***eLife’s* transparent reporting form**

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* You should state whether an appropriate sample size was computed when the study was being designed
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This is a comparative phylogenetic study and does not involve replicates in the sense describe here. All datasets are described and cited in the Methods. All datasets are fully listed in the Supplementary Materials.

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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This is a phylogenetic comparative analysis so these criteria do not apply.

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All data are included in the Supplementary Materials. We will upload R code that implements the statistical analyses described in the Methods to Dryad once the paper is accepted.