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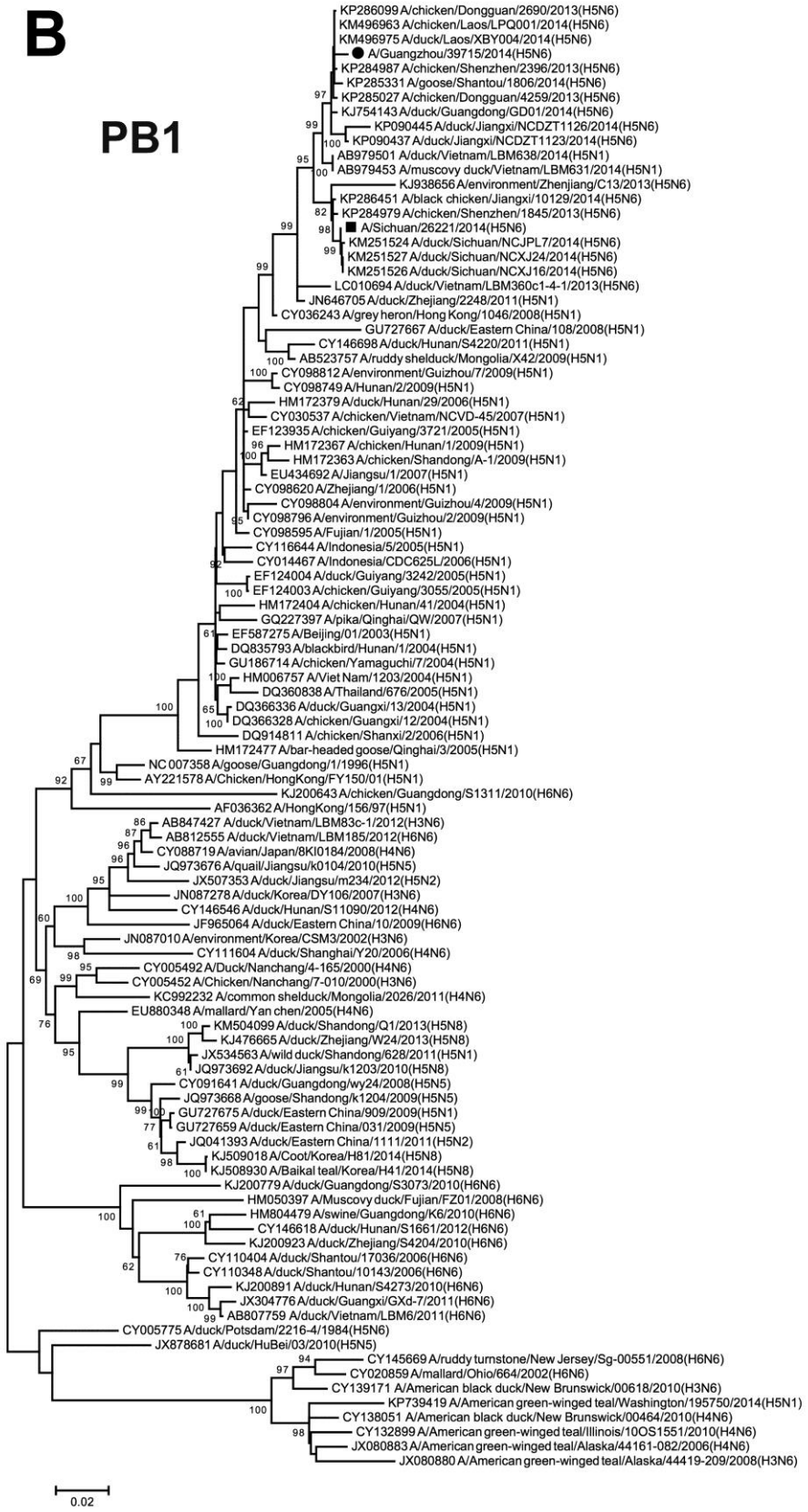
Genetic Characterization of Highly Pathogenic Avian Influenza A(H5N6) Virus, Guangdong, China

Online Technical Appendix 1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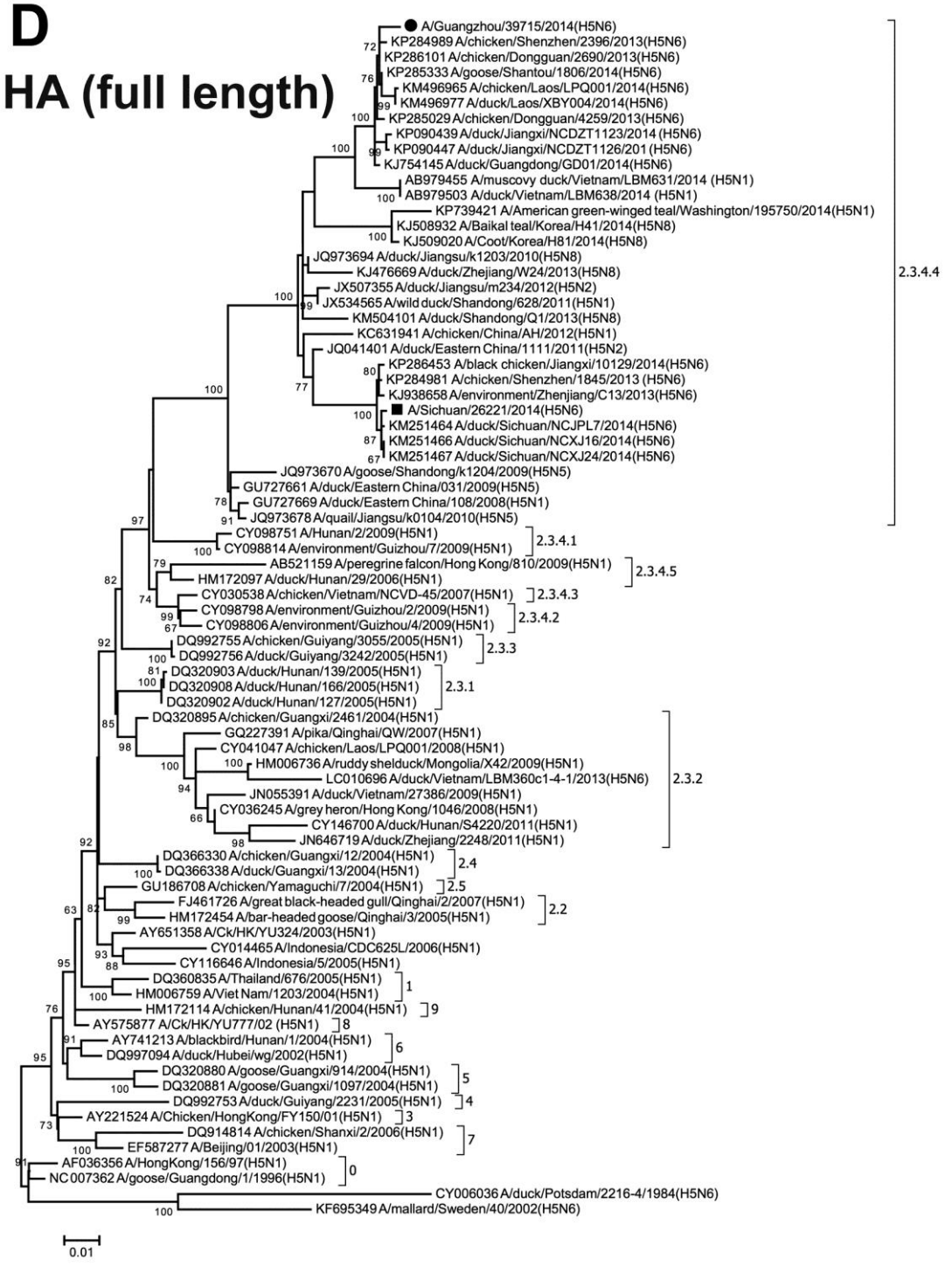
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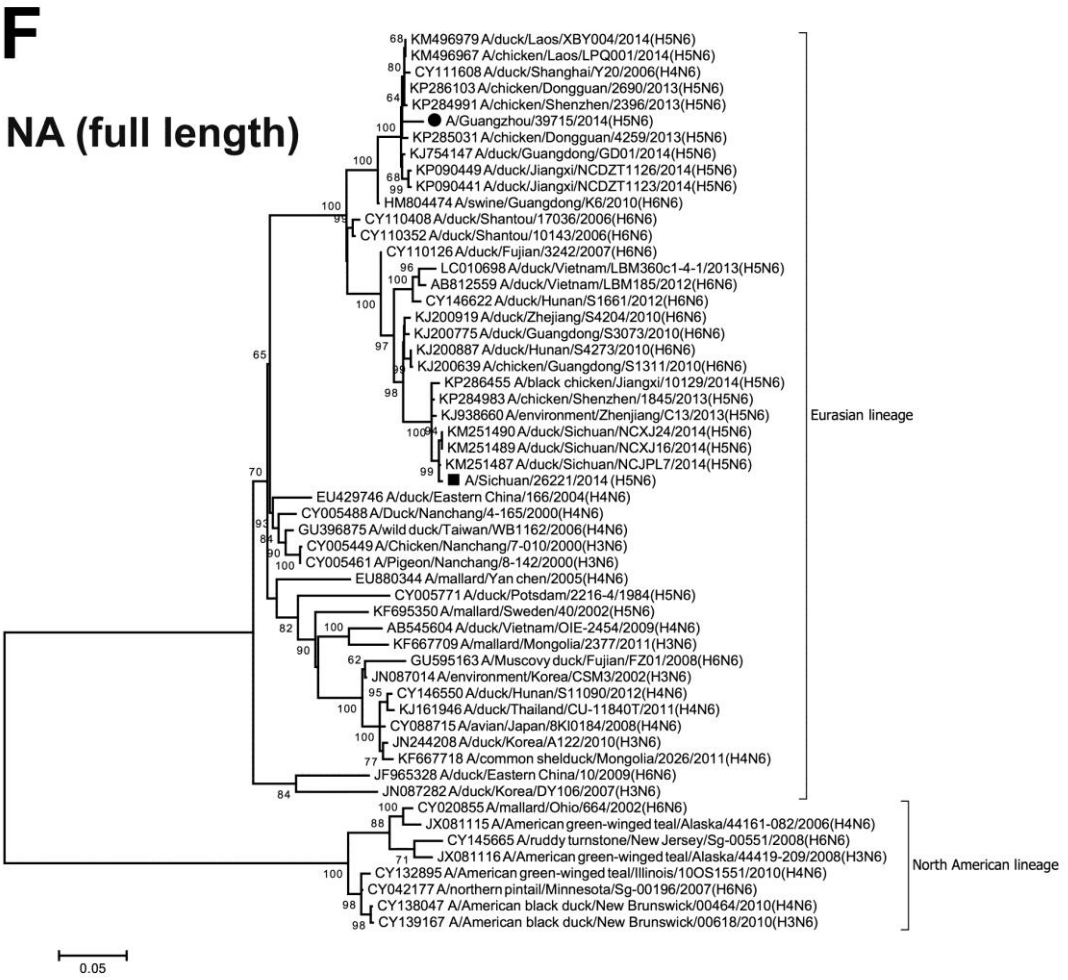
