

Supplementary Material for

Coalescent versus Concatenation Methods and the Placement of *Amborella*
as Sister to Water Lilies

Zhenxiang Xi, Liang Liu, Joshua S. Rest, and Charles C. Davis*

*E-mail: cdavis@oeb.harvard.edu

This PDF file includes:

Figures S1–S11

Tables S1–S8

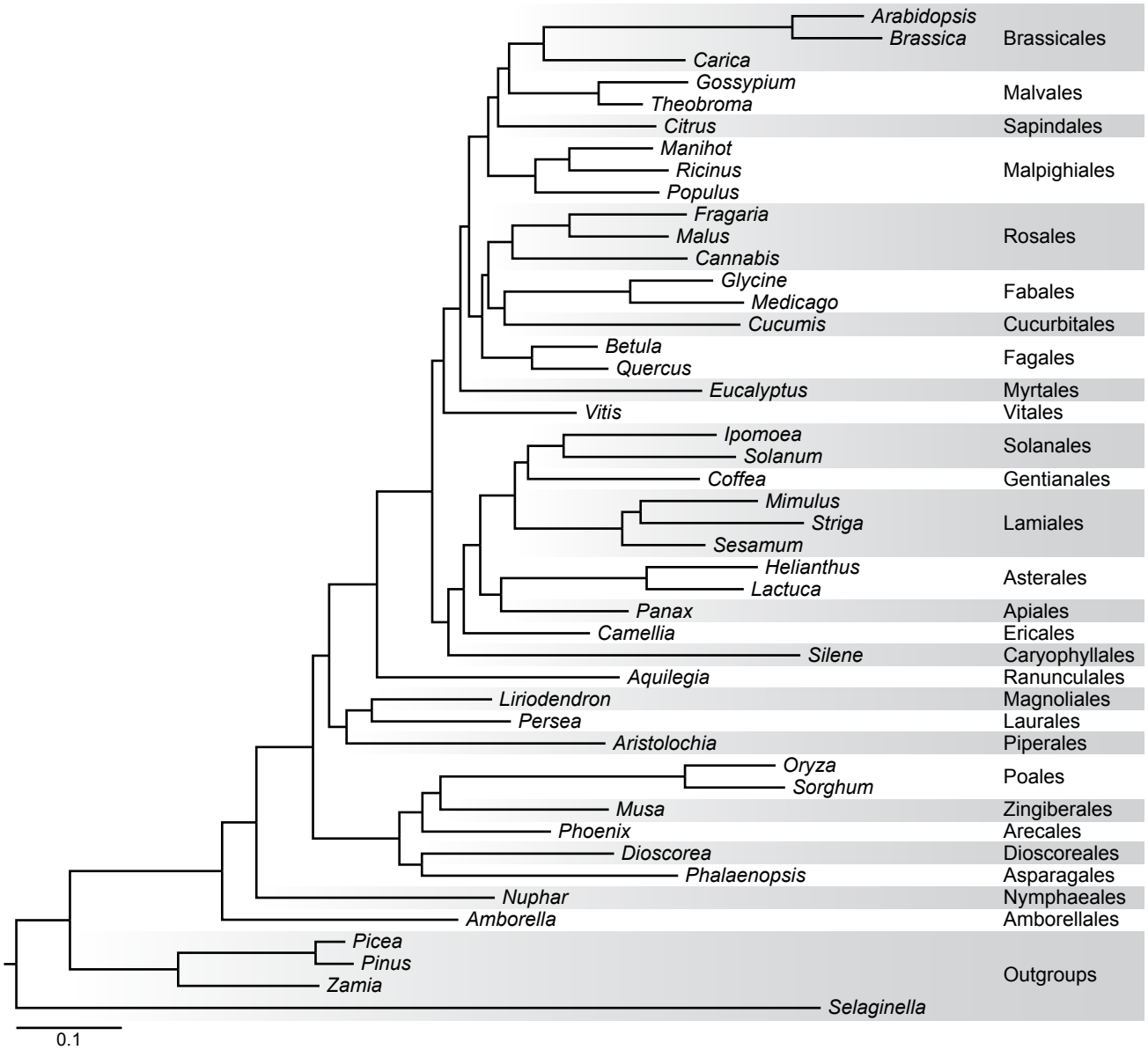


Figure S1. The best-scoring maximum likelihood tree inferred from the 310 nuclear genes using the concatenation method (RAxML with OnePart).

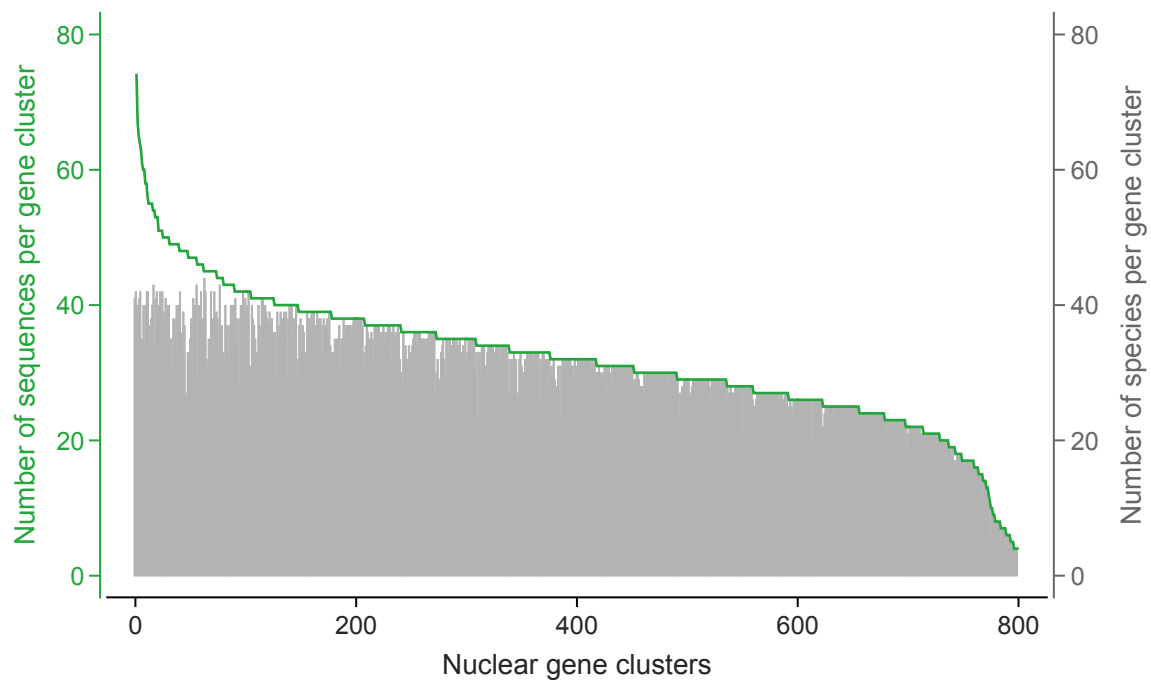


Figure S2. The numbers of sequences and species for each of the 799 nuclear gene clusters that passed our initial criteria for establishing sequence homology. The number of sequences in each gene cluster is shown along the left vertical axis and indicated by a green line, while the number of species in each gene cluster is shown on the right vertical axis indicated by a grey bar.

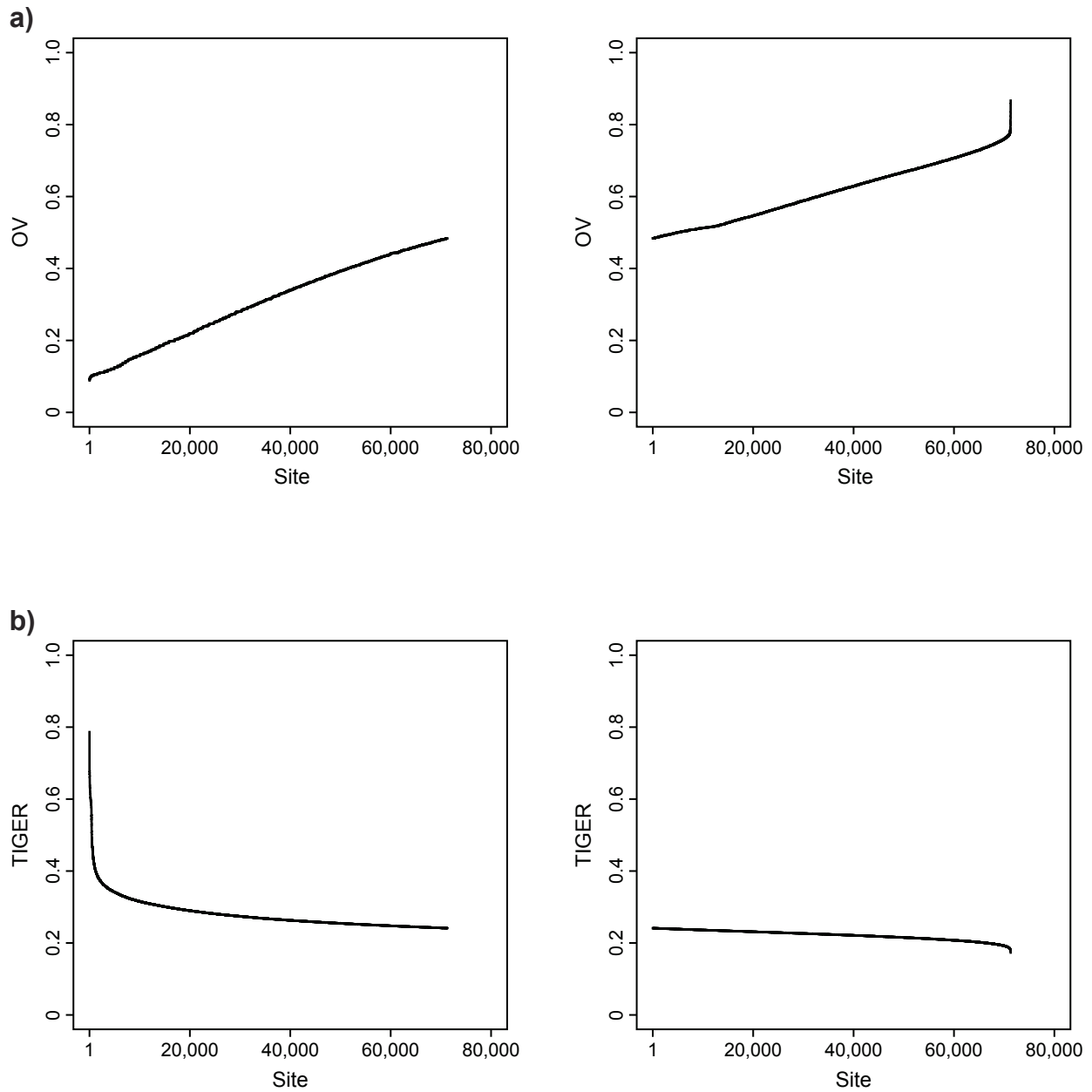


Figure S3. The estimated evolutionary rates for nucleotide sites in the concatenated nuclear matrix. Parsimony informative sites in the concatenated matrix were sorted based on the Observed Variability (OV) method (a) or the Tree Independent Generation of Evolutionary Rates (TIGER) method (b), and subsequently divided into two equal partitions.

