

Supplementary data – Hurt et al. Evidence for the introduction, reassortment and persistence of diverse influenza A viruses in Antarctica

Supplementary Figure legends

Supplementary Figure 1. Map of Antarctica and sampling sites on the Antarctic Peninsula.

Supplementary Figure 2. Maximum-likelihood evolutionary tree of H11-HA sequences showing phylogenetic similarity of the H11 virus, A/Snowy sheathbill/Antarctica/2899/2014 (orange branch), detected in 2014, with the H11N2 viruses detected in Adélie penguins in 2013 (red branches).

Supplementary Figure 3. Maximum-likelihood evolutionary tree of MP sequences showing phylogenetic similarity of the H11 virus, A/Snowy sheathbill/Antarctica/2899/2014 (orange branch), detected in 2014, with the H11N2 viruses detected in Adélie penguins in 2013 (red branches).

Supplementary Figure 4. Maximum-likelihood evolutionary tree of NS sequences showing phylogenetic similarity of the H11 virus, A/Snowy sheathbill/Antarctica/2899/2014 (orange branch), detected in 2014, with the H11N2 viruses detected in Adélie penguins in 2013 (red branches).

Supplementary Figure 5. Maximum-likelihood evolutionary tree of 1,370 H5-HA sequences from avian, equine, human and swine viruses. Blue branches represent

North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 6. Maximum-likelihood evolutionary tree of 405 N5-NA sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 7. Maximum-likelihood evolutionary tree of 2,102 PB2 sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 8. Maximum-likelihood evolutionary tree of 2,102 PB1 sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 9. Maximum-likelihood evolutionary tree of 2,102 PA sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 10. Maximum-likelihood evolutionary tree of 2,102 NP sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 11. Maximum-likelihood evolutionary tree of 2,102 MP sequences from avian, equine, human and swine viruses. Blue branches represent

North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 12. Maximum-likelihood evolutionary tree of 2,102 NS sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 13. Dated evolutionary tree of H5-HA sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 14. Dated evolutionary tree of N5-NA sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 15. Dated evolutionary tree of PB2 sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

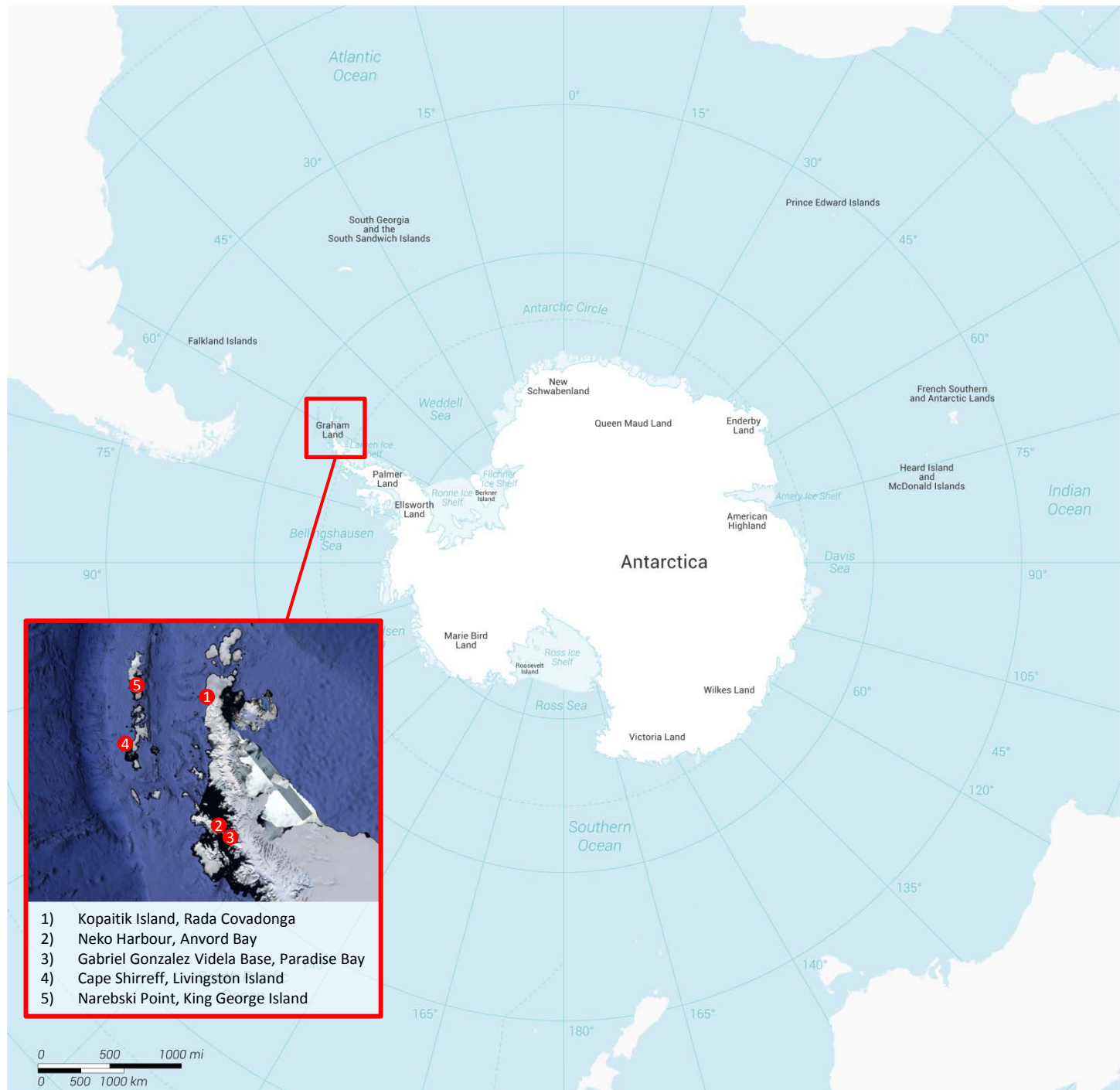
Supplementary Figure 16. Dated evolutionary tree of PB1 sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

