Figure S3.

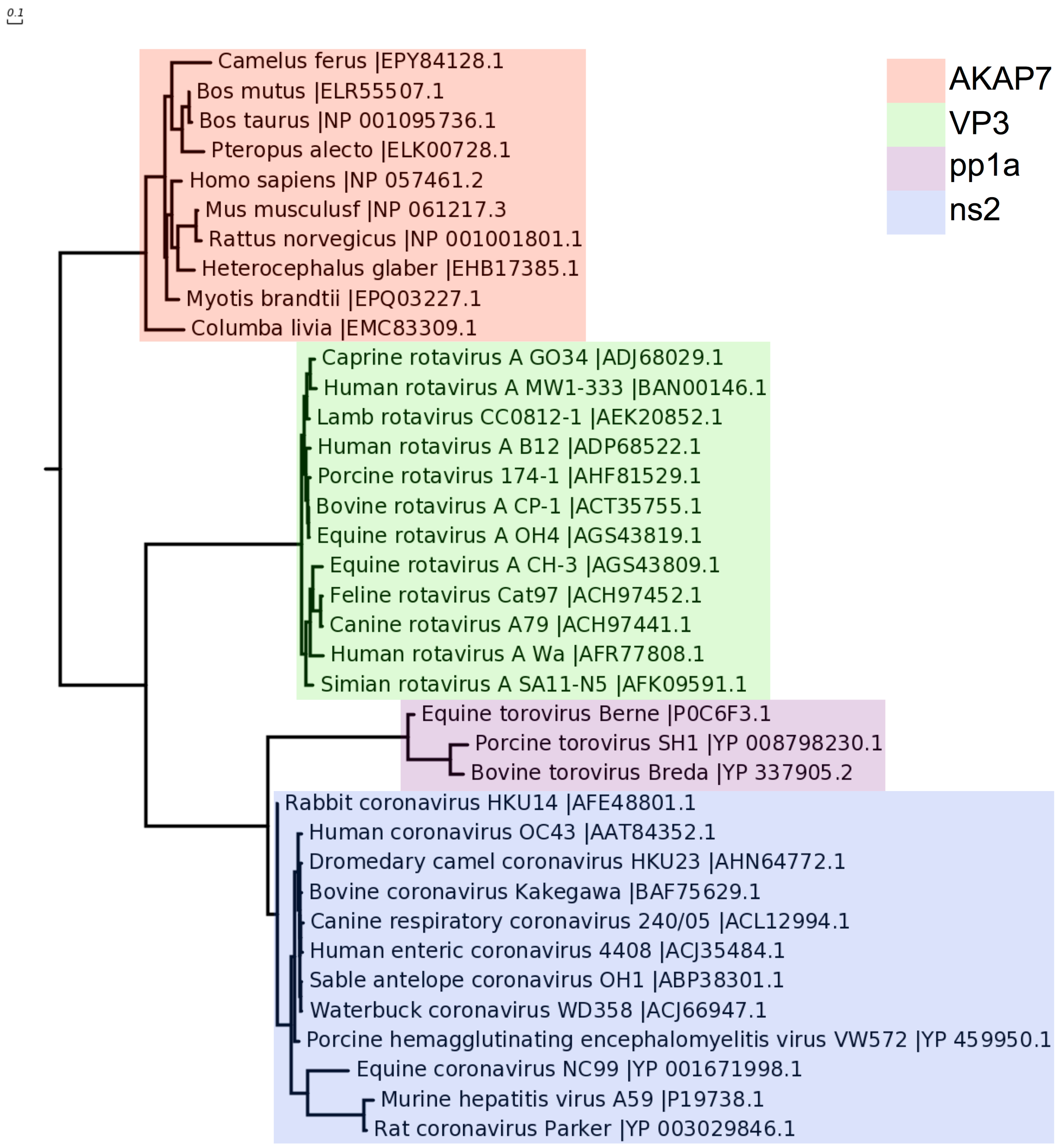

Figure S3. Phylogenetic relationship between 2’,5’-phosphodiesterases of distantly related taxa. Protein sequences of Vertebrate AKAP7, rotavirus VP3, torovirus polyprotein 1a (pp1a) and coronavirus ns2 were analyzed by fast minimum evolution with a maximum sequence difference of 0.9 using the Grishin distance model. The tree is based on a COBALT alignment derived from a PSI Blast search with 3 iterations of Murine hepatitis virus strain A59 ns2 protein NCBI P19738.1.