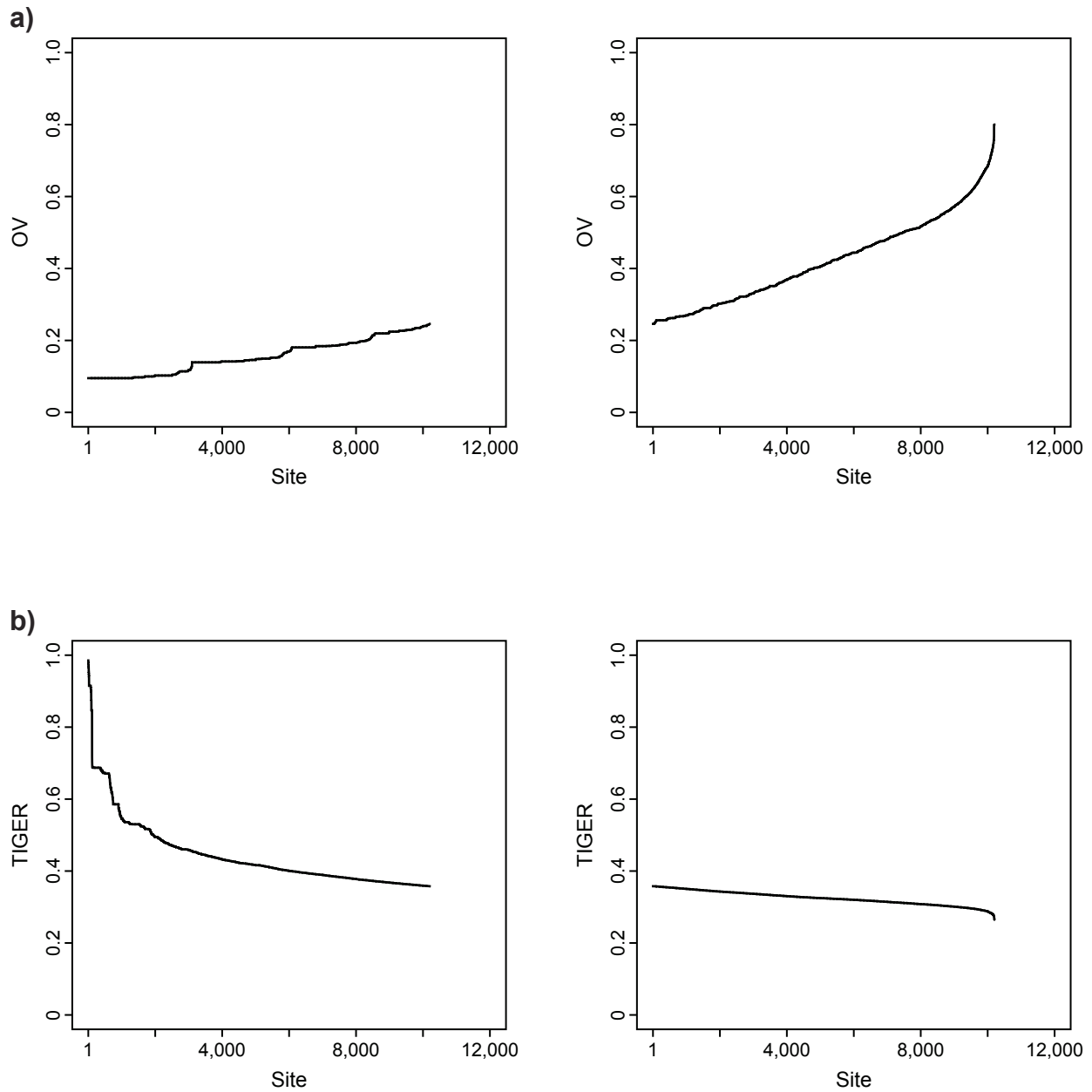


Figure S4. The estimated evolutionary rates for nucleotide sites in the concatenated plastid matrix. Parsimony informative sites in the concatenated matrix were sorted based on the Observed Variability (OV) method (a) or the Tree Independent Generation of Evolutionary Rates (TIGER) method (b), and subsequently divided into two equal partitions.

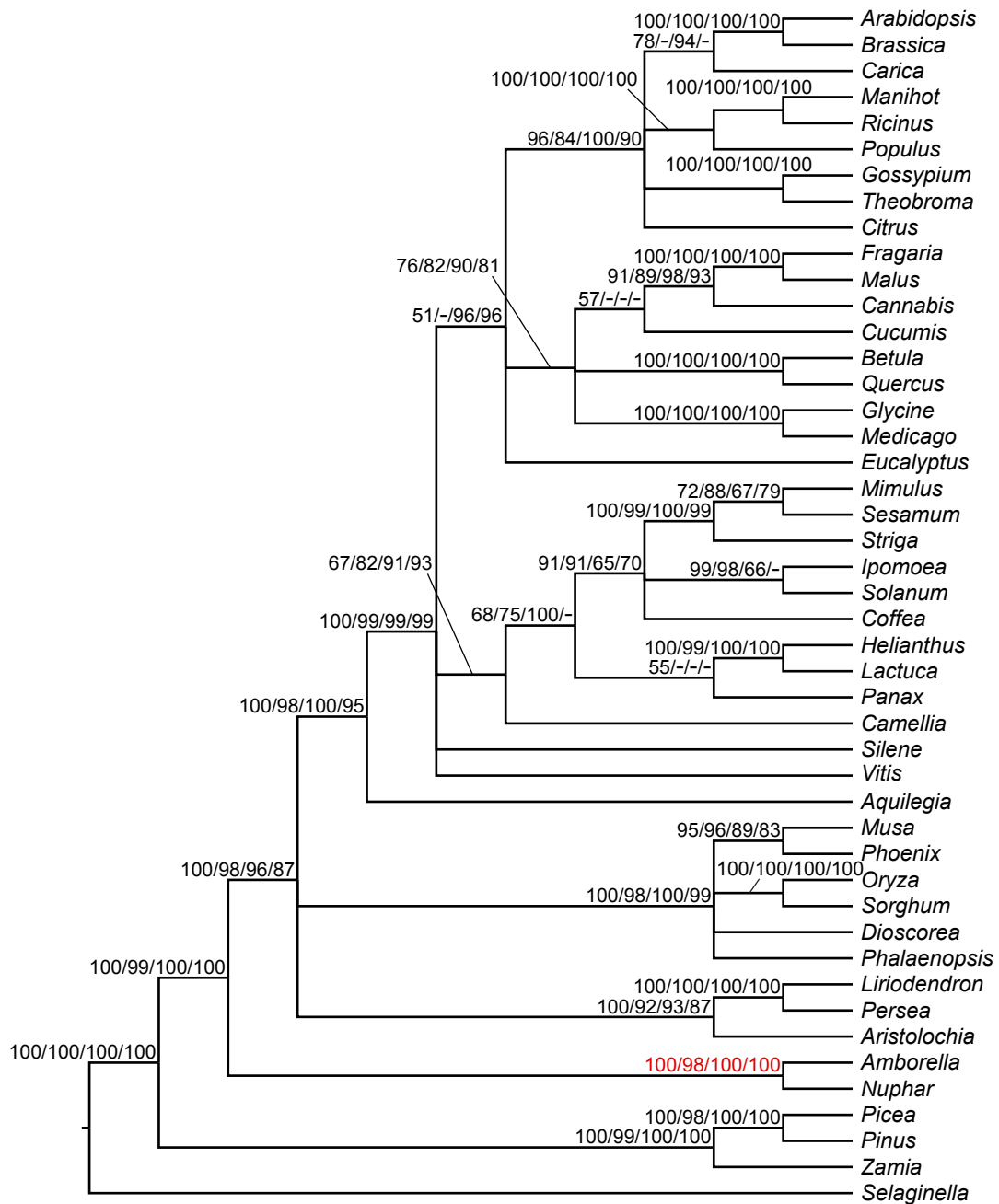


Figure S5. The 50% majority-rule consensus tree inferred from slow nuclear rate partitions using coalescent methods (STAR and MP-EST). The nucleotide rate partitions were determined for 310 nuclear genes using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Bootstrap percentages from OV_STAR /OV_MP-EST/TIGER_STAR/TIGER_MP-EST are indicated above each branch.

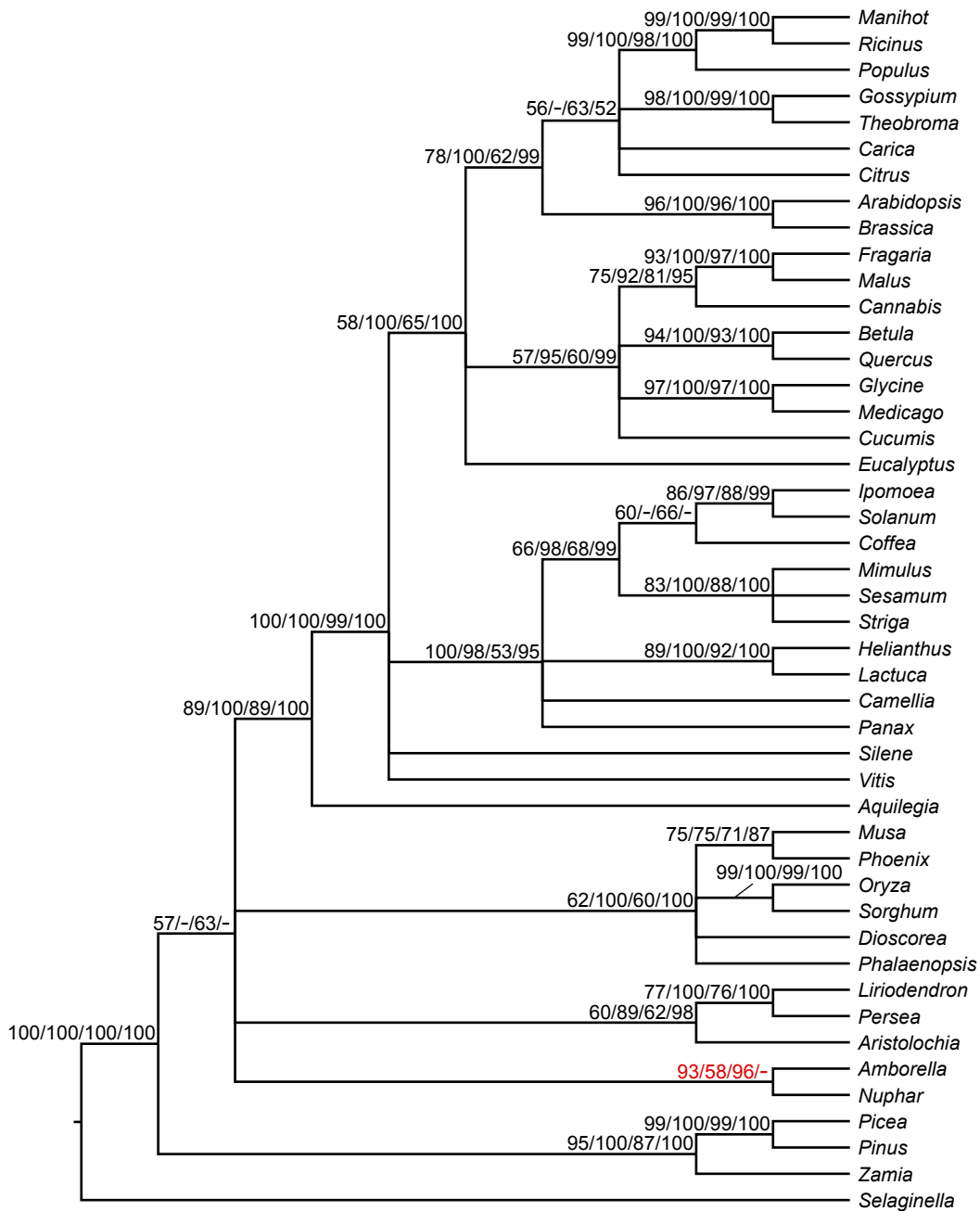


Figure S6. The 50% majority-rule consensus tree inferred from fast nuclear rate partitions using coalescent methods (STAR and MP-EST). The nucleotide rate partitions were determined for 310 nuclear genes using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Bootstrap percentages from OV_MP-EST /OV_STAR/TIGER_MP-EST /TIGER_STAR are indicated above each branch.

