

Supplementary File

Genomic characterisation of a novel avipoxvirus isolated from an endangered northern royal albatross (*Diomedea sanfordi*)

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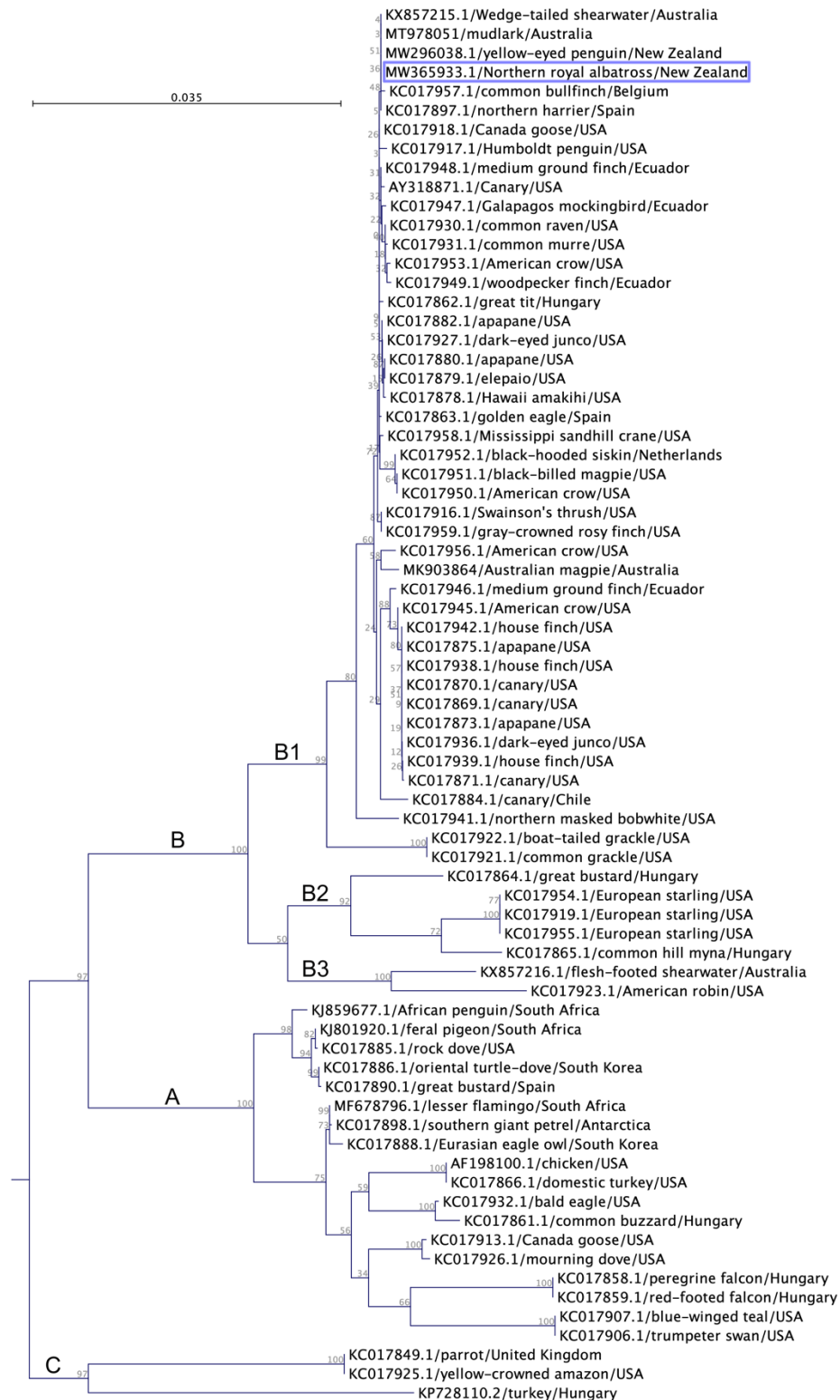


Figure S1: Maximum likelihood (ML) phylogenetic tree from partial nucleotide sequences of the DNA polymerase gene of selected avipoxviruses. Labels at branch tips refer to GenBank accession number/species/country of origin. The numbers on the left show bootstrap values as percentages and the position of ALPV is highlighted using a purple box. The ML tree is displayed as a phylogram. The bootstrap value assigned to a node in the output tree is the percentage (0–100) of the bootstrap resamples which resulted in a tree containing the same subtree as that rooted at the node. According to Gyuranecz *et al* (2013), major clades are designated A, B and C, while B1–B3 represent subclades.

