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:	***2011.003aV***	(to be completed by ICTV officers)

Short title: Lujo virus, a new species in the genus Arenavirus of the Arenaviridae family
(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:

Thomas Briese (thomas.briese@columbia.edu, W. Ian Lipkin (wil2001@columbia.edu), Stuart Nichol (stn1@cdc.gov), Janusz Paweska (januszp@nicd.ac.za), Maria Salvato (msalvato@ihv.umaryland.edu), Michael Buchmeier (m.buchmeier@uci.edu), Remi Charrel (Remi.Charrel@medecine.univ-mrs.fr), Chris Clegg (cleggjcs@yahoo.fr), CJ Peters (cjpeters@utmb.edu), Victor Romanowski (victor@biol.unlp.edu.ar), Igor Lukashevich (ILukashevich@ihv.umaryland.edu), Jean-Paul Gonzalez (jean-paul.gonzalez@ird.fr).

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)	**Arenaviridae SG**

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

Date first submitted to ICTV: 08/08/09
Date of this revision (if different to above):

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	***2011.003aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Arenavirus***
Subfamily:	
Family:	***Arenaviridae***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Lujo virus	FJ952384 - LUJV S-segment FJ952385 - LUJV L-segment

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

Members of an arenavirus species:
- share a specific host in the same species or genus,
- share a similar geographic distribution,
- are / are not an agent of disease in humans,
- share antigenic cross-reactivity,
- show a divergence of no more than 12% in the nucleoprotein amino acid sequence.

Lujo virus was identified in an outbreak of five cases of undiagnosed hemorrhagic fever, four of them fatal, in South Africa after air transfer of a critically ill index case from Zambia. The virus has been provisionally named Lujo virus (LUJV) in recognition of its geographic origins from Lusaka, Zambia and Johannesburg, South Africa, and should be classified as a new species in the genus *Arenavirus* based on:
1) having more than 40% divergence of its deduced nucleoprotein amino acid sequence when compared to other known arenavirus species
2) its capacity to cause severe human disease in conjunction with a probable geographic distribution in Zambia and/or South Africa, from where only arenaviruses without known human pathogenicity are reported.
3) cross-reactivity with a pan-arenavirus antibody cocktail. Specific cross-reactivity to individual other arenavirus species is not characterized.

The host reservoir of Lujo virus is unknown.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Briese, T., J. T. Paweska, L. K. McMullan, S. K. Hutchison, C. Street, G. Palacios, M. L. Khristova, J. Weyer, R. Swanepoel, M. Egholm, S. T. Nichol and W. I. Lipkin (2009) Genetic Detection and Characterization of Lujo Virus, a New Hemorrhagic Fever–Associated Arenavirus from Southern Africa. PLoS Pathog 4(5), e1000455. doi:10.1371/journal.ppat.1000455.

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.

