# S2 Fig for "Traits, phylogeny and host cell receptors predict *Ebolavirus* host status of African mammals"

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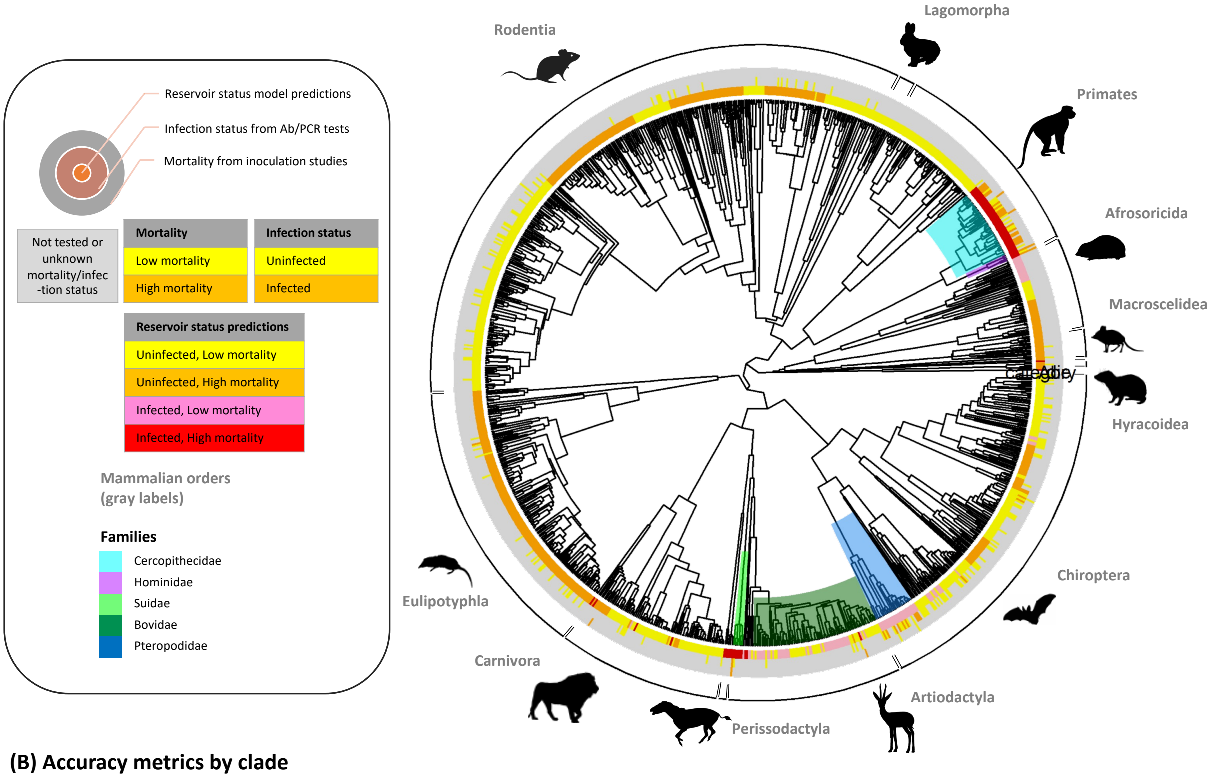
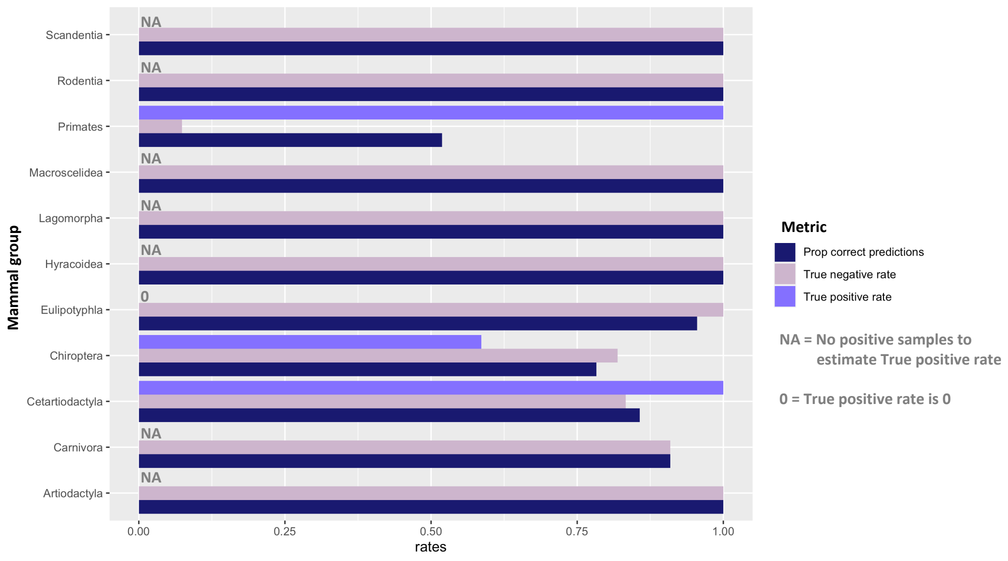
**(A) Reservoir predictions and raw data**



**(B) Accuracy metrics by clade**



**S2 Fig**. Predictions of reservoir status for all known terrestrial African mammals, raw data showing infection status and mortality results for tested species (A). Predictions of reservoir status are based on ridge model predicting mortality of species after exposure to *Ebolavirus* and ridge model predicting infection status of species. Ridge models used trait and phylogenetic eigenvectors as predictors (see main text for more details of models). Accuracy of infection status predictions by mammal clade (B). Silhouettes used are available under Public Domain (https://creativecommons.org/publicdomain/zero/1.0/).