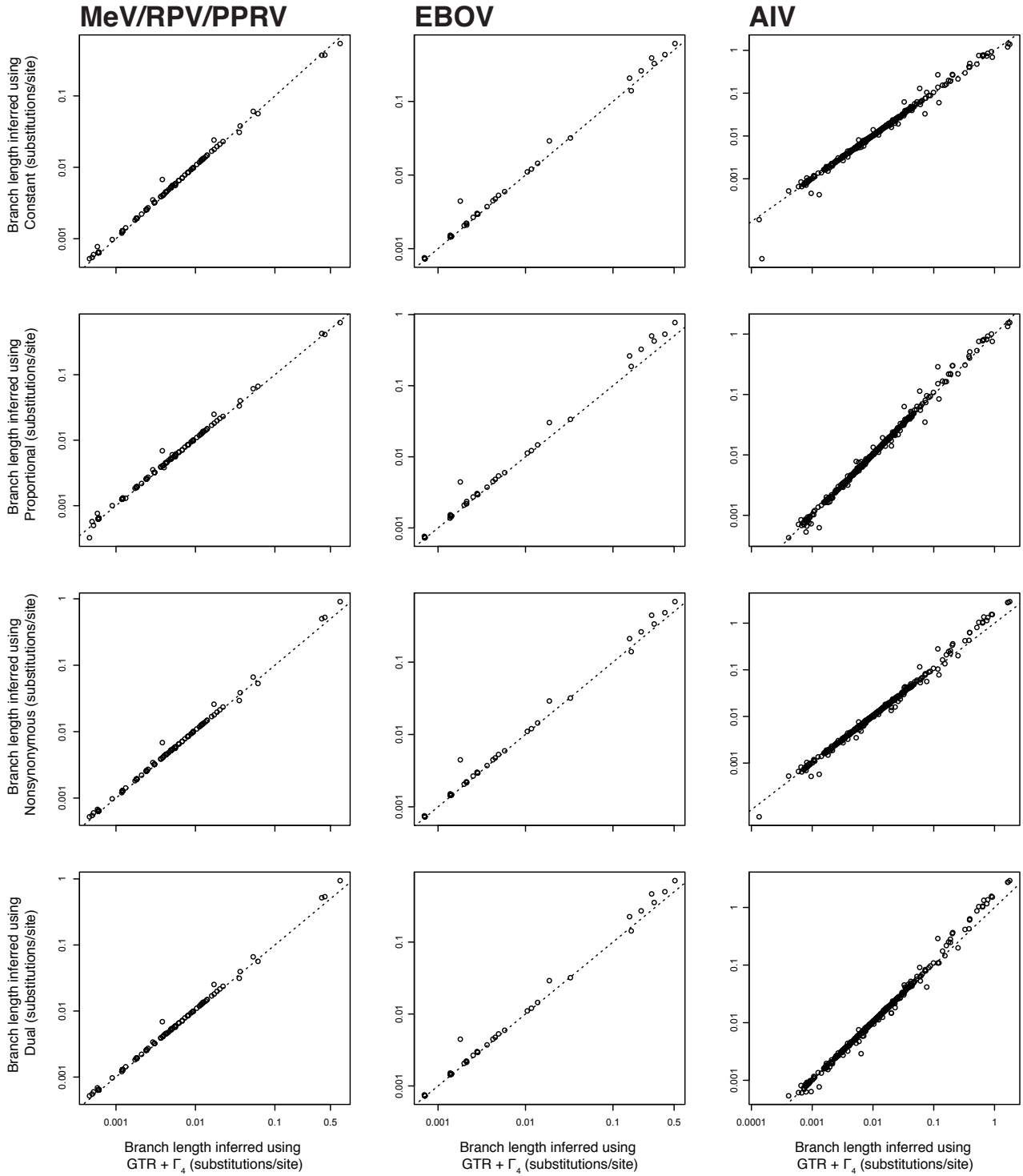SUPPLEMENTARY MATERIAL

FIG. S1.—Effect evolutionary models that differ in their treatment of rate variation on branch length estimates relative to GTR + Γ_4. Each datapoint represents the length of