

Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution

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SUPPLEMENTARY FIGURES 1-6 (pages 2-15)

SUPPLEMENTARY TABLES S1-S3 (pages 16-22)

NOTES S1 – JUSTIFICATION OF FOSSIL CALIBRATIONS (pages 23-44)

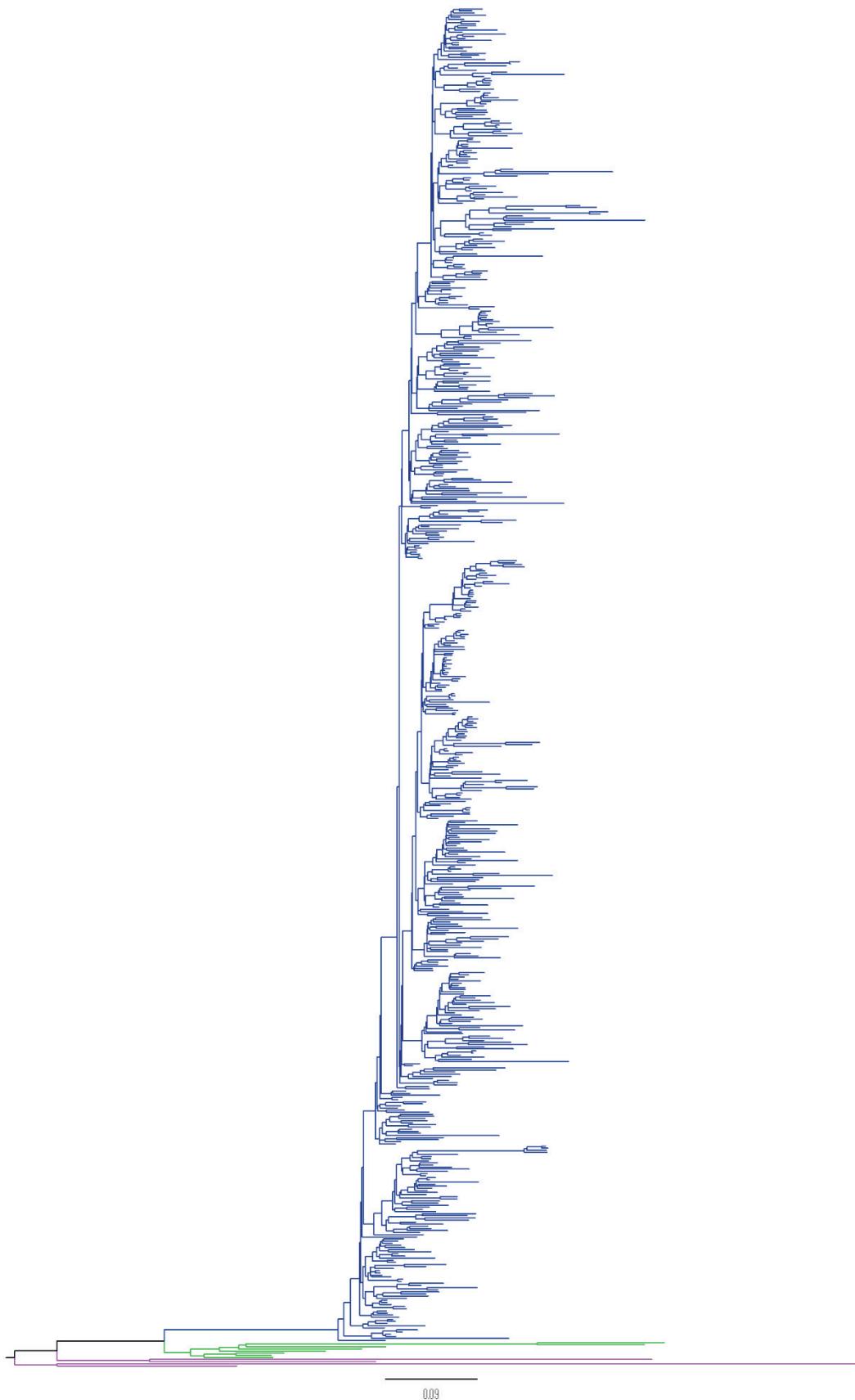


Figure S1. ML Phylogenetic tree from plastid 1st-2nd codon positions for 643 taxa. The Phylogeny was estimated using the GTR+GAMMA model and 1 partition (plastid 1st-2nd). The major lineages of tracheophytes are highlighted: lycophytes and ferns (purple), acrogymnosperms (green) and angiosperms (blue).

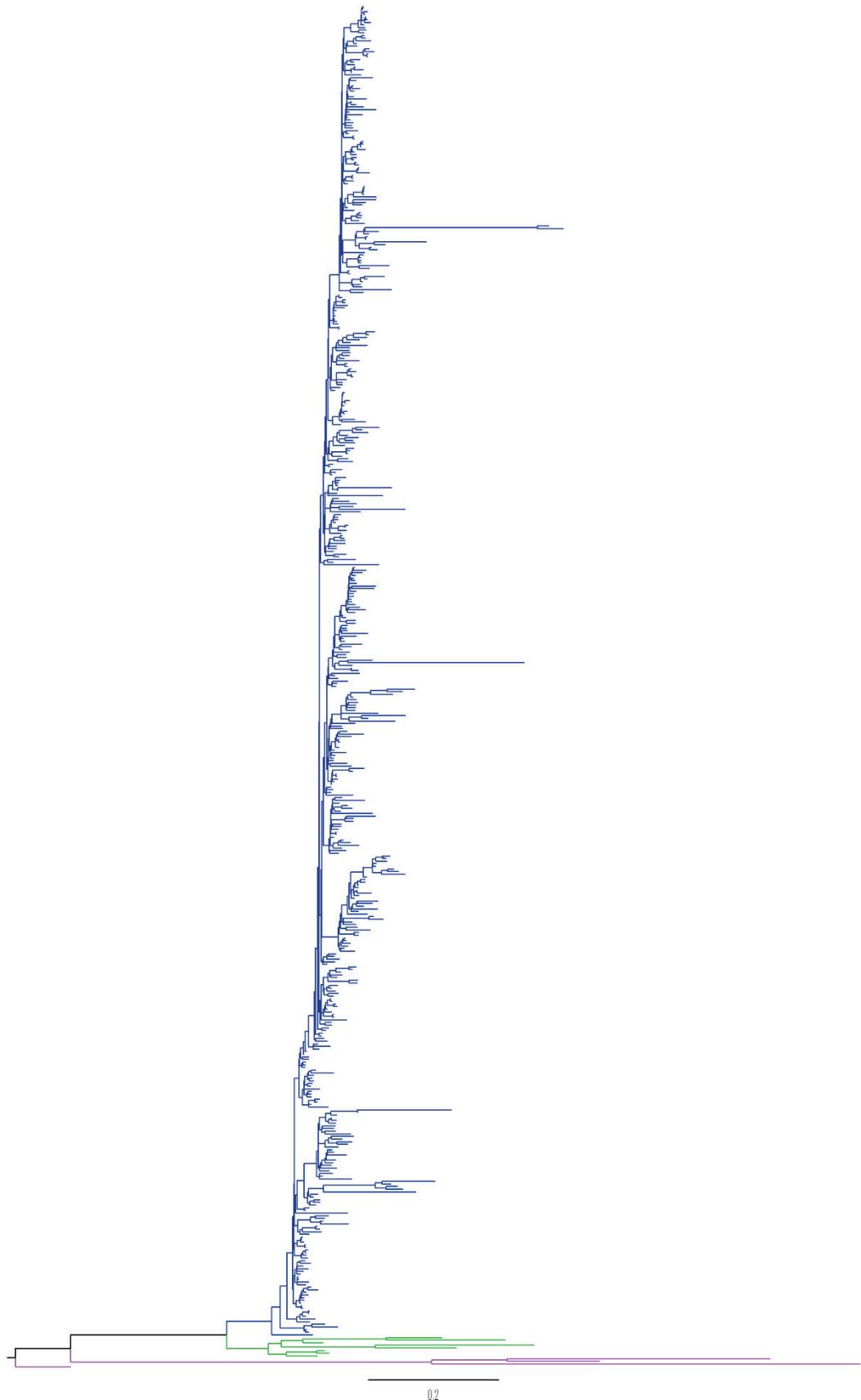


Figure S2. ML Phylogenetic tree from mitochondrial 1st-2nd codon positions for 515 taxa. The Phylogeny was estimated using the GTR+GAMMA model and 1 partition (mitochondrial 1st-2nd). The major lineages of tracheophytes are highlighted: lycophytes and ferns (purple), acrogymnosperms (green) and angiosperms (blue).

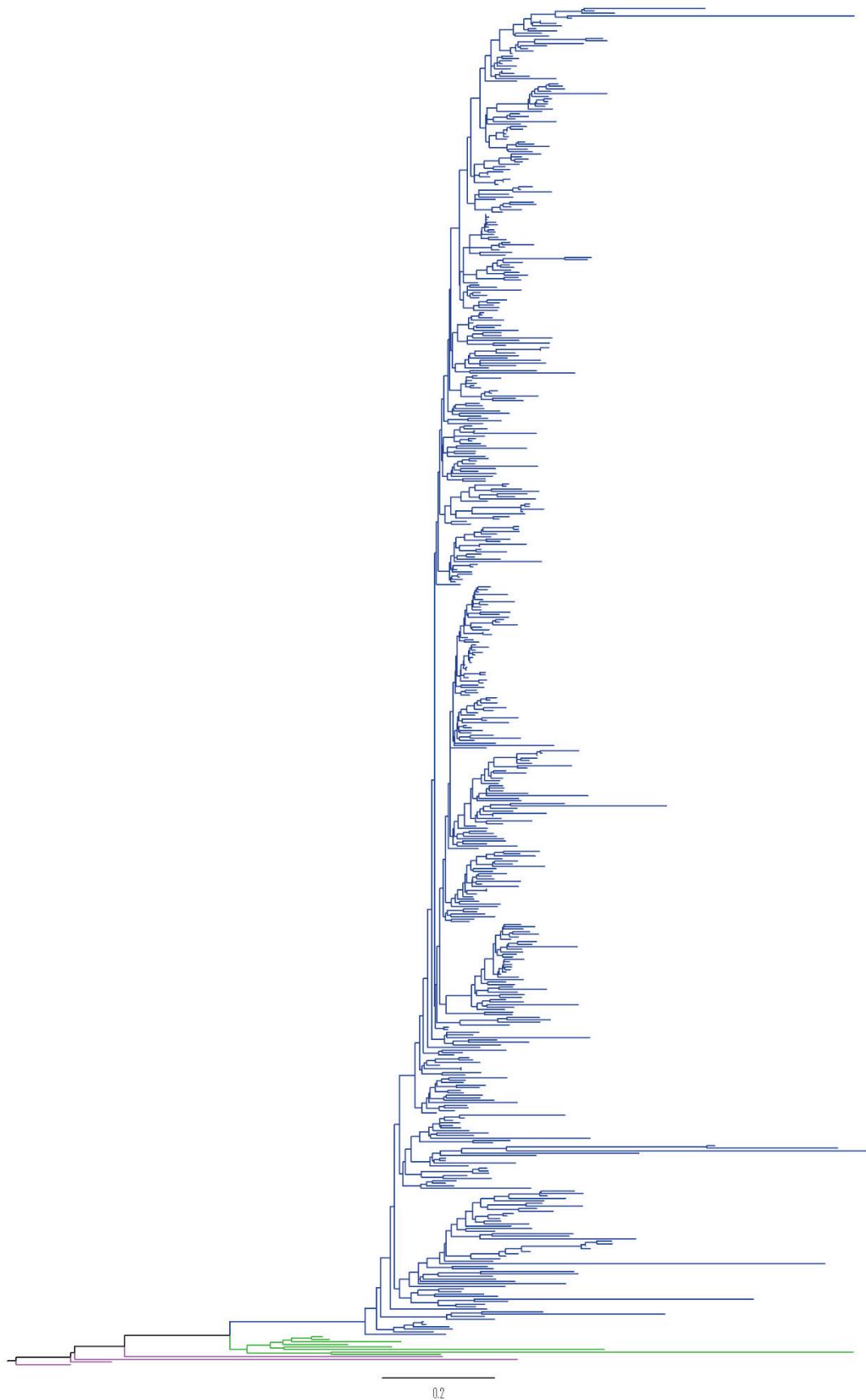


Figure S3. ML Phylogenetic tree from nuclear RNA genes for 540 taxa. The Phylogeny was estimated using the GTR+GAMMA model and 1 partition (nuclear RNA genes). The major lineages of tracheophytes are highlighted: lycophytes and ferns (purple), acrogymnosperms (green) and angiosperms (blue).

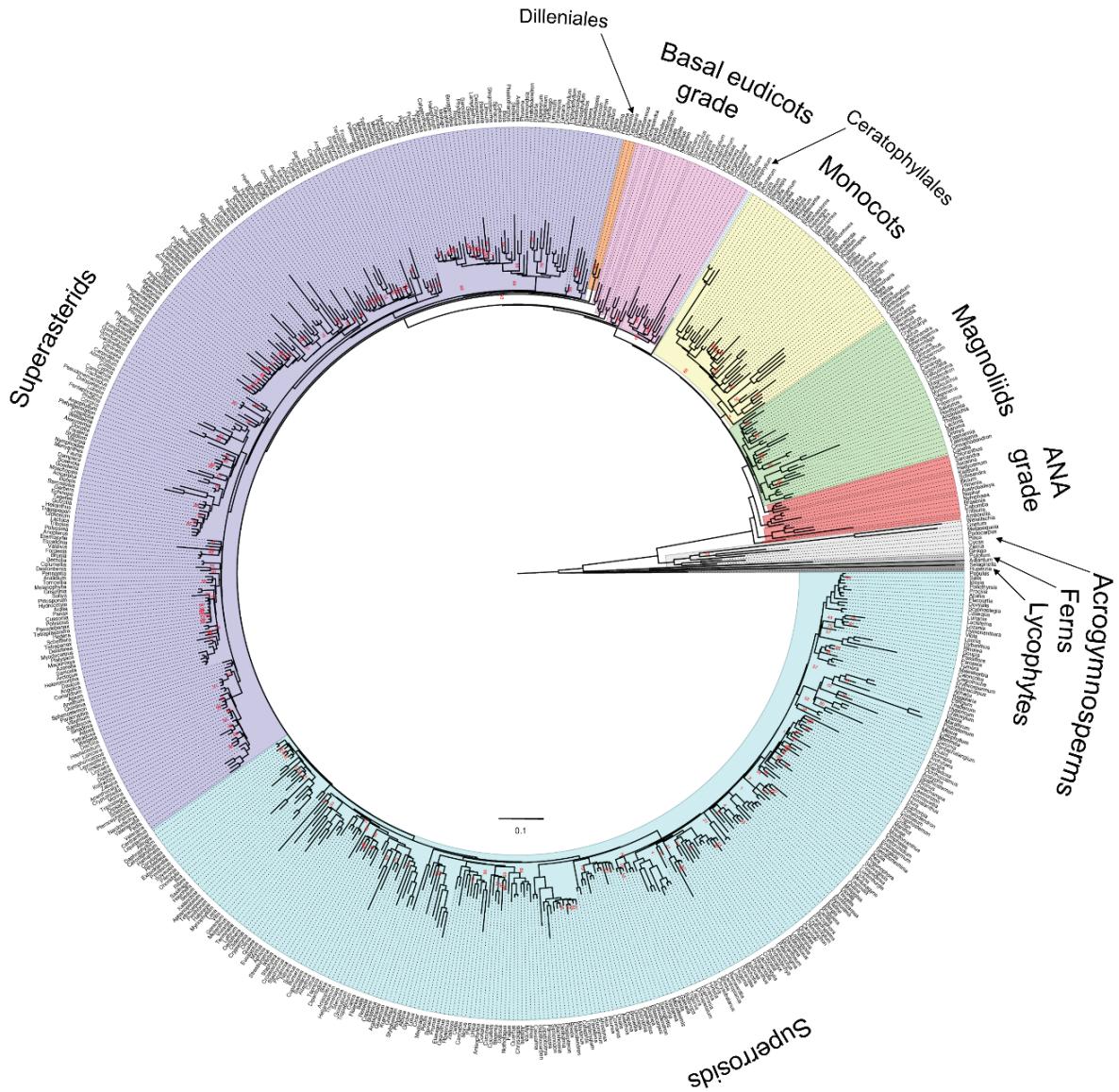


Figure S4. RAxML Phylogenetic tree from the 83 genes and 644 taxa of tracheophytes. The Phylogeny was estimated using the GTR+GAMMA model, using five partitions (plastid 1st-2nd, plastid 3rd, mitochondrial 1st-2nd, mitochondrial 3rd and nuclear RNA genes). Bootstrap support values of 100 % were excluded, while other support values < 100 % are reported directly with red numbers on nodes. The major lineages of tracheophytes and major groups of angiosperms are highlighted: lycophytes (dark grey) and ferns (middle grey), acrogymnosperms (pale grey), ANA grade (red), magnoliids (green), monocots (yellow), Ceratophyllales (pale blue), basal eudicots grade (pink), Dilleniales (orange), superasterids (purple) and superrosids (blue).

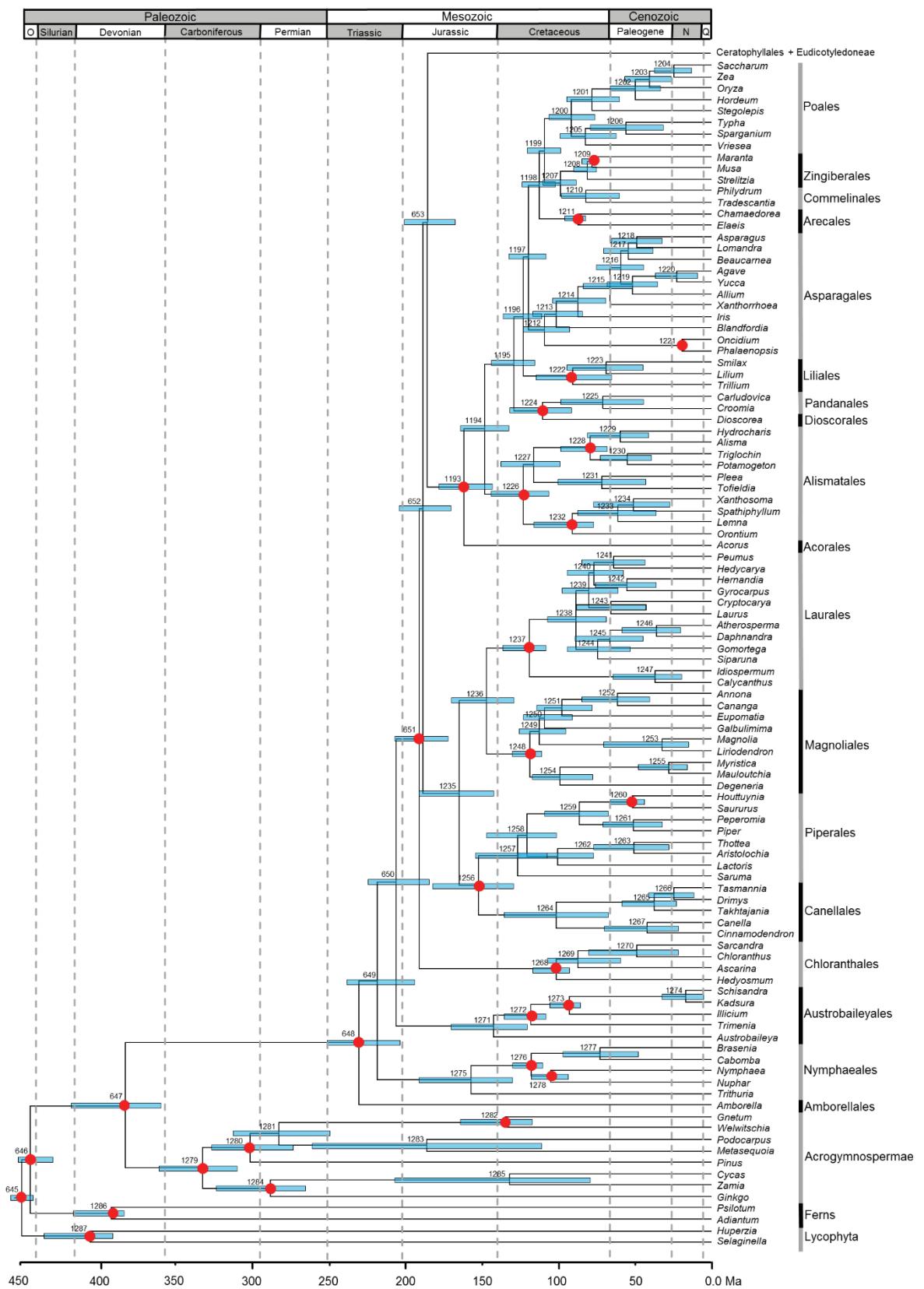


Figure S5. Chronogram of 644 taxa of tracheophytes (from SA-IR-3P). Blue bars represent the 95% HPD credibility intervals for the node ages. Red dots represent calibrated nodes. Divergence times were estimated using calibration strategy A, HKY85+Γ5 substitution model, independent rates model, with the 83 genes subdivided into three partitions: (1) 1st and 2nd codon positions for plastid genes; (2) 1st and 2nd codon positions for mitochondrial genes; and (3) nuclear RNA genes.

