

Supplementary Materials for

**Phylogenetic Inference of H3N2 Canine Influenza A Outbreak
in Ontario, Canada in 2018**

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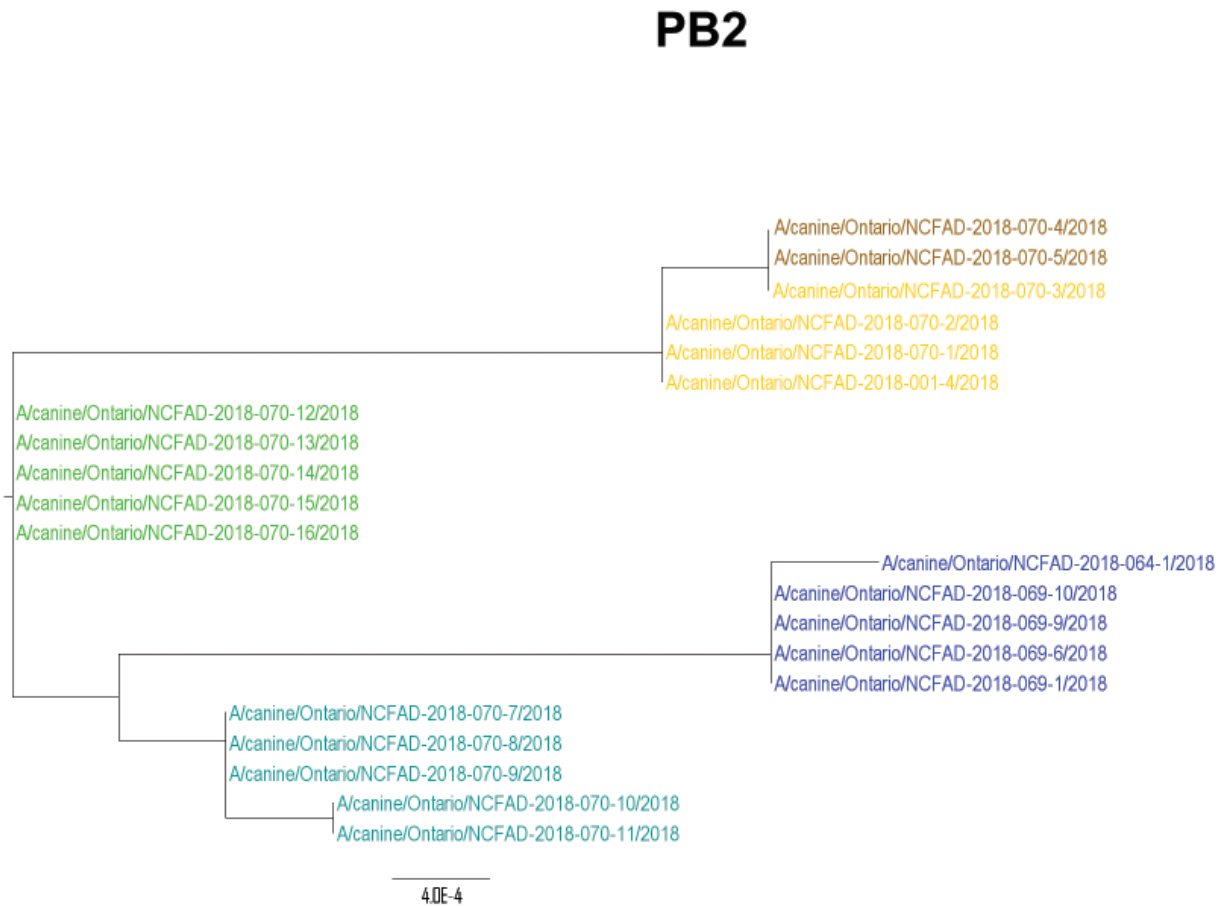
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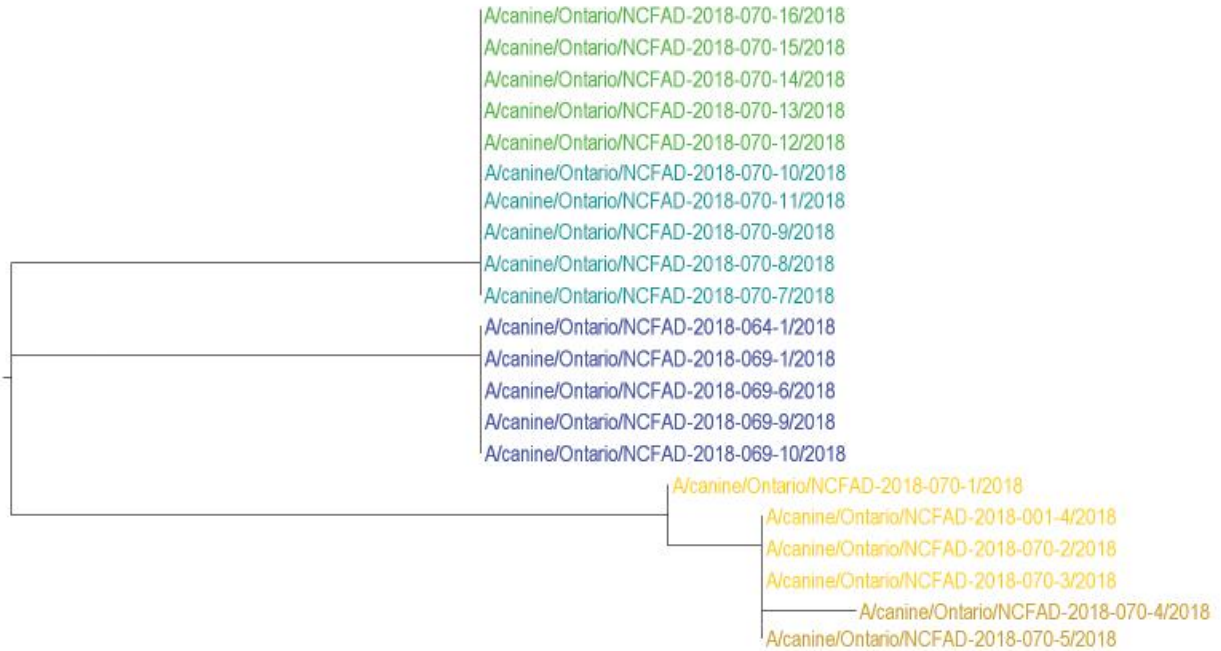
Figs. S1 to S3

