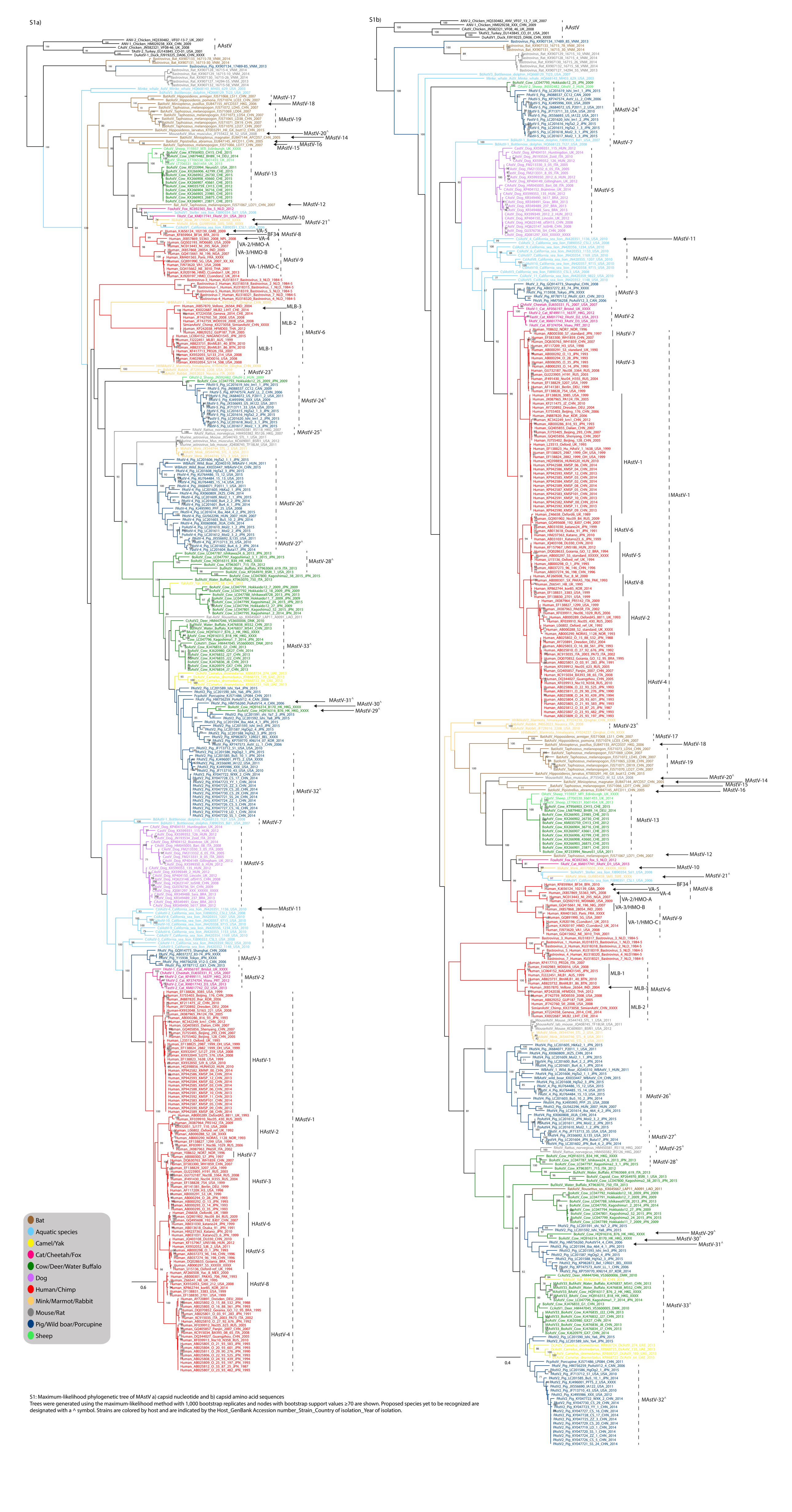

S1: Maximum-likelihood phylogenetic tree of MAstV a) capsid nucleotide and b) capsid amino acid sequences
Trees were generated using the maximum-likelihood method with 1,000 bootstrap replicates and nodes with bootstrap support values ≥70 are shown. Proposed species yet to be recognized are designated with a ^ symbol. Strains are colored by host and are indicated by the Host_GenBank Accession number_Strain_Country of isolation_Year of isolation.