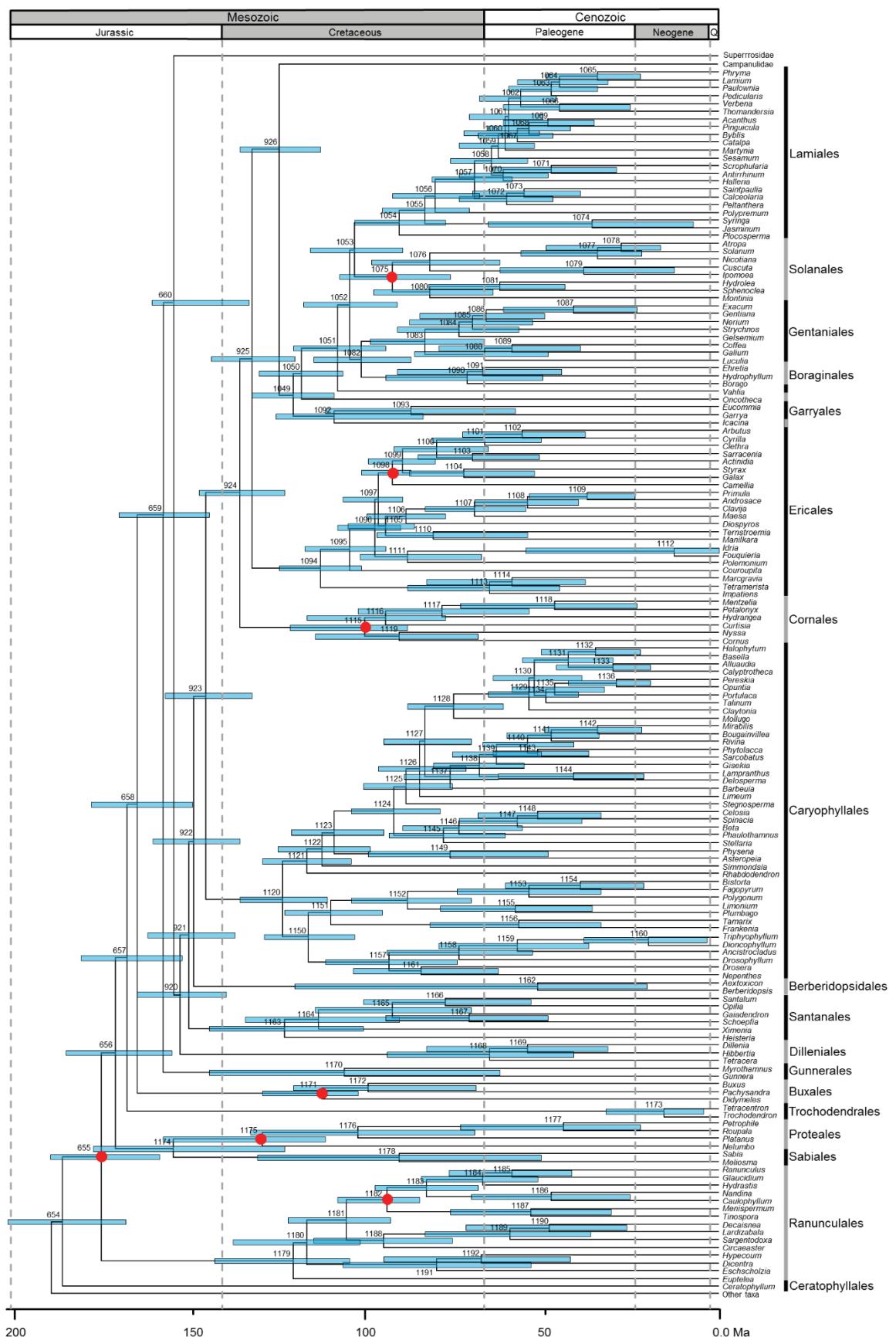


Figure S5.1. Chronogram of 644 taxa of tracheophytes (from SA-IR-3P). Continued

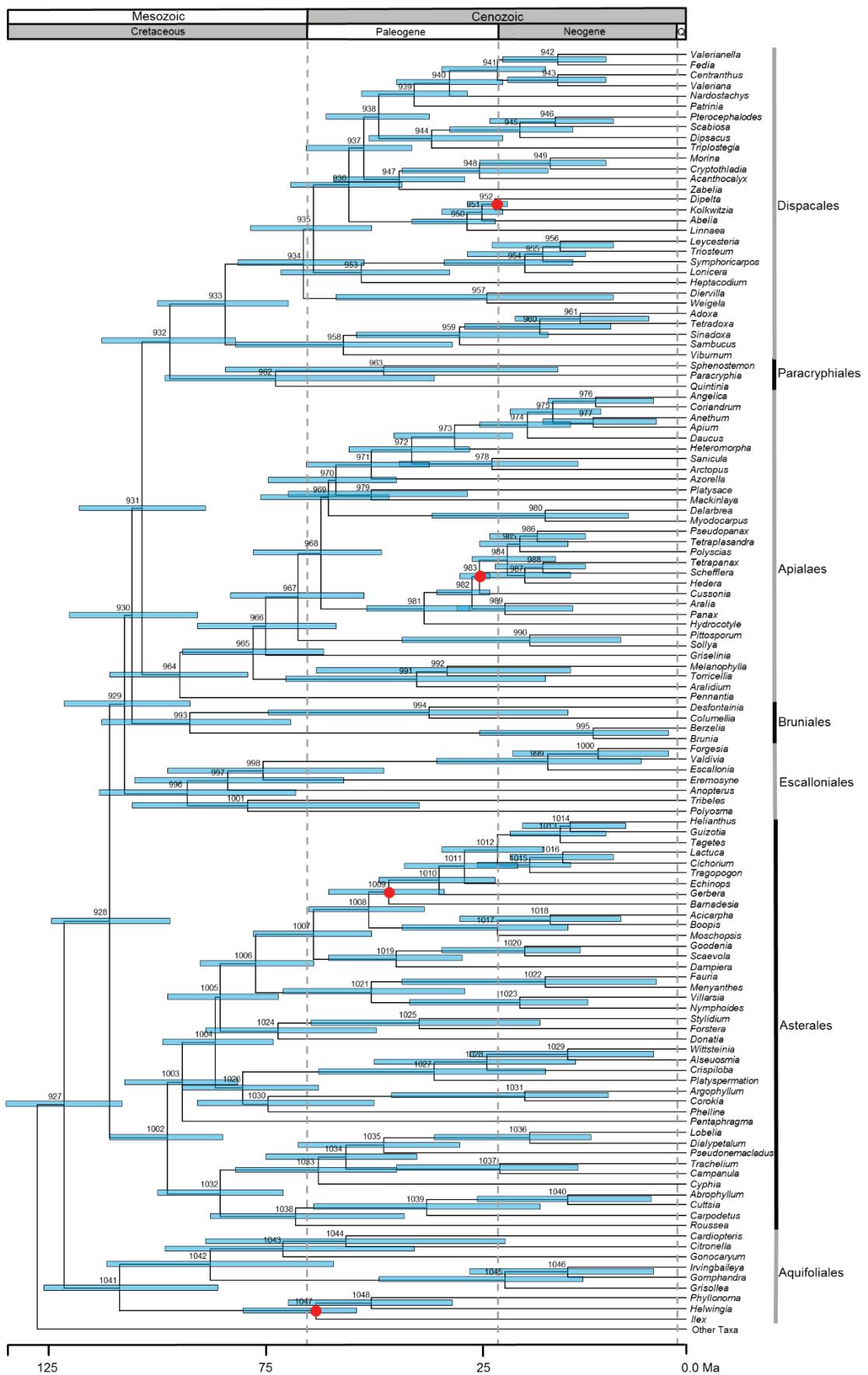


Figure S5.2. Chronogram of 644 taxa of tracheophytes (from SA-IR-3P).

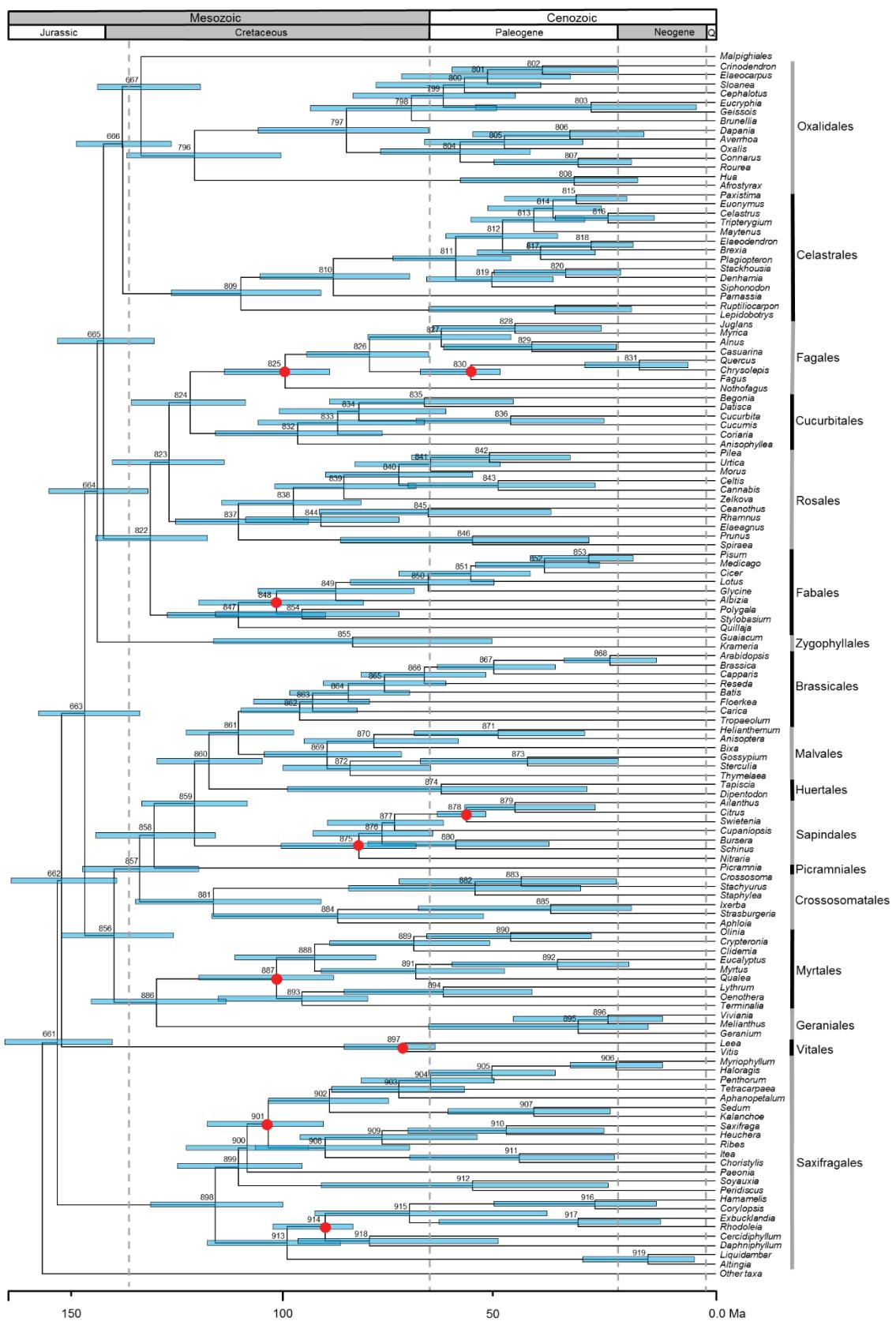


Figure S5.3. Chronogram of 644 taxa of tracheophytes (from SA-IR-3P).

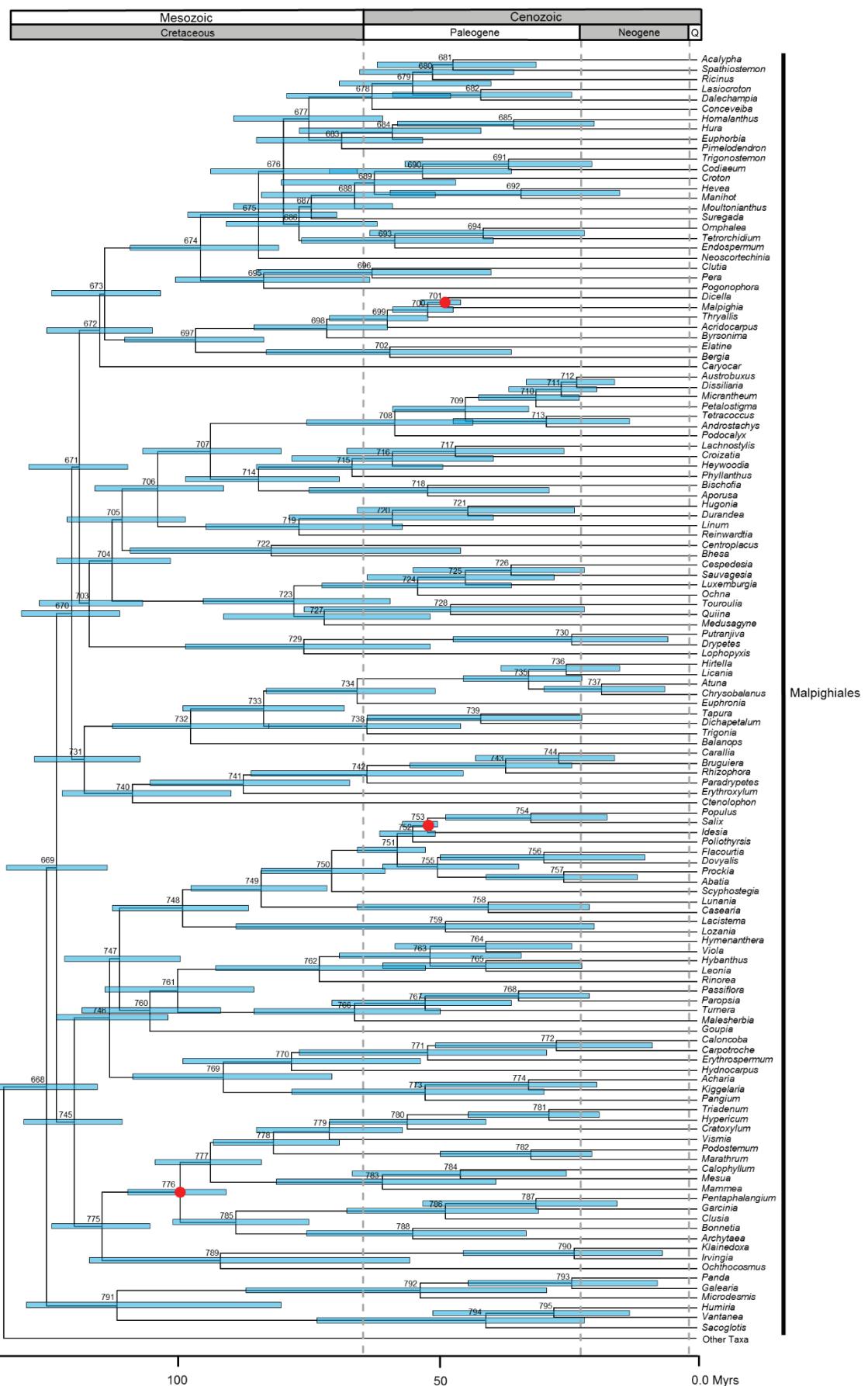


Figure S5.4. Chronogram of 644 taxa of tracheophytes (from SA-IR-3P).

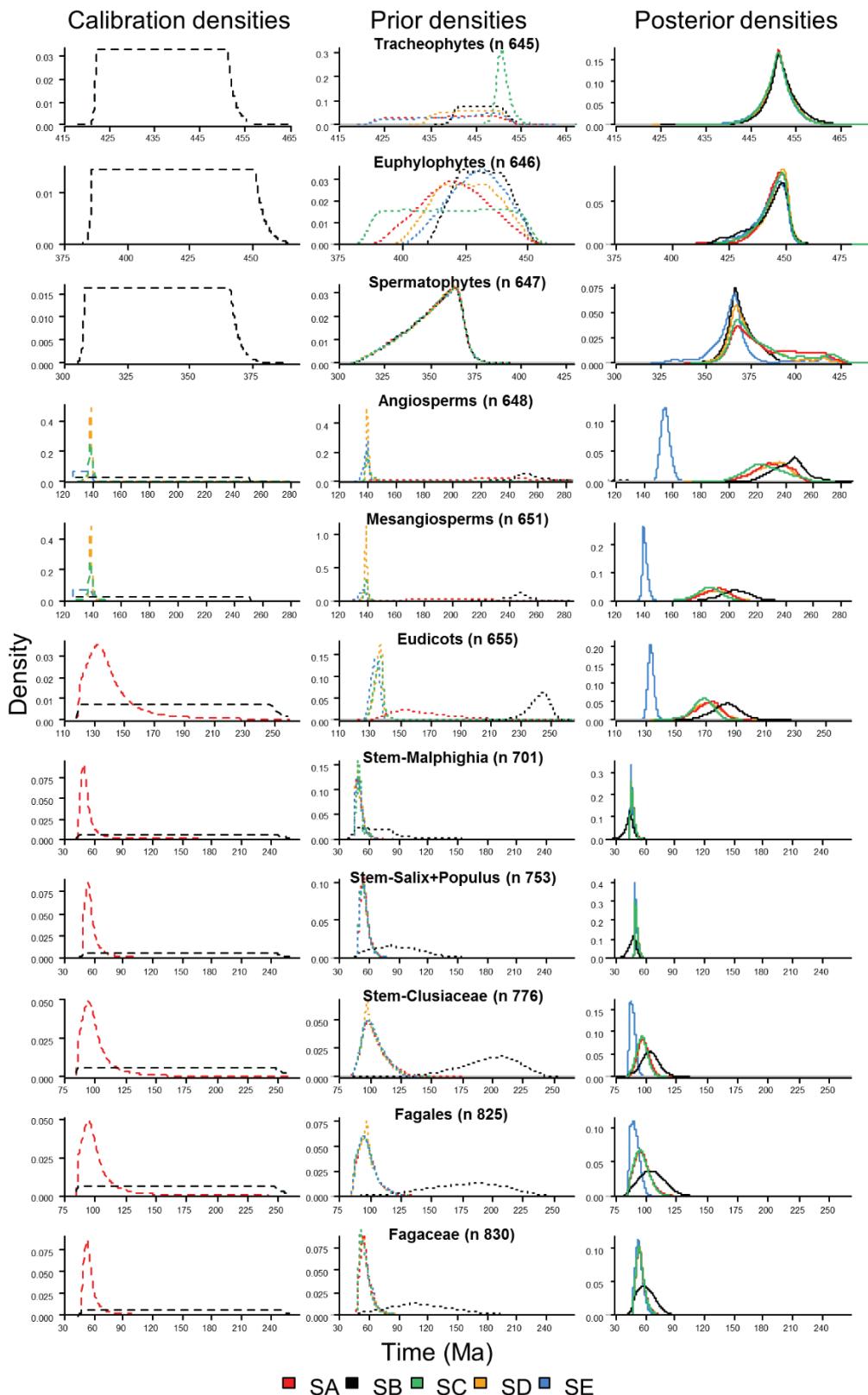


Figure S6. Calibration, prior and posterior densities for 52 calibrated nodes in the tree and for the five calibration strategies. Fossil calibrations are shown as dashed lines, priors as dotted lines and posterior as solid lines. Nodes are numbered as in Supplementary Fig. 1. Estimates were obtained using the HKY85+Γ5 substitution model, independent rates model, with the 83 genes subdivided into three partitions: (1) 1st and 2nd codon positions for plastid genes; (2) 1st and 2nd codon positions for mitochondrial genes; and (3) nuclear RNA genes. Colouring relates to the calibration strategy (SA, SB, SC, SD, SE) as in Figure 1.

