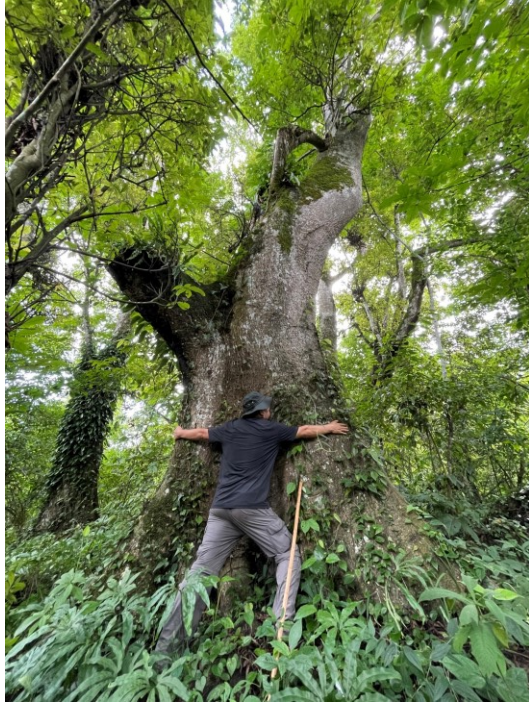


Supplementary Figures and Tables
Supplementary Figures and Legends

Supplementary Figure 1. Sampled tree and the habitats of *C. poilanei*.

(A)



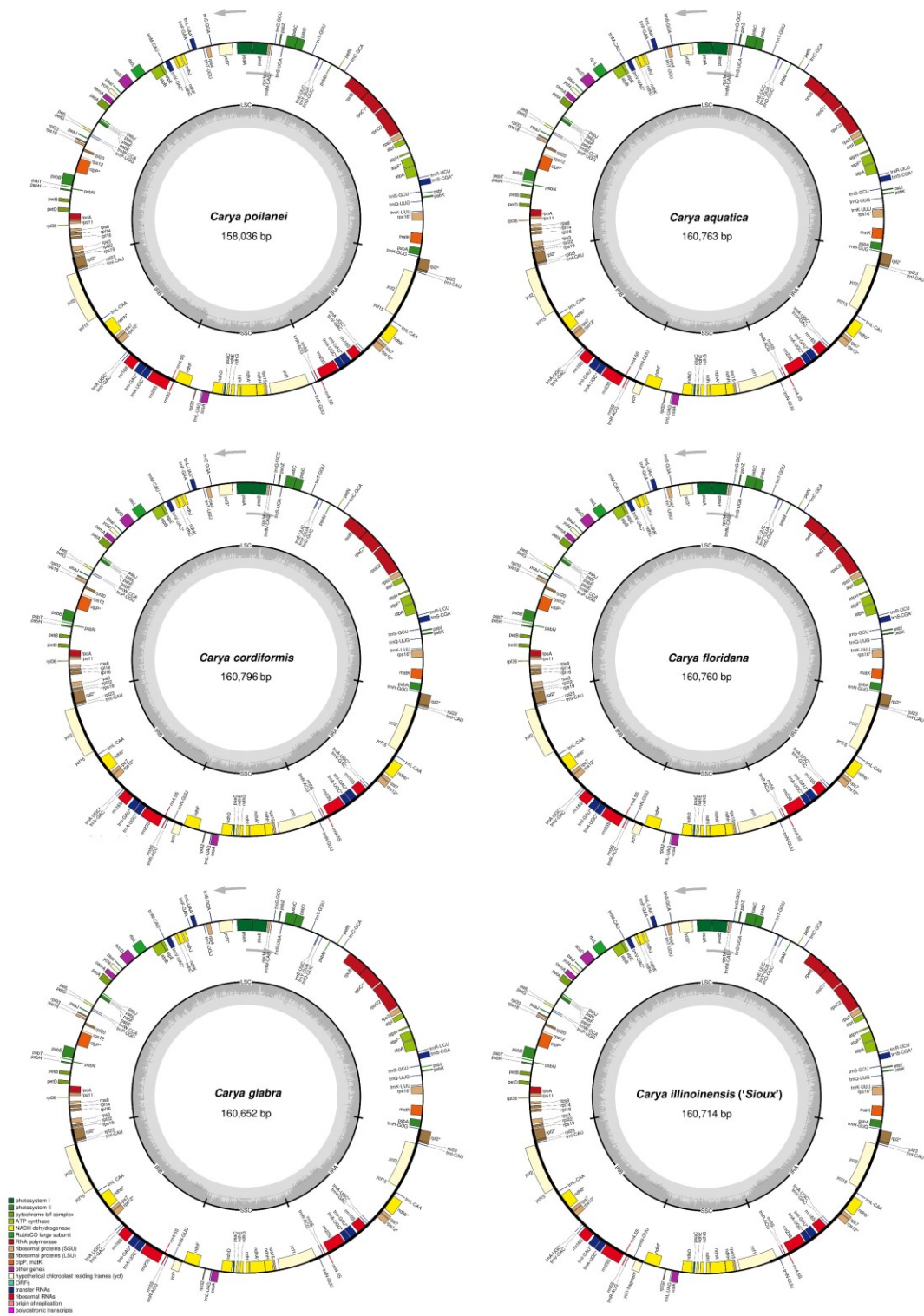
(B)



