Supplementary Figures (Figs. S1-S3)
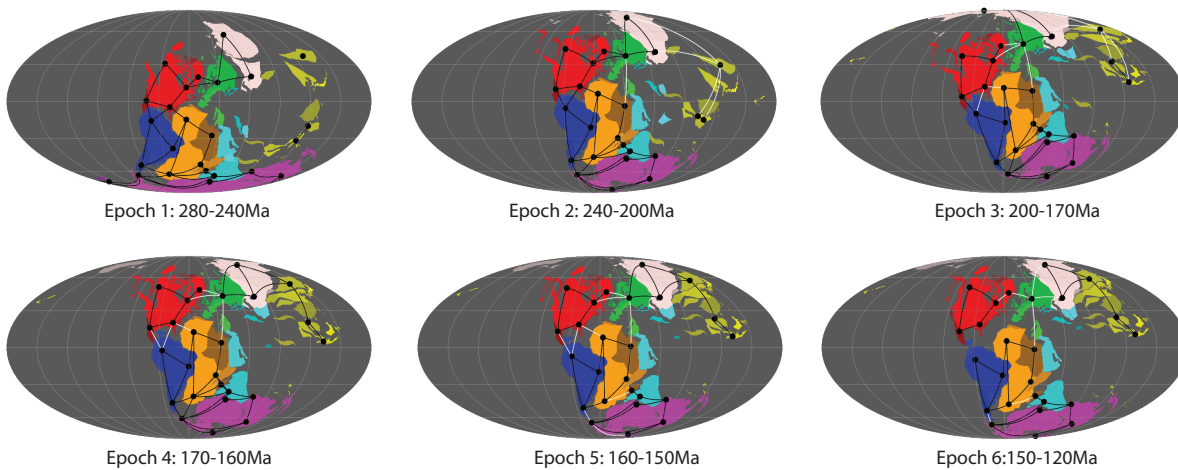

Epoch 1: 280-240Ma

Epoch 2: 240-200Ma

Epoch 3: 200-170Ma

Epoch 4: 170-160Ma

Epoch 5: 160-150Ma

Epoch 6:150-120Ma

Figure S1. "Landis" connectivities between the 25 areas, across the 6 time-slices (epochs) considered here. Area pairs with **high connectivity** are joined by black lines; area pairs with **medium connectivity** are joined by white lines; all other area pairs have **low connectivity**. All panels are from Landis (2016: Fig S8).
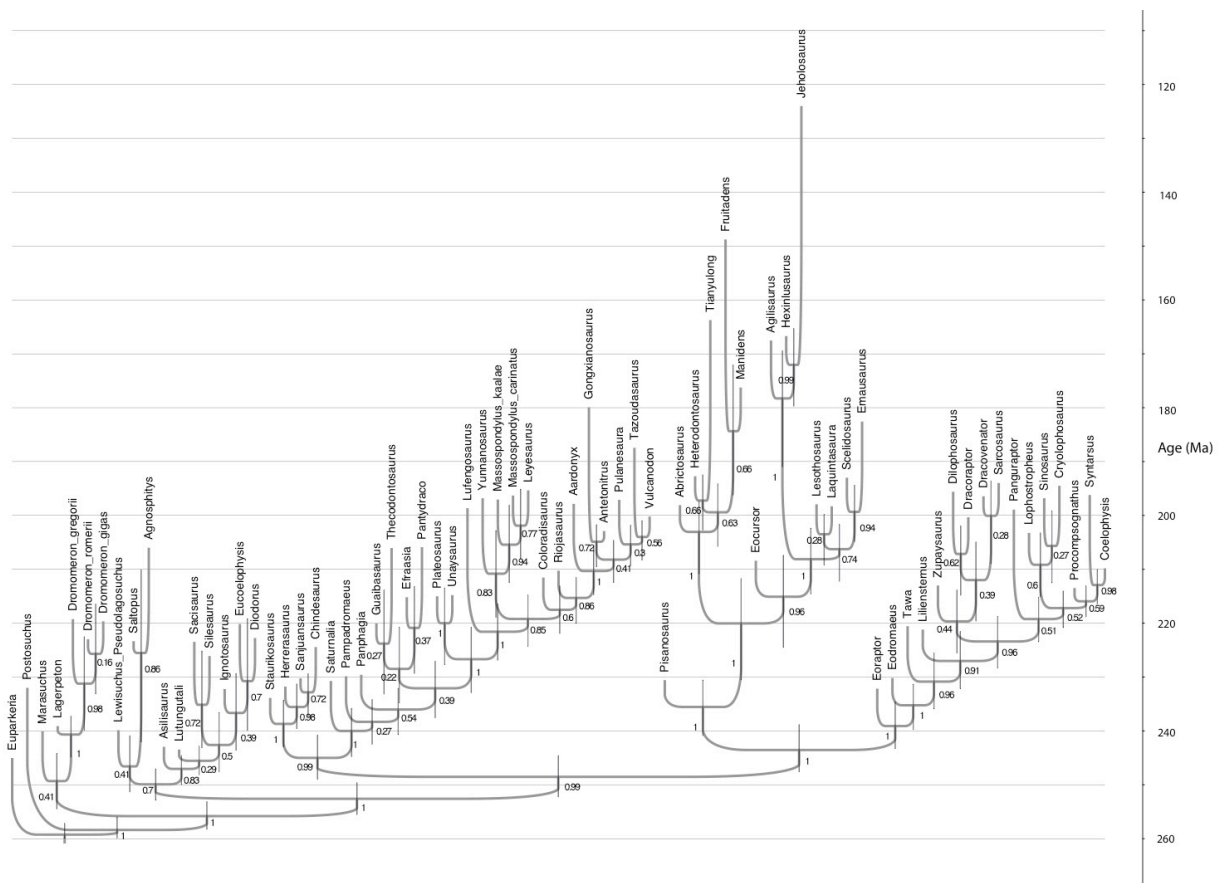

