

**Appendix B from D. San Mauro et al., “Initial Diversification of Living Amphibians Predated the Breakup of Pangaea”
(Am. Nat., vol. 165, no. 5, p. 590)**

Gapped Codon Excluded from the Alignment

A synapomorphic codon insertion was observed in the RAG1 nucleotide sequence of the representatives of our well-defined Hyloidea clade (*Telmatobius bolivianus*, *Litoria caerulea*, *Agalychnis callidryas*, *Hyla meridionalis*, and *Bufo bufo*) with respect to all other amphibians and amniotes. This indel corresponds to that reported by Venkatesh et al. (2001) between positions 637 and 638 of the human RAG1 amino acid sequence and is an amino acid deletion in tetrapods with respect to fishes. Our more comprehensive alignment allowed us to correctly relocate the indel at amino acid position 636–637, where lobe-finned fishes had a serine that is lost in tetrapods but secondarily reevolved in the above-mentioned anuran species, thereby providing further evidence for the monophyly of the group to the exclusion of *Caudiverbera* (which lacks this synapomorphic trait).

Literature Cited in Appendix B

Venkatesh, B., M. V. Erdmann, and S. Brenner. 2001. Molecular synapomorphies resolve evolutionary relationships of extant jawed vertebrates. *Proceedings of the National Academy of Sciences of the USA* 98: 11382–11387.