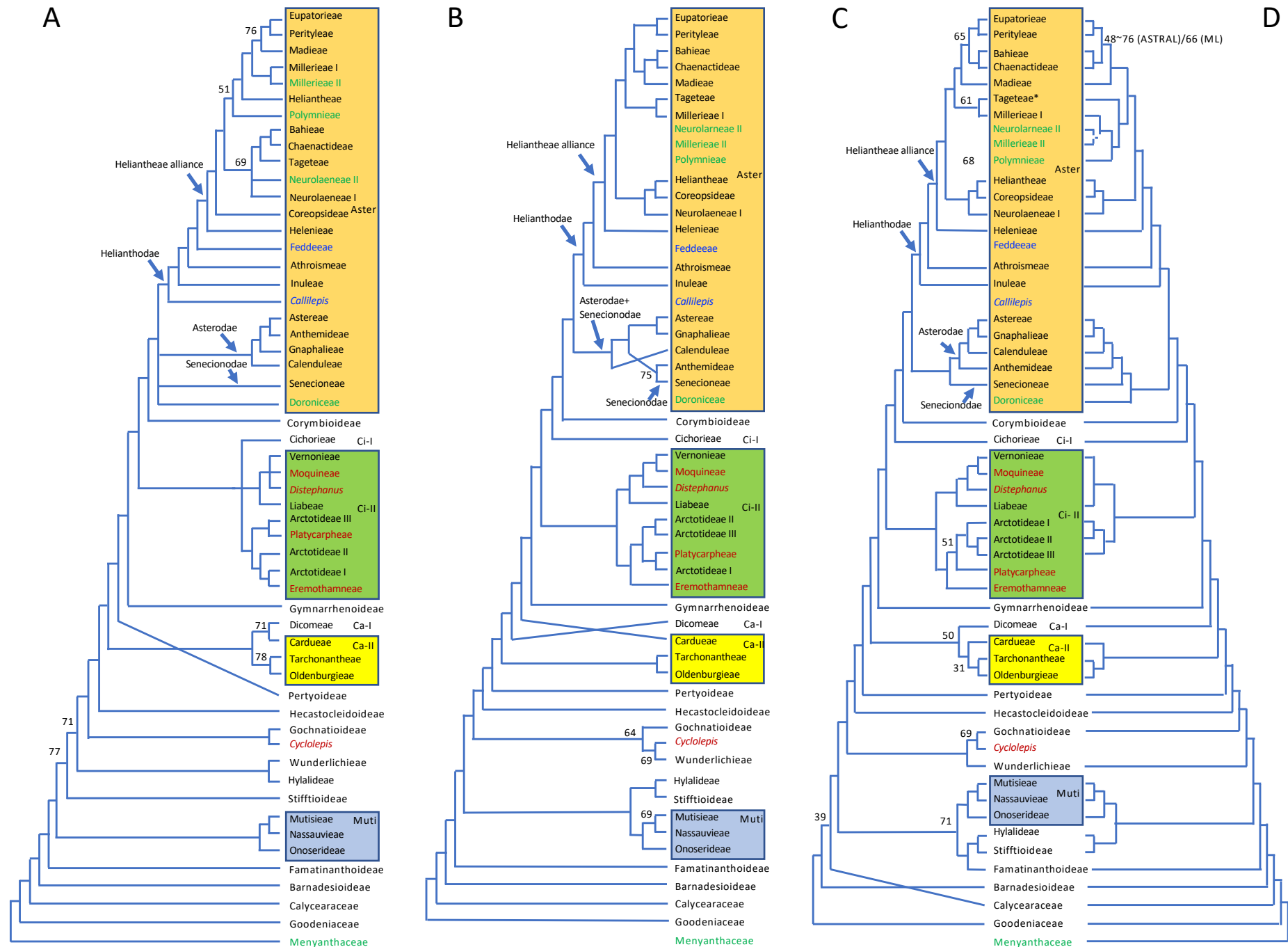


Supplemental Figure S1. Comparison of Asteraceae phylogenies at tribal level.



Plastid tree (modified from Panero 2007, Panero and Funk 2008, Panero et al. 2014, Fu et al. 2016)

ML tree (Mandel et al. 2019)

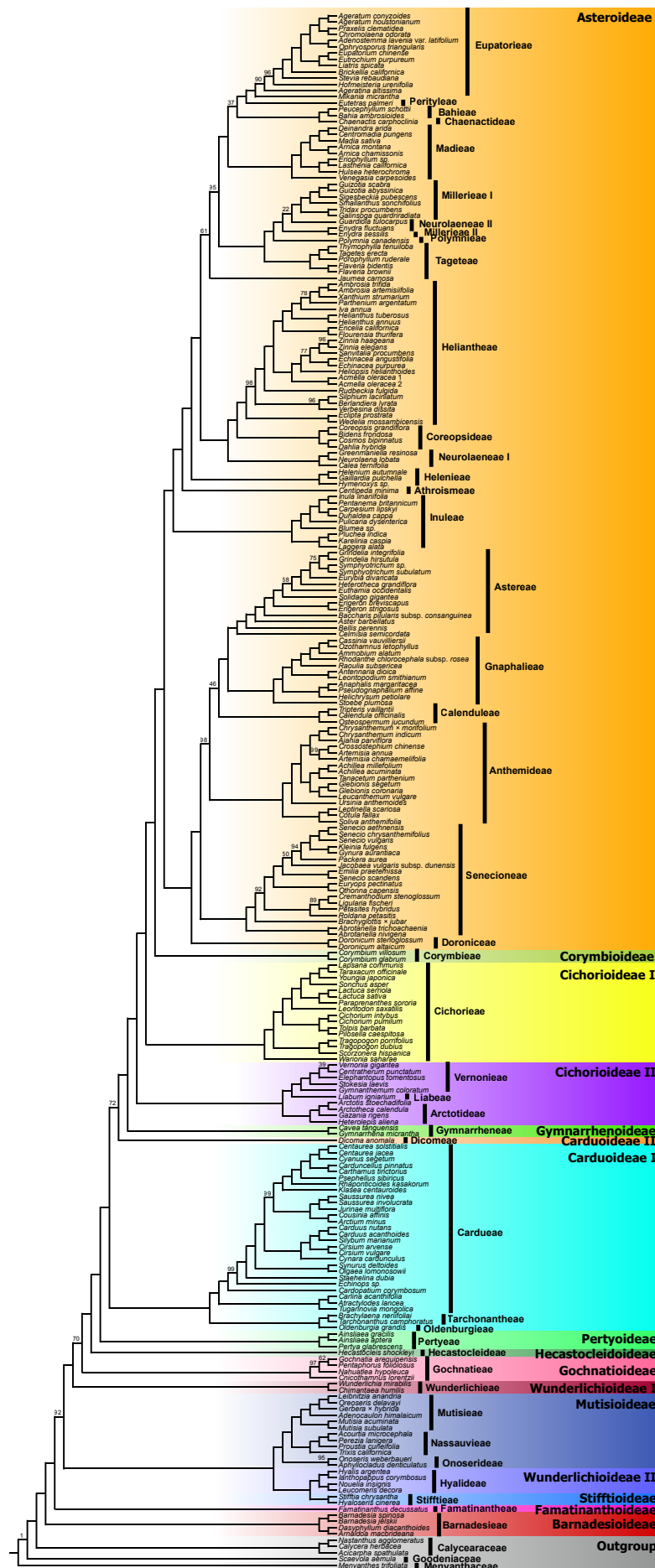
ASTRAL tree
(Mandel et al. 2019)

ASTRAL & ML trees
(This study)

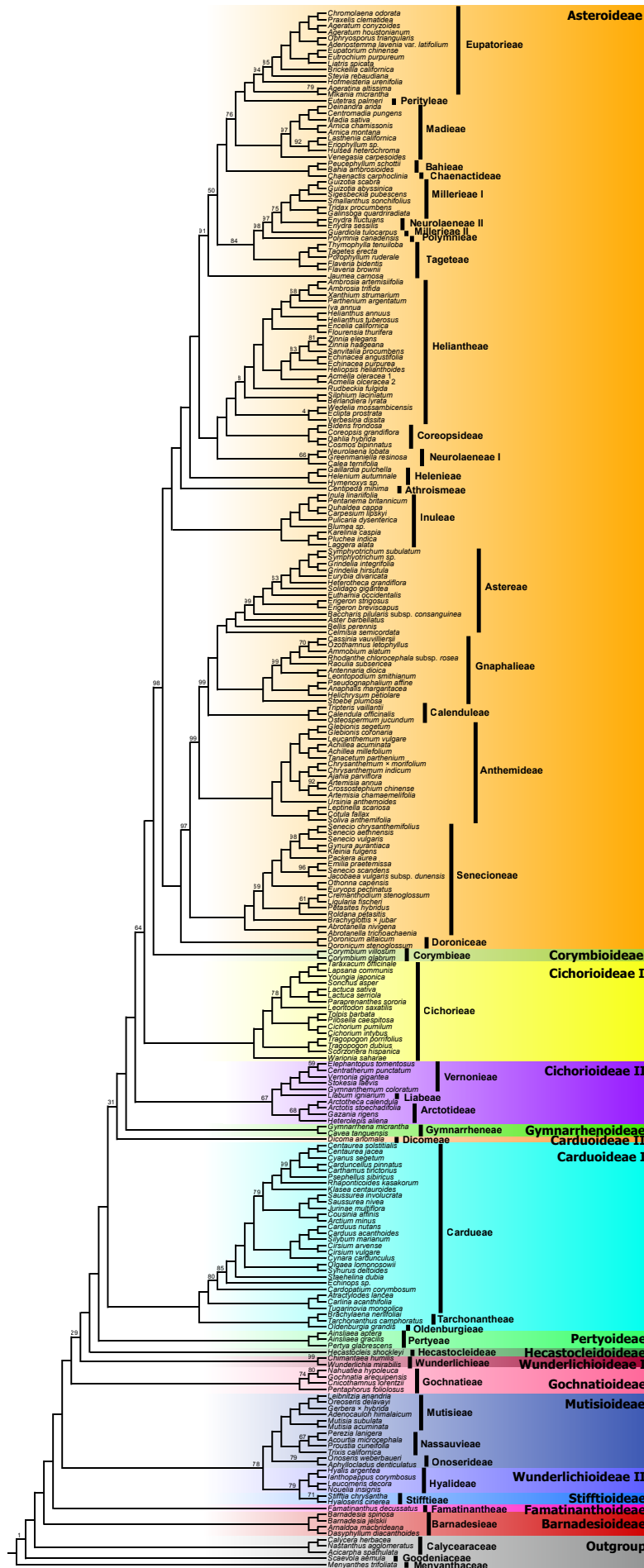
Supplemental Figure 2. An outline for gene selection procedures for multiple gene sets.



Supplemental Figure 3. A coalescent phylogeny of Asteraceae using 847 nuclear genes (set 1 as shown in Supplemental Figure S1).



Supplemental Figure 4. A coalescent phylogeny of Asteraceae using 177 nuclear genes (set 2).



Supplemental Figure 5. A coalescent phylogeny of Asteraceae using 175 nuclear genes (set 3).



Supplemental Figure 6. A coalescent phylogeny of Asteraceae using 1087 nuclear genes (set 4).



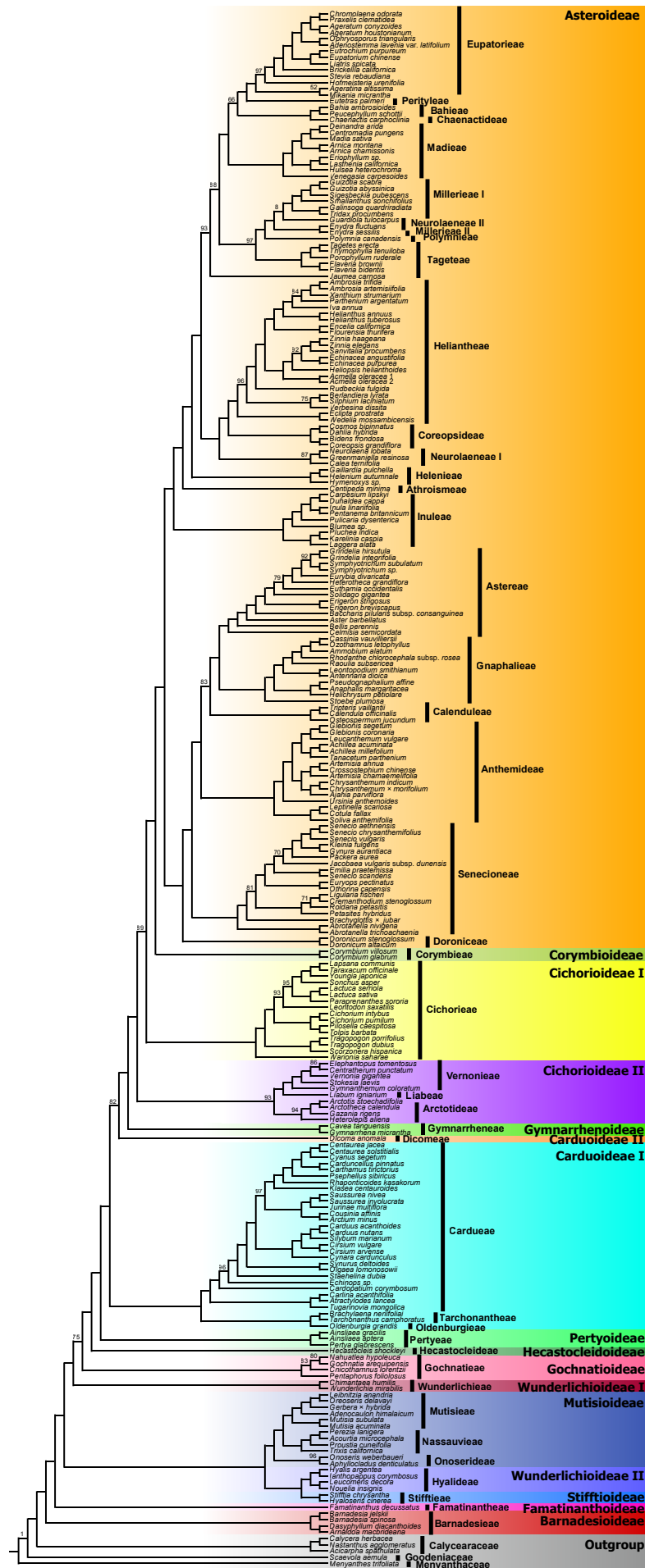
Supplemental Figure 7. A coalescent phylogeny of Asteraceae using 649 nuclear genes (set 5).