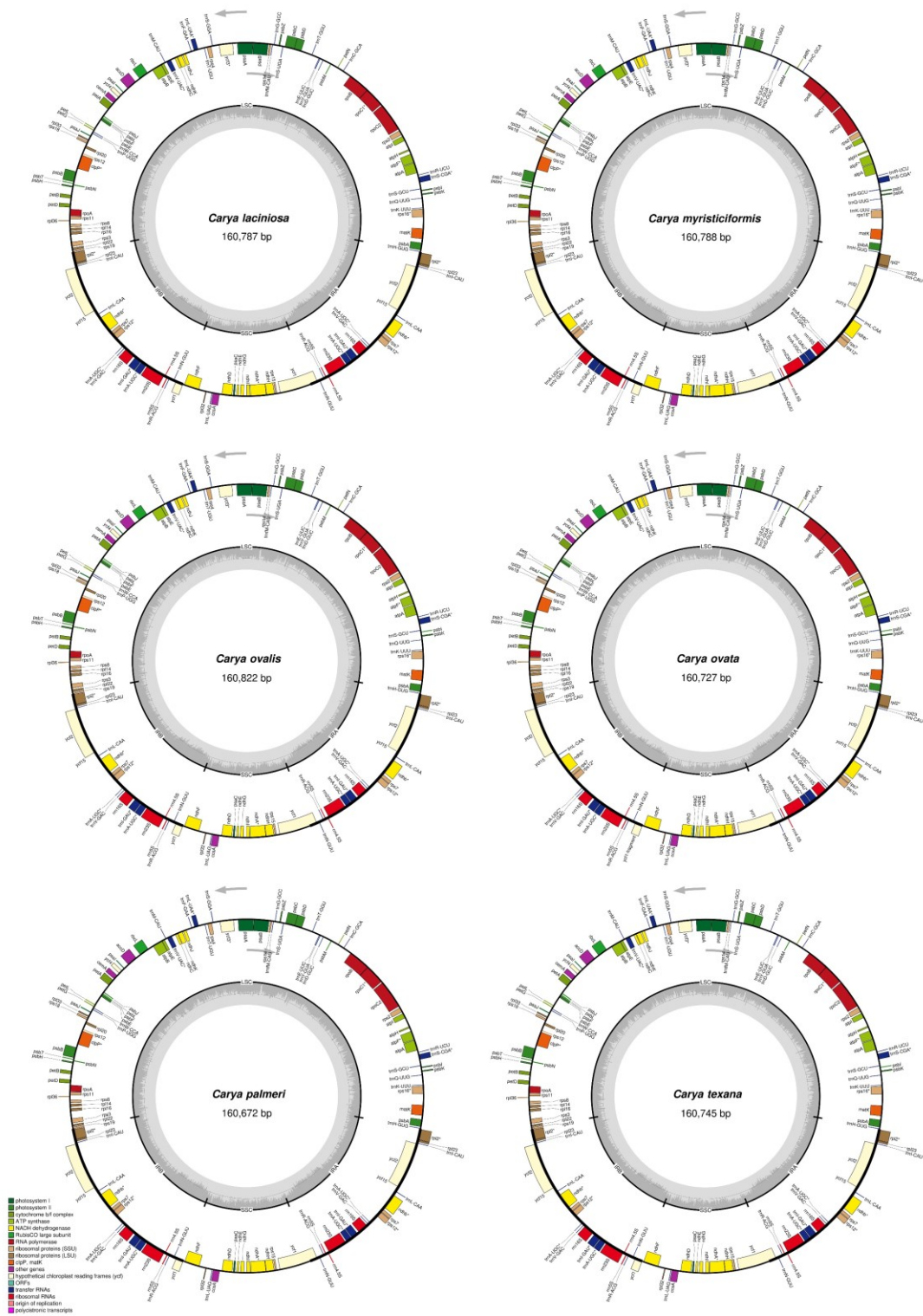
(C)



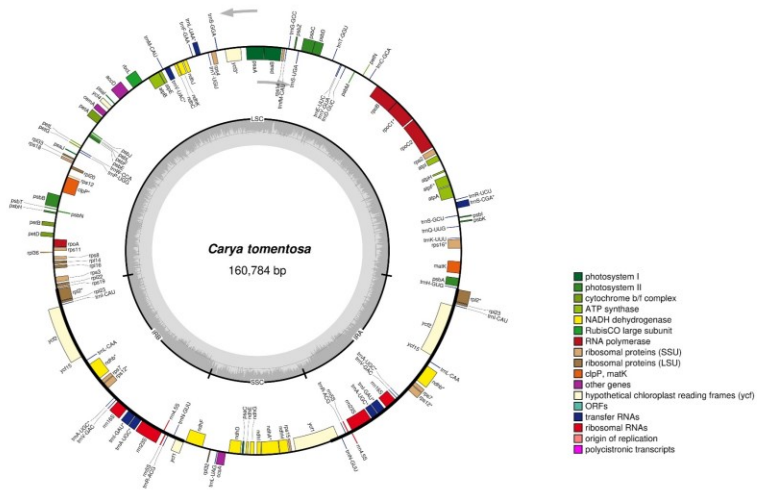
Continued.