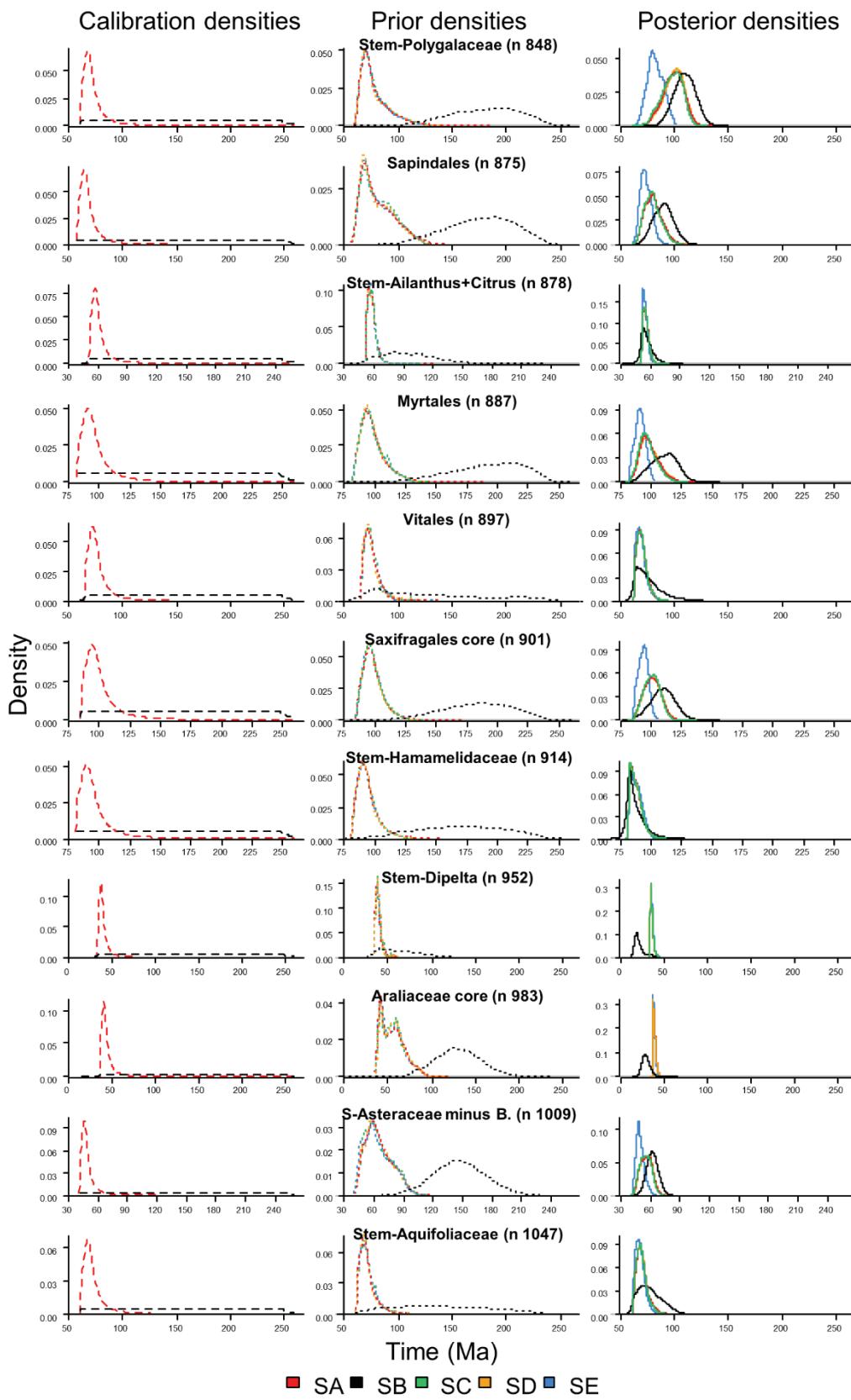


Figure S6.1. Calibration, prior and posterior densities for 52 calibrated nodes in the tree and for the 5 calibration strategies. Continued.

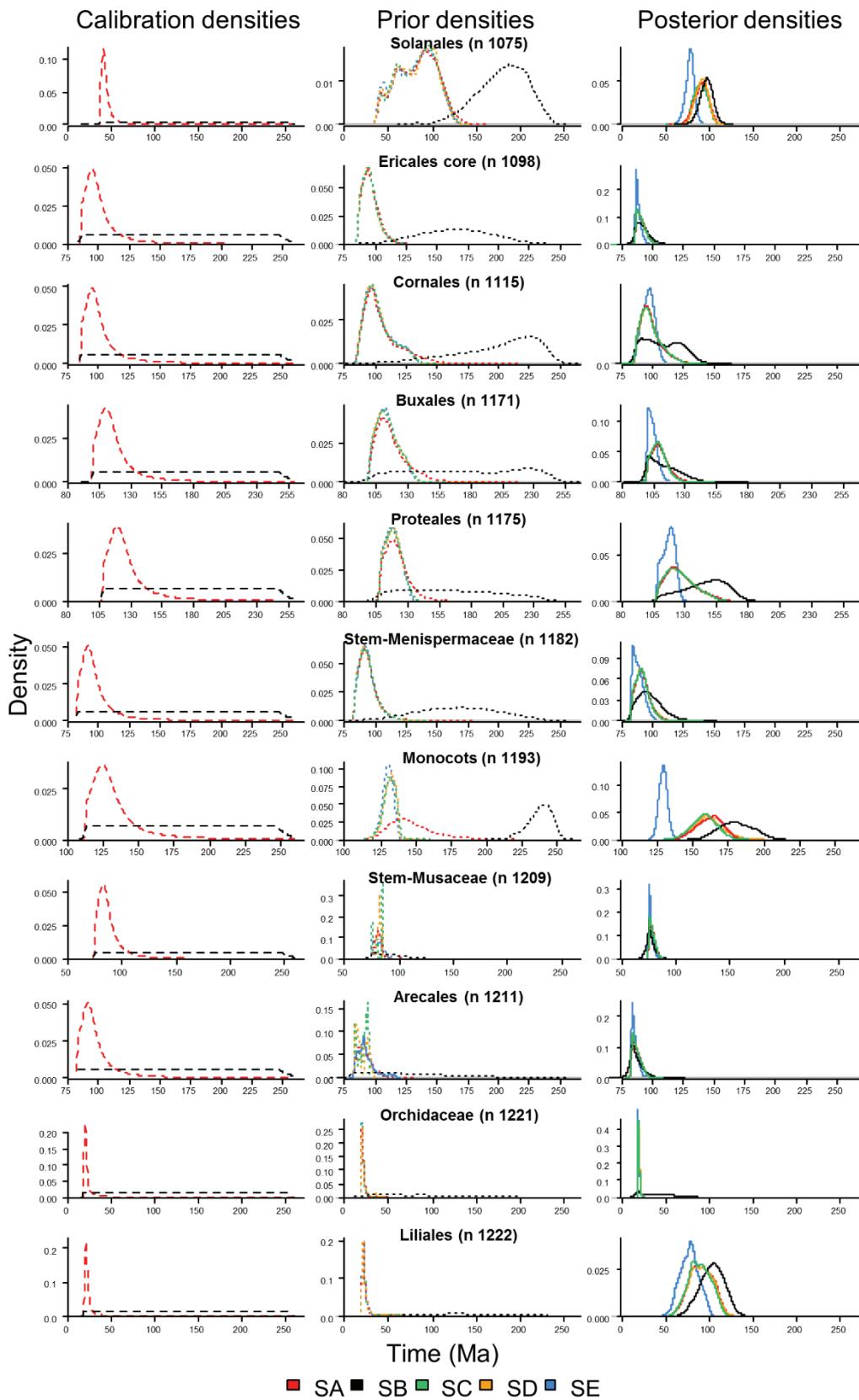


Figure S6.2. Calibration, prior and posterior densities for 52 calibrated nodes in the tree and for the 5 calibration strategies. Continued.

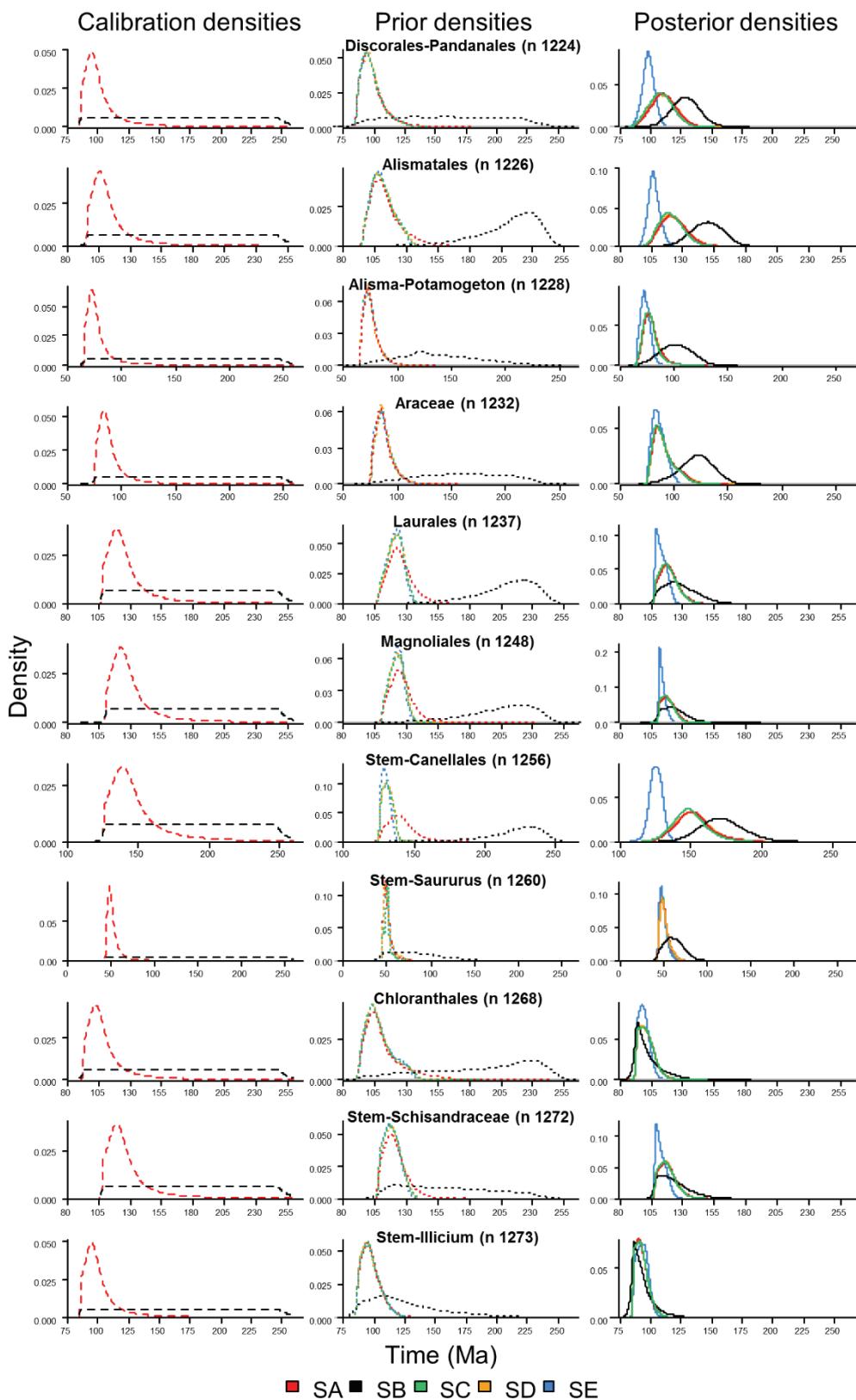


Figure S6.3. Calibration, prior and posterior densities for 52 calibrated nodes in the tree and for the 5 calibration strategies. Continued.

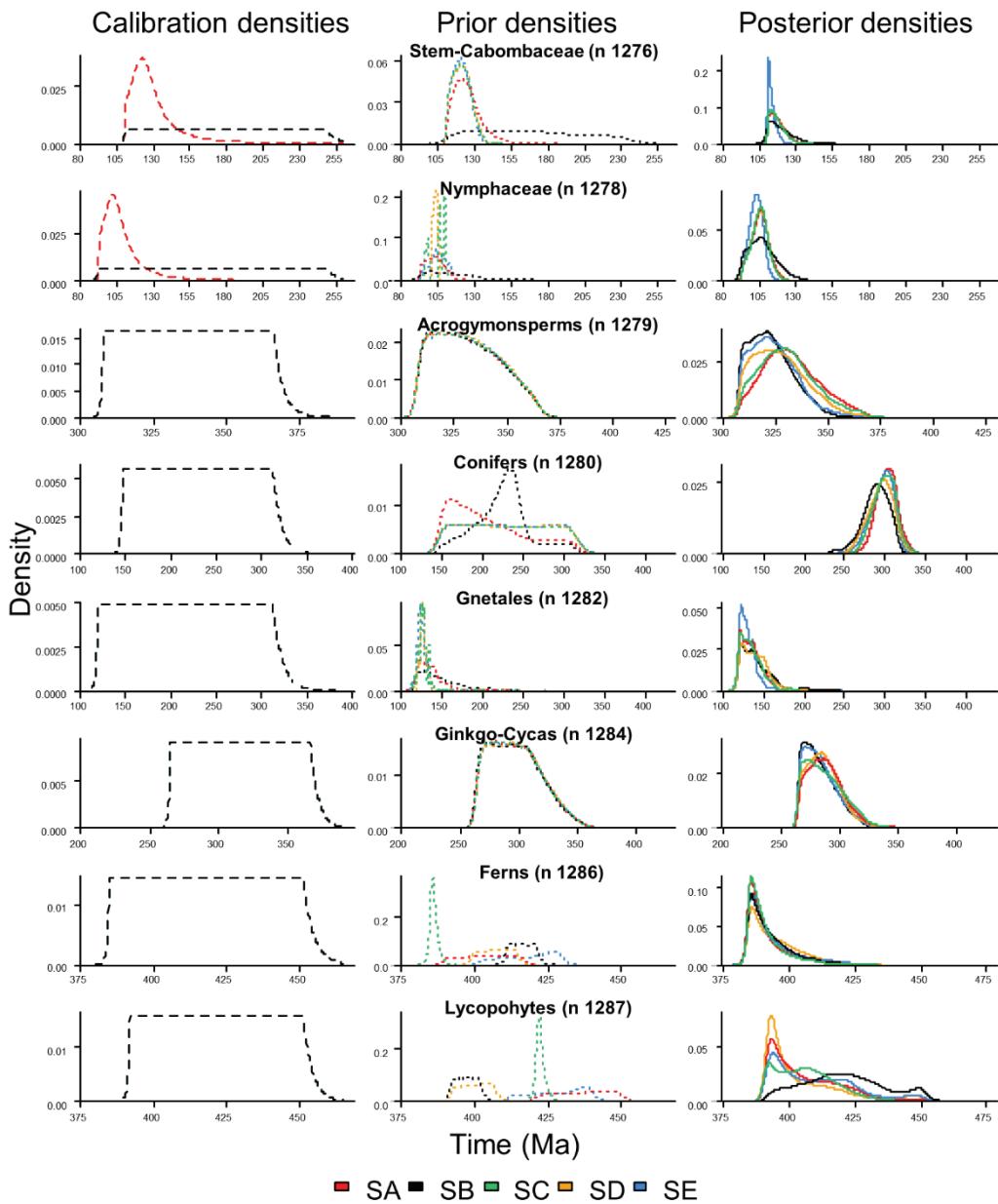


Figure S6.4. Calibration, prior and posterior densities for 52 calibrated nodes in the tree and for the 5 calibration strategies. Continued.

Table S1. List of genes included in the dataset. Tree lengths for each gene were obtained using RAxML under GTR+GAMMA model.

gene	No. taxa	# sites	tree length	gene	No. taxa	# sites	tree length
Plastid Genes				Plastid Genes			
<i>accD</i>	83	1200	7.03	<i>psbJ</i>	109	120	6.26
<i>atpA</i>	110	1518	6.98	<i>psbK</i>	110	126	5.31
<i>atpB</i>	559	1548	21.24	<i>psbL</i>	108	111	2.9
<i>atpE</i>	108	387	7.25	<i>psbM</i>	107	102	4.47
<i>atpF</i>	105	543	7.49	<i>psbZ</i>	106	183	5.06
<i>atpH</i>	110	240	5.62	<i>rbcL</i>	627	1497	43.26
<i>atpI</i>	109	741	7.34	<i>rpl14</i>	109	363	7.04
<i>ccsA</i>	109	672	10.56	<i>rpl16</i>	110	393	8.86
<i>cemA</i>	108	654	7.42	<i>rpl2</i>	100	813	4.49
<i>clpP</i>	102	582	12.32	<i>rpl20</i>	108	336	9.49
<i>infA</i>	77	222	6.42	<i>rpl22</i>	94	318	10.21
<i>matk</i>	588	2421	50.09	<i>rpl23</i>	99	270	3.72
<i>ndhA</i>	102	1086	8.97	<i>rpl32</i>	102	129	10.96
<i>ndhB</i>	98	1530	3.25	<i>rpl33</i>	108	195	7.24
<i>ndhC</i>	100	360	5.76	<i>rpl36</i>	110	108	6.58
<i>ndhD</i>	102	1488	9.71	<i>rpoA</i>	108	978	9.61
<i>ndhE</i>	103	300	8.19	<i>rpoB</i>	108	3207	8.23
<i>ndhF</i>	509	2928	43.81	<i>rpoC1</i>	102	2157	8.08
<i>ndhG</i>	101	525	9.22	<i>rpoC2</i>	398	8604	28.96
<i>ndhH</i>	101	1173	6.9	<i>rps11</i>	109	414	11.43
<i>ndhI</i>	101	465	6.16	<i>rps12</i>	104	369	5.28
<i>ndhJ</i>	100	468	5.55	<i>rps14</i>	109	294	7.51
<i>ndhK</i>	96	855	7.32	<i>rps15</i>	104	255	11.61
<i>petA</i>	108	891	8.72	<i>rps16</i>	95	234	7.35
<i>petB</i>	110	642	6.30	<i>rps18</i>	107	294	10.83
<i>petD</i>	108	471	6.41	<i>rps19</i>	109	273	8.57
<i>petG</i>	110	108	3.99	<i>rps2</i>	107	705	7.54
<i>petL</i>	102	183	3.44	<i>rps4</i>	370	984	16.63
<i>petN</i>	105	87	2.87	<i>rps7</i>	108	465	3.3
<i>psaA</i>	109	2235	6.24	<i>rps8</i>	110	390	8.74
<i>psaB</i>	109	2199	5.62	<i>ycf2</i>	97	3813	5.91
<i>psaC</i>	109	225	5.68	<i>ycf3</i>	108	504	5.74
<i>psaI</i>	107	108	7.15	<i>ycf4</i>	106	549	7.57
<i>psaJ</i>	108	123	6.58	Mitochondrial genes			
<i>psbA</i>	109	1056	4.18	<i>atp1</i>	378	1713	11.03
<i>psbB/N/T/H</i>	343	2073	16.16	<i>matr</i>	480	4236	10.85
<i>psbC</i>	109	1356	6.31	<i>nad5</i>	373	2073	5.60
<i>psbD</i>	109	1056	4.65	<i>rps3</i>	398	3171	21.05
<i>psbE</i>	110	243	5.12	Nuclear RNA genes			
<i>psbF</i>	109	117	2.97	<i>rDNA 18S</i>	501	1769	29.03
<i>psbI</i>	109	105	5.99	<i>rDNA 26S</i>	368	3396	37.04

Table S2. Basic information of data partitions.

