

TABLE S1. Evolutionary rate for various subsets of the Jarvis et al. (2015) data.

Data type	Sum of Branch Lengths <sup>a</sup> (substitutions per site)	Relative Rate <sup>b</sup>
Coding exons, c12	1.26	1
Coding exons, c123	2.48	1.97
UCEs	3.53	2.80
Whole genome	3.80	3.01
Introns	4.91	3.89

<sup>a</sup> The sum of branch lengths for trees downloaded from the newick treefiles in the gigadb dataset described by Jarvis et al. (2015). Only the ingroup branches were considered (i.e., the reptilian outgroup branches were excluded from the sum).

<sup>b</sup> All values are normalized to those for the first and second codon positions

#### REFERENCES

Jarvis E.D., Mirarab S., Aberer A.J., Li B., Houde P., Li C., Ho S.Y.W., Faircloth B.C., Nabholz B., Howard J.T., Suh A., Weber C.C., da Fonseca R.R., Alfaro-Nunez A., Narula N., Liu L., Burt D., Ellegren H., Edwards S.V., Stamatakis A., Mindell D.P., Cracraft J., Braun E.L., Warnow T., Jun W., Gilbert M.T.P., Zhang G., Avian Phylogenomics Consortium. Phylogenomic analyses data of the avian phylogenomics project. *Gigascience*, 2015;4:4.