

Supporting Information from “Time for a rethink: time sub-sampling methods in disparity-through-time analyses”

APPENDIX S1: ADDITIONAL DETAILS OF DATASETS

Beck2014 (Figure A1)

The following taxa were removed because they were in the phylogeny but not the character matrix or vice versa: *Montanalestes*, *Lainodon*, *Kharmarungulatum*, *Alymlestes*.

Brusatte2014 (Figure A2)

We used one randomly selected time-scaled tree from Brusatte et al. (2014). Zero-length branches were replaced with the minimum branch length in the phylogeny. The following taxa were removed because they were in the phylogeny but not the character matrix or vice versa: *Sinraptor dongi*, *Hesperonychus elizabethae*, *Pyroraptor olympius*, *Limenavis patagonica*, *Lithornis*, *Crypturellus undulatus*, *Gallus gallus*, *Crax pauxi*, *Anas platyrhynchos*, *Chauna torquata*, *Epidendrosaurus* and *Kinnareemimus*. The following taxa were removed because they shared no characters in the morphological matrix: *Shanag ashile*, *Atrociraptor marshalli*, *Proceratosaurus bradleyi*, *Incisivosaurus gauthieri*, *Enigmosaurus*, *Nanshiungosaurus brevispinus*, *Xixiasaurus*, *Tsaagan mangas*, *Mirischia*, *Pedopenna*, *Suzhousaurus*, *Juratyran*, *Vorona*, *Bonapartenykus*, *Teratophoneus*, *Gobipteryx*, *Songlingornis*, *Liaoningornis longidigitu* and *Achillesaurus*.

Bapst2016 (Figure A3)

We used the maximum clade credibility tree from Bapst et al. (2016). Zero-length branches were replaced with the minimum branch length in the phylogeny. The following taxa were removed because they were in the phylogeny but not the character matrix or vice versa: *Mei long* and *Mei lon*. The following taxa were removed because they shared no characters in the morphological matrix: *Hagryphus giganteus*, *Atrociraptor marshalli*, *IGM100 1015 UndesDromaeosaurid*, *Dromaeosaurus albertensis*, *Incisivosaurus gauthieri*, *Deinocheirus mirificus*, *Therizinosaurus cheloniformis*, *Anserimimus planinychus* and *Elmisaurus rarus*.

Wright2017 (Figure A4)

We used the maximum clade credibility tree from Wright (2017). To properly timescale the tree we followed the advice of Wright (2017) and divided the branch lengths by the corresponding clock rate (= 0.03517385) and then set the root time to 485.4. Zero-length branches were replaced with the minimum branch length in the phylogeny. No taxa were removed.

