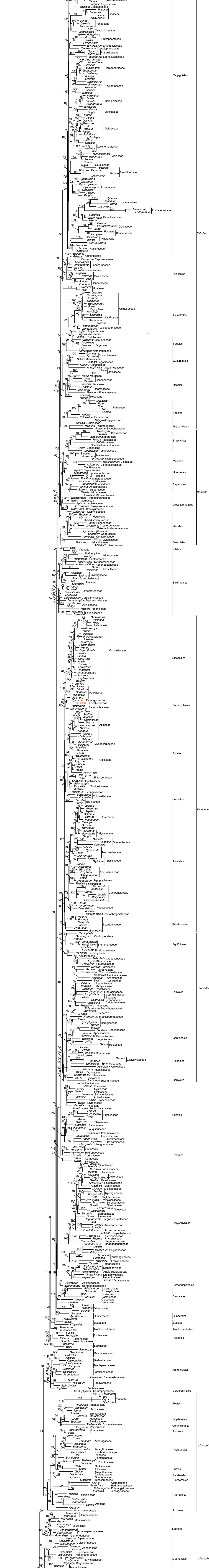
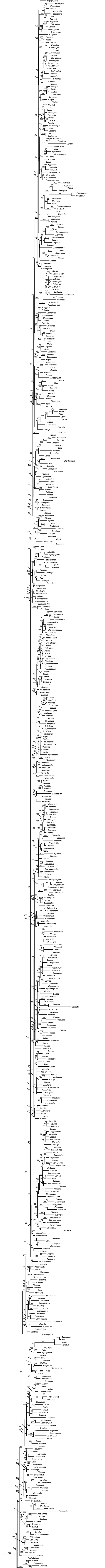


Soltis et al.—*American Journal of Botany* 96(4):704–730, 2009. Data Supplement—page 1
 Soltis, Douglas E., Smith, Nicos C., Cellinese, Kenneth J., Wurdack, David J., Tank, Samuel F., Brockington, Nancy F., Relafio-Rodriguez, Jay B., Walker, Michael J., Moeser, Barbara S., Carlward, Charles D., Bell, Maribeth Luttrell, Sunny C., Davis, Michael J., Sanderson, David, Zhou, Xiansheng, Richard G., Olmstead, Walter S., Judd, Michael J., Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 species. *American Journal of Botany* 98(4): 704–730.

Appendix S2. The maximum likelihood majority rule consensus tree from the 17-gene analysis shown as a phylogenogram. Numbers above branches are bootstrap percentages.

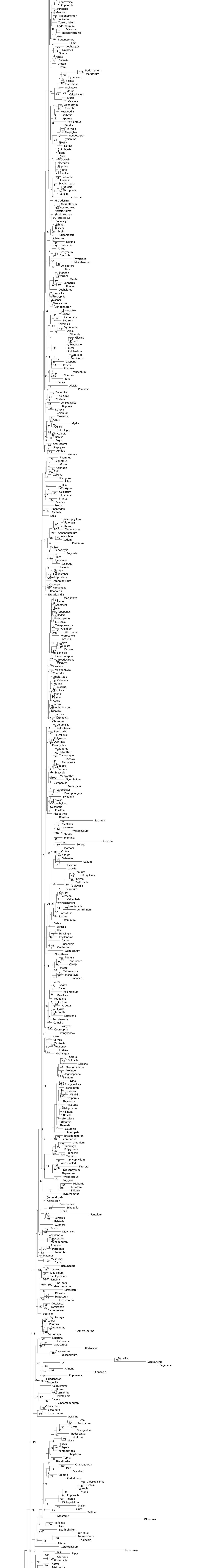


Appendix S3. The maximum likelihood majority-rule consensus from the 13-gene analysis (plastid plus rSSU26S; no mtDNA) shown as a phylogram. Names of the orders and families follow APG III (2009); other names follow Cantino et al. (2007). Numbers above branches are bootstrap percentages.