Other Supplementary Material for this manuscript includes: Table S1 [spreadsheet (.xlsx)]

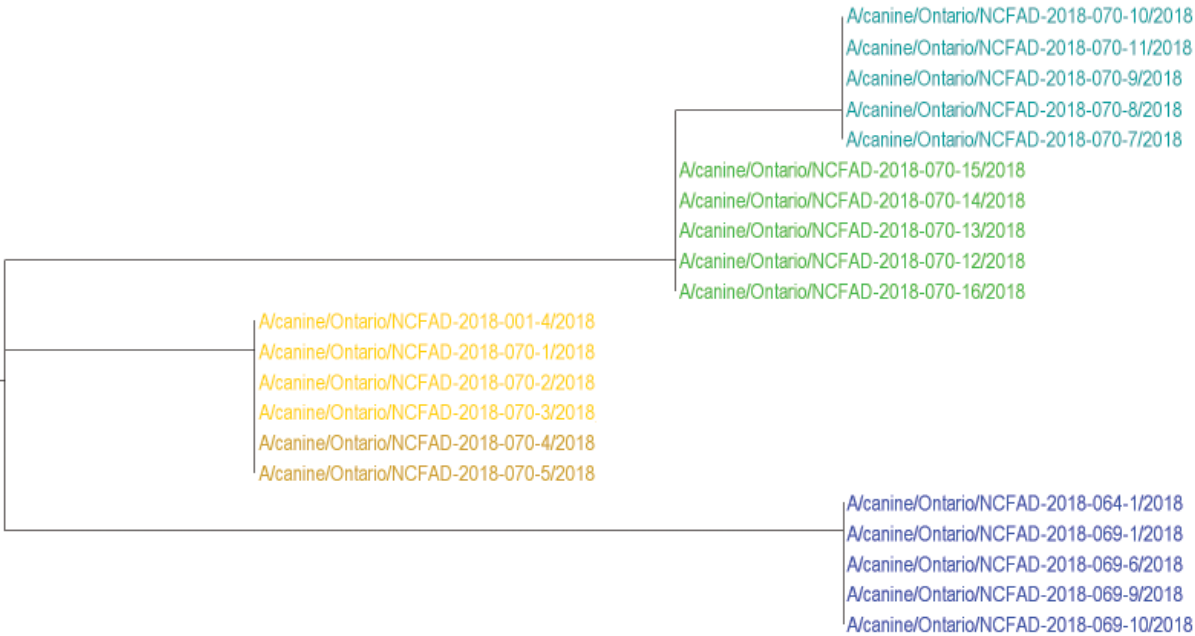
Fig. S1. Maximum Likelihood tree of the individual gene segment of Canadian H3N2 CIVs. Viruses are colored by their epidemiological clusters (yellow for cluster C1; brown for cluster C2; cyan for cluster C3a; green for cluster C3b; and blue for cluster C4). Branch lengths are scaled according to the numbers of nucleotide substitutions per site. The tree is midpoint rooted for clarity.