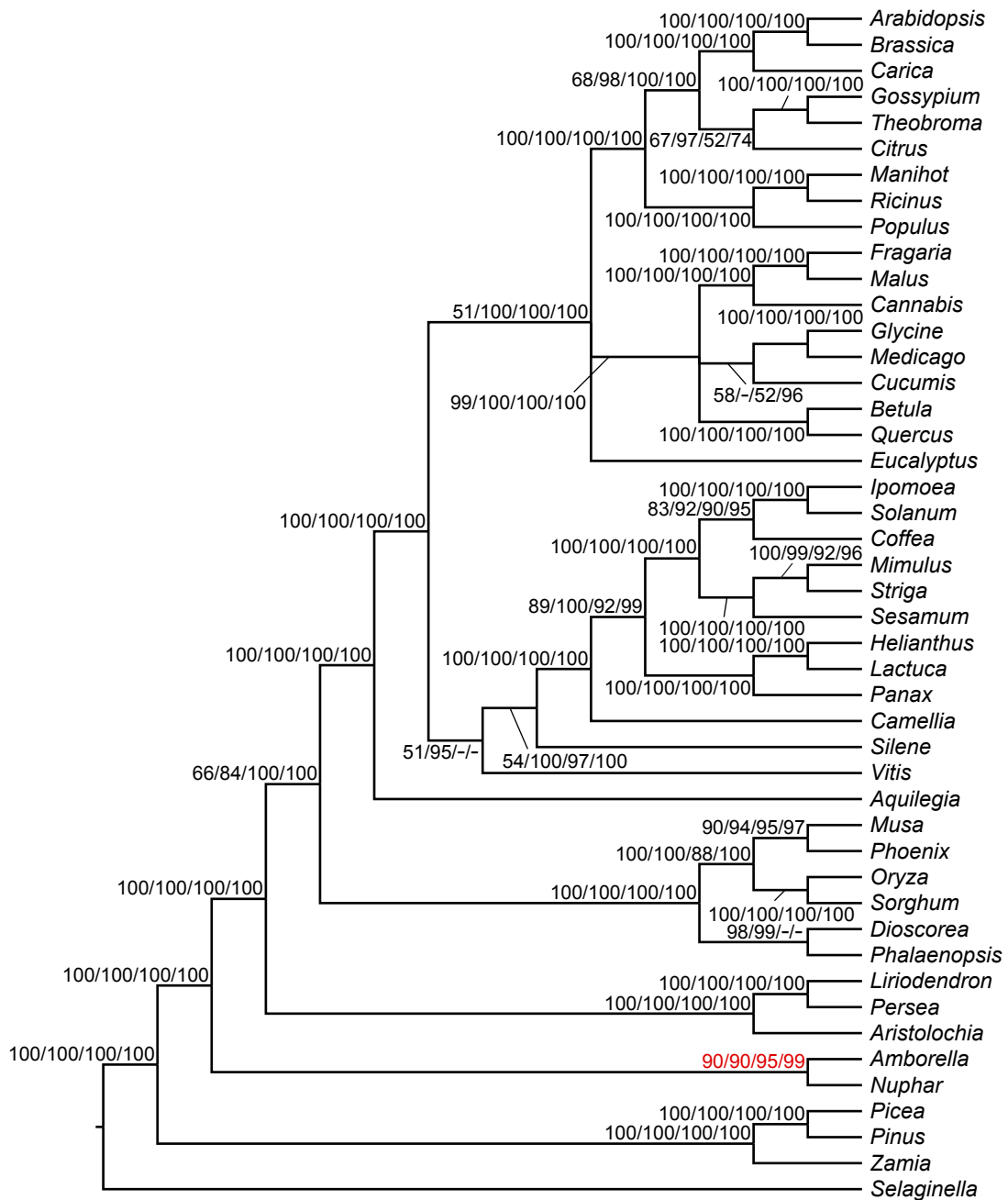


Figure S7. The 50% majority-rule consensus tree inferred from slow nuclear rate partitions using concatenation methods (RAxML and nhPhyML). The nucleotide rate partitions were determined for 310 nuclear genes using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Bootstrap percentages from OV_RAxML /OV_nhPhyML /TIGER_RAxML /TIGER_nhPhyML are indicated above each branch.

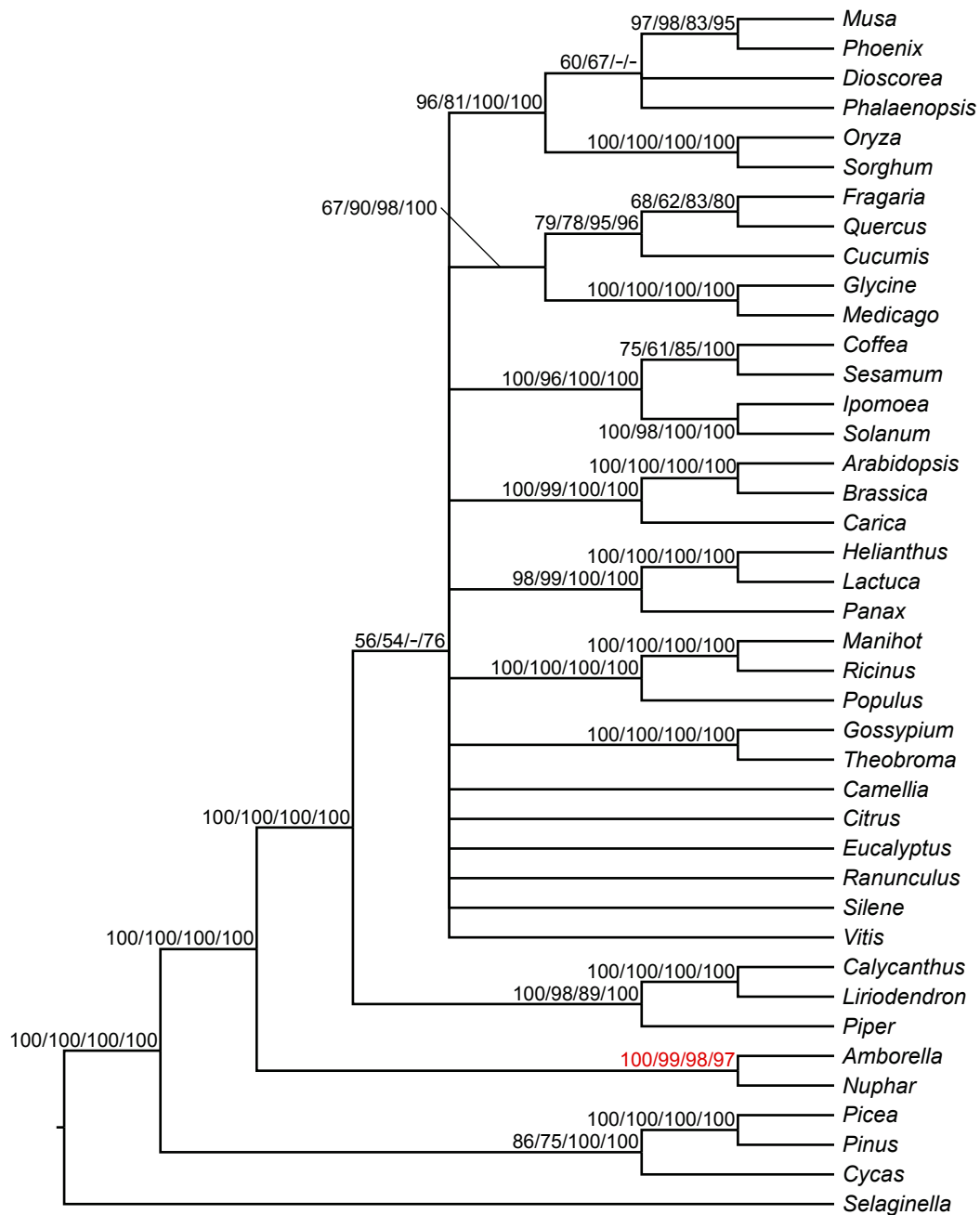


Figure S8. The 50% majority-rule consensus tree inferred from slow plastid rate partitions using concatenation methods (RAxML and nhPhyML). The nucleotide rate partitions were determined for 45 plastid genes using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Bootstrap percentages from OV_RAxML /OV_nhPhyML /TIGER_RAxML /TIGER_nhPhyML are indicated above each branch.

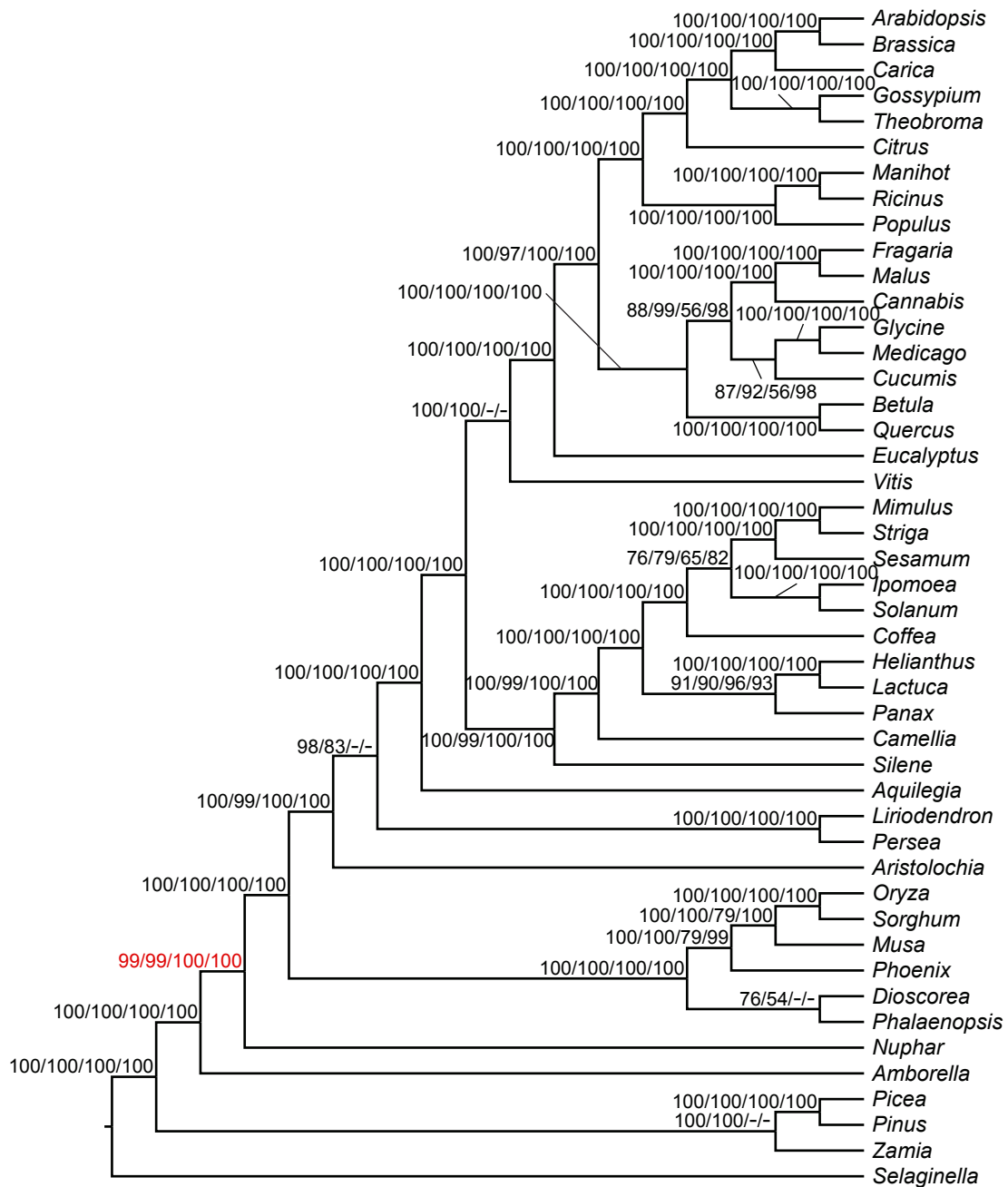


Figure S9. The 50% majority-rule consensus tree inferred from fast nuclear rate partitions using concatenation methods (RAxML and nhPhyML). The nucleotide rate partitions were determined for 310 nuclear genes using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Bootstrap percentages from OV_RAxML /OV_nhPhyML /TIGER_RAxML /TIGER_nhPhyML are indicated above each branch.