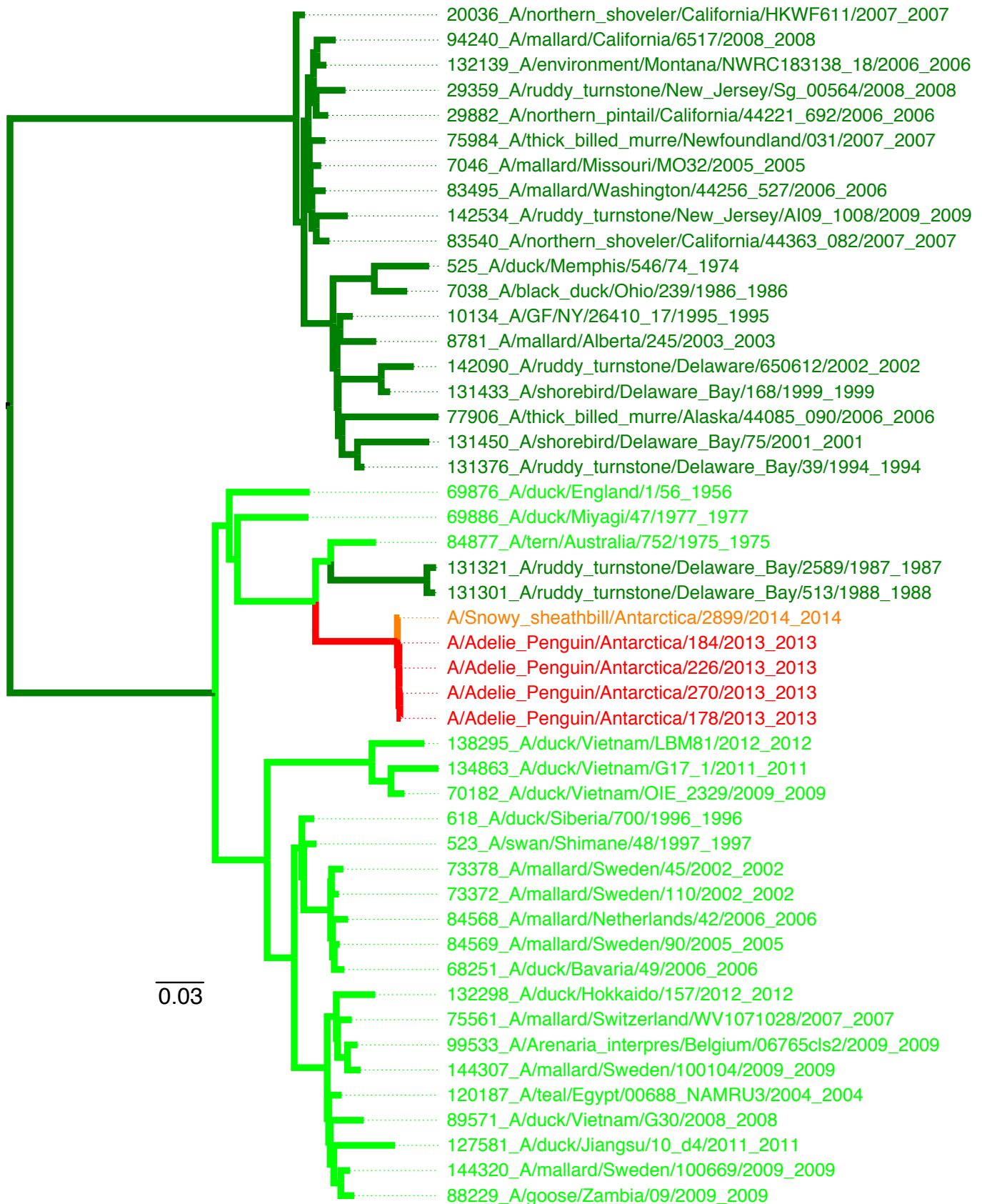
Supplementary Figure 17. Dated evolutionary tree of PA sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 18. Dated evolutionary tree of NP sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 19. Dated evolutionary tree of MP sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.

Supplementary Figure 20. Dated evolutionary tree of NS sequences from avian, equine, human and swine viruses. Blue branches represent North American avian lineages, whereas light green branches denote Eurasian avian lineages.