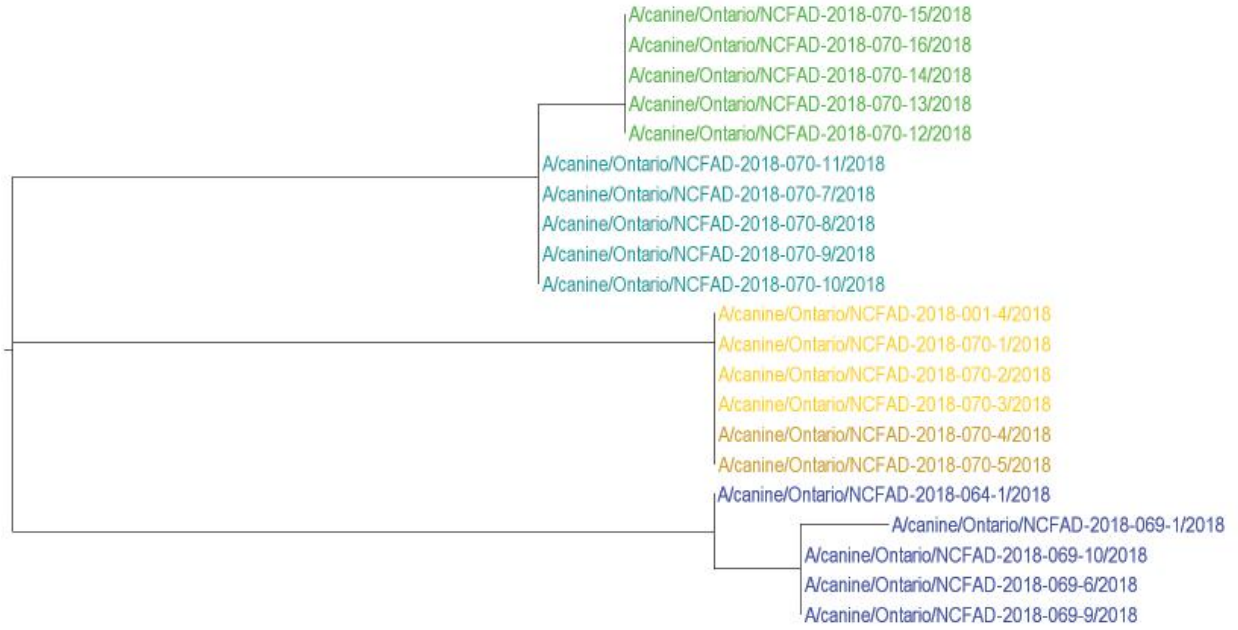
PB1



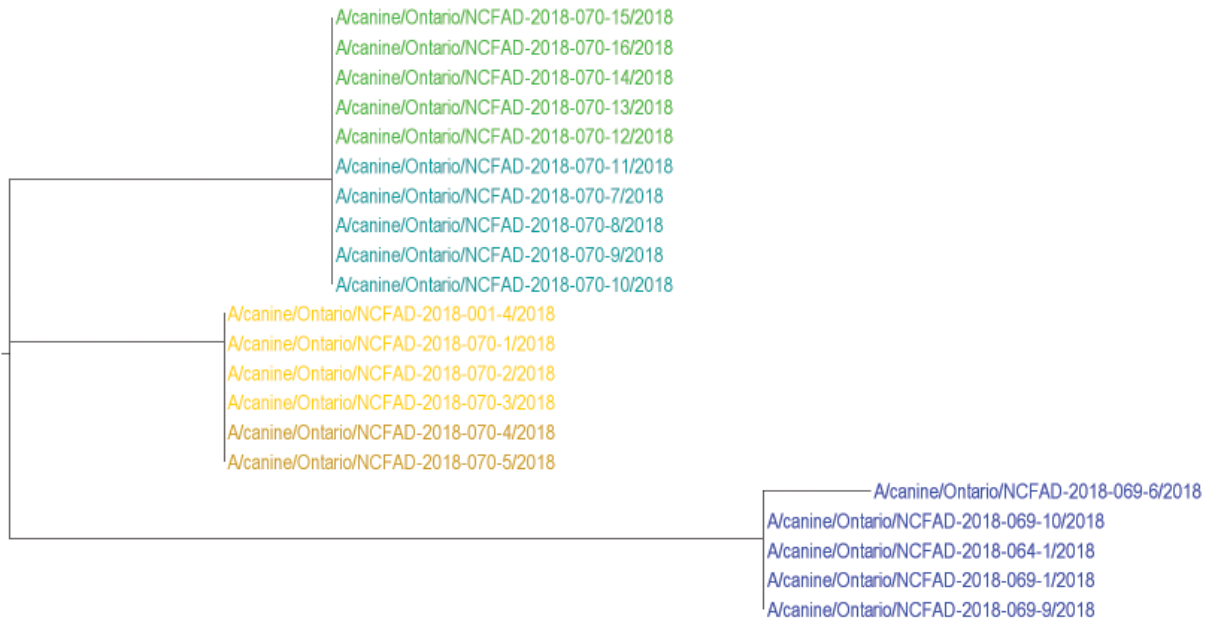
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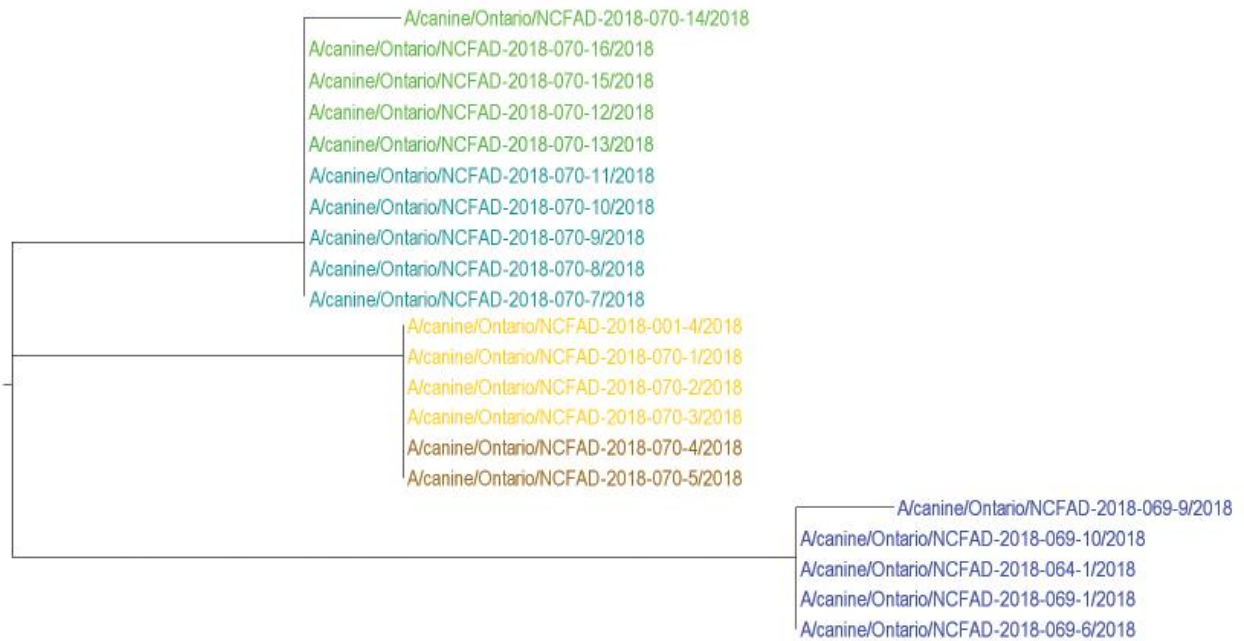
HA