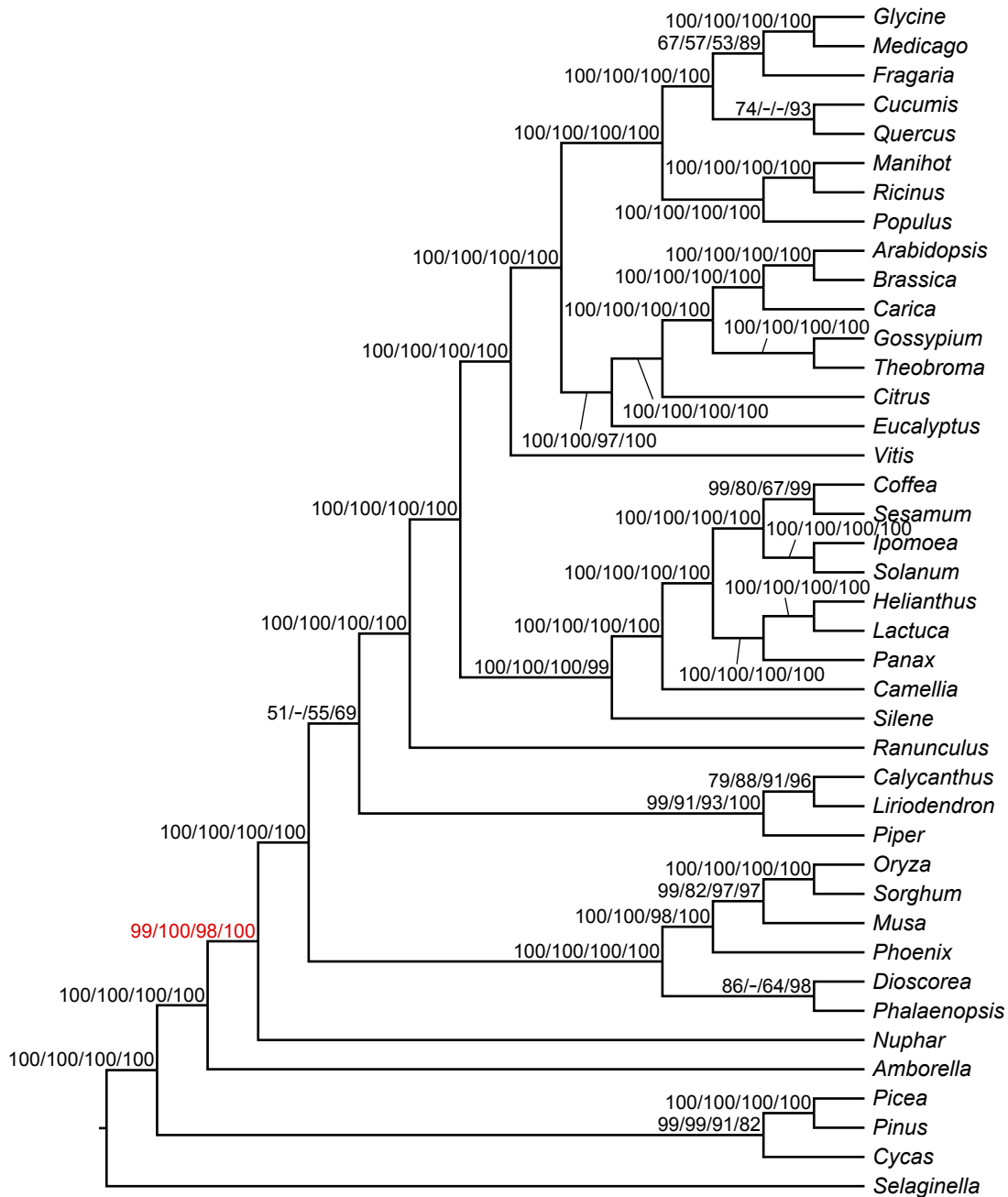


Figure S10. The 50% majority-rule consensus tree inferred from fast plastid rate partitions using concatenation methods (RAxML and nhPhyML). The nucleotide rate partitions were determined for 45 plastid genes using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Bootstrap percentages from OV_RAxML /OV_nhPhyML /TIGER_RAxML /TIGER_nhPhyML are indicated above each branch.

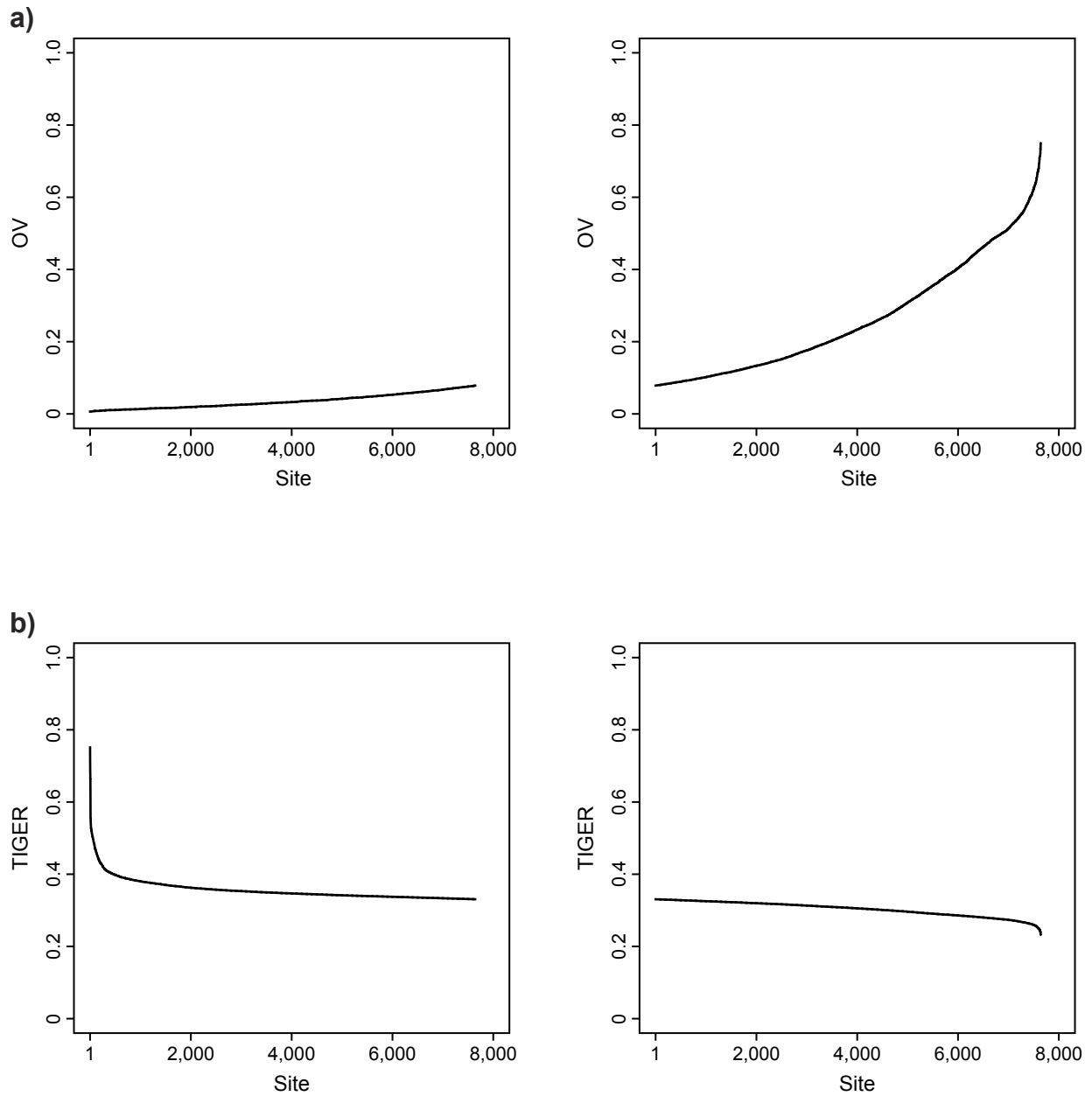


Figure S11. The estimated evolutionary rates for nucleotide sites in the concatenated 17-gene matrix. Parsimony informative sites in the concatenated matrix were sorted based on the Observed Variability (OV) method (a) or the Tree Independent Generation of Evolutionary Rates (TIGER) method (b), and subsequently divided into two equal partitions.

Table S1. Data sources and characteristics of nuclear gene sequences included in our phylogenetic analyses. The nucleotide rate partitions were determined using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Species with coding sequences acquired from whole-genome sequencing projects are highlighted in bold, and species with the lowest and highest GC-contents are highlighted with underlines.

Species	Sources	No. of unigenes included in clustering	No. of genes included in phylogenetic analyses	GC% of all sites	GC% of OV- <i>slow</i> sites	GC% of OV- <i>fast</i> sites	GC% of TIGER- <i>slow</i> sites	GC% of TIGER- <i>fast</i> sites
<i>Amborella trichopoda</i>	[1]	32,987	310	45.3%	46.7%	44.2%	47.0%	44.0%
<i>Aquilegia coerulea</i>	[2]	38,071	272	<u>41.9%</u>	<u>44.0%</u>	<u>35.8%</u>	<u>43.8%</u>	<u>36.3%</u>
<i>Arabidopsis thaliana</i>	[3]	32,768	275	44.9%	46.7%	43.0%	46.9%	42.8%
<i>Aristolochia fimbriata</i>	[1]	22,453	209	46.2%	47.8%	46.5%	48.4%	46.1%
<i>Betula platyphylla</i>	[4]	18,143	159	46.4%	47.2%	48.7%	48.7%	47.2%
<i>Brassica rapa</i>	[2]	37,125	260	47.6%	49.5%	49.4%	50.3%	48.7%
<i>Camellia sinensis</i>	[4]	23,226	90	45.9%	46.9%	46.3%	47.3%	45.8%
<i>Cannabis sativa</i>	[5]	21,526	254	44.3%	45.9%	42.0%	46.3%	41.7%
<i>Carica papaya</i>	[6]	22,398	195	45.3%	46.8%	44.4%	48.0%	43.5%
<i>Citrus sinensis</i>	[2]	43,568	258	45.1%	46.6%	43.9%	47.0%	43.5%
<i>Coffea arabica</i>	[4]	21,210	191	45.3%	46.9%	43.4%	47.8%	43.4%
<i>Cucumis sativus</i>	[2]	26,017	259	44.3%	46.1%	41.8%	46.8%	41.6%
<i>Dioscorea alata</i>	[4]	10,126	97	48.3%	50.2%	50.7%	50.9%	50.1%
<i>Eucalyptus grandis</i>	[2]	41,914	252	49.5%	50.2%	55.1%	51.5%	53.7%
<i>Fragaria vesca</i>	[7]	30,623	177	47.4%	48.1%	49.5%	49.8%	48.0%

<i>Glycine max</i>	[8]	66,967	297	45.8%	47.0%	45.8%	47.7%	45.2%
<i>Gossypium raimondii</i>	[9]	72,555	297	44.4%	46.0%	42.2%	46.4%	41.9%
<i>Helianthus annuus</i>	[4]	25,870	156	45.3%	46.7%	43.9%	47.5%	43.7%
<i>Ipomoea nil</i>	[4]	15,123	129	47.2%	48.8%	47.8%	50.2%	47.0%
<i>Lactuca serriola</i>	[4]	33,756	276	43.2%	44.2%	39.9%	45.0%	39.4%
<i>Liriodendron tulipifera</i>	[1]	27,541	237	47.9%	49.5%	50.7%	50.4%	49.8%
<i>Malus × domestica</i>	[10]	56,646	191	47.9%	49.5%	50.5%	50.7%	49.3%
<i>Manihot esculenta</i>	[11]	32,032	278	44.3%	46.0%	41.9%	46.4%	41.6%
<i>Medicago truncatula</i>	[12]	33,682	209	43.3%	45.4%	39.0%	45.5%	38.9%
<i>Mimulus guttatus</i>	[2]	26,612	274	46.6%	47.9%	47.5%	48.5%	47.0%
<i>Musa acuminata</i>	[13]	30,451	259	48.5%	49.5%	52.7%	51.1%	51.0%
<i>Nuphar advena</i>	[1]	68,266	310	47.2%	48.4%	49.1%	49.4%	48.1%
<i>Oryza sativa</i>	[14]	44,631	279	52.8%	55.1%	61.1%	56.0%	60.1%
<i>Panax ginseng</i>	[4]	10,446	96	45.0%	46.4%	43.2%	47.2%	42.6%
<i>Persea americana</i>	[15]	49,403	258	46.0%	47.2%	46.3%	48.2%	45.4%
<i>Phalaenopsis aphrodite</i>	[4]	12,873	179	46.7%	48.0%	47.9%	48.6%	47.4%
<i>Phoenix dactylifera</i>	[16]	27,374	98	47.3%	48.4%	50.4%	50.1%	48.6%
<i>Picea glauca</i>	[4]	23,693	269	44.5%	45.7%	42.3%	46.8%	41.5%
<i>Pinus taeda</i>	[4]	28,670	235	44.6%	46.2%	42.5%	47.1%	41.6%
<i>Populus trichocarpa</i>	[17]	67,249	294	44.1%	45.8%	41.4%	46.1%	41.1%
<i>Quercus robur</i>	[4]	15,432	143	46.0%	48.3%	45.5%	49.3%	45.1%
<i>Ricinus communis</i>	[18]	26,063	254	43.5%	45.7%	39.3%	45.7%	39.4%
<i>Selaginella moellendorffii</i>	[19]	21,043	310	<u>53.7%</u>	<u>56.8%</u>	<u>61.9%</u>	<u>56.8%</u>	<u>61.8%</u>
<i>Sesamum indicum</i>	[4]	20,162	171	45.7%	47.3%	45.6%	48.1%	44.9%
<i>Silene latifolia</i>	[4]	18,502	189	44.2%	46.2%	41.3%	46.5%	41.3%
<i>Solanum lycopersicum</i>	[20]	29,007	285	43.4%	45.4%	39.4%	45.6%	39.2%