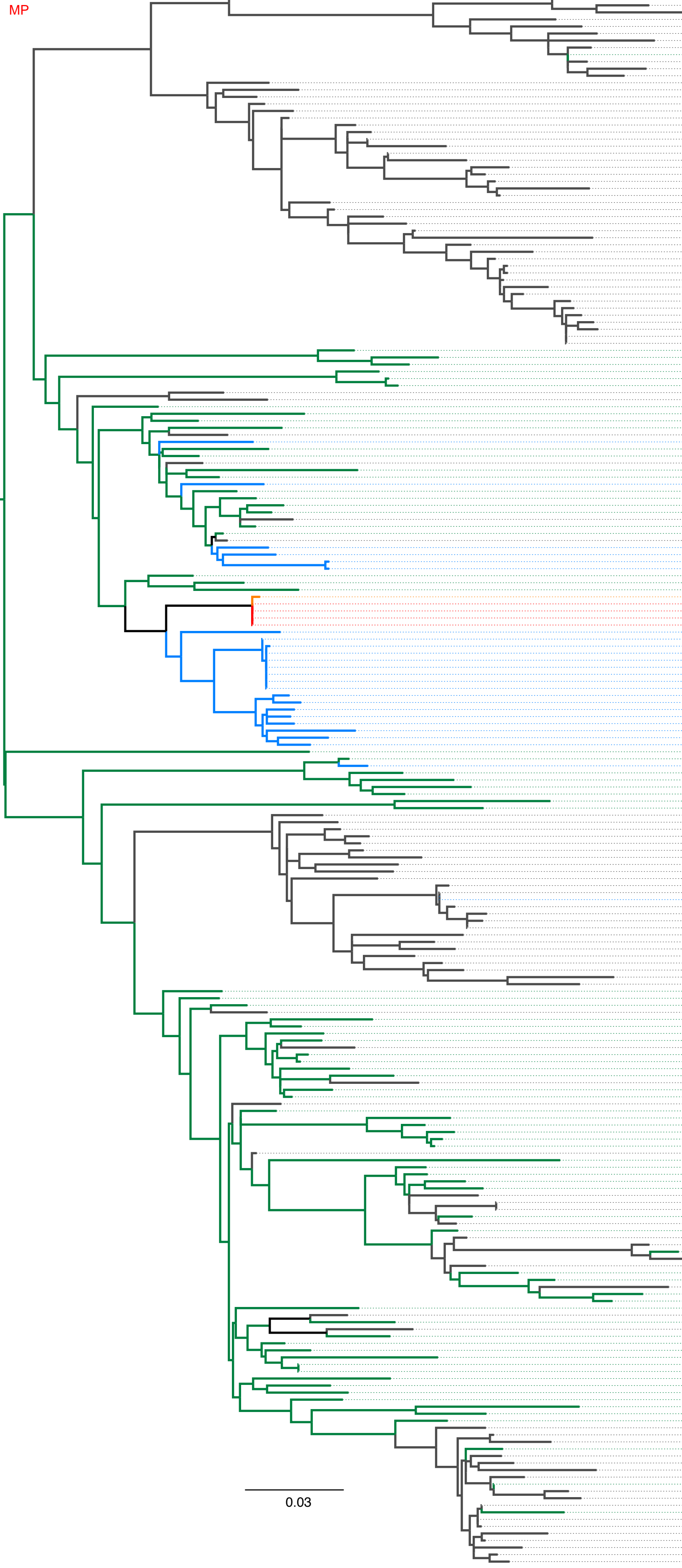


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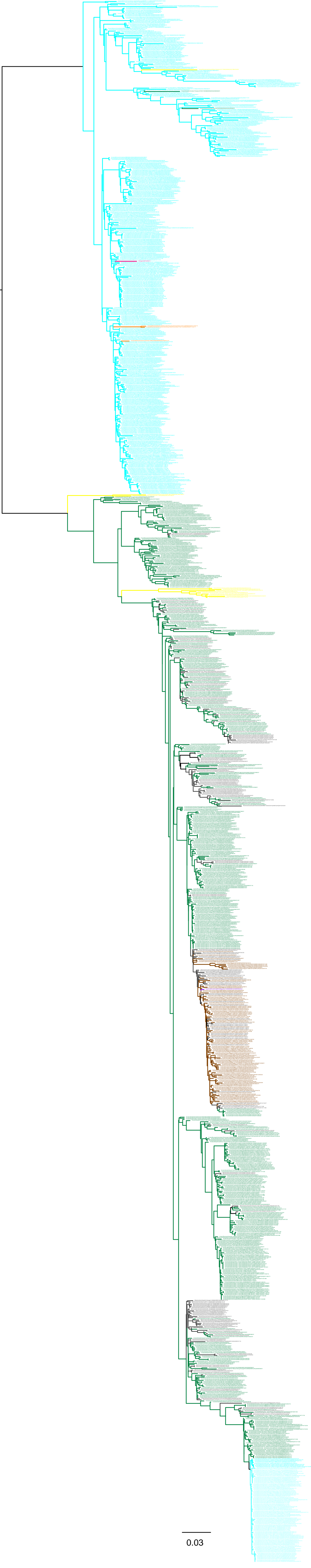
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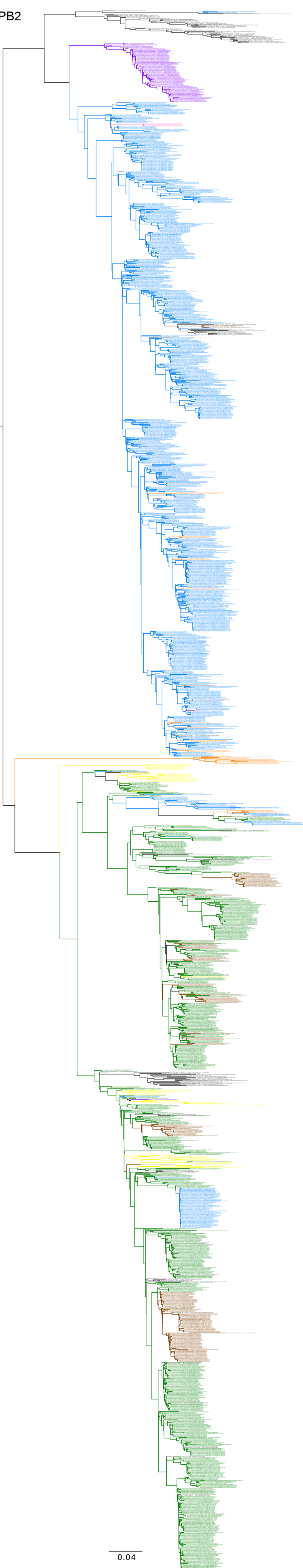
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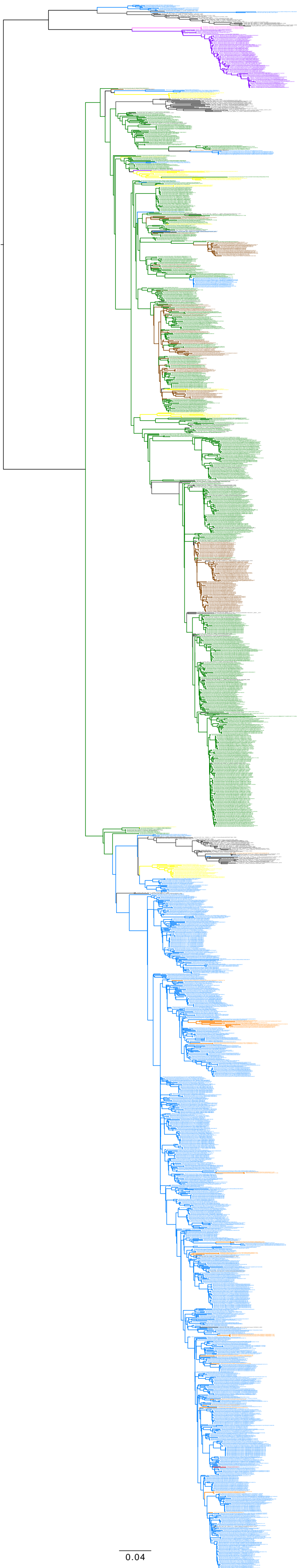


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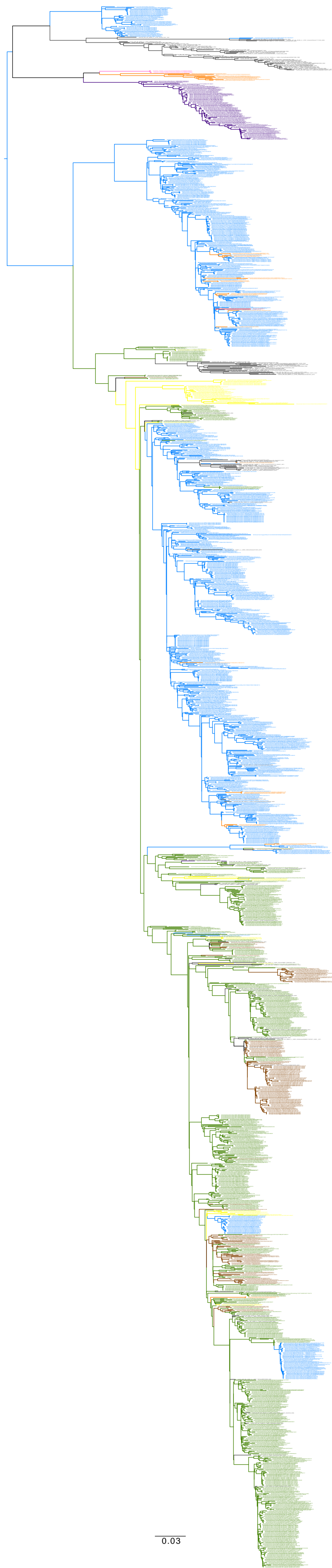


