

Supplemental Information for
**Phylogenomic insights into deep phylogeny of angiosperms based on
broad nuclear gene sampling**

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Table S1. Transcriptome features of *Hedyosmum orientale*

Characteristics	
Number of reads	29,907,986
Number of contigs	26027
Percent GC	45.48%
Contig N50	1311
Medium contig length	723
Average contig length	980
Length range of contigs	297-12774

Table S2. Taxa included in this study

Species name	Family	Order	Groups	Source
<i>Arabidopsis thaliana</i>	Brassicaceae	Brassicales	Rosids	Phytozome
<i>Arabidopsis lyrata</i>	Brassicaceae	Brassicales	Rosids	Phytozome
<i>Capsella rubella</i>	Brassicaceae	Brassicales	Rosids	Phytozome
<i>Brassica rapa</i>	Brassicaceae	Brassicales	Rosids	Phytozome
<i>Eutrema salsugineum</i>	Brassicaceae	Brassicales	Rosids	Phytozome
<i>Cleome serrulata</i>	Cleomaceae	Brassicales	Rosids	Huang et al. 2016a
<i>Carica papaya</i>	Caricaceae	Brassicales	Rosids	Phytozome
<i>Theobroma cacao</i>	Malvaceae	Malvales	Rosids	Phytozome
<i>Gossypium raimondii</i>	Malvaceae	Malvales	Rosids	Phytozome
<i>Citrus sinensis</i>	Rutaceae	Sapindales	Rosids	Phytozome
<i>Citrus clementina</i>	Rutaceae	Sapindales	Rosids	Phytozome
<i>Cedrela sinensis</i>	Meliaceae	Sapindales	Rosids	NCBI
<i>Dimocarpus longan</i>	Sapindaceae	Sapindales	Rosids	NCBI
<i>Stachyurus yunnanensis</i>	Stachyuraceae	Crossosomatales	Rosids	NCBI
<i>Elaeocarpus glabripetalus</i>	Elaeocarpaceae	Oxalidales	Rosids	NCBI
<i>Oxalis corniculata</i>	Oxalidaceae	Oxalidales	Rosids	NCBI
<i>Manihot esculenta</i>	Euphorbiaceae	Malpighiales	Rosids	Phytozome
<i>Ricinus communis</i>	Euphorbiaceae	Malpighiales	Rosids	Phytozome
<i>Rafflesia cantleyi</i>	Rafflesiaceae	Malpighiales	Rosids	NCBI
<i>Linum usitatissimum</i>	Linaceae	Malpighiales	Rosids	Phytozome
<i>Populus trichocarpa</i>	Salicaceae	Malpighiales	Rosids	Phytozome
<i>Euonymus carnosus</i>	Celastraceae	Celastrales	Rosids	NCBI
<i>Tripterygium wilfordii</i>	Celastraceae	Celastrales	Rosids	NCBI

<i>Boehmeria nivea</i>	Urticaceae	Rosales	Rosids	NCBI
<i>Hippophae rhamnoides</i>	Elaeagnaceae	Rosales	Rosids	NCBI
<i>Glycine max</i>	Fabaceae	Fabales	Rosids	Phytozome
<i>Phaseolus vulgaris</i>	Fabaceae	Fabales	Rosids	Phytozome
<i>Cyclobalanopsis glauca</i>	Fagaceae	Fagales	Rosids	NCBI
<i>Corylus avellana</i>	Betulaceae	Fagales	Rosids	NCBI
<i>Juglans regia</i>	Juglandaceae	Fagales	Rosids	NCBI
<i>Myrica rubra</i>	Myricaceae	Fagales	Rosids	NCBI
<i>Eucalyptus grandis</i>	Myrtaceae	Myrtales	Rosids	Phytozome
<i>Paeonia lactiflora</i>	Paeoniaceae	Saxifragales	Rosids	Zeng et al. 2017
<i>Cercidiphyllum japonicum</i>	Cercidiphyllaceae	Saxifragales	Rosids	Zeng et al. 2017
<i>Distylium buxifolium</i>	Hamamelidaceae	Saxifragales	Rosids	NCBI
<i>Santalum album</i>	Santalaceae	Santalales	Rosids	Zeng et al. 2017
<i>Viscum ovalifolium</i>	Viscaceae	Santalales	Rosids	Zeng et al. 2017
<i>Aextoxicon punctatum</i>	Aextoxicaceae	Berberidopsidales	Rosids	Zeng et al. 2017
<i>Berberidopsis beckleri</i>	Berberidopsidaceae	Berberidopsidales	Rosids	The 1KP Project
<i>Parthenocissus tricuspidata</i>	Vitaceae	Vitales	Rosids	Zeng et al. 2017
<i>Cayratia japonica</i>	Vitaceae	Vitales	Rosids	Zeng et al. 2017
<i>Cissus microcarpa</i>	Vitaceae	Vitales	Rosids	NCBI
<i>Ampelopsis cordata</i>	Vitaceae	Vitales	Rosids	NCBI
<i>Leea guineensis</i>	Vitaceae	Vitales	Rosids	NCBI
<i>Vitis vinifera</i>	Vitaceae	Vitales	Rosids	Phytozome
<i>Mimulus guttatus</i>	Phrymaceae	Lamiales	Asterids	Phytozome
<i>Mentha canadensis</i>	Lamiaceae	Lamiales	Asterids	NCBI
<i>Olea europaea</i>	Oleaceae	Lamiales	Asterids	NCBI
<i>Avicennia marina</i>	Acanthaceae	Lamiales	Asterids	NCBI

<i>Orobanche aegyptiaca</i>	Orobanchaceae	Lamiales	Asterids	NCBI
<i>Phyla dulcis</i>	Verbenaceae	Lamiales	Asterids	NCBI
<i>Bothriospermum chinense</i>	Boraginaceae	Boraginales	Asterids	NCBI
<i>Trigonotis peduncularis</i>	Boraginaceae	Boraginales	Asterids	NCBI
<i>Solanum lycopersicum</i>	Solanaceae	Solanales	Asterids	Phytozome
<i>Cuscuta reflexa</i>	Convolvulaceae	Solanales	Asterids	NCBI
<i>Vinca major</i>	Apocynaceae	Gentianales	Asterids	NCBI
<i>Gardenia jasminoides</i>	Rubiaceae	Gentianales	Asterids	Zeng et al. 2017
<i>Ilex chinensis</i>	Aquifoliaceae	Aquifoliales	Asterids	Zeng et al. 2017
<i>Aucuba japonica</i>	Garryaceae	Garryales	Asterids	NCBI
<i>Apium graveolens</i>	Apiaceae	Apiales	Asterids	NCBI
<i>Ligusticum striatum</i>	Apiaceae	Apiales	Asterids	Zeng et al. 2017
<i>Hedera nepalensis</i>	Araliaceae	Apiales	Asterids	NCBI
<i>Dipsacus laciniatus</i>	Caprifoliaceae	Dipsacales	Asterids	NCBI
<i>Lonicera japonica</i>	Caprifoliaceae	Dipsacales	Asterids	NCBI
<i>Valeriana officinalis</i>	Caprifoliaceae	Dipsacales	Asterids	NCBI
<i>Lactuca sativa</i>	Asteraceae	Asterales	Asterids	NCBI
<i>Sonchus asper</i>	Asteraceae	Asterales	Asterids	Huang et al. 2016b
<i>Cirsium vulgare</i>	Asteraceae	Asterales	Asterids	Huang et al. 2016b
<i>Pilosella caespitosa</i>	Asteraceae	Asterales	Asterids	Zeng et al. 2017
<i>Cichorium intybus</i>	Asteraceae	Asterales	Asterids	Huang et al. 2016b
<i>Tagetes erecta</i>	Asteraceae	Asterales	Asterids	Zhang et.al, unpublished
<i>Dahlia pinnata</i>	Asteraceae	Asterales	Asterids	Zeng et al. 2017
<i>Artemisia annua</i>	Asteraceae	Asterales	Asterids	NCBI
<i>Hydrangea macrophylla</i>	Hydrangeaceae	Cornales	Asterids	NCBI
<i>Philadelphus incanus</i>	Hydrangeaceae	Cornales	Asterids	NCBI

<i>Cornus wilsoniana</i>	Cornaceae	Cornales	Asterids	NCBI
<i>Vaccinium corymbosum</i>	Ericaceae	Ericales	Asterids	NCBI
<i>Actinidia arguta</i>	Actinidiaceae	Ericales	Asterids	NCBI
<i>Camellia japonica</i>	Theaceae	Ericales	Asterids	NCBI
<i>Dionaea muscipula</i>	Droseraceae	Caryophyllales	uncertain	NCBI
<i>Phytolacca americana</i>	Phytolaccaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Mirabilis jalapa</i>	Nymphaeaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Tamarix chinensis</i>	Tamaricaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Polygonum runcinatum</i>	Polygonaceae	Caryophyllales	uncertain	NCBI
<i>Stellaria media</i>	Caryophyllaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Opuntia dillenii</i>	Cactaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Alternanthera philoxeroides</i>	Amaranthaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Delosperma cooperi</i>	Aizoaceae	Caryophyllales	uncertain	Zeng et al. 2017
<i>Dillenia indica</i>	Dilleniaceae	Dilleniaceae	uncertain	Zeng et al. 2017
<i>Dillenia turbinata</i>	Dilleniaceae	Dilleniaceae	uncertain	Zeng et al. 2017
<i>Gunnera manicata</i>	Gunneraceae	Gunnerales	core eudicots	Zeng et al. 2017
<i>Buxus sinica</i>	Buxaceae	Buxales	basal eudicots	Zeng et al. 2014
<i>Platanus × acerifolia</i>	Platanaceae	Proteales	basal eudicots	Zeng et al. 2014
<i>Nelumbo nucifera</i>	Nelumbonaceae	Proteales	basal eudicots	NCBI
<i>Meliosma parviflora</i>	Sabiaceae	Sabiaceae	basal eudicots	Zeng et al. 2017
<i>Aquilegia coerulea</i>	Ranunculaceae	Ranunculales	basal eudicots	Phytozome
<i>Nandina domestica</i>	Berberidaceae	Ranunculales	basal eudicots	NCBI
<i>Eschscholzia californica</i>	Papaveraceae	Ranunculales	basal eudicots	NCBI
<i>Ceratophyllum demersum</i>	Ceratophyllaceae	Ceratophyllales	Ceratophyllales	Zeng et al. 2014
<i>Ceratophyllum oryzetorum</i>	Ceratophyllaceae	Ceratophyllales	Ceratophyllales	NCBI
<i>Hedyosmum orientale</i>	Chloranthaceae	Chloranthales	Chloranthales	This study

<i>Chloranthus japonicus</i>	Chloranthaceae	Chloranthales	Chloranthales	NCBI
<i>Sarcandra glabra</i>	Chloranthaceae	Chloranthales	Chloranthales	NCBI
<i>Ascarina rubricaulis</i>	Chloranthaceae	Chloranthales	Chloranthales	The 1KP Project
<i>Cinnamomum camphora</i>	Lauraceae	Lurales	Magnoliids	NCBI
<i>Litsea cubeba</i>	Lauraceae	Lurales	Magnoliids	NCBI
<i>Persea borbonia</i>	Lauraceae	Lurales	Magnoliids	The 1KP Project
<i>Gyrocarpus americanus</i>	Hernandiaceae	Lurales	Magnoliids	The 1KP Project
<i>Peumus boldus</i>	Monimiaceae	Lurales	Magnoliids	The 1KP Project
<i>Gomortega keule</i>	Gomortegaceae	Lurales	Magnoliids	The 1KP Project
<i>Laurelia sempervirens</i>	Atherospermataceae	Lurales	Magnoliids	The 1KP Project
<i>Chimonanthus praecox</i>	Calycanthaceae	Lurales	Magnoliids	NCBI
<i>Magnolia denudata</i>	Magnoliaceae	Magnoliales	Magnoliids	NCBI
<i>Liriodendron chinense</i> × <i>tulipifera</i>	Magnoliaceae	Magnoliales	Magnoliids	NCBI
<i>Eupomatia bennettii</i>	Eupomatiaceae	Magnoliales	Magnoliids	The 1KP Project
<i>Annona muricata</i>	Annonaceae	Magnoliales	Magnoliids	The 1KP Project
<i>Myristica fragrans</i>	Myristicaceae	Magnoliales	Magnoliids	The 1KP Project
<i>Houttuynia cordata</i>	Saururaceae	Piperales	Magnoliids	NCBI
<i>Piper nigrum</i>	Piperaceae	Piperales	Magnoliids	NCBI
<i>Saruma henryi</i>	Aristolochiaceae	Piperales	Magnoliids	The 1KP Project
<i>Aristolochia tagala</i>	Aristolochiaceae	Piperales	Magnoliids	NCBI
<i>Canella winterana</i>	Canellaceae	Canellales	Magnoliids	The 1KP Project
<i>Drimys winteri</i>	Winteraceae	Canellales	Magnoliids	The 1KP Project
<i>Sorghum bicolor</i>	Poaceae	Poales	Monocots	Phytozome
<i>Zea mays</i>	Poaceae	Poales	Monocots	Phytozome
<i>Setaria italica</i>	Poaceae	Poales	Monocots	Phytozome
<i>Panicum virgatum</i>	Poaceae	Poales	Monocots	Phytozome