<i>Sorghum bicolor</i>	[21]	28,211	279	52.7%	55.0%	60.8%	56.0%	59.8%
<i>Striga hermonthica</i>	[4]	14,002	113	48.4%	50.1%	51.6%	50.5%	51.2%
<i>Theobroma cacao</i>	[22]	40,514	287	44.7%	46.3%	42.9%	46.9%	42.4%
<i>Vitis vinifera</i>	[23]	22,014	228	45.3%	46.3%	45.5%	47.5%	44.4%
<i>Zamia vazquezii</i>	[1]	11,104	149	44.9%	46.3%	43.8%	47.3%	43.0%

Reference

- Jiao, Y., Wickett, N.J., Ayyampalayam, S., Chanderbali, A.S., Landherr, L., Ralph, P.E., Tomsho, L.P., Hu, Y., Liang, H., Soltis, P.S., et al. (2011). Ancestral polyploidy in seed plants and angiosperms. *Nature* 473, 97-100.
- Goodstein, D.M., Shu, S.Q., Howson, R., Neupane, R., Hayes, R.D., Fazo, J., Mitros, T., Dirks, W., Hellsten, U., Putnam, N., et al. (2012). Phytozome: a comparative platform for green plant genomics. *Nucleic Acids Res.* 40, D1178-D1186.
- Kaul, S., Koo, H.L., Jenkins, J., Rizzo, M., Rooney, T., Tallon, L.J., Feldblyum, T., Nierman, W., Benito, M.I., Lin, X.Y., et al. (2000). Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* 408, 796-815.
- Duvick, J., Fu, A., Muppirala, U., Sabharwal, M., Wilkerson, M.D., Lawrence, C.J., Lushbough, C., and Brendel, V. (2008). PlantGDB: a resource for comparative plant genomics. *Nucleic Acids Res.* 36, D959-D965.
- van Bakel, H., Stout, J.M., Cote, A.G., Tallon, C.M., Sharpe, A.G., Hughes, T.R., and Page, J.E. (2011). The draft genome and transcriptome of *Cannabis sativa*. *Genome Biol.* 12, R102.
- Ming, R., Hou, S., Feng, Y., Yu, Q., Dionne-Laporte, A., Saw, J.H., Senin, P., Wang, W., Ly, B.V., Lewis, K.L.T., et al. (2008). The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus). *Nature* 452, 991-996.
- Shulaev, V., Sargent, D.J., Crowhurst, R.N., Mockler, T.C., Folkerts, O., Delcher, A.L., Jaiswal, P., Mockaitis, K., Liston, A., Mane, S.P., et al. (2011). The genome of woodland strawberry (*Fragaria vesca*). *Nat. Genet.* 43, 109-116.
- Schmutz, J., Cannon, S.B., Schlueter, J., Ma, J.X., Mitros, T., Nelson, W., Hyten, D.L., Song, Q.J., Thelen, J.J., Cheng, J.L., et al. (2010). Genome sequence of the palaeopolyploid soybean. *Nature* 463, 178-183.
- Paterson, A.H., Wendel, J.F., Gundlach, H., Guo, H., Jenkins, J., Jin, D.C., Llewellyn, D., Showmaker, K.C., Shu, S.Q., Udall, J., et al. (2012). Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres. *Nature* 492, 423-427.
- Velasco, R., Zharkikh, A., Affourtit, J., Dhingra, A., Cestaro, A., Kalyanaraman, A., Fontana, P., Bhatnagar, S.K., Troggio, M., Pruss, D., et al. (2010). The genome of the domesticated apple (*Malus × domestica* Borkh.). *Nat. Genet.* 42, 833-839.
- Prochnik, S., Marri, P., Desany, B., Rabinowicz, P., Kodira, C., Mohiuddin, M., Rodriguez, F., Fauquet, C., Tohme, J., Harkins, T., et al. (2012). The cassava genome: current progress, future directions. *Trop. Plant Biol.* 5, 88-94.

12. Young, N.D., Debelle, F., Oldroyd, G.E.D., Geurts, R., Cannon, S.B., Udvardi, M.K., Benedito, V.A., Mayer, K.F.X., Gouzy, J., Schoof, H., et al. (2011). The *Medicago* genome provides insight into the evolution of rhizobial symbioses. *Nature* 480, 520-524.
13. D'Hont, A., Denoeud, F., Aury, J.-M., Baurens, F.-C., Carreel, F., Garsmeur, O., Noel, B., Bocs, S., Droc, G., Rouard, M., et al. (2012). The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature* 488, 213-217.
14. Ouyang, S., Zhu, W., Hamilton, J., Lin, H., Campbell, M., Childs, K., Thibaud-Nissen, F., Malek, R.L., Lee, Y., Zheng, L., et al. (2007). The TIGR Rice Genome Annotation Resource: improvements and new features. *Nucleic Acids Res.* 35, D883-D887.
15. Jiao, Y., Leebens-Mack, J., Ayyampalayam, S., Bowers, J., McKain, M., McNeal, J., Rolf, M., Ruzicka, D., Wafula, E., Wickett, N., et al. (2012). A genome triplication associated with early diversification of the core eudicots. *Genome Biol.* 13, R3.
16. Al-Dous, E.K., George, B., Al-Mahmoud, M.E., Al-Jaber, M.Y., Wang, H., Salameh, Y.M., Al-Azwani, E.K., Chaluvadi, S., Pontaroli, A.C., DeBarry, J., et al. (2011). *De novo* genome sequencing and comparative genomics of date palm (*Phoenix dactylifera*). *Nat. Biotechnol.* 29, 521-527.
17. Tuskan, G.A., DiFazio, S., Jansson, S., Bohlmann, J., Grigoriev, I., Hellsten, U., Putnam, N., Ralph, S., Rombauts, S., Salamov, A., et al. (2006). The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 313, 1596-1604.
18. Chan, A.P., Crabtree, J., Zhao, Q., Lorenzi, H., Orvis, J., Puiu, D., Melake-Berhan, A., Jones, K.M., Redman, J., Chen, G., et al. (2010). Draft genome sequence of the oilseed species *Ricinus communis*. *Nat. Biotechnol.* 28, 951-956.
19. Banks, J.A., Nishiyama, T., Hasebe, M., Bowman, J.L., Gribskov, M., dePamphilis, C., Albert, V.A., Aono, N., Aoyama, T., Ambrose, B.A., et al. (2011). The Selaginella genome identifies genetic changes associated with the evolution of vascular plants. *Science* 332, 960-963.
20. Sato, S., Tabata, S., Hirakawa, H., Asamizu, E., Shirasawa, K., Isobe, S., Kaneko, T., Nakamura, Y., Shibata, D., Aoki, K., et al. (2012). The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485, 635-641.
21. Paterson, A.H., Bowers, J.E., Bruggmann, R., Dubchak, I., Grimwood, J., Gundlach, H., Haberler, G., Hellsten, U., Mitros, T., Poliakov, A., et al. (2009). The *Sorghum bicolor* genome and the diversification of grasses. *Nature* 457, 551-556.
22. Argout, X., Salse, J., Aury, J.M., Guiltinan, M.J., Droc, G., Gouzy, J., Allegre, M., Chaparro, C., Legavre, T., Maximova, S.N., et al. (2011). The genome of *Theobroma cacao*. *Nat. Genet.* 43, 101-108.
23. Jaillon, O., Aury, J.M., Noel, B., Policriti, A., Clepet, C., Casagrande, A., Choisne, N., Aubourg, S., Vitulo, N., Jubin, C., et al. (2007). The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature* 449, 463-467.

Table S2. Data sources and characteristics of plastid gene sequences included in our phylogenetic analyses. The nucleotide rate partitions were determined using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. Species with the lowest and highest GC-contents are highlighted with underlines.

Species	GenBank accession number	No. of genes included in phylogenetic analyses	GC% of all sites	GC% of OV- <i>slow</i> sites	GC% of OV- <i>fast</i> sites	GC% of TIGER- <i>slow</i> sites	GC% of TIGER- <i>fast</i> sites
<i>Amborella trichopoda</i>	NC_005086	45	39.8%	33.2%	51.4%	34.6%	50.0%
<i>Arabidopsis thaliana</i>	NC_000932	45	38.0%	32.4%	43.7%	33.3%	42.7%
<i>Brassica rapa</i>	NC_016734	45	38.1%	32.5%	43.7%	33.4%	42.8%
<i>Calycanthus floridus</i>	NC_004993	45	40.1%	31.9%	54.7%	33.5%	53.1%
<i>Camellia sinensis</i>	NC_020019	45	38.5%	30.5%	48.0%	32.0%	46.5%
<i>Carica papaya</i>	NC_010323	45	38.9%	31.7%	48.8%	32.7%	47.7%
<i>Citrus sinensis</i>	NC_008334	43	39.8%	33.6%	51.0%	34.9%	49.6%
<i>Coffea arabica</i>	NC_008535	45	38.7%	31.5%	47.9%	33.1%	46.3%
<i>Cucumis sativus</i>	NC_007144	45	38.6%	31.5%	47.0%	32.9%	45.7%
<i>Cycas taitungensis</i>	NC_009618	43	40.5%	39.1%	42.4%	40.6%	41.0%
<i>Dioscorea elephantipes</i>	NC_009601	45	38.5%	31.2%	47.1%	31.8%	46.5%
<i>Eucalyptus grandis</i>	NC_014570	40	38.7%	31.0%	47.6%	31.7%	46.8%
<i>Fragaria vesca</i>	NC_015206	45	39.1%	32.3%	48.7%	33.2%	47.7%
<i>Glycine max</i>	NC_007942	43	<u>37.2%</u>	30.5%	<u>41.3%</u>	31.1%	<u>40.6%</u>
<i>Gossypium raimondii</i>	NC_016668	44	39.3%	32.4%	50.1%	33.5%	49.0%
<i>Helianthus annuus</i>	NC_007977	45	38.8%	31.7%	48.5%	32.8%	47.4%
<i>Ipomoea purpurea</i>	NC_009808	45	39.3%	32.6%	49.0%	33.6%	48.0%

<i>Lactuca sativa</i>	NC_007578	44	38.7%	31.5%	48.5%	32.8%	47.2%
<i>Liriodendron tulipifera</i>	NC_008326	44	39.9%	31.1%	<u>54.9%</u>	32.3%	<u>53.6%</u>
<i>Manihot esculenta</i>	NC_010433	45	38.4%	30.9%	47.3%	31.9%	46.4%
<i>Medicago truncatula</i>	NC_003119	42	37.5%	<u>29.1%</u>	42.0%	<u>31.0%</u>	40.7%
<i>Musa acuminata</i>	EU016983–EU017063	45	38.9%	31.3%	48.9%	32.4%	47.8%
<i>Nuphar advena</i>	NC_008788	45	40.1%	33.9%	52.8%	35.3%	51.4%
<i>Oryza sativa</i>	NC_001320	44	39.7%	33.4%	48.0%	35.5%	46.5%
<i>Panax ginseng</i>	NC_006290	45	39.3%	31.4%	50.9%	33.0%	49.3%
<i>Phalaenopsis aphrodite</i>	NC_007499	35	39.1%	33.2%	46.3%	33.3%	46.5%
<i>Phoenix dactylifera</i>	NC_013991	45	38.8%	30.8%	49.3%	31.9%	48.2%
<i>Picea morrissonicola</i>	NC_016069	32	40.8%	41.0%	43.1%	42.2%	41.8%
<i>Pinus koraiensis</i>	NC_004677	33	40.6%	40.5%	42.5%	41.7%	41.3%
<i>Piper cenocladum</i>	NC_008457	45	39.6%	33.8%	50.0%	34.4%	49.4%
<i>Populus trichocarpa</i>	NC_009143	45	38.6%	31.3%	47.5%	32.1%	46.7%
<i>Quercus rubra</i>	NC_020152	45	39.0%	31.8%	48.9%	32.8%	47.9%
<i>Ranunculus macranthus</i>	NC_008796	45	39.2%	32.2%	49.1%	33.2%	48.1%
<i>Ricinus communis</i>	NC_016736	44	38.5%	31.7%	47.0%	32.8%	45.9%
<i>Selaginella moellendorffii</i>	NC_013086	44	<u>50.8%</u>	<u>53.6%</u>	51.3%	<u>52.1%</u>	52.8%
<i>Sesamum indicum</i>	NC_016433	45	39.1%	31.5%	49.6%	33.1%	48.1%
<i>Silene latifolia</i>	NC_016730	45	38.4%	32.5%	44.7%	33.4%	43.8%
<i>Solanum lycopersicum</i>	NC_007898	45	39.2%	32.1%	49.7%	33.4%	48.5%
<i>Sorghum bicolor</i>	NC_008602	44	39.4%	33.2%	47.3%	35.2%	45.9%
<i>Theobroma cacao</i>	NC_014676	44	38.9%	31.7%	49.5%	32.7%	48.4%
<i>Vitis vinifera</i>	NC_007957	45	38.9%	31.0%	49.7%	32.1%	48.6%

Table S3. Data characteristics for each of the 310 nuclear genes, including the locus ID of *Selaginella moellendorffii* sequence in each gene, the locus ID of *Arabidopsis thaliana* sequence in each gene (if presents), number of species per gene, number of nucleotide sites per gene, and percentage of gaps per gene.