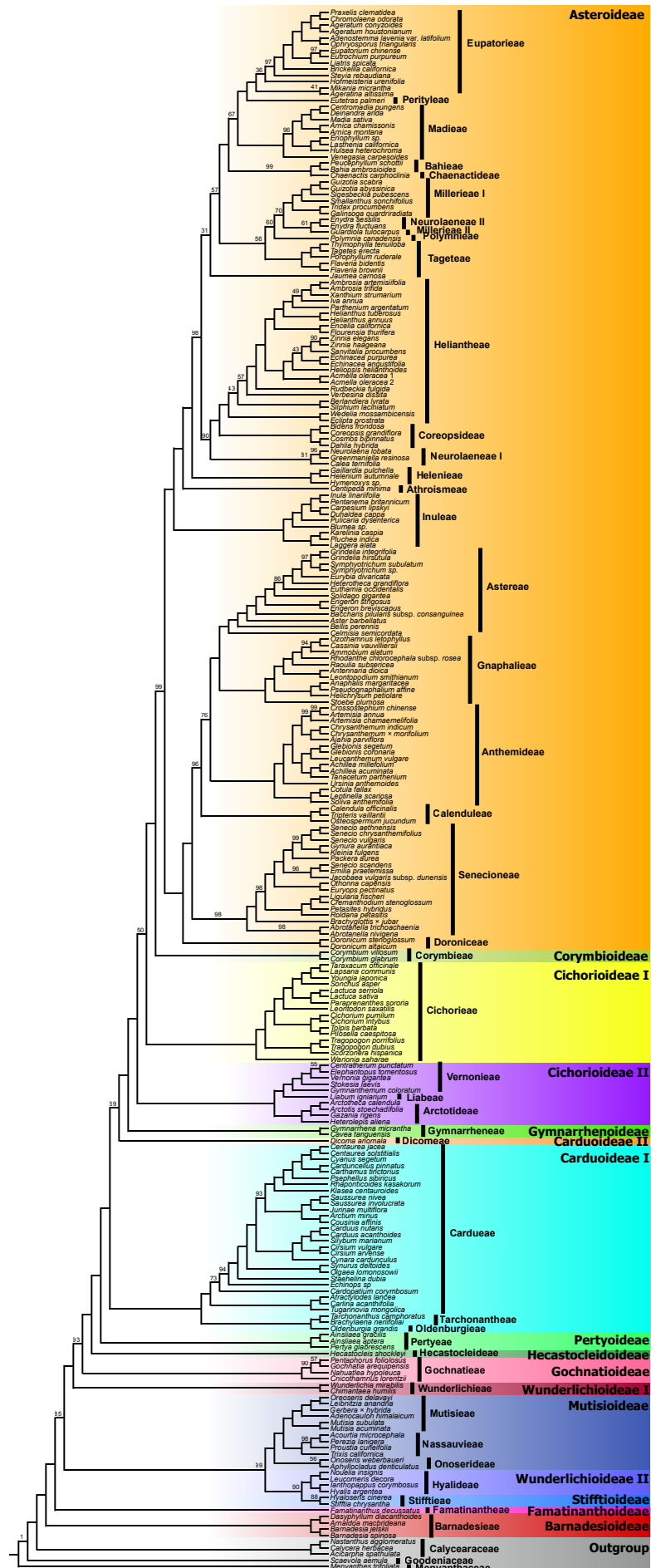
Supplemental Figure 8. A coalescent phylogeny of Asteraceae using 438 nuclear genes (set 6).



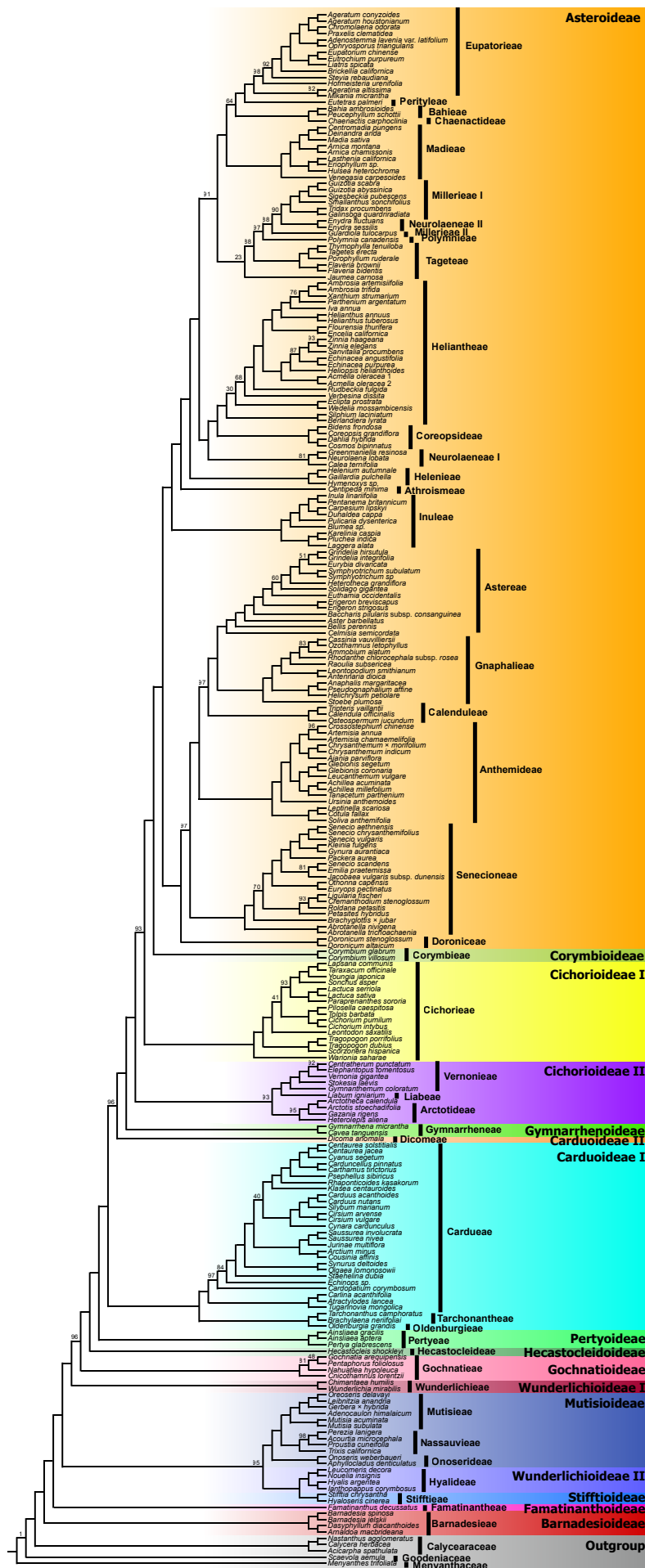
Supplemental Figure 9. A coalescent phylogeny of Asteraceae using 384 nuclear genes (set 7).



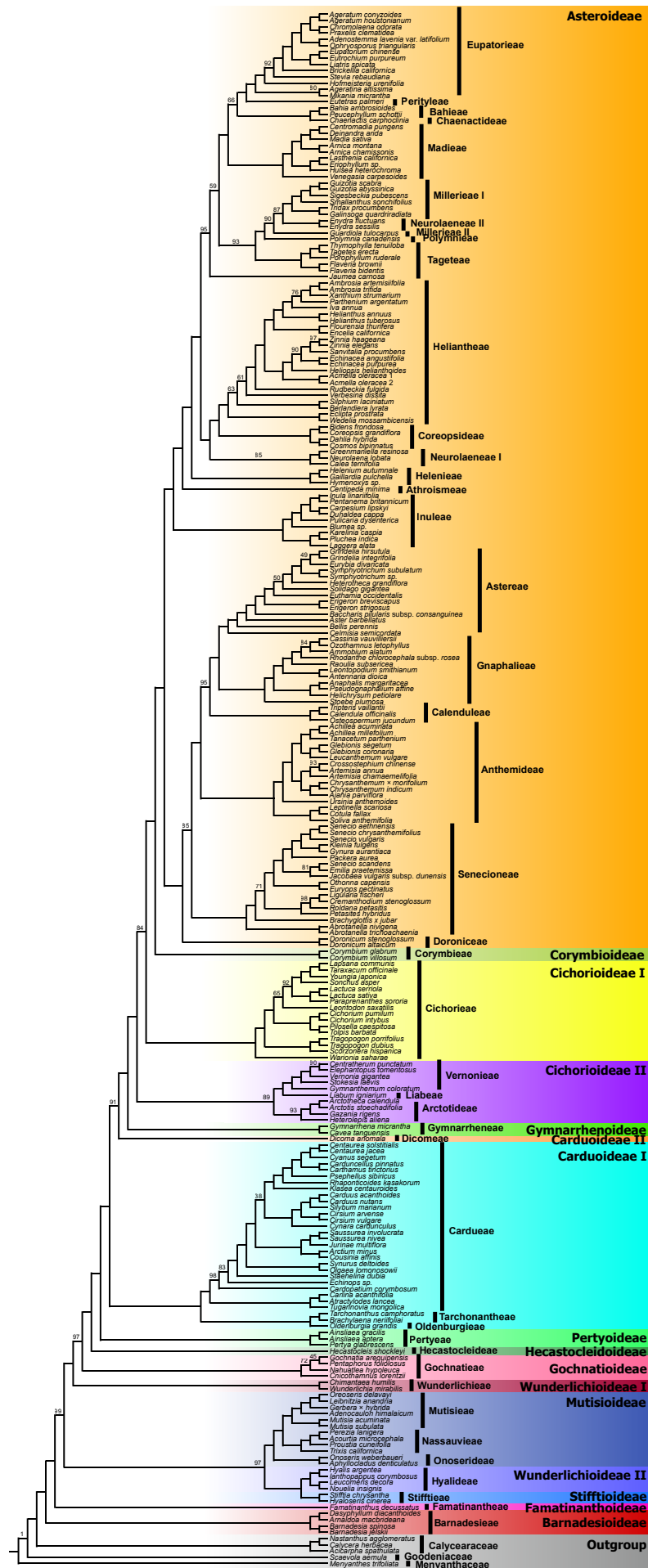
Supplemental Figure 10. A coalescent phylogeny of Asteraceae using 265 nuclear genes (set 8).



Supplemental Figure 11. A coalescent phylogeny of Asteraceae using 202 nuclear genes (set 9)



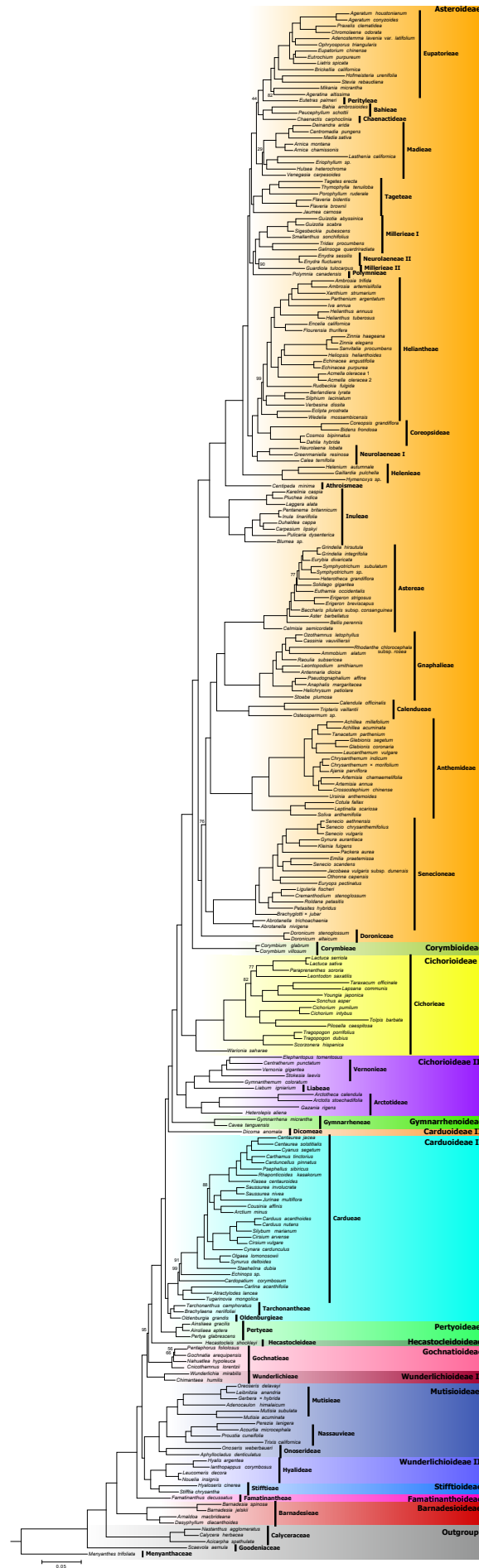
Supplemental Figure 12. A coalescent phylogeny of Asteraceae using 192 nuclear genes (set 11).



Supplemental Figure 13. A coalescent phylogeny of Asteraceae using 192 nuclear genes with 800-1000 bp (set 10).



