

## Corrigendum

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### Undersampling Genomes has Biased Time and Rate Estimates Throughout the Tree of Life

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After publication of this article we discovered that some simulations of trees with 1000 tips had not reached convergence with the program BEAST (10 runs of 20 million generations). When corrected, data scatter and trends in some plots of Fig. 2 changed, and therefore that figure has been replaced online. The results and conclusions are unchanged. The presence of the small sample artifact in even data-rich analyses supports our recommendation that larger data sets are needed to avoid it. In one case, we estimated the impact on speciation rate in two studies (birds and mammals). Although still high (14.5%) after correction, we consider any estimate to be speculative unless simulations are conducted with original data sets and methods. We thank A. Drummond for pointing out that one of the artifacts (Bayesian) we identified is caused by the upwardly skewed variance of branch-lengths near zero.