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:	***2016.020aD***	(to be completed by ICTV officers)

Short title: 1 new species in the genus *Gammaretrovirus*
(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):

Welkin Johnson

Corresponding author with e-mail address:

Welkin Johnson welkin.johnson@bc.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)	Retroviridae SG

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):	August 3, 2016

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

Code	***2016.020aD***	(assigned by ICTV officers)

To create new species within:

Genus:	***Gammaretrovirus***
Subfamily:	***Orthoretrovirinae***
Family:	***Retroviridae***
Order:	

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)**
Koala retrovirus	koala retrovirus (KoRV-A)	AF151794.2

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

Koala retrovirus (KoRV) has canonical features of a gammaretrovirus. In addition to particles with gammaretrovirus morphology, these include a simple genome with no obvious accessory genes; a Gag-Pol polyprotein that uses termination suppression to switch between Gag and Gag-Pol synthesis; a spacer domain analogous to the p12 domain of type species MLV; a Class I reverse transcriptase (RT) protein; and an envelope glycoprotein complex with covalently linked surface (SU) and transmembrane (TM) subunits (Hanger et al., 2000). As with many other gammaretroviruses, KoRV also appears in endogenous forms in its natural host, the Australian koala (Tarlinton et al. 2006, 2008). Endemic KoRV is associated with a high prevalence of leukemia/lymphoma and immunosuppression throughout much of the Australian koala population (reviewed in Denner and Young, 2013).

Among extant gammaretroviruses, KoRV is most closely related to the gibbon ape leukemia virus (GALV) (Hanger et al., 2000). Although closely related to GALV, phylogenetic analysis and sequences recovered from museum specimens have established that KoRV has been in Australian koalas at least since the 19th century, if not longer (Ávila-Arcos et al., 2013). The natural hosts of GALV and KoRV represent different mammalian orders (Primates and Diprotodontia, respectively) and live on different continents. Since the two hosts are separated by deep oceans and on separate continents, it's assumed that interspecies transmission involved at least one intermediate species or human mediated transfer. Based on phylogenetic analysis, KoRV isolates cluster separately from GALV isolates, and are even more divergent from GALV than the woolly monkey sarcoma virus, which is already classified by the ICTV as a separate species (Fig 1). There are distinct KoRV "types"; while KoRV-A uses the koala homolog of PiT-1, which is the receptor used by GALV, KoRV-B and KoRV-J use an entirely different entry receptor, THTR1; differences in receptor usage map to the Receptor Binding Domain of the Env SU protein (Shojima et al.2013; Xu et al.2013).

Classification of KoRV as a distinct species of gammaretrovirus is consistent with four species demarcation criteria that include: differences in gene and genome sequence products, differences in natural host range, differences in pathogenicity, and differences in antigenic properties (9th Report of the ICTV, Part II, page 489).

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Ávila-Arcos, M.C., Ho, S.Y., Ishida, Y., Nikolaidis, N., Tsangaras, K., Hönig, K., Medina, R., Rasmussen, M., Fordyce, S.L., Calvignac-Spencer, S., Willerslev, E., Gilbert, M.T., Helgen, K.M., Roca, A.L., Greenwood, A.D. (2013). One hundred twenty years of koala retrovirus evolution determined from museum skins. Mol. Biol. Evol. 30:299-304.

Denner, J. and Young, P. (2013). Koala retroviruses: characterization and impact on the life of koalas. Retrovirology 10:108.

Hanger, J. J., Bromham, L. D., McKee, J. J., O_Brien,T. M. and Robinson, W. F. (2000). The nucleotide sequence of koala (*Phascolarctos cinereus*) retrovirus: a novel type C endogenous virus related to gibbon ape leukemia virus. J. Virol. 74:4264-4272.

Shojima, T. et al.(2013). Identification of a novel subgroup of Koala retrovirus from Koalas in Japanese zoos. J. Virol. 87:9943-9948.

Tarlinton, R., Meers, J., Young, P. (2006). Retroviral invasion of the koala genome. Nature 442:79-81.

Tarlinton, R., Meers, J., Young, P. (2008) Biology and evolution of the endogenous koala retrovirus. Cell. Mol. Life Sci. 65:3413-3421.

Xu, W. et al. (2013). An exogenous retrovirus isolated from koalas with malignant neoplasias in a US zoo. PNAS. 110:11547-11552.

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.