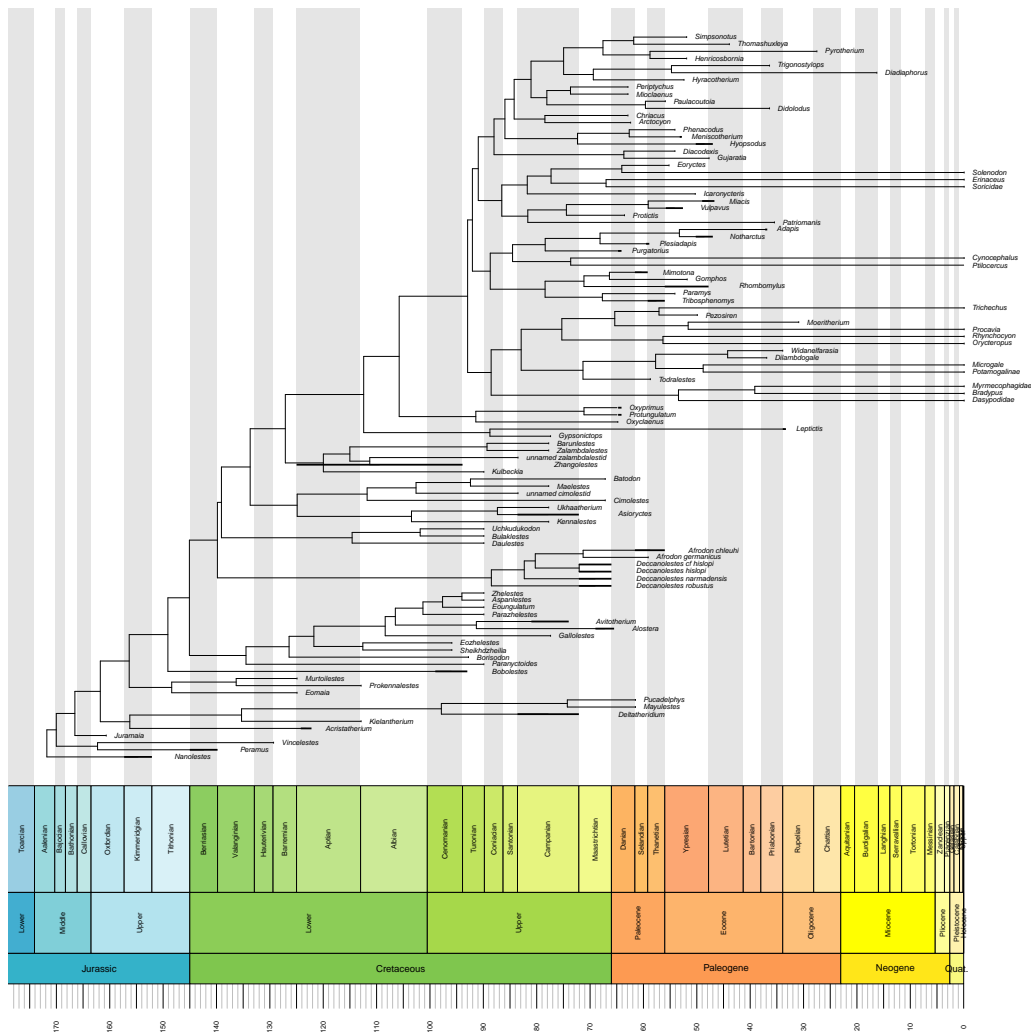


Figure A1: Phylogeny from Beck & Lee (2014).