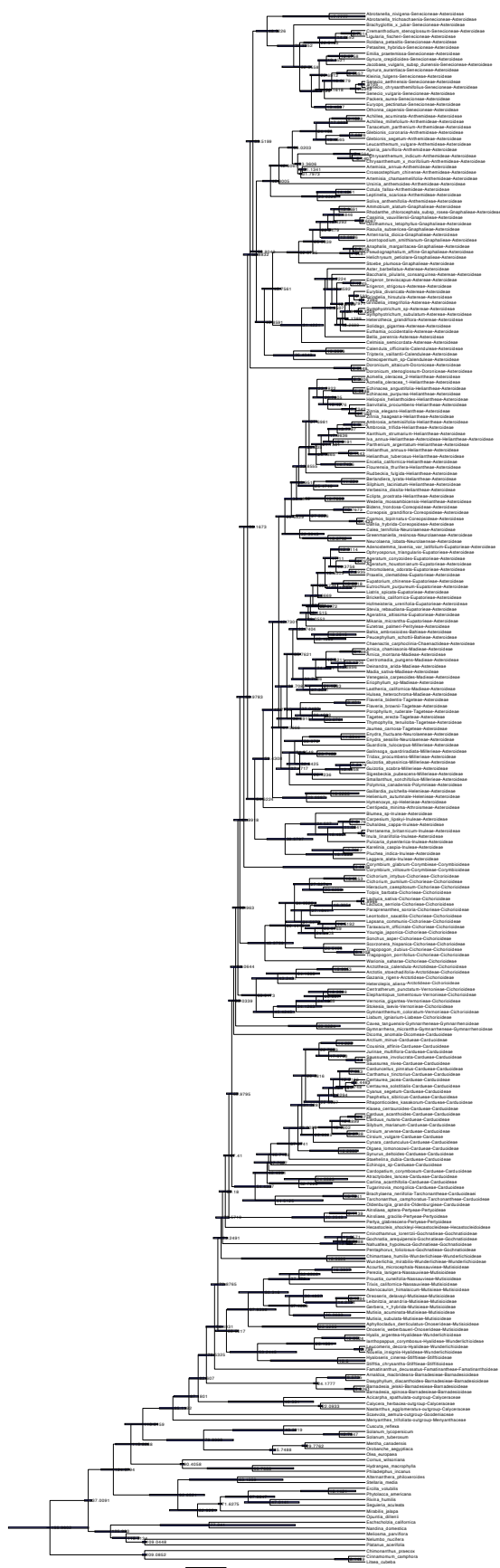
Supplemental Figure 14. A Maximum Likelihood phylogeny of Asteraceae using 192 genes (set 11)



Supplemental Figure 16. Divergence times estimated using r8s (set 1).



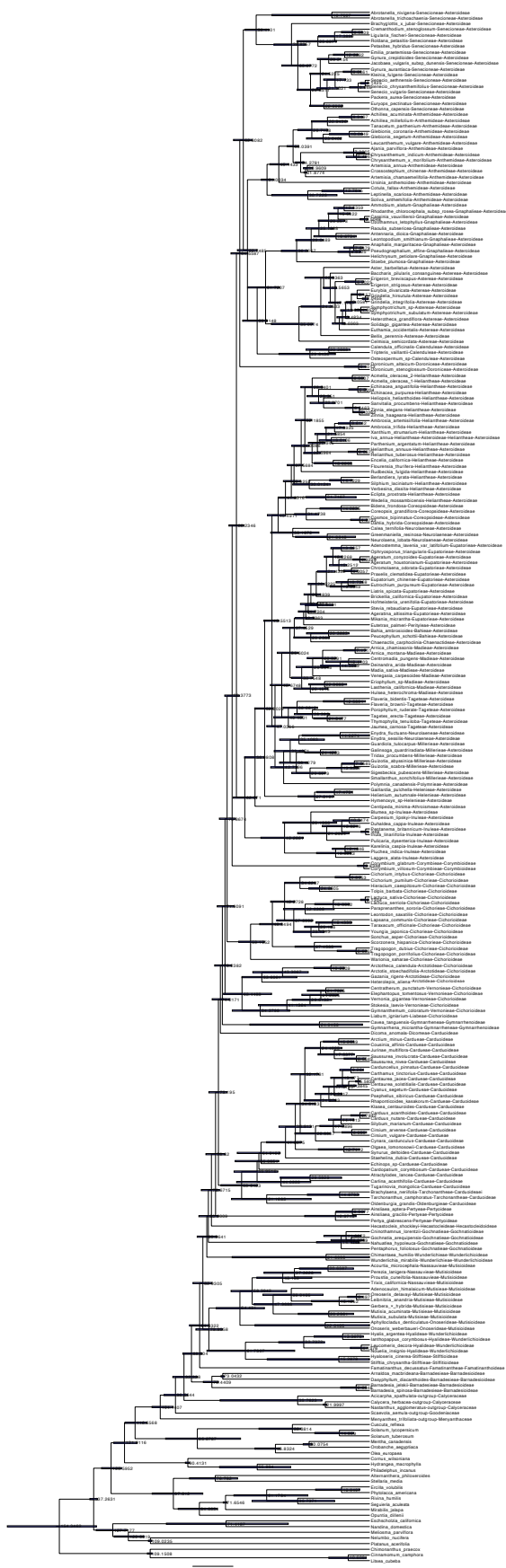
Supplemental Figure 17. Divergence times estimated using BEAST (set 1).



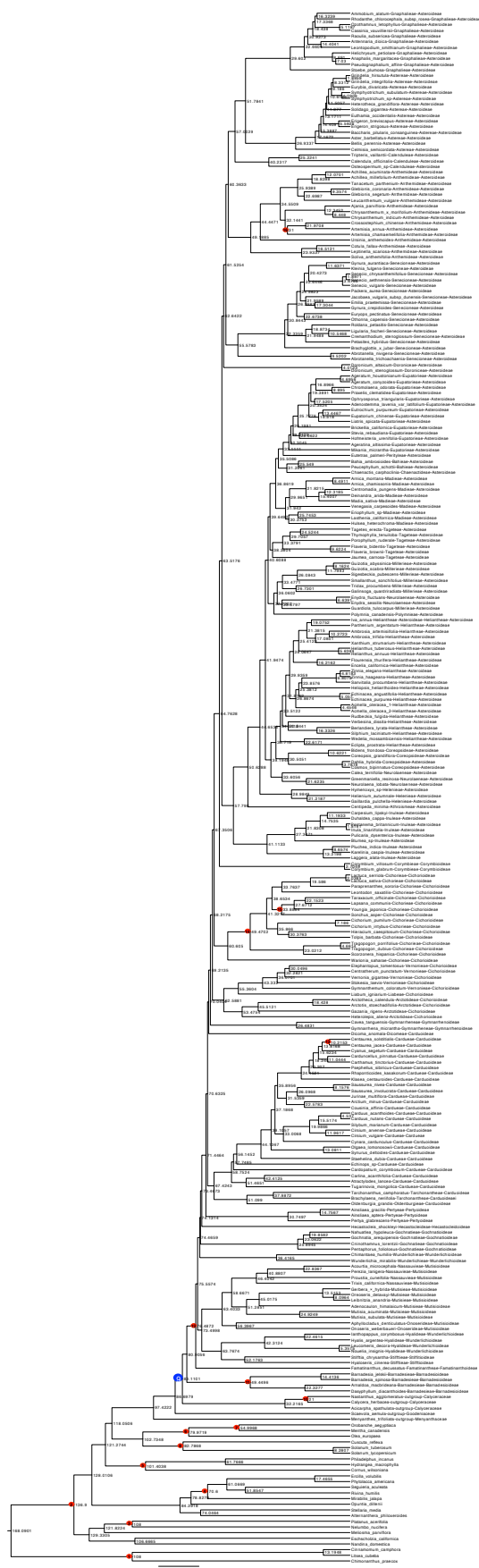
Supplemental Figure 18. Divergence times estimated using r8s (set 2).



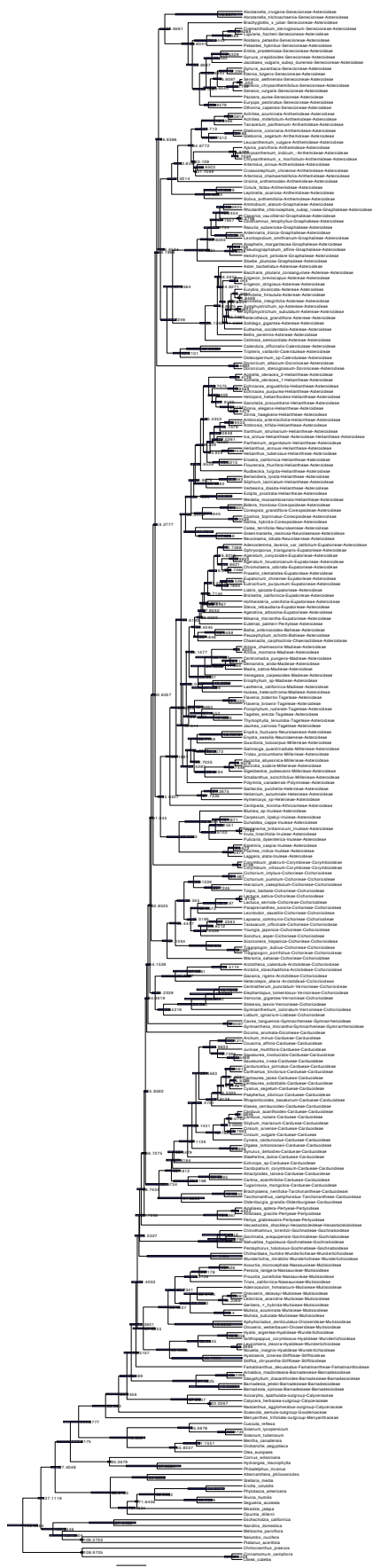
Supplemental Figure 19. Divergence times estimated using BEAST (set 2).



Supplemental Figure 20. Divergence times estimated using r8s (set 3).



Supplemental Figure 21. Divergence times estimated using BEAST (set 3).



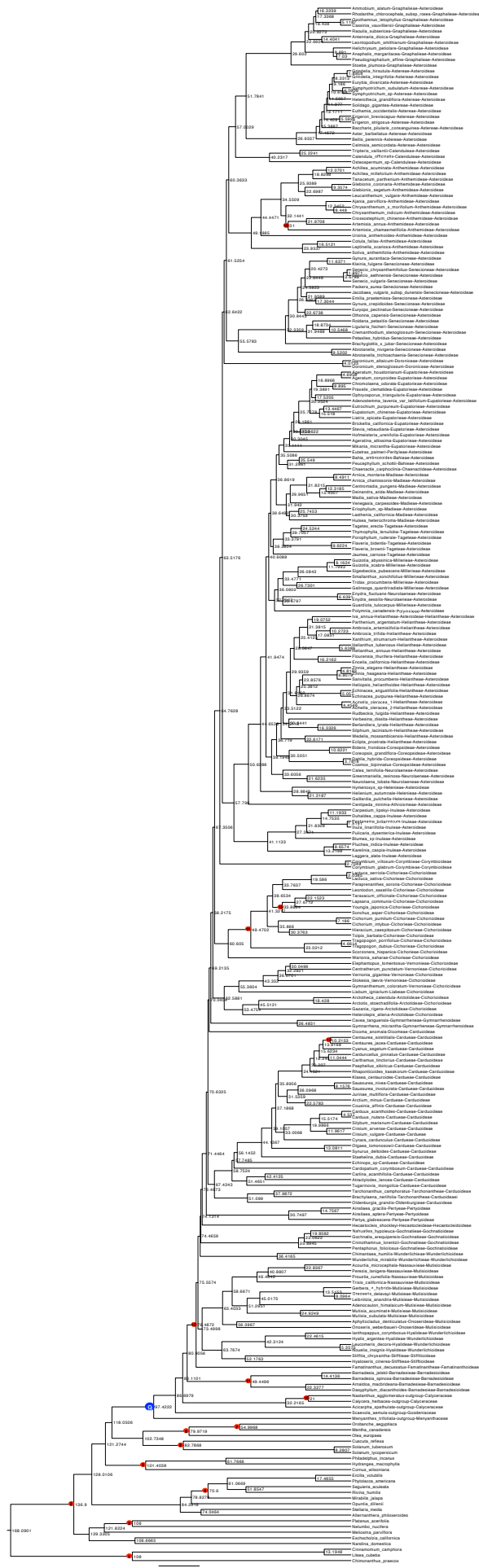
Supplemental Figure 22. Divergence times estimated using r8s (set 4).



Supplemental Figure 23. Divergence times estimated using BEAST (set 4).



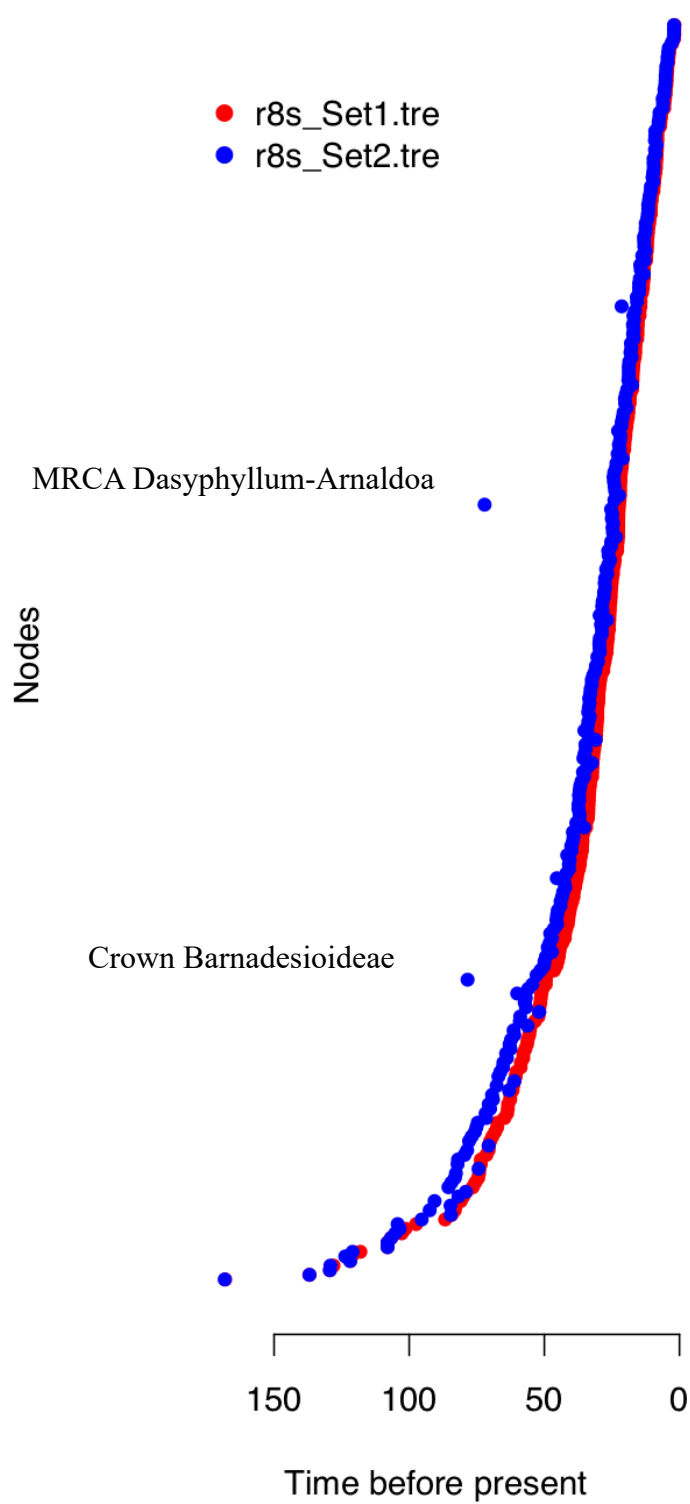
Supplemental Figure 24. Divergence times estimated using r8s (set 5).



