

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2023.014M*** |  |
| **Short title:** Create two new species in genus *Mammarenavirus* (*Bunyavirales*: *Arenaviridae*) | | |
|  | | |

**Author(s) and email address(es)**

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**Corresponding author**

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| Cuypers LN |

**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Arenaviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Arenaviridae* Study Group | 13 | 0 | 0 |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| N/A | N/A | N/A |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

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| N/A |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2023.014M.N.v1.Mammarenavirus\_2nsp |

**Abstract**

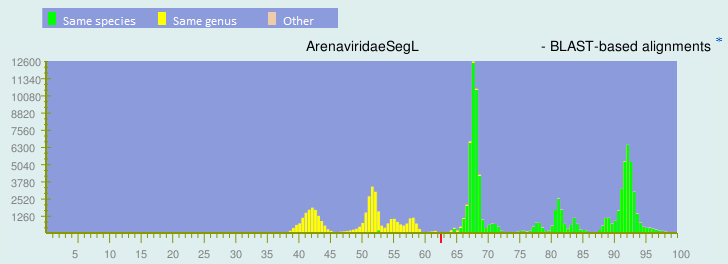
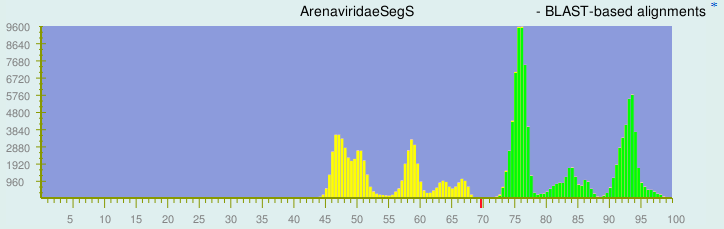
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| We propose the establishment of two new species in arenavirid genus *Mammarenavirus* to accommodate Berega and Songea viruses discovered in woodland grammomys in Tanzania. |

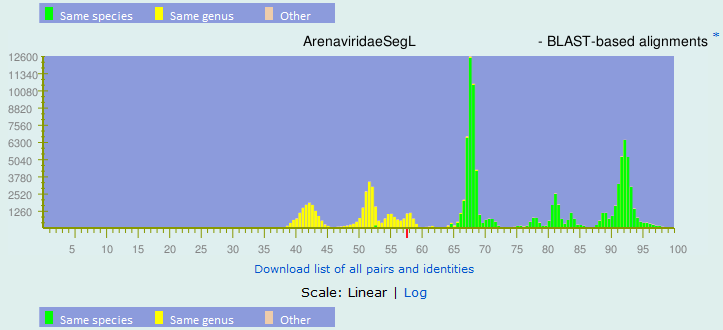
**Text of proposal**

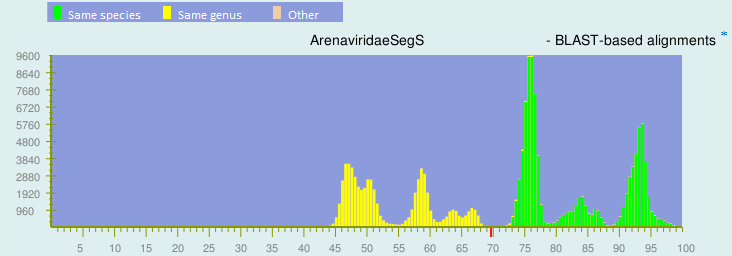
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| --- | --- |
| |  | | --- | | Two distinct mammarenaviruses were detected in woodland grammomys (murid *Grammomys surdaster* (Thomas and Wroughton, 1908; sensu Musser & Carleton 2005 and Bryja et al. 2017) in Tanzania: one in a kidney sample from (TZ31109) trapped at Lilondo (Songea Rural District) and another in a salivary gland sample (TZ33709) trapped at Berega (Kilosa District). Metagenomic sequencing was performed on a TZ31109 dried blood sample, yielding a complete mammarenavirus genome sequence, and on the TZ33709 salivary gland sample, yielding a coding-complete mammarenavirus genome sequence that misses a few non-coding nucleotides at all ends except the 3’ end of the S segment (Cuypers et al. 2023). Both viruses meet the ICTV *Arenaviridae* Study Group’s criteria to each be considered members of new mammarenavirus species. We therefore propose the establishment of the species *Mammarenavirus songeaense* (for the first virus, named Songea virus [SOGV]) and *Mammarenavirus beregaense* (for the second virus, named Berega virus [BEGV]) after the district and the locality where they were discovered, respectively.  The best PASC hit for both SOGV genome segments is Solwezi virus (S segment: 70%, L segment: 63%; Figure 1), which is also Songea virus’s sister in the *L* and *NP* trees (Figure 2). A Geneious alignment of the two NP amino acids sequences reveals a pairwise identity of 83%.  The best PASC hit for BEGV is Mariental virus (S segment) (70% identity) and BEGV clusters with Mariental virus in the *NP*, *GPC*,and *L* phylogenetic tree below (Figure 2). | |