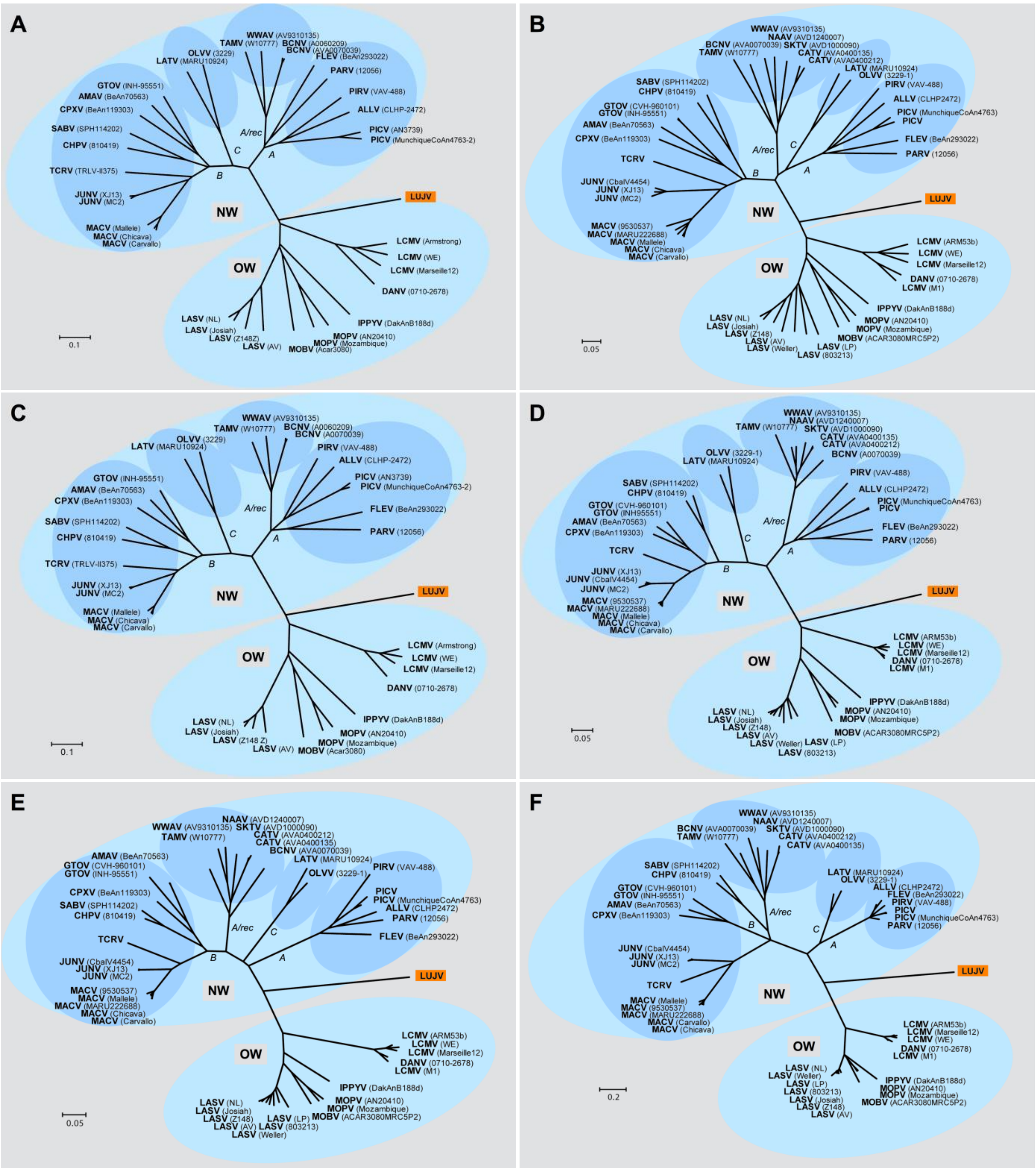

Figure 3: **Phylogenetic analyses of LUJV.** Phylogenetic relationships of LUJV were inferred based on full L (**A**) and S segment nucleotide sequence (**B**), as well as on deduced amino acid sequences of L (**C**), NP (**D**), Signal/G2 (**E)** and G1 (**F)** ORF's. Phylogenies were reconstructed by neighbor-joining analysis applying a Jukes-Cantor model; the scale bar indicates substitutions per site; robust boostrap support for the positioning of LUJV was obtained in all cases (>98% of

1000 pseudoreplicates). GenBank Accession numbers for reference sequences are: ALLV CLHP2472 (AY216502, AY012687); AMAV BeAn70563 (AF512834); BCNV AVA0070039 (AY924390, AY922491), A0060209 (AY216503); CATV AVA0400135 (DQ865244), AVA0400212 (DQ865245); CHPV 810419 (EU, 260464, EU260463); CPXV BeAn119303 (AY216519, AF512832); DANV 0710-2678 (EU136039, EU136038); FLEV BeAn293022 (EU627611, AF512831); GTOV INH-95551 (AY358024, AF485258), CVH-960101 (AY497548); IPPYV DakAnB188d (DQ328878, DQ328877); JUNV MC2 (AY216507, D10072), XJ13 (AY358022, AY358023), CbalV4454 (DQ272266); LASV LP (AF181853), 803213 (AF181854), Weller (AY628206), AV (AY179171, AF246121), Z148 (AY628204, AY628205), Josiah (U73034, J043204), NL (AY179172, AY179173); LATV MARU10924 (EU627612, AF485259); LCMV Armstrong (AY847351), ARM53b (M20869), WE (AF004519, M22138), Marseille12 (DQ286932, DQ286931), M1 (AB261991); MACV Carvallo (AY619642, AY619643), Chicava (AY624354, AY624355), Mallele (AY619644, AY619645), MARU222688 (AY922407), 9530537 (AY571959); MOBV ACAR3080MRC5P2 (DQ328876, AY342390); MOPV AN20410 (AY772169, AY772170), Mozambique (DQ328875, DQ328874); NAAV AVD1240007 (EU123329); OLVV 3229-1 (AY216514, U34248); PARV 12056 (EU627613, AF485261); PICV (K02734), MunchiqueCoAn4763 (EF529745, EF529744), AN3739 (AF427517); PIRV VAV-488 (AY216505, AF277659); SABV SPH114202 (AY358026, U41071); SKTV AVD1000090 (EU123328); TAMV W10777 (EU627614, AF512828); TCRV (J04340, M20304); WWAV AV9310135 (AY924395, AF228063).