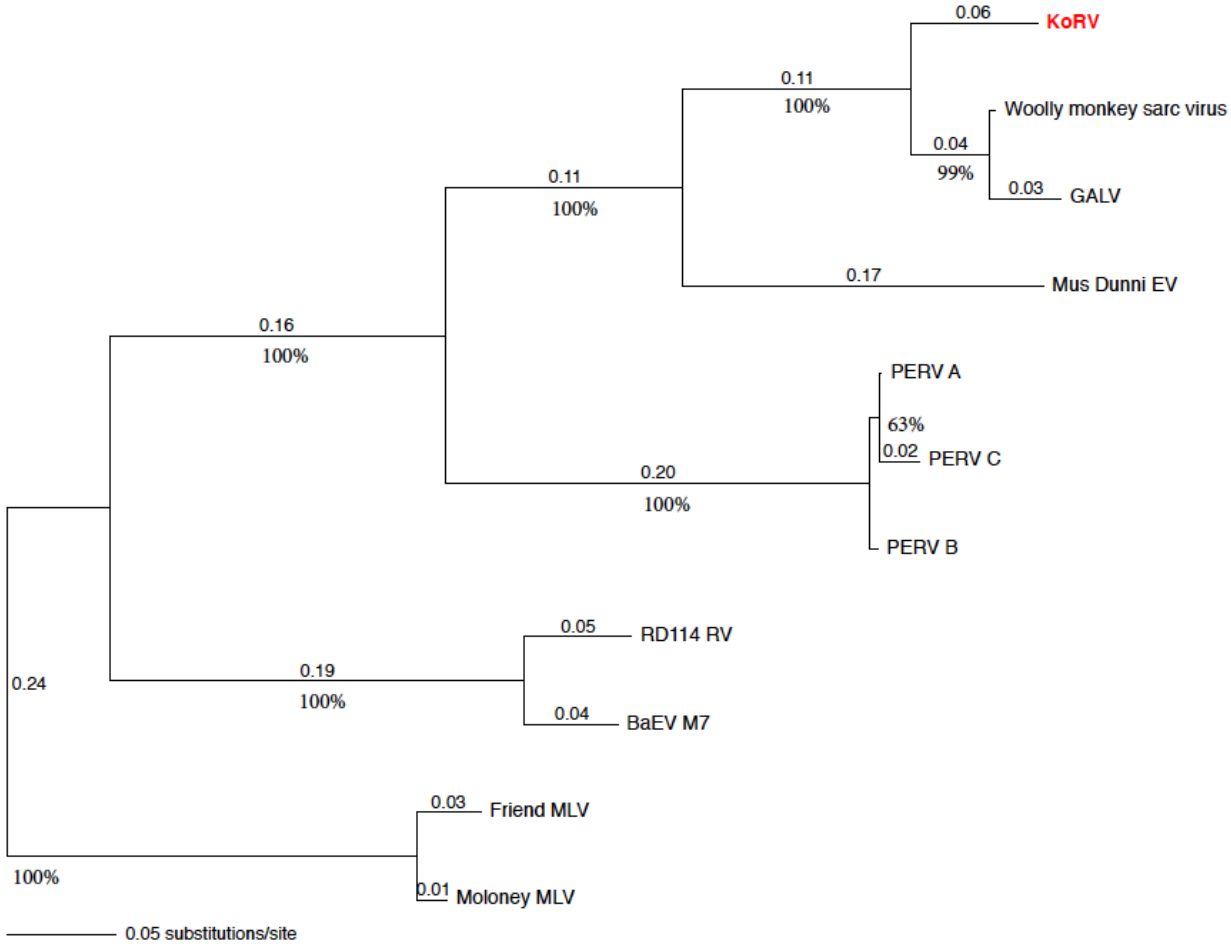

Figure 1. Relationship of koala retrovirus (KoRV) to other gammaretroviruses. Tree was generated using an alignment of the reverse transcriptase domain of the Pol protein sequence, and using the Likelihood criterion and heuristic search setting in PAUP*. Bootstrap values (%) are based on 100 replicates. The murine gammaretroviruses Friend MLV and Moloney MLV were designated as a monophyletic outgroup to root the tree. The same topology was also obtained using a distance-based method (Neighbor-Joining, not shown).
Input taxa include koala retrovirus (KoRV acc.# gb|AHY24803.1); woolly monkey sarcoma virus (gb|ALV83312.1); gibbon ape leukemia virus (GALV, ref|NP_056790.1); Mus dunni endogenous virus (gb|AAC31805.1); porcine endogenous retrovirus types A, B and C (PERV-A gb|AAM29192.1, PERV-B gb|AAM29194.1, and PERV-C gb|ABL74442.1); RD114 (dbj|BAM17307.1, an endogenous gammaretrovirus of cats); baboon endogenous virus (BAEV ref|YP_009109692.1); Friend murine leukemia virus (Friend MLV ref|NP_040333.1); Moloney murine leukemia virus (Moloney MLV ref|NP_057933.2).