Partition	No. taxa	# sites	ML tree lenght	alpha
Nucleotide partitions				
Plastid 1 st & 2 nd	643	41021	22.541	0.519
Plastid 3 rd	643	20360	47.605	1.180
Mitochondrial 1 st & 2 nd	515	5690	13.666	0.473
Mitochondrial 3 rd	515	2878	22.82	0.776
Nuclear rDNA	540	5081	39.546	0.372
All partitions concatenated as a single partition	644	75030	29.41	0.486
Amino acid partitions				
Plastid proteins	643	21579	46.563	0.521
Mitochondrial proteins	515	3731	23.003	0.610
Tree length (sum of branch lengths) and gamma shape parameter (α) were estimated using RAxML under the GTR+GAMMA model for nucleotide partitions, the CPREV+GAMMA for plastid proteins and WAG+GAMMA for mitochondrial proteins.				

Table S3. Summary of Fossil calibrations used in this study in million years before the present.

Node	Clade	Stem/Crown	Minimum divergence time (Ma)	Maximum divergence time (Ma)
645	Tracheophytes	Crown	422 (\dagger <i>Zosterophyllum</i> sp)	451 (oldest occurrence of trilete spores)
646	Euphyllophytes	Crown	385.57 (\dagger <i>Rellimia thomsonii</i>)	451 (oldest occurrence of trilete spores)
647	Spermatophytes	Crown	308.14 (\dagger <i>Cordaites iowensis</i>)	365.63 (base of Vco zone which contains the first seeds)
648	Angiosperms	Crown	125.9 (tricolpate pollen)	247.3 (sediments below the oldest occurrence of angiosperm like pollen which are devoid of such pollen)
651	Mesangiosperms	Crown	125.9 (tricolpate pollen)	247.3 (sediments below the oldest occurrence of angiosperm like pollen which are devoid of such pollen)
655	Eudicots	Crown	119.6 (\dagger <i>Hyrcantha decussata</i>)	—
701	<i>Malpighia</i>	Stem	44.83 (\dagger <i>Perisyncolporites pokornyi</i>)	—
753	<i>Salix</i> plus <i>Populus</i>	Stem	48.57 (\dagger <i>Pseudosalix handleyi</i>)	—
776	Clusiaceae	Stem	85.8 (\dagger <i>Paleoclusia chevalieri</i>)	—
825	Fagales	Crown	85.8 (\dagger <i>Nothofagioides senectus</i>)	—
830	Fagaceae	Crown	47.6 (\dagger <i>Fagus langevinii</i>)	—
848	Polygalaceae	Stem	61.6 (\dagger <i>Paleosecuridaca curisiae</i>)	—
875	Sapindales	Crown	59.24 (\dagger <i>Dipteronia brownii</i>)	—
878	<i>Ailanthus</i> plus <i>Citrus</i>	Stem	51.83 (\dagger <i>Ailanthus confucii</i>)	—
887	Myrtales	Crown	83.3 (\dagger <i>Esqueiria futabensis</i>)	—
897	Vitales	Crown	65.5 (\dagger <i>Indovitis chitaleyae</i>)	—
901	Saxifragales core	Crown	85.8 (\dagger <i>Divisestylus brevistamineus</i> and \dagger <i>D. longistamineus</i>)	—
914	Hamamelidaceae	Stem	82 (\dagger <i>Androdecidua endressii</i>)	—
952	<i>Dipelta</i>	Stem	33.7 (\dagger <i>Diplodipelta reniptera</i>)	—
983	Araliaceae core	Crown	37.3 (\dagger <i>Dendropanax eocenensis</i>)	—
1009	Asteraceae minus	Stem	41.5 (\dagger <i>Tubulifloridites antipodica</i>)	—
1047	Aquifoliaceae	Stem	61.6 (\dagger <i>Ilex hercynica</i>)	—
1075	Solanales	Crown	37.3 (\dagger <i>Solanites crassus</i>)	—
1098	Ericales core	Crown	85.8 (\dagger <i>Paleoenkianthus sayrevillensis</i>)	—
1115	Cornales	Crown	85.8 (\dagger <i>Tylerianthus crossmanensis</i>)	—
1171	Buxales	Crown	100.1 (\dagger <i>Spanomera marylandensis</i>)	—
1175	Proteales	Crown	107.59 (\dagger <i>Sapindopsis variabilis</i> , \dagger <i>Aquia brookensis</i> and \dagger <i>Palatonocarpus brookensis</i>)	—
1182	Menispermaceae	Stem	83.41 (\dagger <i>Prototinomiscium testudinarum</i> and \dagger <i>P. vangerowii</i>)	—
1193	Monocots	Crown	112.6 (\dagger <i>Liliacidites</i>)	—
1209	Musaceae	Stem	74.6 (\dagger <i>Spirematospermum chandlerae</i>)	—
1211	Arecales	Crown	83.41 (\dagger <i>Sabalites carolinensis</i>)	—
1221	Orchidaceae	Crown	17.82 (\dagger <i>Meliorchis caribea</i>)	—
1222	Liliales	Crown	18.7 (\dagger <i>Luzuriaga contortus</i>)	—
1224	Dioscoreales—Pandanales	Crown	85.8 (\dagger <i>Mabelia connatifila</i>)	—
1226	Alismatales	Crown	96.24 (\dagger <i>Mayoa portugallica</i>)	—
1228	<i>Alisma</i> — <i>Potamogeton</i>	Crown	66 (\dagger <i>Cardstonia tolmanii</i>)	—
1232	Araceae	Crown	76 (\dagger <i>Lysichiton austriacus</i>)	—
1237	Laurales	Crown	107.59 (\dagger <i>Virginianthus calycanthoides</i> and \dagger <i>Cohongarootonia hispida</i>)	—
1248	Magnoliales	Crown	110.87 (\dagger <i>Schenkeriphyllum glanduliferum</i> and \dagger <i>Endressinia brasiliiana</i>)	—
1256	Canellales	Stem	125.9 (\dagger <i>Walkeripollis gabonensis</i>)	—
1260	<i>Saururus</i>	Stem	44.3 (\dagger <i>Saururus tuckerae</i>)	—
1268	Chloranthaeles	Crown	92.8 (\dagger <i>Pennipolis</i> sp.)	—
1272	Schisandraceae	Stem	107.59 (\dagger <i>Anacostia virginianensis</i>)	—
1273	<i>Illicium</i>	Stem	85.44 (\dagger <i>Illiciospermum pusillum</i>)	—
1276	Cabombaceae	Stem	110.97 (\dagger <i>Pluricarpellaria peltata</i>)	—
1278	Nymphaeaceae	Crown	92.8 (\dagger <i>Monetanithus mirus</i>)	—
1279	Acrogymnospermae	Crown	308.14 (\dagger <i>Cordaites iowensis</i>)	365.63 (base of Vco zone which contains the first seeds)
1280	Conifers	Crown	147 (\dagger <i>Rissikia media</i>)	312.38 (sediments bearing \dagger <i>Cordaites iowensis</i>)
1282	Gnetales	Crown	119.6 (\dagger <i>Eoantha zherikhinii</i>)	312.38 (sediments bearing \dagger <i>Cordaites iowensis</i>)
2284	<i>Ginkgo</i> — <i>Cycas</i>	Crown	264.7 (\dagger <i>Crossozamia</i>)	365.63 (base of Vco zone which contains the first seeds)
1286	Ferns	Crown	384.71 (\dagger <i>Ibyka amphikoma</i>)	451 (oldest occurrence of trilete spores)
1287	Lycopophytes	Crown	392.1 (\dagger <i>Leclercquia complexa</i>)	451 (oldest occurrence of trilete spores)

Nodes are numbered as in Figure S2. Fossil taxa are indicated by a dagger (\dagger) before their names.

Table S4. The 95% HPD limits of posterior divergence times for selected nodes in the vascular plant tree under the 5 calibration strategies in millions of years before the present.

Node	Clade	SA-IR-3P		SB-IR-3P		SC-IR-3P		SD-IR-3P		SE-IR-3P		Composite	
		Min.	Max.	Min.	Max.								
645*	Tracheophytes	444	458	444	460	443	458	443	458	442	458	442	458
646*	Euphylophytes	433	455	424	455	430	454	430	455	427	453	427	455
647*	Spermatophytes	360	418	356	387	359	422	356	413	340	418	340	422
648*	Angiosperms	206	253	219	266	201	255	203	256	149	162	149	256
651*	Mesangiosperms	173	208	183	225	168	203	171	210	138	145	138	210
655*	Eudicots	156	186	164	201	152	181	155	188	129	137	129	188
661	Superrosids	136	160	141	173	134	157	136	162	118	126	118	162
662	Rosids	135	159	140	172	133	155	135	160	117	125	117	160
668	Malpighiales	113	132	115	144	111	130	113	133	100	110	100	133
701*	Stem- <i>Malpighia</i>	44	51	35	53	44	51	45	51	44	51	44	51
753*	Stem- <i>Salix</i> plus <i>Populus</i>	48	55	38	55	48	55	48	55	48	54	48	55
776*	Stem-Clusiaceae	88	107	88	117	88	105	88	107	85	93	85	107
796	Oxidales	100	134	105	144	99	132	100	134	86	110	86	134
809	Celastrales	89	123	93	133	88	122	89	123	78	104	78	123
825*	Fagales	86	108	86	123	86	108	86	108	85	98	85	108
830*	Fagaceae	48	64	46	78	48	64	48	64	48	62	48	64
832	Cucurbitales	76	113	80	121	75	111	77	113	65	96	65	113
837	Rosales	92	122	97	132	91	120	91	122	81	104	81	122
847	Fabales	88	124	98	136	87	122	89	124	77	103	77	124
848*	Stem- <i>Polygalaceae</i>	79	116	90	128	78	114	80	117	69	96	69	117
855	Zygophyllales	50	112	52	118	49	111	49	112	43	95	43	112
862	Brassicales	81	107	84	115	78	104	81	107	69	90	69	107
869	Malvales	71	102	76	110	71	101	72	103	61	88	61	103
874	Huertales	28	96	30	103	28	94	29	97	23	81	23	97
875*	Sapindales	66	96	71	107	66	95	66	96	64	84	64	96
878*	Stem- <i>Ailanthus</i> plus <i>Citrus</i>	52	62	47	69	52	62	52	62	52	60	52	62
881	Crossosomatales	90	132	97	144	89	130	91	133	81	111	81	133
887*	Mytales	84	114	89	130	84	112	85	115	83	99	83	115
895	Geriales	14	48	8	50	12	52	7	60	9	41	9	60
897*	Vitales	63	80	58	105	63	80	62	80	62	79	62	63
898	Saxifragales	97	126	100	142	97	125	97	127	94	111	94	127
901*	Saxifragales core	87	113	89	128	88	112	88	114	86	100	86	114
914*	Stem-Hamamelidaceae	81	97	75	104	81	97	81	97	81	97	81	97
921	Superasterids	135	159	140	171	133	156	135	161	116	126	116	161
924	Asterids	121	145	127	156	120	143	121	146	107	118	107	146
933	Dispinales	75	100	77	106	74	98	74	99	67	87	67	100
952*	Stem-Dipelta	34	40	13	36	34	40	34	40	34	40	34	40
962	Paracryphiales	50	100	52	105	49	99	49	99	43	88	43	100
964	Apiales	83	109	85	115	82	108	83	109	74	93	74	109
983*	Araliaceae core	37	42	21	38	37	42	37	42	37	42	37	42
993	Bruniales	76	111	78	117	75	110	76	112	67	95	67	112
996	Escalloniales	76	112	79	118	75	110	77	112	66	96	66	112
1002	Asterales	87	109	90	116	86	108	87	109	77	93	77	109
1009*	Stem-Asteraceae minus <i>Barnadesia</i>	45	67	51	74	45	66	45	67	42	58	42	67
1041	Aquifoliales	90	122	94	130	89	120	90	123	83	103	83	123
1047*	Stem- <i>Aquifoliaceae</i>	62	81	60	99	62	80	62	81	62	76	62	81
1054	Lamiales	76	101	81	108	75	100	76	101	67	86	67	101
1075*	Solanales	75	105	81	111	75	105	77	105	66	88	66	105
1083	Gentianales	65	97	70	103	64	96	65	97	57	81	57	93
1090	Boraginales	49	93	51	97	48	91	49	93	43	79	43	93
1093	Garryales	58	111	62	118	57	109	59	111	50	94	50	111
1094	Ericales	99	122	100	130	99	121	99	122	94	105	94	122
1098*	Ericales core	85	98	83	103	85	98	85	98	85	93	85	98
1115*	Cornales	85	115	84	134	85	115	85	116	86	105	86	116
1120	Caryophyllales	109	133	112	142	107	131	109	133	94	109	94	133
1162	Berberidopsidales	18	111	16	118	18	111	18	110	17	100	17	111
1163	Santanales	100	142	107	153	99	140	101	143	87	115	87	143
1168	Dilleniales	39	91	44	96	39	88	40	93	33	74	33	93
1170	Gunnerales	62	143	69	155	63	141	63	144	55	116	55	144
1171*	Buxales	99	124	96	138	99	122	99	123	99	112	99	124
1173	Trochodendrales	3	29	4	30	3	28	3	28	2	24	2	29
1175*	Proteales	108	151	110	173	108	148	107	150	108	125	107	151
1178	Sabiales	48	126	49	140	45	125	48	127	41	110	41	127
1179	Ranunculales	101	137	103	152	101	136	101	138	96	123	96	138

1182*	Stem-Menispermaceae	83	103	81	118	83	103	83	104	82	97	82	104
1193*	Monocots	144	179	159	203	141	176	141	181	123	135	123	181
1200	Poales	76	106	74	114	72	104	78	108	64	94	64	108
1208	Zingiberales	75	89	71	93	75	88	75	89	74	84	74	89
1209*	Stem- <i>Musaceae</i>	74	84	68	87	74	84	74	84	74	81	74	84
1210	Commeliniales	62	99	62	106	55	98	58	100	52	90	52	100
1211*	Arecales	82	95	77	99	82	94	82	94	82	91	82	95
1212	Asparagales	94	123	100	136	93	121	93	124	85	105	85	124
1221*	Orchidaceae	18	21	13	76	18	21	18	22	18	21	18	22
1222*	Liliales	66	115	75	129	65	113	65	115	58	98	58	115
1224*	Dioscoreales-Pandanales	91	131	105	152	90	128	90	131	89	108	89	131
1225	Pandanales	45	99	48	113	44	97	45	99	38	86	38	99
1226*	Alismatales	105	143	125	172	105	140	104	143	98	116	98	95
1228*	<i>Alisma-Potamogeton</i>	66	94	74	128	66	92	66	95	66	82	66	95
1232*	Araceae	76	112	88	151	76	111	76	113	76	98	76	113
1235	Magnoliidae	141	190	155	212	141	185	141	190	128	140	128	190
1237*	Laurales	107	134	107	153	107	132	107	133	107	121	107	134
1248*	Magnoliales	110	129	108	142	110	128	110	129	109	120	109	129
1256*	Stem-Canellales	128	179	143	203	127	174	128	179	117	134	117	179
1257	Piperales	106	152	115	171	105	148	106	152	95	120	95	152
1260*	Stem- <i>Saururus</i>	44	63	43	84	44	63	44	63	44	59	44	63
1264	Canellales	67	135	70	154	67	131	67	134	61	112	61	135
1268*	Chloranthales	92	113	88	126	92	113	92	113	92	107	92	113
1271	Austrobaileyales	119	167	119	180	119	165	119	167	115	135	115	167
1272*	Stem-Schisandraceae	107	132	105	148	107	132	107	132	107	121	107	132
1273*	Stem- <i>Illicium</i>	85	103	80	112	85	104	85	103	85	101	85	104
1275	Nymphaeales	128	189	129	198	128	185	129	188	119	140	119	189
1276*	Stem- <i>Cabombaceae</i>	110	128	107	138	110	128	110	128	109	119	109	128
1278*	Nymphaeae	93	116	91	126	93	116	93	116	94	111	93	116
1279*	Acrogymnosperms	308	357	307	342	308	355	307	351	307	345	307	357
1280*	Conifers	274	327	254	318	271	325	264	322	265	321	265	327
1282*	Gnetales	116	160	113	184	115	161	116	166	115	151	115	166
1284*	<i>Ginkgo-Cycas</i>	264	317	263	310	264	318	263	313	263	311	263	317
1286*	Ferns	383	413	382	411	383	409	383	415	383	415	383	413
1287*	Lycophtyes	390	430	395	452	391	432	389	443	390	444	389	443

Nodes are numbered as in Figure S2. The 52 calibrated nodes are represented by (*) and nodes in bold characters represent major angiosperm orders. Posterior times are the 95% HPD CI, estimated using the HKY85+ Γ_5 substitution model, IR rate model, with the 83 genes subdivided into three partitions: (1) 1st and 2nd codon positions for plastid genes; (2) 1st and 2nd codon positions for mitochondrial genes; and (3) nuclear RNA genes. Composite: 95% high posterior density credibility interval (HPD CI) is a composite of the 95% HPD credibility intervals across all calibration strategies, except calibration strategy B (SB).