Genes	<i>Selaginella</i> ID	<i>Arabidopsis</i> ID	No. of species	No. of sites	Gaps%
Cluster1436	441012	AT1G79590.2	37	687	0.5%
Cluster1508	403773	-	37	921	0.1%
Cluster1544	268311	-	26	1050	0.2%
Cluster1669	158309	AT4G27690.1	29	891	0.9%
Cluster1716	115313	AT1G18070.1	28	1503	1.3%
Cluster1744	270531	-	30	561	0.0%
Cluster1757	231593	AT3G56190.1	36	864	0.4%
Cluster1808	76404	-	30	426	0.7%
Cluster1809	420519	-	30	765	0.8%
Cluster1818	145865	AT5G66510.1	33	810	1.5%
Cluster1857	109700	AT5G14030.1	37	585	2.4%
Cluster1883	149251	-	31	789	1.0%
Cluster1985	231474	-	28	684	1.7%
Cluster2026	167618	AT2G37940.1	31	942	1.1%
Cluster2039	270833	AT3G47810.2	37	555	0.4%
Cluster2123	141259	AT5G02040.2	37	624	0.5%
Cluster2124	89663	AT5G13710.2	31	1035	0.6%
Cluster2135	78115	-	37	882	0.2%
Cluster2187	269383	-	33	972	0.1%
Cluster2188	151778	AT1G15470.1	31	1026	1.6%
Cluster2196	146763	AT3G12800.1	35	888	0.4%
Cluster2239	84888	AT2G39970.1	35	957	0.9%
Cluster2246	233612	-	33	1059	0.7%
Cluster2280	266778	-	33	1155	1.2%
Cluster2317	271043	AT3G02720.1	32	1149	0.4%
Cluster2399	178739	AT1G11680.1	35	1431	0.5%
Cluster2403	267769	AT5G64250.2	37	963	1.0%
Cluster2421	270930	AT2G27020.1	40	687	0.0%
Cluster2427	179125	AT3G60880.2	33	1092	2.7%
Cluster2445	423144	AT3G54890.1	38	732	1.3%
Cluster2455	171051	AT4G25630.1	27	795	0.8%
Cluster2461	74817	-	30	1011	1.4%
Cluster2508	160411	AT1G61520.3	38	786	0.6%
Cluster2556	166040	AT1G30630.1	38	852	0.6%
Cluster2565	172686	-	26	1392	0.0%
Cluster2572	73428	AT4G04640.1	22	1122	1.4%
Cluster2573	90697	AT2G38960.1	22	1350	2.8%
Cluster2606	403082	AT3G20000.1	35	921	0.2%
Cluster2607	139849	AT3G02780.1	27	699	0.1%
Cluster2626	82341	AT2G04690.1	30	570	0.4%
Cluster2634	96969	AT1G12050.1	34	1248	0.5%
Cluster2653	88464	-	33	411	2.5%
Cluster2673	231325	AT1G65650.1	37	981	1.2%
Cluster2703	163805	AT3G27280.1	36	834	0.5%
Cluster2733	178059	AT4G12790.2	36	798	2.3%
Cluster2742	164521	AT2G31350.1	35	912	1.7%
Cluster2743	90623	AT3G51840.1	32	1230	0.8%
Cluster2769	173172	AT5G46630.2	37	1308	2.1%
Cluster2803	268105	-	31	669	0.0%
Cluster2814	183263	AT1G28490.1	30	705	0.7%
Cluster2825	234811	AT3G05710.2	32	933	0.7%
Cluster2842	154330	AT1G64520.1	44	795	0.7%
Cluster2855	88496	AT3G59990.3	27	1311	4.8%

Cluster2865	177367	AT3G27740.1	35	1260	2.4%
Cluster2868	146417	AT1G09330.1	35	549	1.4%
Cluster2878	103272	AT3G07950.1	36	921	1.6%
Cluster2900	90273	AT5G04850.1	38	708	1.4%
Cluster2918	124123	AT3G09350.1	36	1068	0.8%
Cluster2943	161472	AT5G57655.2	26	1431	0.4%
Cluster2950	405873	AT5G40670.1	35	822	2.3%
Cluster2958	443337	-	32	744	0.7%
Cluster2984	166088	AT4G03280.1	37	678	0.7%
Cluster2985	82841	-	29	957	0.2%
Cluster3010	133041	AT5G08160.1	31	1005	0.2%
Cluster3035	444262	AT1G50670.1	36	621	0.0%
Cluster3040	165154	AT4G05530.1	38	756	0.3%
Cluster3049	139450	AT3G57340.2	31	1116	4.0%
Cluster3054	438632	AT3G56130.1	33	654	5.0%
Cluster3071	106498	-	27	687	1.5%
Cluster3078	167575	AT5G14250.1	31	1251	1.1%
Cluster3082	75154	AT5G22950.1	30	681	0.5%
Cluster3120	266613	AT3G10230.1	28	1512	2.9%
Cluster3122	140411	AT3G56740.1	34	876	0.7%
Cluster3126	437541	AT2G33340.2	33	1530	0.3%
Cluster3134	145221	AT5G12210.2	28	939	0.6%
Cluster3150	181288	AT1G09870.1	32	1386	0.9%
Cluster3160	141330	AT4G24550.2	30	1350	1.1%
Cluster3172	269010	AT5G01990.1	29	1227	0.8%
Cluster3177	227548	AT3G13230.1	34	669	1.8%
Cluster3208	166200	AT3G01850.1	35	633	0.6%
Cluster3212	231938	AT5G11500.1	35	633	0.0%
Cluster3215	173359	AT1G01910.4	33	1050	0.7%
Cluster3239	153526	AT1G10840.1	38	987	0.7%
Cluster3261	157954	AT3G05280.1	40	825	1.6%
Cluster3270	444756	AT3G03160.1	35	390	0.1%
Cluster3279	104803	AT1G21870.1	36	1020	2.0%
Cluster3282	232038	AT2G18040.1	28	354	0.6%
Cluster3308	158876	AT5G42790.1	37	768	0.6%
Cluster3309	110005	AT2G32080.1	35	822	1.0%
Cluster3315	73440	AT1G22920.1	26	1056	0.2%
Cluster3317	123489	AT1G13910.1	29	948	0.6%
Cluster3320	268686	AT3G22845.1	39	603	0.1%
Cluster3334	154248	AT1G80360.1	37	1170	2.0%
Cluster3337	155397	-	21	552	0.4%
Cluster3339	146440	AT3G14080.1	33	375	0.0%
Cluster3350	167542	AT1G74210.1	25	1140	1.2%
Cluster3361	73696	AT4G02620.1	35	387	0.6%
Cluster3368	268792	-	32	774	1.2%
Cluster3371	143805	-	30	864	0.7%
Cluster3380	167610	-	35	888	0.7%
Cluster3382	97708	AT5G64000.1	26	1161	7.4%
Cluster3414	140847	AT1G77750.1	34	429	5.6%
Cluster3451	229314	AT2G38710.1	40	624	1.9%
Cluster3454	109399	AT3G62600.1	34	1029	1.4%
Cluster3463	120943	AT2G14110.1	29	489	0.1%
Cluster3466	99026	AT3G07090.1	33	720	0.6%
Cluster3470	431378	AT3G22290.1	33	1008	1.3%
Cluster3509	65451	-	28	1116	3.4%
Cluster3520	411677	AT4G38570.1	35	672	0.9%
Cluster3566	154794	AT4G33250.1	41	660	1.0%
Cluster3573	418702	AT3G50960.1	32	681	0.7%
Cluster3583	146325	AT3G02590.1	35	792	0.2%
Cluster3618	185086	AT5G64350.1	41	333	0.1%
Cluster3619	438896	AT3G13200.1	38	681	0.5%
Cluster3626	87975	AT2G05830.1	30	1065	0.8%
Cluster3643	234665	AT5G02280.1	42	417	0.2%
Cluster3676	118760	AT4G20410.1	37	807	0.8%
Cluster3682	270288	AT1G30070.2	39	651	1.1%

Cluster3719	76878	AT1G53580.2	28	720	0.3%
Cluster3722	230609	AT2G34470.2	38	786	0.8%
Cluster3725	81847	-	30	735	0.3%
Cluster3777	107381	-	19	501	0.9%
Cluster3783	97230	AT5G61500.1	32	936	0.8%
Cluster3805	90000	AT1G66740.1	32	534	1.0%
Cluster3809	141745	AT4G32175.1	38	681	0.4%
Cluster3810	77840	AT3G21640.1	33	1095	2.1%
Cluster3820	266600	AT4G01320.1	35	1245	0.5%
Cluster3826	236819	AT5G15750.1	40	543	0.6%
Cluster3856	439290	AT5G27830.4	37	699	3.3%
Cluster3873	76414	AT5G52210.2	37	609	1.1%
Cluster3876	148310	AT1G12410.1	37	804	0.6%
Cluster3881	442455	AT5G12190.1	43	363	0.7%
Cluster3886	173060	AT5G48630.1	31	735	1.2%
Cluster3912	148966	AT4G30260.1	33	822	2.0%
Cluster3946	123078	AT1G21690.1	37	996	0.4%
Cluster3959	171147	AT5G49510.2	37	570	2.2%
Cluster3974	123928	AT3G10670.1	34	894	2.4%
Cluster4085	115580	AT2G26060.1	34	1047	1.6%
Cluster4088	235312	AT5G14800.1	39	795	0.1%
Cluster4095	235070	AT5G50960.1	29	1008	0.9%
Cluster4105	228154	AT3G07760.2	39	372	0.3%
Cluster4188	78109	AT3G06060.1	29	939	0.6%
Cluster4191	73689	AT3G23620.1	35	936	0.4%
Cluster4200	413610	AT5G16800.2	27	759	0.9%
Cluster4212	168418	AT3G05000.1	39	522	0.8%
Cluster4216	91736	-	32	423	2.3%
Cluster4219	73953	AT5G55940.1	35	609	0.6%
Cluster4235	66840	AT3G15460.1	33	915	1.2%
Cluster4242	75169	AT5G60340.1	38	498	0.4%
Cluster4246	150177	AT3G51140.1	27	843	3.2%
Cluster4276	144908	AT5G09920.1	40	411	0.6%
Cluster4302	55512	AT5G35460.1	26	1134	4.6%
Cluster4324	110731	AT1G51160.2	41	504	1.2%
Cluster4331	98270	AT1G20575.1	34	714	0.2%
Cluster4344	430064	AT3G57280.1	28	657	4.0%
Cluster4363	406072	AT3G16565.2	32	696	0.6%
Cluster4384	49133	AT3G23490.1	37	450	0.3%
Cluster4396	270168	AT5G11770.1	30	636	2.7%
Cluster4414	79490	AT4G06599.1	34	981	0.6%
Cluster4473	141946	AT2G28900.1	33	438	0.1%
Cluster4486	91405	AT1G03900.1	37	774	0.4%
Cluster4514	177574	AT3G25920.1	36	714	0.5%
Cluster4562	271067	AT5G52980.1	32	609	1.1%
Cluster4577	270804	AT2G19940.1	32	1104	0.5%
Cluster4580	102449	AT4G09070.1	39	645	1.0%
Cluster4643	100915	-	31	438	0.1%
Cluster4649	175633	AT3G22660.1	32	864	2.9%
Cluster4682	86206	AT1G08490.1	19	1314	0.4%
Cluster4712	170435	AT5G51020.1	38	780	1.6%
Cluster4717	155351	AT2G41250.1	23	861	6.9%
Cluster4740	267328	AT1G77290.2	31	789	0.0%
Cluster4745	148698	-	34	747	0.4%
Cluster4772	99428	AT2G14260.1	30	1131	3.2%
Cluster4779	271344	-	36	516	0.4%
Cluster4785	91805	AT2G19560.1	30	1230	1.1%
Cluster4791	169883	-	37	681	0.2%
Cluster4795	177094	AT1G14360.1	37	981	0.5%
Cluster4828	113878	AT2G19790.1	39	423	1.3%
Cluster4840	177496	AT3G12050.1	35	1035	1.5%
Cluster4886	233015	AT4G24440.2	36	315	0.1%
Cluster4893	142363	AT1G33490.1	33	531	1.5%
Cluster4916	110629	AT3G11945.1	25	1155	3.4%
Cluster4942	160384	AT4G36530.2	36	1104	2.7%