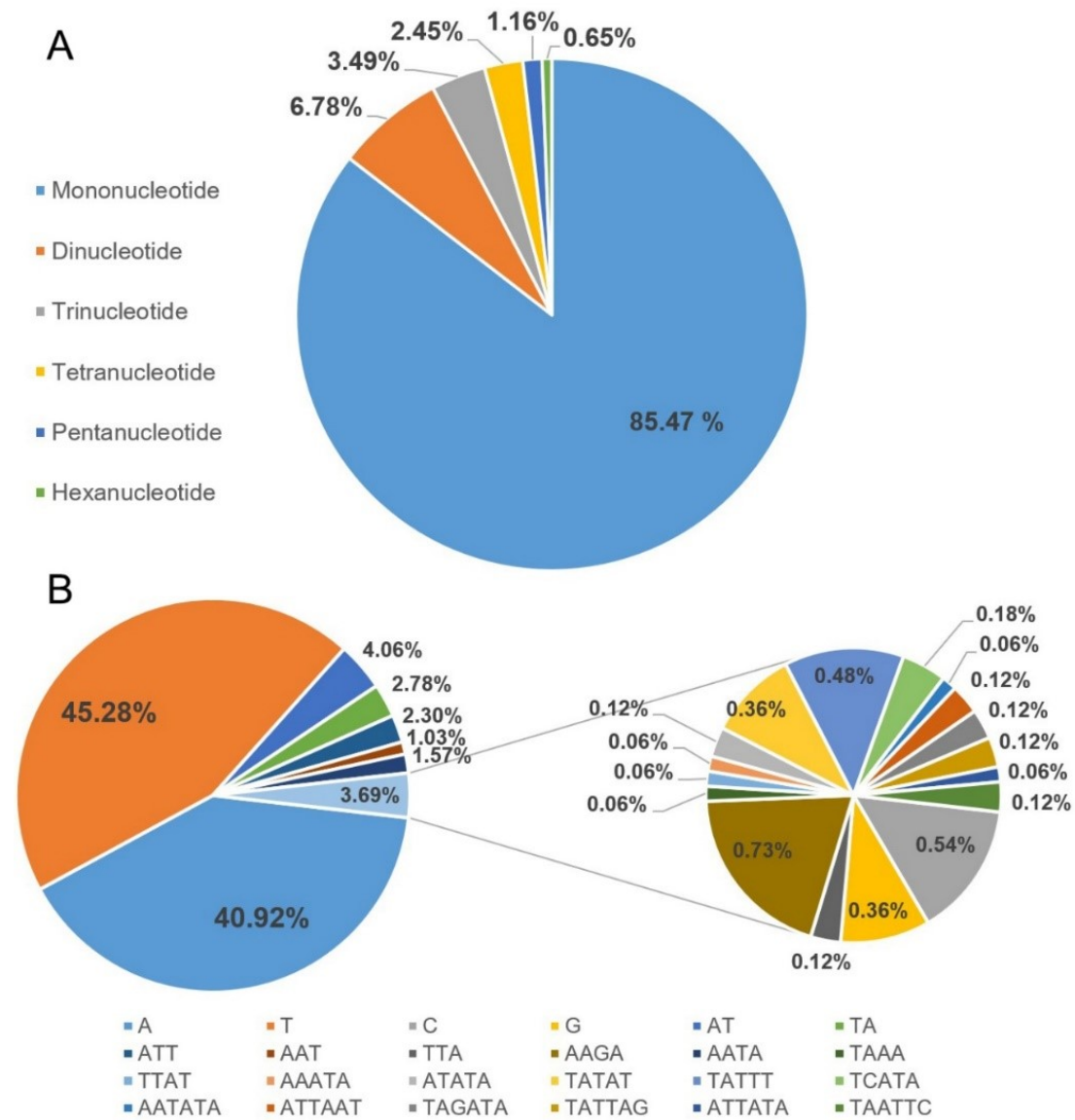
Continued.



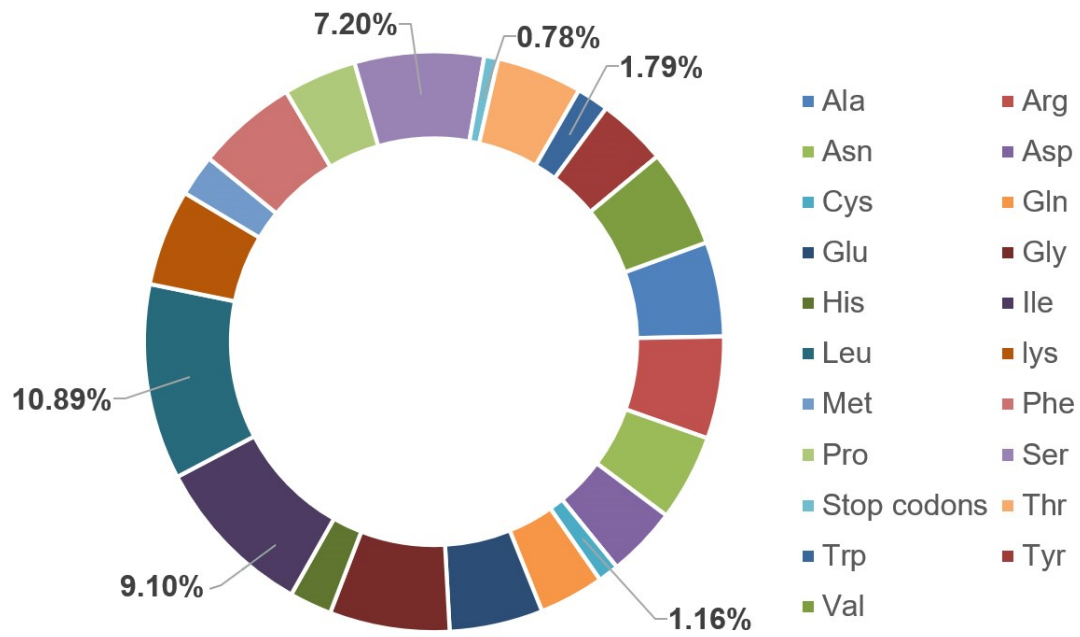
Continued.



Supplementary Figure 4. Statistics of SSR types. A, SSR types and their proportions in *Carya* plastomes. B, The detailed statistics of SSR types in *Carya* plastomes.