Table S5. The 95% HPD limits of posterior divergence times, in millions of years before the present, for selected nodes in the vascular plant tree under different partition strategies, AR rate model, birth-death parameters and excluding lycophytes and ferns.

node	Clade	SA-IR-1P	SA-IR-MP	SA-AR-3P	SA-IR-3P-EP	SA-IR-3P-BD1	SA-IR-3P-BD2
645*	Tracheophytes	437	457	443	458	437	456
646*	Euphylophytes	418	452	430	454	422	451
647*	Spermatophytes	341	375	355	389	344	371
648*	Angiosperms	223	263	213	261	230	265
651*	Mesangiosperms	184	222	177	211	189	216
655*	Eudicots	164	196	159	187	166	188
661	Superrosids	143	167	140	160	138	154
662	Rosids	141	165	138	158	137	153
668	Malpighiales	118	138	114	131	109	121
701*	<i>Stem-Malpighia</i>	45	53	44	52	44	50
753*	<i>Stem-Salix plus Populus</i>	49	58	48	55	49	55
776*	Stem-Clusiaceae	91	115	89	107	85	93
796	Oxidales	104	140	105	135	116	130
809	Celastrales	95	131	90	123	100	116
825*	Fagales	86	111	86	109	94	115
830*	Fagaceae	48	67	48	64	51	80
832	Cucurbitales	67	113	78	112	85	110
837	Rosales	91	125	91	120	100	118
847	Fabales	87	129	89	124	91	116
848*	<i>Stem-Polygalaceae</i>	79	123	80	117	86	112
855	Zygophyllales	48	124	50	111	66	111
862	Brassicales	76	110	82	107	78	100
869	Malvales	70	108	74	103	77	98
874	Huertales	29	103	31	98	54	101
875*	Sapindales	65	99	68	98	77	100
878*	<i>Stem-Ailanthus plus Citrus</i>	52	63	52	62	52	64
881	Crossosomatales	83	134	84	131	111	130
887*	Myrtales	84	117	86	116	84	104
895	Geriales	85	134	12	58	110	130
897*	Vitales	62	84	63	81	63	100
898	Saxifragales	101	137	96	126	108	134
901*	Saxifragales core	88	119	87	114	94	122
914*	<i>Stem-Hamamelidaceae</i>	81	101	81	94	89	118
921	Superasterids	141	166	138	159	138	155
924	Asterids	127	151	123	144	126	141
933	Dispinales	84	111	76	100	95	111
952*	<i>Stem-Dipelta</i>	34	42	34	40	34	41
962	Paracryphiales	38	106	45	97	84	110
964	Apiales	89	117	85	110	101	115
983*	Araliaceae core	37	44	37	43	38	59
993	Bruniales	77	121	74	111	99	117
996	Escalloniales	74	120	79	112	103	118
1002	Asterales	97	122	89	109	92	108
1009*	<i>Stem-Asteraceae minus Barnadesia</i>	47	77	46	68	53	72
1041	Aquifoliales	91	129	90	121	109	126
1047*	<i>Stem-Aquifoliaceae</i>	61	83	62	81	66	105
1054	Lamiales	82	109	76	100	86	102
1075*	Solanales	78	112	77	104	93	109
1083	Gentianales	69	103	65	96	79	99
1090	Boraginales	37	95	48	90	77	98
1093	Garryales	45	110	55	107	91	118
1094	Ericales	103	130	100	123	101	118
1098*	Ericales core	85	104	85	99	86	101
1115*	Cornales	86	125	85	114	107	133
1120	Caryophyllales	116	143	112	134	106	122
1162	Berberidopsidales	18	105	18	94	64	138
1163	Santanales	93	145	103	145	117	142
1168	Dilleniales	36	109	36	85	37	88
1170	Gunnerales	66	162	72	150	104	147
1171*	Buxales	99	131	99	124	102	144
1173	Trochodendrales	5	55	4	30	18	73
1175*	Proteales	108	156	108	148	150	176
1178	Sabiales	37	133	47	125	91	154
1179	Ranunculales	105	157	102	141	107	156
1182*	<i>Stem-Menispermaceae</i>	83	108	83	106	83	118
1193*	Monocots	141	184	146	179	154	182
1200	Poales	76	108	74	105	84	101
1208	Zingiberales	75	90	75	87	75	86

1209*	Stem-Musaceae	74	86	74	84	74	83	74	85	74	85	74	84
1210	Commelinales	47	96	52	96	80	99	57	103	62	99	61	99
1211*	Arecales	82	96	82	95	82	90	82	96	82	95	82	95
1212	Asparagales	90	124	92	122	105	120	99	130	95	124	94	123
1221*	Orchidaceae	18	23	18	21	18	21	18	22	18	22	18	21
1222*	Liliales	51	120	66	114	88	115	69	122	67	117	66	114
1224*	Dioscoreales-Pandanales	87	132	89	126	109	130	92	139	90	132	92	131
1225	Pandanales	33	101	45	98	72	109	47	104	44	99	45	99
1226*	Alismatales	101	140	105	141	121	147	109	154	106	145	106	144
1228*	<i>Alisma-Potamogeton</i>	66	91	66	95	66	83	67	105	67	96	67	96
1232*	Araceae	76	108	76	114	91	130	76	122	76	114	76	115
1235	Magnoliidae	135	188	140	183	179	207	147	201	144	192	144	195
1237*	Laurales	108	136	108	133	123	162	108	138	108	135	108	134
1248*	Magnoliales	110	134	110	128	117	157	110	133	110	130	110	129
1256*	Stem-Canellales	118	169	127	170	169	201	134	190	130	180	130	186
1257	Piperales	96	142	108	148	113	169	111	160	108	154	108	156
1260*	Stem-Saururus	44	61	44	62	44	72	44	65	44	63	44	64
1264	Canellales	70	137	68	131	124	179	70	140	68	136	68	136
1268*	Chloranthales	92	121	92	114	93	144	92	114	92	114	92	113
1271	Austrobaileyales	115	175	119	168	132	192	120	174	119	170	119	169
1272*	Stem-Schisandraceae	107	135	107	133	109	153	107	135	107	134	107	133
1273*	Stem- <i>Illicium</i>	85	107	85	103	85	114	85	103	85	104	85	103
1275	Nymphaeales	124	197	125	185	145	208	132	202	130	193	129	196
1276*	Stem-Cabombaceae	110	135	110	128	110	137	110	130	110	129	110	129
1278*	Nymphaeaceae	93	116	93	116	94	124	93	118	93	116	93	116
1279*	Acrogymnosperms	307	346	307	345	306	326	310	362	307	343	308	355
1280*	Conifers	217	314	265	323	262	309	278	328	268	320	267	328
1282*	Gnetales	116	169	117	164	116	170	116	161	117	156	115	153
1284*	<i>Ginkgo-Cycas</i>	263	313	263	305	273	315	264	319	263	312	263	311
1286*	Ferns	383	411	383	410	383	405	N/A	N/A	383	398	384	413
1287*	Lycopophytes	391	423	390	445	392	441	N/A	N/A	392	447	390	428

Nodes are numbered as in Figure S2. The 52 calibrated nodes are represented by (*) and nodes in bold characters represent major angiosperm orders. Posterior times are the 95% HPD CI, estimated using the HKY85+ Γ_5 substitution model, and calibration strategy A (SA). 1P, the tree partitions analysed as a single partition; MP, mixed partitions of plastid proteins, mitochondrial proteins and nuclear RNA genes; IR, independent rates model; AR autocorrelated rates model and birth-death parameters adjusted to generate a tree with long internal branches and short tip branches (BD1) and large node ages with nodes close to the root (BD2). N/A: not applicable.

NOTES S1 – Justification of fossil calibrations

Node 645 | CG Tracheophyta | MRCA: Lycophyta-Euphylophyta | 422 Ma – 451 Ma.

Fossil taxon and specimen. Clarke et al. [1] based their calibration of this node on *Zosterophyllum* sp. [US384-8137; University of Saskatchewan Collec but more accurate timescale but more accurate timescale tions, Canada] from Bathurst Island [2].

Phylogenetic justification. Following Clarke et al. (2011), the *Zosterophyllum* sp. from Bathurst Island (Kotyk et al. 2002) is unequivocally zosterophyll given its possession of reniform sporangia, sporangia that dehisce along their distal margins, and laterally inserted sporangia. All *Zosterophyllum* species are total group Lycopsida [3].

Minimum age. 422 Ma.

Maximum age. 451 Ma.

Age justification. *Zosterophyllum* sp. on Bathurst Island [2] co-occurs with conodont *Ozarkodina douroensis*, which is restricted to the Ludlow (as O. n. sp. B in [4-7]. Thus, a minimum age interpretation can be derived from the top of the Ludlow, dated to 423.0 Ma ± 1.0 Myr, thus 422.0 Ma. The soft maximum constraint, following Clarke et al. [1], is based on the oldest occurrences of trilete spores, known from the Qusaiba-1 core from the Quasim Formation of northern Saudi Arabia [8]. Thus, we establish our soft maximum for Tracheophyta at 451 Ma. The very oldest records precede the earliest occurrences of the *Acanthochitina barbata*, opening the possibility that they occur in the preceding *Tanuchitina fistulosa* biozone, though *T. fistulosa* does not occur. The oldest stratigraphic records within the core co-occur with the chitinozoan *Armoricochitina nigerica*, known to extend into the Caradoc, to within the biozone characterized by *Fungochitina spinifera* (= *Fungochitina fungiformis*) [9]. The base of the *F. spinifera* zone falls within the *Dicranograptus clingani* Biozone (*Dicellograptus morrisi* subzone) [10], the base of which is estimated at 451 Ma [11].

Node 646 | CG Euphylophytes | MRCA: Ferns-Spermatophyta | 385.571 Ma – 451 Ma.

Fossil taxon and specimen. *Rellimia thomsonii* from the Panther Mountain Formation of New York [12] [335.34; Paleobotanical Collection of the State University of New York at Bingham].

Phylogenetic justification. Magallón et al. [13] identified *Ibyka amphikoma* [14] as the oldest record of the pteridophyte lineage based on phylogenetic analyses undertaken by Kenrick and Crane [3].

Minimum age. 384.71 Ma.

Maximum age. 451 Ma.

Age justification. Clarke et al. [1] proposed *Rellimia thomsonii*, an aneurophytalean progymnosperm from the Panther Mountain Formation of New York [12], as the oldest record of crown Euphylophyta. The Panther Mountain Formation is equivalent to the Ludlowville and Skaneateles formations [1], which occur below the Moscow Formation of New York [15], making *Rellimia thomsonii* older than *Ibyka amphikoma* [1]. The Ludlowville-Moscow formation boundary falls deep within the Lower varcus zone [16] and, therefore, below the *rhenanus-ansatus* biozonal boundary [17], at the very least, which has been dated to 386.25 Ma ± 0.679 Myr, yielding a minimum constraint of 385.571 Ma. The soft maximum constraint, following Clarke et al. [1], is based on the oldest occurrences of trilete spores, known from the Qusaiba-1 core from the Quasim Formation of northern Saudi Arabia [8]. The very oldest records precede the earliest occurrences of the *Acanthochitina barbata*, opening the possibility that they occur in the preceding *Tanuchitina fistulosa* biozone, though *T. fistulosa* does not occur. The oldest stratigraphic records within the core co-occur with the chitinozoan *Armoricochitina nigerica*, known to extend into the Caradoc, to within the biozone characterized by *Fungochitina spinifera* (= *Fungochitina fungiformis*) [9]. The base of the *F. spinifera* zone falls within the *Dicranograptus clingani* Biozone (*Dicellograptus morrisi* Subzone) [10] et al., 2008 [11], the base of which is estimated at 451 Ma (Cooper and Saddler 2012). Thus, we establish our soft maximum for Tracheophyta at 451 Ma.

Discussion. Magallón et al. [13] established a minimum age constraint using *Ibyka amphikoma*, based on the Givetian-Frasnian boundary, for which they provided a date of 385 Ma, though this has since been revised to 382.7 Ma ± 1 Myr [17]. *Ibyka amphikoma* was recovered from the Manorkill Shale Member, which is a lateral equivalent of the Windom Member, within the Moscow Formation of New York [18, 19], which falls fully within the *ansatus* conodont Biozone [20, 21] the top of which is dated to 385.41 Ma ± 0.7 Myr [17], thus, yielding a minimum age constraint of 384.71 Ma, younger than the minimum age of *Rellimia thomsonii*.

Node 647 | CG Spermatophytes | MRCA: Ginkgo-Austrobuxus | 308.14 Ma – 365.629 Ma.

Fossil taxon and specimen. *Cordaites iowensis* [UIC 12,233: University of Illinois at Chicago; OUPH 9616-9742: Ohio University Paleobotanical Herbarium, Department of Botany, Ohio University, Athens, Ohio] from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa [22].

Phylogenetic justification. Clarke *et al.* [1] identify cordaitian coniferophytes as the oldest records of the crown group of the spermatophyte clade. The oldest whole plant reconstruction is *Cordaites iowensis* from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa [22].

Minimum age. 308.14 Ma.

Maximum age. 365.629 Ma.

Age justification. Janousek and Pope [23] argue that the Laddsdale Coal is equivalent to the Bluejacket Coal of Oklahoma, which occurs as part of the Bluejacket Sandstone Member, underlying the Inola Limestone, part of the Inola Cyclothem of the Krebs subgroup of the Cherokee Group, characterized by the occurrence of the conodonts *Idiognathodus amplificus*, *Idiognathodus podolskensis* and *Neognathodus asymmetricus* [24]. The Inola cyclothem falls fully within the *Idiognathodus amplificus*/ *Idiognathodus obliquus* biozone [25]. This is indicative of the *Neognathodus medexultimus*-*Streptognathodus concinnus* (Pc10) biozone, certainly older than the *Neognathodus roundyi* – *Streptognathodus cancellatus* (Pc11) biozone [25, 26]. The base of Pc10 is bracketed by an older age constraint of $312.01\text{ Ma} \pm 0.37\text{ Myr}$ and the base of Pc11 is bracketed by a younger age constraint of $308.5\text{ Ma} \pm 0.36\text{ Myr}$ in the Composite Standard of Davydov *et al.* [26], yielding a minimum constraint of 308.14 Ma.

The soft maximum constraint follows Clarke *et al.* [1] who based theirs on the first records of seeds in the form of preovules that satisfy the criteria of the seed habit, which occur in the Upper Fammenian (Late Devonian) VCo Spore Biozone [27], a well documented example of which being *Elkinsia polymorpha* [28]; *E. polymorpha* has been recovered from the Hampshire Formation, West Virginia, from which the palynomorphs *Grandispora cornuta*, *Retispora macroreticulata*, *Retusotriletes phillipsii* and *Rugospora radiata* have been reported [29], which substantiate assignment to the VCo Biozone [30]. The VCo biozone is not directly dated but its base falls within the *Palmatolepis trachytera* conodont biozone [31], the base of which is dated to $364.19\text{ Ma} \pm 1.439\text{ Myr}$ [17], yielding a soft maximum constraint on the divergence of crown Spermatophyta at 365.629 Ma.

Node 648 | CG Angiosperms | MRCA: *Amborella-Austrobuxus* | 125.9 Ma – 247.3 Ma.

Fossil taxon and specimen. Tricolporate pollen grain [BRN 126] from the Cowleaze Chine Member of the Vectis Formation of the Isle of Wight [32].

Phylogenetic justification. Following Clarke *et al.* [1], our minimum age constraint is based on the earliest occurrences Fischer's rule tricolporate pollen, and knowledge of the distribution of tricolporate pollen across the phylogeny of angiosperms [33].

Minimum age. 125.9 Ma.

Maximum age. 247.3 Ma.

Age justification. Following Clarke *et al.* [1], the Cowleaze Chine Member of the Vectis Formation of the Isle of Wight (Hughes & McDougall, 1990) occurs within the M1n polarity chron at the top of the Barremian, dated as $126.3\text{ Ma} \pm 0.4\text{ Myr}$ [34]. The soft maximum age constraint is based on sediments devoid of angiosperm-like pollen below their first report in the Middle Triassic, thus, the base of the Anisian, dated to $247.1\text{ Ma} \pm 0.2\text{ Myr}$ [35], thus, 247.3 Ma.

Discussion. The recently described *Euanthus panii* [36], *Juraherba boda* [37] and *Yuhania dahugouensis* [38] from the Jiulongshan Formation were considered but not assigned. At the current stage, the age of the formation appears to be still not fully settled despite most experts agree on a middle Jurassic age (see [37, 38]), whereas the assignment to extant lineages also required further investigation using phylogenetic approaches to confirm the proposed relationships of *Juraherba* to Hydatellaceae - which are the sister to the remaining Nymphaeales lineage (node 1276) and *Yuhania* to monocots.

Node 651 | CG Mesangiosperms | MRCA: *Chloranthus-Austrobuxus* | 125.9 Ma – 247.3 Ma.

Fossil taxon and specimen. Tricolporate pollen grain [BRN 126] from the Cowleaze Chine Member of the Vectis Formation of the Isle of Wight. [32].

Phylogenetic justification. Following Clarke *et al.* [1], our minimum age constraint is based on the earliest occurrences Fischer's rule tricolporate pollen, and knowledge of the distribution of tricolporate pollen across the phylogeny of angiosperms [33].

Minimum age. 125.9 Ma.

Maximum age. 247.3 Ma.

Age justification. Following Clarke *et al.* [1], the Cowleaze Chine Member of the Vectis Formation of the Isle of Wight [32] occurs within the M1n polarity chron at the top of the Barremian, dated as $126.3\text{ Ma} \pm 0.4\text{ Myr}$ [34]. The soft maximum age constraint is based on sediments devoid of angiosperm-like pollen below their first report in the Middle Triassic, thus, the base of the Anisian, dated to $247.1\text{ Ma} \pm 0.2\text{ Myr}$ [35], thus, 247.3 Ma.

Node 655 | CG Eudicots | MRCA: *Dicentra-Austrobuxus* | 119.6 Ma.

Fossil taxon and specimen. *Hyrcantha decussata* [NJU-DES02001: Geological Institute, Chinese Academy of Sciences, Beijing], from the lower part of the Yixian Formation, Jehol Group, Liaoning Province, China [39].

Phylogenetic justification. Similar to *Leefructus* from the Yixian formation of the Lower Cretaceous of China, *Hyrcantha* is considered to be a stem group representative of the Ranunculales [40].

Minimum age. 119.6 Ma.

Age justification. The main fossil bearing beds have been dated and may be as old as 129.2 Ma [41], however, in the absence of knowledge of the position of the fossils within the stratigraphy, relative to the sources of the absolute dates, a minimum age constraint can be derived from the Jiufontang Formation which overlies it.

⁴⁰Ar/³⁹Ar dating of a number of samples from the Jiufontang Formation has yielded an age of 120.3 ± 0.7 Ma for the volcanic tuffs [42], establishing a minimum constraint of 119.6 Ma.

Node 701 | SG Malpighia | MRCA: *Dicella-Malpighia* | 44.83 Ma.

Fossil taxon and specimen. *Perisyncolporites pokornyi* [UFP65: Paleobotanical Collection of the Florida Museum of Natural History, University of Florida: Gainesville, Florida, USA] from central Colombia [43].

Phylogenetic justification. Assigned to Malpighiales [43, 44]. Based on morphological similarities, the fossils are considered as reliable assigned to the stem of the stigmaphyllloid clade [45].

Minimum age. 44.83 Ma.

Age justification. The minimum age of *Perisyncolporites pokornyi* is best constrained in sections in central Colombia which Jaramillo and Dilcher [43] integrated into a graphic correlation composite standard and, on this basis, were able to establish its first occurrence as within the Lower Eocene. This composite standard has been refined and calibrated to absolute time by Jaramillo et al. [46] who provide a date of 44.83 Ma for the first appearance of *Perisyncolporites pokornyi*.

Node 753 | SG *Salix* plus *Populus* | MRCA: *Idesia-Salix* | 48.57 Ma.

Fossil taxon and specimen. *Pseudosalix handleyi* [UMNH PB-1: Utah Museum of Natural History, Salt Lake City, USA] from lacustrine shales of the Parachute Creek Member of the Green River Formation in the vicinity of Bonanza, Utah, USA [47].

Phylogenetic justification. Our node assignment follows the currently accepted interpretation of the fossil record of Salicaceae [48].

Minimum age. 48.57 Ma.

Age justification. The Parachute Creek Member reaches into C22n magnetozone [49], the minimum age of which can be established from the base of the succeeding C21r, dated to 48.57 Ma in the combined age model of Vandenberghe et al. [50].

