

## Supplementary information to

# “First Detection and Frequent Occurrence of Equine Hepacivirus in Horses on the African Continent”

## Authors

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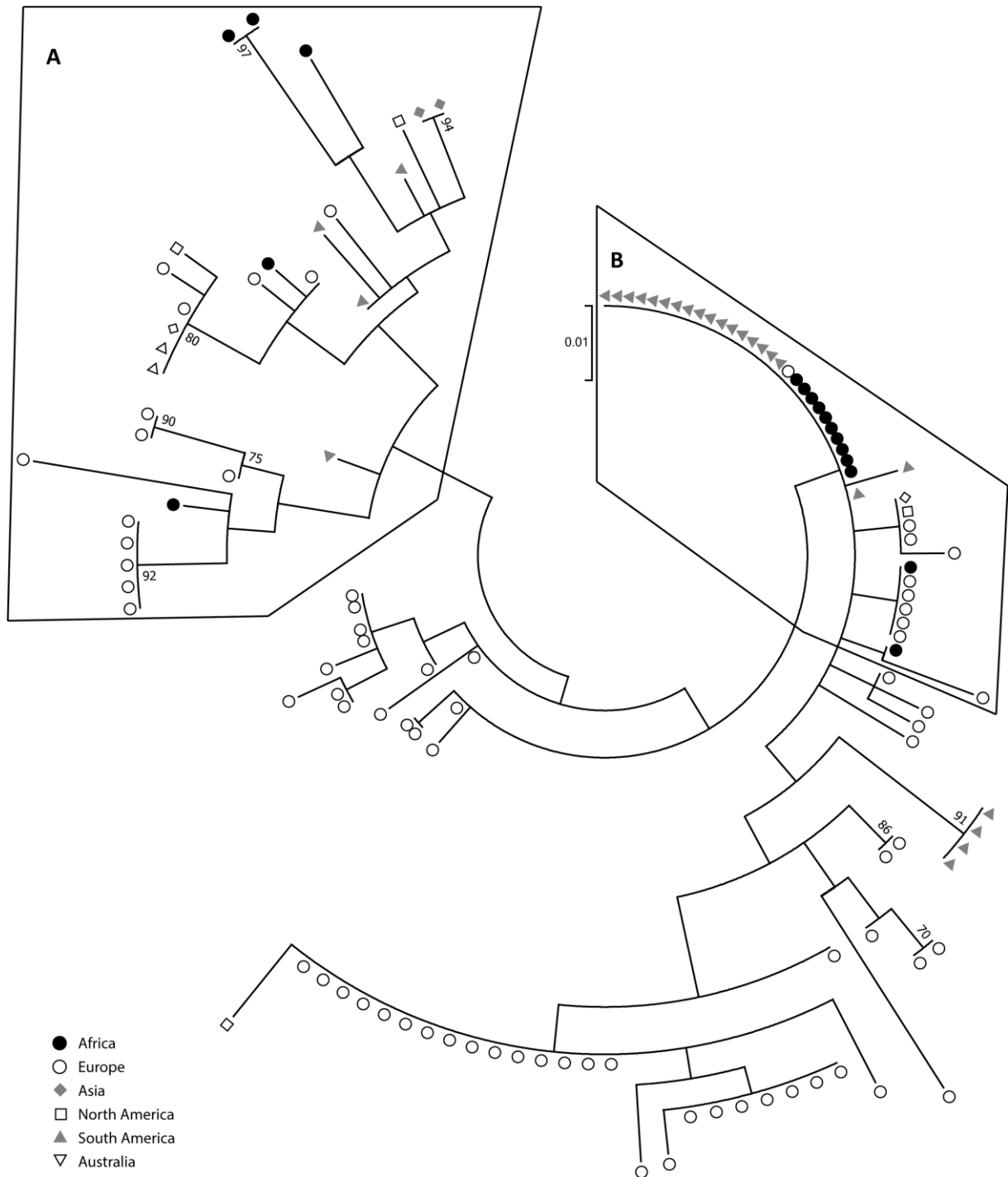
