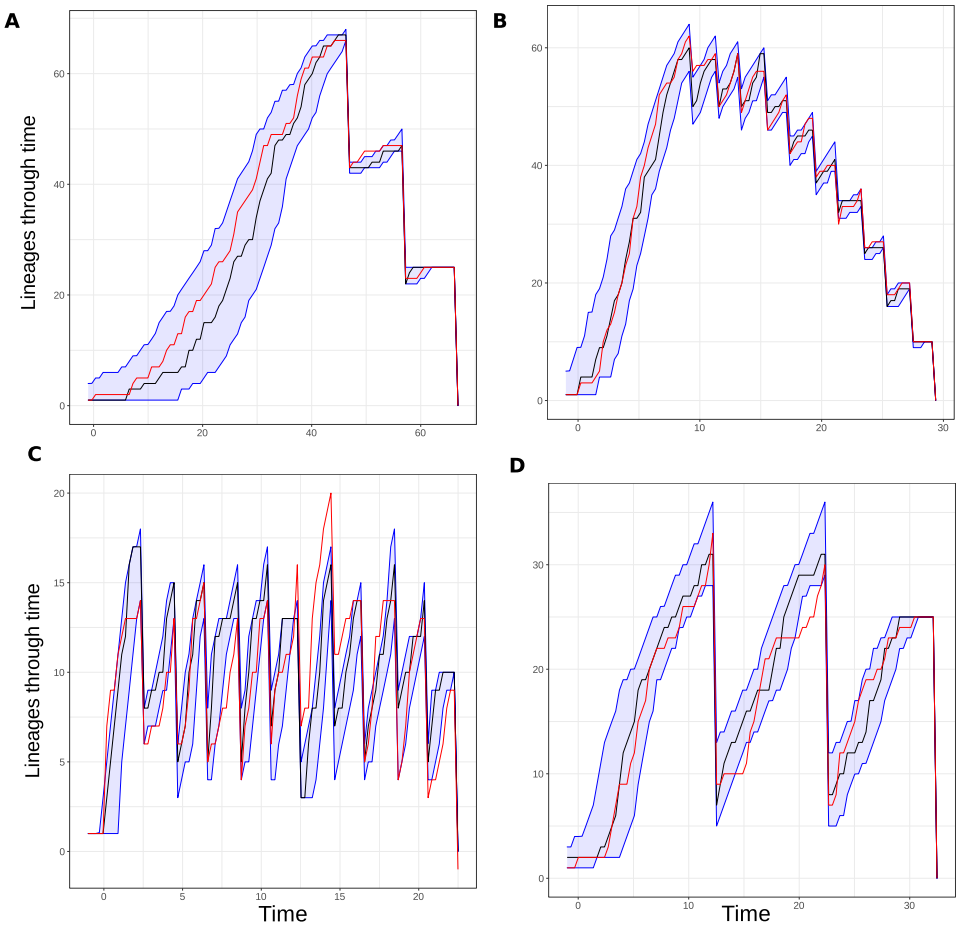

Figure S1: Estimated (black) and true (red) lineages through time for four simulation scenarios in (To et al., 2015) . Plots A-D correspond to different simulation scenarios corresponding to labels 750_3_25, 750_11_10, 995_3_25, and 995_11_10 in (To et al., 2015) .