Node 776 | SG Clusiaceae | MRCA: *Clusia-Hypericum* | 85.8 Ma.

Fossil taxon and specimen. *Paleoclusia chevalieri* [CUPC 1192: L. H. Bailey Hortorium Paleobotanical Collection, Cornell University, Ithaca, NY, USA] from the Old Crossman locality, New Jersey, USA [51].

Phylogenetic justification. The phylogenetic interpretation follows Ruhfels [52].

Minimum age. 85.8 Ma.

Age justification. Clarke et al. [1] argued that a minimum constraint on the age of this deposit could be established from Santonian-Campanian Boundary, however, Massoni et al. [53] argue that a tighter correlation can be established with better rocks attributable to the CC13-14 Nannofossil zones in South Carolina, indicating a minimum age of $86.3 \text{ Ma} \pm 0.5 \text{ Myr}$, thus, 85.8 Ma.

Node 825 | CG Fagales | MRCA: *Nothofagus-Fagus* | 85.8 Ma.

Fossil taxon and specimen. *Nothofagidites senectus* [GSV 61898: Mines Department of Victoria, Melbourne, Australia] from the Bass and Gippsland Basins, Australia [54].

Phylogenetic justification. These microfossils are widely considered to be Nothofagaceae which in turn are the sister to the remaining Fagales clade [55].

Minimum age. 85.8 Ma.

Age justification. The first appearance of *Nothofagidites senectus* defines the base of the *Nothofagidites senectus* Palynozone, which coincides with the Coniacian-Santonian Boundary, which is dated to $86.3 \text{ Ma} \pm 0.5 \text{ Myr}$ [34], affording a minimum age constraint of 85.8 Ma.

Node 830 | CG Fagaceae | *Fagus-Quercus* | 47.6 Ma.

Fossil taxon and specimen. *Fagus langevini* [UWBM 97583: Burke Museum, Seattle, Washington, USA] preserved as impressions and carbonaceous films in a siliceous shale in an unnamed formation within the Kamloops Group at the McAbee Locality near the town of Cache Creek, British Columbia [57].

Phylogenetic justification. This fossil is accepted as a stem group representative of the genus *Fagus* [58].

Minimum age. 47.6 Ma.

Age justification. Ashes within the 30 metre sequence of fossiliferous shales have yielded dates based on K-Ar geochronology, ranging between $52\text{ Ma} \pm 2\text{ Myr}$ and $49\text{ Ma} \pm 2\text{ Myr}$ [59]. Correlation based on facies and pollen biostratigraphy establish an Ypresian age for the fossil assemblage, compatible with the aged from the intercalated ashes. Therefore, a minimum age constraint can be established on the Ypresian-Lutetian Boundary which has been dated to $47.8\text{ Ma} \pm 0.2\text{ Myr}$ based on the combined age model of Vandenberghe et al. [50], thus, 47.6 Ma.

Node 848 | SG Polygalaceae | MRCA: *Polygala-Medicago* | 61.6 Ma.

Fossil taxon and specimen. *Paleosecuridaca curisii* [PP34562: Field Museum, Chicago, IL, USA], described by from the Sentinel Butte Formation at the Almont site in Morton County, central North Dakota [62].

Phylogenetic justification. The phylogenetic relationships were clarified by Pigg [61].

Minimum age. 61.6 Ma.

Age justification. The age of the Sentinel Butte Formation has been assigned to the Tiffanian 3 based on mollusk and mammal-based biostratigraphy, but the most concrete age evidence is based on palynostratigraphy, assigned the Almont Site sediments of the Sentinel Butte Formation to Pollen Zone 5 of the late Palaeocene [63]. In the absence of further constraint we establish a minimum age for *Paleosecuridaca curisii* based on the Palaeocene-Eocene boundary, dated to 61.6 Ma in the combined age model of Vandenberghe et al. [50].

Node 875 | CG Sapindales | MRCA: *Citrus-Nitraria* | 59.24 Ma.

Fossil taxon and specimen. *Dipteronia brownii* [UF 15740E-23086: Florida Museum of Natural History, Gainesville FL, USA] from the Paleocene Fort Union Formation at Hell's Half Acre, Wyoming [64].

Phylogenetic justification. This fossil is assigned to the extant genus *Dipteronia* which belongs to the subfamily Hippocantanoideae of the family Sapindaceae. The extant genus is considered a Tertiary relict having two extent species endemic to China [65, 66]. Being a possible stem group representative of the extant genus nested in the Sapindales provided the framework for this assignment.

Minimum age. 59.24 Ma.

Age justification. *Dipteronia brownii* occurs within the P4 Pollen Zone in the type section of Nichols and Ott [67], which falls fully within Magnetic Anomaly Zone C26r [68], the end of which is dated to 59.24 Ma in the combined age model of Vandenberghe et al. [50].

Node 878 | SG Ailanthus plus Citrus | MRCA: *Ailanthus-Swietenia* | 51.83 Ma.

Fossil taxon and specimen. *Ailanthus confucii* (senior synonym of *Ailanthus lesquereuxi*) [DMNH 7879: Denver Museum of Natural History, Denver CO, USA] from the Fossil Butte fish quarries of the Green River Formation near Kemmerer, Wyoming [69].

Phylogenetic justification. This fossil is accepted to belong to the extant genus *Ailanthus* and can be therefore assigned to this clade [69].

Minimum age. 51.83 Ma.

Age justification. The Fossil Butte Member of the Green River Formation is bounded minimally by the C23r magnetozone [49], the minimum age of which can be established from the base of the succeeding C23n, dated to 51.83 Ma in the combined age model of Vandenberghe et al. [50].

Node 887 | CG Myrtales | MRCA: *Myrtus-Oenothera* | 83.3 Ma.

Fossil taxon and specimen. *Esqueiria futabensis* [PP45419: Field Museum, Chicago IL, USA] from two levels in the Futaba Group exposed in Fukushima Prefecture, northeastern Honshu, Japan [70].

Phylogenetic justification. The phylogenetic relationships have been established by several authors [71].

Minimum age. 83.3 Ma.

Age justification. One locality, considered Coniacian, occurs in the Asamigawa Member of the Ashizawa Formation, on a tributary of the Kitaba River in Kamikitaba, Hirono-machi. Unfortunately, no material evidence has been presented to substantiate this age assignment (Takahashi et al. [70], among others, merely cite the presence of unspecified Coniacian ammonites). The second locality is in the middle part of the Tamayama Formation, on the Kohisa River, Kohisa, Ouhisa machi, northeast of Iwaki City. The Asamigawa Formation is the lowermost formation in the Futaba Group, and is overlain by the Kasamatsu Formation, in turn overlain by the Tamayama Formation. The age of the Tamayama Formation is substantiated on the presence of *Inoceramus amakusensis* [70], which is restricted to the Santonian [72]. Thus, a minimum age constraint may be established on the Santonian-Campanian Boundary, dated as $83.6\text{ Ma} \pm 0.3\text{ Myr}$ [34], thus, 83.3 Ma.

Node 897 | CG Vitales | MRCA: *Vitis-Leea* | 65.508 Ma.

Fossil taxon and specimen. *Indovitis chitaleyae* [UF19279-56220: Florida Museum of Natural History (UF) Gainesville, Florida, USA] preserved as fruits and seeds in chert from Deccan Intertrappean beds exposed in a

quarry near the village of Mahurzari, India about 14 km from Nagpur, along with young fruits with intact seeds and isolated mature seeds from a series of localities including Mohgaonkalan in Chhindwara District and Ambabagholi in Baitul District, both in Madhya Pradesh, and Shiblea in Yeotmal District, Maharashtra [73].

Phylogenetic justification. The phylogenetic relationships of this fossil have been clarified previously [73].

Minimum age. 65.508 Ma

Age justification. A minimum constraint on the age of *Indovitis chitaleyae* can be established on minimum age of Deccan volcanism, which has been constrained to 65.535 Ma ± 0.027 Myr [74], thus, 65.508 Ma.

Node 901 | CG Saxifragales core | MRCA: *Haloragis-Itea* | 85.8 Ma.

Fossil taxon and specimen. *Divisestylus brevistamineus* [CUPC 1340: L. H. Bailey Hortorium Paleobotanical Collection, Cornell University, Ithaca NY, USA], flowers described from the Old Crossman locality, New Jersey, USA [75].

Phylogenetic justification. The phylogenetic relationships of this fossil have been clarified previously [75].

Minimum age. 85.8 Ma

Age justification. Clarke et al. [1] argued that a minimum constraint on the age of this deposit could be established from Santonian-Campanian Boundary, however, Massoni et al. [53] argue that a tighter correlation can be established with better rocks attributable to the CC13-14 Nannofossil zones in South Carolina, indicating a minimum age of 86.3 Ma ± 0.5 Myr, thus, 85.8 Ma.

Node 914 | SG Hamamelidaceae | MRCA: *Daphniphyllum-Rhodoleia* | 82.00 Ma.

Fossil taxon and specimen. *Androdecidua endressii* [PP45947: Field Museum, Chicago IL, USA] from the Buffalo Creek Member of the Gaillard Formation in the south pit (Allon Quarry) of the Atlanta Sand and Supply Company in Gaillard, Georgia, ca. 9.5 km southeast of Roberta in Crawford County [76].

Phylogenetic justification. The phylogenetic relationships were carefully discussed by the authors introducing the taxon [76].

Minimum age. 82.00 Ma

Age justification. Christopher correlated this deposit to nannofossil zone CC17 based on its palynoflora, though the evidence on which this is based was not presented. CC17 ranges in age from Late Santonian to Early Campanian and the CC17-18 boundary falls within the *Scaphites hippocrepis* II ammonoid biozone, dated to 82.00 Ma [34].

Node 952 | SG Dipelta | *Dipelta-Kolkwitzia* | 33.71 Ma.

Fossil taxon and specimen. *Diplodipelta reniptera* [UM 33621: University of Michigan, Ann Arbor MI, USA] from the Florissant Formation, Mormon Cr, Ruby, CO, USA [78].

Phylogenetic justification. Based on the distribution of morphological characters in the phylogeny of Caprifoliaceae, this fossil is considered to be sister to the genus *Dipelta* which provide in turn the arguments for this assignment [78, 79].

Minimum age. 33.71 Ma.

Age justification. The Florissant Formation has been correlated with the early Chron C13r, based on its reversed polarity and a $^{40}\text{Ar}/^{39}\text{Ar}$ date of 34.07 Ma ± 0.10 Myr from the upper part of the section [80, 81]. The minimum age for the Florissant flora can be established on the C13r-C13n boundary, which has been dated to 33.71 Ma, based on the combined age model in Vandenberghe et al. [50].

Node 983 | CG Araliaceae core | MRCA: *Cussonia-Tetralpasandra* | 37.3 Ma.

Fossil taxon and specimen. *Dendropanax eocenensis* [W1107: Indiana University paleobotanical collection] from the Claiborne Formation at Warman Clay Pit (2 miles west of Como), Tennessee, USA.

Phylogenetic justification. Phylogenetic relationships were discussed by Martinez-Millan [82].

Minimum age. 37.3 Ma.

Age justification. The Claiborne Formation is commonly attributed a middle Eocene age, but material evidence is rarely presented in support this. Taylor [83] provides a summary of the palynostratigraphic evidence, citing Elsik as supporting a middle Eocene age based on juglandaceous palynomorphs including *Plicatopollis*, *Platycarya*, *Platycaryapollenites*, *Carya* and *Casuarinidites*. Their presence may be indicative of a late Eocene age, though they occur in low frequency and, thus, Taylor [83] argues instead for a Middle Eocene age based on the presence of *Nuxpollenites terminalis* and *Amanoa* type palynomorphs in even the uppermost Claiborne Formation [84]. Thus, we establish a minimum age constraint on the age of *Solanites crassus* based on the Bartonian-Priabonian Boundary, dated to 37.8 Ma ± 0.5 Myr based on the combined age model of Vandenberghe et al. [50], thus, 37.3 Ma.

Node 1009 | SG Asteraceae minus Barnadesia | MRCA: *Barnadesia-Helianthus* | 41.5 Ma.

Fossil taxon and specimen. *Tubulifloridites antipodica* from onshore deposits taken from a paleochannel at Koingnaas, on the west coast of South Africa.

Phylogenetic justification. This fossil is accepted to belong to the Barnadesioides despite its actual placement in the subfamily is ambiguous but this is not a challenge to our analyses^{82,85}.

Minimum age. 41.5 Ma.

Age justification. These occurrences are, described to occur alongside the planktic forams *Globigerinatheka index* and *Turborotalia centralis* [85]. *Globigerinatheka index* is known to range from 42.9 - 34.3 Ma [86], but *Turborotalia centralis* is a junior synonym of *Turborotalia pomeroli*, which is known to range from 42.4-41.5 Ma [86]. Thus, the minimum age constraint on *Tubulifloridites antipodica* is 41.5 Ma. The newly described *Tubulifloridites lilliei* arguably slightly predates the other fossils of this palynological genus in its age⁵⁸.

Node 1047 | SG Aquifoliaceae | MRCA: *Ilex- Phyllonoma* | 61.6 Ma.

Fossil taxon and specimen. *Ilex hercynica* [MAI, Nr. 6004: Zentralsammlung Zentrales Geologisches Institut Berlin] described from Walkmühle in Gonna, Germany [87-89].

Phylogenetic justification. Phylogenetic relationships were discussed by Martinez-Millan [82].

Minimum age. 61.6 Ma

Age justification. Knobloch et al. [90] assert an early Palaeocene age range for *Ilex hercynica*, affording a minimum constraint of 61.6 Ma based on the Danian-Salandian Boundary and the combined age model of Vandenbergh et al. [50].

Node 1075 | CG Solanales | MRCA: *Solanum-Montinia* | 37.3 Ma.

Fossil taxon and specimen. *Solanites crassus* [USNM-39949: Smithsonian Institution National Museum of Natural History, Washington DC, USA] from Holly Springs Sand in the Claiborne Formation at Mill Creek, at a railroad cut north of Shandy, Hardeman County, Tennessee, USA [91].

Phylogenetic justification. The phylogenetic interpretation of the fossil record of Solanales have been explored recently including the fossil incorporated here .

Minimum age. 37.3 Ma.

Age justification. The Claiborne Formation is commonly attributed a middle Eocene age, but material evidence is rarely presented in support this. Taylor [83] provides a summary of the palynostratigraphic evidence, citing Elsik [84] as supporting a middle Eocene age based on juglandaceous palynomorphs including *Plicatopollis*, *Platycarya*, *Platycaryapollenites*, *Carya* and *Casuarinidites*. Their presence may be indicative of a late Eocene age, though they occur in low frequency and, thus, Taylor [83] argues instead for a Middle Eocene age based on the presence of *Nuxpollenites terminalis* and *Amanoa* type palynomorphs in even the uppermost Claiborne Formation [84]. Thus, we establish a minimum age constraint on the age of *Solanites crassus* based on the Bartonian-Priabonian Boundary, dated to 37.8 Ma ± 0.5 Myr based on the combined age model of Vandenbergh et al. [50], thus, 37.3 Ma,

Node 1098 | CG Ericales core | MRCA: *Arbutus-Camellia* | 85.8 Ma.

Fossil taxon and specimen. *Paleoenkianthus sayrevillensis* [CUPC 1100: L. H. Bailey Hortorium, Cornell University, Ithaca NY, USA] from the South Amboy Fire Clay of the Raritan Formation, of which outcrops are exposed in the Old Crossman Clay Pit in Sayreville, New Jersey.

Phylogenetic justification. The phylogenetic relationships of this fossil has been tested based on morphological evidence [93].

Minimum age. 85.8 Ma

Age justification. Clarke et al. [1] argued that a minimum constraint on the age of this deposit could be established from Santonian-Campanian Boundary, however, Massoni et al. [53] argue that a tighter correlation can be established with better rocks attributable to the CC13-14 Nannofossil zones in South Carolina, indicating a minimum age of 86.3 Ma ± 0.5 Myr, thus, 85.8 Ma.

Node 1115 | CG Cornales | MRCA: *Cornus-Petalyonyx* | 85.8 Ma.

Fossil taxon and specimen. *Tylerianthus crossmanensis* [CUPC 1047: L. H. Bailey Hortorium, Cornell University, Ithaca NY, USA] from the South Amboy Fire Clay of the Raritan Formation, of which outcrops are exposed in the Old Crossman Clay Pit in Sayreville, New Jersey [94].

Phylogenetic justification. The phylogenetic relationships of this fossil have been clarified [95, 96].

Minimum age. 85.8 Ma

Age justification. Clarke et al. [1] argued that a minimum constraint on the age of this deposit could be established from Santonian-Campanian Boundary, however, Massoni et al. [53] argue that a tighter correlation can be established with better rocks attributable to the CC13-14 Nannofossil zones in South Carolina, indicating a minimum age of 86.3 Ma ± 0.5 Myr, thus, 85.8 Ma.

Node 1171 | CG Buxales | MRCA: *Didymoles-Buxus* | 100.1 Ma.

Fossil taxon and specimen. *Spanomera marylandensis* [PP42978: Field Museum, Chicago IL, USA] described by Drinnan et al. from the Potomac Formation at West Brothers clay pit, east of Washington, DC, Prince Georges County, eastern Maryland (late Albian), assigned to Palynozone IIB.

Phylogenetic justification. Based on similarities in the inflorescences and the striate tricolporate pollen, this fossil is likely related to the extant Buxaceae [98].

Minimum age. 100.1 Ma

Age justification. In the absence of further constraint on where within Zone IIB *Spanomera marylandensis* was recovered, we take the upper age constraint on the age of this zone to establish a minimum age constraint. Massoni et al. [53] argued that deposits lower within IIB were middle Albian, but Hochuli et al. [99] have demonstrated that at least some of Zone IIB is Upper Albian. Thus, we establish our minimum age constraint on the Albian-Cenomanian Boundary, dated to 100.5 Ma 0.4 Myr [34].

Node 1175 | CG Proteales | *Nelumbo-Platanus* | 107.59 Ma.

Fossil taxon and specimen. *Aquia brookensis* [PP4295: Field Museum, Chicago IL, USA] described by Crane et al. [100] from the Potomac Formation at Bank, near Brooke, Virginia, USA.

Phylogenetic justification. Doyle [98] recognized *Aquia* (combination of *Sapindopsis variabilis*, *Platanocarpus brookensis*, *Aquia brookensis*) as a stem group member of the genus *Platanus* and the widespread Albian leaf fossil *Nelumbites* as related to the genus *Nelumbo*.

Minimum age. 107.59 Ma

Age justification. Palynological correlations place Brooke in lower Subzone II-B, for which Massoni et al. [53] provide a very detailed biostratigraphic justification for a middle Albian age, to which we refer readers. Thus, a minimum constraint for Proteales may be established on the middle-late Albian Boundary, which coincides with the base of the *Diploceras cristatum* Biozone, dated to 107.59 Ma [34].

Node 1182 | SG Menispermaceae | MRCA: *Menispermum-Ranunculus* | 83.41 Ma.

Fossil taxon and specimen. *Prototinomiscium testudinarum* and *P. vangerowii* from Klikov Formation, Czech Republic [89].

Phylogenetic justification. The phylogenetic relationships of the fossil were clarified in a study testing them as calibration points for divergence time estimates of Menispermaceae [101].

Minimum age. 83.41 Ma

Age justification. An Upper Turonian-Santonian age was established for the Klikov Formation by Pacltova [102] and Knobloch [103]. Thus, a minimum constraint can be established on the Santonian-Campanian Boundary, coincident with the base of the *Scaphites Leei III* Zone, dated to $83.64 \text{ Ma} \pm 0.23 \text{ Myr}$ [34], thus, 83.41 Ma.

Node 1193 | CG Monocots | MRCA: *Acorus-Saccharum* | 112.6 Ma.