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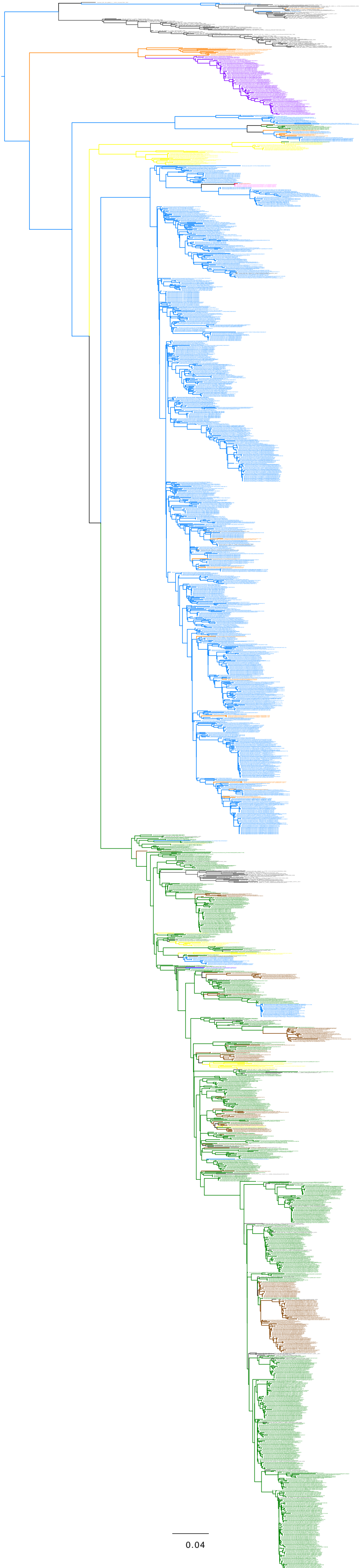
PB1



PA

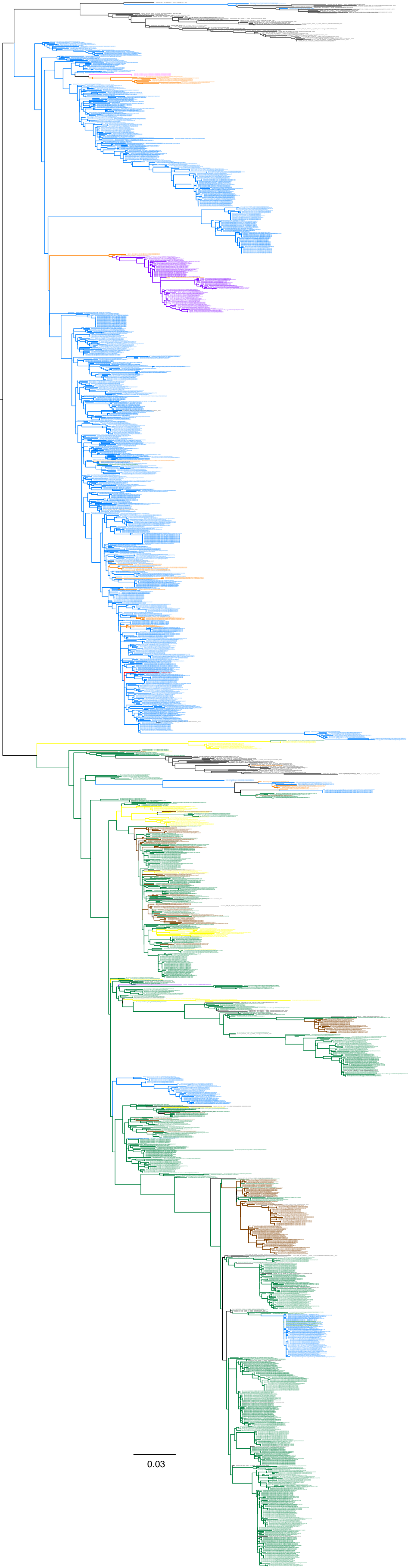


NP

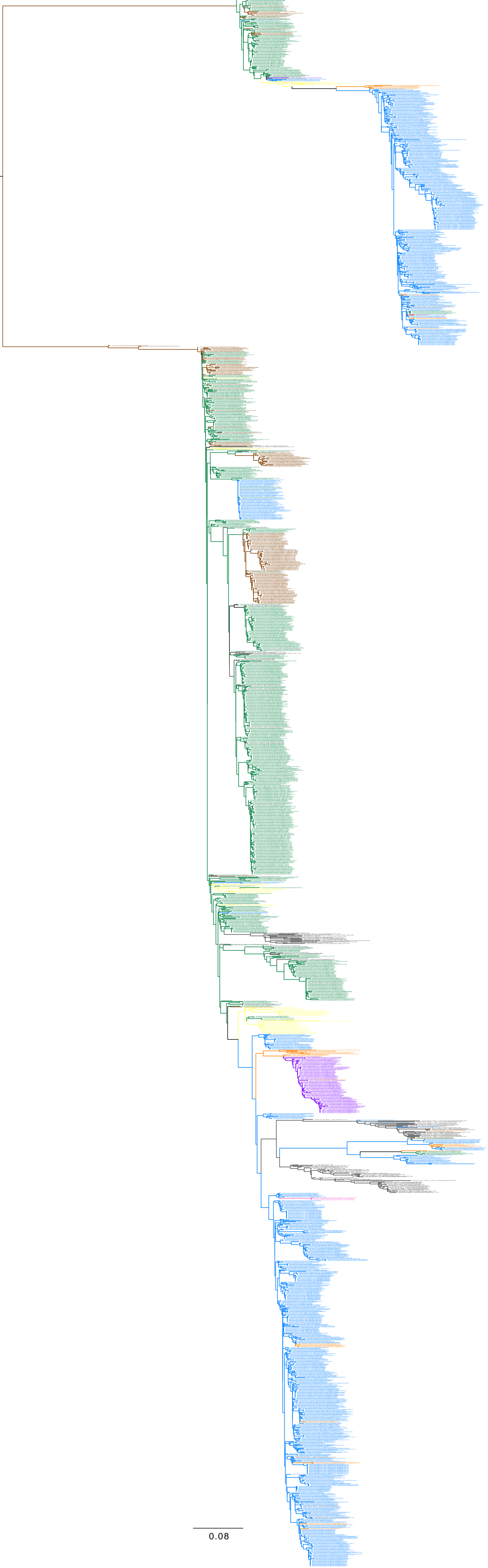


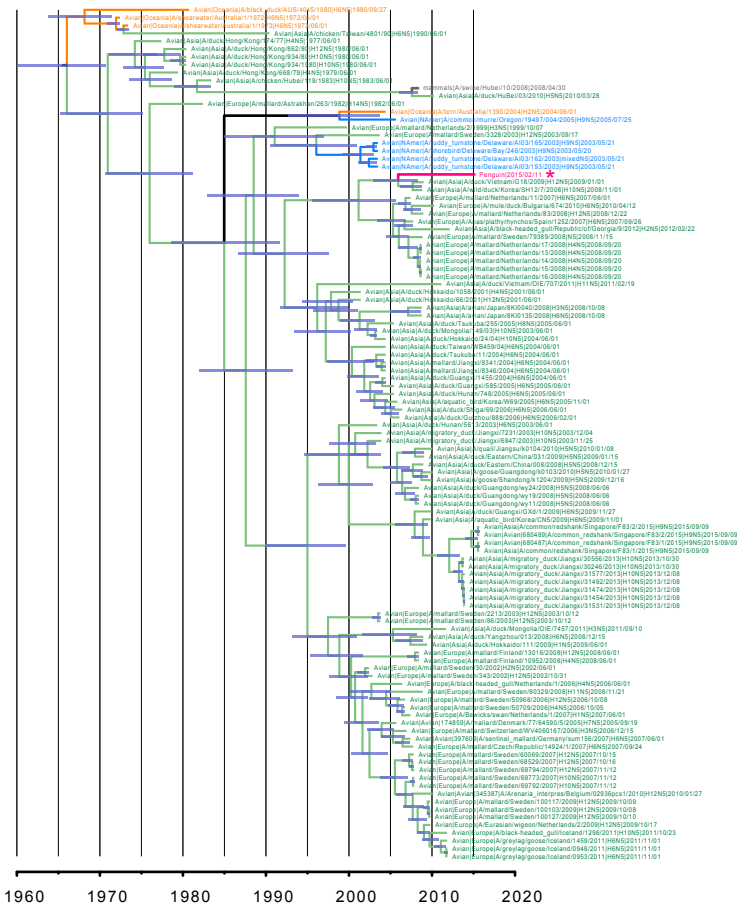
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MP