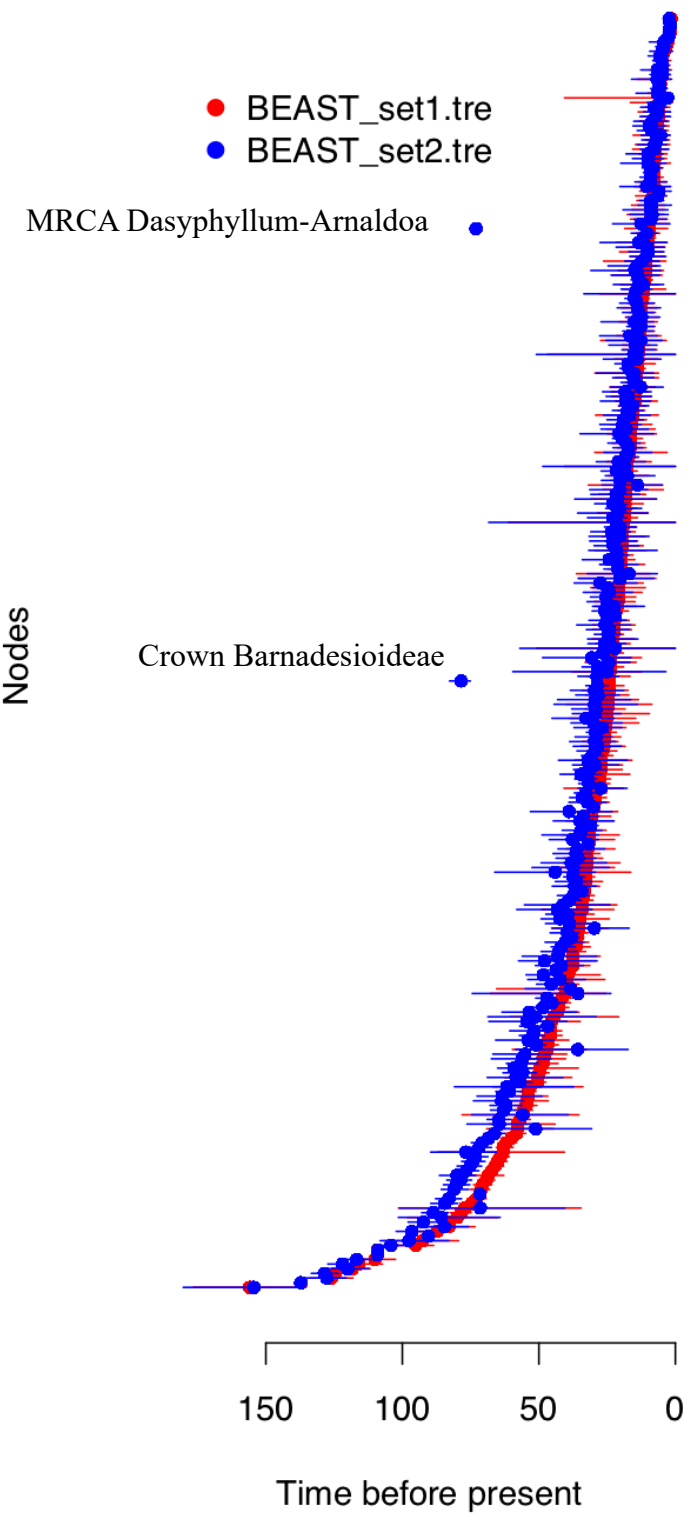
Supplemental Figure 25. Divergence times estimated using BEAST (set 5).



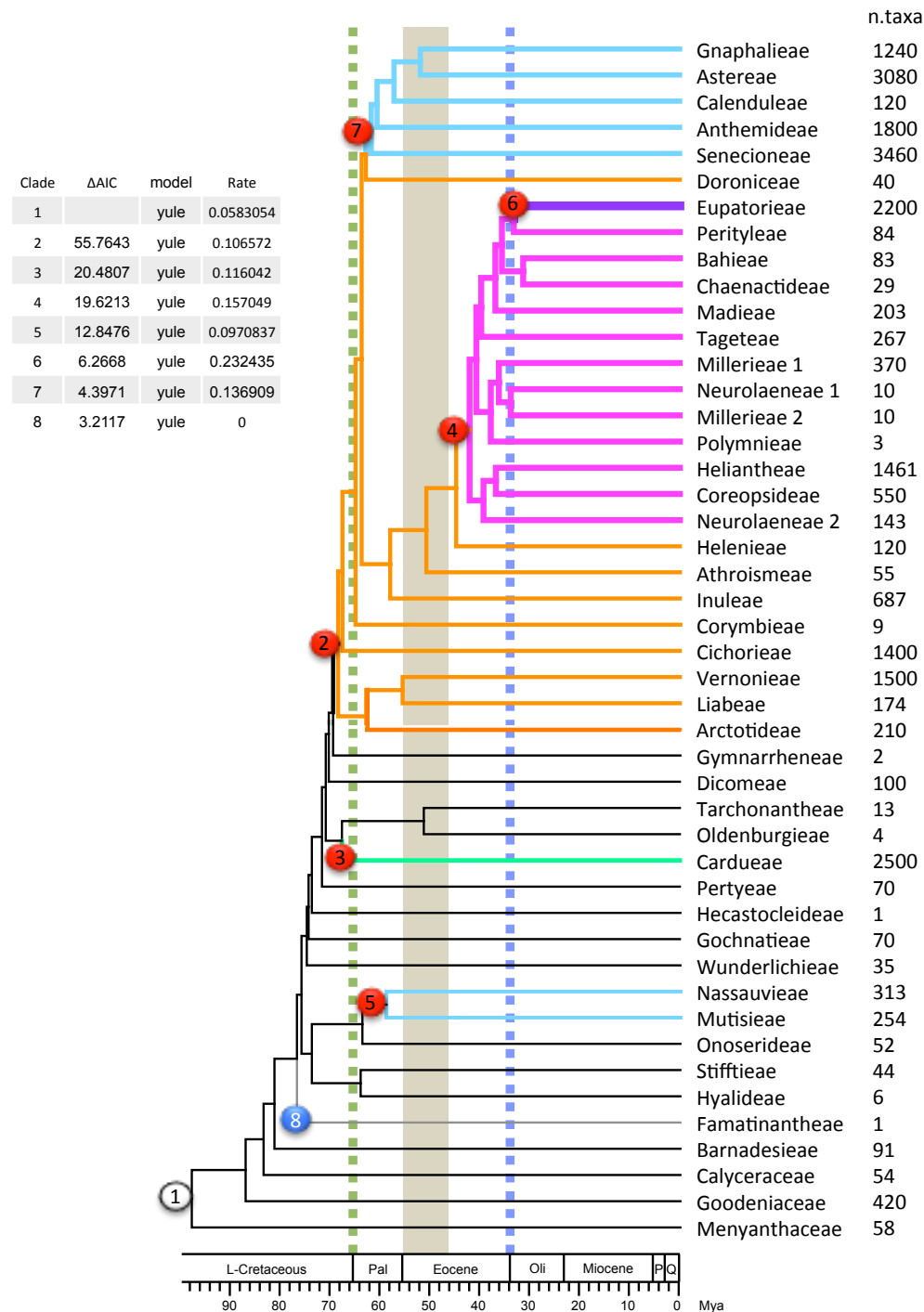
Supplemental Figure 26. Comparing ages with calibration sets 1 and 2 using r8s.



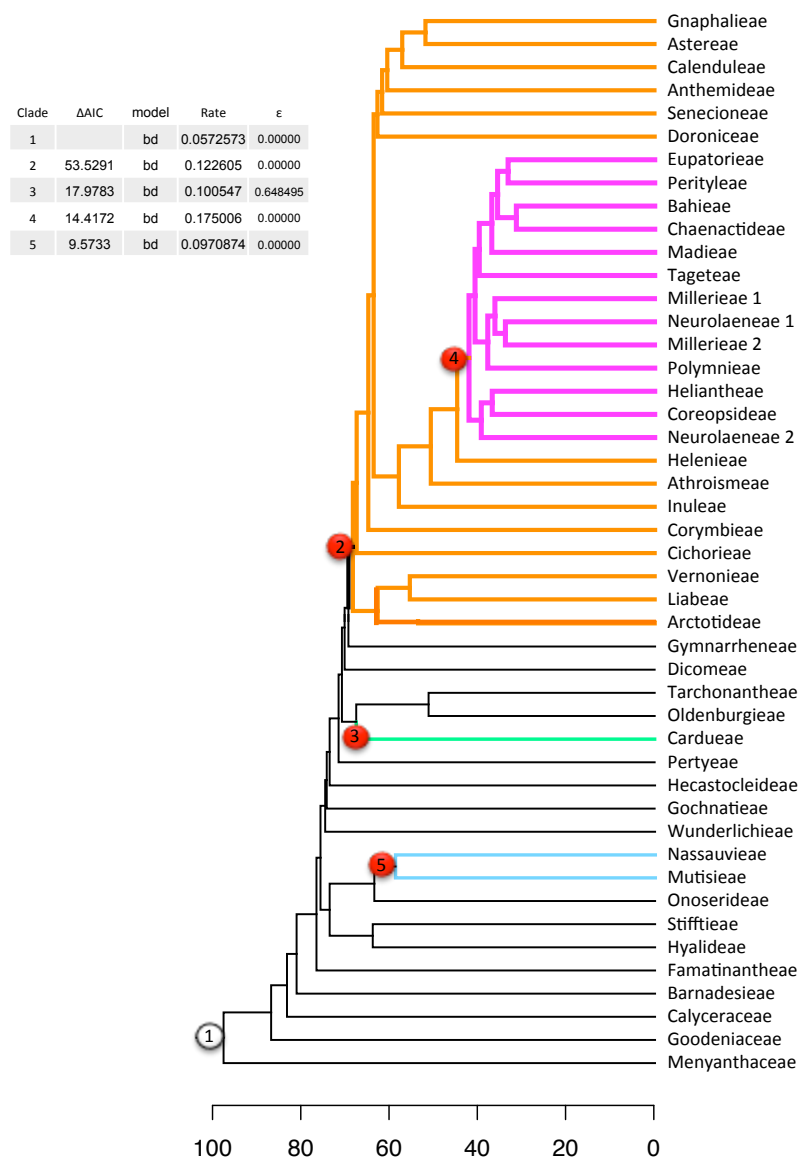
Supplemental Figure 27. Comparing ages with calibration sets 1 and 2 using BEAST.



Supplemental Figure S28. Net diversification rate shift analyzed by MEDUSA under mixed model.

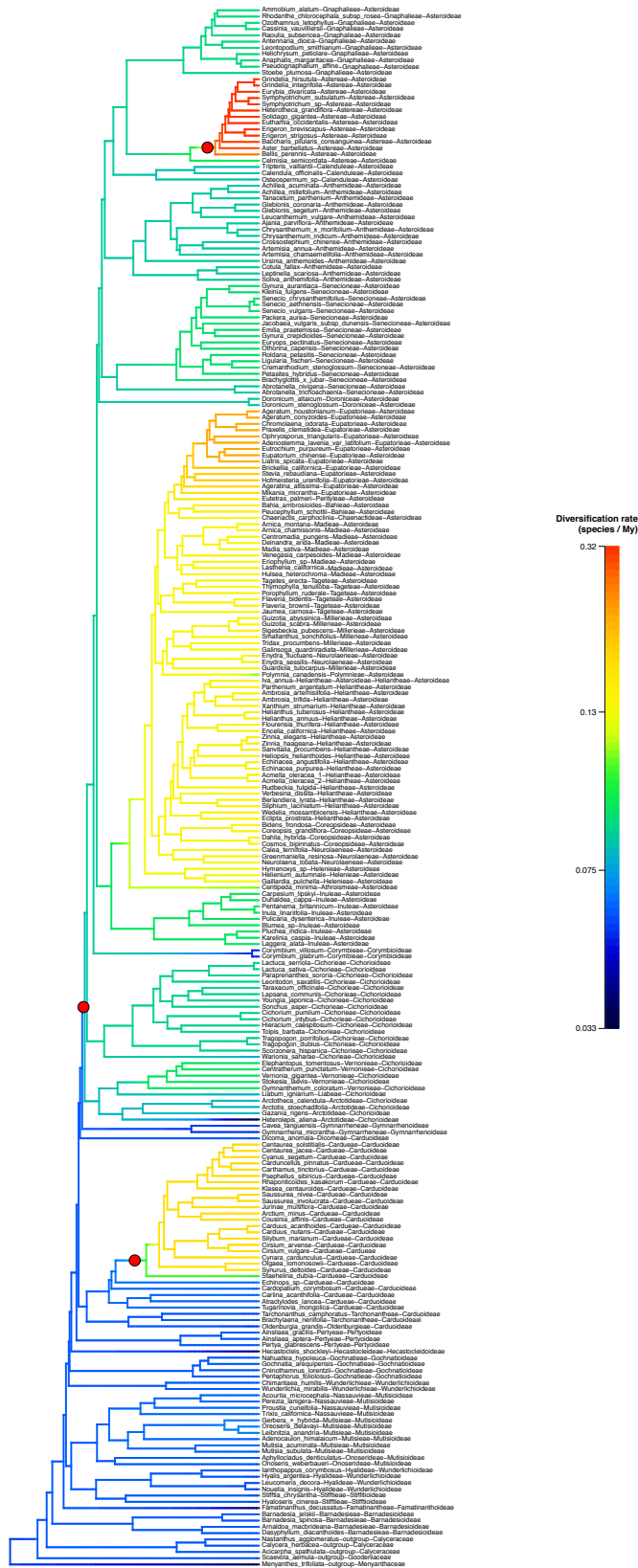


Supplemental Figure S29. Net diversification rate shift analyzed by MEDUSA under birth-death model.