NP



NA



M

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	A/canine/Ontario/NCFAD-2018-070-9/2018
	A/canine/Ontario/NCFAD-2018-070-8/2018
	A/canine/Ontario/NCFAD-2018-070-7/2018
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A/canine/Ontario/NCFAD-2018-070-13/2018	
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A/canine/Ontario/NCFAD-2018-070-4/2018
A/canine/Ontario/NCFAD-2018-070-5/2018

Fig. S2. Maximum clade credibility tree. Time-scaled phylogenies (dates on the horizontal axis) inferred using Bayesian MCMC analysis. Denotations are the same as in Fig. S1. Phylogenetic clusters are denoted as I to IV.

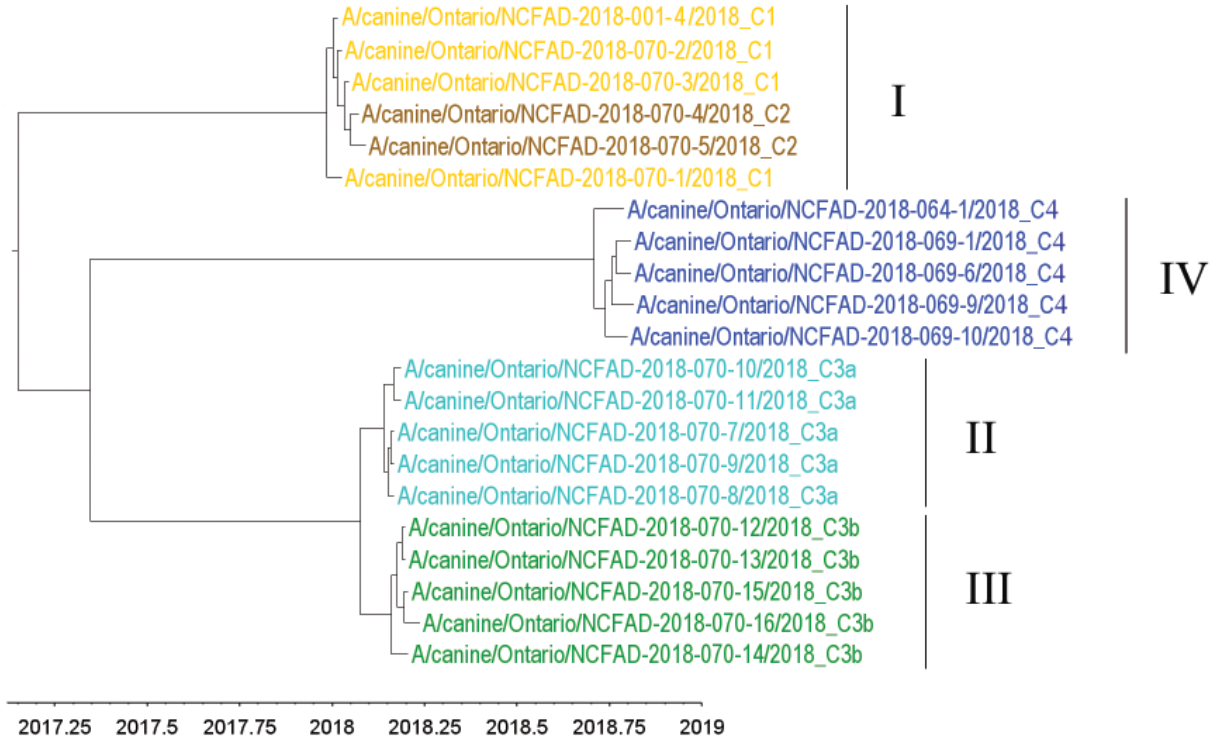
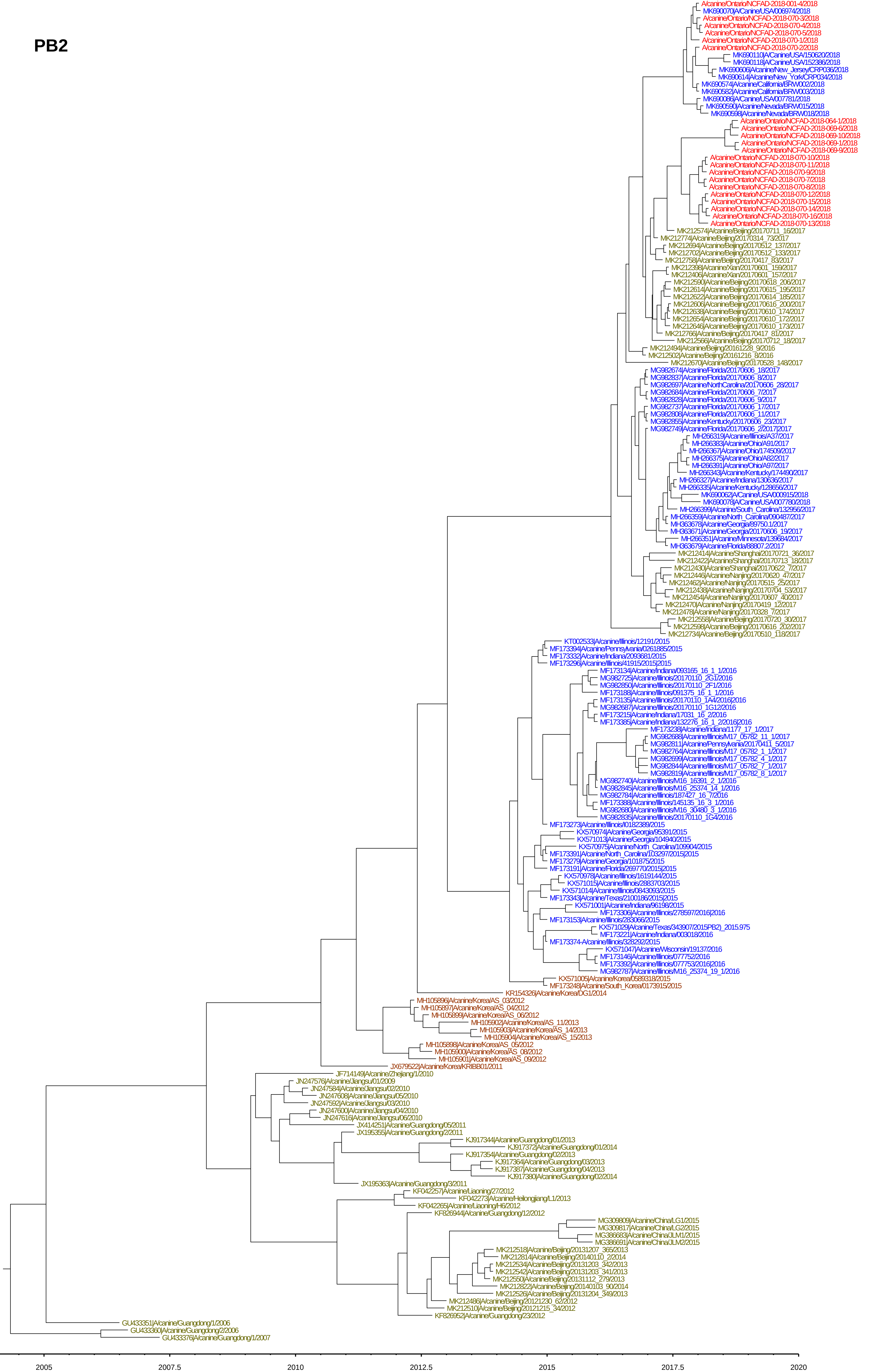
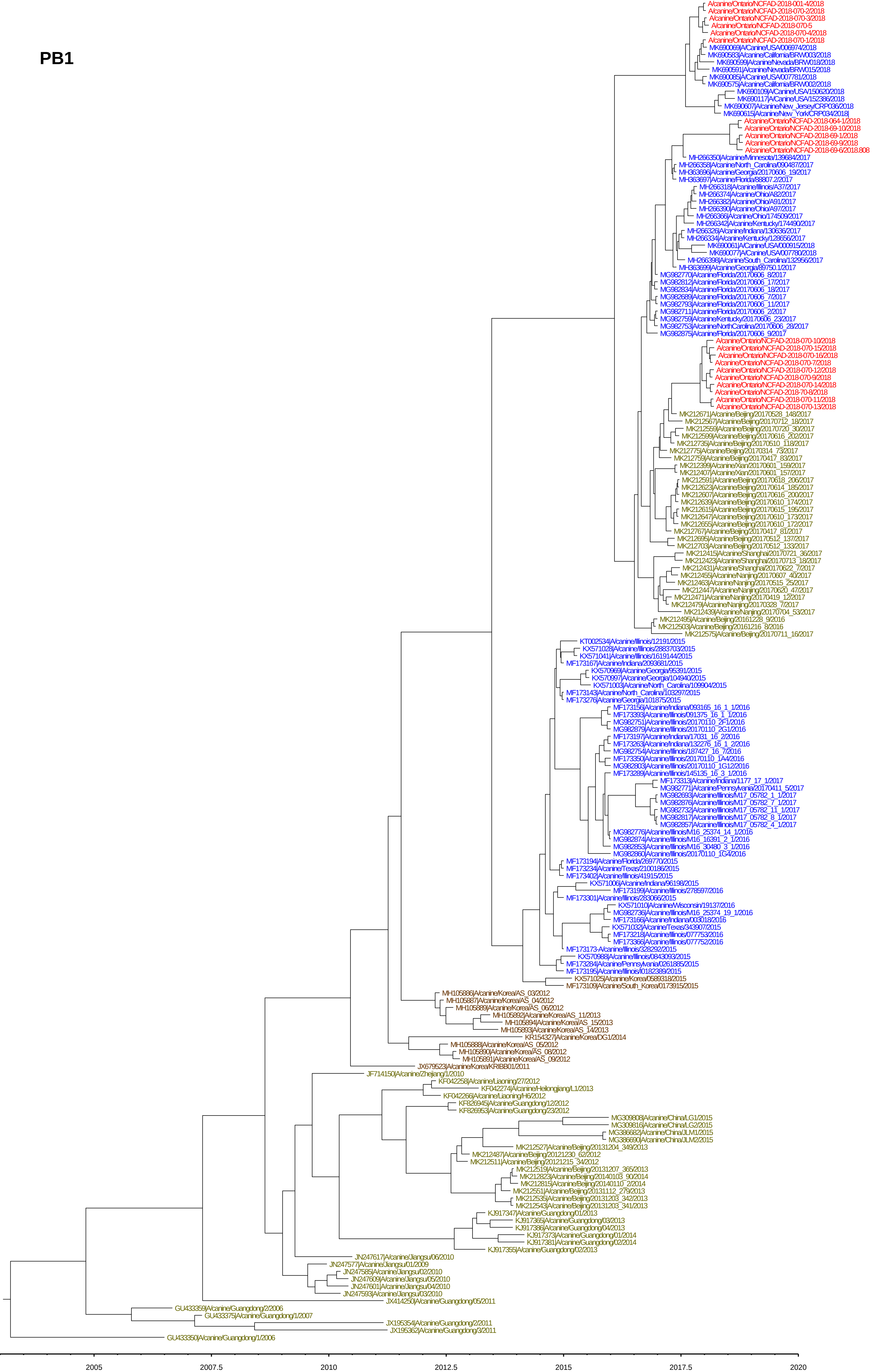


