

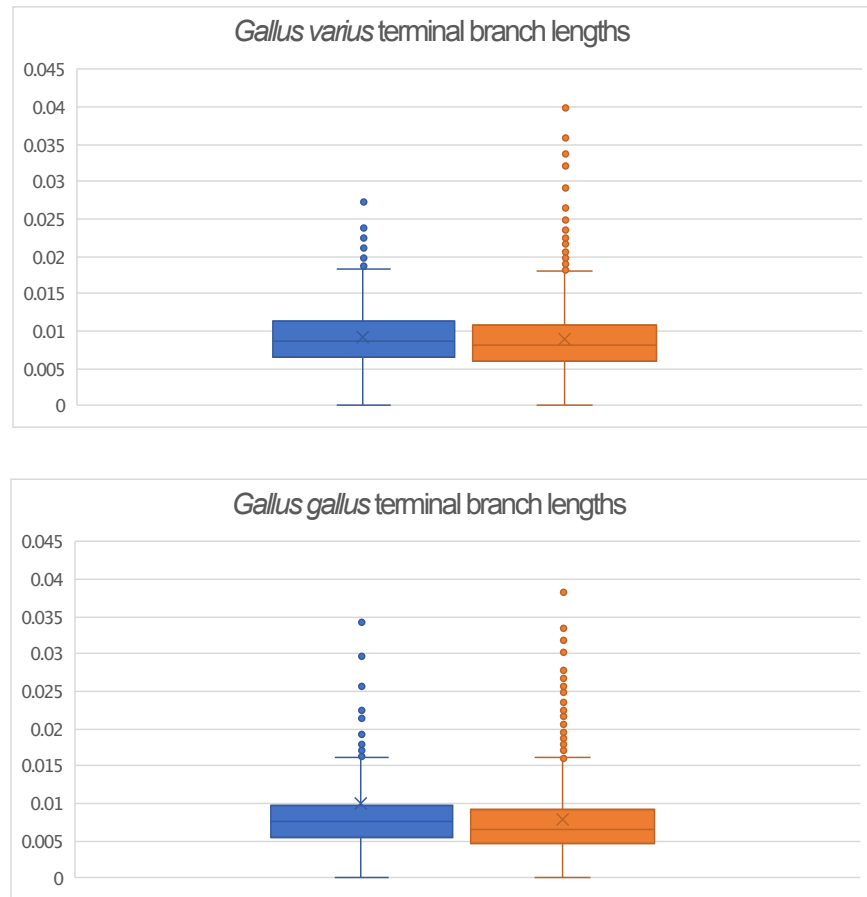


Figure S1. The distribution of terminal branch lengths for selected *Gallus* species are independent of topology. This page: gene trees were divided into those with a *G. varius* - *G. gallus* clade (shown to the left in blue; $n = 532$) and those without a *G. varius* - *G. gallus* clade (shown to the right in orange; $n = 2,014$) and the branch lengths (in substitutions per site) were examined. A prediction of very recent gene flow (i.e., gene flow that might be related to the domestication of *G. gallus*) is an excess of very short branches in trees that have a *G. varius* - *G. gallus* clade; this is not evident. The top panel shows terminal branch lengths for *G. varius* and the bottom shows terminal branch lengths for *G. gallus*. Next page: similar graphs for *G. sonneratii* and *G. gallus*. Organization of that panel is similar to the panel on this page, with the trees that have a *G. sonneratii* - *G. gallus* clade shown on the left (in blue; $n = 404$) and those without the clade shown on the right (in orange; $n = 2,142$). The prediction for very recent gene flow for these species is similar to those for *G. varius* and *G. gallus*; no excess for evident for this species either. These figures are based on 2,546 gene trees generated using introns with at least 10 parsimony informative sites; three outlier trees with very long *G. gallus* branches were omitted.

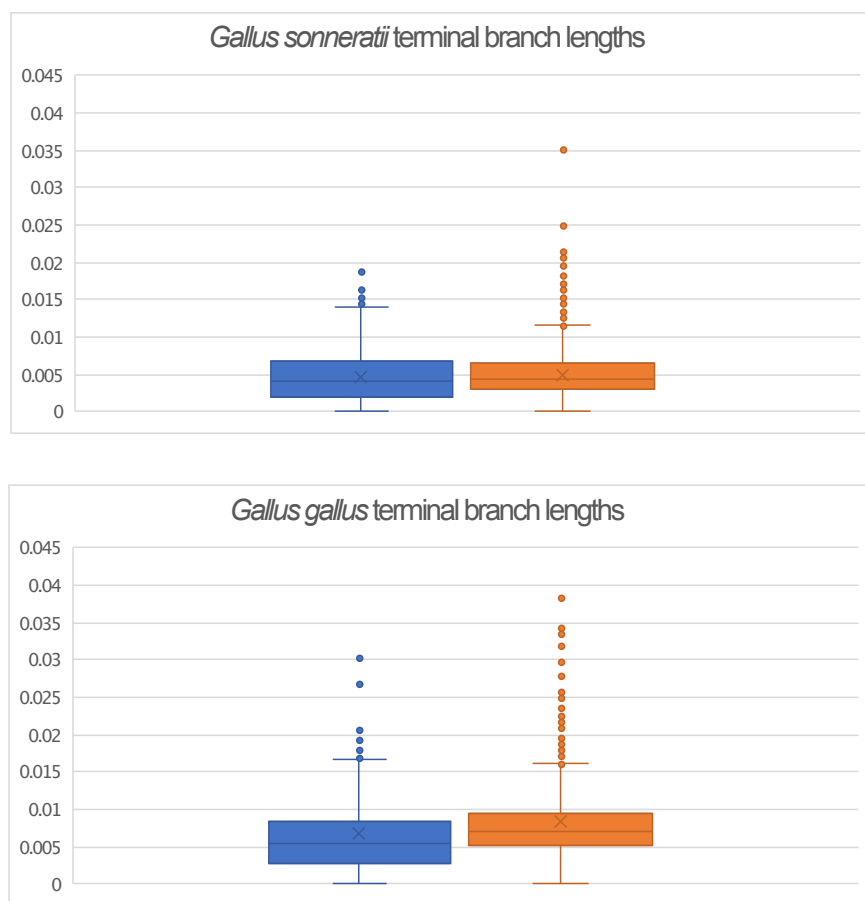


Figure S1. The distribution of terminal branch lengths for selected *Gallus* species are independent of topology, continued. These panels show the data for *G. sonneratii* and *G. gallus*. See previous page for details