

## **SUPPORTING INFORMATION**

**DATA S1.** Raw character matrix. Modifications from the original codification appear in bold.

**TABLE S1.** List of characters and character states considered in phylogenetic analysis. Modifications from the original codification appear in bold.

**TEXT S1.** Data matrix (Nexus format) of PAUP analysis.

**TEXT S2.** Tree file (Newick format) of *strap* analysis.

**TEXT S3.** Ages file (R package paleotree format) of *strap* analysis.