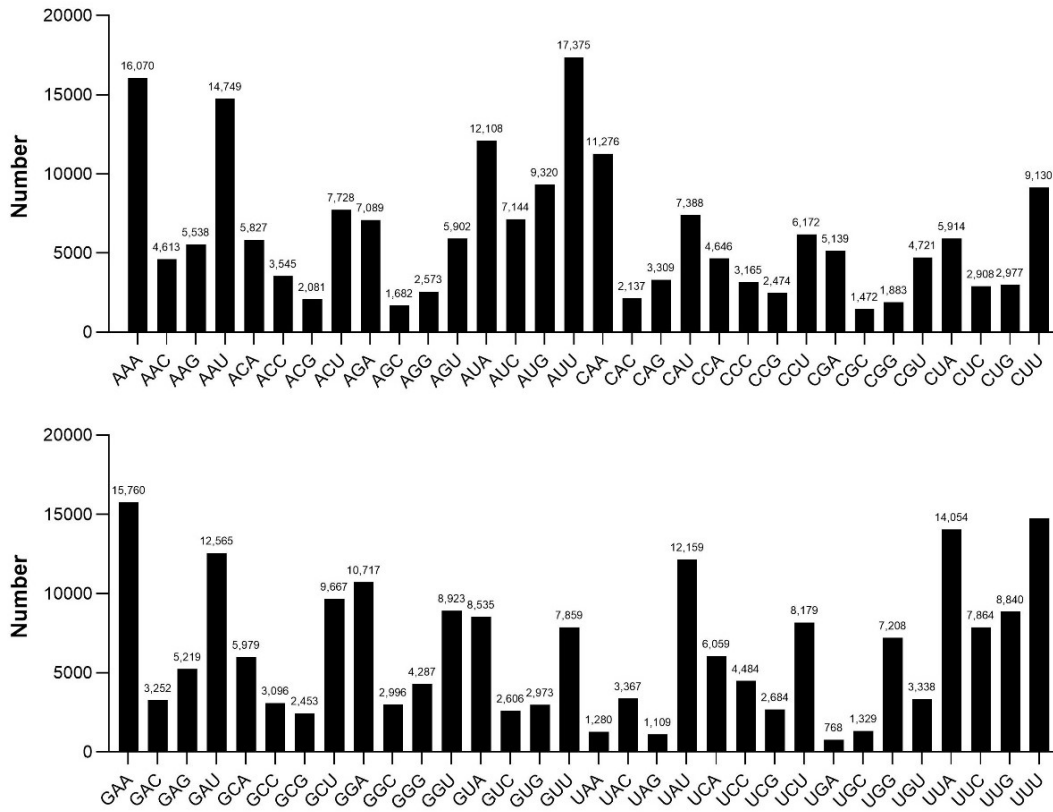


Supplementary Figure 5. Proportion of amino acids in *Carya* plastomes.

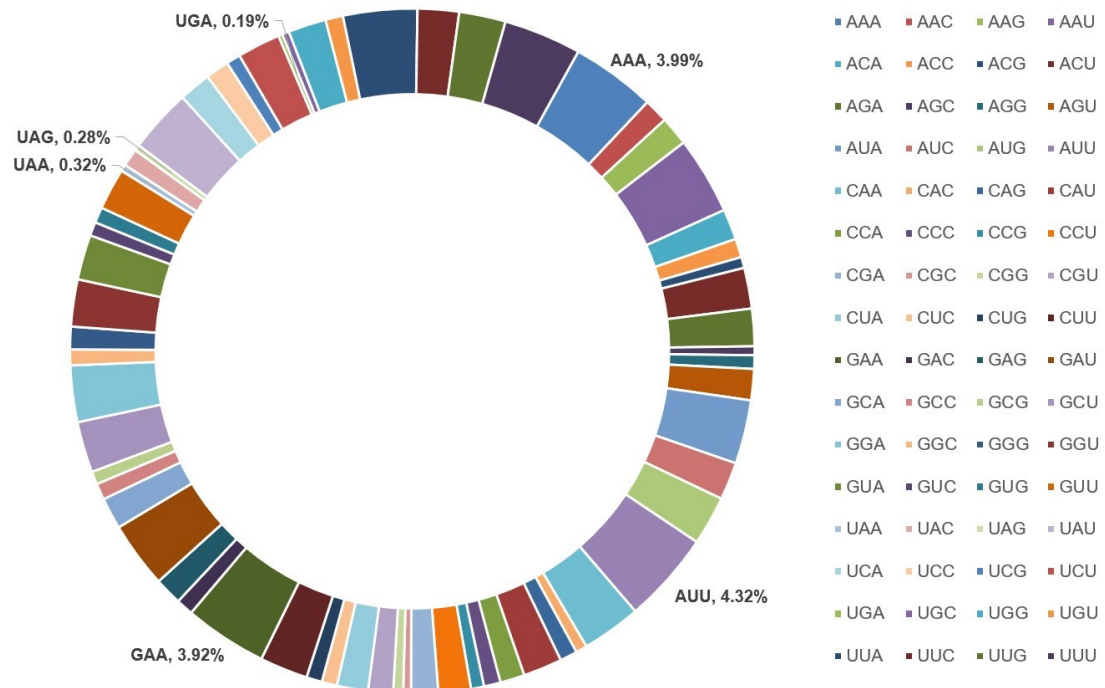


Supplementary Figure 6. Codon number (A) and usage statistics (B) of *Carya* plastomes.