<i>Oryza sativa</i>	Poaceae	Poales	Monocots	Phytozome
<i>Brachypodium distachyon</i>	Poaceae	Poales	Monocots	Phytozome
<i>Acorus calamus</i>	Acoraceae	Acorales	Monocots	NCBI
<i>Acorus americanus</i>	Acoraceae	Acorales	Monocots	The 1KP Project
<i>Alisma plantago-aquatica</i>	Alismataceae	Alismatales	Monocots	NCBI
<i>Pinellia ternata</i>	Araceae	Alismatales	Monocots	NCBI
<i>Spirodela polyrhiza</i>	Araceae	Alismatales	Monocots	Phytozome
<i>Trachycarpus fortunei</i>	Arecaceae	Arecales	Monocots	NCBI
<i>Sabal bermudana</i>	Arecaceae	Arecales	Monocots	The 1KP Project
<i>Yucca filamentosa</i>	Asparagaceae	Asparagales	Monocots	NCBI
<i>Asparagus officinalis</i>	Asparagaceae	Asparagales	Monocots	NCBI
<i>Iris japonica</i>	Iridaceae	Asparagales	Monocots	NCBI
<i>Dioscorea opposita</i>	Dioscoreaceae	Dioscoreales	Monocots	NCBI
<i>Dioscorea villosa</i>	Dioscoreaceae	Dioscoreales	Monocots	The 1KP Project
<i>Lilium brownii</i>	Liliaceae	Liliales	Monocots	NCBI
<i>Smilax bona-nox</i>	Smilacaceae	Liliales	Monocots	The 1KP Project
<i>Colchicum autumnale</i>	Colchicaceae	Liliales	Monocots	The 1KP Project
<i>Pandanus utilis</i>	Pandanaceae	Pandanales	Monocots	NCBI
<i>Canna indica</i>	Cannaceae	Zingiberales	Monocots	NCBI
<i>Musa acuminata</i>	Musaceae	Zingiberales	Monocots	Phytozome
<i>Illicium henryi</i>	Schisandraceae	Austrobaileyales	Basal angiosperm	NCBI
<i>Cabomba caroliniana</i>	Cabombaceae	Nymphaeales	Basal angiosperm	NCBI
<i>Nuphar advena</i>	Nymphaeaceae	Nymphaeales	Basal angiosperm	NCBI
<i>Amborella trichopoda</i>	Amborellaceae	Amborellales	Basal angiosperm	Phytozome
<i>Ginkgo biloba</i>	Ginkgoaceae	Ginkgoales	Gymnosperms	Phytozome
<i>Pinus taeda</i>	Pinaceae	Pinales	Gymnosperms	NCBI

Table S3. Estimated ages of major angiosperm clades.

Clade	Strategy A	Strategy B	Strategy C	The subset (64 taxa)
	Mean age (95% HPD) (Ma)	Mean age (95% HPD) (Ma)	Mean age (95% HPD) (Ma)	Mean age (95% HPD) (Ma)
Angiosperms	240.2 (255.08 - 222.2)	237.02 (252.45 - 216.94)	239.53 (258.44 - 216.67)	232.95 (254.31 - 205.97)
Mesangiospermae	178.82 (192.16 - 166.44)	180.21 (194.01 - 167.12)	181.70 (196.02 - 168.25)	-
Magnoliids	159.16 (170.73 - 147.14)	158.94 (171.58 - 146.92)	159.95 (172.51 - 147.21)	151.02 (171.12 - 131.11)
Monocots	160.52 (174.64 - 145.71)	162.85 (176.7 - 148.67)	163.76 (178.16 - 149.15)	-
Eudicots	129.17 (131.06 - 127.79)	129.16 (131 - 127.78)	129.15 (130.89 - 127.64)	128.36 (129.66 - 126.72)
Eudicots - Ceratophyllales	151.81 (163.89 - 140.63)	151.51 (164.03 - 140.24)	152.52 (165.42 - 140.89)	-
Core eudicots	121.07 (123.78 - 118.48)	121.07 (123.62 - 118.26)	121.14 (123.76 - 118.6)	120.83 (123.97 - 126.72)
Berberidopsidales - rest eudicots	119.40 (122.05 - 116.59)	119.39 (122.14 - 116.62)	119.45 (122.08 - 116.68)	118.31 (121.85 - 114.86)
Caryophyllales - Asterids	115.44 (118.61 - 112.3)	115.44 (118.56 - 112.31)	115.47 (118.54 - 112.32)	113.07 (117.3 - 108.71)
Asterids	110.30 (114.29 - 106.23)	110.32 (114.28 - 106.36)	110.24 (114.23 - 106.05)	107.30 (112.12 - 102.19)
Santalales - Superrosids	116.56 (119.50 - 113.58)	116.55 (119.42 - 113.6)	116.61 (119.51 - 113.68)	114.95 (118.58 - 110.93)
Vitales - (Rosids + Saxifragales)	114.56 (117.56 - 111.24)	114.57 (117.68 - 111.55)	114.64 (117.71 - 111.55)	112.65 (116.54 - 108.17)
Rosids - Saxifragales	112.51 (115.83 - 109.16)	112.52 (115.75 - 109.36)	112.59 (115.81 - 109.28)	109.89 (114.26 - 105.22)
Rosids	108.04 (111.61 - 104.35)	108.07 (111.77 - 104.5)	108.18 (111.81 - 104.59)	104.68 (109.85 - 99.54)

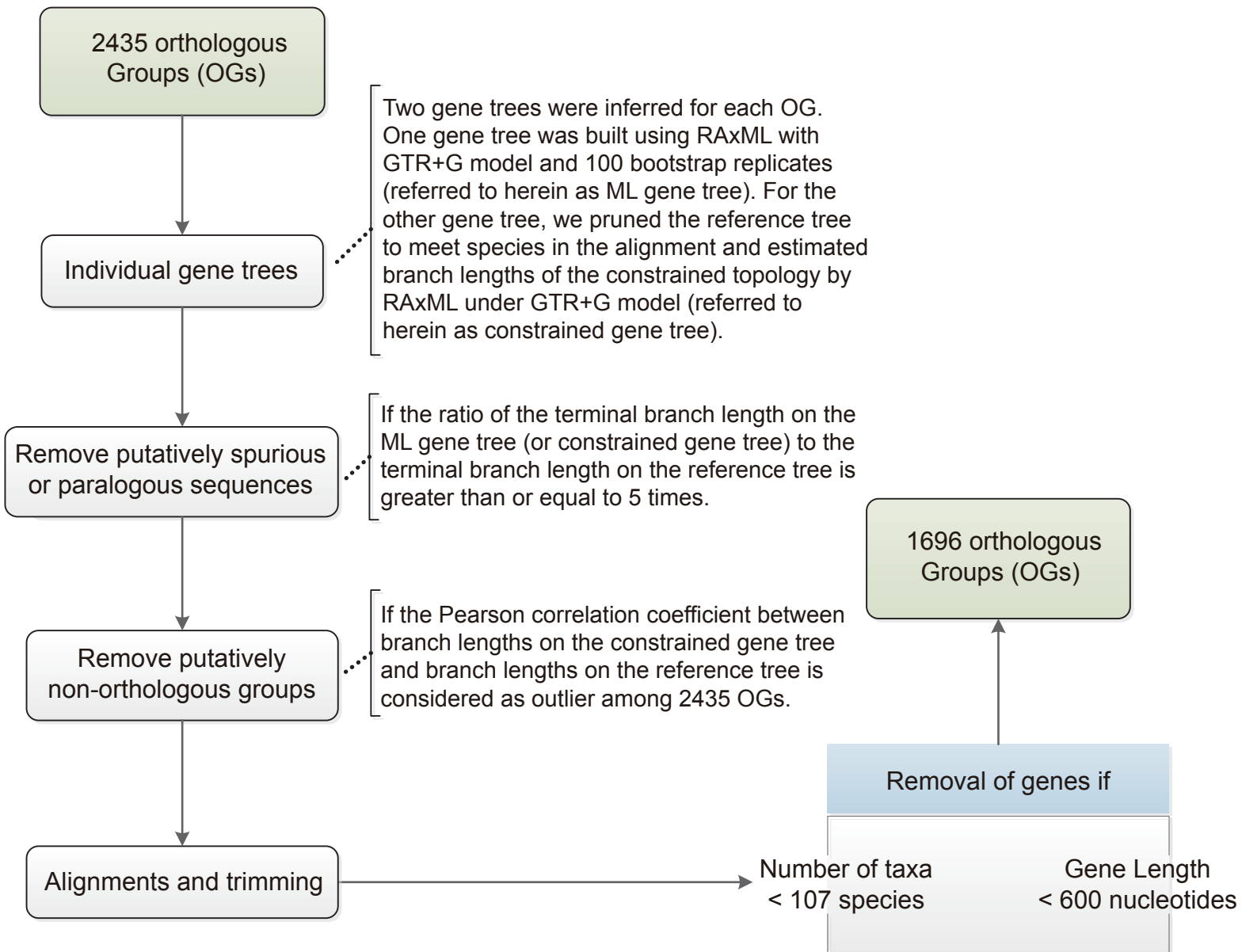


Fig. S1. The workflow of paralogue-filtering strategy.

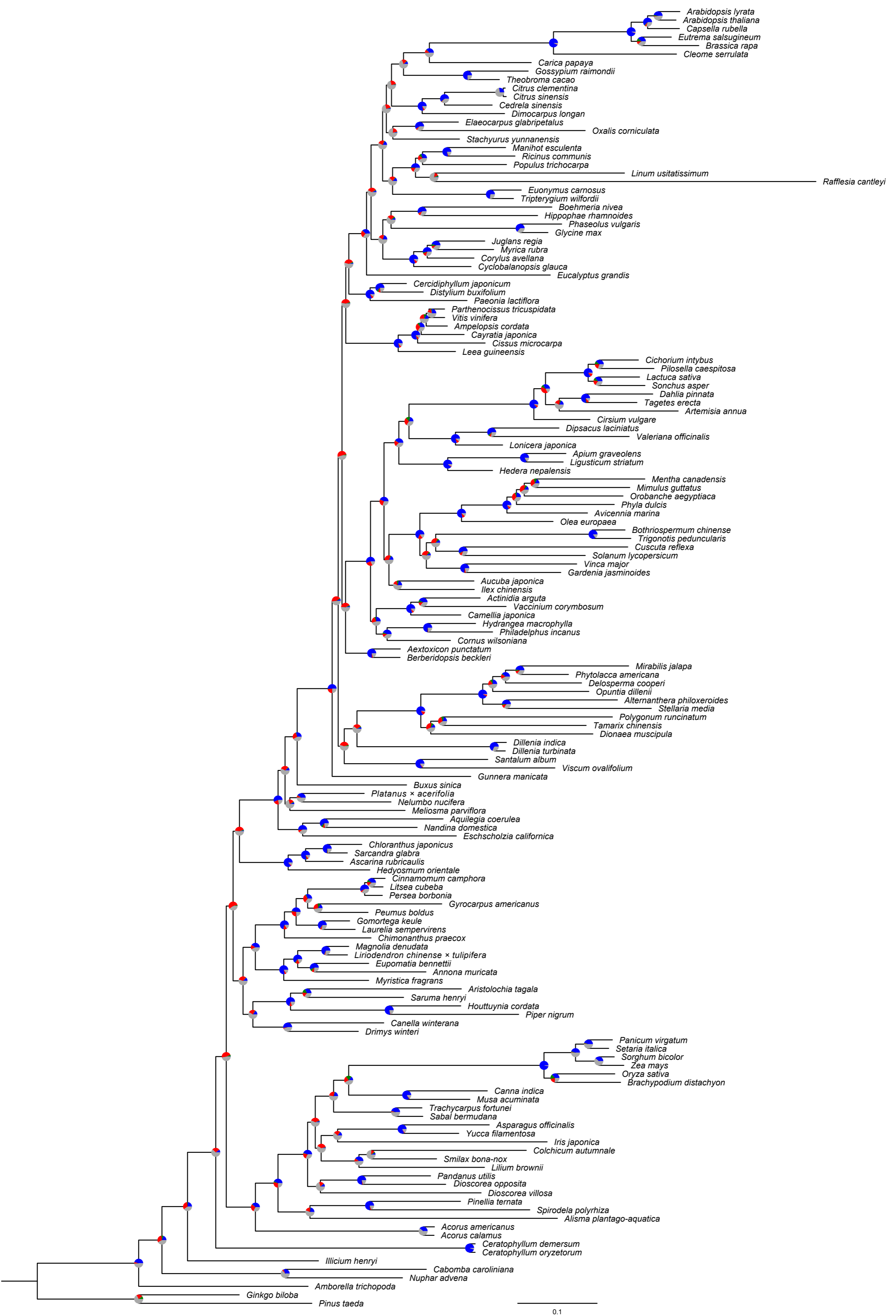


Figure S2 The concatenation-based species tree of 1594-genes data with summary of gene tree concordance and conflict. The pie charts at each node present the proportion of gene tree concordance and conflict. Pie chart color coding: blue—the fraction of gene trees that are concordant with the species tree; green—fraction of gene trees supporting the second most common topology; red—fraction of gene trees supporting all other alternative conflicting partitions; gray—fraction of gene trees with <50% bootstrap support at that node. The branch lengths in coalescent units were estimated by ASTRAL.

