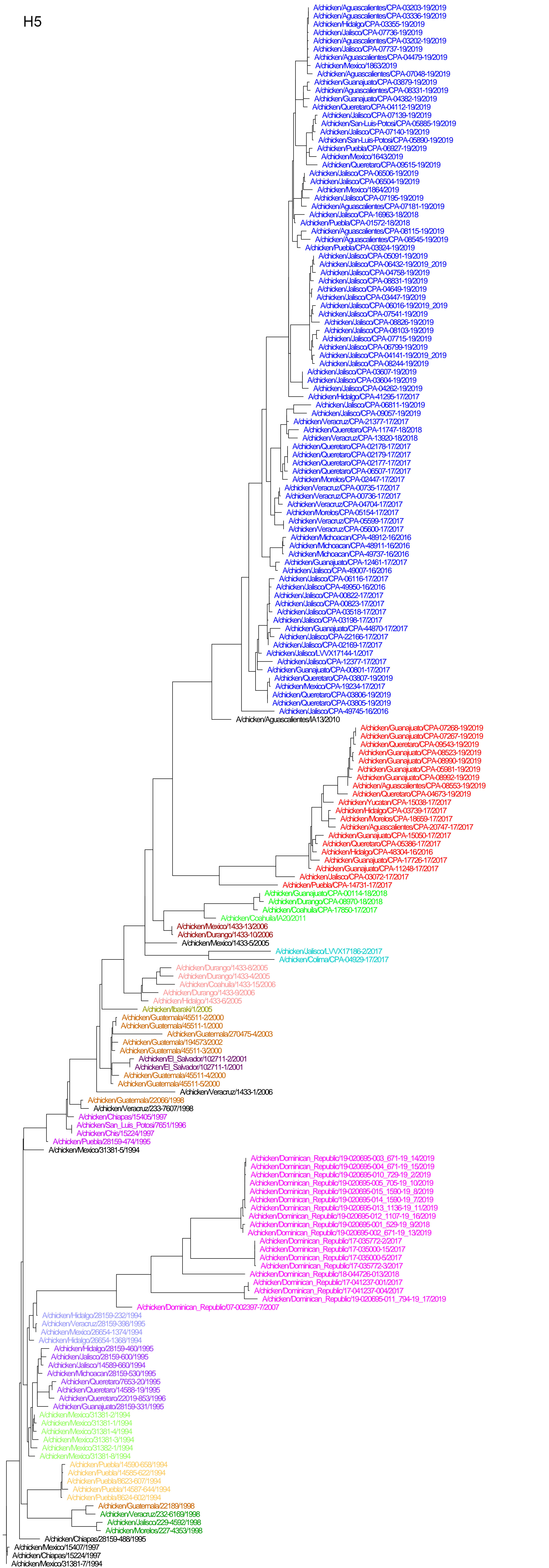
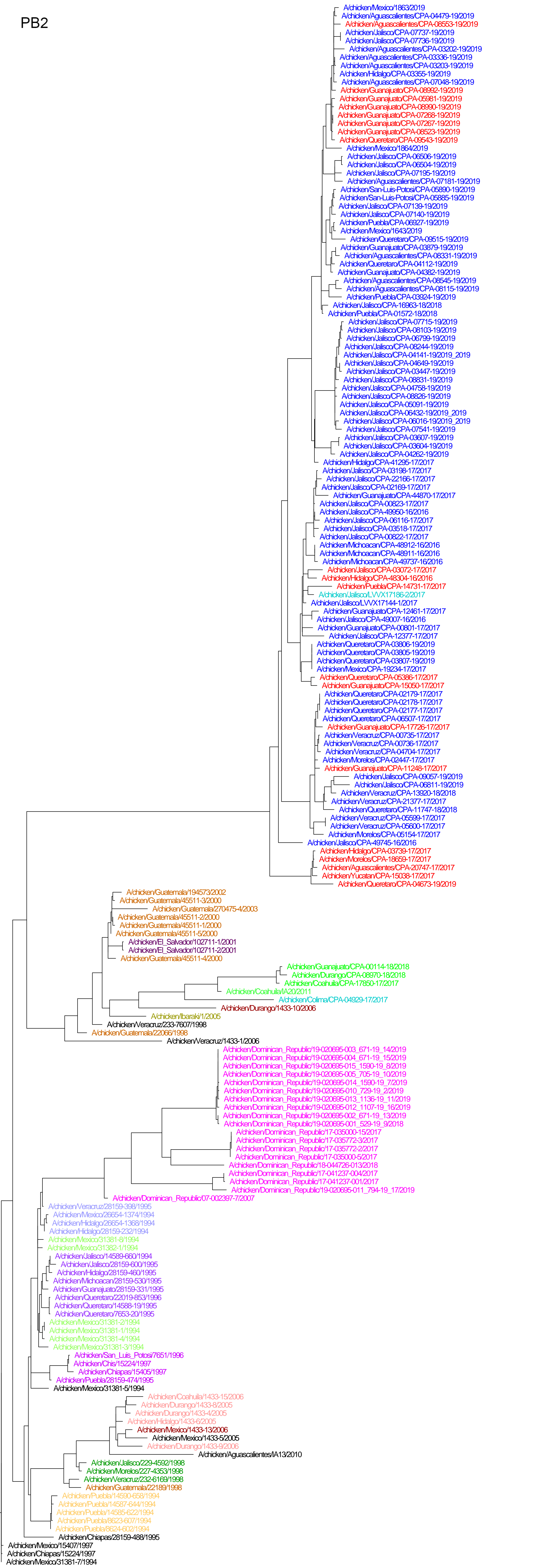