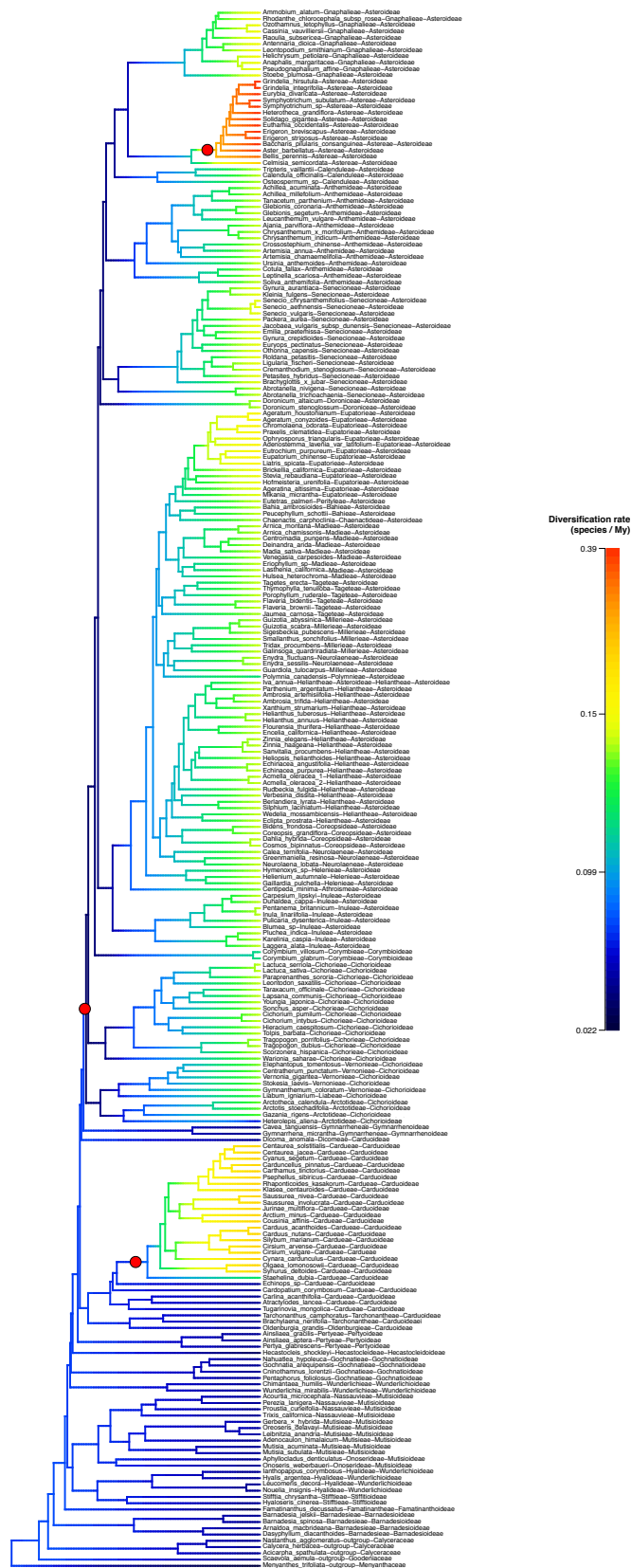


Supplemental Figure 30. Shift configuration of net diversification rates with the highest maximum a posteriori (MAP) probability (“the best shift configuration”) as a result of BAMM analyses.

(a) Time-constant algorithm

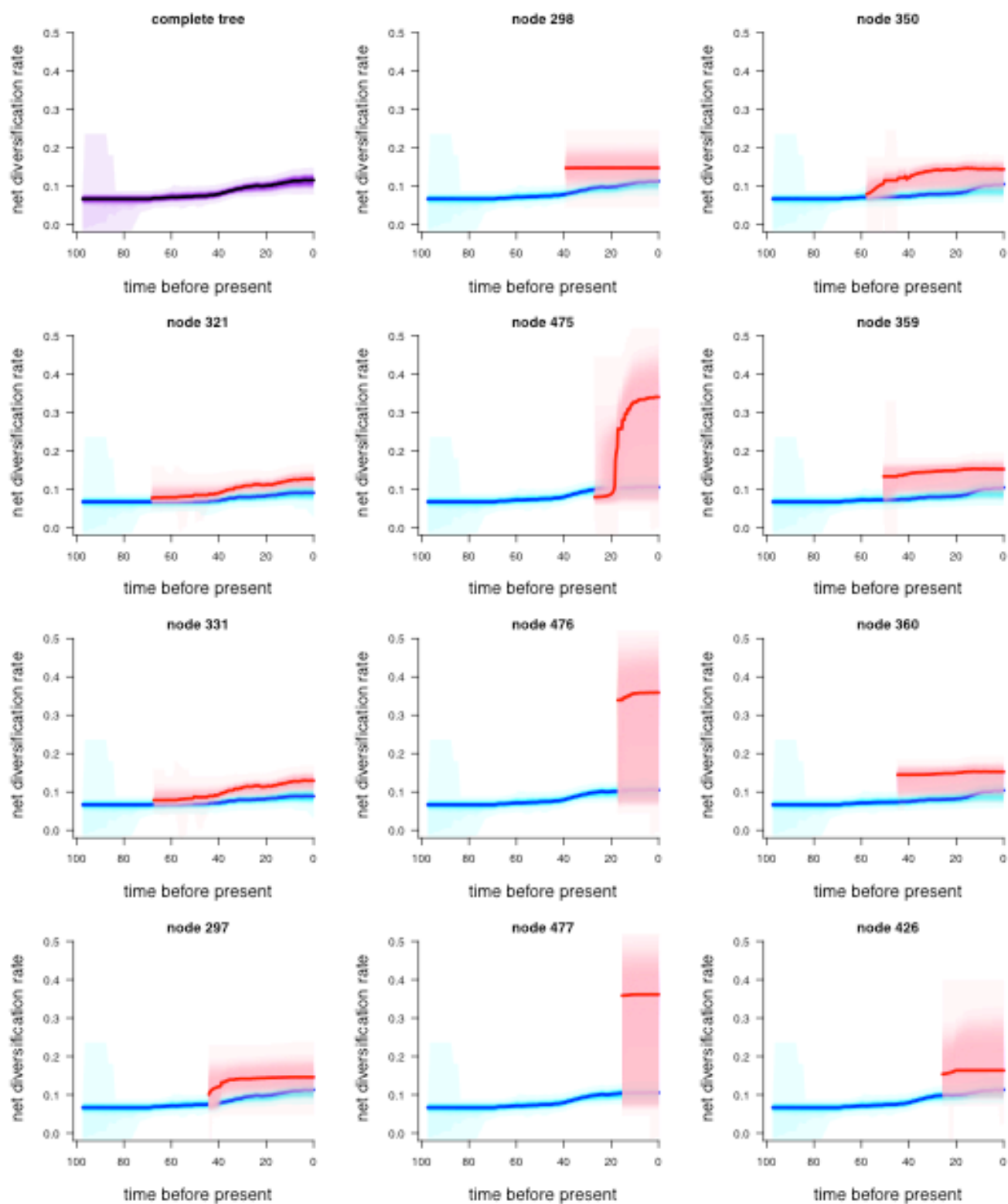


(b) Time-variable algorithm



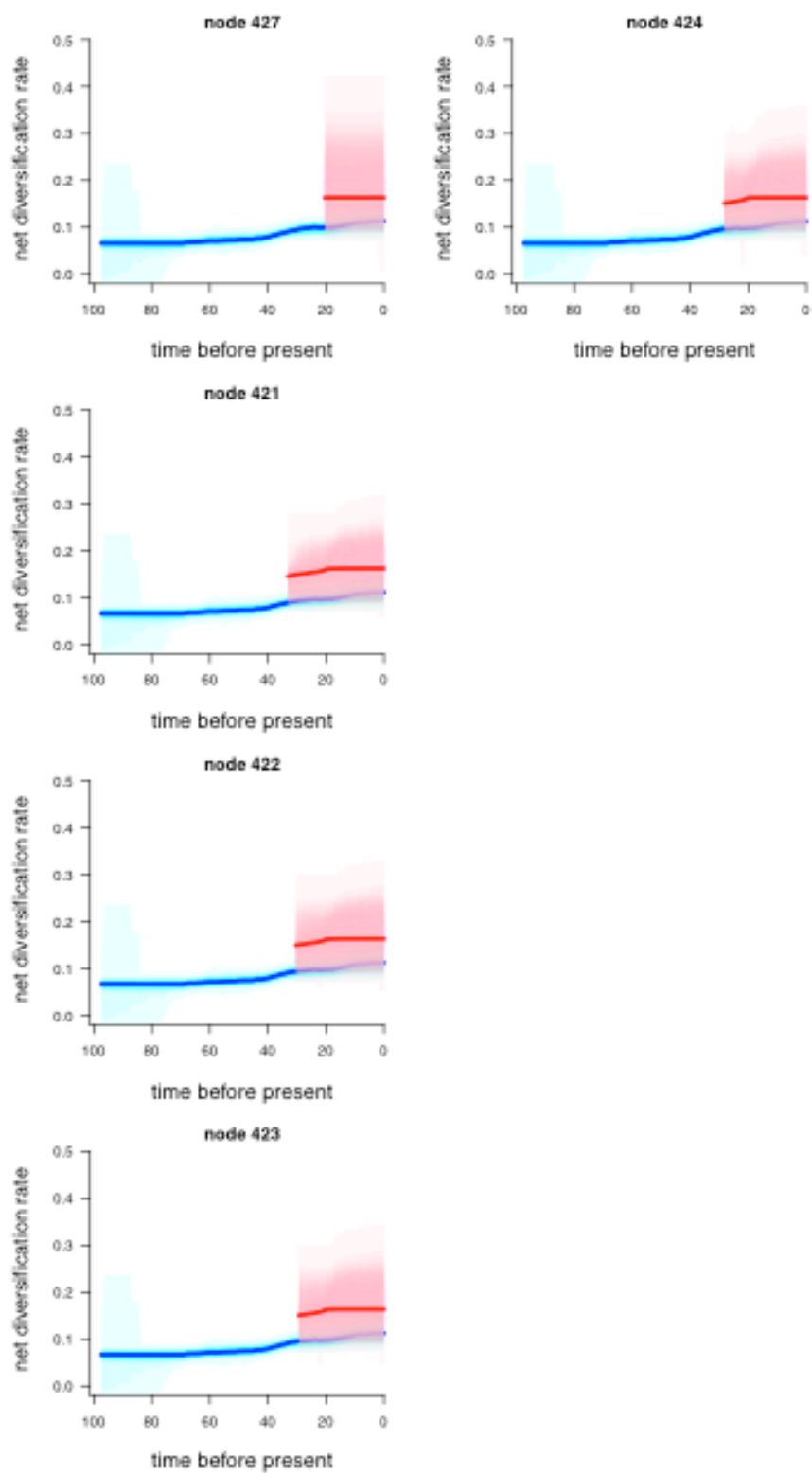
Supplemental Figure S31. Rate-through-time (RTT) plots of net diversification rates estimated by BAMM.