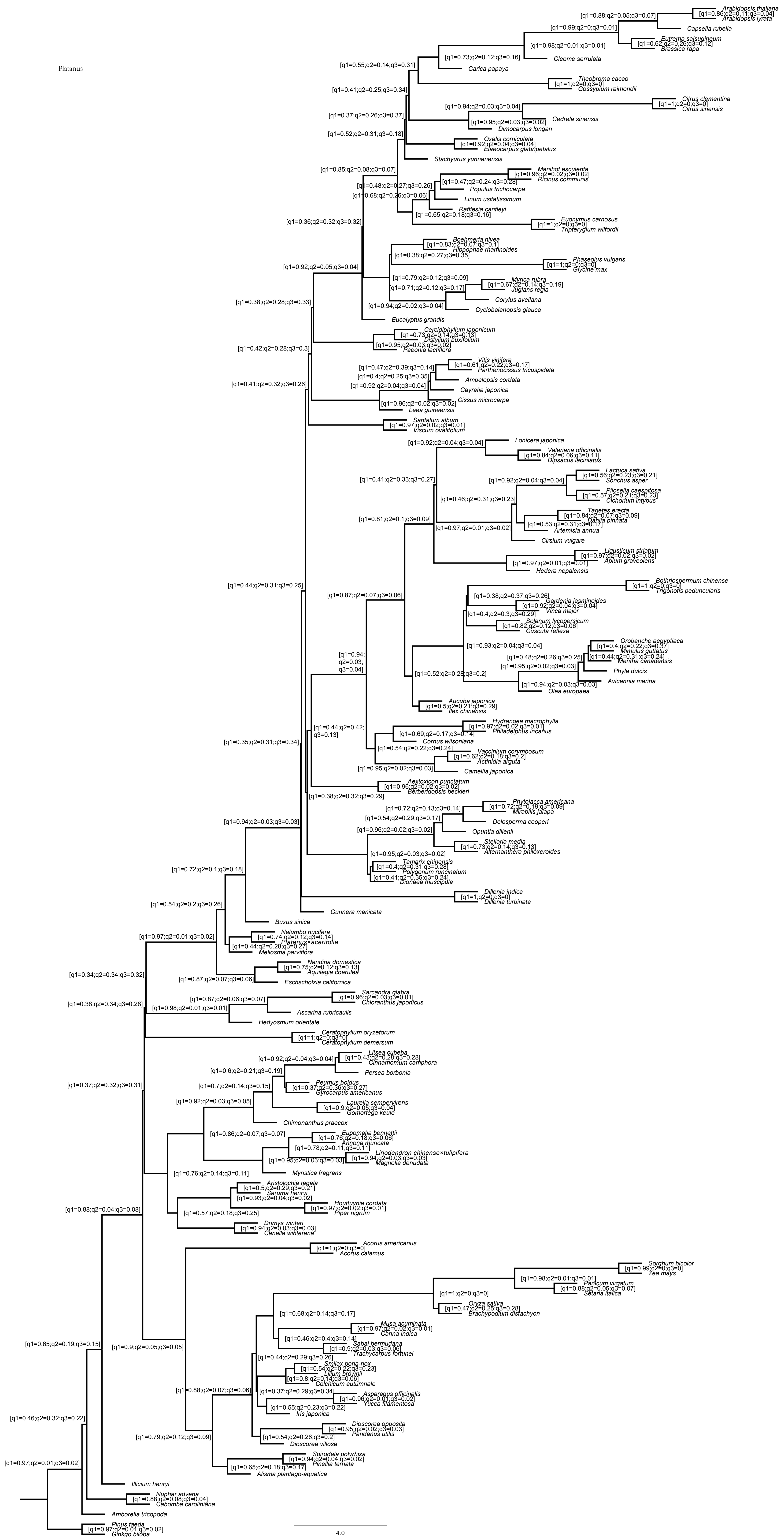


Figure S3 The quartet score for the coalescent-based species tree of 1594 genes. 'q1', 'q2', 'q3' show quartet support for the topology of current species tree, the first alternative, and the second alternative, respectively.

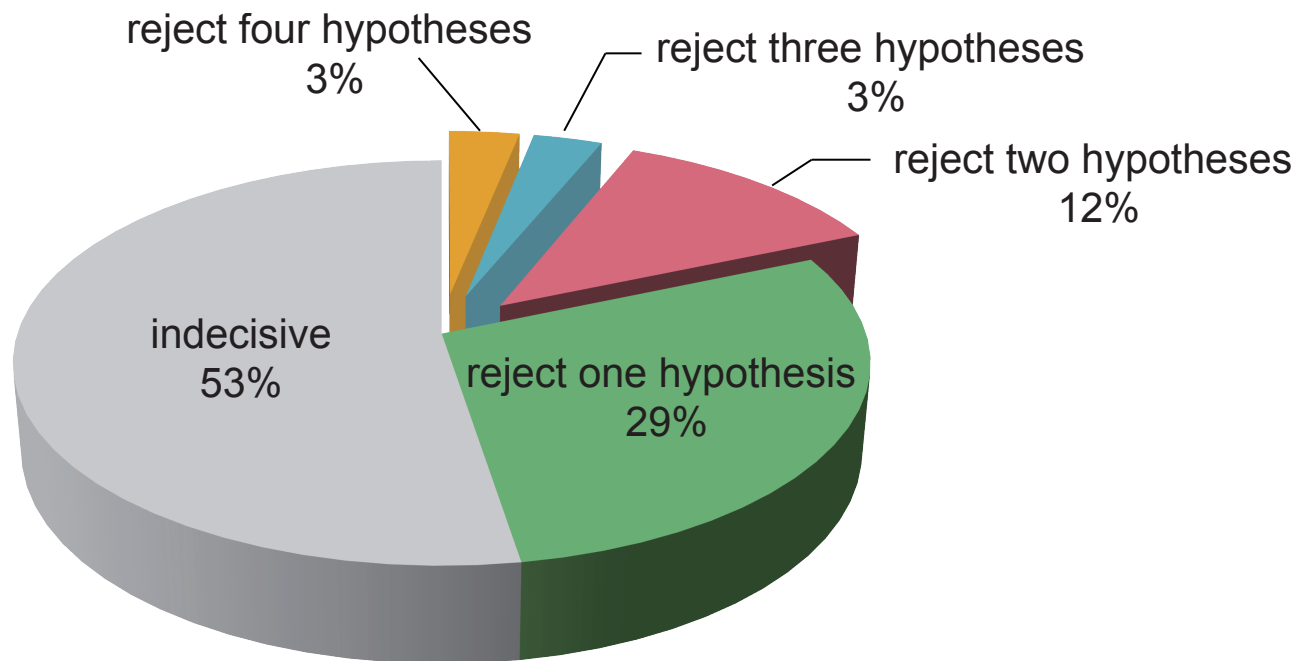


Fig. S4 Results from phylogenetic signal analyses by using AU test. These results show that insufficient phylogenetic signals are prevalent in 1594-gene data.

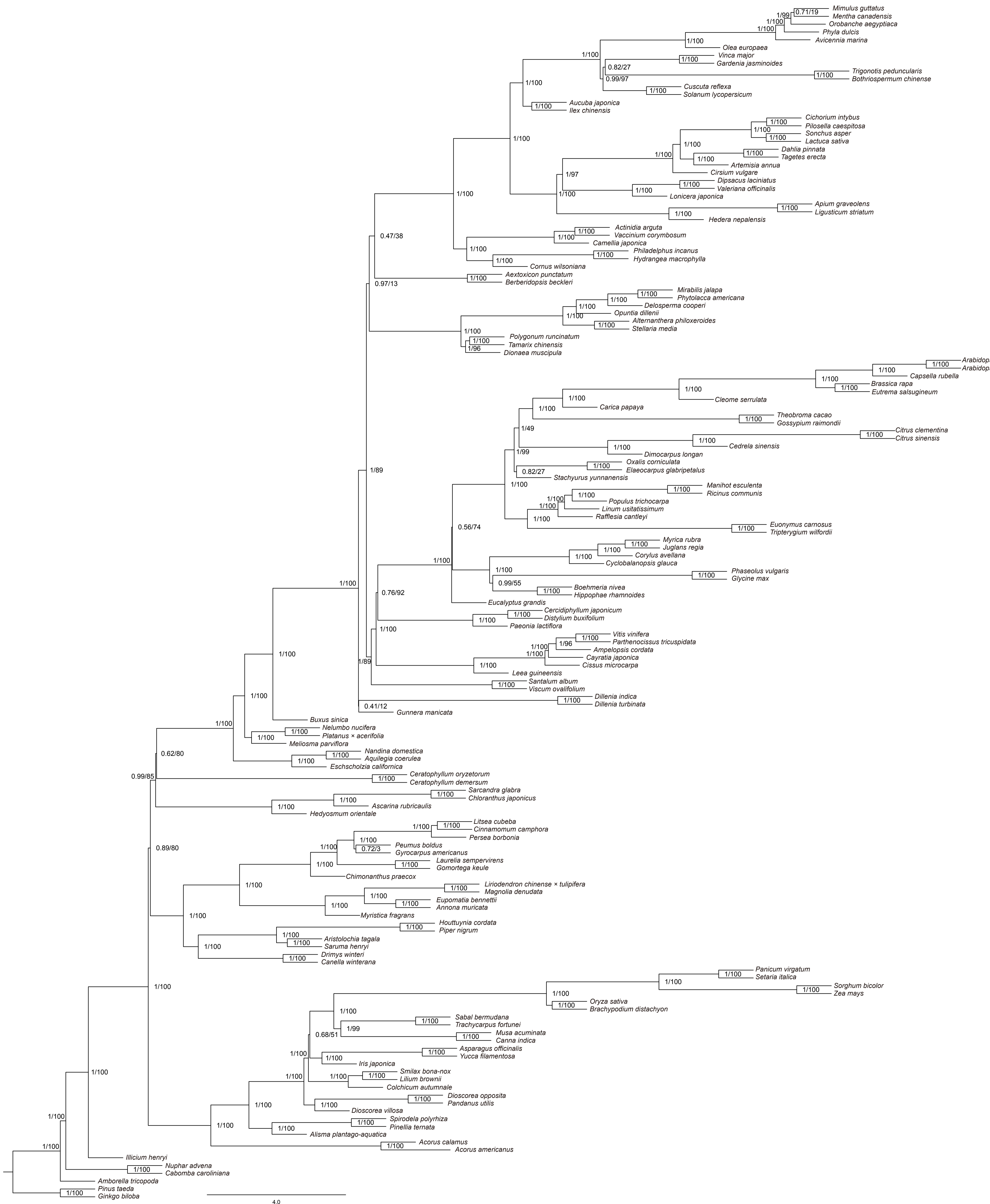
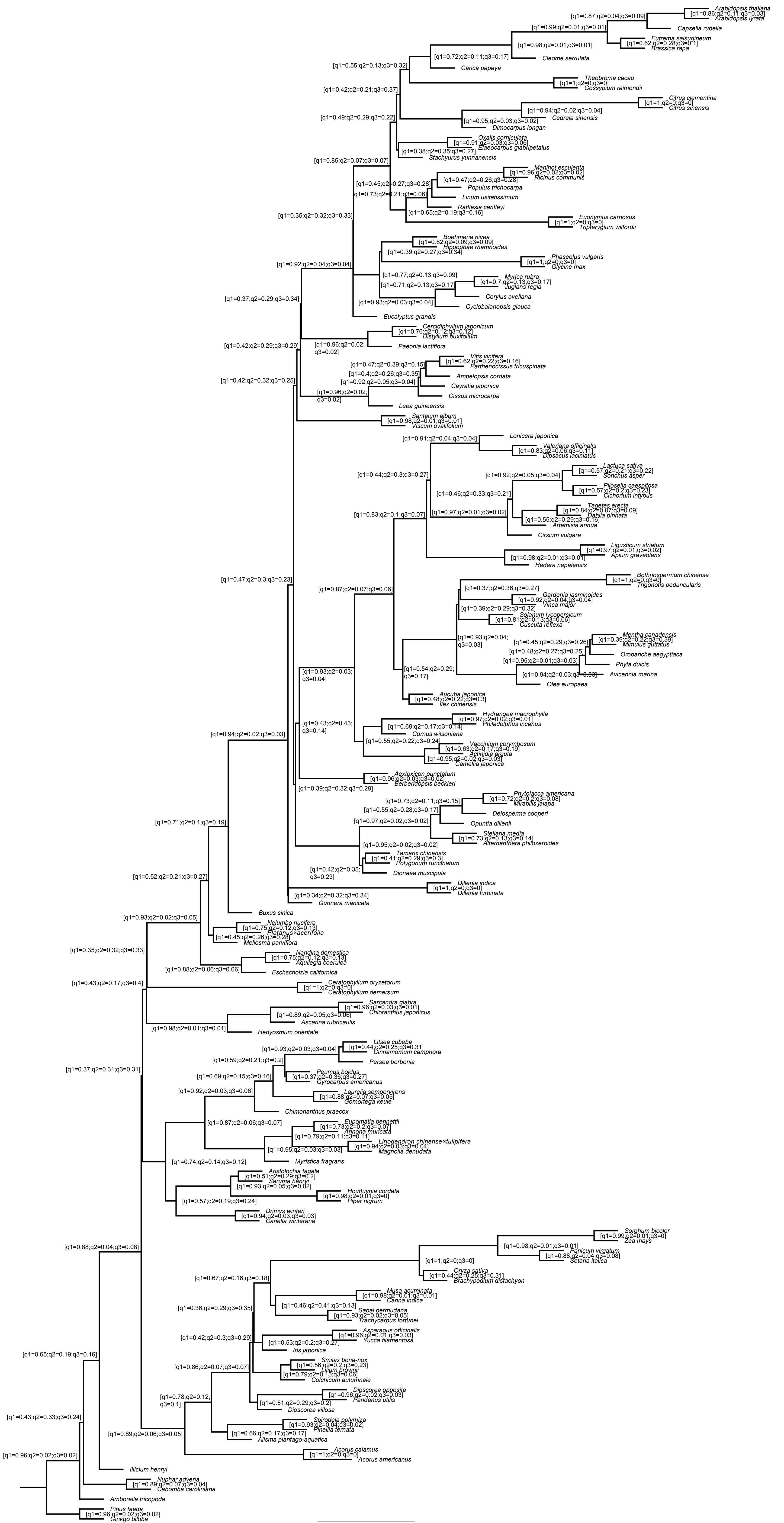


Fig. S5 The coalescent-based species tree was inferred by ASTRAL using 756 genes. Numbers associated with nodes are support values obtained by the posterior probability (PP on the left) and the multilocus bootstrapping (BS on the right).