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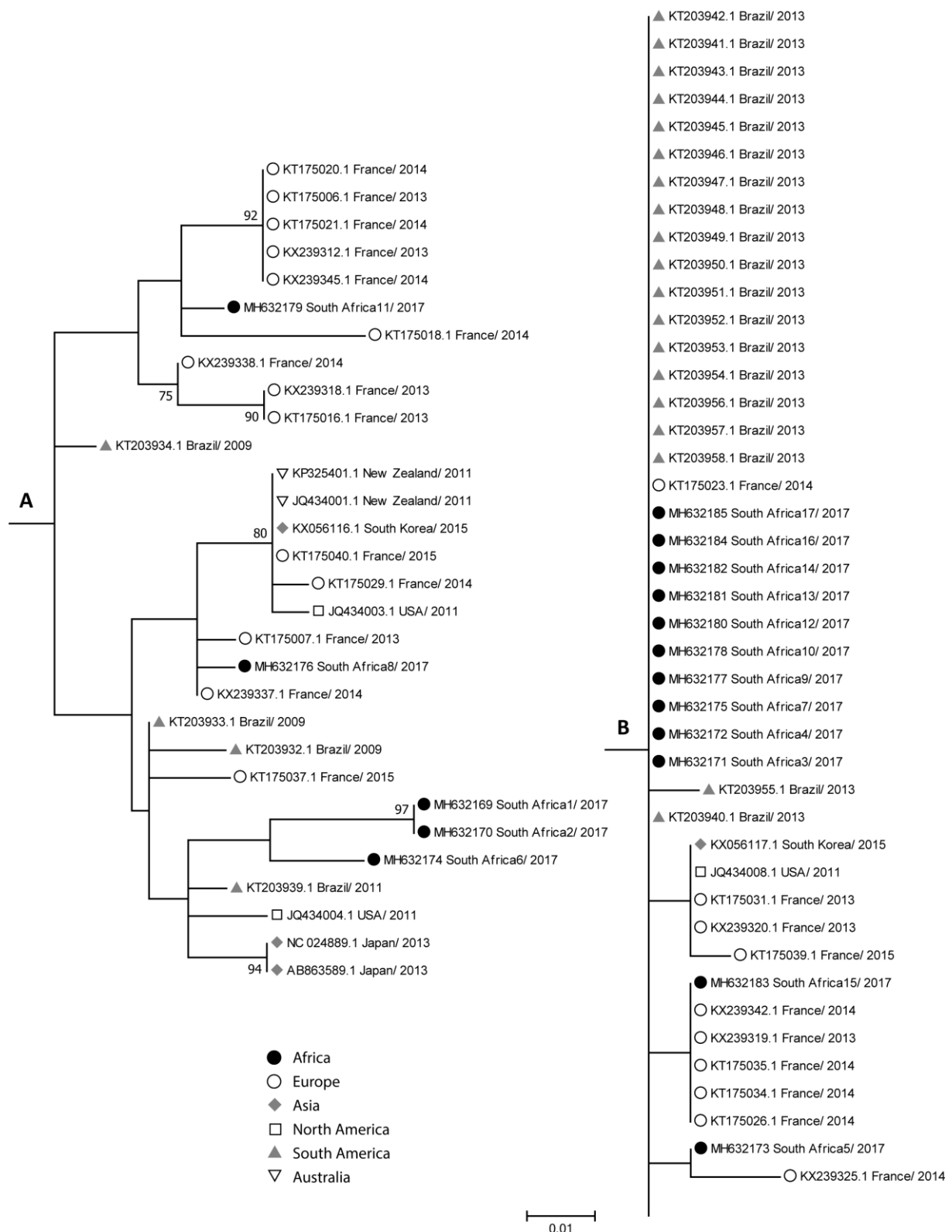
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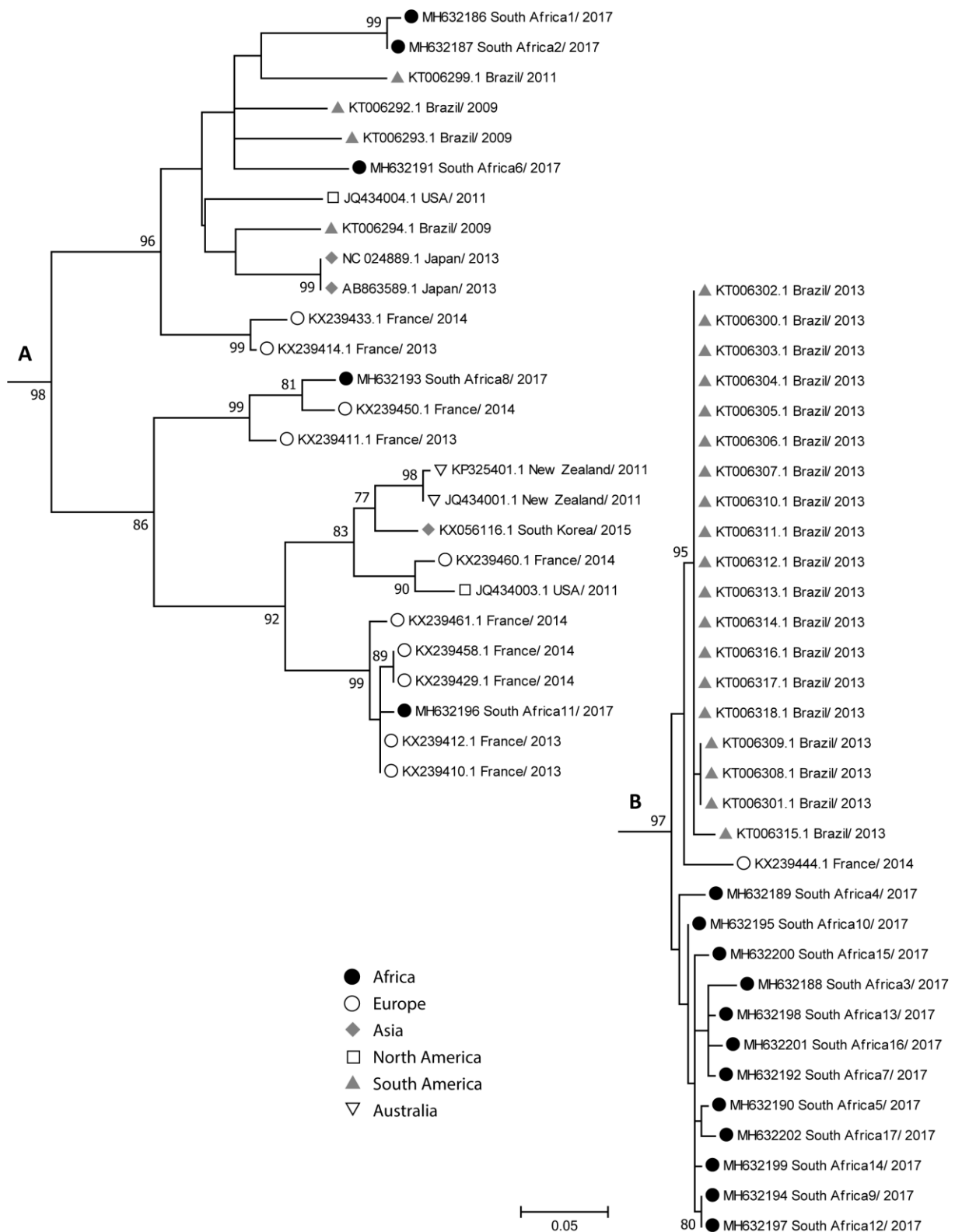