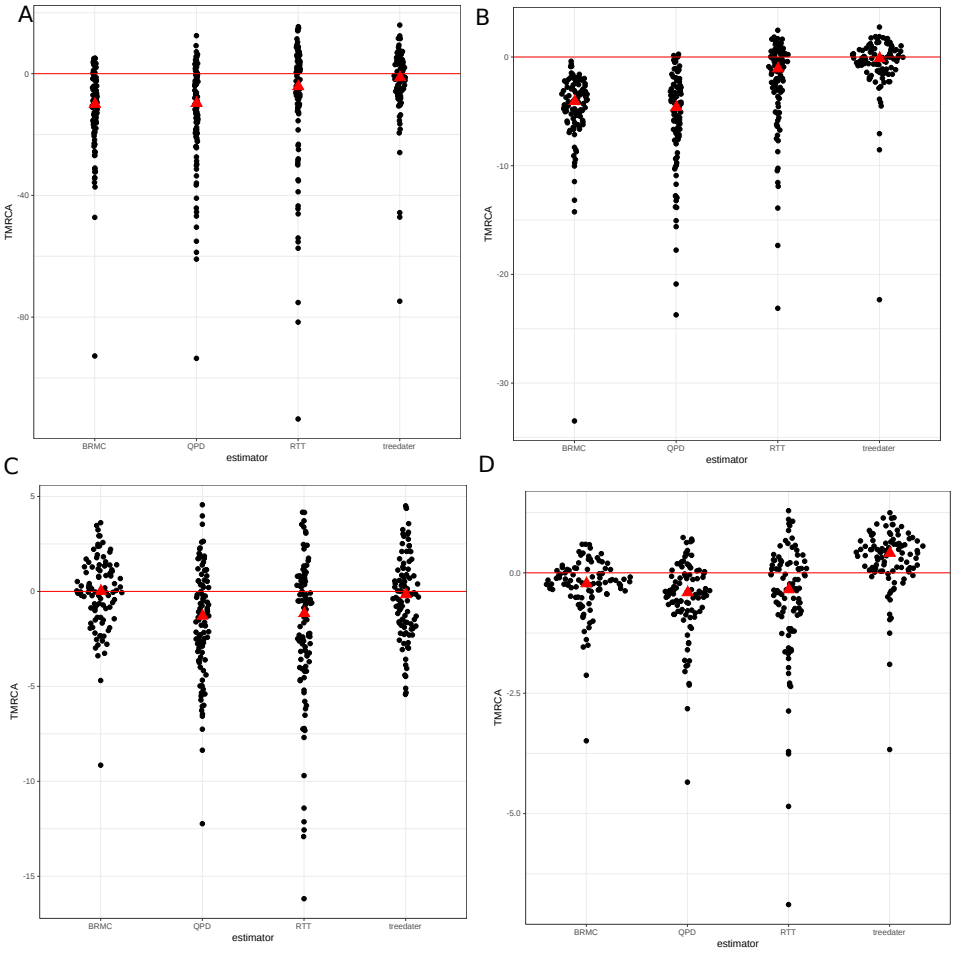

Figure S2: Estimated TMRCA four simulation scenarios in (To et al., 2015) . Each point is based on a single simulation replicate. Plots A-D correspond to different simulation scenarios corresponding to labels 750_3_25, 750_11_10, 995_3_25, and 995_11_10 in (To et al., 2015) .

