with SH-like branch support). Branches with <80% support have been collapsed. The phylogenetic tree was rooted using cyclovirus reverse complemented genome sequences. New taxa are highlighted in red and taxa for which we are proposing a new species name are highlighted in blue font.

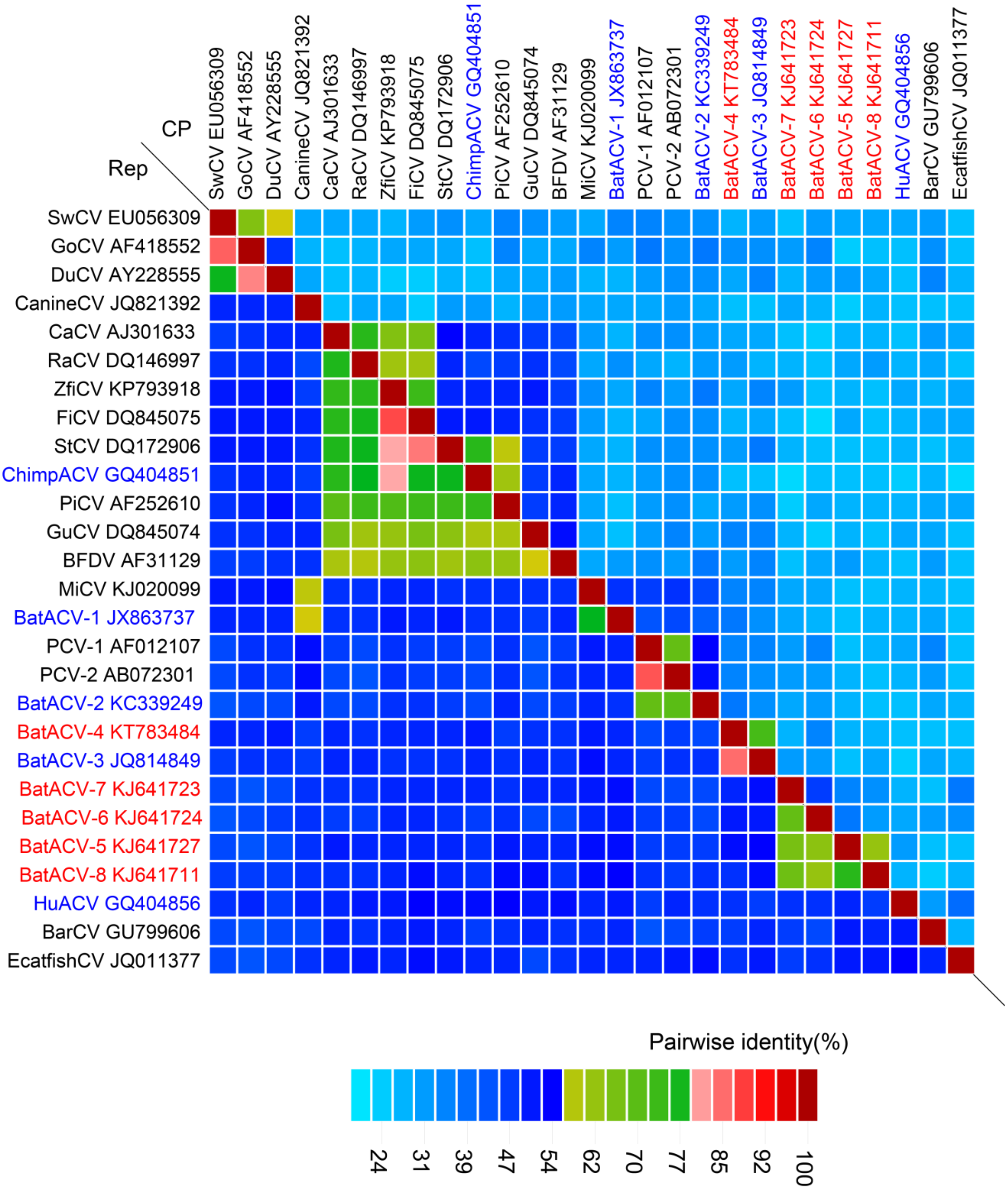

Figure 3: Two-by-two pairwise identity plot of the replication-associated (Rep) and capsid (CP) protein sequences constructed using SDT v1.2 (Muhire et al., 2014) with a ‘three colour’ profile. The 5 new taxa are highlighted in red and taxa for which we are proposing a new species name are highlighted in blue font.

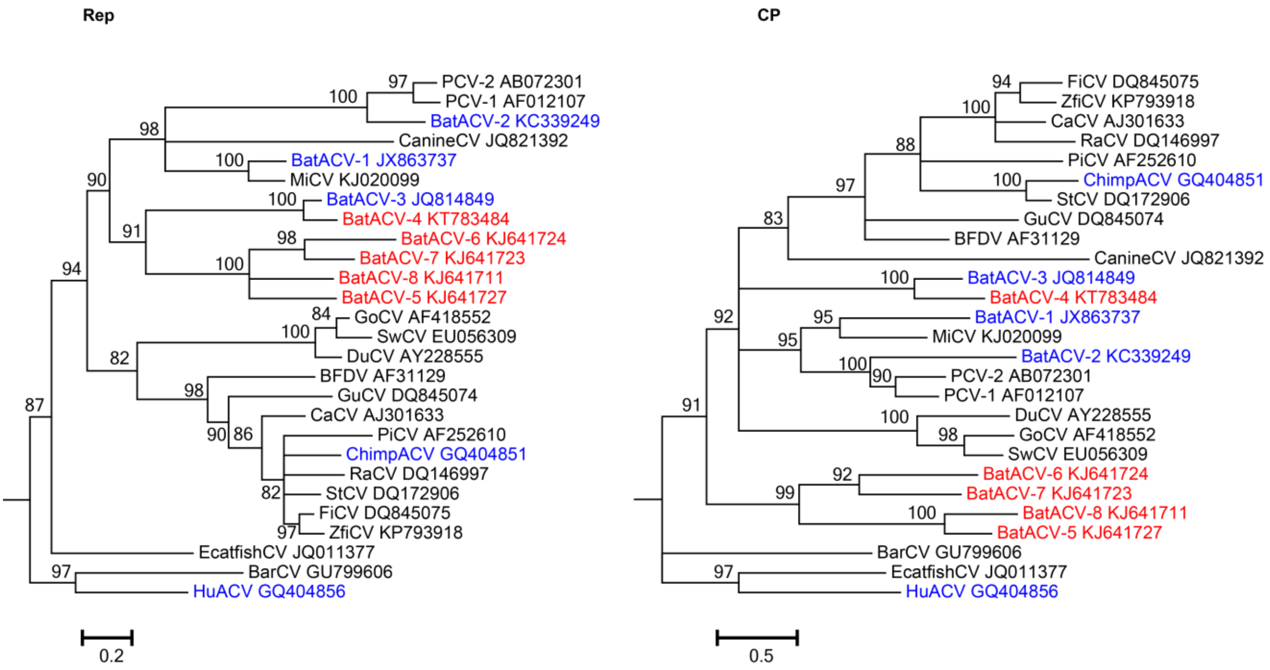

Figure 4: Maximum likelihood phylogenetic tree of the representative circovirus replication-associated (Rep) and capsid (CP) protein sequences. The ML tree was inferred with PHYML using the LG model of substitution (with SH-like branch support). Branches with <80% support have been collapsed. Rep and CP phylogenetic trees were rooted with cyclovirus sequences. New taxa are highlighted in red and taxa for which we are proposing a new species name are highlighted in blue font.