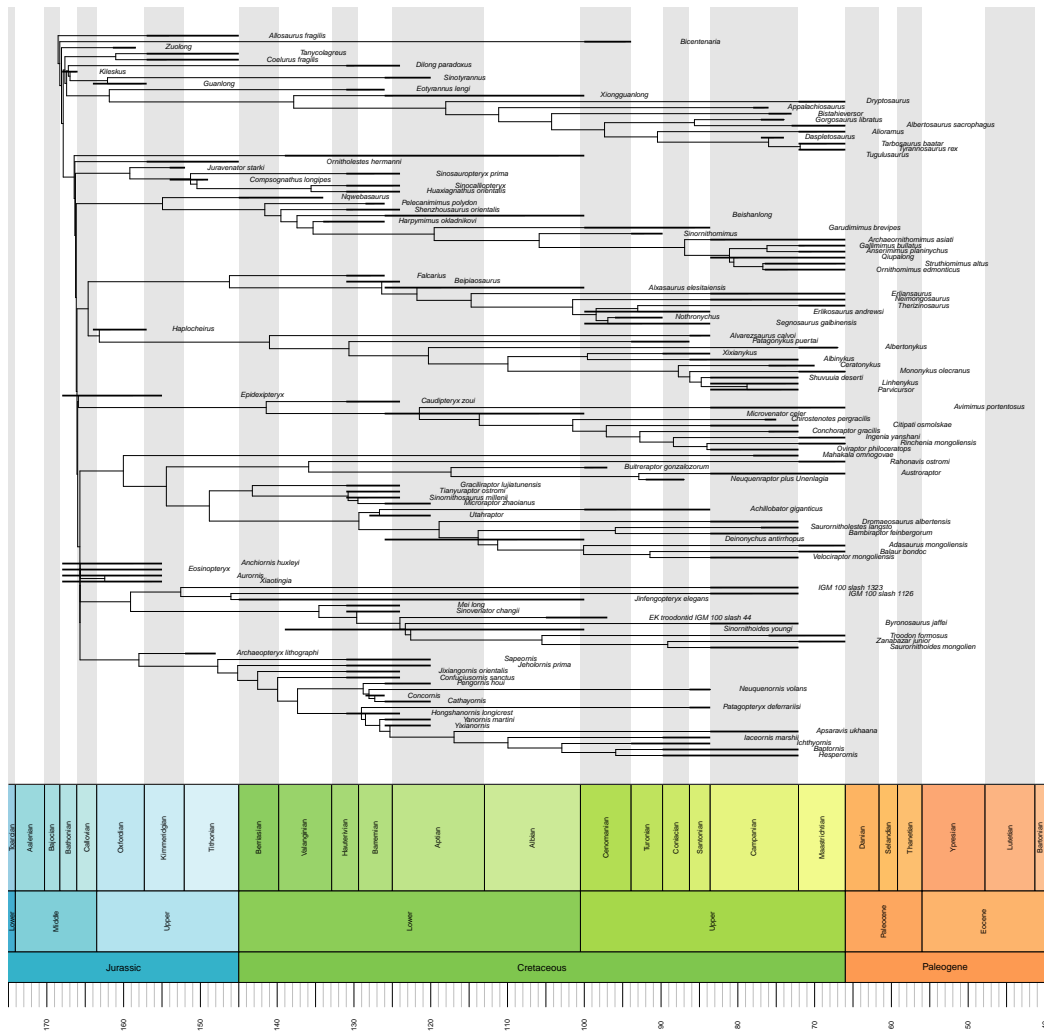


Figure A2: Phylogeny from Brusatte et al. (2014). This is one randomly selected tree from the time-scaled trees in the paper.

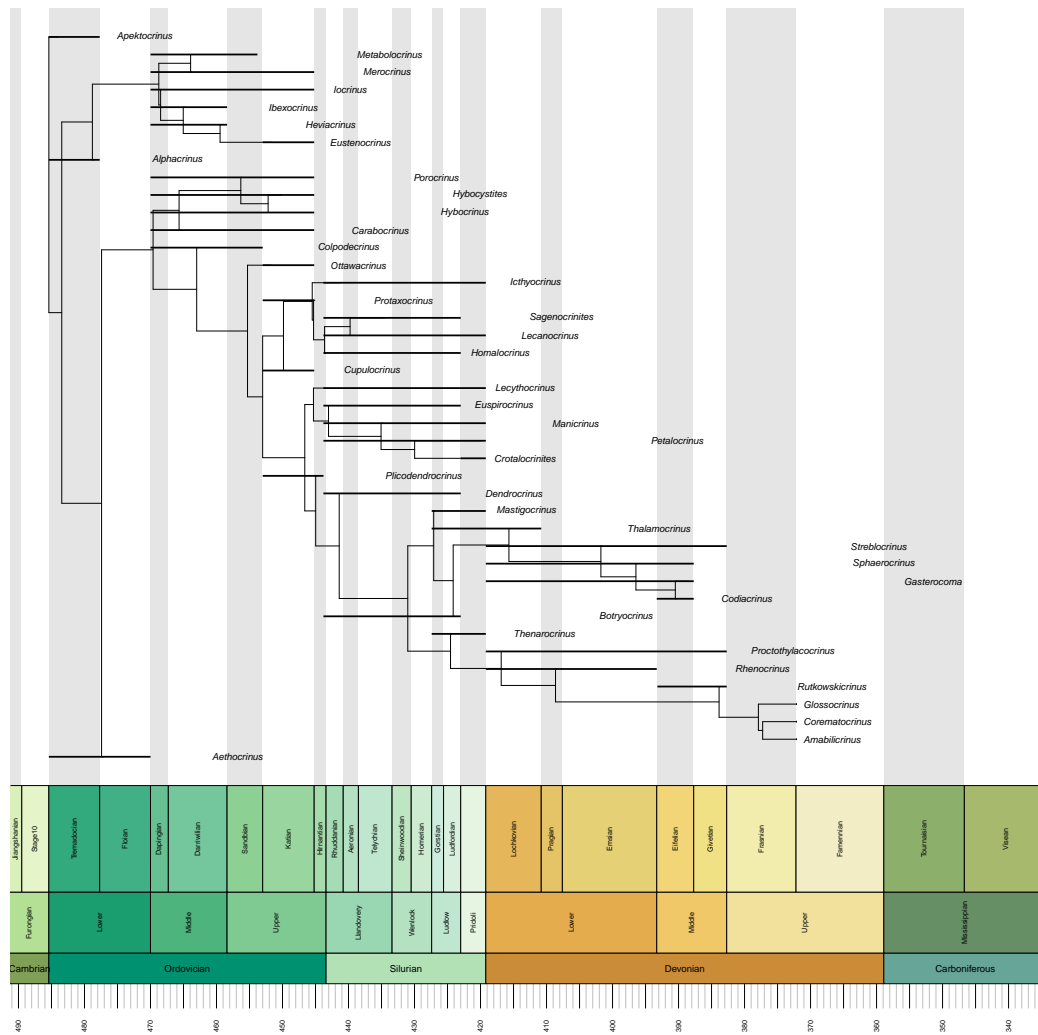


Figure A4: This is the maximum clade credibility tree from Wright (2017).