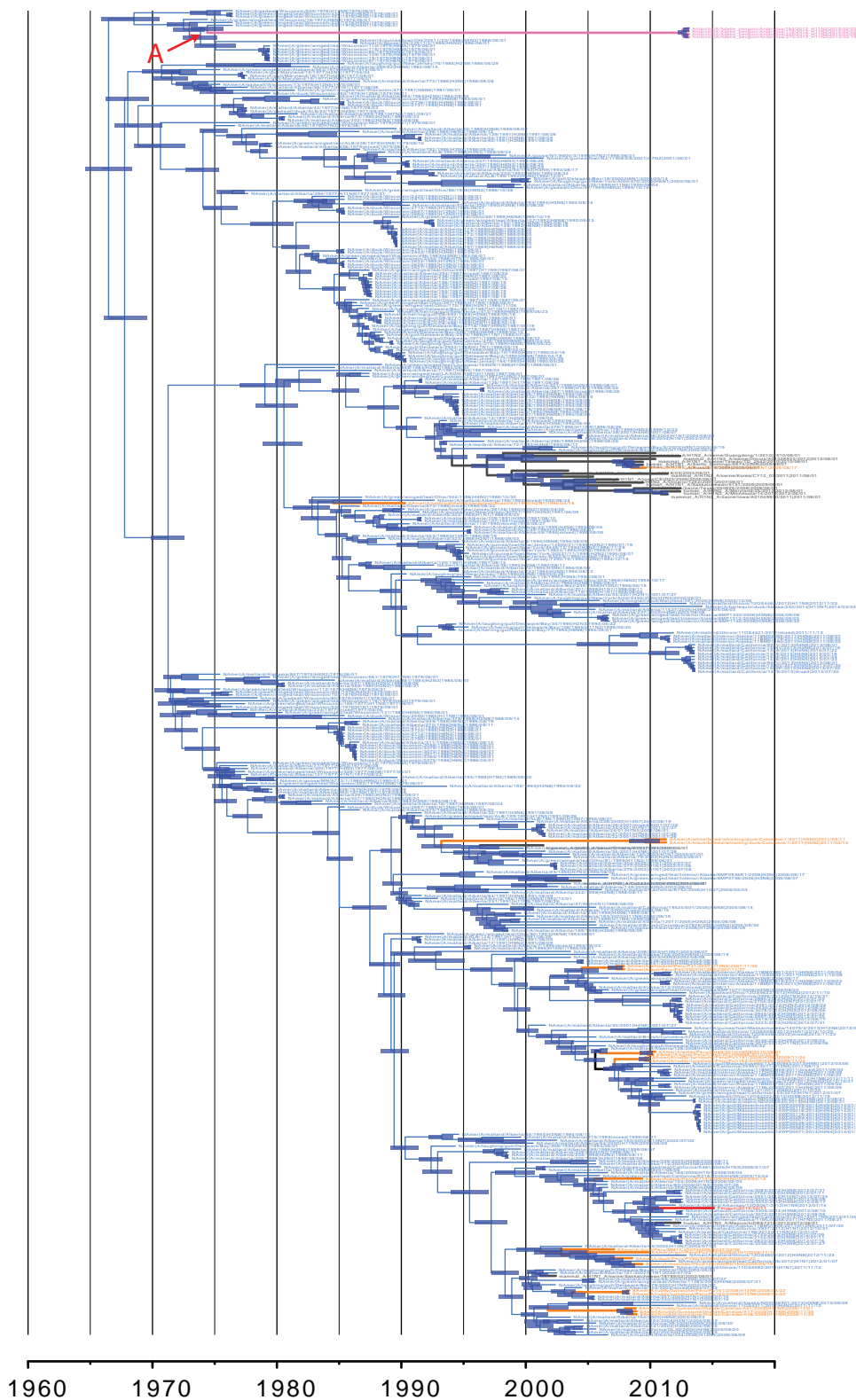


NS

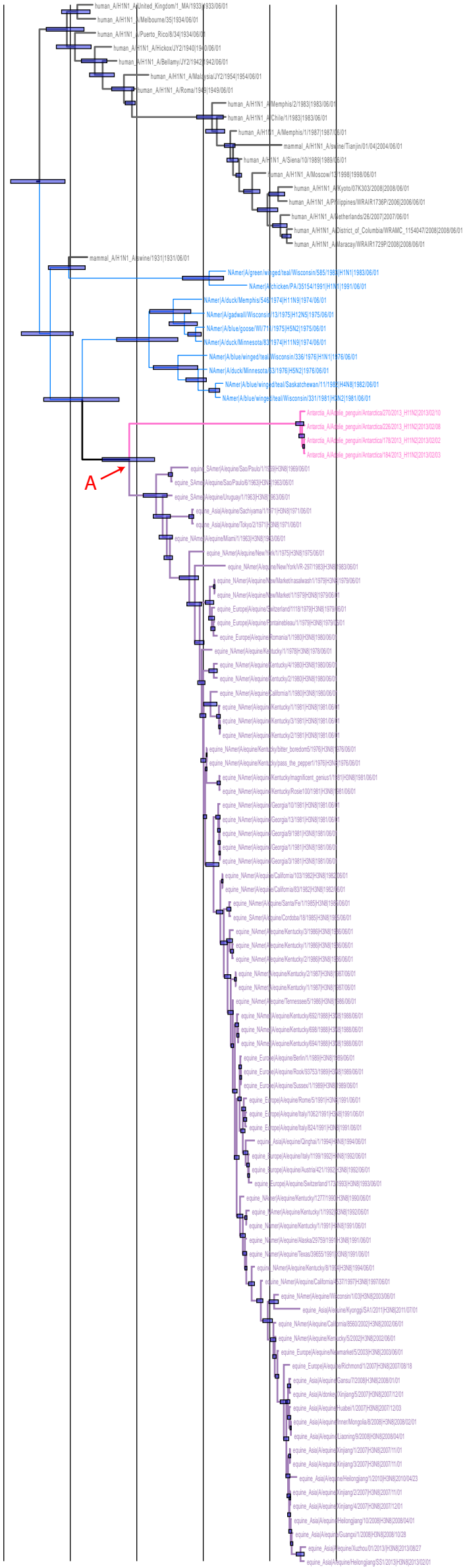




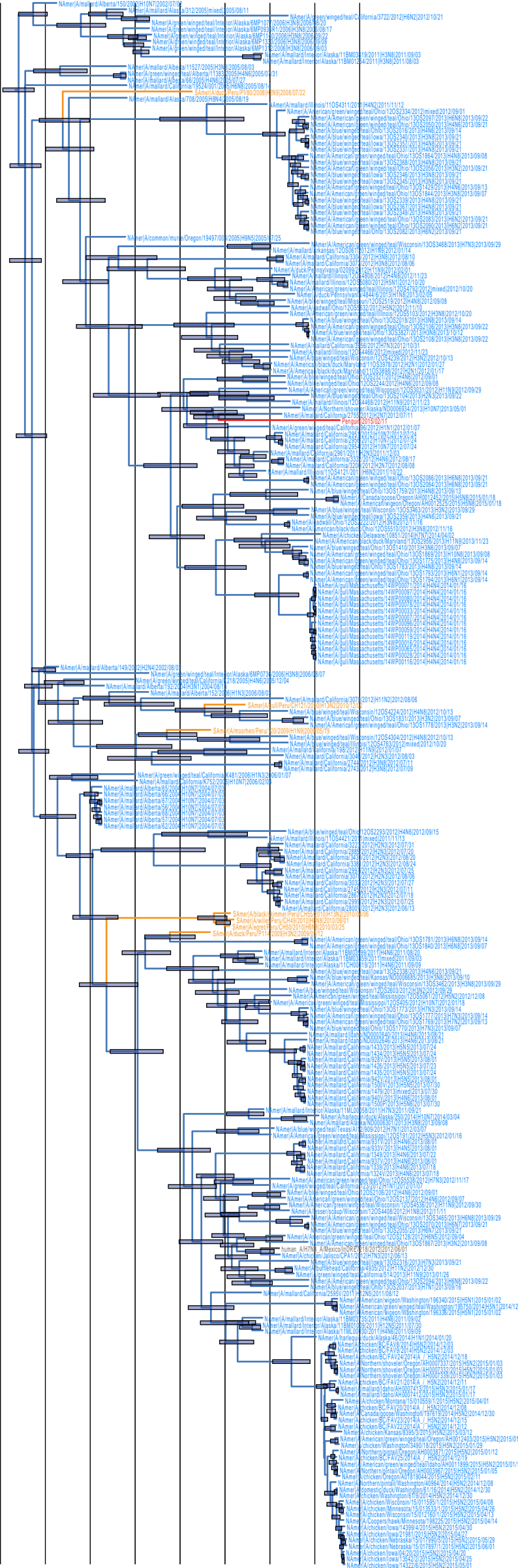