Figure S2. Phylogenetic incongruence analysis. ML trees for each genomic segment were inferred from 189 full-genome H5N2 viruses using RAxML. The phylogenies of segments are colored according to the origin of their HA. The phylogenetic position of each sequence was traced across all seven trees.

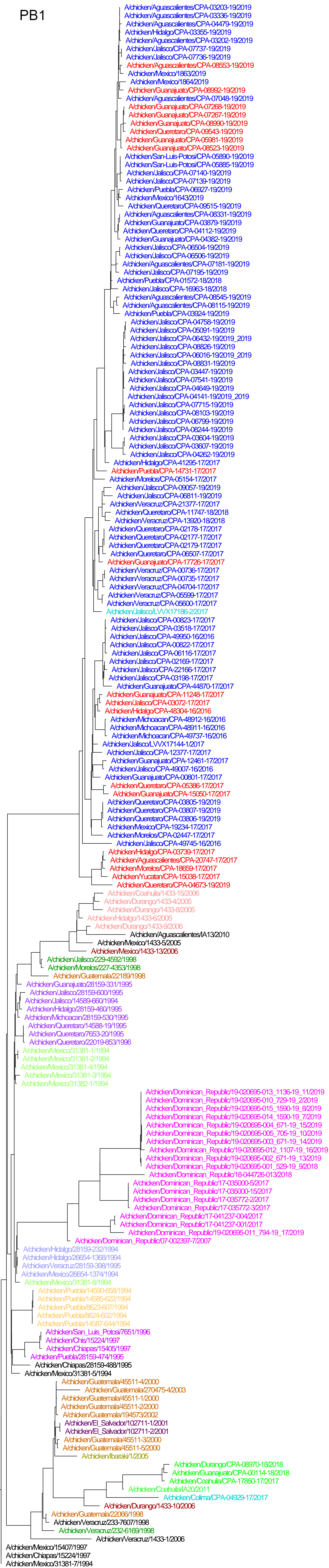
H5



0.004



PB1



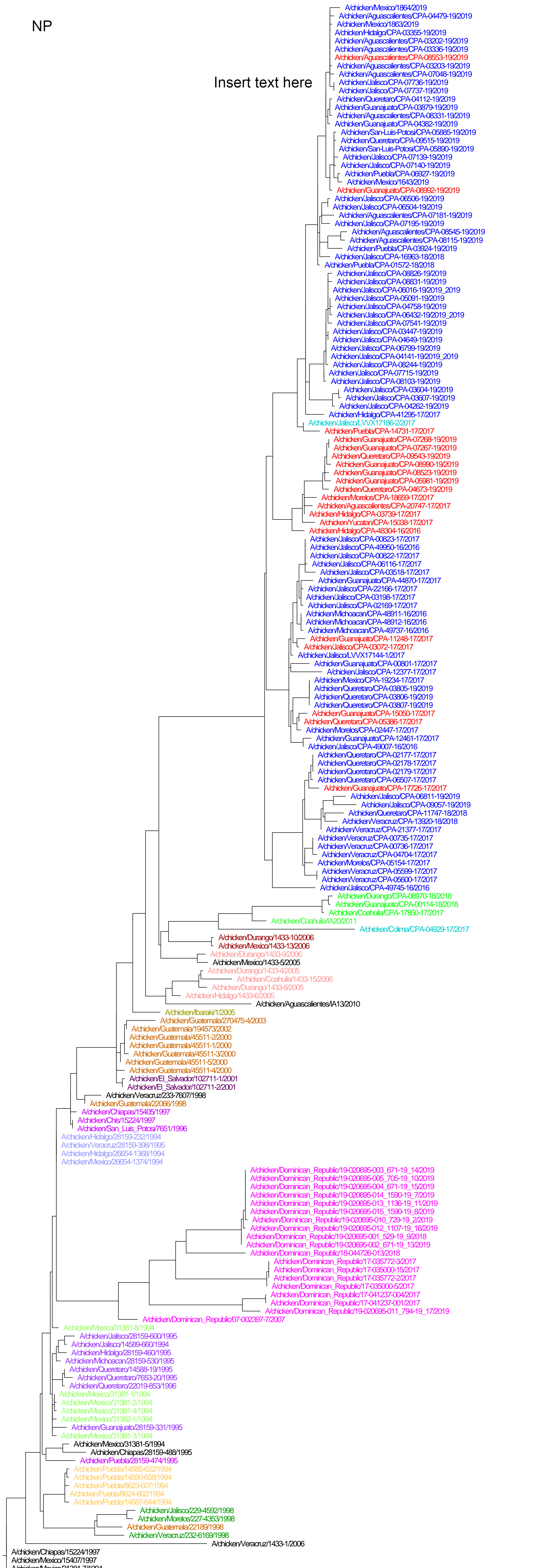
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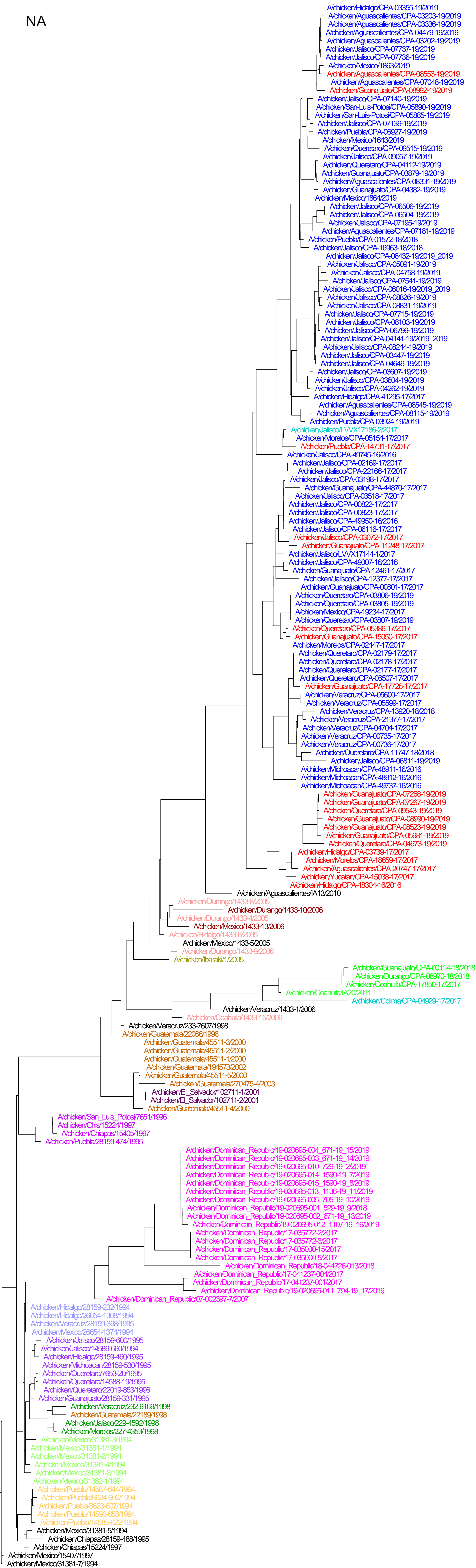
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