Supplementary Figure

Bones hold the key to DNA virus history and epidemiology

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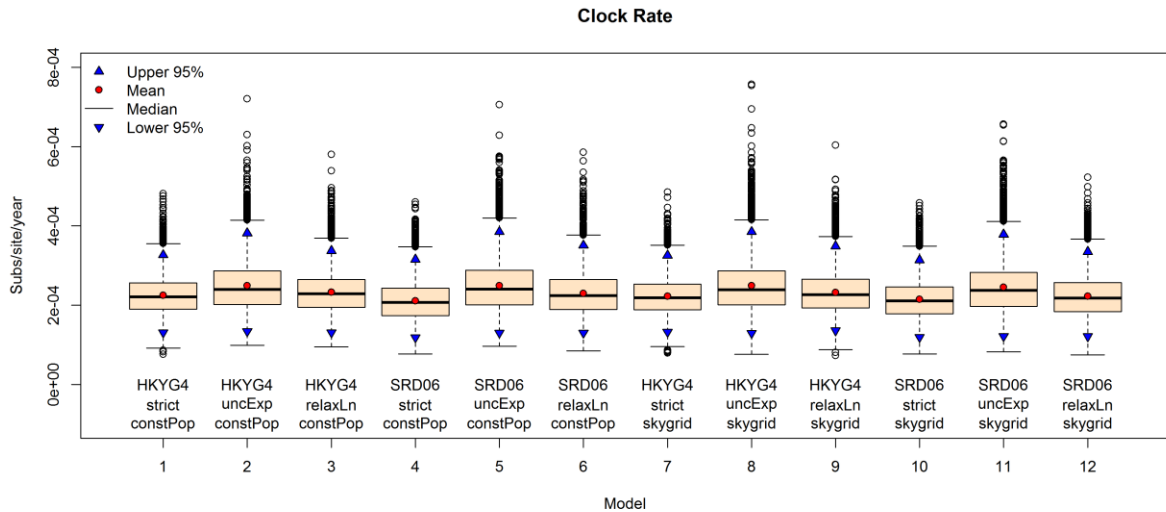
Supplementary Fig. S1. **Overall clock rate estimates for Genotype 1, 2 & 3 using several models with BEAST**. Clock models tested were the strict clock ('strict', models 1, 4, 7, 10); uncorrelated exponential clock ('uncExp', models 2, 6, 8, 11); and uncorrelated relaxed lognormal clock ('relaxLn', models 3, 6, 9, 12). Models 1-3, and 7-9 additionally use the HKY nucleotide substitution model with site to site rate variation (HKYG4) and models 4-6 and 10-12 use the SRD06 codon partitioned substitution model. Models 1-6 also use a constant population coalescent model ('constPop'), whereas models 7-12 use a Skygrid flexible effective population size prior model with 10 bins over 300 years ('skygrid'). The model quoted in the main text is model 4, with the SRD06 substitution model, strict clock and constant population size.