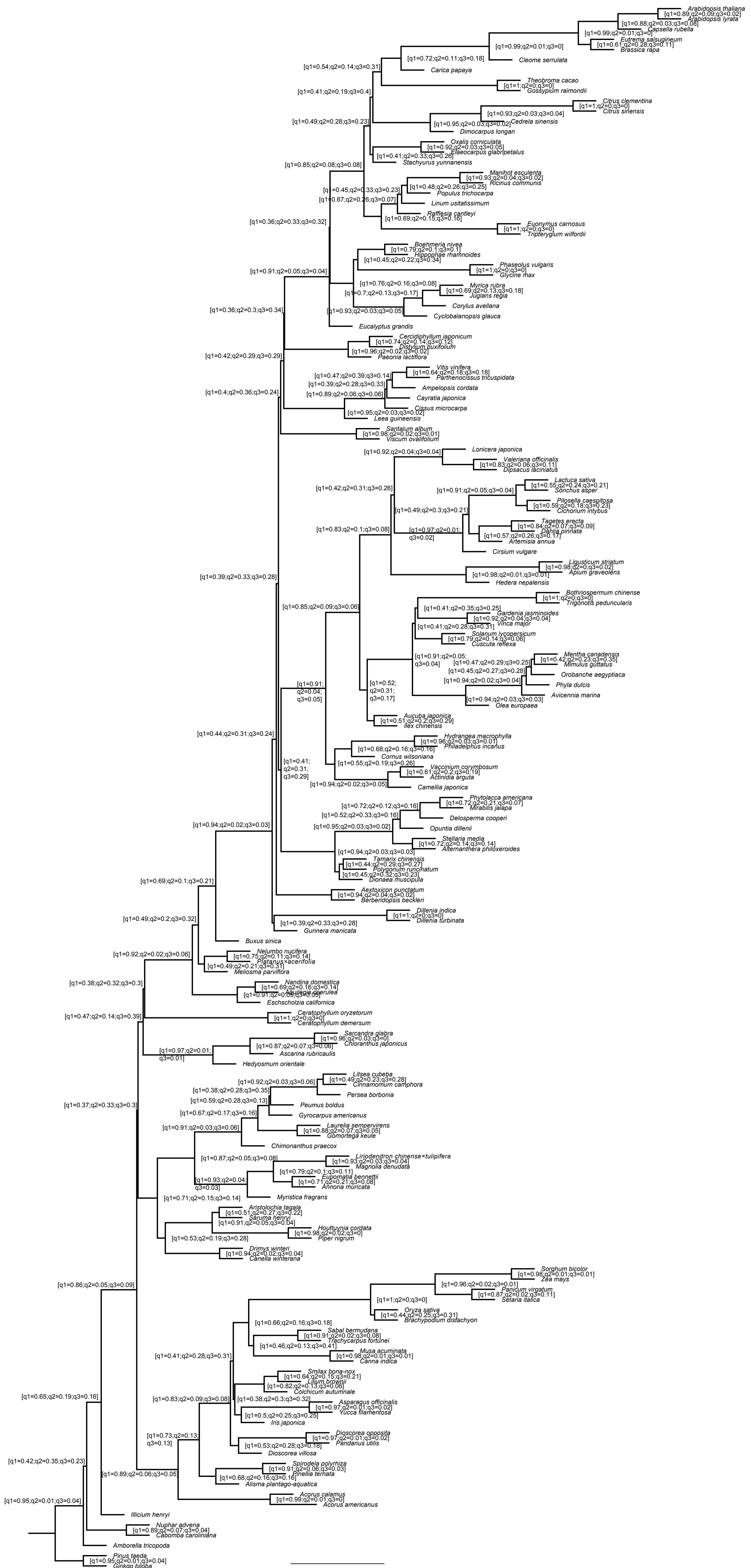


Figure S7 The quartet score for the coalescent-based species tree of 296 genes. 'q1', 'q2', 'q3' show quartet support for the topology of current species tree, the first alternative, and the second alternative, respectively.



Figure S8 The coalescent-based species tree was inferred by ASTRAL using 838 genes. Numbers associated with nodes are support values obtained by the posterior probability (PP on the left) and the multilocus bootstrapping (BS on the right).

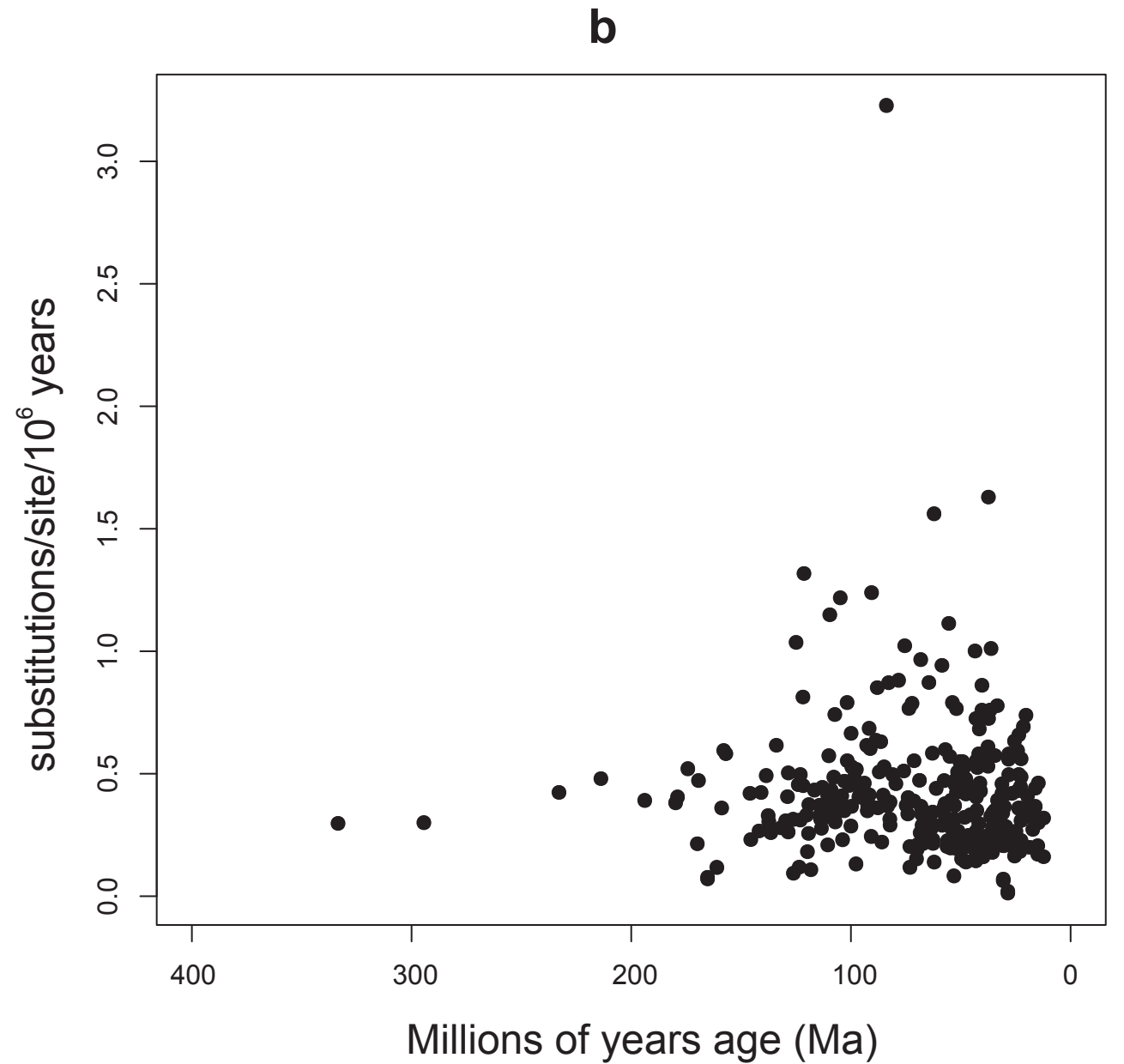
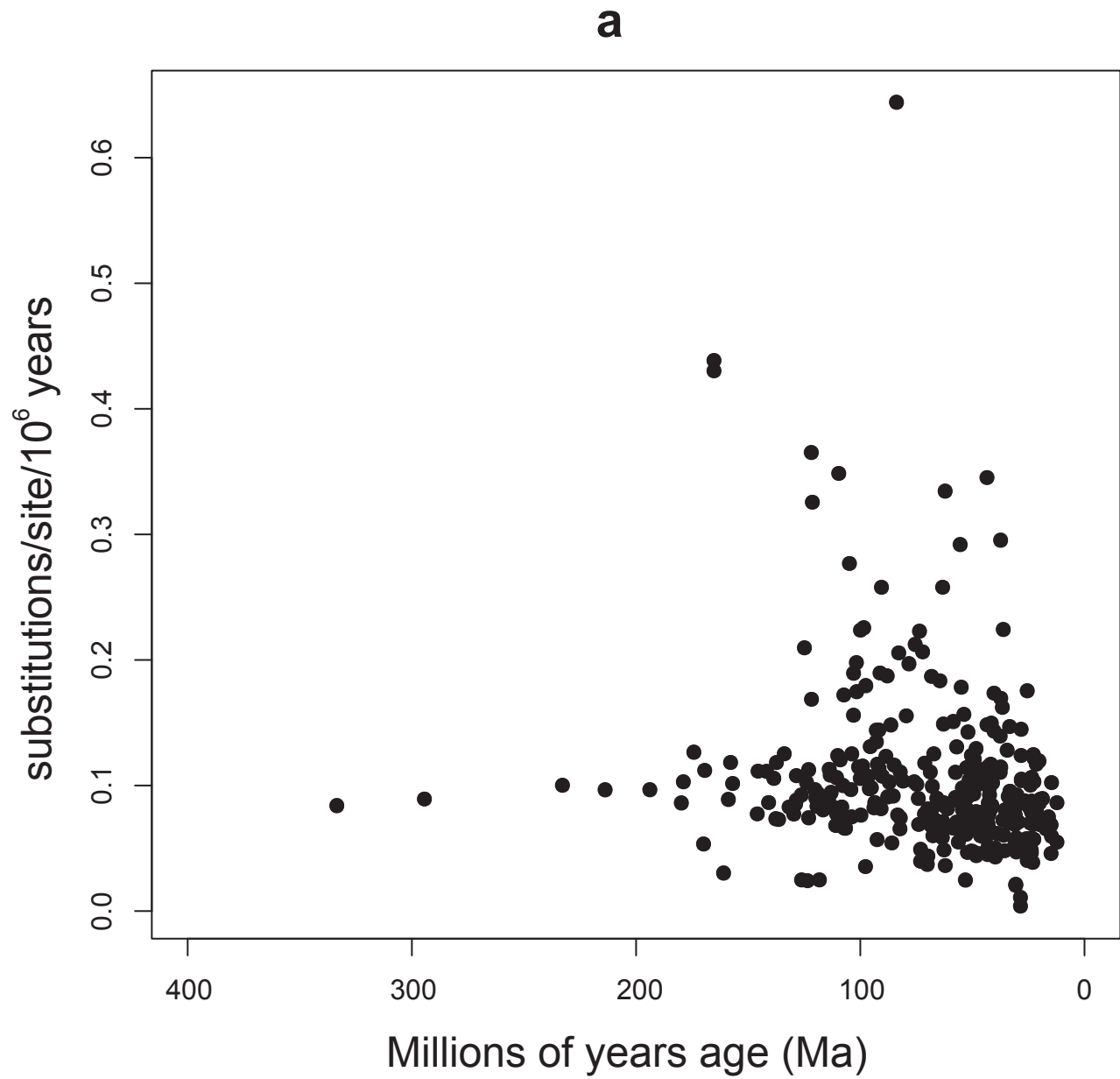


Fig.S9 Branch-specific substitution rates plotted against the midpoint ages of these branches, for (a) first and second codon positions, and (b) third codon positions. Both the rates and ages were estimated using Strategy A in MCMCTree.