PB2 (penguin H11N2 and novel penguin H5N5)



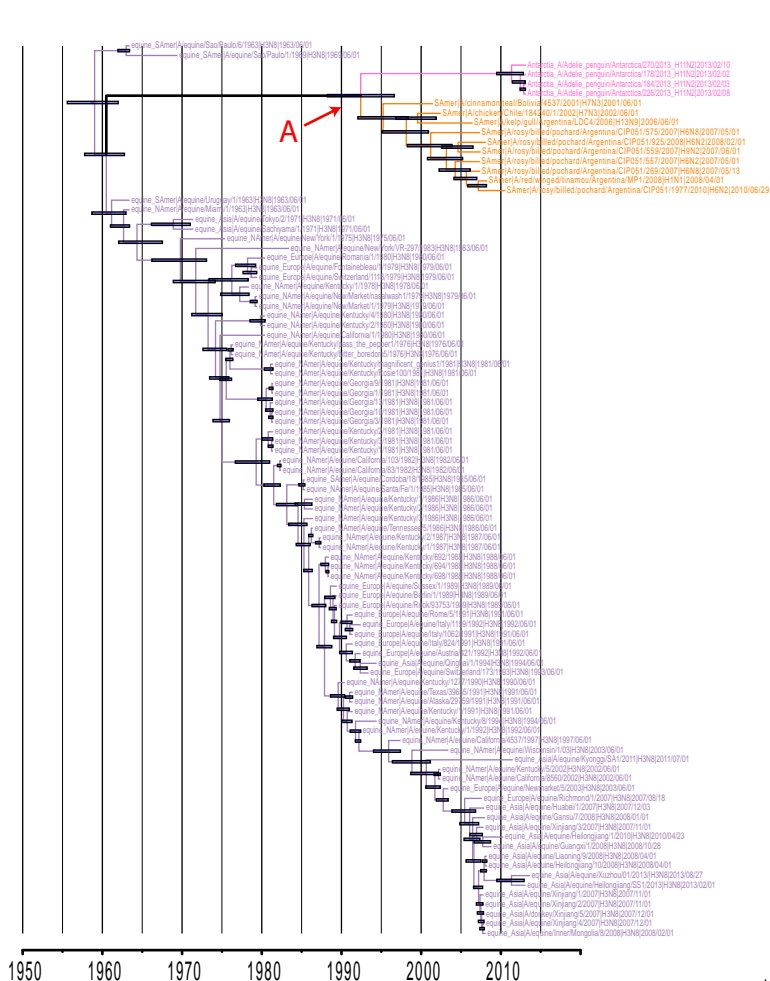
PB1 (penguin H11N2)



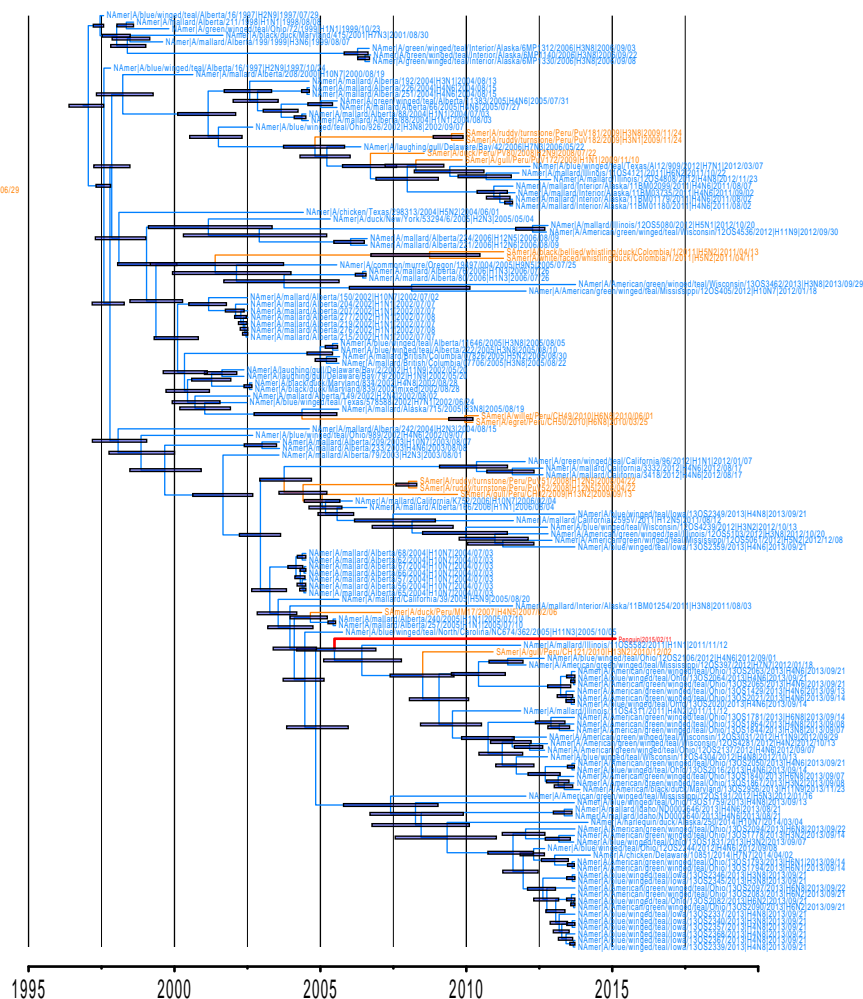
PB1 (novel penguin H5N5)