**Supplementary Fig. 1** Maximum-likelihood phylogeny based on partial 5'UTR sequences of EHV-1. In addition to sequences obtained from South African foals, the phylogenetic tree contains sequences for EHV-1 retrieved from GenBank, as described in the Materials and Methods section. The analysis involved 130 nucleotide sequences. All positions containing gaps and missing data were eliminated, whereby a total of 184 positions were included in the final dataset. Bootstrap values <70% are not shown. The symbol legend indicates symbols and the corresponding continent which a sequence originated from. The scale bar illustrates the number of substitutions per site. Framed sections, including sequences obtained in this study, are illustrated in detail in supplementary Fig. 2.



**Supplementary Fig. 2** Detailed views of the complete phylogenetic tree based on partial 5'UTR sequences of EqHV. (A-B) Each panel illustrates a part of the complete tree, including the accession number, country and year of each sequence. Additionally, sequences acquired in the present study are labelled with the number of the foal which the isolate originated from (refer to Table 3). The symbol legend indicates symbols and the corresponding continent which a sequence originated from. The scale bar illustrates the number of substitutions per site.





**Supplementary Fig. 4** Detailed views of the complete phylogenetic tree based on partial NS5B sequences of EqHV. (A-B) Each panel illustrates a part of the complete tree, including the accession number, country and year of each sequence. Additionally, sequences acquired in the present study are labelled with the number of the foal which the isolate originated from (refer to Table 3). The symbol legend indicates symbols and the corresponding continent which a sequence originated from. The scale bar illustrates the number of substitutions per site.