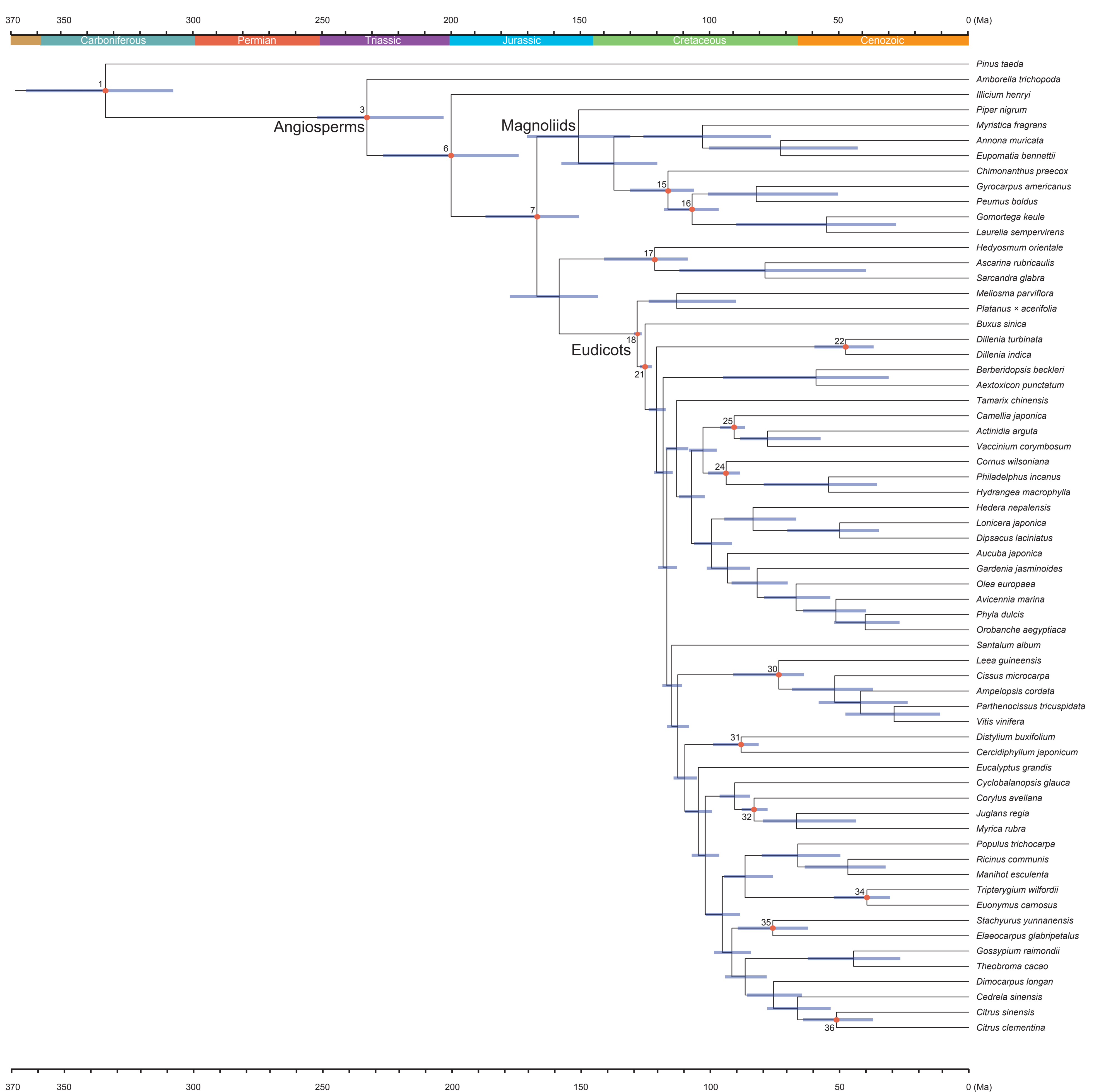


Fig. S10 Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 296 genes from 64 taxa (remove all current or ancestrally herbaceous taxa), with 18 fossil calibrations and an uncorrelated relaxed clock, in MCMCTREE. Fossil constraints are shown with red dots, and the details of fossils were available in the supplementary materials. Horizontal bars represent 95% credibility intervals.

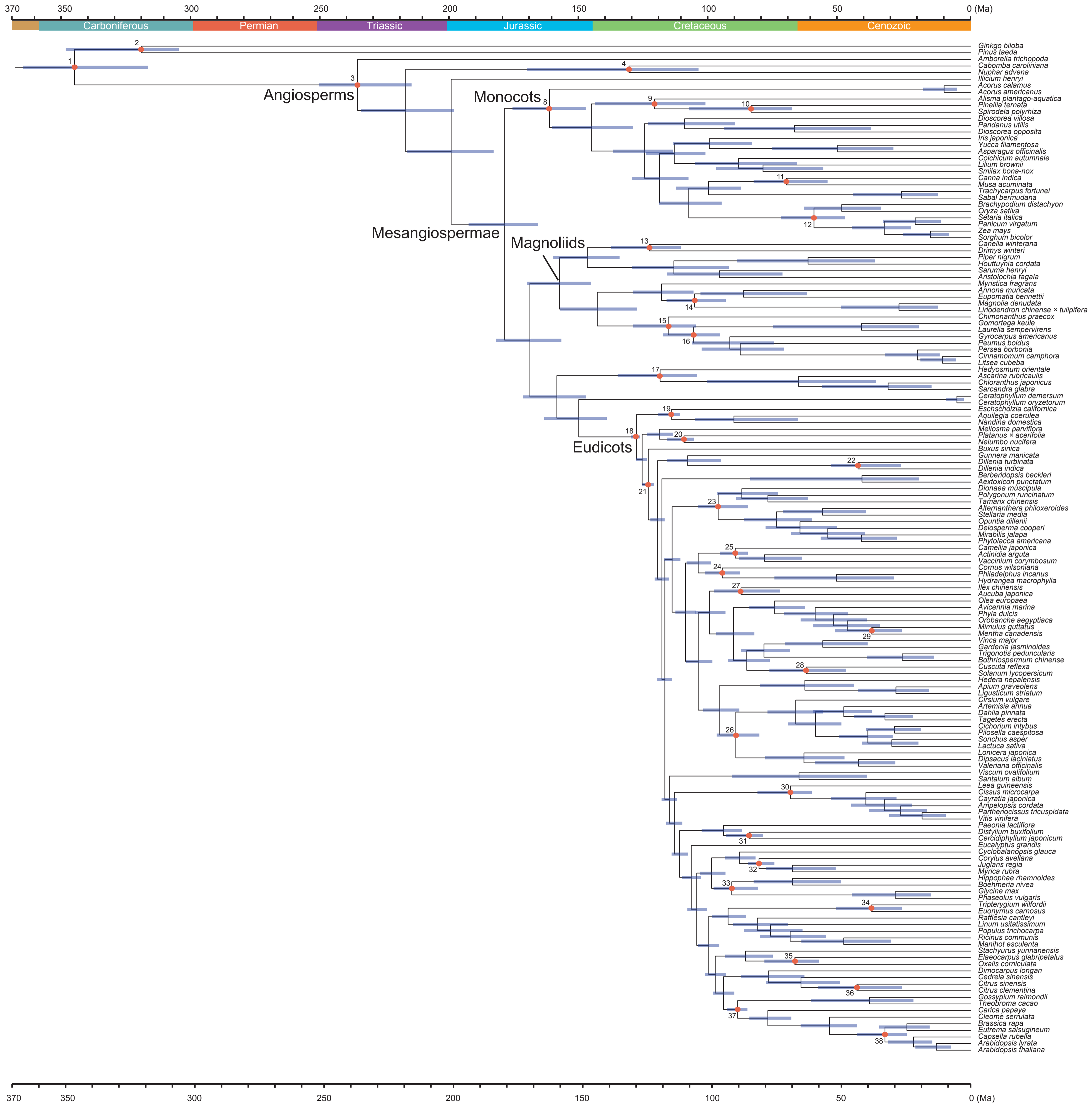


Fig. S11 Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 296 genes from 153 taxa, with 35 fossil calibrations (strategy B: reduce three calibration nodes: Node 5, Node 6 and Node 7) and an uncorrelated relaxed clock, in MCMCTREE. Fossil constraints are shown with red dots, and the details of fossils were available in the supplementary materials. Horizontal bars represent 95% credibility intervals.

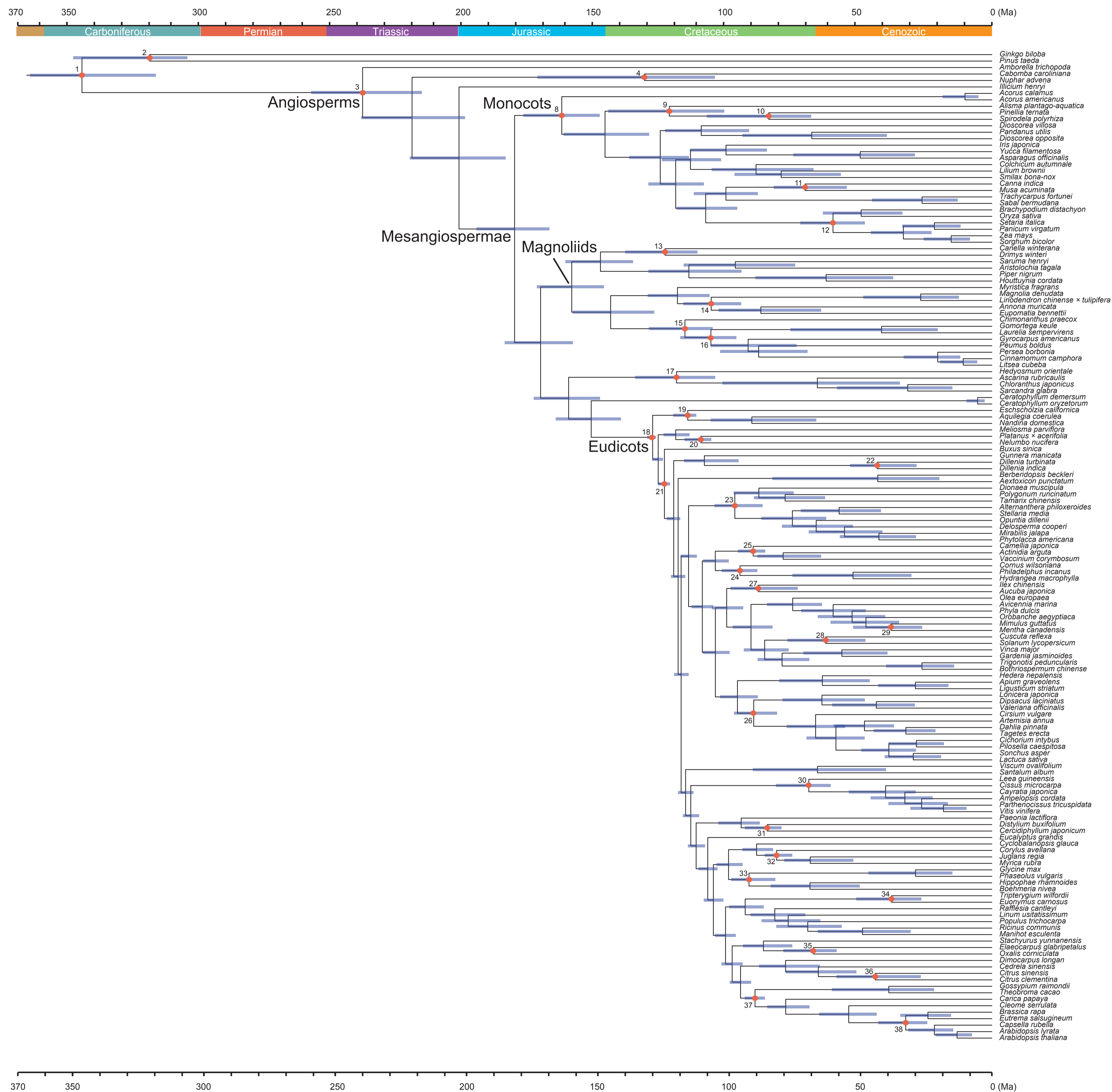


Fig. S12 Chronogram depicting the angiosperm evolutionary timescale, as estimated using Bayesian analysis of 296 genes from 153 taxa, with 35 fossil calibrations (strategy C: reduce three calibration nodes (Node 5, Node 6 and Node 7) and decrease the minimum fossil constraint of crown angiosperms) and an uncorrelated relaxed clock, in MCMCTREE. Fossil constraints are shown with red dots, and the details of fossils were available in the supplementary materials. Horizontal bars represent 95% credibility intervals.

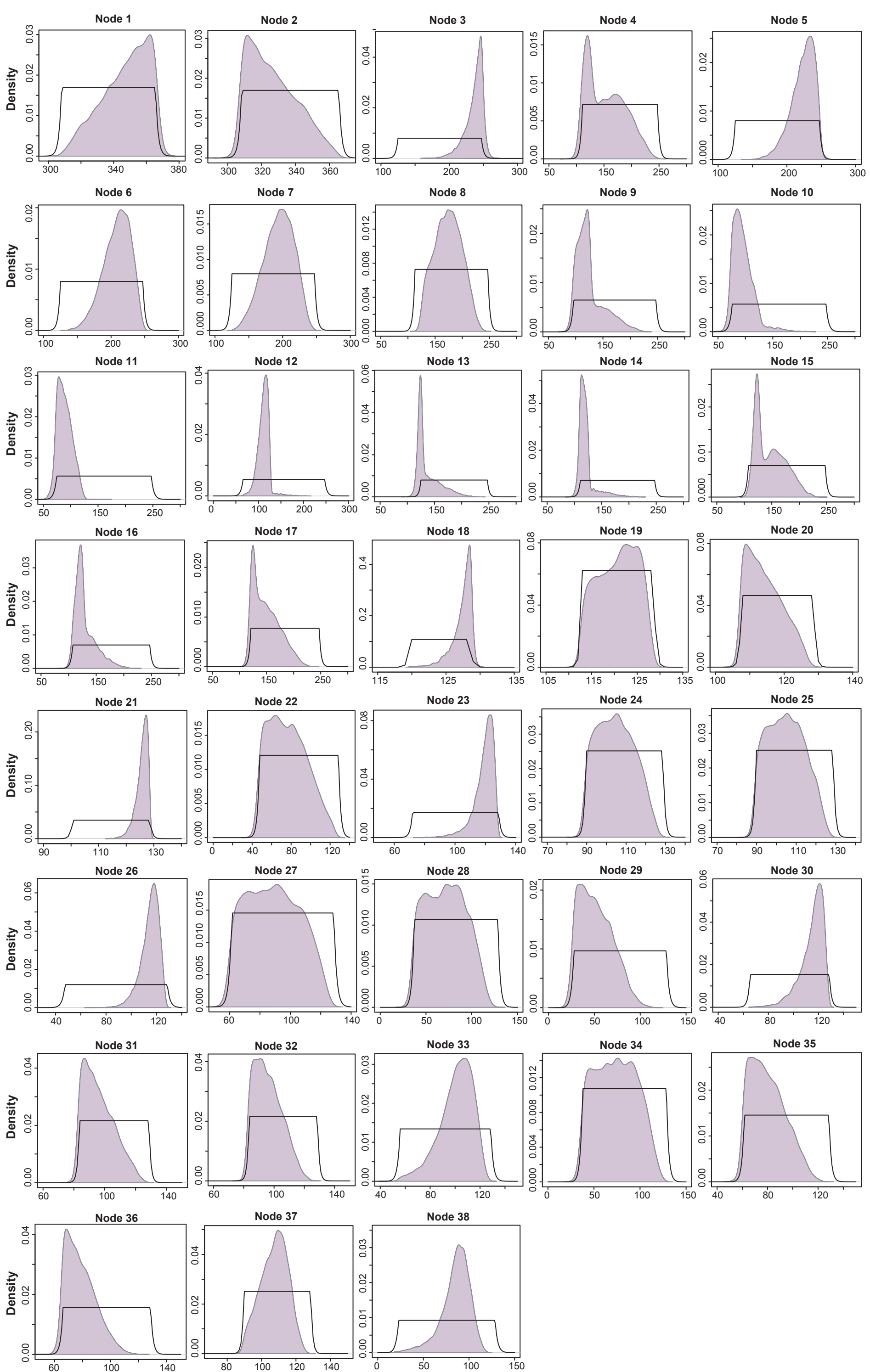


Fig. S13. Comparison of the age distributions on the 38 calibrated nodes for the specified priors (black line) and effective priors (purple) using uniform prior distributions on the coalescent-based species tree.