(a) Time-constant algorithm



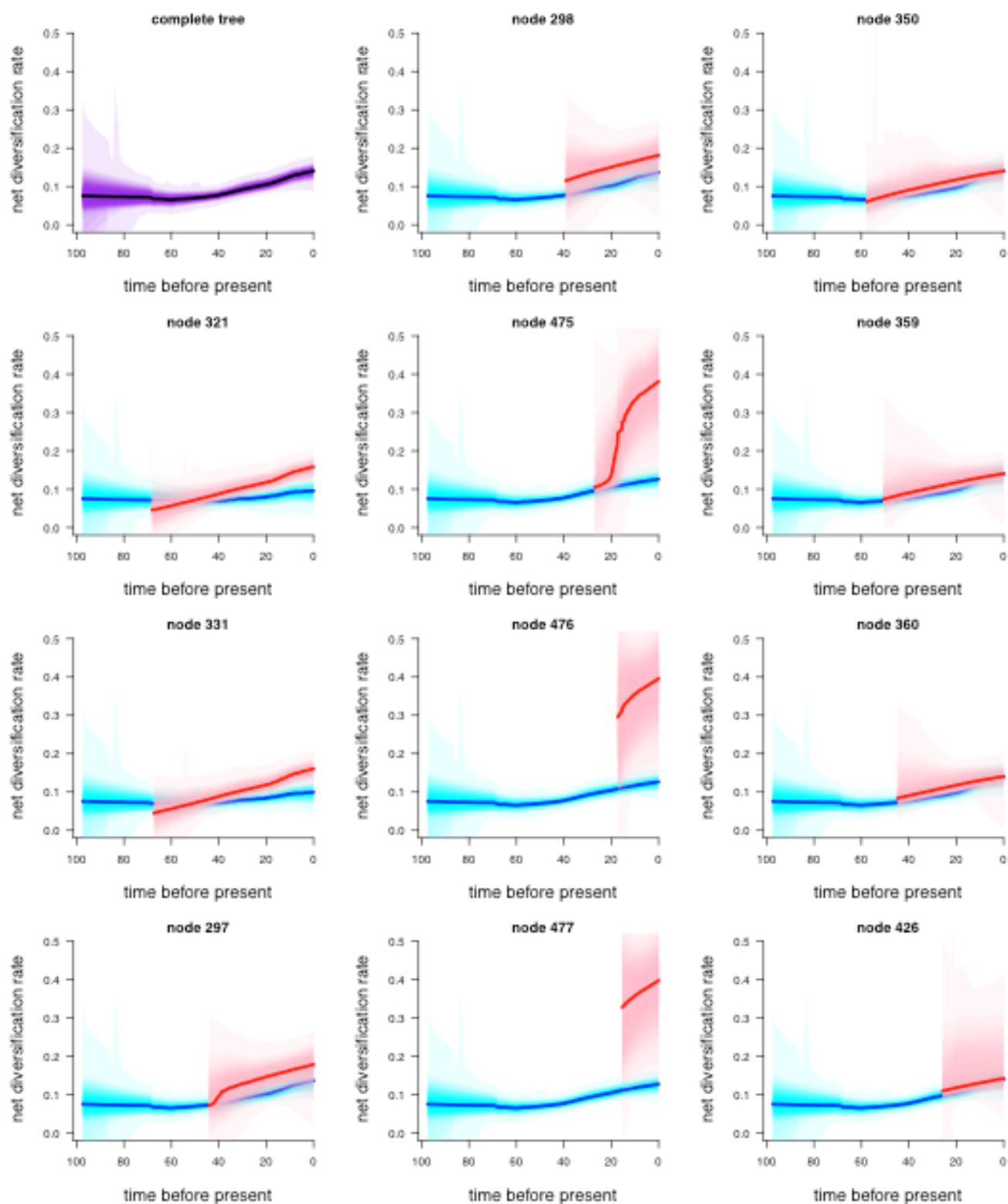
Supplemental Figure S31. continue

(b) Time-constant algorithm continue



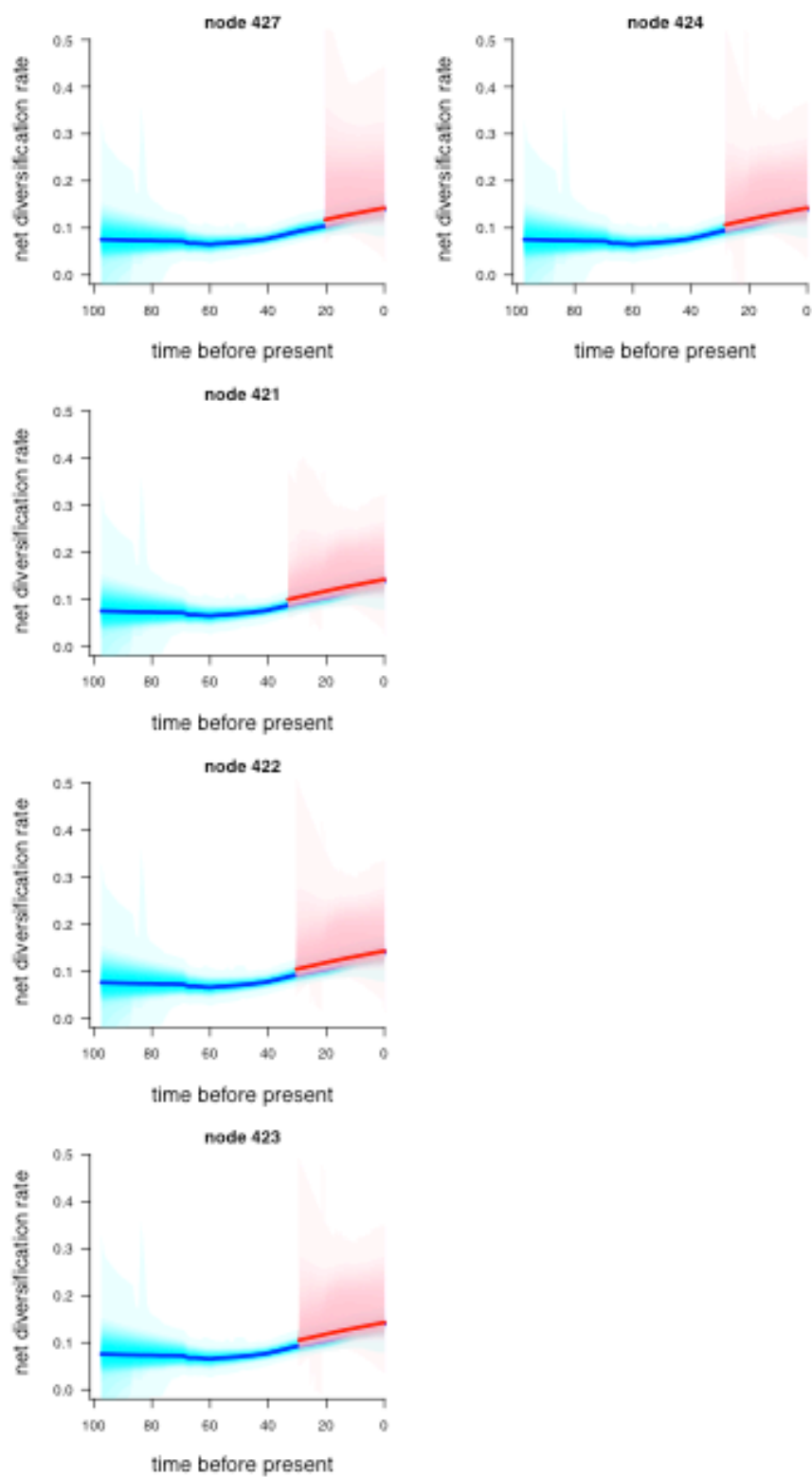
Supplemental Figure S31. Continue

(c) Time-variable algorithm

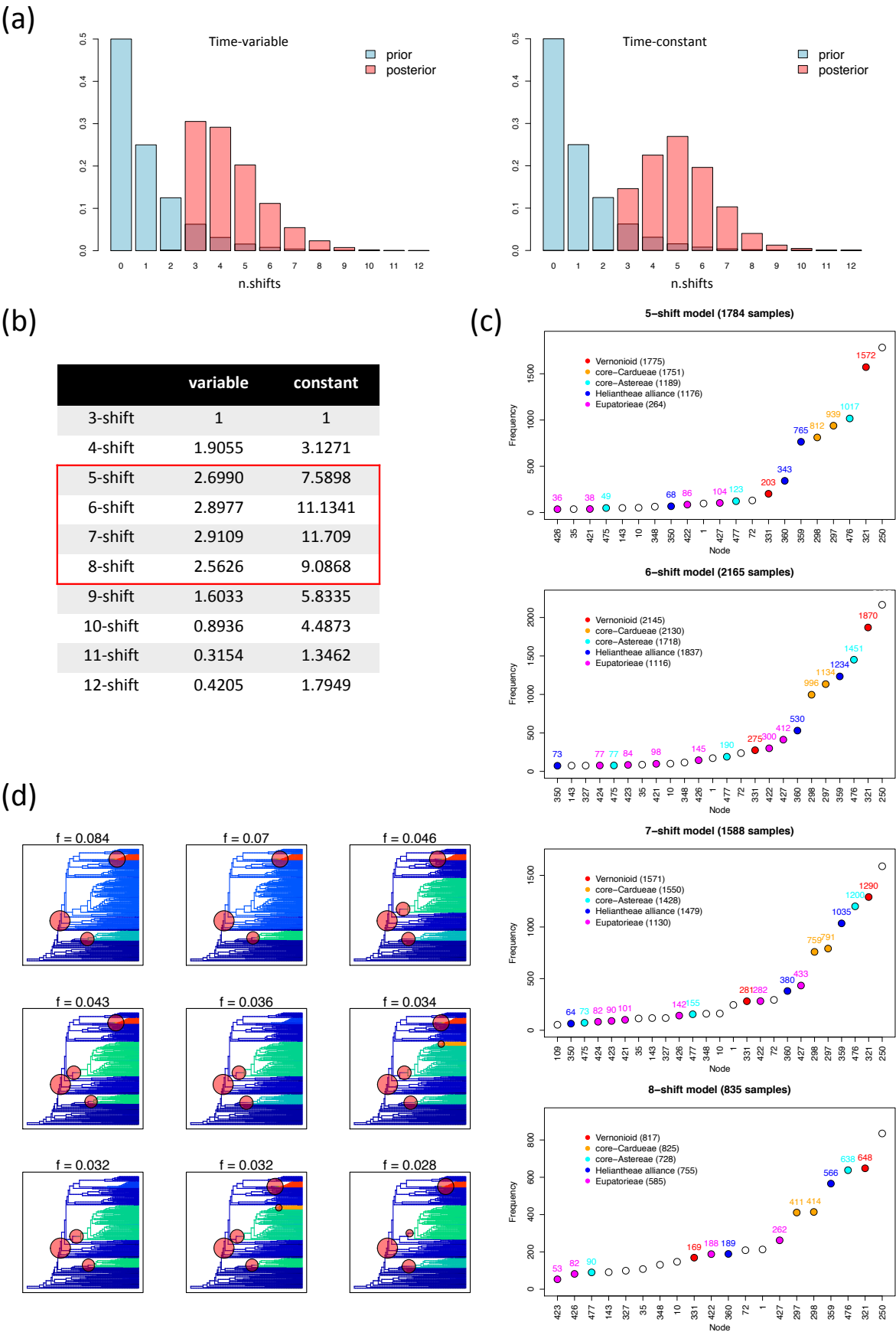


Supplemental Figure S31. Continue

(d) Time-variable algorithm continue

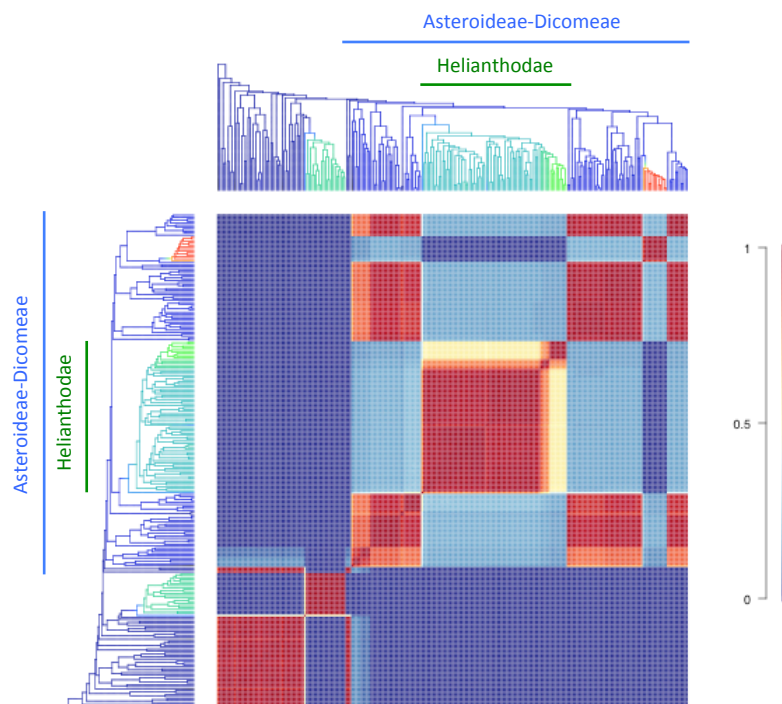


Supplemental Figure 32. In-depth investigation on the shift positions from BAMB

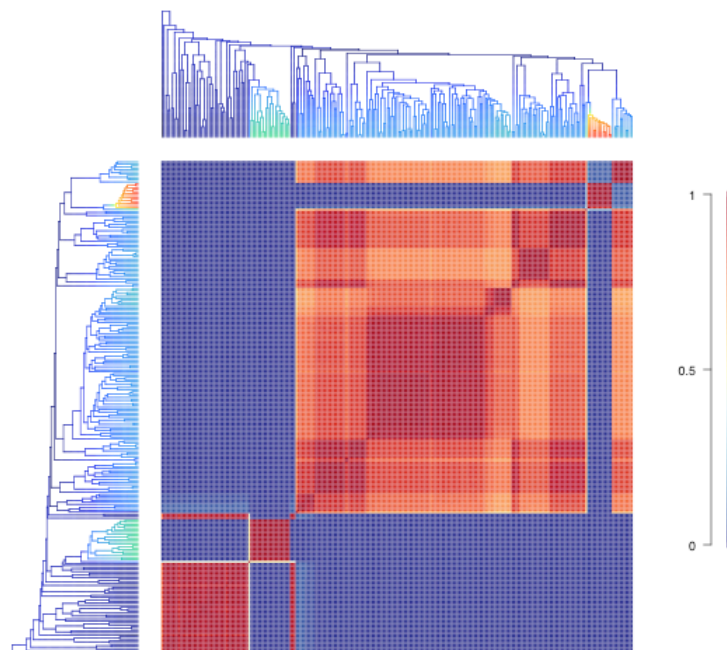


Supplemental Figure S33. Cohorts of net diversification rates by BAMM.