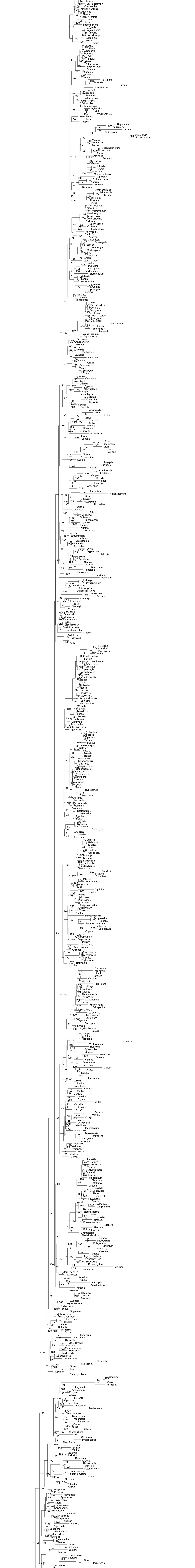


Appendix S4. The maximum likelihood majority-rule consensus from the rDNA analysis (18S/26S) shown as a phylogram. Numbers above branches are bootstrap percentages.

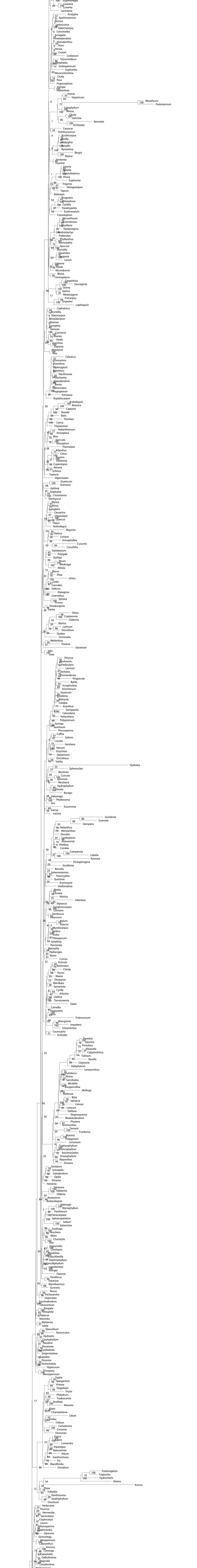
Hugonia



Appendix S5. The maximum likelihood majority-rule consensus from the cpDNA analysis shown as a phylogram. Numbers above branches are bootstrap percentages.

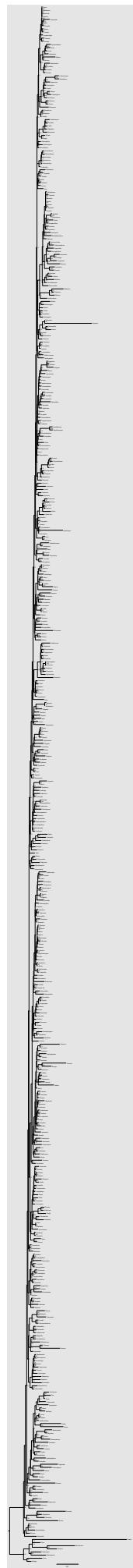


Appendix S6. The maximum likelihood majority-rule consensus tree from the mtDNA analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



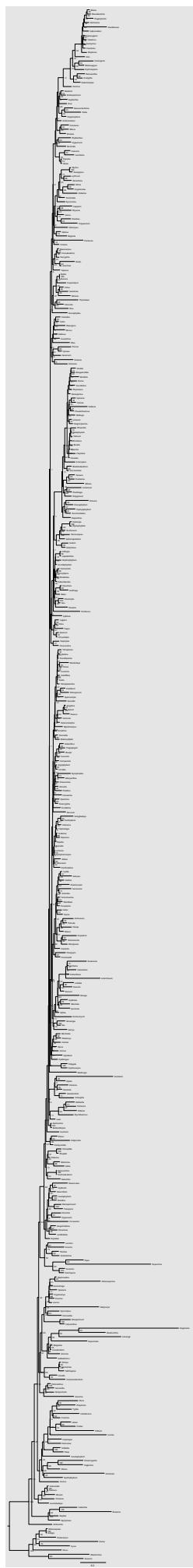
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S7. The maximum likelihood majority-rule consensus from the 18S rDNA analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