Detailed analyses for divergence time estimation

The gap between molecular ages and the oldest fossil records of angiosperms (Early Cretaceous) has triggered many researches in recent years. Fossil calibrations provide the fundamental information for the estimates of absolute times and rates in molecular clock dating analyses. The placement of the fossil on the tree is most important to all strategies. The widely used crown-angiosperm constraints were tricolpate pollen grains from the Barremian-Aptian boundary (~125 Ma), which was unequivocally related to the eudicot clade (Magallón et al., 2015; Coiro et al. 2019). These fossils may represent the limitations of the fossil record, but may also be uninformative. Obviously, they are ‘too young’ for the crown node of angiosperms. We employed three calibration strategies to test the influence of these fossils for the gap between molecular age and fossil evidence of angiosperms. In strategy A (the main analyses that are described in Results), all 38 fossil constraints were used to calibrate the timetree. For strategy B, we removed three calibration nodes (Node 5, Node 6 and Node 7). For strategy C, we further decreased the minimum fossil constraint of crown angiosperms on the basis of strategy B. We ran the MCMCTree analyses for both strategy B and strategy C and inferred highly congruent ages for crown angiosperms (strategy B: 252.45 - 216.94 Ma, Supplementary fig.S11; strategy C: 258.44 - 216.67 Ma, Supplementary fig.S12). Despite tricolpate pollen grains are likely to provide limited information for this node, we chose to use these fossils to calibrate the minimum constraint of angiosperms for replenishing fossil information as much as possible. Comparing the molecular ages between strategy A and strategy B, two different strategies both supported a pre-Cretaceous origin of angiosperms, but more calibration points produced a narrower 95% credible interval width (strategy A: 255.08 - 222.2 Ma; strategy B: 252.45 - 216.94 Ma). Fewer calibration nodes tended to increase the variance of age estimates remarkably (Salomo et al., 2017). We used the results of strategy A as our main analyses.

Through a series of simulations, Beaulieu et al. (2015) demonstrated that the potential biases caused by rate heterogeneity between herbaceous and woody species tended to generate the older age estimates, especially there were large shifts in branch

rates among early-diverging lineages of angiosperms. However, Foster et al. (2017) indicated that estimated divergence ages without herbaceous lineages were congruent with other analyses. Salomo et al. (2017) also considered the rate heterogeneity, and the results didn't show great influence of rates on the crown node of angiosperms. We evaluated the impacts of rate heterogeneity between herbaceous and woody species. First, we checked shifts in branch rates in the results of our main MCMCTree analysis. The branch rates from our main MCMCTree analyse were plotted against the midpoint ages of branches by the R package NELSI v0.21 (Ho et al., 2015). The rategrams for each locus (Supplementary fig. S9) didn't show large shifts in the early branches of angiosperms, implying that rate changes between early-diverging angiosperm species had little fluctuation. Besides, in order to further eliminate the impact of rate heterogeneity among these two different kinds of groups, we divided 153 species into woody perennials and herbaceous annuals, and reconstructed their ancestral states by using the `make.simmap` function (R package Phytools v0.6-60, Revell 2012). Then, all lineages that are currently and were ancestrally herbaceous were removed, as faster rates might be expected in herbaceous annuals. We ran MCMCTree analyses for the reduced dataset (64 taxa), and obtained the highly similar ages of crown angiosperms with the main analyses (254.31 - 205.97 Ma, Supplementary fig. S10) after removing all herbaceous annuals. The heterogeneous rates across a phylogenetic tree have little effect for the age of crown angiosperms in our data set.

In summary, our divergence time estimations are robust and support a pre-Cretaceous origin of angiosperms. To explain the mystery of the gap between molecular age and fossil evidence of angiosperms, we need to make future efforts not only in developing new molecular methods, but also in making the fossil records more abundant.

Phylogenetic and age justifications for fossil calibrations

We implemented three maximum age constraints:

(1) 365.629 Ma for Node 1 and Node 2, the soft maximum constraint which follows Morris et al. (2018) is based on the first records of seeds in the form of preovules that satisfy the criteria of the seed habit.

(2) 247.2 Ma for Node 3 ~ Node 16, the soft maximum constraint which follows Morris et al. (2018) is based on sediments devoid of angiosperm-like pollen below their first report in the Middle Triassic.

(3) 128.63 Ma for Node 17 ~ Node 38. The age constraint is based on the maximum age of the oldest potential age of tricolpate pollen (the earliest unequivocal angiosperm fossils, Hughes and McDougall 1990), from the middle Atherfield Wealden Bed 35 of the Cowleaze Chine Member, Vectis Formation (Hughes and McDougall 1990) which occurs within the M1n polarity chron in the Late Barremian (Clarke et al. 2011). And the base of the M1n chron is approximately correlated with the base of the *Gerhardtia sartousi* Biozone, dated at 128.63 Ma (Morris et al. 2018).

Node 1 | CG Spermatophyta | 308.14 Ma – 365.629 Ma.

Fossil taxon and specimen. *Cordaixylon iowensis* [OUPH 9616-9742 and UIC 12,233: Ohio University Paleobotanical Herbarium, Department of Botany, Ohio University, Athens, Ohio] from coal balls from the Laddsdale Coal, Lower Cherokee Group, Desmoinesian (upper Moscovian – Kasimovian), Middle – Upper Pennsylvanian (Carboniferous), near What Cheer, Iowa (Trivett 1992).

Phylogenetic justification. Clarke et al. (2011) confirm cordaitean coniferophytes as the oldest records of the crown group of the Acrogymnospermae clade. Afterwards, they rely on cordaitean taxa that are known from whole-plant reconstructions which have informed cladistic analyses, the oldest of which is *Cordaixylon iowensis* from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa (Trivett 1992).

Minimum age. 308.14 Ma

Maximum age. 365.629 Ma

Age justification. Following Morris et al. (2018) and Barba-Montoya et al. (2018), we use 308.14 Ma as the minimum constraint of *Cordaixylon iowensis* and 365.625 Ma as the maximum age of this node.

Node 2 | CG Gymnosperm | 308.14 Ma – 365.629 Ma.

Fossil taxon and specimen. *Cordaixylon iowensis* [OUPH 9616-9742 and UIC 12,233: Ohio University Paleobotanical Herbarium, Department of Botany, Ohio University, Athens, Ohio] from coal balls from the Laddsdale Coal, Lower Cherokee Group, Desmoinesian (upper Moscovian – Kasimovian), Middle – Upper Pennsylvanian (Carboniferous), near What Cheer, Iowa (Trivett 1992).

Phylogenetic justification. Clarke et al. (2011) confirm cordaitean coniferophytes as the oldest records of the crown group of the Acrogymnospermae clade. Afterwards, they rely on cordaitean taxa that are known from whole-plant reconstructions which have informed cladistic analyses, the oldest of which is *Cordaixylon iowensis* from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa (Trivett 1992).

Minimum age. 308.14 Ma

Maximum age. 365.629 Ma

Age justification. Following Morris et al. (2018) and Barba-Montoya et al. (2018), we use 308.14 Ma as the minimum constraint of *Cordaixylon iowensis* and 365.625 Ma as the maximum age of this node.

Node 3 | CG Angiospermae | 125 Ma – 247.2 Ma.

Fossil taxon and specimen. Tricolpate pollen grain from sample BRN 126 of the middle Atherfield Wealden Bed 35, corresponding to the mid- to late Barremian in the Early Cretaceous succession in southern and eastern England (Hughes and McDougall 1990).

Phylogenetic justification. Magallón et al. (2015) identify that the oldest fossil

tricolpate pollen grains lack any distinctive features to link them to a particular living group within eudicots and these grains should be used to calibrate the stem node of eudicots. As there are no confirmed fossils which are older than them within Angiospermae, Tricolpate pollen grain is regarded as the earliest unequivocal evidence of angiosperms.

Minimum age. 125 Ma

Maximum age. 247.2 Ma

Age justification. Following Morris et al. (2018), we use 125 Ma as the minimum constraint of tricolpate pollen grain and 247.2 Ma as the maximum age of this node.

Node 4 | SG Cabombaceae | 110.87 Ma – 247.2 Ma.

Fossil taxon and specimen. *Pluricarpellatia peltata* [MB. Pb. 2000/80: Museum of Natural History, Berlin, Germany], from the Crato Formation of Brazil (Mohr et al. 2008).

Phylogenetic justification. Taylor et al. (2008) identify *Pluricarpellatia peltata* is the member of *Cabomba*.

Minimum age. 110.87 Ma

Maximum age. 247.2 Ma

Age justification. Following Barba-Montoya et al. (2018), we use 110.87 Ma as the minimum constraint of *Pluricarpellatia peltata*.

Node 5 | Nymphaeales – [Austrobaileyales + Mesangiospermae] | 125 Ma – 247.2 Ma.

Fossil taxon and specimen. Tricolpate pollen grain from sample BRN 126 of the middle Atherfield Wealden Bed 35, corresponding to the mid- to late Barremian in the Early Cretaceous succession in southern and eastern England (Hughes and McDougall 1990).

Phylogenetic justification. Magallón et al. (2015) identify that the oldest fossil tricolpate pollen grains lack any distinctive features to link them to a particular living group within eudicots and these grains should be used to calibrate the stem node of

eudicots. However, there are no confirmed fossils which are older than those within this group. Tricolpate pollen grain is the earliest unequivocal evidence of this group.

Minimum age. 125 Ma

Maximum age. 247.2 Ma

Age justification. Following Morris et al. (2018), we use 125 Ma as the minimum constraint of tricolpate pollen grain and 247.2 Ma as the maximum age of this node.

Node 6 | Austrobaileyales – Mesangiospermae | 125 Ma – 247.2 Ma.

Fossil taxon and specimen. Tricolpate pollen grain from sample BRN 126 of the middle Atherfield Wealden Bed 35, corresponding to the mid- to late Barremian in the Early Cretaceous succession in southern and eastern England (Hughes and McDougall 1990).

Phylogenetic justification. Magallón et al. (2015) identify that the oldest fossil tricolpate pollen grains lack any distinctive features to link them to a particular living group within eudicots and these grains should be used to calibrate the stem node of eudicots. However, there are no confirmed fossils which are older than those within this group. Tricolpate pollen grain is the earliest unequivocal evidence of this group.

Minimum age. 125 Ma

Maximum age. 247.2 Ma

Age justification. Following Morris et al. (2018), we use 125 Ma as the minimum constraint of tricolpate pollen grain and 247.2 Ma as the maximum age of this node.

Node 7 | CG Mesangiospermae | 125 Ma – 247.2 Ma.

Fossil taxon and specimen. Tricolpate pollen grain from sample BRN 126 of the middle Atherfield Wealden Bed 35, corresponding to the mid- to late Barremian in the Early Cretaceous succession in southern and eastern England (Hughes and McDougall 1990).

Phylogenetic justification. Magallón et al. (2015) identify that the oldest fossil tricolpate pollen grains lack any distinctive features to link them to a particular living group within eudicots and these grains should be used to calibrate the stem node of

eudicots. However, there are no confirmed fossils which are older than them within Mesangiospermae. Tricolpate pollen grain is the earliest unequivocal evidence of Mesangiospermae.

Minimum age. 125 Ma

Maximum age. 247.2 Ma

Age justification. Following Morris et al. (2018), we use 125 Ma as the minimum constraint of tricolpate pollen grain and 247.2 Ma as the maximum age of this node.

Node 8 | CG Monocots | 113 Ma – 247.2 Ma.

Fossil taxon and specimen. *Liliacidites* sp. A [palynological slide 71-8-1d], from the Potomac Group, Albian Zone I (Early Cretaceous), at the Trent's Reach Locality, Virginia, USA (Hickey and Doyle 1977; Doyle et al. 2008).

Phylogenetic justification. By using a morphological data set of basal angiosperms and assuming relationships among living taxa derived from morphological and molecular data, Doyle et al. (2008) support a monocot affinity for *Liliacidites*. The pollen assigned to *Liliacidites* can represent the stem of monocots (Doyle et al. 2008). Morris et al. (2018) consider it as the oldest secure record of the monocot total group.

Minimum age. 113 Ma

Maximum age. 247.2 Ma

Age justification. Morris et al. (2018) use the Aptian-Albian boundary to calibrate these earliest records of *Liliacidites*, according to the absence of further stratigraphic constraint. Thus, we use 113 Ma to calibrate the minimum age of this node (International Chronostratigraphic Chart, v.2019/05).

Node 9 | CG Alismatales | 96.24 Ma – 247.2 Ma.

Fossil taxon and specimen. *Mayoa portugallica* [S136663: Swedish Museum of Natural History Palaeobotanical Collection], from the Torres Vedras flora of the Figueira da Foz Formation (Friis et al. 2004).

Phylogenetic justification. Following Friis et al. (2004), *Mayoa portugallica* is assigned to the tribe Spathiphyllaeae of the extant monocotyledonous family Araceae.

Similarly, Magallón et al. (2013) propose that these striate and inaperturate pollen grains of *Mayoa portugallica* are similar in detail to those of Monsteroideae (Araceae), such as *Holochlamys* and *Spathiphyllum*. We here use it to calibrate the crown group of Alismatales.