**Supporting evidence**

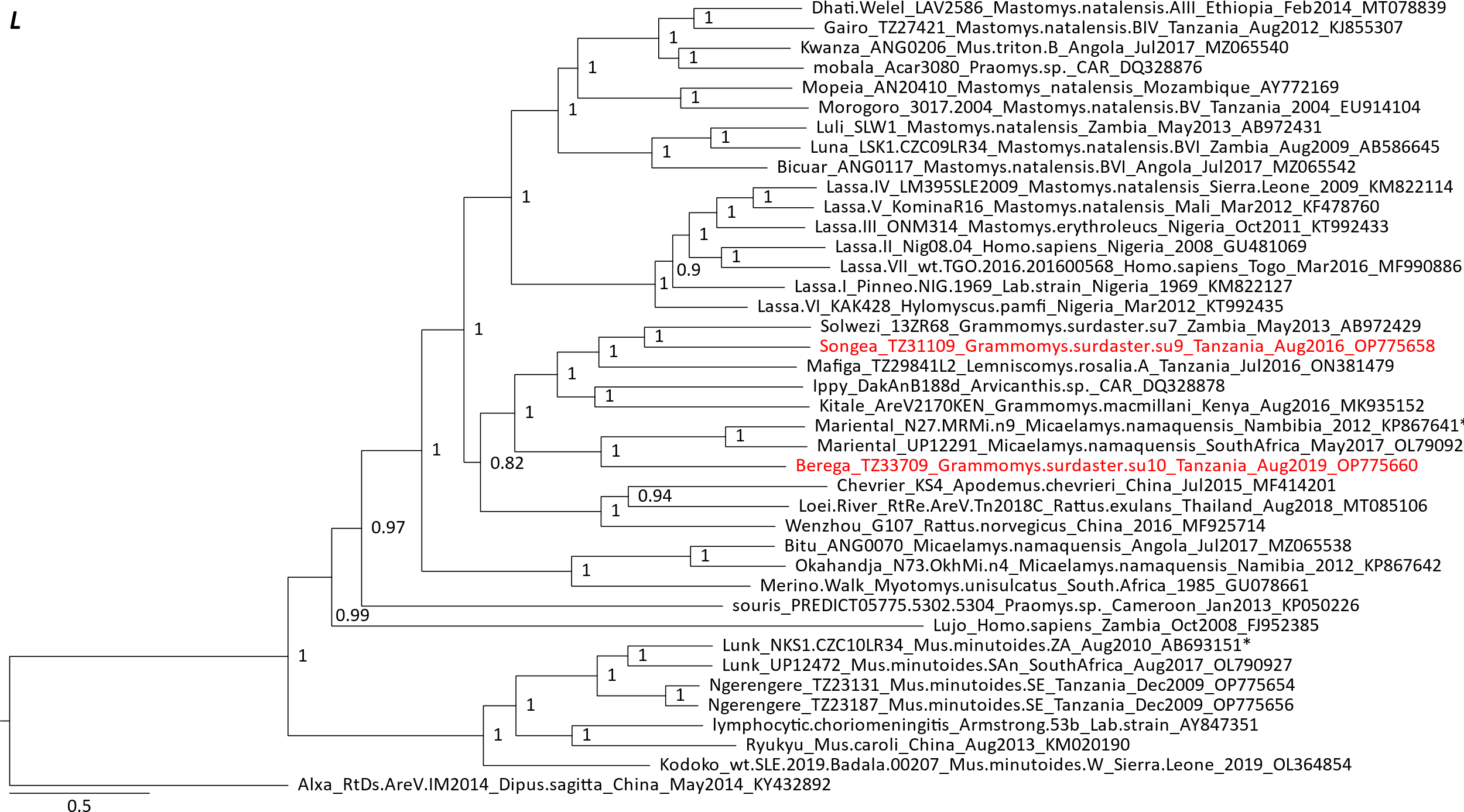
**Figure 1.** PAirwise Sequence Comparison analyses performed through the online webtool available at https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi.