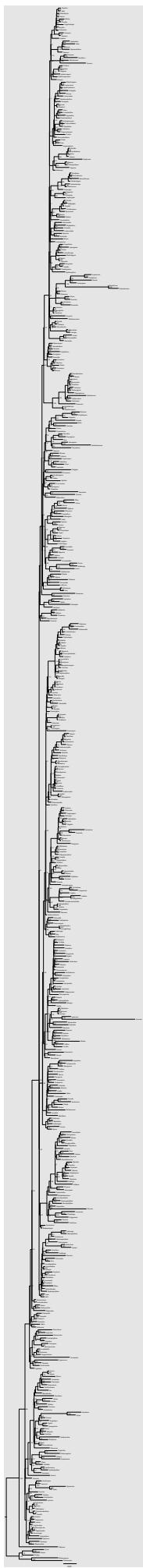
Soltis et al—*American Journal of Botany*
98(4):704-730. 2011. – Data Supplement S8 – page
1
Soltis, Douglas E., Stephen A. Smith, Nico
Cellinese, Kenneth J. Wurdack, David C. Tank,
Samuel F. Brockington, Nancy F. Refulio-
Rodriguez, Jay B. Walker, Michael J. Moore,
Barbara S. Carlsward, Charles D. Bell, Maribeth
Latvis, Sunny Crawley, Chelsea Black, Diaga
Diouf, Zhenxiang Xi, Catherine A. Rushworth,
Matthew A. Gitzendanner, Kenneth J. Sytsma,
Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis,
Michael J. Sanderson, Reed S. Beaman, Richard G.
Olmstead, Walter S. Judd, Michael J. Donoghue,
and Pamela S. Soltis. Angiosperm phylogeny: 17
genes, 640 taxa. *American Journal of Botany* 98(4):
704-730.

Appendix S8. The maximum likelihood
majority-rule consensus from the 26S rDNA
analysis shown as a phylogram. Numbers
above branches are bootstrap percentages.



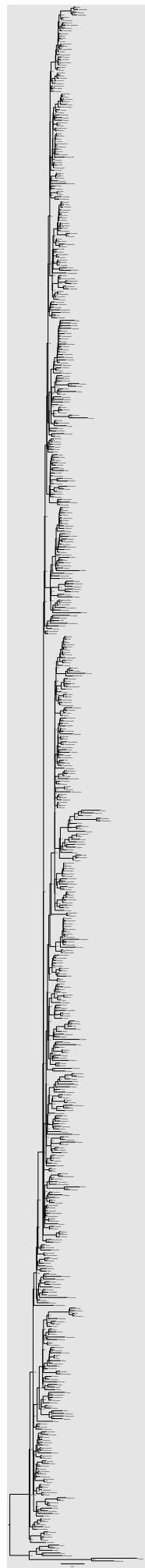
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704-730.

Appendix S9. The maximum likelihood majority-rule consensus from the *atpB* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlswald, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S10. The maximum likelihood majority-rule consensus from the *matK* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



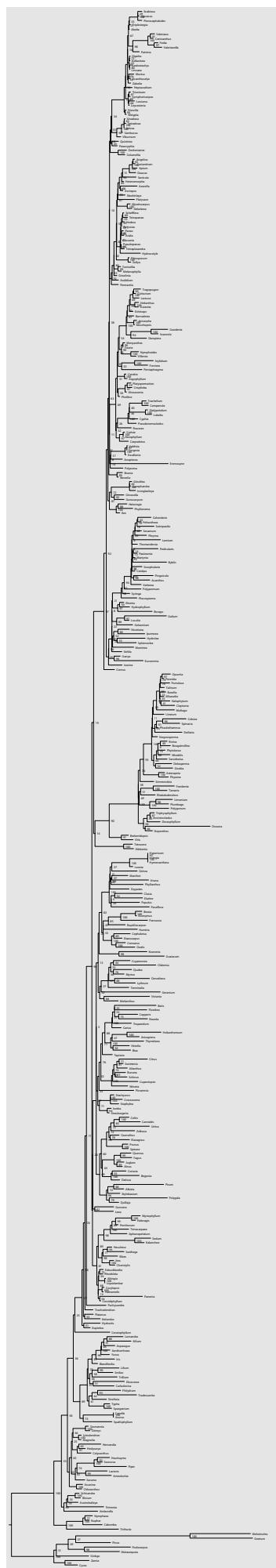
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S11. The maximum likelihood majority-rule consensus from the *ndhF* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



Soltis, Douglas E., Stephen A. Smith,
Nico Cellinese, Kenneth J. Wurdack,
David C. Tank, Samuel F. Brockington,
Nancy F. Refulio-Rodriguez, Jay B.
Walker, Michael J. Moore, Barbara S.
Carlsward, Charles D. Bell, Maribeth
Latvis, Sunny Crawley, Chelsea Black,
Diaga Diouf, Zhenxiang Xi, Catherine A.
Rushworth, Matthew A. Gitzendanner,
Kenneth J. Sytsma, Yin-Long Qiu, Khidir
W. Hilu, Charles C. Davis, Michael J.
Sanderson, Reed S. Beaman, Richard G.
Olmstead, Walter S. Judd, Michael J.
Donoghue, and Pamela S. Soltis.
Angiosperm phylogeny: 17 genes, 640
taxa. *American Journal of Botany* 98(4):
704–730.