Minimum age. 96.24 Ma

Maximum age. 247.2 Ma

Age justification. Barba-Montoya et al. (2018) consider that an unequivocal minimum age is provided by the appearance of ostracod *Fossocytheridea merlensis* in the overlying Canecas Formation, attributable to the base of the Middle Cenomanian, which coincides with the base of the Conlinoveras gilberti Zone, dated to 96.24 Ma.

Node 10 | CG Araceae | 76.0 Ma – 247.2 Ma.

Fossil taxon and specimen. *Lysichiton (Araciphyllites) austriacus* [NHMW 1999B0057/0183: Natural History Museum, Vienna, Austria], from the Grünbach Formation of Austria (Bogner et al. 2007).

Phylogenetic justification. Bogner et al. (2007) confirm that the fossil is a representative member of the subfamily Orontioideae (family Araceae).

Minimum age. 76 Ma

Maximum age. 247.2 Ma

Age justification. Following Barba-Montoya et al. (2018), we use 76.0 Ma as the minimum age of this node, corresponding to the UC15-UC16 boundary.

Node 11 | SG Musaceae | 74.6 Ma – 247.2 Ma.

Fossil taxon and specimen. Isolated seeds and groups of seeds assigned to *Spirematospermum chandlerae* (Friis 1988), from the Neuse River locality, Black Creek Formation, southwest of Goldsboro, Wayne County, North Carolina, USA.

Phylogenetic justification. Following Barba-Montoya et al. (2018), they use *Spirematospermum chandlerae* to calibrate the stem node of Musaceae based on previous studies. We use it to constraint the stem node of Musaceae.

Minimum age. 74.6 Ma

Maximum age. 247.2 Ma

Age justification. Following Barba-Montoya et al. (2018), we use 74.6 Ma as the minimum age of this node, corresponding to the age of Black Creek Formation.

Node 12 | CG Poaceae | 66.0 Ma– 247.2 Ma .

Fossil taxon and specimen. *Changii indicum* [Holotype: slide 13160; Coordinates: Q-14-3], from coprolites from Red clays, Lameta Formation, Pisdura East and Pisdura South (Prasad et al. 2011).

Phylogenetic justification. Prasad et al. (2011) reveal that *Changii indicum* is most likely a member of the Oryzeae. Iles et al. (2015) identify that it is suitable for dating the stem node of Oryzeae or the crown node of Ehrhartoideae.

Minimum age. 66.0 Ma

Maximum age. 247.2 Ma

Age justification. Following Iles et al. (2015), we use the upper boundary of the Maastrichtian as the minimum age of *Changii indicum* (International Chronostratigraphic Chart, v.2019/05), according as it was recovered from dinosaur coprolites in horizons containing dinosaur bones.

Node 13 | SG Winteraceae | 125 Ma – 247.2 Ma.

Fossil taxon and specimen. Dispersed pollen tetrads assigned to *Walkeripollis gabonensis* described by Doyle et al. (1990) from sample 2963 (939-944 m) in the N'Toum No. 1 well, Gabon, from the upper part of Elf-Aquitaine palynozone C-VII.

Phylogenetic justification. Doyle and Endress (2010) use a morphological dataset for living basal angiosperms to assess the most parsimonious positions of early angiosperm fossils on cladograms of Recent plants. They confirm that *Walkeripollis gabonensis* is sister to Winteraceae, which can be used to calibrate the Winteraceae stem group.

Minimum age. 125 Ma

Maximum age. 247.2 Ma

Age justification. The more recent data (Doyle et al. 1990; Doyle 1992) suggest that

Walkeripollis gabonensis may be late Barremian. We here use 125 Ma as the minimum constraint of *Walkeripollis gabonensis*, corresponding to the upper boundary of the Barremian (International Chronostratigraphic Chart, v.2019/05).

Node 14 | CG Magnoliineae | 110.87 Ma – 247.2 Ma.

Fossil taxon and specimen. *Endressinia brasiliانا* Mohr and Bernardes-de-Oliveira (Mohr and Bernardes-de-Oliveira 2004) [MB. PB. 2001/1455; Museum of Natural History, Institute of Paleontology, Berlin, Germany] consists of a branching axis with attached simple, narrowly ovate leaves and several terminal small flowers, from the Crato Formation, Brazil.

Phylogenetic justification. By summarizing the results of other studies, Massoni et al. (2015) conclude that *Endressinia brasiliانا* provides a safe minimum age for the crown node of Magnoliineae .

Minimum age. 110.87 Ma

Maximum age. 247.2 Ma

Age justification. Massoni et al. (2015) propose a minimum age for *Endressinia brasiliانا* corresponding to the Aptian-Albian boundary, we here use 110.87 Ma as the minimum constraint of this node (Morris et al. 2018).

Node 15 | CG Laurales | 107.59 Ma – 247.2 Ma.

Fossil taxon and specimen. *Virginianthus calycanthoides* Friis, Eklund, Pedersen and Crane (Friis et al. 1994a) [PP43703], from the Albian of Puddledock, Virginia.

Phylogenetic justification. Friis et al. (1994a) support *Virginianthus calycanthoides* as the stem lineage of Calycanthaceae, while Crepet et al. (2005) consider it as the sister lineage of entire Laurales or core Laurales (entire Laurales except Calycanthaceae). Although the most parsimonious position of *Virginianthus calycanthoides* remains controversial, Massoni et al. (2015) believe *Virginianthus* provides a minimum age for the crown node of Laurales following the result of Doyle et al. (2008).

Minimum age. 107.59 Ma

Maximum age. 247.2 Ma

Age justification. Massoni et al. (2015) consider *Virginianthus* is of middle Albian age and use the middle-late Albian boundary to calibrate the minimum age for *Virginianthus*. We here use 107.59 Ma to constrain the minimum age of the Laurales's crown node.

Node 16 | CG core Laurales | 107.59 Ma – 247.2 Ma.

Fossil taxon and specimen. *Cohongarootonia hispida* von Balthazar, Crane, Pedersen, and Friis (von Balthazar et al. 2011), from the Puddledock Flora.

Phylogenetic justification. Massoni et al. (2015) believe that *Cohongarootonia hispida* provides a minimum age for the crown node of core Laurales (entire Laurales excluding Calycanthaceae).

Minimum age. 107.59 Ma

Maximum age. 247.2 Ma

Age justification. Massoni et al. (2015) consider that *Cohongarootonia hispida* is of middle Albian age, and they use the middle-late Albian boundary to calibrate the minimum age for it. We here use 107.59 Ma to constrain the minimum age of the core Laurales's crown node.

Node 17 | SG *Hedyosmum* | 121 Ma – 247.2 Ma.

Fossil taxon and specimen. Trigonous flowers/fruits with attached *Asteropollis* pollen from the Torres Vedras locality, Estremadura Region, Portugal (Friis et al. 1994b, 1999).

Phylogenetic justification. Based on substantial morphological and structural similarities of the flowers and attached pollen with extant *Hedyosmum* (Friis et al. 1994b, 1999), and combining with the phylogenetic result of Eklund et al. (2004), it can represent a crown group member or stem representative of *Hedyosmum* (Magallón et al. 2015).

Minimum age. 121 Ma

Maximum age. 247.2 Ma

Age justification. The Torres Vedras locality is considered to correspond to the late Barremian to early Aptian (Heimhofer et al. 2007). Magallón et al. (2015) use 120.7 Ma (the lower third part of the Aptian) as its minimum age. Hence, we use 121 Ma (the lower third part of the Aptian) as its minimum age (International Chronostratigraphic Chart, v.2019/05).

Node 18 | CG Eudicots | 119.6 Ma – 128.63 Ma.

Fossil taxon and specimen. *Hyrcantha decussata* [NJU-DES02-001: Geological Institute, Chinese Academy of Sciences, Beijing], from the lower part of the Yixian Formation, Jehol Group, Aptian (Early Cretaceous), from the Liaoning Province, China (Dilcher et al. 2006).

Phylogenetic justification. *Hyrcantha karatscheensis* from western Kazakhstan and the species *Hyrcantha decussata* have many fairly similar characteristics. Dilcher et al. (2006) report that there is great similarity among *Hyrcantha karatscheensis*, *Hyrcantha decussata* and *Sinocarpus decussatus* Leng et Friis. Moreover, these taxa should be combined with the genus *Hyrcantha*. And *Hyrcantha* could be considered as a stem lineage of Ranunculaceae (Wang et al.2016). Following Morris et al. (2018), we here use *Hyrcantha decussata* to calibrate the stem node of Ranunculales (crown node of Eudicots).

Minimum age. 119.6 Ma

Maximum age. 128.63 Ma

Age justification. Morris et al. (2018) establish a minimum constraint of 119.6 Ma based on the Jiufontang Formation.

Node 19 | CG Ranunculales | 113 Ma – 128.63 Ma.

Fossil taxon and specimen. *Teixeiraea lusitanica*, spec. nov., von Balthazar, Pedersen and Friis (von Balthazar et al. 2005) [S125001 (from sample vale de Agua 364)], from the Farmalicao locality of the Figueira da Foz Formation.

Phylogenetic justification. Floral morphology and pollen structure of *Teixeiraea lusitanica* suggest a closer relationship to Ranunculales (von Balthazar et al. 2005).

Magallón et al. (2015) consider it to be a stem lineage member of the least inclusive clade which included all these extant families. Hence, we use it to constrain crown node of Ranunculales.

Minimum age. 113 Ma

Maximum age. 128.63 Ma

Age justification. Friis et al. (2011) identify that *Teixeiraea lusitanica* was from the late Aptian, and Magallón et al. (2015) use the upper boundary of the Aptian as the minimum age. Following these analyses, we here use 113 Ma to calibrate the minimum constraint of this node (International Chronostratigraphic Chart, v.2019/05).

Node 20 | CG Proteales | 107.59 Ma – 128.63 Ma.

Fossil taxon and specimen. *Aquila brookensis* [PP4295: Field Museum, Chicago IL, USA] described by Crane et al. (1993) from the Potomac Formation at Bank, near Brooke, Virginia, USA.

Phylogenetic justification. Doyle (2015) identifies *Aquila* (including *Sapindopsis variabilis*, *Platanocarpus brookensis*, *Aquila brookensis*) as a stem group member of the genus *Platanus*.

Minimum age. 107.59 Ma

Maximum age. 128.63 Ma

Age justification. From Barba-Montoya et al. (2018), they establish a minimum constraint for Proteales corresponding to the middle-late Albian Boundary. Thus, we here use 107.59 Ma as the minimum constraint of this node.

Node 21 | SG Buxales | 100.5 Ma – 128.63 Ma.

Fossil taxon and specimen. *Spanomera marylandensis* sp. nov. [PP42978: Field Museum, Chicago IL, USA] (Drinnan et al. 1991), from Elk Neck beds, Potomac Group, Mauldin Mountain, northeastern Maryland, USA.

Phylogenetic justification. Drinnan et al. (1991) identify *Spanomera marylandensis* as a member of *Spanomera*, and morphological and structural features of *Spanomera* suggest a relationship with Buxaceae. Doyle and Endress (2010) confirm that the best

position of *Spanomera* is sister to Buxaceae.

Minimum age. 100.5 Ma

Maximum age. 128.63 Ma

Age justification. *Spanomera marylandensis* sp. nov. was from the late Albian Patapsco Formation (Drinnan et al. 1991) and we use the upper limit of the Albian as the minimum constraint of this node (International Chronostratigraphic Chart, v.2019/05).

Node 22 | CG Dilleniales | 47.8 Ma – 128.63 Ma.

Fossil taxon and specimen. Seeds similar to *Hibbertia* and *Tetracera* (Chandler 1964), from the Early Eocene of England, UK.

Phylogenetic justification. The phylogenetic relationships of these seeds have been clarified by Magallón et al. (2015), considering them as the crown node of Dilleniaceae.

Minimum age. 47.8 Ma

Maximum age. 128.63 Ma

Age justification. Following Magallón et al. (2015), we use the upper boundary of the Early Eocene (47.8 Ma) to constrain the minimum age of this node (International Chronostratigraphic Chart, v.2019/05).

Node 23 | CG Caryophyllales | 72.1 Ma – 128.63 Ma.

Fossil taxon and specimen. Fossil infructescences and fruits assigned to *Coahuilacarpon phytolaccoides* Cevallos-Ferriz, Estrada-Ruiz et Pérez-Hernández, from the Cerro del Pueblo Formation, Coahuila, Mexico (Cevallos-Ferriz et al. 2008) [Colección Nacional de Paleontología, Instituto de Geología, Universidad Nacional Autónoma de México, catalogue no. IGM-PB 1244].

Phylogenetic justification. Cevallos-Ferriz et al. (2008) report the fossil *Coahuilacarpon phytolaccoides* has many similar morphological and anatomical characters with those found in Caryophyllales, particularly in Phytolaccaceae.

Minimum age. 72.1 Ma

Maximum age. 128.63 Ma

Age justification. The plants represented by infructescences contained in the sediments grew during the late Campanian based on its stratigraphic position and sedimentary correlation (Cevallos-Ferriz et al. 2008). Thus, we use the upper boundary of the Campanian as the minimum constraint of this node (International Chronostratigraphic Chart, v.2019/05).

Node 24 | SG Hydrangeaceae | 89.8 Ma – 128.63 Ma.

Fossil taxon and specimen. Flowers assigned to *Tylerianthus crossmanensis* Gandolfo, Nixon et Crepet, sp. nov. Generic, from Old Crossman Pit, Raritan Formation, New Jersey, USA (Gandolfo et al. 1998a) [CUPC 1047].