Fossil taxon. The earliest records of *Liliacidites* occur at the Trent's Reach Locality of the Potomac Group, attributable to the Albian Zone I [99].

Phylogenetic justification. Doyle et al. [104] identified pollen referred to the genus *Liliacidites* (but not *Similipollis*) as representative of the monocot stem, making it the oldest secure record of the monocot total group (see [98]).

Minimum age. 112.6 Ma.

Age justification. In the absence of further stratigraphic constraint, these earliest records of *Liliacidites* can be constrained in age by the Aptian-Albian Boundary, dated to $113.0 \text{ ma} \pm 0.4 \text{ Myr}$, thus, 112.6 Ma.

Discussion. Doyle et al. [104] highlight that, despite decades of sampling of the Hauterivian and Barremian of England, no clear representatives of *Liliacidites* pollen have been recovered [105], perhaps implying that the earliest records from the Albian are a close approximation of their antiquity. Because of the position of monocots in our molecular tree we consider *Liliacidites* to be nested within monocots, and use it to calibrate the monocot crown node.

Node 1209 | SG Musaceae | MRCA: *Musa-Maranta* | 74.6 Ma.

Fossil taxon and specimen. *Spirematospermum chandlerae* has been described from isolated seeds and groups of seeds from the Neuse River locality, Black Creek Formation, southwest of Goldsboro, Wayne County, North Carolina, USA.

Phylogenetic justification. The phylogenetic relationships of this fossil have discussed in previous studies [106].

Minimum age. 74.6 Ma.

Age justification. Widely reported, but not evidenced as Late Cretaceous (Early Campanian) in age [107], the Black Creek Formation has been assigned to the *Exogyra ponderosa* Biozone which occurs beneath the *Didymoceras cheyennense* Tethyan ammonoid biozone [108], the base of which is dated to 74.6 Ma [34].

Node 1211 | CG Arecales | MRCA: *Elaeis-Chamaedorea* | 83.41 Ma.

Fossil taxon and specimen. *Sabalites carolinensis* [PAL 175717/P 38208: Smithsonian Museum of Natural History; Washington DC, USA] described from the Middendorf Arkose Member of Black Creek Formation near Langley, Aiken County, South Carolina [109].

Phylogenetic justification. The phylogenetic relationships of this fossil have discussed in Hertweck et al. [106] and Iles et al. .

Minimum age. 83.41 Ma

Age justification. Berry's view that the Middendorf was merely a distinct facies within the Black Creek Formation, rather than a stratigraphically distinct unit, has been rejected. Sohl and Owens [111] subdivided the Upper Cretaceous of Carolina coastal plain into three lithostratigraphic units, the Middendorf, Black Creek and Peedee Formations, raised the Black Creek to group status and subdivided this into three unconformity-bound formations, viz. in stratigraphic sequence, the Tar Heel, Bladen and Donoho Creek formations. Evidently, *Sabalites carolinensis* was recovered from what is now recognized as the Middendorf Formation, and a minimum age constraint can be established on the boundary between the Middendorf and Tar Heel Formations. The Middendorf is commonly considered Santonian in age, however, little material evidence has been presented in support of this, in part a consequent of the complex history of stratigraphic divisions at outcrop, in subsurface and offshore [112]. Habib and Miller [113] established an age 'not younger than Campanian' on the basis of dinoflagellate biostratigraphy, but following the stratigraphic scheme outlined Campbell and Grohn [112], the Middendorf is older than the Shepherd Grove Formation and, therefore, following the stratigraphy of Christopher and Prowell [108], must be no younger than Santonian. Thus, we may established a minimum age constraint on the *Sabalites carolinensis* based on the Santonian-Campanian Boundary, coincident with the base of the *Scaphites leei III* Zone, dated to 83.64 Ma ± 0.23 Myr [34], thus, 83.41 Ma.

Node 1221 | CG Orchidaceae | MRCA: *Oncidium-Phaelanopsis* | 17.82 Ma.

Fossil taxon and specimen. *Meliorchis caribea* [MCZ-31141: Museum of Comparative Zoology (Harvard University), Cambridge MA, USA], recovered from a mine east of Santiago, Cordillera Septentrional, Dominican Republic [114].

Phylogenetic justification. This amber fossil is composed of a pollinium attached to the wing of a stingless bee showing some similarities to the extant genus *Ligeophila* [114]. Pollinium structure provide unequivocal evidence for the occurrence of Orchidaceae a this time.

Minimum age. 17.82 Ma.

Age justification. The age of Dominican Amber has been the subject of much speculation, but its dating has been best constrained on the basis of planktic forams, to late Early to early Middle Miocene [115] who list a series of biostratigraphically important species of planktic foraminifera, the stratigraphic ranges of which are not entirely compatible. However, the contemporaneous sediments contain including *Catapsydrax dissimillis*, the last appearance of which has been dated to 17.62 Ma [86], providing a minimum constraint on the age of *Meliorchis caribea*.

Node 1222 | CG Lillales | *Trillium-Lilium* | 18.7 Ma.

Fossil taxon and specimen. *Luzuriaga contortus* [L24916: Palynological Type Collection of th eNew Zealand Institute of Geological and Nuclear Sciences], based on leaf remains, from the Foulden Hill Diatomite, near Middlemarch, Otago, New Zealand [116].

Phylogenetic justification. The preserved structure show high similarity to structures observed in extend this of the genus *Luzuriaga* and therefore the fossil is assigned unequivocally to the Alstromeriaceae .

Minimum age. 18.7 Ma.

Age justification. The deposit has been well studied and its maximum age is constrained by radiometric dating to 23.3 Ma ± 0.2 Ma [117]. The deposit has been attributed to the Waitakian, but a minimum age constraint must also encompass evidence of early Otaian elements of the flora and fauna, including *Assamiapollenites incognitus* which extends into the Otaian *Proteacidites isopogiformis* Zone [118]. The Otaian-Altonian Boundary has been dated to 18.7 Ma [119, 120].

Node 1224 | CG Dioscoreales-Pandanales| MRCA: *Dioscorea-Croomia* | 85.8 Ma.

Fossil taxon and specimen. *Mabelia connatifila* [CUPC 1255: L. H. Bailey Hortorium Paleobotanical Collection, Cornell University, Ithaca NY, USA] from the South Amboy Fire Clay Member of the Raritan Formation at the Old Crossman clay pit in Sayreville, New Jersey, USA [121].

Phylogenetic justification. The phylogenetic assignment is based on the phylogenetic hypothesis reconstructed by Gandolfo et al. [121].

Minimum age. 85.8 Ma.

Age justification. Clarke et al. [1] argued that a minimum constraint on the age of this deposit could be established from Santonian-Campanian Boundary, however, Massoni et al. [53] argue that a tighter correlation can be established with better rocks attributable to the CC13-14 Nannofossil zones in South Carolina, indicating a minimum age of 86.3 Ma ± 0.5 Myr, thus, 85.8 Ma.

Node 1226 | CG Alismatales | MRCA: *Orontium-Hydrocharis* | 96.24 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 [122], as the oldest record of crown-Alismatales.

Phylogenetic justification. Magallón et al. [13] argue that these striate and inaperturate pollen grains are similar to those of Monsteroideae (Araceae), such as *Holochlamys* and *Spathiphyllum*.

Minimum age. 96.24 Ma

Age justification. The Torres Vedras flora has been considered Late Barremian to Early Aptian in age [71, 123]. However, recent evidence suggests that they are considerably younger, within the ‘Upper Almargem’ Formation overlying a late Aptian to early Albian unconformity [124]. Despite the uncertainty, 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 [125, 126], which coincides with the base of the Conlinoveras *gilberti* Zone, dated to 96.24 Ma [34].

Node 1228 | MRCA: *Alisma-Potamogeton* | 66 Ma.

Fossil taxon and specimen. *Cardstonia tolmanii* [UAPC-ALTA S55138: University of Alberta Paleobotanical Collections] from the St. Mary River Formation [127].

Phylogenetic justification. Ridley and Stockey (2004) provided a convincing argument that this fossil shows closest similarity to extant genera of Alismatales. This interpretation is accepted here.

Minimum age. 66 Ma.

Age justification. Riley and Stockey [127] attribute *Cardstonia tolmanii* to the Late Campanian–Early Maastrichtian (Upper Cretaceous), though there is little direct evidence to support this. However, the St. Mary River Formation is chronostratigraphically equivalent to the Horseshoe Canyon Formation into which it intergrades and which in turn is constrained minimally by the C30n magnetozone [128], the top of which is slightly older than the Maastrichtian–Paleogene Boundary, dated to 66.0 Ma [34].

Node 1232 | CG Araceae | MRCA: *Orontium-Xanthosoma* | 76 Ma.

Fossil taxon and specimen. *Lysichiton (Araciphylletes) austriacus* [NHMW 1999B0057/0183: Natural History Museum, Vienna, Austria], from the Grünbach Formation of Austria, is the oldest record of this clade [129, 130]

Phylogenetic justification. This fossil was interpreted as closely related to extant species of the Orontioideae (family Araceae) by Bogner et al. [129]. This assignment is supported by the occurrence of several putative related fossil taxa at around the same time [131].

Minimum age. 76 Ma.

Age justification. The Grunbach Formation can be attributed to the *Globotruncata elevata* planktic foram biozone and the UC15 calcareous nannofossil biozone [130, 132]. The overlying Piesting Formation has been attributed to the UC16 nannofossil biozone [130, 132] and, thus, the age of the Grunbach Flora can be constrained by the UC15-UC16 boundary which is estimated to be 76 Ma [34].

Node 1237 | CG Laurales | MRCA: *Laurus-Calycanthus* | 107.59 Ma.

Fossil taxon and specimen. *Virginianthus calycanthoides* [PP43703: Field Museum, Chicago IL, USA] from the Albian of Puddledock, Virginia [133].

Phylogenetic justification. Doyle and colleagues [104, 134] identify *Virginianthus calycanthoides* from the Albian of Puddledock, Virginia [133], as the sister group to Calycanthaceae, or to the remaining Laurales, in either instance the oldest record of crown Laurales. Massoni et al. [53] also recognise *Cohongarootonia hispida* from the Puddledock Flora [135] as the oldest record of the total group comprised of Lauraceae, Monimiaceae, and Hernandiaceae, in other words the crown node of the clade of Laurales excluding Calycanthaceae [53]. We accept both of these as records of crown-Laurales, deeming evidence of their membership of more derived clades as insufficiently robust to be used as a basis for calibration.

Minimum age. 107.59 Ma.

Age justification. Massoni et al. [53] reason that the sediments in the Puddledock Locality are definitively early Albian based on the presence of reticulate tricolporate pollen and *Clavatipollenites rotundus* (aff. *Retimonocolpites dividuus* [136] but not striate tricolpates, which occur later in the early Albian.

Node 1248 | CG Magnoliales | MRCA: *Magnolia*-*Myristica* | 110.87 Ma.

Fossil taxon and specimen. *Endressinia brasiliiana* [MB. PB. 2001/1455: Museum of Natural History, Institute of Paleontology, Berlin, Germany], from the Crato Formation of Brazil [137].

Phylogenetic justification. Masson et al. identify both *Schenkeriphyllum glanduliferum* and *Endressinia brasiliiana*, both from the Crato Formation of Brazil [137, 138], as the oldest records of crown Magnoliineae, the sister clade of Myristicaceae, based on the phylogenetic analyses [98, 134, 138].

Minimum age. 110.87 Ma.

Age justification. Clarke et al. [1] argued that the age of the Crato Formation could not be constrained to being definitively older than Albian based on pollen [140], ostracod [141], and dinoflagellate [142] biostratigraphy and, in the absence of further evidence, established a minimum constraint on the Albian-Cenomanian boundary. Massoni et al. [53] argued for an Aptian age for the Crato Formation based on evidence from Heimhofer and Hochuli [142] but, unfortunately, these authors do not present evidence that can discriminate against a possible early Albian age for the Crato Formation, as acknowledged by Mohr et al. [138]. While the evidence suggests at worst, an early Albian age for the Crato Formation, and so it is possible to derive a minimum age interpretation for the Formation based on the Early-Middle Albian Boundary, which coincides approximately with the base of the *Douvilleiceras mammillatum* ammonite biozone, dated to 110.87 Ma [34].

Discussion. *Archaeanthus linnenbergii* was recognized as a further putative stem group Magnoliaceae but it is younger than *Endressinia* [53, 98].

Node 1256 | SG Canellales | MRCA: *Piper*-*Canella* | 125.9 Ma.

Fossil taxon and specimen. *Walkeripollis gabonensis* [Single-pollen grain preparation 2963-27: University of California (Berkeley) Museum of Paleontology], Cocobeach sequence near N'Toum, Gabon [53].

Phylogenetic justification. Massoni et al. [53] identify *Walkeripollis gabonensis* as the oldest record of Canellales, based on phylogenetic of pollen grain characters that resolve this pollen species as stem-Winteraceae [134], one of the two families that comprise Canellales, based on the presence of permanent tetrads, rounded aperture shape, as well as characteristic pore sculpture.

Minimum age. 125.9 Ma.

Age justification. Massoni et al. [53] establish a pre-Aptian age for *Walkeripollis gabonensis* based on the correlation of its occurrence in the Elf-Aquitaine palynological Subzone C-VIIc of the Cocobeach sequence near N'Toum, Gabon, to better-dated late Barremian sequences elsewhere. Thus, a minimum age constraint is established on the Barremian-Aptian boundary that has been dated to 126.3 Ma \pm 0.4 Myr, thus, 125.9 Ma.

Discussion. Massoni et al. [53] proposed records of more derived clades within Canellales (e.g. *Appomattoxia*, including the pollen of *Tucanopolis* and *Transitoripollis* types, from the Puddledock, Virginia [143], and Torres Vedras, Portugal [71, 144]). However, these are not sufficiently convincing to use as a basis for calibration. For example, *Appomattoxia* maybe more closely related to *Ceratophyllum* and Chloranthaceae [98].

Node 1260 | SG Saururus | MRCA: *Saururus*-*Houttuynia* | 44.3 Ma.

Fossil taxon and specimen. *Saururus tuckerae* [UAPC P1631 Bbot a: University of Alberta (Edmonton) Paleobotanical Collections] from the Middle Eocene Princeton Chert, British Columbia, Canada.

Phylogenetic justification. Massoni et al. [53] follow Smith and Stockey [145] in identifying *Saururus tuckerae* as the oldest record of total group *Saururus*. Based on tens of flowers and a partial inflorescence, the flower structure and pollen are characteristic of Saururaceae (Piperales), and phylogenetic analyses resolved *S. tuckerae* as the sister clade to extant *Saururus* [145].

Minimum age. 44.3 Ma.

Age justification. The Princeton Chert is part of the Allenby Formation which has been the subject of a number of absolute dating studies yielding age estimates of 48 Ma \pm 2 Myr [146, 147], between 47 Ma \pm 2 Myr and 50 Ma \pm 2 Myr [148], between 46.2 Ma \pm 1.9 Myr and 49.4 Ma \pm 2 Myr [149], and 52.08 Ma \pm 0.12 Myr [150] for the Allenby Formation. We follow Massoni et al. [53] in basing our minimum constraint based on the youngest age Interpretation of the youngest radiometric age estimate, viz. 44.3 Ma

Node 1268 | CG Chloranthales | MRCA: *Chloranthus*-*Hedyosmum* | 92.8 Ma.

Fossil taxon and specimen. *Pennipolis* plant [151] based on material from Vale de Agua, Buarcos, Portugal [152].

Phylogenetic justification. *Pennipolis* was found as sister to the crown group Chloranthaceae [153], whereas the Aptian to Cernomanina *Asteropollis* mesofossils may represent both crown and stem group Chloranthaceae [98].

Minimum age. 92.8 Ma.

Age justification. Clarke et al. [1] established a minimum age for Vale de Agua, which is assigned to the Figueira da Foz Formation [154-156] based on the overlying Costa d'Arnes Formation, the oldest ammonites in

which include *Calycoceras naviculare* [157], indicative of the naviculare biozone, the dating of which in error of the top of the Cenomanian, dated $93.6 \text{ Ma} \pm 0.8 \text{ Myr}$ [34], thus, 92.8 Ma.

Discussion. Other early Cretaceous fossils with possible relationships to Chloranthaceae, such as *Zlatkcarpus* and *Canrightia* are younger than *Pennipolis* [98].

Node 1272 | SG Schisandraceae | MRCA: *Trimenia-Kadsura* | 107.59 Ma.

Fossil taxon and specimen. *Anacostia virginiensis* based on material from Kenilworth, Maryland, Puddledock, Virginia .

Phylogenetic justification. The assignment is based on the result of maximum parsimony based reconstruction of the phylogenetic relationships of this fossil to extant angiosperms that recovered this taxon as nested between *Trimenia* and the clade comprising *Illicium* and *Schisandra* [153].

Minimum age. 107.59 Ma.

Age justification. Massoni et al. [53] reason that the sediments in the Puddledock Locality are definitively early Albian based on the presence of reticulate tricolpate pollen and *Clavatipollenites rotundus* (aff.

Retimonocolpites dividuus [136]) but not striate tricolpates, which occur later in the early Albian. Therefore, they constrain minimally the age of the *A. virginiensis* by the Middle-late Albian boundary, which coincides with the base of the *Diploceras cristatum* biozone which has been dated to 107.59 Ma [34].

Discussion. *Anacostia*, reportedly from the early and middle Albian of Buarcos, Famalicão, and Vale de Agua (Portugal), Puddledock (Virginia, USA), and Kenilworth (Maryland, USA) was recognized as the oldest fossil record of the Austrobaileyales [98, 153]. Doyle and Endress [153] identified *Anacostia portugallica* and *A. teixeirae* as early Albian and, therefore the oldest species belonging to this lineage. However, the minimum age interpretation of these localities the Figueira da Foz Formation cannot be constrained minimally to more than 92.8 Ma (see above). However, the minimum age constraint on *A. virginiensis* from the Puddledock Locality is older.

Node 1273 | SG *Illicium* | MRCA: *Illicium-Schisandra* | 85.44 Ma.

Fossil taxon and specimen. *Illiciospermum pusillum* [1700b-127: Komarov Botanical Institute, St. Petersburg, Russia.], known from seeds from the Cenomanian-Turonian of Kazakhstan [158].

Phylogenetic justification. *Illiciospermum pusillum*, known from seeds that preserve a structure resembling the strophiole of *Illicium* [158].

Minimum age. 85.44 Ma.

Age justification. There is a paucity of evidence supporting the age interpretation of the Sarbay Quarry near Rudnyy, Kustanay Region, north-western Kazakhstan. Frumin and Friis (1996) describe the sediments, including the plant-bearing bed, as belonging to the Shet-Irgiz Formation of Cenomanian-Turonian age [159], overlain by marine sands of the Santonian-Campanian Ayat Suite containing *Inoceramus cardissoides* [159]. The *Inoceramus cardissoides* Zone falls fully within the *Sigalia carpatica* Planktic foraminiferal Zone [160], the range end of which is dated to 85.44 Ma [34].

Node 1276 | SG Cabombaceae | MRCA: *Nymphaea-Cabomba* | 110.87 Ma.

Fossil taxon and specimen. *Pluricappellatia peltata* [MB.Pb. 2000/80: Museum of Natural History, Berlin, Germany], from the Crato Formation of Brazil [161]

Phylogenetic justification. *Pluricappellatia peltata* has been considered phylogenetically and resolved as members of the lineage leading to *Cabomba* after it diverged from *Nymphaea* [162].

Minimum age. 110.87 Ma.