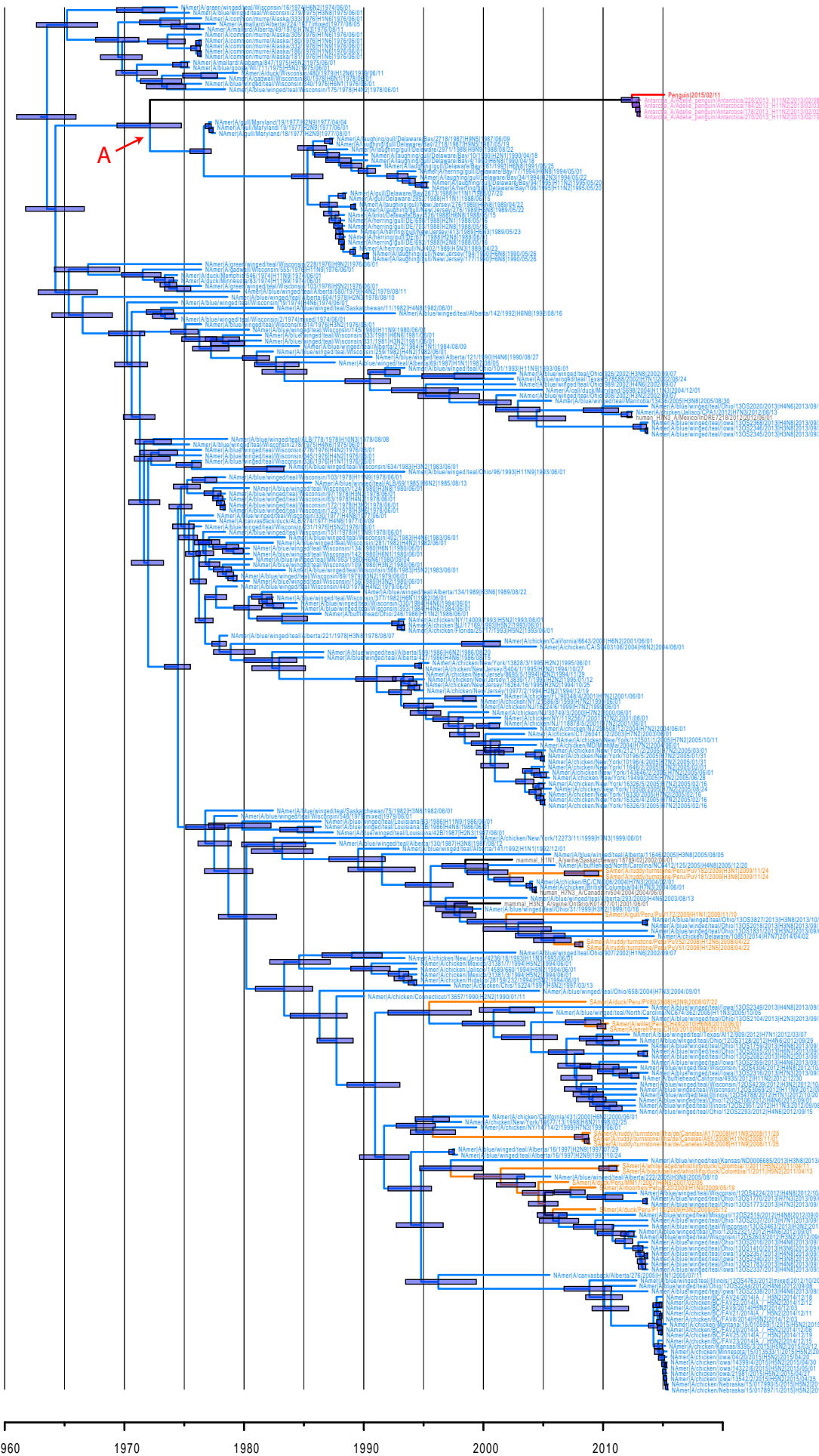
PA (Antarctica H11N2 lineage)



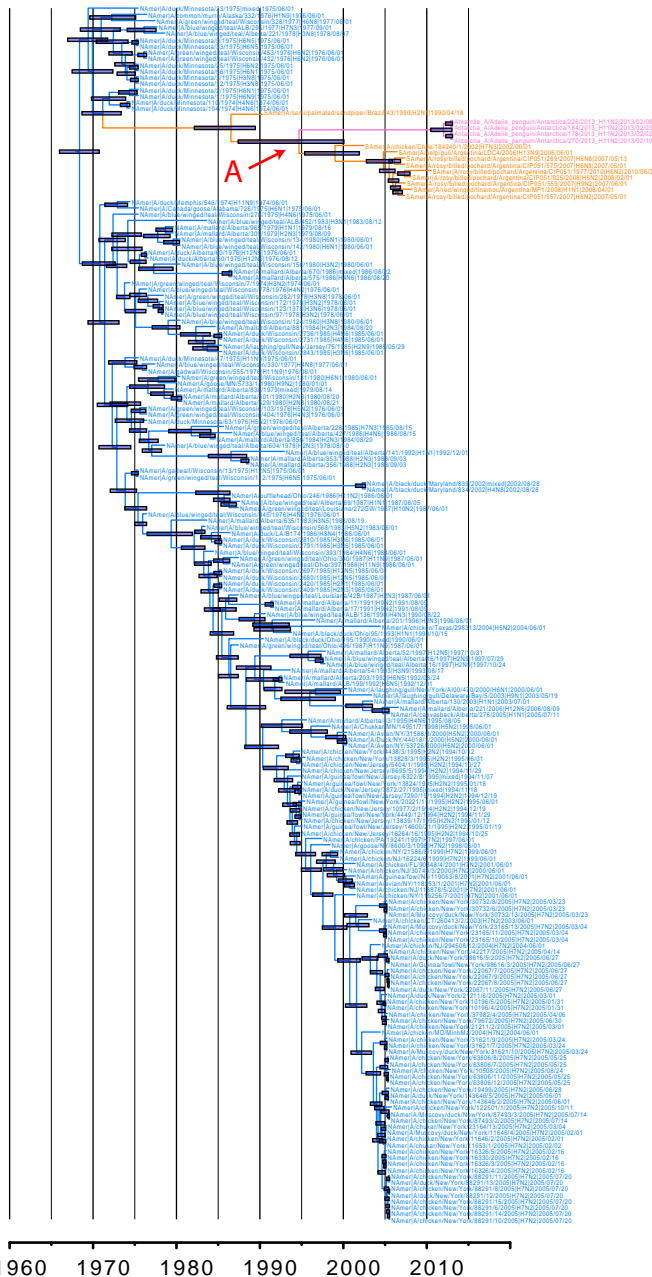
PA (new penguin H5N5)