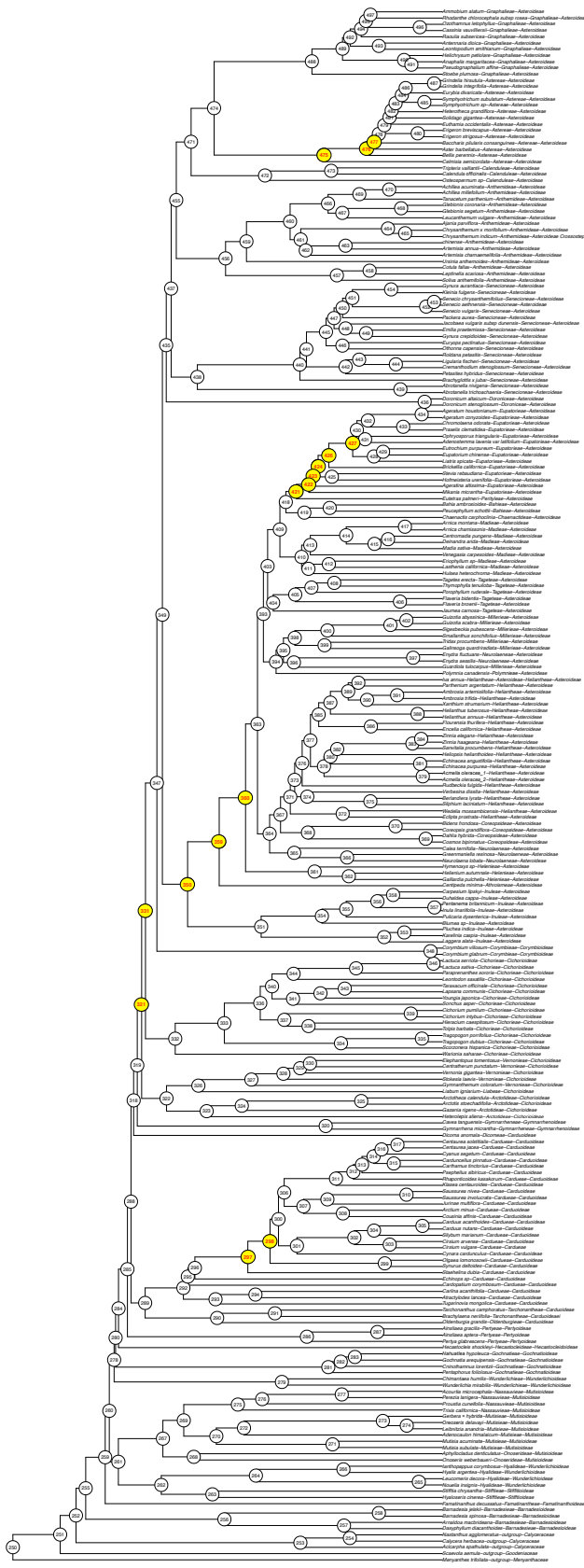
(a) Time-constant algorithm



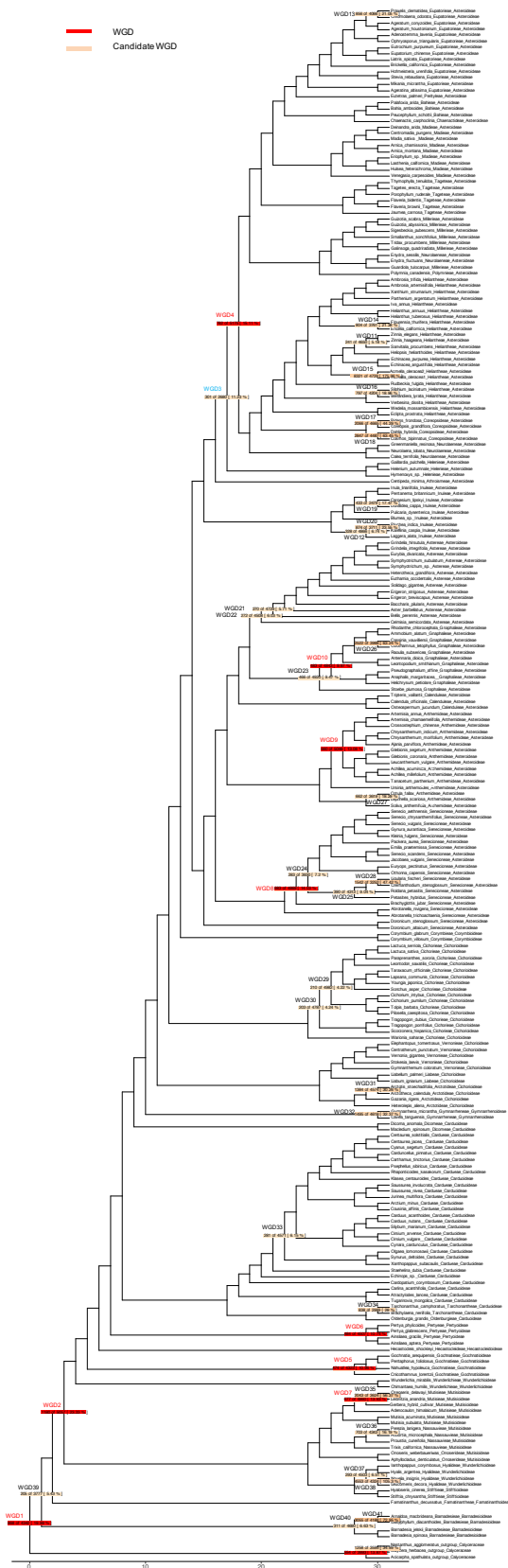
(b) Time-variable algorithm



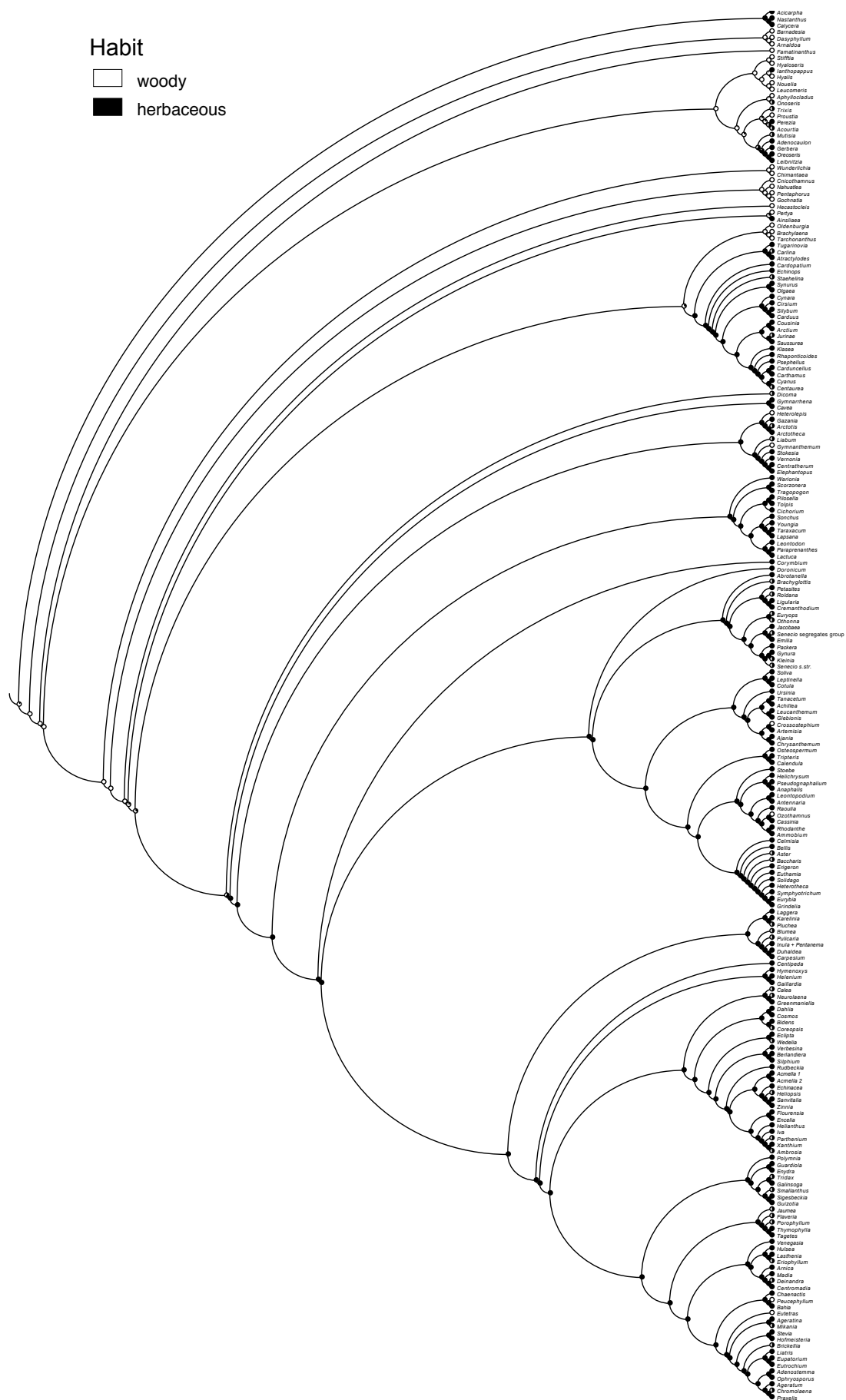
Supplemental Figure 34. Identification of nodes in BAMM analyses.



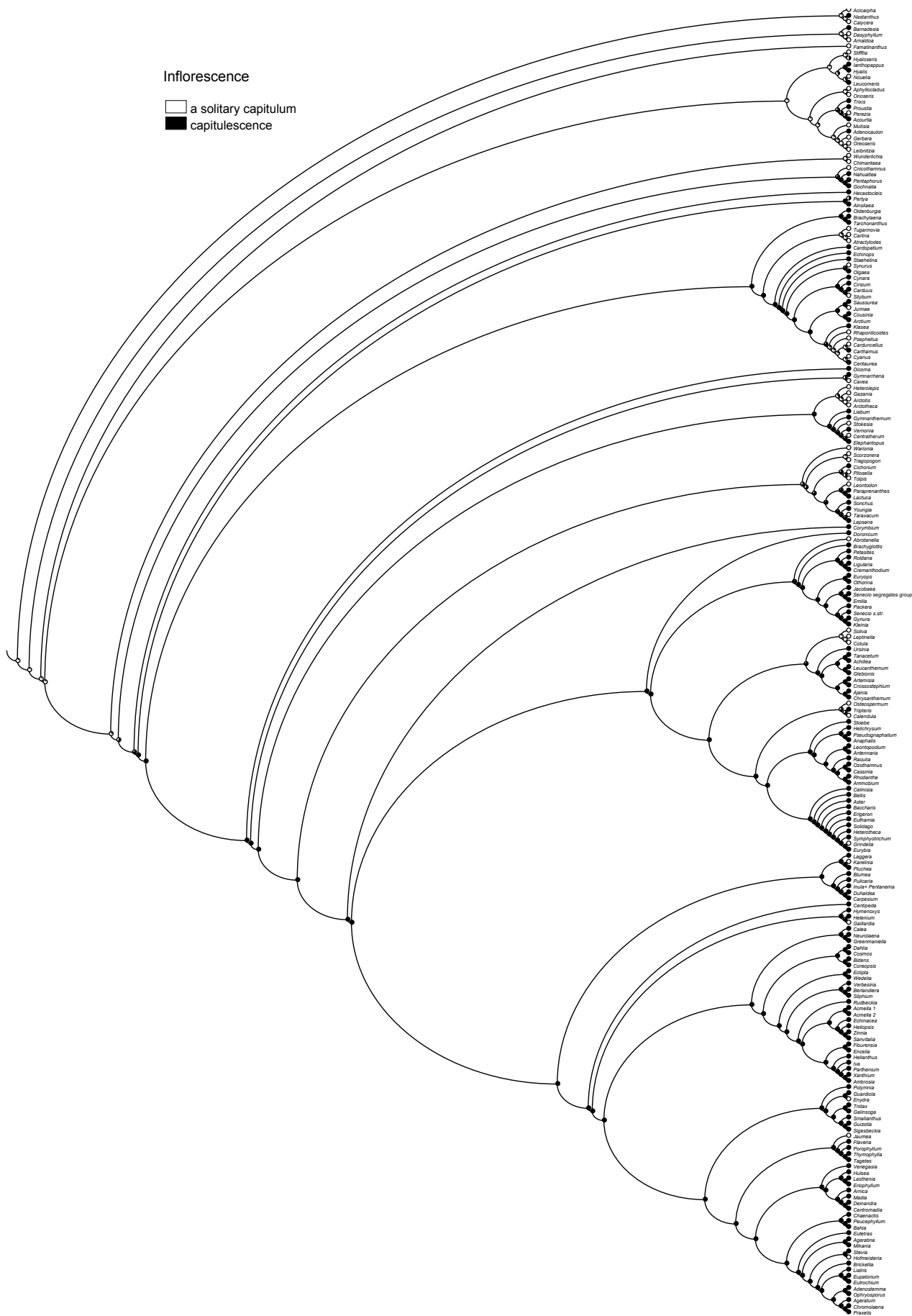
Supplemental Figure 35. A summary of detected (candidate) whole genome duplication event.