Appendix S12. The maximum likelihood majority-rule consensus from the *psbBNTH* (four genes) analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



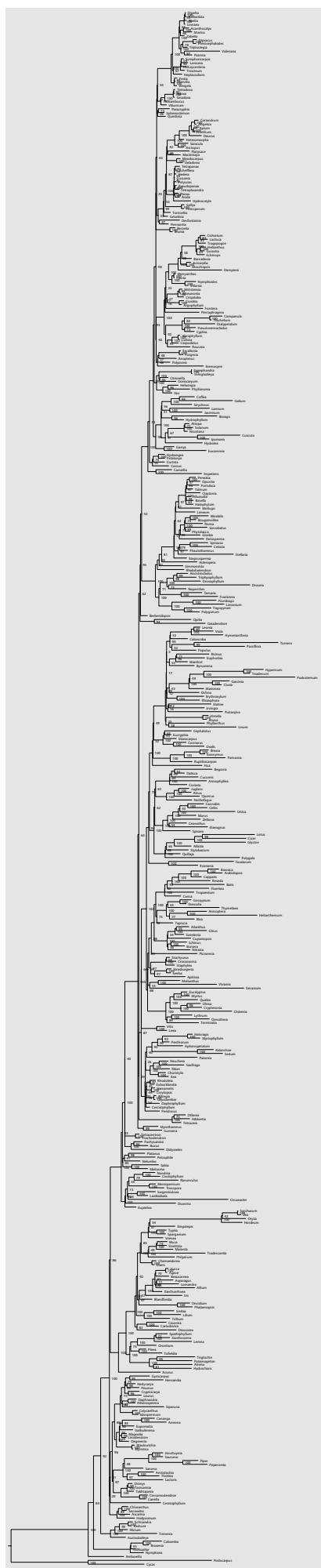
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S13. The maximum likelihood majority-rule consensus from the *rbcL* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704-730.

Appendix S14. The maximum likelihood majority-rule consensus from the *rpoC2* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



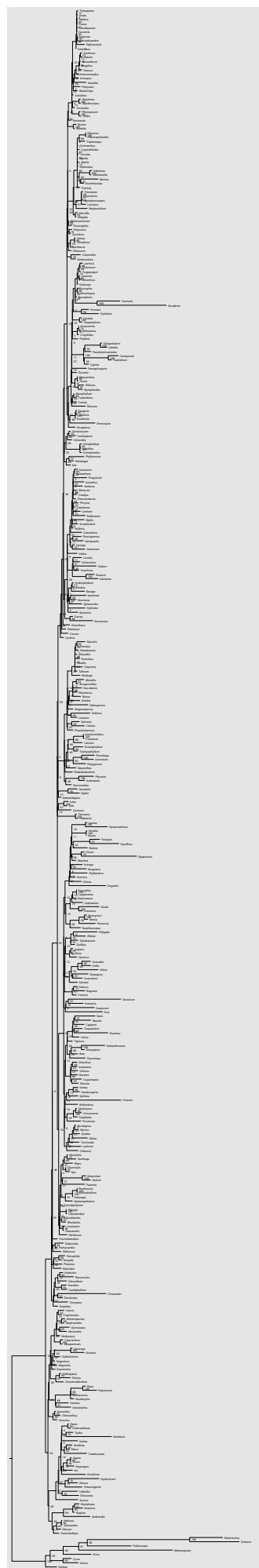
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S15. The maximum likelihood majority-rule consensus from the *rps16* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