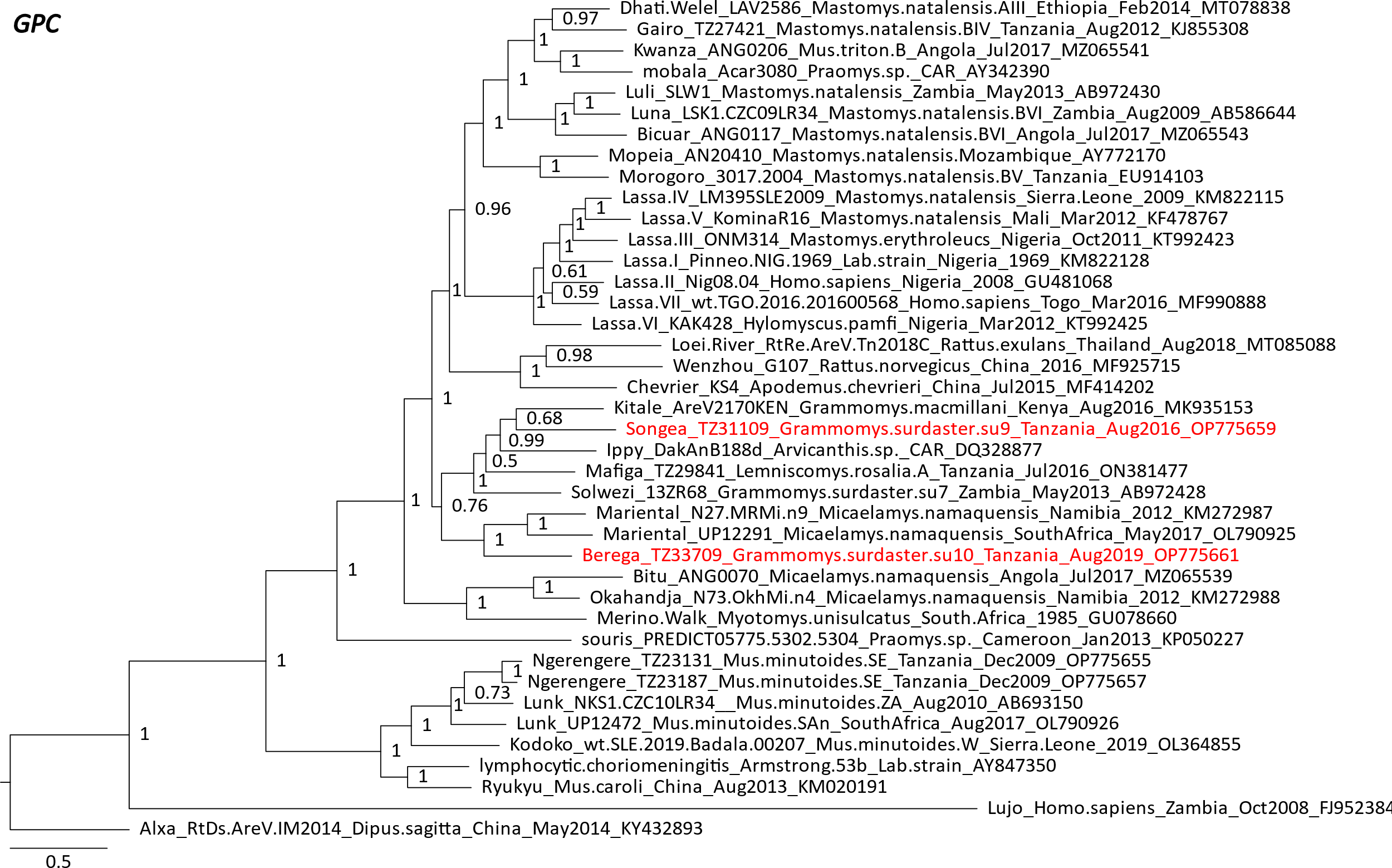
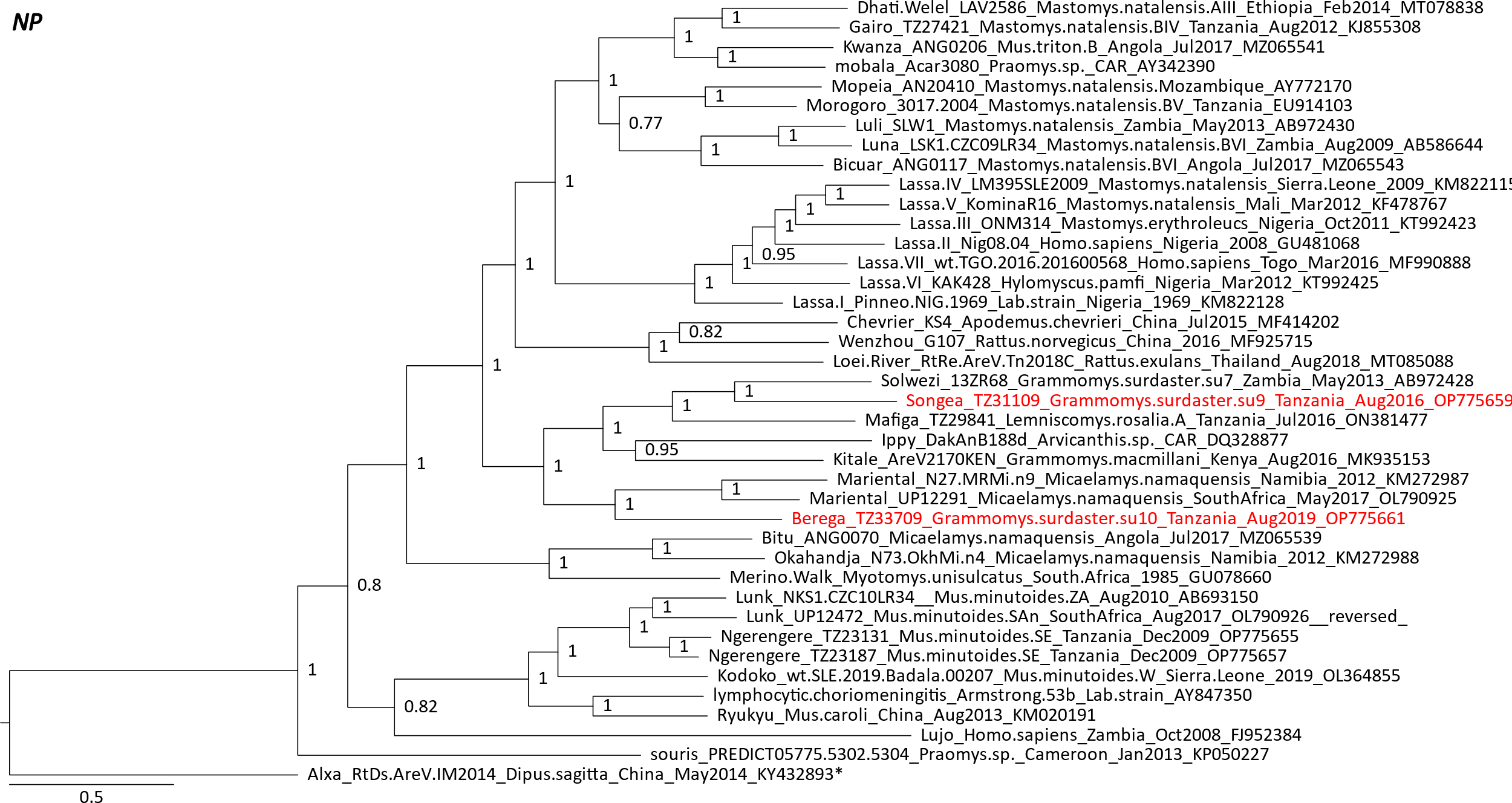
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**Figure 2.** *L*, *NP* and *GPC* gene phylogenetic trees rooted with Alxa virus. The trees were inferred with MrBayes v3.2.7a with codon partitioning and a GTR+G nucleotide substitution model. In two independent runs four chains ran for 2,000,000 generations with a burn-in of 25%. Average standard deviations of split frequencies were examined for convergence, as were parameter effective sample sizes and trace patterns in Tracer (<https://beast.community/tracer>). Trees were visualized in FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>). Posterior probabilities are indicated at the nodes and the scale bars indicate the number of nucleotide substitutions per site. Asterisks indicate that sequences were slightly modified from the corresponding GenBank sequences to improve translation alignment: a suspected chimaeric region of KP867641 was masked (Těšíková et al., 2021), one N was added at position 7,074 in AB693151 to restore the reading frame and enable a longer sequence (Cuypers et al. 2022), and the first four nucleotides of KY432893 were cut so the Alxa virus *NP* sequence starts with a start codon (Cuypers et al. 2022).





**References**

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