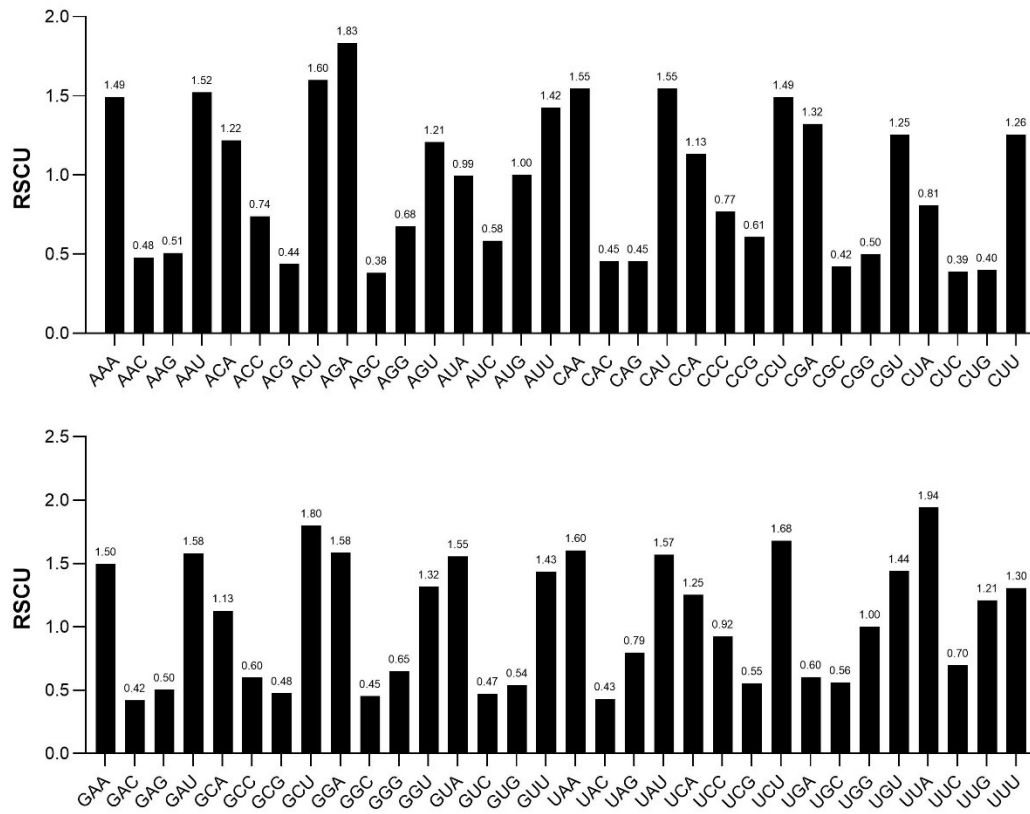
(A)



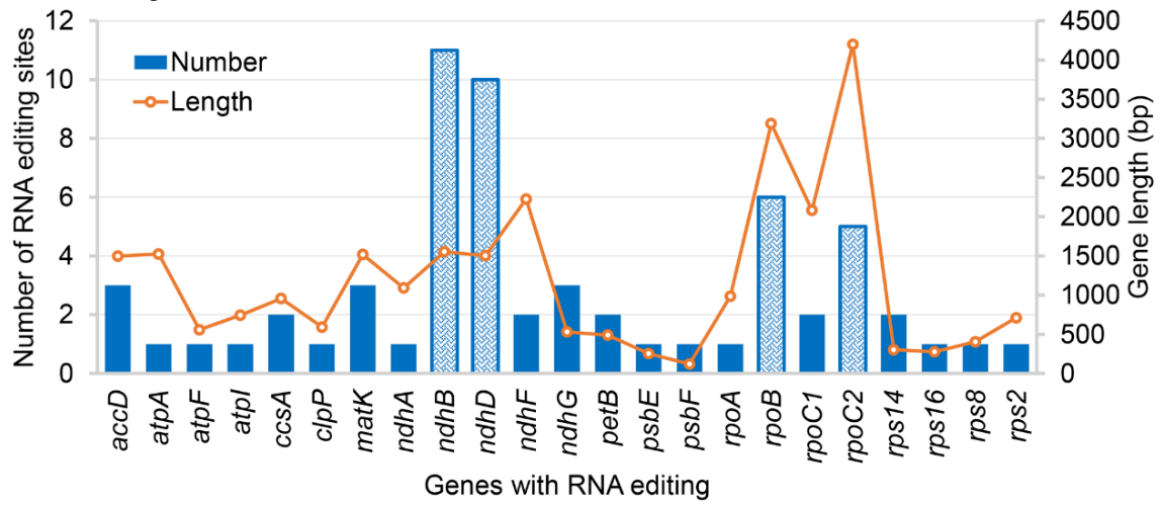
(B)



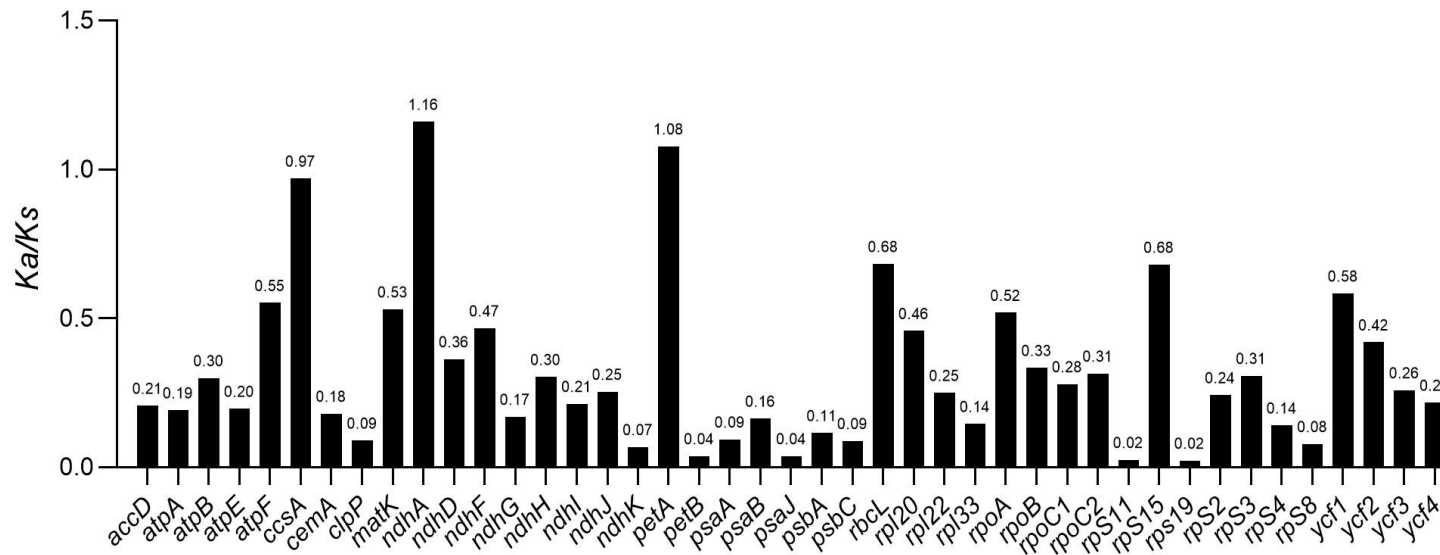
Supplementary Figure 7. Codon RSCU value of *Carya* plastomes.