Cluster4945	139300	AT4G06676.1	26	744	0.3%
Cluster4963	106159	AT1G02680.1	34	378	0.7%
Cluster4970	167838	AT5G44730.1	36	741	0.2%
Cluster4999	80529	AT4G27490.1	37	729	0.2%
Cluster5016	438442	AT2G25280.1	37	870	0.1%
Cluster5034	75337	AT2G15400.1	38	954	1.4%
Cluster5055	79269	AT5G14600.1	29	930	1.9%
Cluster5181	227629	-	28	825	0.5%
Cluster5183	85922	AT1G72175.1	38	543	1.4%
Cluster5212	165081	AT5G60540.1	35	747	1.9%
Cluster5228	130333	AT2G19350.1	40	306	0.2%
Cluster5246	49683	AT4G34700.1	38	327	0.2%
Cluster5287	74617	AT3G12030.1	37	543	0.4%
Cluster5309	84283	AT2G36300.1	31	711	0.5%
Cluster5327	74672	AT1G29990.1	36	387	0.4%
Cluster5360	403066	AT2G26540.1	26	891	2.9%
Cluster5378	269334	AT2G27450.1	40	870	1.5%
Cluster5419	71455	AT5G03080.1	38	609	1.5%
Cluster5452	227238	AT3G28140.1	31	546	0.7%
Cluster5456	403901	AT4G19003.2	36	531	0.6%
Cluster5460	85283	AT5G39250.1	39	729	1.0%
Cluster5461	232741	AT4G16265.1	36	312	0.0%
Cluster5470	438712	AT1G78190.1	42	366	0.3%
Cluster5495	76023	AT5G63440.2	34	663	0.1%
Cluster5520	6403	AT5G11340.1	40	489	1.1%
Cluster5528	228033	AT5G19590.1	30	330	2.0%
Cluster5536	98142	AT3G16190.1	33	546	0.5%
Cluster5541	82731	AT1G25682.1	33	885	0.4%
Cluster5545	101073	AT1G17890.3	32	918	0.3%
Cluster5564	270683	AT3G04780.1	34	522	0.2%
Cluster5567	270732	AT3G44890.1	38	555	1.8%
Cluster5568	403374	AT2G37330.1	35	756	0.5%
Cluster5580	54978	AT1G43580.1	34	1245	0.5%
Cluster5621	438744	AT3G02950.1	38	720	0.9%
Cluster5630	423950	AT5G66930.2	37	648	1.5%
Cluster5655	92343	AT2G39550.1	30	1008	0.5%
Cluster5663	410867	AT1G36980.1	37	405	0.1%
Cluster5664	105120	AT5G18070.1	29	1641	1.6%
Cluster5676	230282	AT4G30820.2	36	573	3.3%
Cluster5681	442381	AT4G27120.2	32	885	2.4%
Cluster5691	174737	AT4G27700.1	33	690	2.0%
Cluster5723	185060	AT4G07390.1	35	699	1.2%
Cluster5726	430901	AT2G43030.1	27	798	5.9%
Cluster5751	130493	AT3G09960.1	23	906	0.4%
Cluster5768	79688	AT5G50440.1	37	633	0.4%
Cluster5771	172574	AT1G64850.1	35	489	0.4%
Cluster5793	95614	AT5G01230.1	29	945	0.9%
Cluster5808	132775	AT5G42850.1	35	384	0.6%
Cluster5824	269565	AT4G37000.1	27	918	3.2%
Cluster5831	106195	AT5G43280.1	35	801	1.4%
Cluster5838	145922	AT1G63780.1	34	876	0.1%
Cluster5840	67460	AT4G27350.1	32	813	1.8%
Cluster5846	232928	AT4G16710.2	35	531	2.1%
Cluster5857	232025	AT4G31790.2	31	813	0.2%
Cluster5928	444080	AT5G12320.1	34	453	3.0%
Cluster5933	146341	AT3G10970.1	32	1077	1.1%
Cluster5936	79877	AT5G48180.1	34	918	0.7%
Cluster5939	271184	-	31	828	1.1%
Cluster5944	440387	AT1G05720.1	38	471	4.1%
Cluster5971	270181	AT1G28140.1	30	810	1.4%
Cluster5976	175887	AT5G38890.1	30	558	0.1%
Cluster5984	81108	AT3G51610.1	34	591	0.8%
Cluster6021	170924	AT5G64180.1	38	417	0.4%
Cluster6022	170698	AT2G21150.1	27	1002	2.0%
Cluster6025	423378	AT3G18790.1	33	876	1.0%

Cluster6042	57444	AT2G38270.1	33	888	3.6%
Cluster6073	109689	AT5G11680.1	38	603	1.1%
Cluster6087	49639	AT1G77350.1	38	360	0.8%
Cluster6115	77895	AT5G53310.1	31	666	2.8%
Cluster6127	119017	AT2G20930.1	35	414	0.4%
Cluster6154	73417	AT3G04880.1	31	852	0.4%
Cluster6158	78465	AT4G15770.1	37	561	1.1%
Cluster6223	182295	AT2G29020.1	40	375	0.7%
Cluster6228	410874	AT3G15090.1	30	1089	1.2%
Cluster6244	185868	AT3G63140.1	33	1188	1.8%
Cluster6255	227421	AT1G16740.1	40	372	1.7%
Cluster6268	159329	AT4G37200.1	32	768	3.6%
Cluster6282	232997	AT5G65000.1	31	972	1.7%
Cluster6289	440510	AT1G33810.1	42	411	1.3%
Cluster6291	145440	AT1G14810.1	32	1119	2.3%
Cluster6312	127479	AT4G29870.1	36	510	2.0%
Cluster6327	83318	AT2G34460.1	29	792	1.4%
Cluster6338	79311	AT5G64730.1	38	882	1.7%
Cluster6342	85659	AT5G57900.1	36	879	1.4%
Cluster6355	112137	AT2G07340.1	40	375	0.7%
Cluster6356	165272	AT1G04630.1	38	426	0.4%
Cluster6374	107348	AT1G05190.1	35	672	0.8%
Cluster6396	77174	AT5G21060.2	27	1119	0.9%
Cluster6519	150245	AT3G23400.1	28	786	1.4%
Cluster6589	142186	AT1G13690.1	36	492	0.4%
Cluster6606	127051	AT2G46890.1	35	906	0.5%
Cluster6635	440803	AT5G64160.1	34	483	2.1%
Cluster6664	235018	AT4G28830.1	35	615	1.1%
Cluster6695	409585	AT3G59390.2	27	783	1.0%
Cluster6733	270742	AT2G35450.1	28	1017	5.9%
Cluster6758	89039	AT1G29260.1	35	942	1.2%
Cluster6764	93986	AT3G18940.1	34	840	0.5%
Cluster6795	75622	AT4G38495.1	39	369	0.6%
Cluster6807	186360	AT4G27540.1	29	600	2.5%
Cluster6808	98666	AT2G26680.1	30	966	2.5%
Cluster6833	139765	AT3G24730.1	36	447	1.4%
Cluster6889	402197	AT3G52220.1	35	654	1.2%
Cluster6959	170430	AT5G03455.1	38	381	0.5%
Cluster6965	101071	AT4G16510.1	35	660	0.7%
Cluster6967	118824	AT5G65860.2	28	954	0.7%
Cluster6980	231365	AT5G23220.1	31	576	1.3%
Cluster7030	168321	AT5G37290.1	35	522	0.6%
Cluster7129	92107	AT3G16990.1	35	669	2.3%
Cluster7188	93003	AT3G09085.1	32	321	0.4%
Cluster7282	419577	AT2G19385.1	29	969	6.1%
Cluster7308	406972	AT5G17610.1	31	363	2.6%
Cluster7335	94581	AT1G10030.1	29	384	1.9%
Cluster7393	84379	-	27	363	1.2%
Cluster7458	79372	AT3G59520.1	28	813	1.1%
Cluster7488	418784	AT3G25545.1	31	660	4.9%
Cluster7499	412944	-	25	669	2.5%
Cluster7514	121160	AT1G47750.1	32	672	1.2%
Cluster7544	123418	AT1G14300.1	29	987	0.5%
Cluster7557	37399	AT3G29280.1	28	516	3.8%
Cluster7617	403279	AT5G24020.1	32	897	0.7%
Cluster7687	85641	AT1G80190.1	28	582	0.7%
Cluster7771	80277	AT1G62730.1	30	903	1.2%
Cluster8027	96579	AT1G21840.1	23	777	6.7%
Cluster8101	229401	AT2G17705.1	33	375	0.7%
Cluster8346	110563	AT3G53220.1	31	363	0.6%
Cluster8563	407908	AT3G62880.2	25	315	3.6%
Cluster8972	75086	-	16	618	2.2%

