

Additional file 3: Figure S2: Comparing the performance of GTR+I+ Γ model distance correction in the coding and non-coding gene segments

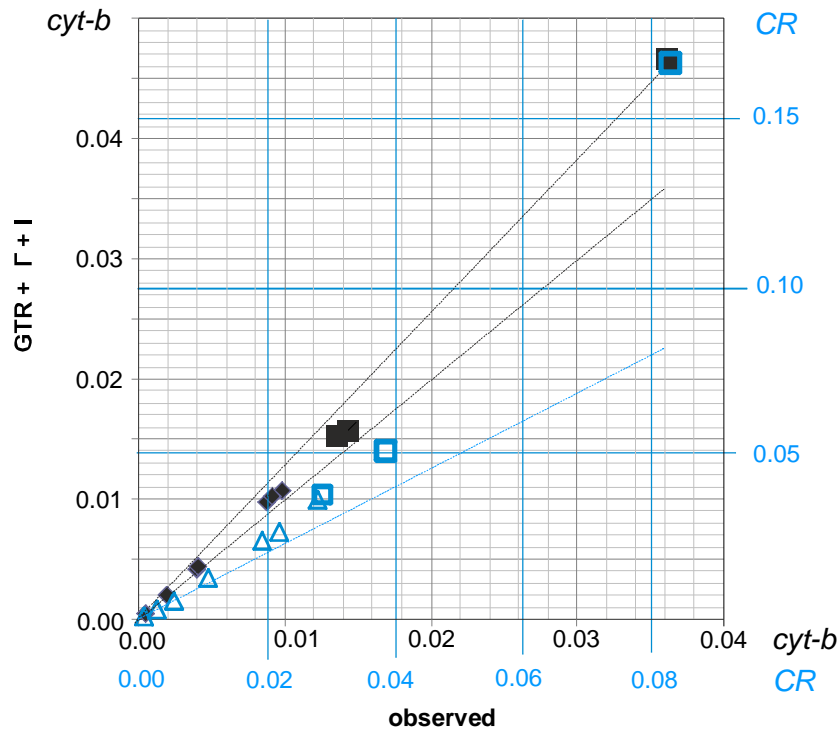


Figure S2: Comparing the performance of GTR+I+ Γ model distance correction in the coding and non-coding gene segments

The GTR+I+ Γ model distance correction in the coding (*cyt-b*, filled symbols) and non-coding (*CR*, open blue symbols) gene segments when “deep calibration” by interspecies reference is used. For each gene, observed vs. corrected distances are plotted. The corrected GTR+I+ Γ values are from Table 2, the corresponding observed values are close to the π diversity values: diamonds and triangles are the group-wise averages for the geographical subsets, the squares are inter- and intraspecies basal distances. The markers are plotted on different scales (black for *cyt-b*, blue for *CR*) so that the interspecies distance estimates coincide (upper right corner). The figure illustrates that if the interspecies distance is used for setting a time scale, and if a time-dependence of the rate is expected to cause age overestimation of recent events, such a bias would be considerably smaller for *CR* than for *cyt-b*, even if *CR* generally evolves faster and is thought to show more irregular patterns.