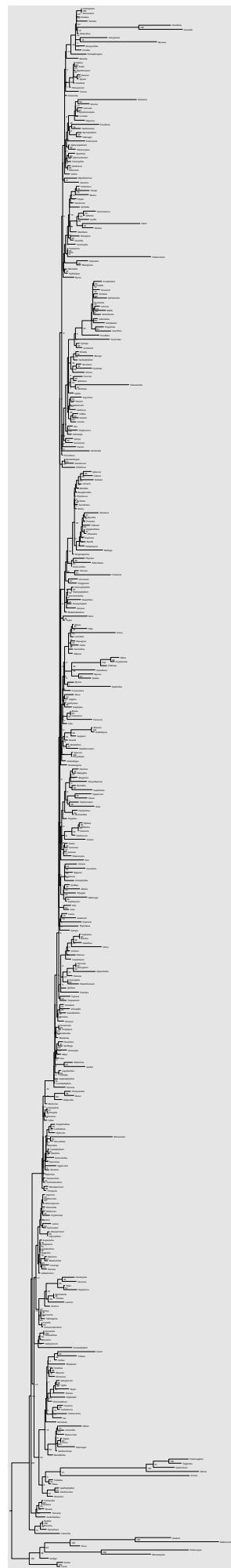
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704-730.

Appendix S16. The maximum likelihood majority-rule consensus from the *rps4* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



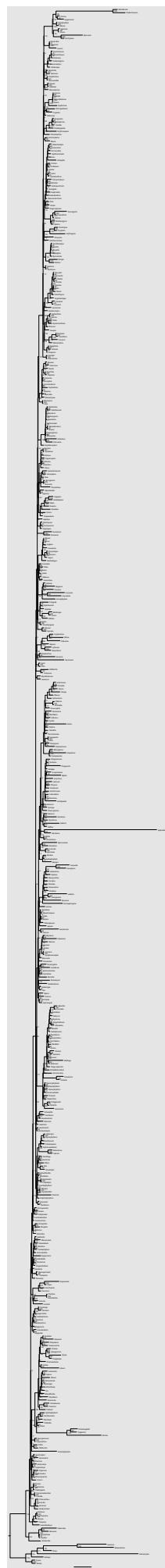
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S17. The maximum likelihood majority-rule consensus from the *atp1* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



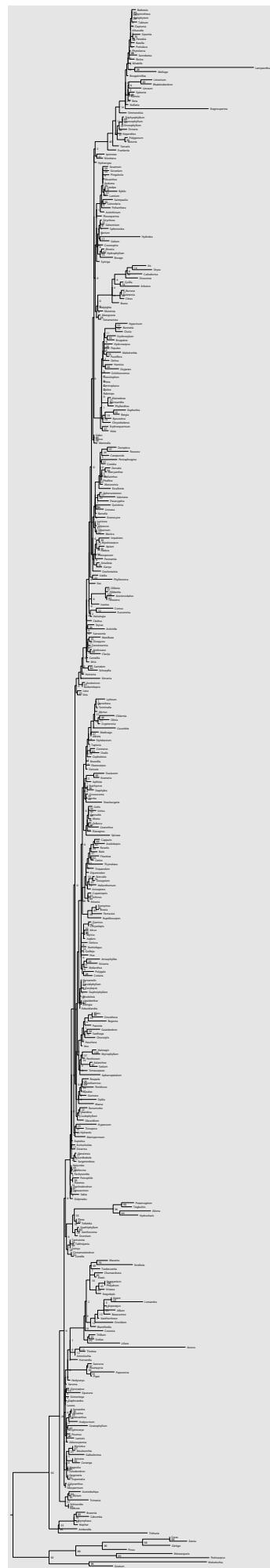
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S18. The maximum likelihood majority-rule consensus from the *matR* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlsward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704-730.

Appendix S19. The maximum likelihood majority-rule consensus from the *nad5* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