Phylogenetic justification. Gandolfo et al. (1998a) compare the characters of these flowers assigned to *Tylerianthus crossmanensis* with those of extant flowers (from several families of the saxifragalean complex). They find that these flowers have a close relationship with extant members of the Saxifragaceae and Hydrangeaceae. Magallón et al. (2015) consider *Tylerianthus crossmanensis* to be related to Hydrangeaceae and use it to calibrate the stem node of Hydrangeaceae.

Minimum age. 89.8 Ma

Maximum age. 128.63 Ma

Age justification. Gandolfo et al. (1998a) identify that *Tylerianthus crossmanensis* is dated back to the Turonian on the basis of palynology. We here use the upper boundary of the Turonian as the minimum age of this fossil (International Chronostratigraphic Chart, v.2019/05).

Node 25 | CG Ericales | 89.8 Ma – 128.63 Ma.

Fossil taxon and specimen. *Pentapetalum trifasciculandricus* Martínez-Millán, Crepet et Nixon gen.et sp.nov. (Martínez-Millán et al. 2009), from Old Crossoman Clay Pit locality of Sayreville, New Jersey [Holotype: part CUPC579 and counterpart CUPC591].

Phylogenetic justification. Martínez-Millán et al. (2009) compare *Pentapetalum*

trifasciculandricus with extant taxa by using traditional methods of identification and support a relation with the Theaceae (*Stewartia*). However, the phylogenetic analyses propose a different view and support another relationship to the Ternstroemiaceae/Pentaphylacaceae. Magallón et al. (2015) follow the explicit phylogenetic results that are consistent with other assignments, and use *Pentapetalum trifasciculandricus* to calibrate the crown node of Ericales.

Minimum age. 89.8 Ma

Maximum age. 128.63 Ma

Age justification. *Pentapetalum trifasciculandricus* is dated back to the Turonian of New Jersey in North America (Martínez-Millán et al. 2009). We here use the upper boundary of the Turonian as the minimum age of this fossil (International Chronostratigraphic Chart, v.2019/05).

Node 26 | SG Asteraceae | 47.5 Ma – 128.63 Ma.

Fossil taxon and specimen. *Raiguenrayun cura* Barreda, Katinas, Passalia & Palazzesi sp. nov. (Barreda et al. 2012), from Río Pichileufú fossil-bearing strata, Huitara Formation, Argentina [Specimen MLG 1156: ‘Museo del Lago Gutiérrez Dr. Rosendo Pascual de Geología y Paleontología’ Villa Los Coihues, San Carlos de Bariloche, Río Negro Province, Argentina].

Phylogenetic justification. The extinct taxa *Raiguenrayun cura* doesn’t match exactly any living member of the family. This taxa is closely related to the root of Asteraceae and is the oldest well-dated member of Asteraceae (Barreda et al. 2012).

Minimum age. 47.5 Ma

Maximum age. 128.63 Ma

Age justification. Wilf et al. (2005) constrain the age of Río Pichileufú fossil-bearing strata about 47.46 ± 0.05 Ma based on radiometric data. Thus, we use 47.5 Ma as the minimum age of this fossil.

Node 27 | SG Aquifoliaceae | 61.6 Ma – 128.63 Ma .

Fossil taxon and specimen. Seed assigned to *Ilex hercynica* Mai, from Gonna,

Germany (Mai 1970) [MAI, Nr. 6004: Zentralsammlung Zentrales Geologisches Institut Berlin].

Phylogenetic justification. The seeds assigned to *Ilex hercynica* can be used as the reliable fossils of Aquifoliaceae (Martínez-Millán et al. 2010). Magallón et al. (2015) use it to calibrate the stem node of Aquifoliaceae.

Minimum age. 61.6 Ma

Maximum age. 128.63 Ma

Age justification. Martínez-Millán et al. (2010) consider the fossil *Ilex hercynica* as the member of the Early Paleocene fossils. We use the upper boundary of the Early Paleocene (Danian) to calibrate the minimum age of this node (International Chronostratigraphic Chart, v.2019/05).

Node 28 | CG Solanales | 37.3 Ma – 128.63 Ma.

Fossil taxon and specimen. *Solanites crassus* [USNM-39949: Smithsonian Institution National Museum of Natural History, Washington DC, USA], from Holly Springs sand, Mill Creek, railroad cut north of Shandy, Hardeman County, Tenn (Berry 1930).

Phylogenetic justification. Berry (1930) find that these flowers assigned to *Solanites crassus* resemble those of several genera of the Solanaceae and they are clearly referable to this family.

Minimum age. 37.3 Ma

Maximum age. 128.63 Ma

Age justification. From Barba-Montoya et al. (2018), they use 37.3 Ma to constrain the minimum age of *Solanites crassus* based on the combined age model of Vandenberghe et al. (2012).

Node 29 | SG Lamiaceae | 27.82 Ma – 128.63 Ma.

Fossil taxon and specimen. Fruits assigned to *Ajuginucula smithii* Reid et Chandler and *Melissa parva* Reid et Chandler (Reid and Chandler 1926), from Bembridge, England.

Phylogenetic justification. Martínez-Millán et al. (2010) propose that the fruits from the Bembridge flora in England are the oldest fossils of Lamiaceae. We here use them to calibrate the node between Lamiaceae and Phrymaceae.

Minimum age. 27.82 Ma

Maximum age. 128.63 Ma

Age justification. Martínez-Millán et al. (2010) identify these fossils from the Early-Middle Oligocene. Thus, we use 27.82 Ma as the minimum constraint of this node, corresponding to the upper boundary of Early Oligocene (International Chronostratigraphic Chart, v.2019/05).

Node 30 | CG Vitaceae | 65.508 Ma – 128.63 Ma.

Fossil taxon and specimen. Fruits and seeds assigned to *Indovitis chitaleyae* (Manchester et al. 2013) [UF19279-56220: Florida Museum of Natural History (UF) Gainesville, Florida, USA], from serial sections and peels of chert from the Deccan Intertrappean beds of central India.

Phylogenetic justification. *Indovitis chitaleyae* is conformed closely to extant *Vitis* in a suite of characters and it is the oldest known fossil occurrence of Vitaceae (Manchester et al. 2013).

Minimum age. 65.508 Ma

Maximum age. 128.63 Ma

Age justification. From Barba-Montoya et al. (2018), they consider that the minimum age of *Indovitis chitaleyae* can be constrained by the minimum age of Deccan volcanism, which is constrained to 65.535 Ma \pm 0.027 Myr (Schoene et al. 2015), thus, 65.508 Ma.

Node 31 | SG Hamamelidaceae | 83.6 Ma – 128.63 Ma.

Fossil taxon and specimen. Flowers assigned to *Allonia decandra* Magallón-Puebla, Herendeen & Endress [PP44595: Paleobotanical Collections of the Field Museum, Chicago], and to *Androdecidua endressi* Magallón, Herendeen & Crane, from the Allon locality, Buffalo Creek Member, Gaillard Formation, Georgia, USA

(Magallón-Puebla et al. 1996; Magallón et al. 2001).

Phylogenetic justification. Magallón-Puebla et al. (1996) identify that *Allonia* is closely related to the extant genus *Maingaya* based on morphological characters. Magallón et al. (2001) suggest a relationship between *Androdecidua* and Hamamelidaceae. Following Magallón et al. (2015), they consider these two genera as the sister taxa to *Hamamelis* and use them to calibrate the crown node of Hamamelidaceae. We here use these fossils to calibrate the node between Hamamelidaceae and Cercidiphyllaceae.

Minimum age. 83.6 Ma

Maximum age. 128.63 Ma

Age justification. From Magallón et al. (2015), they use the upper boundary of the Santonian to constraint the minimum age of this fossil, thus we use 83.6 Ma corresponding to this boundary (International Chronostratigraphic Chart, v.2019/05).

Node 32 | SG Juglandaceae plus Myricaceae | 83.6 Ma – 128.63 Ma.

Fossil taxon and specimen. Three types of fossil flowers and fruits that are referred to *Caryanthus* (Sims et al. 1999), from the upper Santonian (Upper Cretaceous) Buffalo Creek Member of the Gaillard Formation in central Georgia, USA.

Phylogenetic justification. Sims et al. (1999) identify these types of fossil flowers and fruits (from the Gaillard Formation in central Georgia, USA) are referred to *Caryanthus*. Magallón et al. (2015) consider that *Caryanthus* is more closely related to Rhoipteleaceae, Myricaceae and Juglandaceae, and they use these fossils to calibrate the stem node of the clade including Juglandaceae and Myricaceae.

Minimum age. 83.6 Ma

Maximum age. 128.63 Ma

Age justification. These types of fossil flowers and fruits are identified from the upper Santonian by Sims et al. (1999). We here use 83.6 Ma, corresponding to the upper boundary of the Santonian, as the minimum age of this node (International Chronostratigraphic Chart, v.2019/05).

Node 33 | SG Fabaceae | 56.0 Ma – 128.63 Ma.

Fossil taxon and specimen. Infructescence and fruits assigned to *Leguminocarpon gardneri* (Herendeen and Crane 1992), from the Reading Formation, England.

Phylogenetic justification. Herendeen and Crane (1992) find some features observed in *Leguminocarpon gardneri* are similar with those of different genera within Caesalpinioideae. Magallón et al. (2015) use it to calibrate the stem node of Fabaceae.

Minimum age. 56.0 Ma

Maximum age. 128.63 Ma

Age justification. Herendeen and Crane (1992) confirm these infructescence and fruits assigned to *Leguminocarpon gardneri* are dated back to the Paleocene. Hence, we use 56.0 Ma to calibrate the minimum age of this node, corresponding to the boundary of the Paleocene (International Chronostratigraphic Chart, v.2019/05).

Node 34 | CG Celastraceae | 37.8 Ma – 128.63 Ma.

Fossil taxon and specimen. Leaves of *Celastrus* from the Green River Flora, USA (MacGinitie 1969).

Phylogenetic justification. Only leaf fossils have been reported in Celastraceae (Taylor 1990). The phylogenetic relationships of these leaves have been discussed by Magallón et al. (2015).

Minimum age. 37.8 Ma

Maximum age. 128.63 Ma

Age justification. MacGinitie (1969) identifies that these leaves assigned to *Celastrus* are dated back to Middle Eocene. Hence, we use 37.8 Ma to calibrate the minimum age of this node, corresponding to the boundary of the Middle Eocene (International Chronostratigraphic Chart, v.2019/05).

Node 35 | SG Elaeocarpaceae | 61.6 Ma – 128.63 Ma.

Fossil taxon and specimen. *Sloanea ungeri* (Heer) Manch. & Z. Kvaček comb. n. (Manchester and Kvaček 2009), from the Great Plains regions of North America, in

sediments from early Paleocene (Puercan) to late Paleocene (Tiffanian) of Wyoming and Montana; and from the Early Eocene of the Wind River Formation.

Phylogenetic justification. Manchester and Kvaček (2009) confirm that fruits assigned to *Sloanea ungeri* have a close relationship with those of extant *Sloanea*, in terms of shape and number of valves. We use these fossils to calibrate the node between Elaeocarpaceae and Oxalidaceae.

Minimum age. 61.6 Ma

Maximum age. 128.63 Ma

Age justification. From Magallón et al. (2015), they use the upper boundary of the Danian (Lower Paleocene) to constrain the minimum age of this fossil, then we use 61.6 Ma corresponding to this boundary (International Chronostratigraphic Chart, v.2019/05).

Node 36 | CG Rutaceae | 66.0 Ma – 128.63 Ma.

Fossil taxon and specimen. Seeds assigned to *Rutaspermum biornatum* Knobloch & Mai from Walbeck, Germany, corresponding to the Maastrichtian (Knobloch & Mai, 1986).

Phylogenetic justification. The phylogenetic relationships of these seeds have been discussed by Magallón et al. (2015). They acknowledge that these seeds are the oldest representatives of Rutaceae and use them to calibrate the crown node of Rutaceae.

Minimum age. 66.0 Ma

Maximum age. 128.63 Ma

Age justification. From Magallón et al. (2015), they use the upper boundary of the Maastrichtian to constrain the minimum age of this fossil, then we use 66.0 Ma corresponding to this boundary (International Chronostratigraphic Chart, v.2019/05).

Node 37 | SG Brassicales | 89.8 Ma – 128.63 Ma.

Fossil taxon and specimen. Flowers assigned to *Dressiantha bicarpelata* Gandolfo, Nixon & Crepet (Gandolfo et al. 1998b), from the Old Crossman Clay Pit, Raritan Formation, New Jersey, USA.

Phylogenetic justification. The fossil species has unique suite of characters that are found in extant families of the Order Capparales. Hence, *Dressiantha bicarpelata* constitutes the oldest fossil record for this order (Gandolfo et al. 1998b). Magallón et al. (2015) consider it as a stem or crown member of Brassicales. We here use it to calibrate the stem node of Brassicales.

Minimum age. 89.8 Ma

Maximum age. 128.63 Ma

Age justification. The fossils were collected from outcrops of the Raritan Formation and the age of the formation was calculated as Turonian (Gandolfo et al. 1998b). Therefore, we use the upper boundary of the Turonian as the minimum constraint of this node.

Node 38 | CG Brassicaceae | 23.03 Ma – 128.63 Ma.

Fossil taxon and specimen. Fruits assigned to *Thlaspi primaevum* Becker (Becker 1961), from the Ruby River Basin, Montana, USA.

Phylogenetic justification. Becker (1961) assigned *Thlaspi primaevum* to the extant genus *Thlaspi* (Brassicaceae), and Beilstein et al. (2010) further support this justification.

Minimum age. 23.03 Ma

Maximum age. 128.63 Ma

Age justification. *Thlaspi primaevum* is an Oligocene fossil with angustiseptate winged fruits from the Ruby Basin Flora of southwestern Montana (Becker 1961; Beilstein et al. 2010). Thus, we use the upper boundary of the Oligocene as the minimum constraint of this node (International Chronostratigraphic Chart, v.2019/05).

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