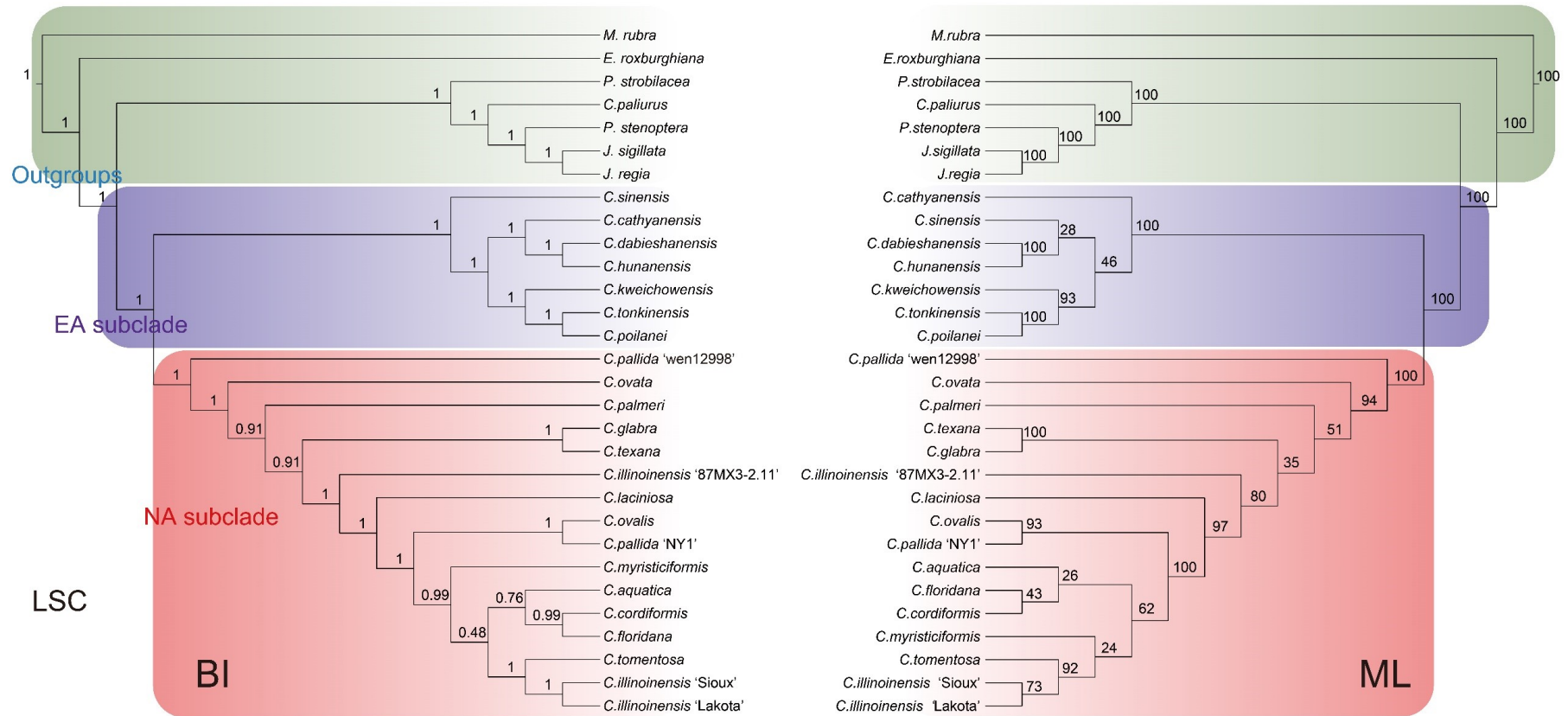
Supplementary Figure 8. RNA editing sites in the protein-coding genes of *Carya* plastomes. The genes with relatively large number, including *ndhB*, *ndhD*, *rpoB*, and *rpoC2*, were highlighted by different blue grid fill.



