

The following supplement accompanies the article

Identification, molecular and phylogenetic analysis of poxvirus in skin lesions of southern right whale

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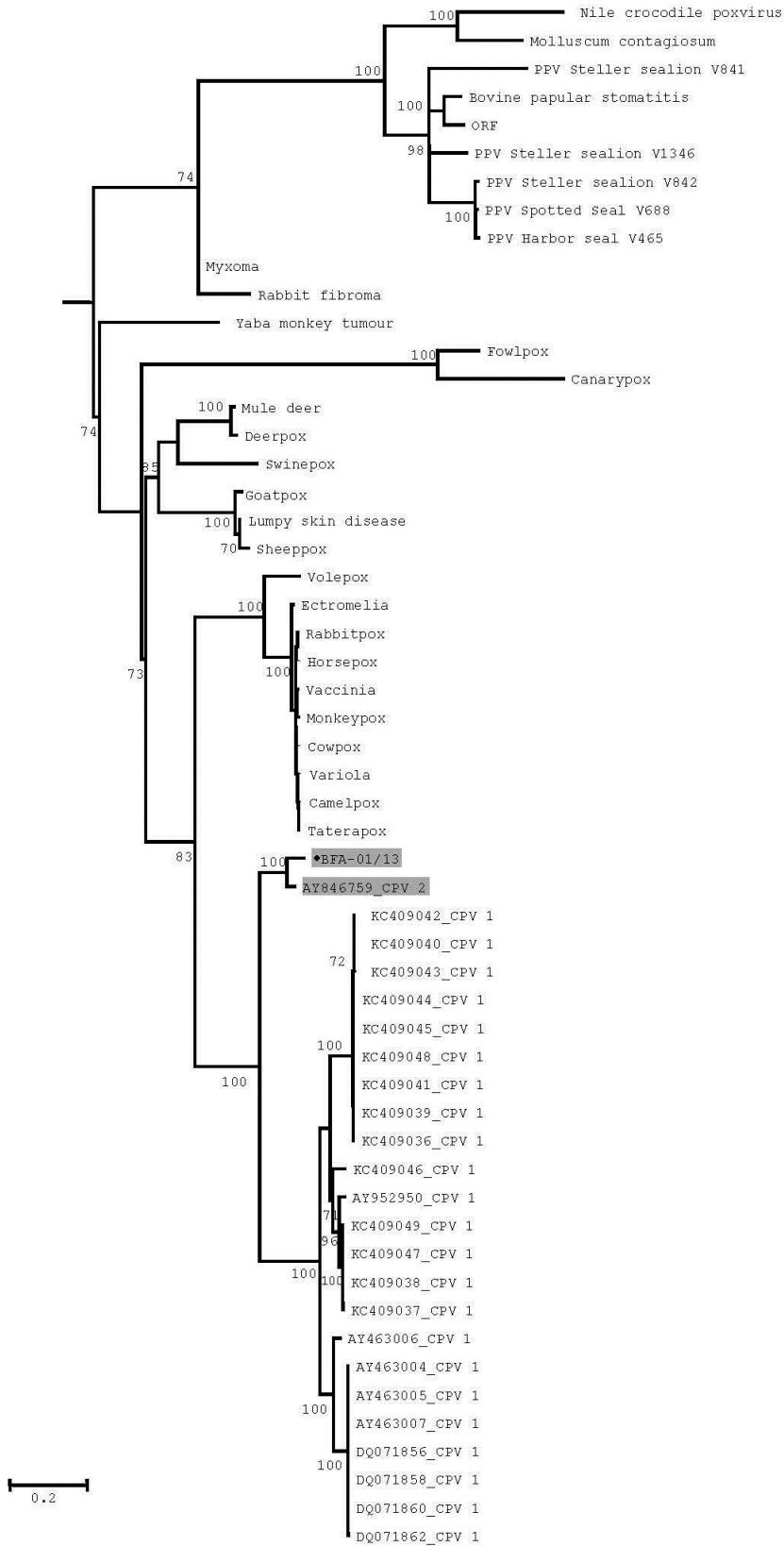
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Supplement.

Figure S1. Phylogenetic tree from the DNA polymerase analysis for Maximum likelihood method (GTR+G+I model). The CPV 2 sequences are shown in grey. For identification of CPV sequences, accession numbers from DNA polymerase, are detailed in the taxon name. Bootstrap values higher than 70% are indicated in the nodes. CPV= Cetacean Poxvirus. The bar scale estimates the number of substitutions per site.

Figure S2. Phylogenetic tree from the DNA topoisomerase I analysis for Maximum likelihood method (GTR+G model). The CPV 2 sequences are shown in grey. For identification of CPV sequences, accession numbers from DNA topoisomerase I are detailed in the taxon name. Bootstrap values higher than 70% are indicated in the nodes. CPV= Cetacean Poxvirus. The bar scale estimates the number of substitutions per site.



Supplementary material. Figure S1