Cluster3172 X X X - X X - X - X X X - - X X - - X X - X X X X X X X - X - - - X - X X - X X X - X X -
Cluster3177 X X X X - - - X X X - X X X - X X X X X X X X - X - - X X X X X X X X X X X X - X X X X - X X X X -
Cluster3208 X X X X - - - X X X - - X X - X X X X X X X X X X X X - X - X X X X X X X X X X X X X X - X X
Cluster3212 X X X - - X - X X X - X - X - X X X X - X
Cluster3215 X X X X X X - X X X - X - X X X X - - X - X X - X
Cluster3239 X X X X X X - X X - X X - X X X X - X X X X - X
Cluster3261 X X X - X X X X X X - X X X - X
Cluster3270 X - X - - X - - - X - X X - X
Cluster3279 X X X - - X - X X X X - X X X X - - X
Cluster3282 X X X - - X X - X X - - X - X - X - X X X X X - X X X - X X - - - X X - - X X X X - X X X - X X X
Cluster3308 X X X X - X - - X X X - X
Cluster3309 X X X - - X - X X X X - X - X - X
Cluster3315 X - X X - - - X X X - - - - - X - - X X - X - X
Cluster3317 X X X - - - X X - - X - - X - - X - - - X X X X - X X X - X X X - X X X - X X X - X X X - X X X X
Cluster3320 X X X - X X - - X X X X - X
Cluster3334 X X X - X X - X - X
Cluster3337 X - - - - - - - - - - - X - X X X - X X - - X - X X X - X - X X X - X - X - - - X - - - X - - X
Cluster3339 X X X X X X - X - X - X X X X - X X X X X X - X - X X X - X X - X X X X - X X X - X X X - X X X - X X X
Cluster3350 X X X - X - X X X - X - - X - X X - - X X X X - X - - X X X X - X - - - X - - - X - - X X X - X X X
Cluster3361 X X X - X X - - X X X X - - X X X X - - X X X X - X - X
Cluster3368 X - - - - - X X X X - X X - X
Cluster3371 X X - X X - - X - X X - X - X - X X X X - X X X X X X X X - X X - X - X X X X - X X X - - X X X - X X X
Cluster3380 X X - X X - - X X X X X - X X X X X X - X X X X X X - X X X X X X - X X X X X X X X X X X X X X X X
Cluster3382 X X X - - X - X X X - - - - X X X - - X - - X - - X X - - X X X X - X - X X X X - X X X X - X X X
Cluster3414 X X X - - X - X - X X X X - X
Cluster3451 X X X - X
Cluster3454 X X X X X X - X X X - X X X - X X - - X X X X X X X X X X X X - X - X X X X X X X X - X X X - X X X
Cluster3463 X X X - - X - - - - - - - - X - - X - - X
Cluster3466 X X X - - X - X X - - - - X X - X X - - X
Cluster3470 X X X X - X - X - X X X X - - X X X X - - X X X X X X - X - - - X X X X - X X X X - X X X X X X X
Cluster3509 X X - X X - X X X X - X - X X X X - - X X - X X X X X - - - X X X X - - X X - X X X - X X X - X X X
Cluster3520 X X X X X X X X - X - X - X - X X - - X X X X X X X X X X X X - X X - X X X X X X X X - X X X - X X X
Cluster3566 X X X X X X X X - X X X X X X X X - X X X X X X X X X X X X - X X X X X X X X - X X X X X X X X
Cluster3573 X X X X - X - X X X - X - - X X X - X - - X X X X X - X X - X X X X - X X X - X X X - X X X - X X X
Cluster3583 X X X X - X - - X X X X - X X X - - X X X X - X X X X - X
Cluster3618 X X X X X X X - X X X - X
Cluster3619 X X X - X - X - X X X X X - X X X - X
Cluster3626 X X X - X X X X X X - - X X X - - - X X X X X X - - X - - X X X X X X - - X X X X X X - - X X X
Cluster3643 X X X X X X X X X X X X X X - X X X X - X
Cluster3676 X X X X X - X X - X X X X X - X X X X - X X X X - X X X - X X X X X X X X - X X X - X X X X X X
Cluster3682 X X X X - X - - - X X X X X - X
Cluster3719 X X X - X - X X X X - X - X - - X X X - - X X X X - - X X X X - - X X X X - - X X X X - X X X
Cluster3722 X X X - - X X X X X X X X X X X X - X X X X X X X X - X - X X X X X X X X X X X X X X X X X X
Cluster3725 X X - - - - X - X X X - X
Cluster3777 X - - - - - X - - - - X - - - X - - - X X X - X X - - X X - - X X X - X X - - - - X - - - X
Cluster3783 X X X X X - X X X - X - X - - X - - X - - X X X - X - - X X X X - X X - - X X X X - X X X X X X X
Cluster3805 X X X X X X - X X - X X - - X X - X X X - X X X X - X X X X - X X X - X X X X - X X X X - X X X
Cluster3809 X X X X X - X - X X X X X - X X - X
Cluster3810 X X X - X - X - X X X X - X - X X - X X X - X X X X X X X X - - X X X X - X X X X X X X X - X X X
Cluster3820 X X X X X - X - X X X - X X X X - - X X X X X X X X X X - X - X - X X X X X X X X X X X X X X X
Cluster3826 X X X X X - X - X
Cluster3856 X X X X X - X X X - X - - - X
Cluster3873 X X X X X - X - X X X - X
Cluster3876 X X X X - X - X X X X X X X X X X X X - X - X X - X X X X - X X X X - X X X X X X X X X X X X
Cluster3881 X X X X X - X X X - X
Cluster3886 X X X - X - X - X X X - - X X X - X X X - X X X X - X X X X - - X X X X - X X X - X X X X
Cluster3912 X X X - X - X X X - X - - - X X - - X X X - X
Cluster3946 X X X - X X X - X - X - X X X X - X
Cluster3959 X X X X X - X X X X - X X X X - X
Cluster3974 X X X - X - - X X X - X - X - X X X X X X X - X X X - X X X - X X X X X X X X X X X X X X X
Cluster4085 X X X X X - - X X X - X - X X X - - X X - X X X X X X X - X X - X X X - X X X X X X X X X X X
Cluster4088 X X X - X X X X X X - - X X X X X X X X X X X X X X X X X X - X X X - X X X X X X X X X X X
Cluster4095 X X X X X - X - - - X X X - - - X X X X X X X X X X - X - X - X X X - X X X - X X X X
Cluster4105 X X X X X - X - X X X X - X X X X - X X X X - X
Cluster4188 X - X X - X - X X X X X - X - X X X X - X X X X - X X X X - X X X X - - X - - - X X X - - -
Cluster4191 X X X X X - X X X - X X X - X X X X - - X X X X - X
Cluster4200 X X X - X X X X - X - X - - - X - - - X - X X X X X X - X - - - X - X X - - X X X X -
Cluster4212 X X X - X X X - X - X - X X X X - X
Cluster4216 X - - X X - X - X X - X - X X X X - - X X X X X - X X X X X X - X X X X X X X X X X X X
Cluster4219 X X X - X - X X X X - X X X X - - X X - X X X - X X - - X X X X X X - X X X X X X X X X X X
Cluster4235 X X X X X - - X X - - - X X X X - - X - X X X X X X X - - X X X X X X X X X X X X X X X X
Cluster4242 X X X X - X - - - X X X X X X - X
Cluster4246 X X X - X - - X - X X X - X - X X - X X X X X X X - - X X - - X X X X X X X X X X X X
Cluster4276 X X X X X X X X X X X X X X X X X X X - X X X X - X X X - X X X X X X X X - X X X X
Cluster4302 X - X - X X - X - X - X - X X - - X X - X - X X X - - - X - X X X X X X X X X X X X
Cluster4324 X X X X X - X X X X - X X X X - X X X - X
Cluster4331 X X X - - X - X - X - X - X X X X X X X - X X X X X X X - X X X - X X - X X X - X X X
Cluster4344 X X X - X - X - X X - X - X X X X X X X - - X X X - X - X X X - - - X - X X - X X X -
Cluster4363 X X X - - X X - X - - - X X X X X X - X - - X X X X X X X X X - X X X - - X X - X X X
Cluster4384 X X X X X - X X - X X X X X X X X X X - X - X X X X X X X - X X X - X X X - X X X - X X X
Cluster4396 X - - - X - X - X X - X X X X X X X - - X X - X X X - X X X - X X X X X X X - X X
Cluster4414 X X X - - X - X X X - X - X X X - - X X X X - X X X X X X X - X X X - X X X - X X X
Cluster4473 X X X - X X - X X X X - X X X X - X X X X - X X X X X X - X X X X - X X X - - X - X X
Cluster4486 X X X X - X - X X X X X - X X X X X X X X X X X X X - X X X - X X X - X X X - X X X
Cluster4514 X X X X - X - X X X X X X X X X X X X X X X X X X - X - X X X - X X X - X X X - X X X
Cluster4562 X X X - X - X X X - - - X X X X - X X X - X X X X X X X X X - X X - X X X - - X X X X
Cluster4577 X X X - X - - - X X X - X - X X - - X - X X X X X X X - X X X X - X X X X X X X X X X
Cluster4580 X X X X X X X X X X X X - X X X X X X X X X X X X X - X X X X X X X X X X X X X X
Cluster4643 X - X - - X X - X X - X X - X X X X - X X X X - X X X - X X X - X X X - X X X X X X
Cluster4649 X X - X X - X X X - X - X X X X - - X - X X X - X X - X X - X X X X X X X X X X
Cluster4682 X - X - X X - X - X - - - - X X - - X - - - - X X X X - - X X - - X X - X - - -
Cluster4712 X - - X X X X - X X X - X - X X X X X X X X - X X X X X X X X - X X X X X X X X X X X X

Table S5. Data characteristics for each of the 45 plastid genes, including number of species per gene, number of nucleotide sites per gene, and percentage of gaps per gene.

Gene	No. of species	No. of sites	Gaps%
<i>atpA</i>	41	1518	0.1%
<i>atpB</i>	41	1494	0.3%
<i>atpE</i>	41	399	0.1%
<i>atpF</i>	41	549	0.0%
<i>atpI</i>	41	732	0.2%
<i>ccsA</i>	41	954	0.6%
<i>clpP</i>	41	582	0.1%
<i>matK</i>	41	1506	0.6%
<i>ndhA</i>	37	1077	0.4%
<i>ndhB</i>	38	1500	0.2%
<i>ndhC</i>	38	360	0.0%
<i>ndhD</i>	38	1497	0.0%
<i>ndhF</i>	38	2217	0.6%
<i>ndhG</i>	38	528	0.0%
<i>ndhH</i>	38	1179	0.0%
<i>ndhI</i>	38	495	0.3%
<i>ndhJ</i>	38	477	0.5%
<i>ndhK</i>	36	672	0.6%
<i>petA</i>	40	957	0.0%
<i>petB</i>	41	702	7.1%
<i>petD</i>	41	474	0.0%
<i>psaA</i>	41	2247	0.0%
<i>psaB</i>	41	2202	0.0%
<i>psbA</i>	41	1041	0.0%
<i>psbB</i>	41	1476	0.0%
<i>psbC</i>	41	1383	0.0%
<i>psbD</i>	41	1059	0.0%
<i>rbcL</i>	41	1425	0.0%
<i>rpl2</i>	40	819	0.2%
<i>rpl14</i>	41	366	0.0%
<i>rpl16</i>	41	402	0.4%
<i>rpl22</i>	35	339	3.1%
<i>rpoA</i>	41	975	1.2%
<i>rpoB</i>	41	3204	0.1%

<i>rpoC1</i>	40	2040	0.4%
<i>rpoC2</i>	39	4050	0.9%
<i>rps3</i>	41	651	0.2%
<i>rps4</i>	40	603	0.1%
<i>rps7</i>	41	465	0.0%
<i>rps8</i>	41	396	0.2%
<i>rps11</i>	41	396	0.4%
<i>rps14</i>	39	300	0.0%
<i>ycf2</i>	34	6816	1.9%
<i>ycf3</i>	40	504	0.1%
<i>ycf4</i>	39	552	0.0%

Table S7. Estimated index of substitution saturation (I_{SS}) for each rate partition with different operational taxonomic units (OTUs). The rate partitions were decided using the Observed Variability (OV) method or the Tree Independent Generation of Evolutionary Rates (TIGER) method. For each OTU, the critical I_{SS} value was estimated assuming a pectinate ($I_{SS,C1}$) or symmetrical ($I_{SS,C2}$) topology, and the p -value was inferred using the two-tailed t -test.

Data	Sorting criteria	Rate partitions	No. of sites	OTUs	I_{SS}	$I_{SS,C1}$	P -value	$I_{SS,C2}$	P -value
Nuclear genes (46 species)	OV	<i>slow</i>	71,295	4	0.898	0.855	0.0000	0.859	0.0000
				8	0.791	0.782	0.2965	0.857	0.0000
				16	0.743	0.705	0.0000	0.844	0.0000
				32	0.728	0.601	0.0000	0.819	0.0000
		<i>fast</i>	71,295	4	1.110	0.855	0.0000	0.859	0.0000
				8	0.986	0.782	0.0000	0.857	0.0000
				16	0.935	0.705	0.0000	0.844	0.0000
				32	0.918	0.601	0.0000	0.819	0.0000
	TIGER	<i>slow</i>	71,295	4	0.952	0.855	0.0000	0.859	0.0000
				8	0.832	0.782	0.0000	0.857	0.0000
				16	0.781	0.705	0.0000	0.844	0.0000
				32	0.764	0.601	0.0000	0.819	0.0000
		<i>fast</i>	71,295	4	1.056	0.855	0.0000	0.859	0.0000
				8	0.946	0.782	0.0000	0.857	0.0000
				16	0.898	0.705	0.0000	0.844	0.0000
				32	0.883	0.601	0.0000	0.819	0.0000
Plastid genes (41 species)	OV	<i>slow</i>	10,199	4	0.291	0.846	0.0000	0.857	0.0000
				8	0.291	0.763	0.0000	0.845	0.0000
				16	0.299	0.677	0.0000	0.849	0.0000
				32	0.310	0.571	0.0000	0.817	0.0000

	<i>fast</i>	10,199	4	0.584	0.846	0.0000	0.857	0.0000
			8	0.565	0.763	0.0000	0.845	0.0000
			16	0.565	0.677	0.0000	0.849	0.0000
			32	0.571	0.571	0.9910	0.817	0.0000
TIGER	<i>slow</i>	10,199	4	0.289	0.846	0.0000	0.857	0.0000
			8	0.290	0.763	0.0000	0.845	0.0000
			16	0.298	0.677	0.0000	0.849	0.0000
			32	0.308	0.571	0.0000	0.817	0.0000
	<i>fast</i>	10,199	4	0.586	0.846	0.0000	0.857	0.0000
			8	0.565	0.763	0.0000	0.845	0.0000
			16	0.565	0.677	0.0000	0.849	0.0000
			32	0.572	0.571	0.8731	0.817	0.0000

Table S8. Estimated index of substitution saturation (I_{SS}) for the most conserved 5,000 sites from the concatenated nuclear gene matrix. For each operational taxonomic unit (OTU), the critical I_{SS} value was estimated assuming a pectinate ($I_{SS,C1}$) or symmetrical ($I_{SS,C2}$) topology, and the p -value was inferred using the two-tailed t -test.

Data	No. of sites	OTUs	I_{SS}	$I_{SS,C1}$	P-value	$I_{SS,C2}$	P-value
Nuclear genes (46 species)	5,000	4	0.685	0.842	0.0000	0.850	0.0000
		8	0.605	0.767	0.0000	0.846	0.0000
		16	0.570	0.680	0.0000	0.832	0.0000
		32	0.559	0.565	0.0119	0.811	0.0000