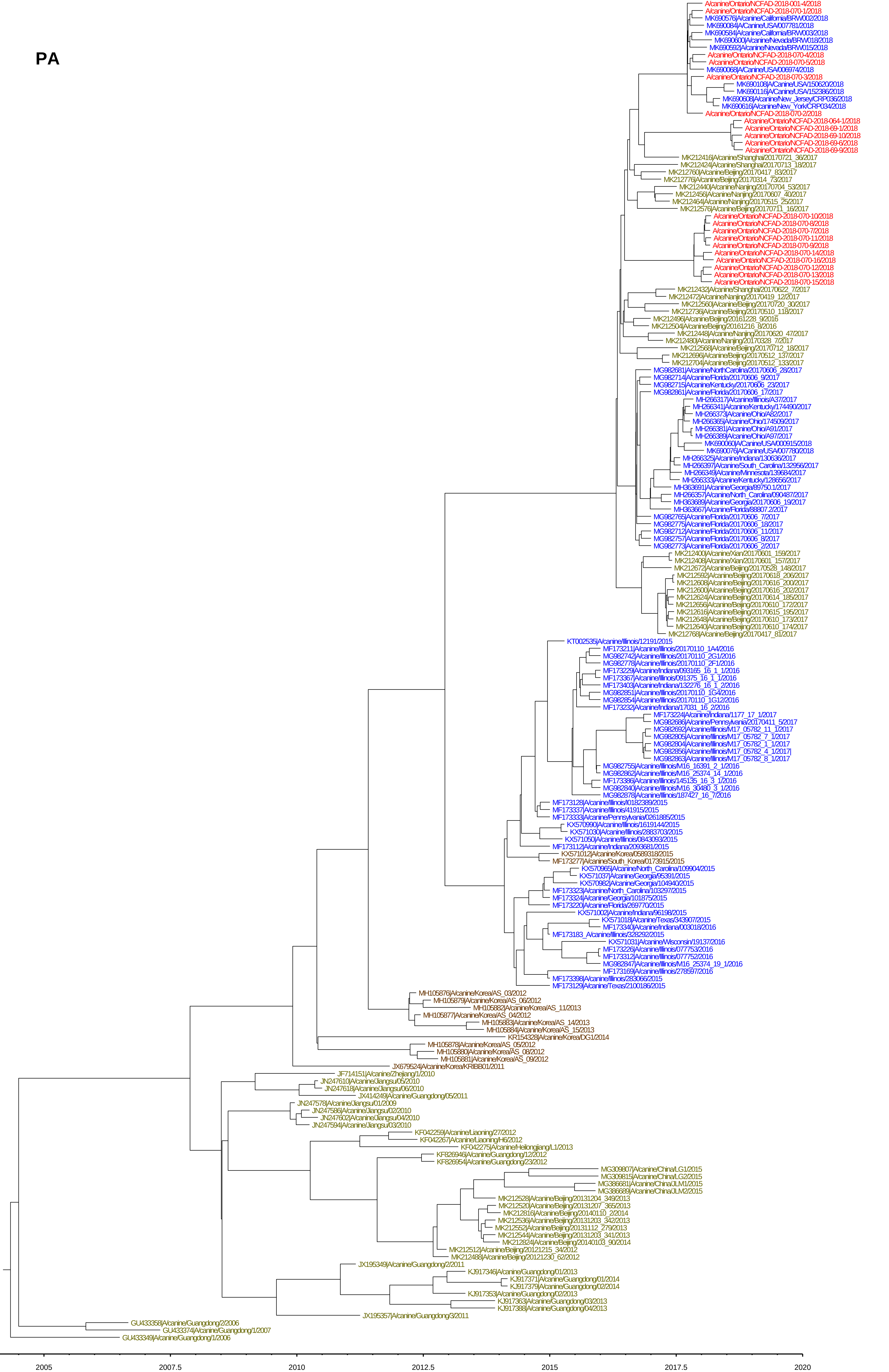
Fig. S3. Maximum clade credibility tree inferred for the individual gene segment of 183 H3N2 CIVs. Sequences are colored according to the country of origin. Red, Canada; blue, the United States; green, China; brown, South Korea.