Age justification. Clarke et al. [1] argued that the age of the Crato Formation could not be constrained to being definitively older than Albian based on pollen [140], ostracod [141], and dinoflagellate [142] biostratigraphy and, in the absence of further evidence, established a minimum constraint on the Albian-Cenomanian boundary. Massoni et al. [53] argued for an Aptian age for the Crato Formation based on evidence from Heimhofer and Hochuli [142] but, unfortunately, these authors do not present evidence that can discriminate against a possible early Albian age for the Crato Formation, as acknowledged by Mohr et al. [138]. While the evidence suggests, at worst, an early Albian age for the Crato Formation, it is possible to derive a minimum age interpretation for the Formation based on the Early-Middle Albian Boundary, which coincides approximately with the base of the *Douvilleiceras mammillatum* ammonite biozone, dated to 110.87 Ma [34].

Discussion. Magallon et al. [13] derive a minimum constraint from *Monetianthus mirus* which they recognize as a representative of the Nymphaeaceae stem lineage and, thus, use it as the basis of a minimum constraint on the age of total-group Nymphaeaceae at 125 Ma. However, Clarke et al. [1] demonstrated that the minimum age of the host deposit, Vale de Água, Portugal [163, 164] is 93.9 Ma [34]. However, there are other, potentially older records of Nymphaeaceae and, more specifically, the crown clade circumscribed by *Nymphaea-Cabomba*.

Clarke et al. [1] identified much older, but more equivocal records, as well as the oldest unequivocal records, viz. *Pluricappellatia peltata* from the Crato Formation of Brazil [161] and *Scutifolium jordanicum* from the

Jarash Formation (Kurnub Group) of Jordan [162], both of which have been considered phylogenetically and resolved as members of the lineage leading to *Cabomba* after it diverged from *Nymphaea* [162]. *Scutifolium jordanicum* was used to establish a minimum age for crown-Nymphaeales at 105 Ma by Smith et al. [165], and for total-group Cabombaceae at 105 Ma by Zanne et al. [166]. The Jarash Formation can be dated minimally to 95 Ma ($96.1 \text{ Ma} \pm 1.1 \text{ Myr}$ in [167]), but the Crato Formation is older.

Node 1278 | CG Nymphaeaceae | MRCA: *Nymphaea* - *Nuphar* crown | 92.8 Ma.

Fossil taxon and specimen. *Monetianthus mirus* [S122015: Palaeobotanical Collectons, Swedish Museum of Natural History, Stockholm, Sweden] from Vale de Agua, Portugal [164].

Phylogenetic justification. Doyle and Endress [153] identify *Monetianthus mirus*, a coalified flower from Vale de Agua, Portugal, as a stem member of the clade Barclaya-Nymphaeoideae, to the exclusion of *Nuphar*.

Minimum age. 92.8 Ma.

Age justification. Clarke et al. [1] established a minimum age for Vale de Agua, which is assigned to the Figueira da Foz Formation [154-156], based on the overlying Costa d'Arnes Formation, the oldest ammonites in which include *Calycoceras naviculare* [157], indicative of the *naviculare* Biozone, the dating of which in error of the top of the Cenomanian, dated $93.6 \text{ Ma} \pm 0.8 \text{ Myr}$ [34], thus, 92.8 Ma.

Node 1279 | CG Acrogymnosperms | MRCA: *Ginkgo-Pinus* | 308.14 Ma – 365.629 Ma.

Fossil taxon and specimen. *Cordaites iowensis* [UM4616: University of Michigan and Illinois Geological Survey, Ann Arbor MI, USA] from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa, USA [22].

Phylogenetic justification. Clarke et al. [1] identify cordaitean coniferophytes as the oldest records of the *Ginkgo-Pinus* clade, the oldest whole plant reconstruction of which is *Cordaites iowensis* from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa [22].

Minimum age. 308.14 Ma.

Maximum age: 365.629 Ma.

Age justification. Janousek and Pope [23] argue that the Laddsdale Coal is equivalent to the Bluejacket Coal of Oklahoma, which occurs as part of the Bluejacket Sandstone Member, underlying the Inola Limestone, part of the Inola Cyclothem of the Krebs subgroup of the Cherokee Group, characterized by the occurrence of the conodonts *Idiognathodus amplificus*, *Idiognathodus podolskensis* and *Neognathodus asymmetricus* [24]. The Inola cyclothem falls fully within the *Idiognathodus amplificus*/ *Idiognathodus obliquus* biozone [25]. This is indicative of the *Neognathodus medexultimus*-*Streptognathodus concinnus* (Pc10) biozone, certainly older than the *Neognathodus roundyi* – *Streptognathodus cancellatus* (Pc11) biozone [25, 26]. The base of Pc10 is bracketed by an older age constraint of $312.01 \text{ Ma} \pm 0.37 \text{ Myr}$ and the base of Pc11 is bracketed by a younger age constraint of $308.5 \text{ Ma} \pm 0.36 \text{ Myr}$ in the Composite Standard of Davydov et al. [26], yielding a minimum age constraint of 308.14 Ma. A soft maximum is based upon the first appearance of seeds in the form of preovules which are attributable to the spermatophyte stem, the oldest interpretation of which is 365.629 Ma (see Spermatophyta).

Discussion. Zanne et al. [166] derive a minimum constraint from *Emporia lockardii* at 290.0 Ma which they recognize as a member of crown-Acrogymnospermae within a phylogenetic concept of the group in which, as here, cycads and *Ginkgo* comprise a clade.

Node 1280 | CG Conifers | MRCA: *Pinus-Metasequoia* | 147 Ma - 312.38 Ma.

Fossil taxon and specimen. *Araucaria mirabilis* [NHM V. 30953: Natural History Museum, London, UK], represented by cones, from Cerro Cuadrado petrified forest, La Matilde Formation, Patagonia, Argentina [168-171].

Phylogenetic justification. These fossils possess a ‘vascular plexus’ at the ovule base, ovuliferous scale vascularization, two vascular strands to the conescale complex and an embryo with two cotyledons, all characters established to distinguish *Araucaria* section *Bunya* of the Araucariaceae [170, 172], to which only extant *Araucaria bidwillii* belongs.

Minimum age. 147 Ma.

Maximum age: 312.38 Ma.

Age justification. The age of La Matilde Formation is poorly constrained as the stratigraphy is complex, although the volcanic deposits do allow radiometric dating. La Matilde Formation is overlain by volcanics dated to $157 \text{ Ma} \pm 10 \text{ Myr}$ [173], and thus the minimum constraint on the divergence of crown Cupressophyta, total group Cupressophyta and crown Coniferae is 147 Ma. A soft maximum constraint can be based on *Cordaites iowensis*, a cordaitean coniferophyte from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa [22], is the oldest whole plant reconstruction for Coniferae. Janousek and Pope [23] argue that the Laddsdale Coal is equivalent to the Bluejacket Coal of Oklahoma, which occurs as part of the Bluejacket Sandstone Member, underlying the Inola Limestone, part of the Inola Cyclothem of the Krebs subgroup of the Cherokee Group, characterized by the occurrence of the conodonts *Idiognathodus amplificus*, *Idiognathodus podolskensis* and *Neognathodus asymmetricus* [24]. The Inola cyclothem falls fully within the *Idiognathodus amplificus*/ *Idiognathodus obliquus* biozone [25]. This is indicative of the *Neognathodus medexultimus*-*Streptognathodus concinnus* (Pc10) biozone, certainly older than the *Neognathodus roundyi* – *Streptognathodus cancellatus* (Pc11) biozone [25, 26]. The base of Pc10 is bracketed by an older age constraint of $312.01 \text{ Ma} \pm 0.37 \text{ Myr}$ and the base of Pc11 is bracketed by a younger age constraint of $308.5 \text{ Ma} \pm 0.36 \text{ Myr}$ in the Composite Standard of Davydov et al. [26], yielding a minimum age constraint of 308.14 Ma. A soft maximum is based upon the first appearance of seeds in the form of preovules which are attributable to the spermatophyte stem, the oldest interpretation of which is 365.629 Ma (see Spermatophyta).

Cherokee Group, characterized by the occurrence of the conodonts *Idiognathodus amplificus*, *Idiognathodus podolskensis* and *Neognathodus asymmetricus* [24]. The Inola cyclothem falls fully within the *Idiognathodus amplificus*/ *Idiognathodus obliquus* biozone [25]. This is indicative of the *Neognathodus medexultimus*-*Streptognathodus concinnus* (Pc10) biozone, certainly older than the *Neognathodus roundyi* – *Streptognathodus cancellatus* (Pc11) biozone [25, 26]. The base of Pc10 is bracketed by an older age constraint of 312.01 Ma ± 0.37 Myr and the base of Pc11 is bracketed by a younger age constraint of 308.5 Ma ± 0.36 Myr in the Composite Standard of Davydov et al. [26], yielding a soft maximum of 312.38 Ma.

Discussion. This is the fundamental divergence of Coniferae into Cupressophyta, Gnetales and Pinaceae. The oldest secure records of the gnepine total group occur within the Yixian Formation of Liaoning, China, the minimum age of which is 121.8 Ma (see [1]). The oldest possible records of Cupressophyta total group include Triassic *Rissikia media* (Townrow, 1967) but it lacks the Podocarpaceae diagnostic feature of one ovule per cone scale, instead possessing two [1]. Other Triassic-Jurassic records are equally problematic [174-176].

Node 1282 | CG Gnetales | MRCA: *Gnetum-Welwitschia* | 119.6 Ma – 312.38 Ma.

Fossil taxon and specimen. *Eoantha zherikhinii* [Repository of the Institute of Biology and Pedology, Vladivostok, Russia], from the Zaza Formation at the Baisa locality in the upper reaches of the Vitim River in Lake Baikal [177].

Phylogenetic justification. This fossil is assigned as a representative of the Gnetales because of the presence of an ovule with a an exending micropylar tube similar to extend Gnetales and the presence of polypligate pollen of *Ephedritopes*-type (see [178]). *Eoantha* is one out of several Early Cretaceous fossils unequivocally assigned to the crown Gnetales [179]

Minimum age. 119.6 Ma.

Maximum age. 312.38 Ma.

Age justification. The Zaza Formation can be correlated with the Turga Formation, also of Transbaikalia based principally on common elements of their floral assemblages, including *Asteropollis asteroides*, *Dicotylophyllum pusillum*, *Baisa hirsuta*, *Podozamites*, *Schizolepis*, *Pseudolarix*, *Phoenicopsis*, *Czekanowskia rigida* and *Sphenobaiera* [177, 180-182]. The age of the Turga flora and Formation is based on the chronological distribution of *Asteropollis* type pollen, but correlation with the Yixian Formation of China is also supported strongly [180], allowing for refinement of the *Asteropollis*-derived ages. Correlation between Turga and Yixian is based on similarities in the floral assemblages of these two formations, with the shared presence of the species *Baisa hirsuta*, *Botrychites reheensis*, *Neozamites verchojanensis*, *Pityolepis pseudotsugaoides*, *Brachiphyllum longispicum*, *Scarbugia hili*, *Ephedrites chenii*, *Carpolithus multiseminalis*, *Carpolithus pachythelis*, *Schizolepis*, *Baiera*, *Coniopteris*, *Ginkoites*, *Pityocladus*, *Pityospermum* and *Elatocladus* [177, 180, 183]. The shared presence of *Asteropollis asteroides* in Turga and Zaza can be used to constrain their age. The last appearance of *Asteropollis* pollen is in Antarctica [184] and is dated to the end-Campanian, at the latest 72.1 Ma ± 0.2 [34]. This minimum may be constrained further based on the correlation of the Zaza Formation through the Turga Formation to the Yixian Formation. The main fossil bearing beds in the Yixian Formation have been recently dated and may be as old as 129.2 Ma [41], however, in the absence of knowledge of the position of the fossils within the stratigraphy, relative to the sources of the absolute dates, a minimum age constraint can be derived from the Jiufontang Formation which overlies it. $^{40}\text{Ar}/^{39}\text{Ar}$ dating of a number of samples from the Jiufontang Formation has yielded an age of 120.3 ± 0.7 Ma for the volcanic tuffs [42], establishing a minimum constraint of 119.6 Ma for the age of the Yixian, Formation and, thus ultimately the Zaza Formation.

A soft maximum constraint can be based on *Cordaites iowensis*, a cordaitean coniferophyte from the Laddsdale Coals (Cherokee Group, Desmoinesian) near What Cheer, Iowa [22], is the oldest whole plant reconstruction for Coniferae. Janousek and Pope [23] argue that the Laddsdale Coal is equivalent to the Bluejacket Coal of Oklahoma, which occurs as part of the Bluejacket Sandstone Member, underlying the Inola Limestone, part of the Inola Cyclothem of the Krebs subgroup of the Cherokee Group, characterized by the occurrence of the conodonts *Idiognathodus amplificus*, *Idiognathodus podolskensis* and *Neognathodus asymmetricus* [24]. The Inola cyclothem falls fully within the *Idiognathodus amplificus*/ *Idiognathodus obliquus* biozone [25]. This is indicative of the *Neognathodus medexultimus*-*Streptognathodus concinnus* (Pc10) biozone, certainly older than the *Neognathodus roundyi* – *Streptognathodus cancellatus* (Pc11) biozone [25, 26]. The base of Pc10 is bracketed by an older age constraint of 312.01 Ma ± 0.37 Myr and the base of Pc11 is bracketed by a younger age constraint of 308.5 Ma ± 0.36 Myr in the Composite Standard of Davydov et al. [26], yielding a soft maximum of 312.38 Ma.

Node 1284 | MRCA: *Ginkgo-Cycas* | 264.7 Ma – 365.629 Ma.

Fossil taxon and specimen. *Crossozamia chinensis* [GP0027: Beijing Graduate School, China Institute of Mining, Beijing, China], Lower Shihhotse Formation at Simugedong, Dongshan (East Hills), Taiyuan, north China [185].

Phylogenetic justification. Nagalingum et al. [186] identify *Crossozamia* as the oldest record of the *Cycas* lineage, based on megasporophylls that exhibit similarity to extant *Cycas* [185]. They argue against the interpretation of *Crossozamia* as the sister lineage of *Cycas* based on the presence of an estipulate leaf base and a terminal pinna found in the seedlings [187], instead favouring its assignment to the cycad stem. The arguments presented clearly raise doubts about the assignment of *Crossozamia* to crown-cycads, however, they do not provide definitive evidence of its exclusion from this clade and so *Crossozamia* may more appropriately be assigned to the cycad total group (i.e. we cannot discriminate between a stem or crown-cycad affinity based on the available evidence). In either instance, *Crossozamia* is the oldest record of the minimal clade comprised of *Ginkgo* and *Cycas*.

Minimum age. 264.7 Ma.

Maximum age. 365.629 Ma.

Age justification. The Lower Shihhotse Formation at Simugedong, Dongshan (East Hills), Taiyuan, north China [185] has been established biostratigraphically as Roadian-Wordian (middle Permian) [188] and, thus a minimum age constraint can be established on the Wordian-Capitanian Boundary which has been dated to 265.1 Ma \pm 0.4 Myr [189]. Thus, the minimum age constraint on the *Cycas-Ginkgo* clade is 264.7 Ma. A soft maximum is based upon the first appearance of seeds in the form of preovules which are attributable to the spermatophyte stem, the oldest interpretation of which is 365.629 Ma (see Spermatophyta).

Node 1286 | CG Ferns | MRCA: *Psilotum-Adiantum* | 384.71 Ma – 451 Ma.

Fossil taxon and specimen. *Ibyka amphikoma* was recovered from the Manorkill Shale Member at Schoharie Creek directly below the spillway of Gilboa dam, Gilboa, Schoharie County, New York, Gilboa [14].

Phylogenetic justification. *Ibyka amphikoma* [14] is the oldest record of the equisetopsid lineage based on the phylogenetic analyses undertaken by Kenrick and Crane [3].

Minimum age. 384.71 Ma.

Maximum age. 451 Ma.

Age justification. *Ibyka amphikoma* was recovered from the Manorkill Shale Member, which is a lateral equivalent of the Windom Member, within the Moscow Formation of New York [18, 19], which falls fully within the *ansatus* conodont Biozone [20, 21] the top of which is dated to 385.41 Ma \pm 0.7 Myr, thus, yielding a minimum age constraint of 384.71 Ma. The soft maximum constraint, following Clarke et al. [1], is based on the oldest occurrences of trilete spores, known from the Qusaiba-1 core from the Quasim Formation of northern Saudi Arabia [8]. The very oldest records precede the earliest occurrences of the *A. barbata*, opening the possibility that they occur in the preceding *Tanuchitina fistulosa* biozone, though *T. fistulosa* does not occur. The oldest stratigraphic records within the core co-occur with the chitinozoan *Armoricochitina nigerica*, known to extend into the Caradoc, to within the biozone characterized by *Fungochitina spinifera* (= *Fungochitina fungiformis*) [9]. The base of the *F. spinifera* Zone falls within the *Dicranograptus clingani* Biozone (*Dicellograptus morrisi* Subzone) [10], the base of which is estimated at 451 Ma [11]. Thus, we establish our soft maximum for Tracheophyta at 451 Ma.

Discussion. Magallón et al. [13] established a minimum age constraint based on *Ibyka amphikoma* using the Givetian-Frasnian boundary, for which they provided a date of 385 Ma, though this has since been revised to 382.7 Ma \pm 1 Myr [17]. However, we provide a more detailed stratigraphic justification for the age of *I. amphikoma* which allows for an older minimum age constraint.

Node 1287 | CG Lycophytes | MRCA: *Huperzia-Selaginella* | 392.1 Ma – 451 Ma.

Fossil taxon and specimen. *Leclercquia complexa* [CW092 (07 – 061): Collections of the Centre for Palynological Studies, Department of Animal and Plant Sciences, University of Sheffield, UK], from Campbellton Formation outcropping on the south shore of the Restigouche River, between Dalhousie and Campbellton, New Brunswick, eastern Canada [190].

Phylogenetic justification. Kenrick and Crane [3] identified *Leclercquia complexa* as the oldest member of Isoetopsida and crown Lycopodiophyta. This interpretation is supported by spore characteristics analysed phylogenetically by Wellman et al. [190].

Minimum age. 392.1 Ma.

Maximum age. 451 Ma.

Age justification. A Late Emsian age is often cited for the New Brunswick occurrences of identified *Leclercquia complexa* and, indeed, the *Stockmensella-Leclercquia* macroplant Biozone spans all but the earliest Emsian [17]. However, Wellman et al. [190] attribute their own material of *Leclercquia complexa* to the middle of the *Emphanisporites annulatus* – *Camarozonotriletes sextantii* Spore Assemblage Biozone which falls within the early part of the Emsian. In either instance, the earliest records of *Leclercquia complexa* fall fully within the Emsian, the end of which is dated to 393.3 Ma \pm 1.2 Myr [17], yielding a minimum constraint of 392.1 Ma. The soft maximum constraint, following Clarke et al. (2011), is based on the oldest occurrences of trilete spores, known from the Qusaiba-1 core from the Quasim Formation of northern Saudi Arabia [8]. The very oldest

records precede the earliest occurrences of the *A. barbata*, opening the possibility that they occur in the preceding *Tanuchitina fistulosa* biozone, though *T. fistulosa* does not occur. The oldest stratigraphic records within the core co-occur with the chitinozoan *Armoricochitina nigerica*, known to extend into the Caradoc, to within the Biozone characterized by *Fungochitina spinifera* (= *Fungochitina fungiformis*) [9]. The base of the *F. spinifera* Zone falls within the *Dicranograptus clingani* Biozone (*Dicellograptus morrisi* Subzone) [10], the base of which is estimated at 451 Ma [11]. Thus, we establish our soft maximum for Tracheophyta at 451 Ma. **Discussion.** Magallon et al. [13] cite a minimum age of 385 Ma, based on the Middle-Upper Devonian Boundary, but our more detailed stratigraphy allows for an older minimum age interpretation of *Leclercquia complexa*.

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