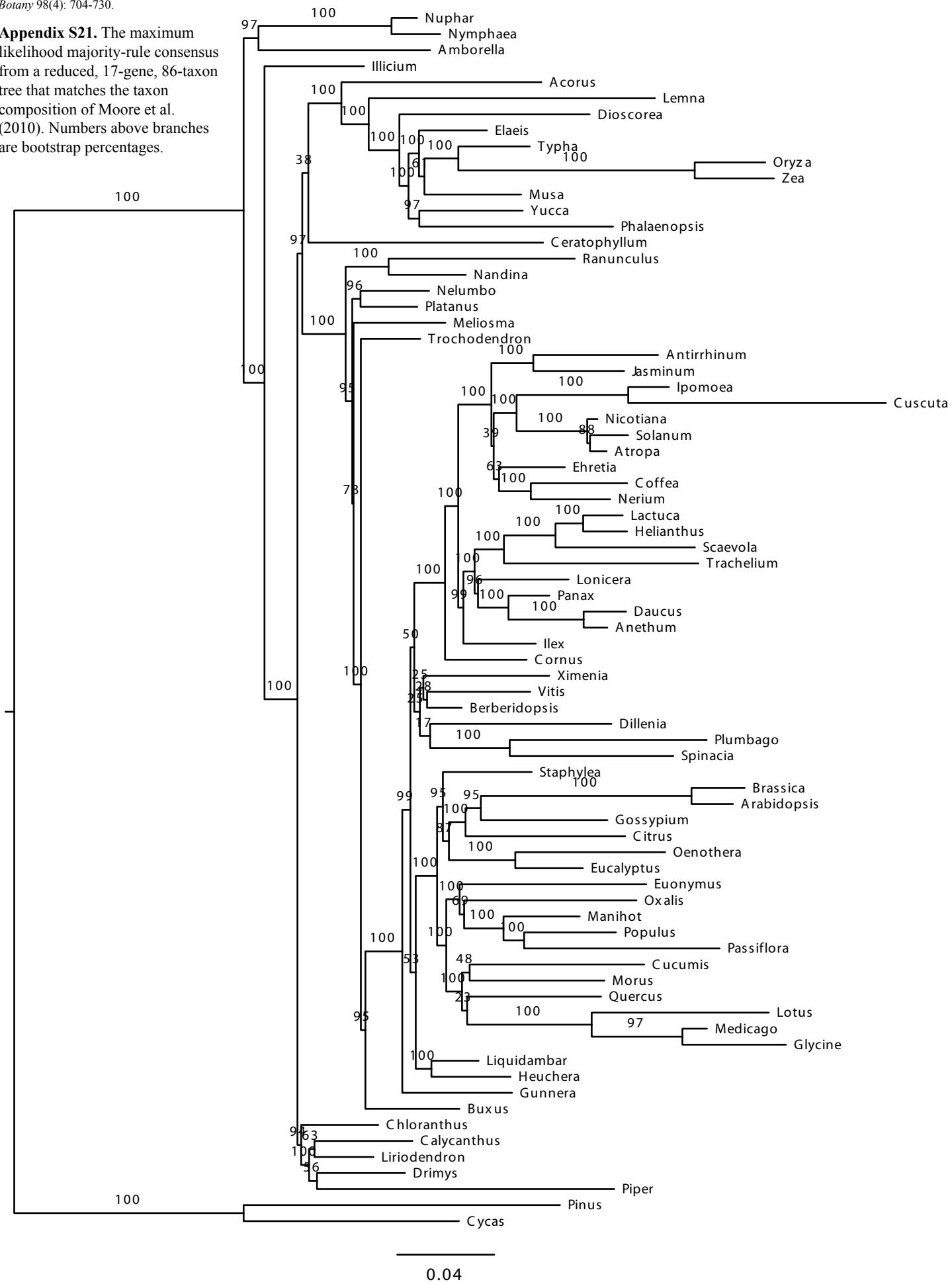
Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704-730.

Appendix S20. The maximum likelihood majority-rule consensus from the *rps3* analysis shown as a phylogram. Numbers above branches are bootstrap percentages.



Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Refulio-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlswald, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Diaga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S21. The maximum likelihood majority-rule consensus from a reduced, 17-gene, 86-taxon tree that matches the taxon composition of Moore et al. (2010). Numbers above branches are bootstrap percentages.



Soltis, Douglas E., Stephen A. Smith, Nico Cellinese, Kenneth J. Wurdack, David C. Tank, Samuel F. Brockington, Nancy F. Reffuto-Rodriguez, Jay B. Walker, Michael J. Moore, Barbara S. Carlward, Charles D. Bell, Maribeth Latvis, Sunny Crawley, Chelsea Black, Draga Diouf, Zhenxiang Xi, Catherine A. Rushworth, Matthew A. Gitzendanner, Kenneth J. Sytsma, Yin-Long Qiu, Khidir W. Hilu, Charles C. Davis, Michael J. Sanderson, Reed S. Beaman, Richard G. Olmstead, Walter S. Judd, Michael J. Donoghue, and Pamela S. Soltis. Angiosperm phylogeny: 17 genes, 640 taxa. *American Journal of Botany* 98(4): 704–730.

Appendix S22. The maximum parsimony majority-rule consensus resulting from the 17-gene analysis with mtDNA removed for *Polyosma*. Bootstrap values (500 replicates) are given above branches; majority-rule consensus values below 100 are below branches.

Majority rule