Figure S2. Timscaled phylogeny from tip-dated phylogenetic analysis, excluding biogeographic information. Note position of *Dracovenator* beside the (geographically remote) *Sarcosaurus*.
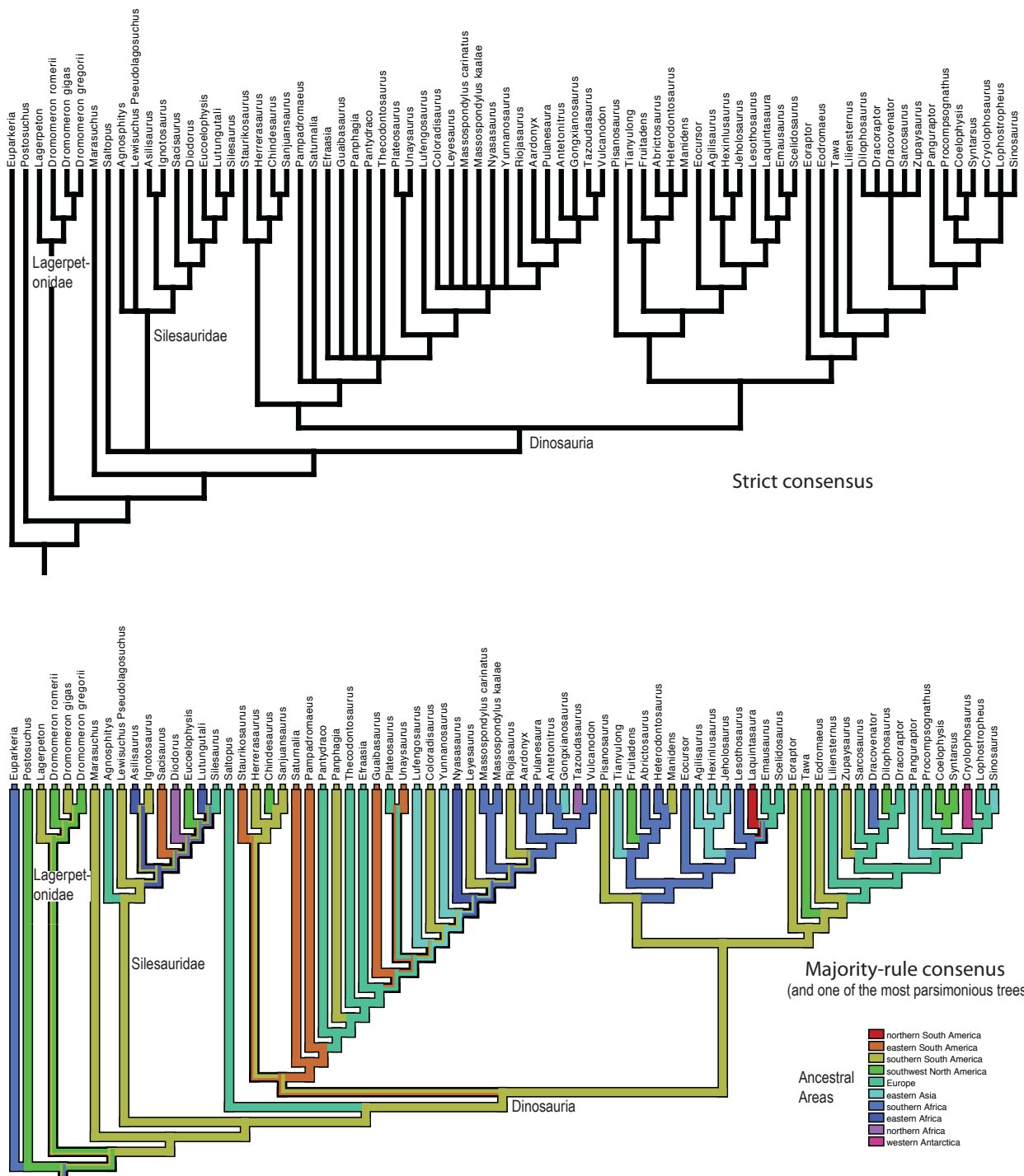
Figure S3. Parsimony analysis of the morphological data in [14] using PAUP* (Swofford 2003). (A) Strict consensus of 128 000 sampled most-parsimonious trees of length 1734. (B) Majority Rule consensus of 128 000 sampled most-parsimonious trees of length 1734. This tree is identical to one of the MPTs. Biogeographic areas is optimised on this tree using parsimony and treating "locality" as an unordered multistate character. Branches are colour-coded by inferred locality, and equally-parsimonious states for a particular branch are shown as multiple colours (vertical stripes).