a single branch of the measles/rinderpest/peste-des-petits ruminants virus (MeV/RPV/PPRV), Ebola virus (EBOV), or avian influenza virus (AIV) phylogeny. Dashed lines are an x = y reference.
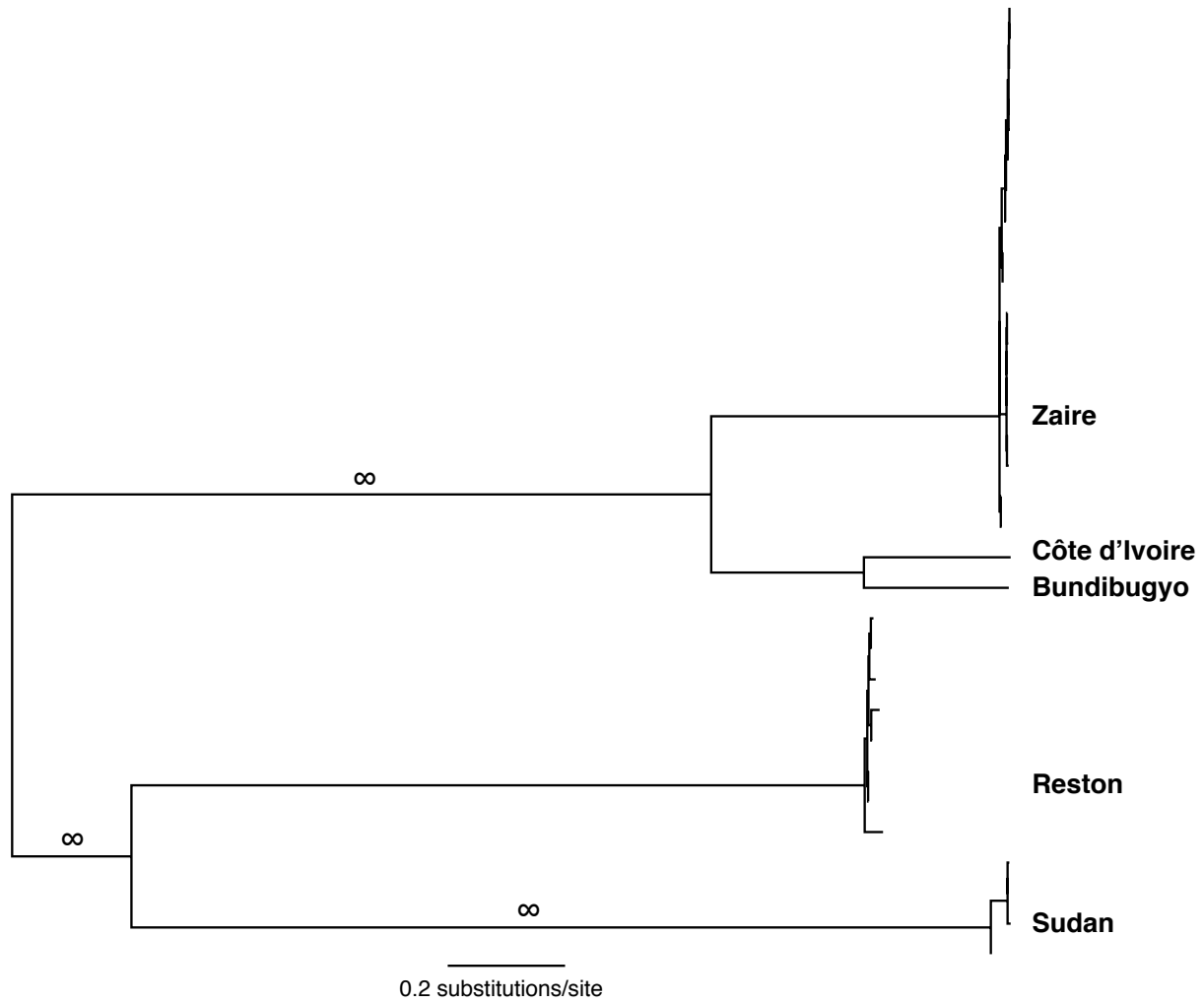
Zaire