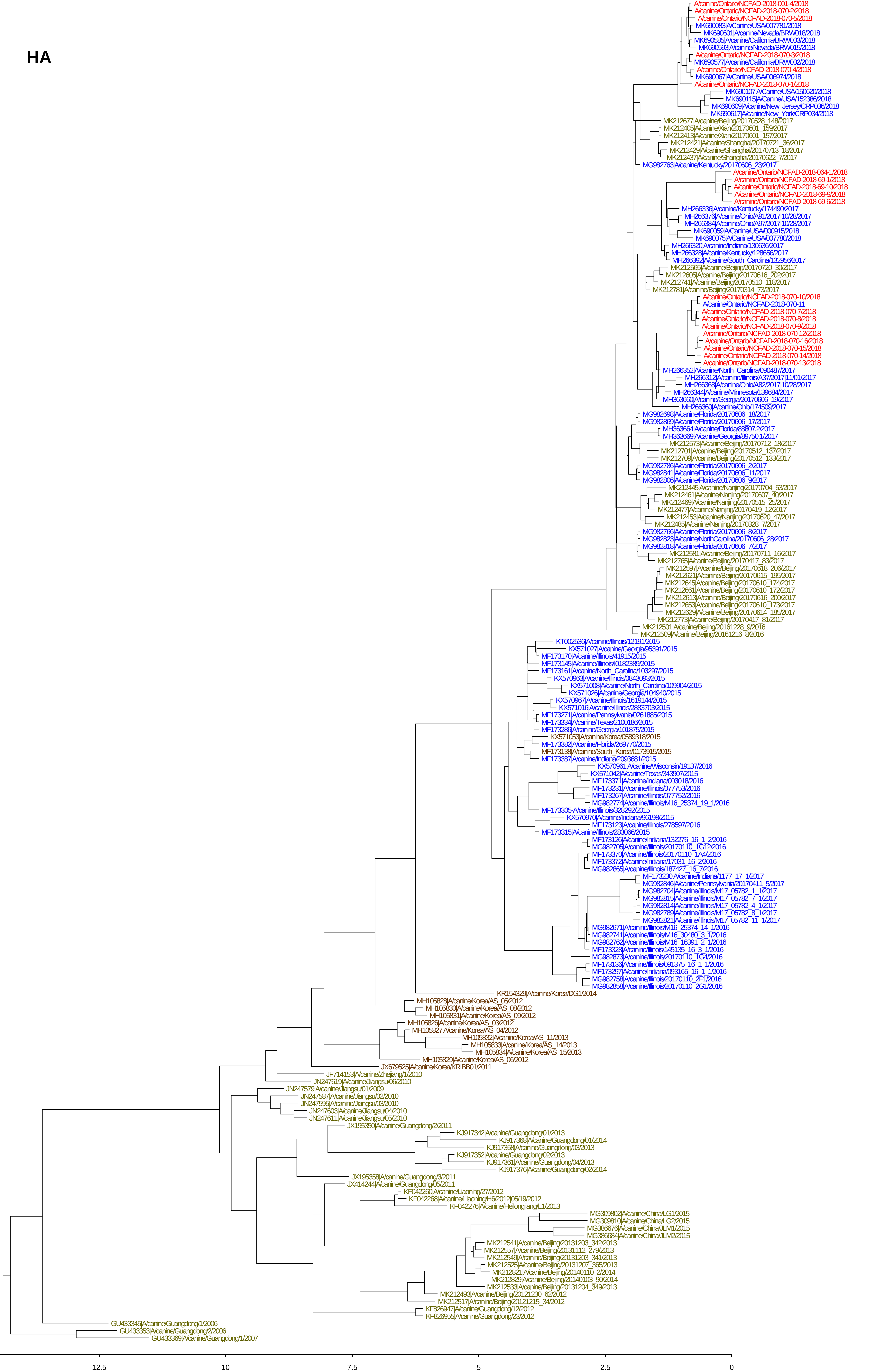
PB1



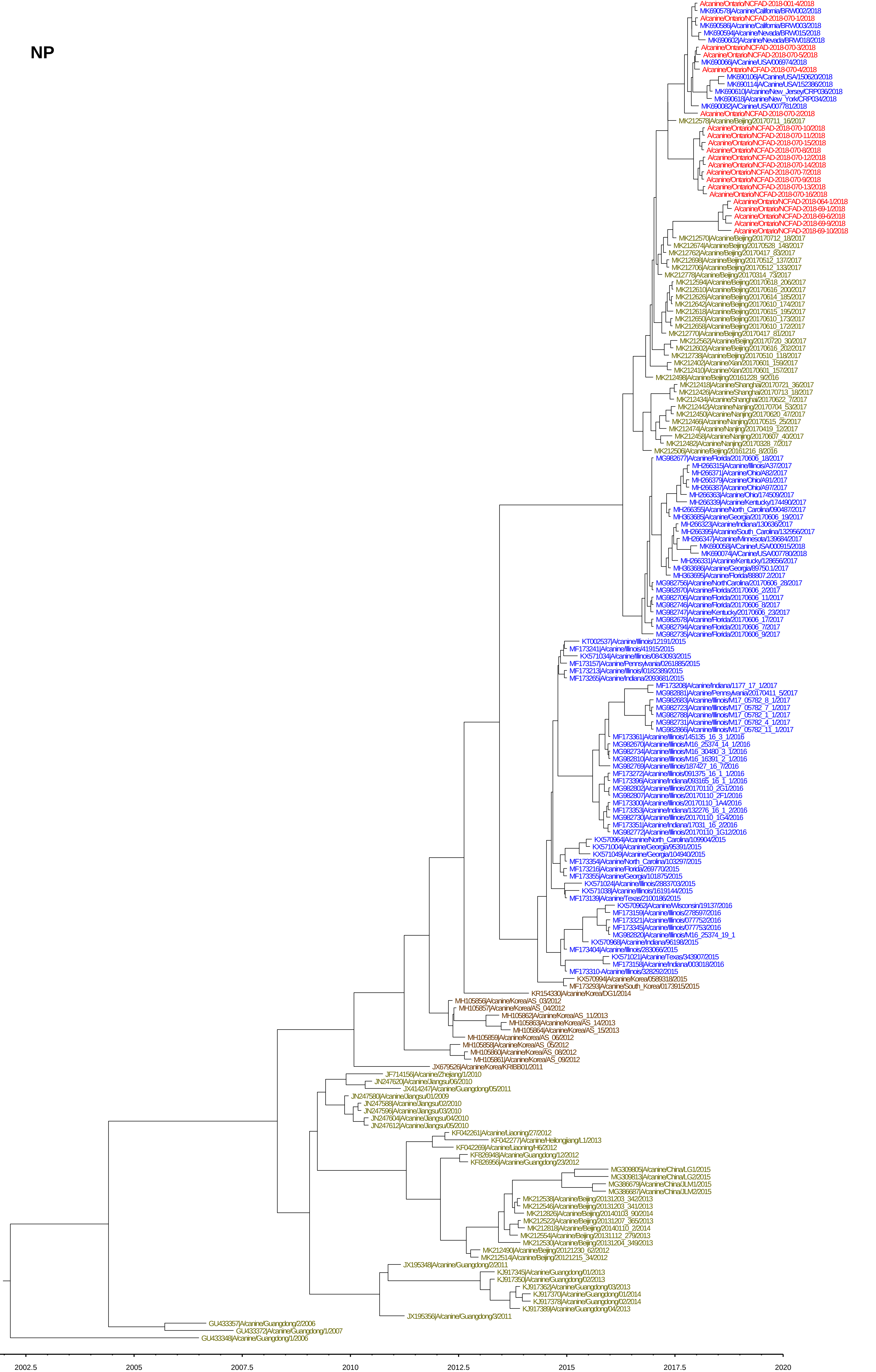
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