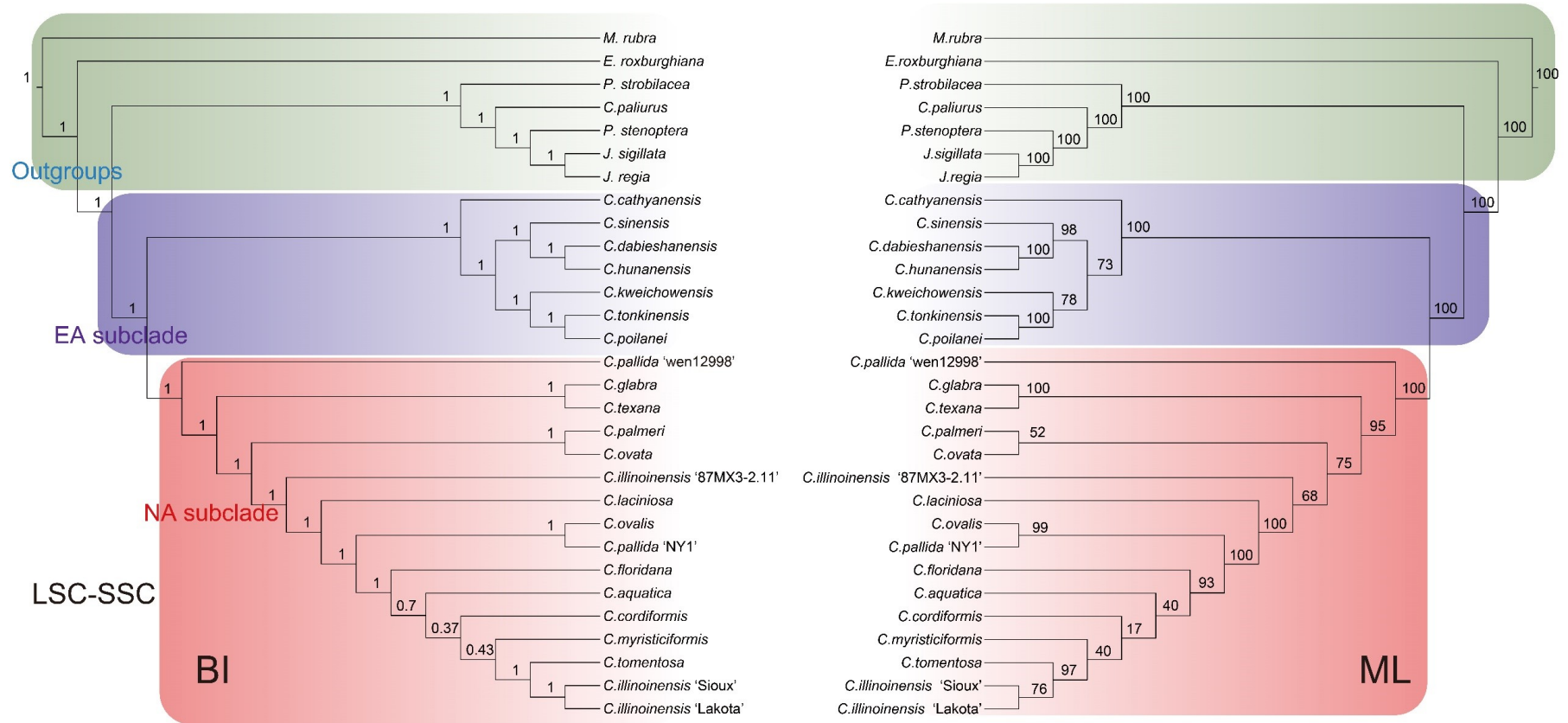
Supplementary Figure 9. Comparison of Ka/Ks (ω) values of protein-coding genes in *Carya* plastomes. Only the ω values not equal to zero are shown.



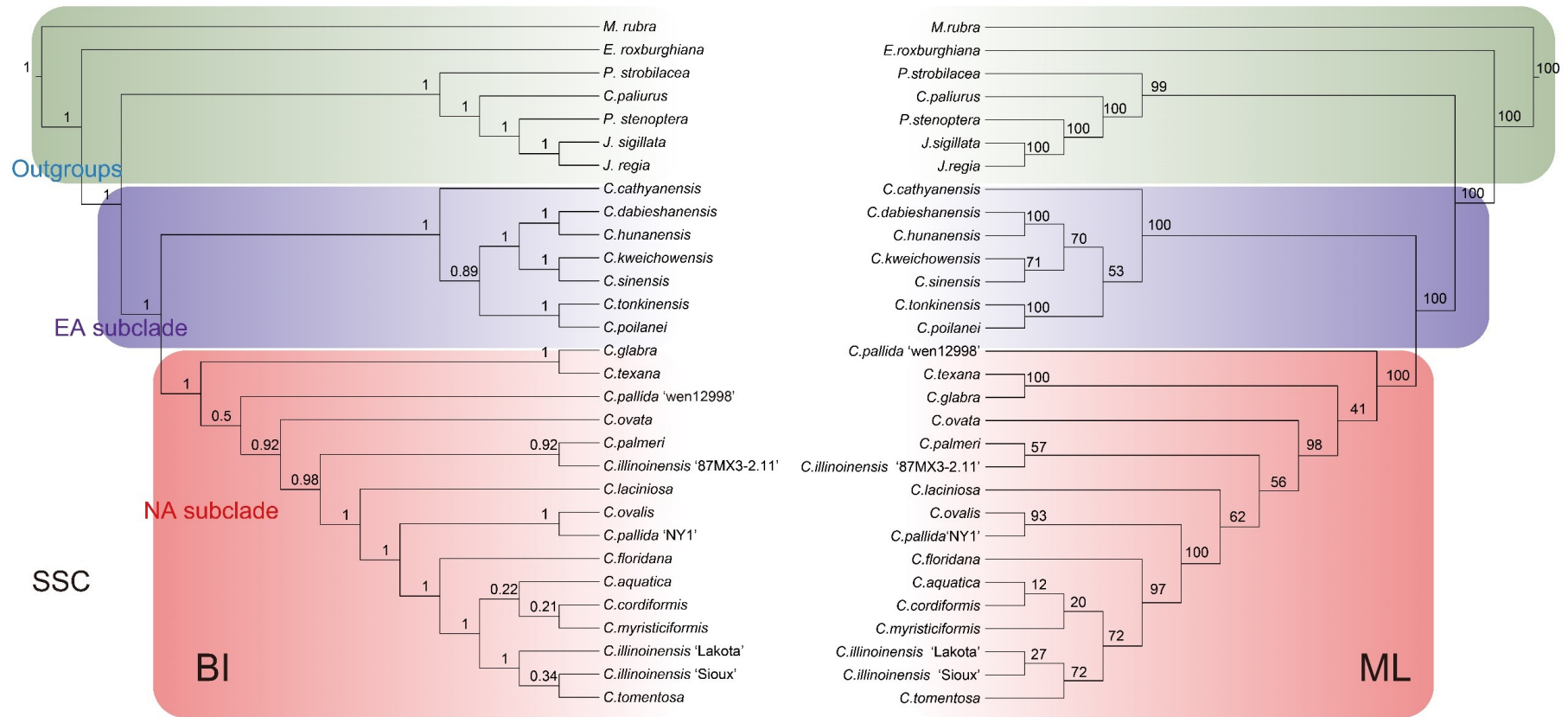
Supplementary Figure 10 . Phylogenetic trees of *Carya* species and representative species in other genera of Juglandaceae inferred from the datasets of LSC regions using Bayesian Inference (BI) and Maximum likelihood methods. The posterior probability (PP) and bootstrap (BS) values that supported each node are shown above the branches. The colors in green, light purple and pink indicate the outgroups, EA and NA *Carya* species, respectively.