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CY110352 A/duck/Shantou/10143/2006(H6N6)
CY110126 A/duck/Fujian/3242/2007(H6N6)
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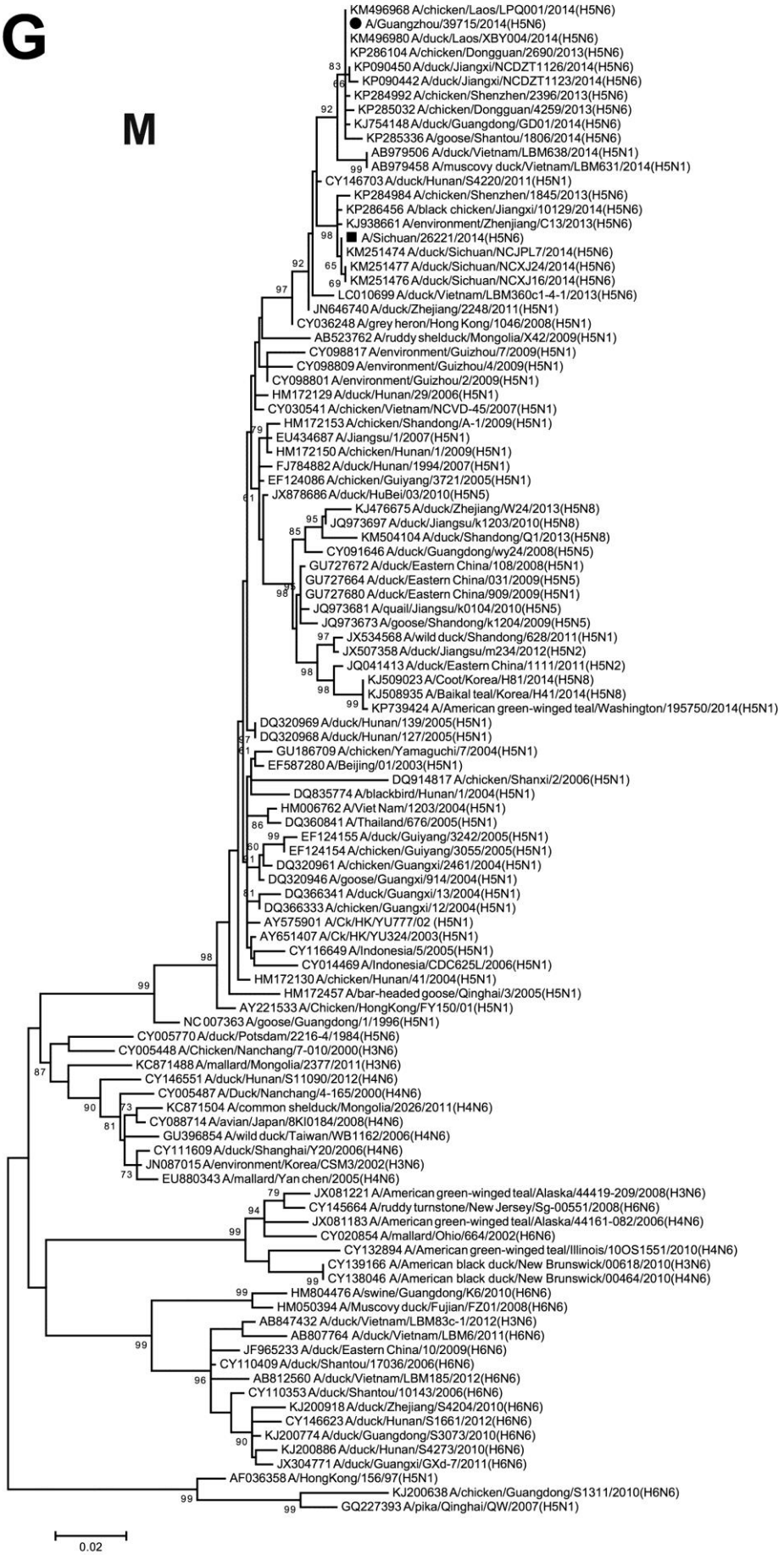
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0.02

Full phylogenetic trees of polymerase basic (PB2) (Technical Appendix Figure 1A), PB1 (Technical Appendix Figure 1B), polymerase acidic (PA) (Technical Appendix

Figure 1C), hemagglutinin (HA) (Technical Appendix Figure 1D), nucleoprotein (NP) (Technical Appendix Figure 1E), neuraminidase (NA) (Technical Appendix Figure 1F), M (Technical Appendix Figure 1G), and nonstructural (NS) (Technical Appendix Figure 1H) genes. Maximum-likelihood trees were constructed by using the general time reversible + gama distribution + invariant sites (GTR + Γ + I) model in MEGA 6.06 (http://www.megasoftware.net). Bootstrap values were calculated on 1,000 replicates; only values >60% are shown. A/Guangzhou/39715/2014 and A/Sichuan/26221/2014 are marked by a circle and a square, respectively. Scale bars indicate nucleotide substitutions per site.