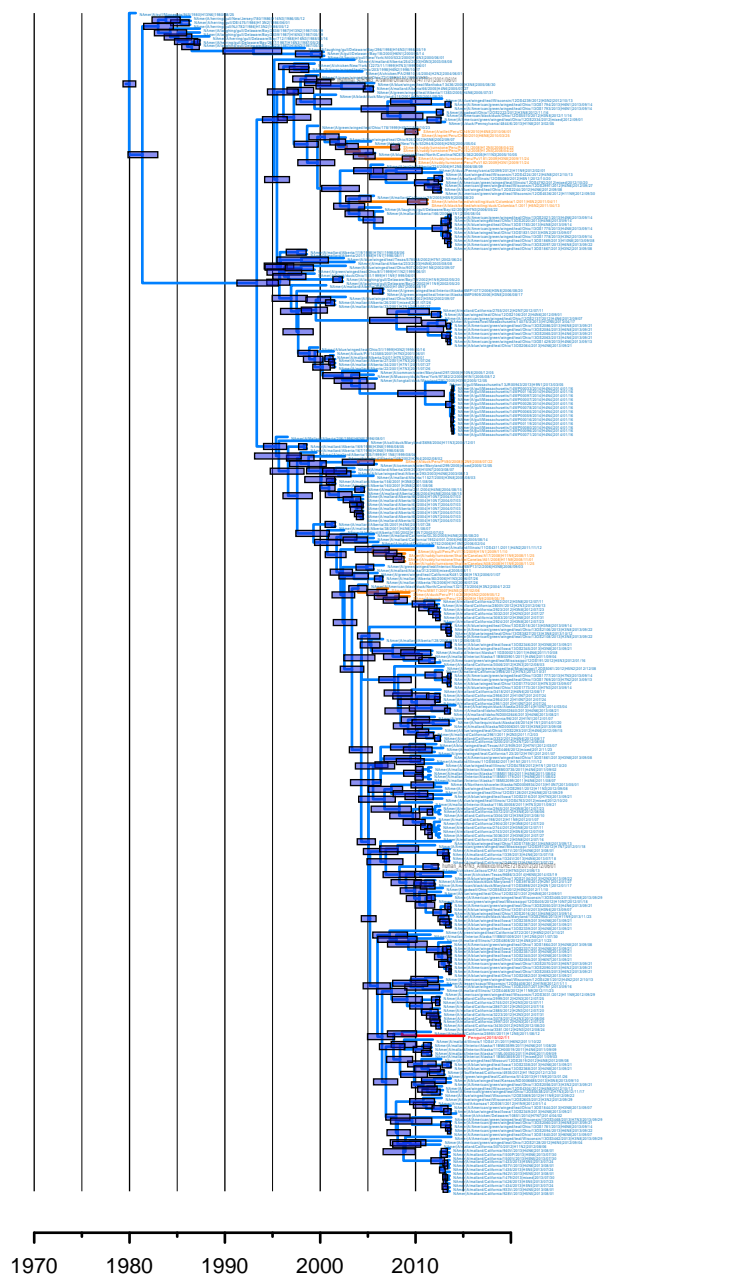
NP (penguin H11N2 and novel penguin H5N5)



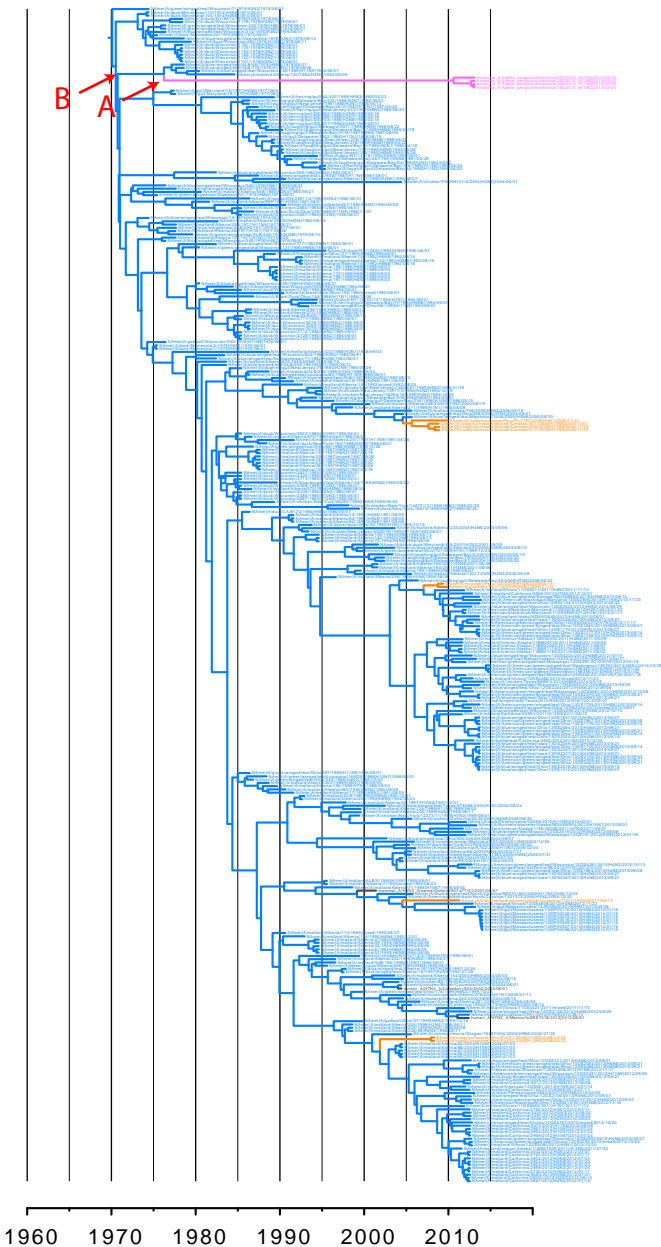
MP (penguin H11N2)



MP (novel penguin H5N5)



NS (penguin H11N2)



NS (novel penguin H5N5)