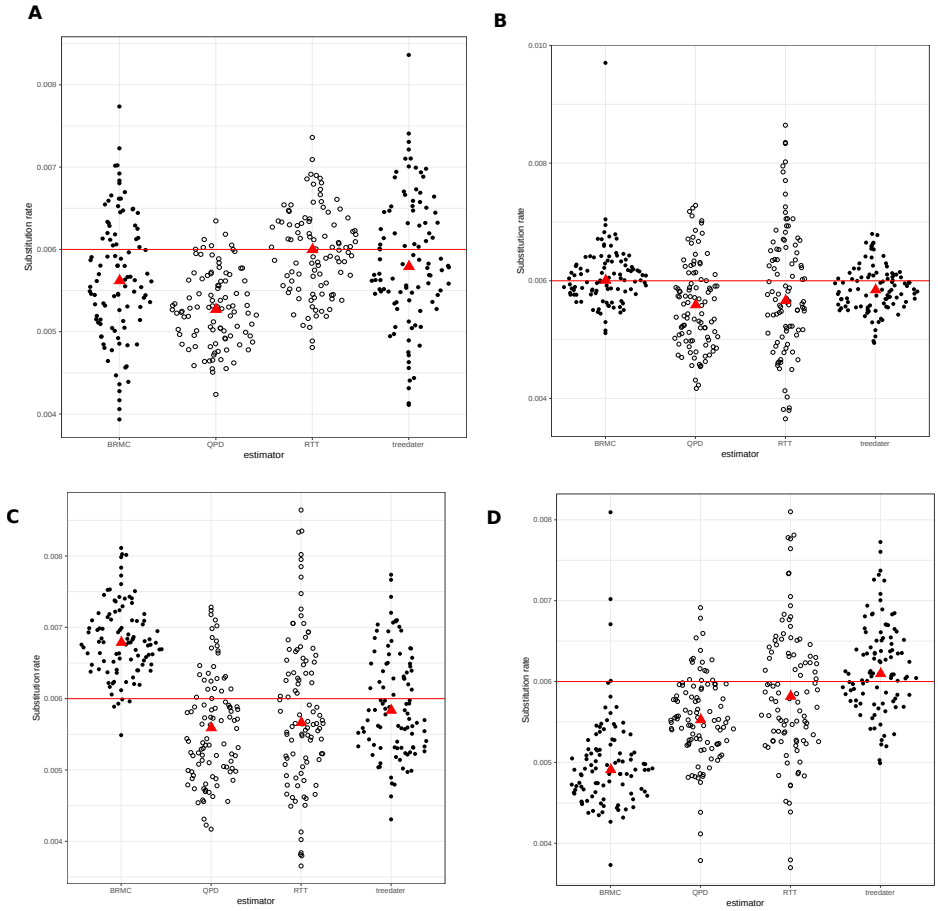

Figure S3: Comparison of estimated mean substitution rates using *treedater* and several other methods using the simulations in (To et al., 2015) . Plots A-D correspond to different simulation scenarios corresponding to labels 750_3_25, 750_11_10, 995_3_25, and 995_11_10 in (To et al., 2015) . Note that estimates with RTT and QPD were recycled from an earlier publication ((To et al., 2015)) and are shown with unfilled points.

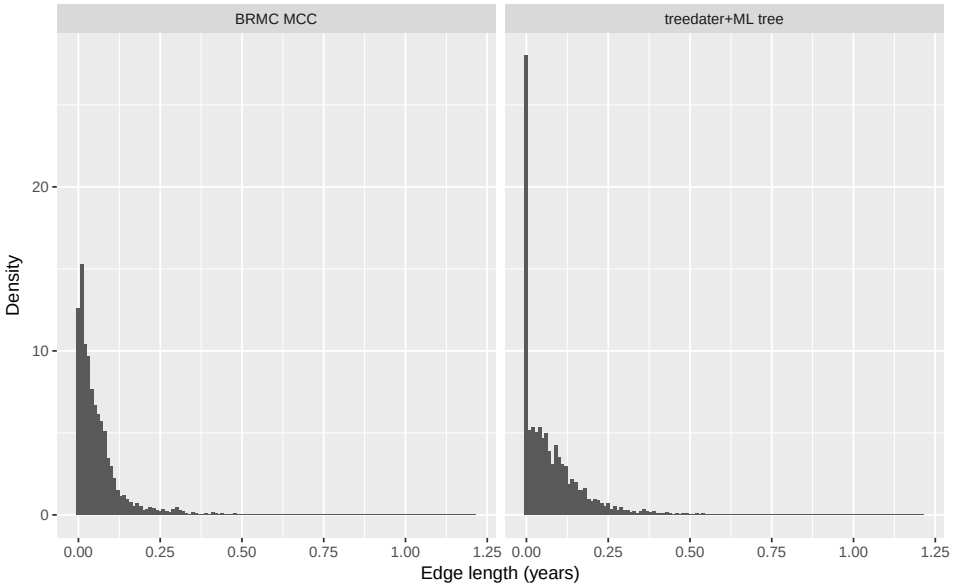

Figure S4: Comparison of the distribution of edge lengths (in years) obtained from the maximum clade clade credibility tree and from treedater applied to a maximum likelihood tree, both reconstructed from the 1610-sequence Ebola virus dataset. The maximum likelihood tree has a large number of zero-length branches that are absent in the Bayesian reconstruction.