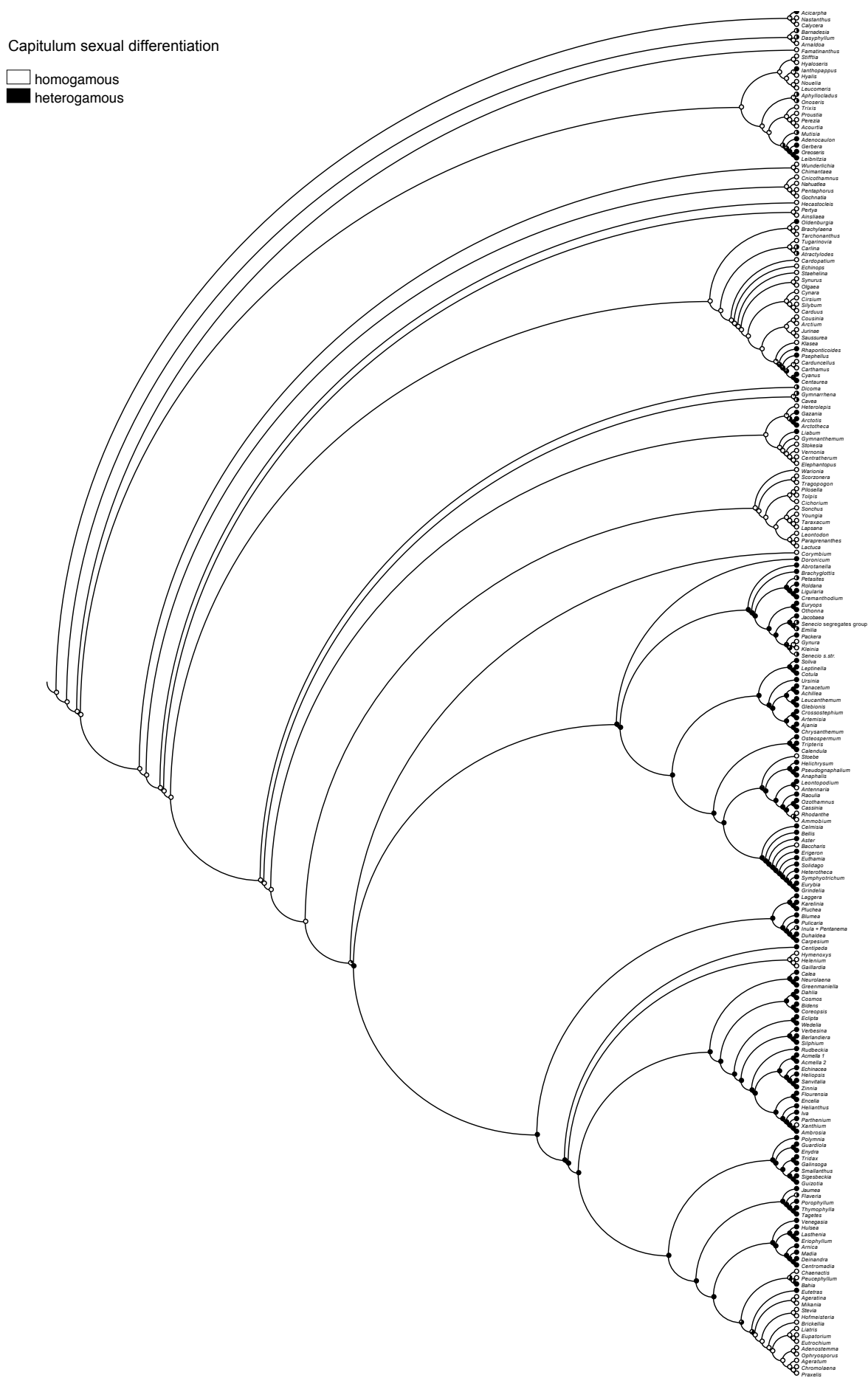
Supplemental Figure 36. Ancestral character reconstruction of habit.



Supplemental Figure 37. Ancestral character reconstruction of inflorescence.

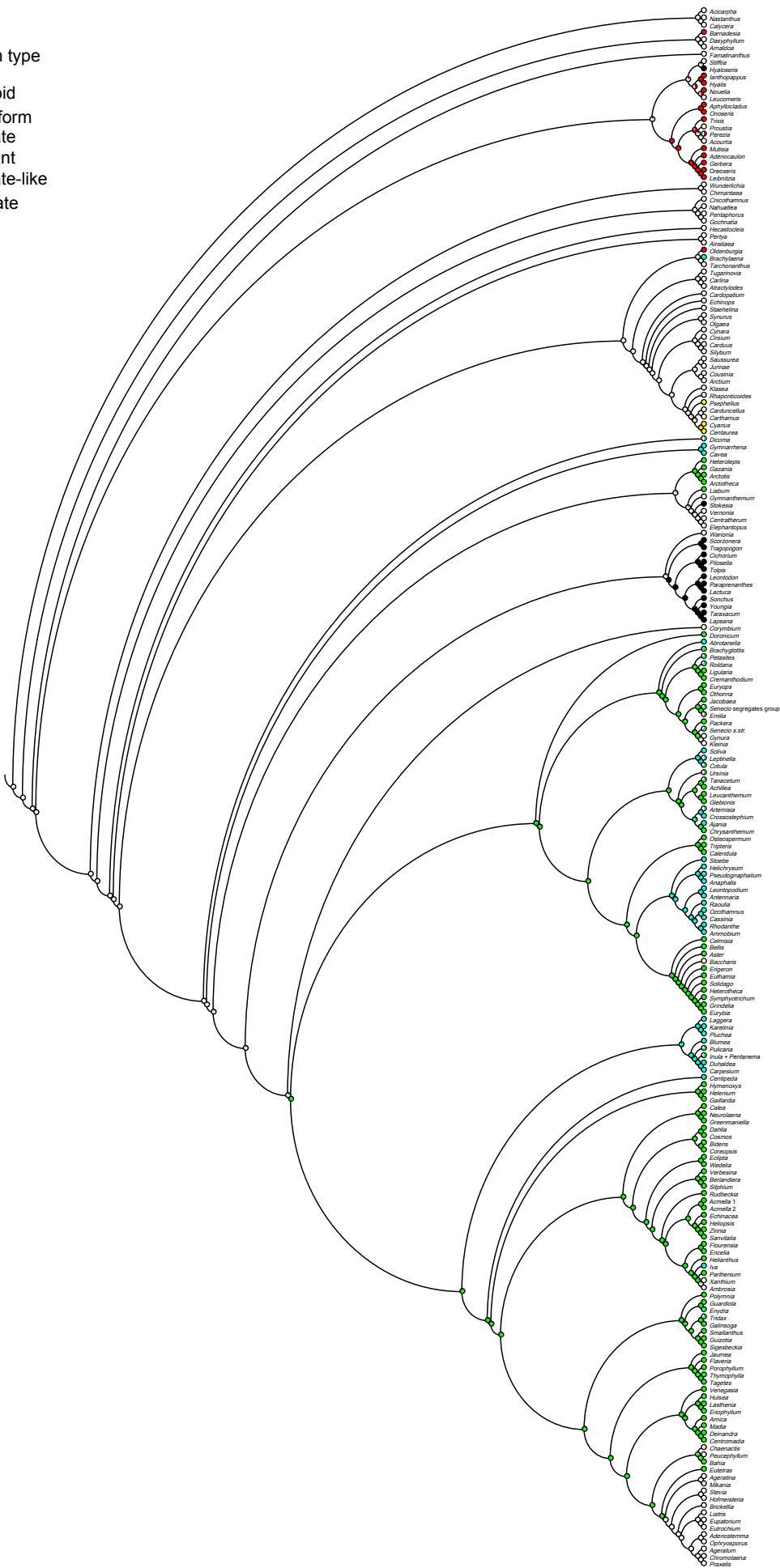


Supplemental Figure 38. Ancestral character reconstruction of capitulum sexual differentiation.

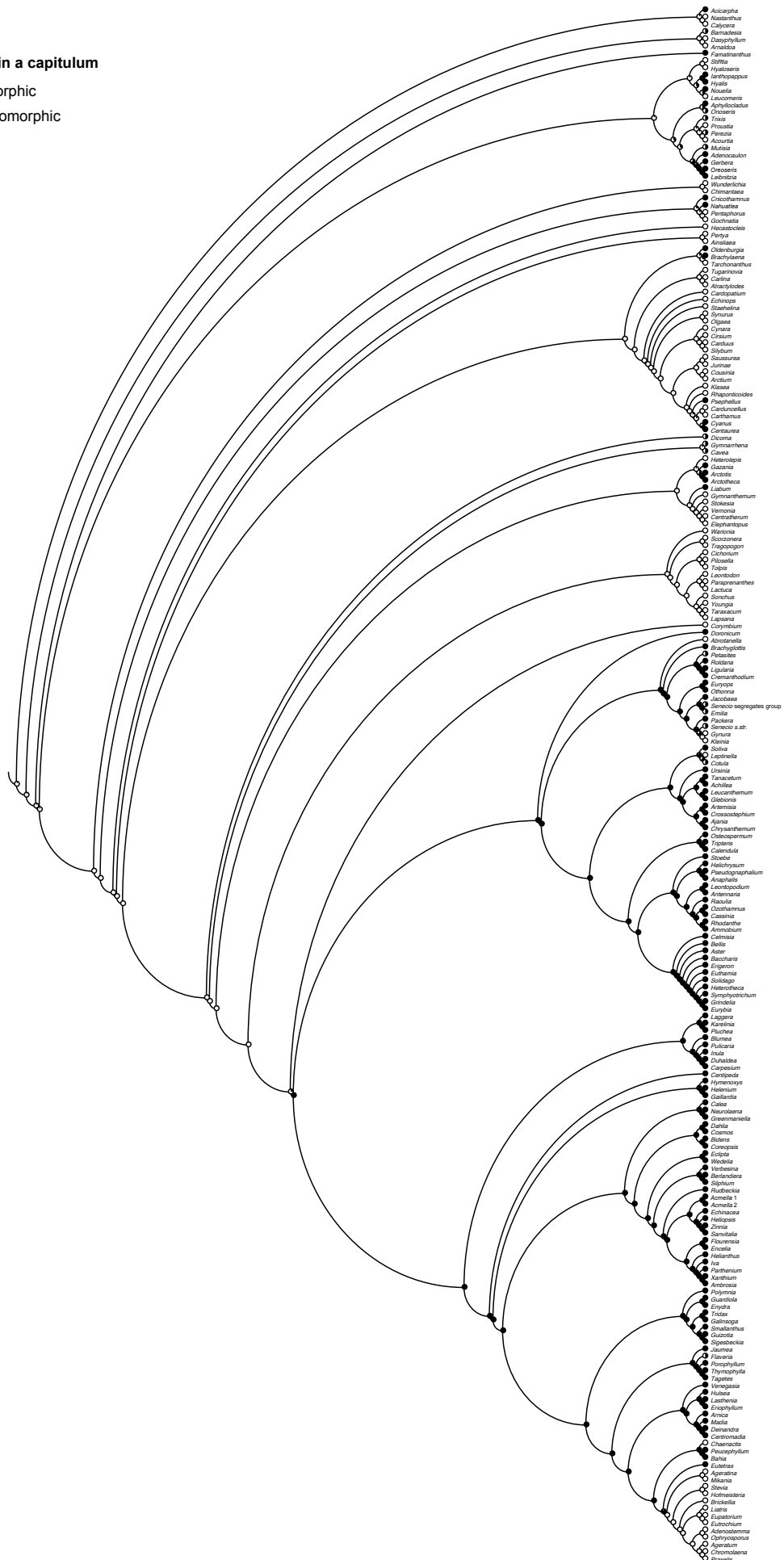


Supplemental Figure 39. Ancestral character reconstruction of capitulum type.

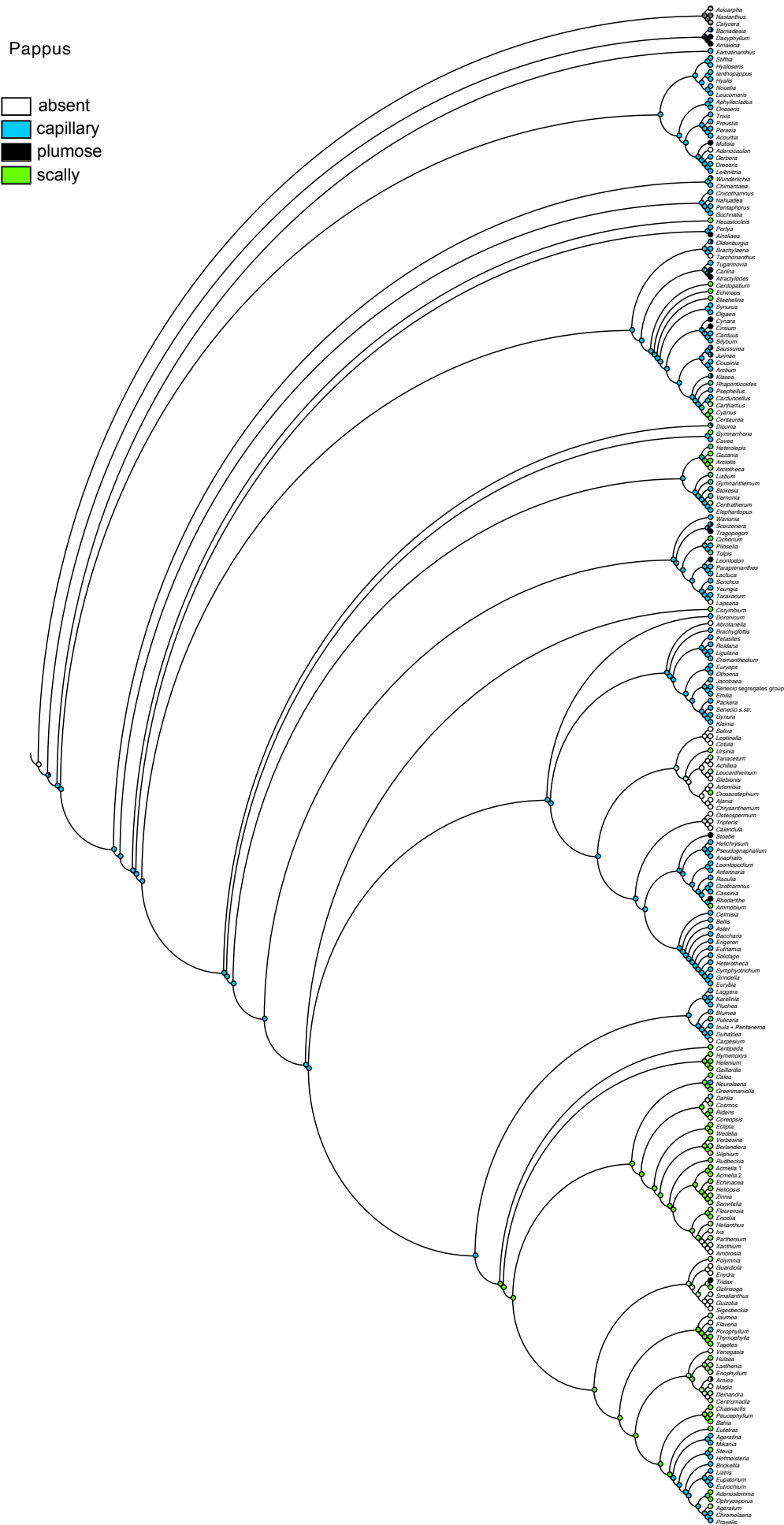
- Capitulum type
- discoïd
 - disciform
 - radiate
 - radiant
 - radiate-like
 - ligulate



Supplemental Figure 40. Ancestral character reconstruction of corollas in a capitulum.



Supplemental Figure 41. Ancestral character reconstruction of pappus.



Supplemental Figure 42. Ancestral character reconstruction of receptacular bracts.