∞

Côte d'Ivoire

Bundibugyo

∞

Reston

∞

Sudan

0.2 substitutions/site

Fɪɢ. S2.—Maximum clade credibility phylogeny for Ebola virus glycoprotein gene with branch lengths inferred under Dual+Lineage (8-rate) model. Branch lengths with near saturation at synonymous sites are rescaled for ease of viewing and marked as infinity. Ebola subtypes are labeled. Tree is rooted according to the GTR + Γ_4 topology.
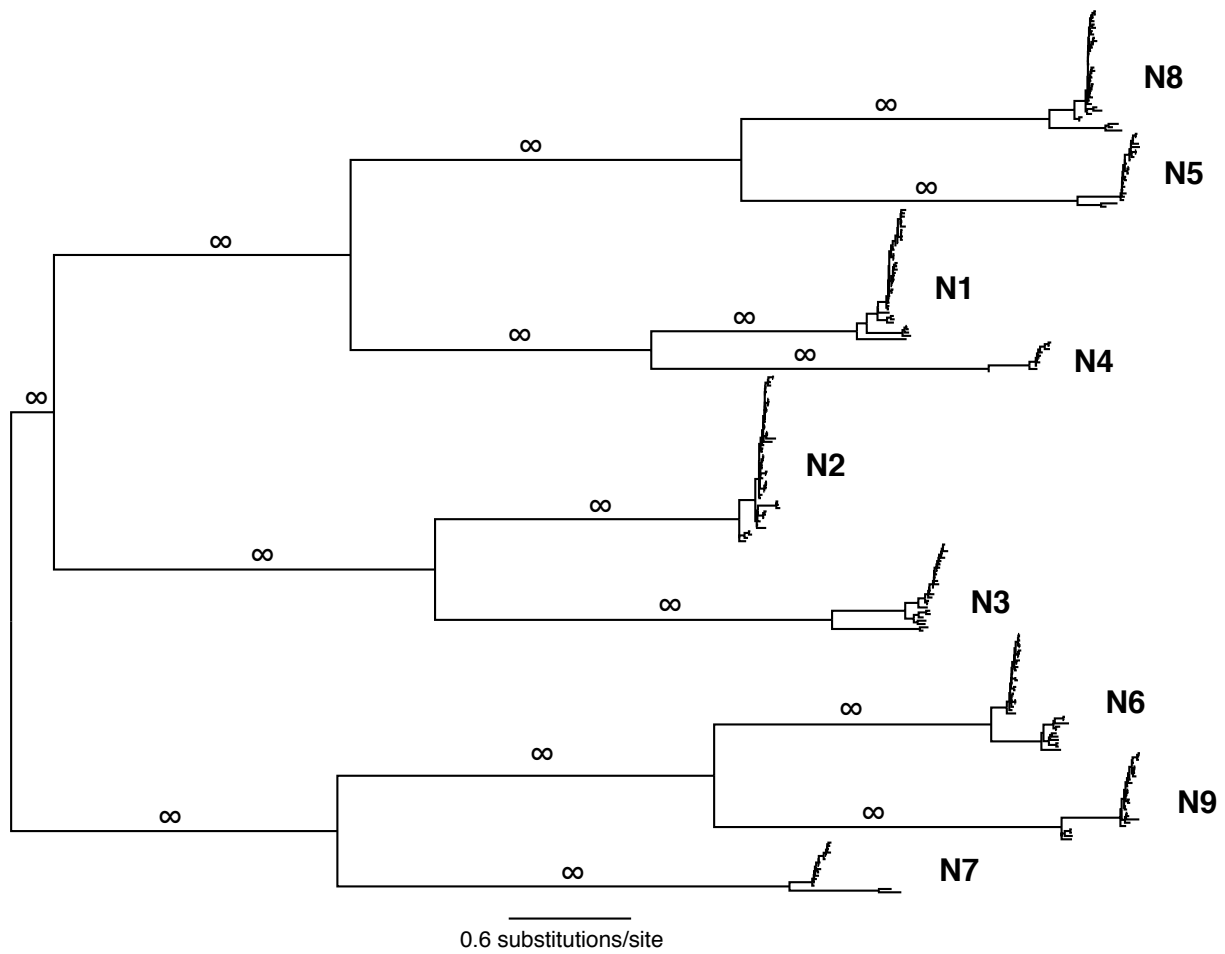
FIG. S3.—Maximum clade credibility phylogeny for avian influenza virus neuraminidase gene with branch lengths inferred under Dual+Lineage (2-rate) model. Branch lengths with near saturation at synonymous sites are rescaled for ease of viewing and marked as infinity. Avian influenza virus neuraminidase serotypes are labeled. Tree is rooted according to the GTR + Γ_4 topology.