





**Fig. 2.** Family-level phylogenetic relationships in passerines reconciled from concatenation and coalescent analyses (connects to bottom of Fig. 1 at the circled star). Biogeographic reconstruction including fossil taxa (Inset, tree) yields identical ancestral areas for crown lineages of passerines, suboscines, and oscines (also *SI Appendix, Fig. S8*). Plei., Pleistocene; Plio., Pliocene.

clock rates among lineages ranged from 0.28 to 0.44 across analyses, with 95% credible interval limits as low as 0.24 and as high as 0.48, suggesting that our choice of a relaxed clock model was appropriate. This level of rate heterogeneity across the tree is

lower than those reported in recent avian phylogenomic studies that sampled more broadly across extant birds (4, 43). Removal of some or most fossil calibrations did not significantly change divergence time estimates at uncalibrated nodes but had mixed effects