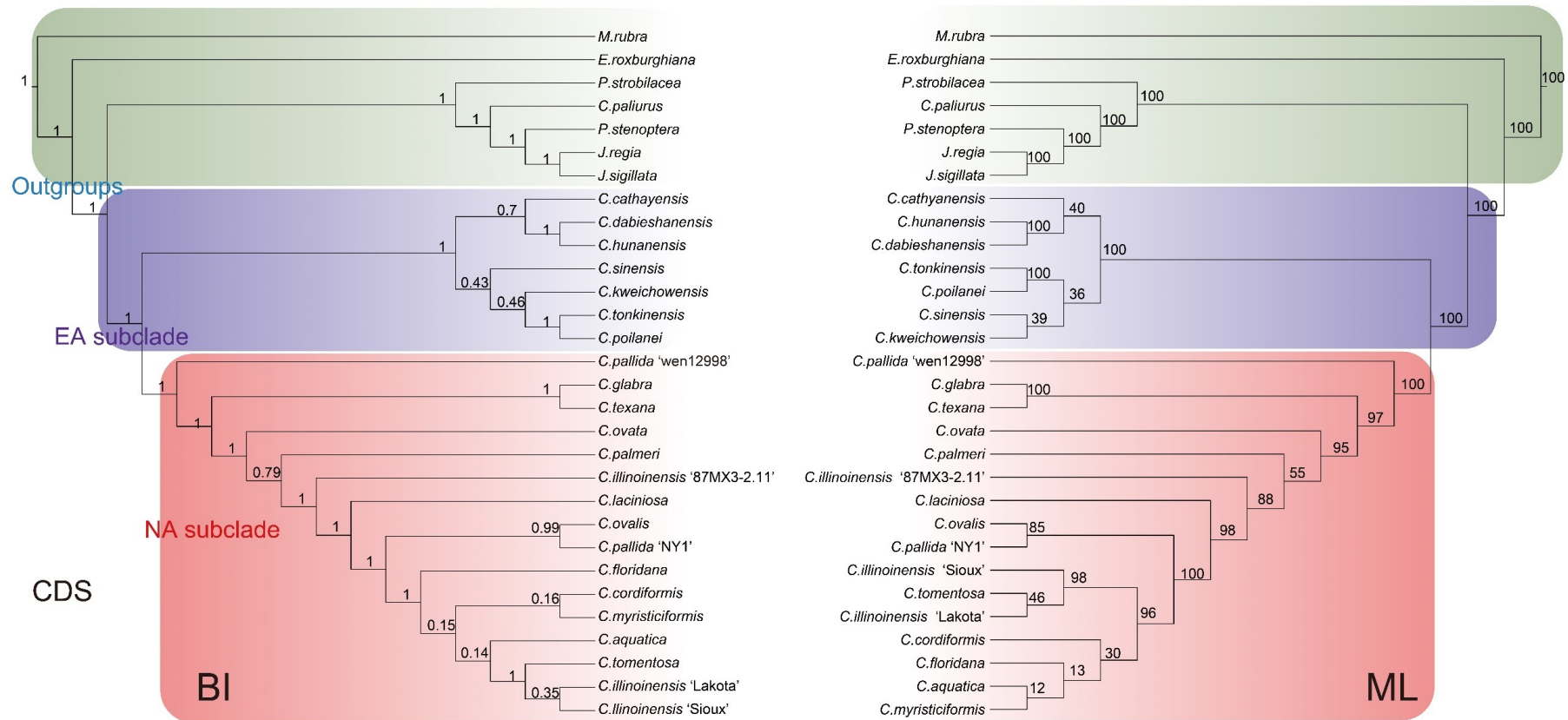
Supplementary Figure 11. Phylogenetic trees of *Carya* species and representative species in other genera of Juglandaceae inferred from the datasets of LSC-SSC regions using Bayesian Inference (BI) and Maximum likelihood methods. The posterior probability (PP) and bootstrap (BS) values that supported each node are shown above the branches. The colors in green, light purple and pink indicate the outgroups, EA and NA *Carya* species, respectively.



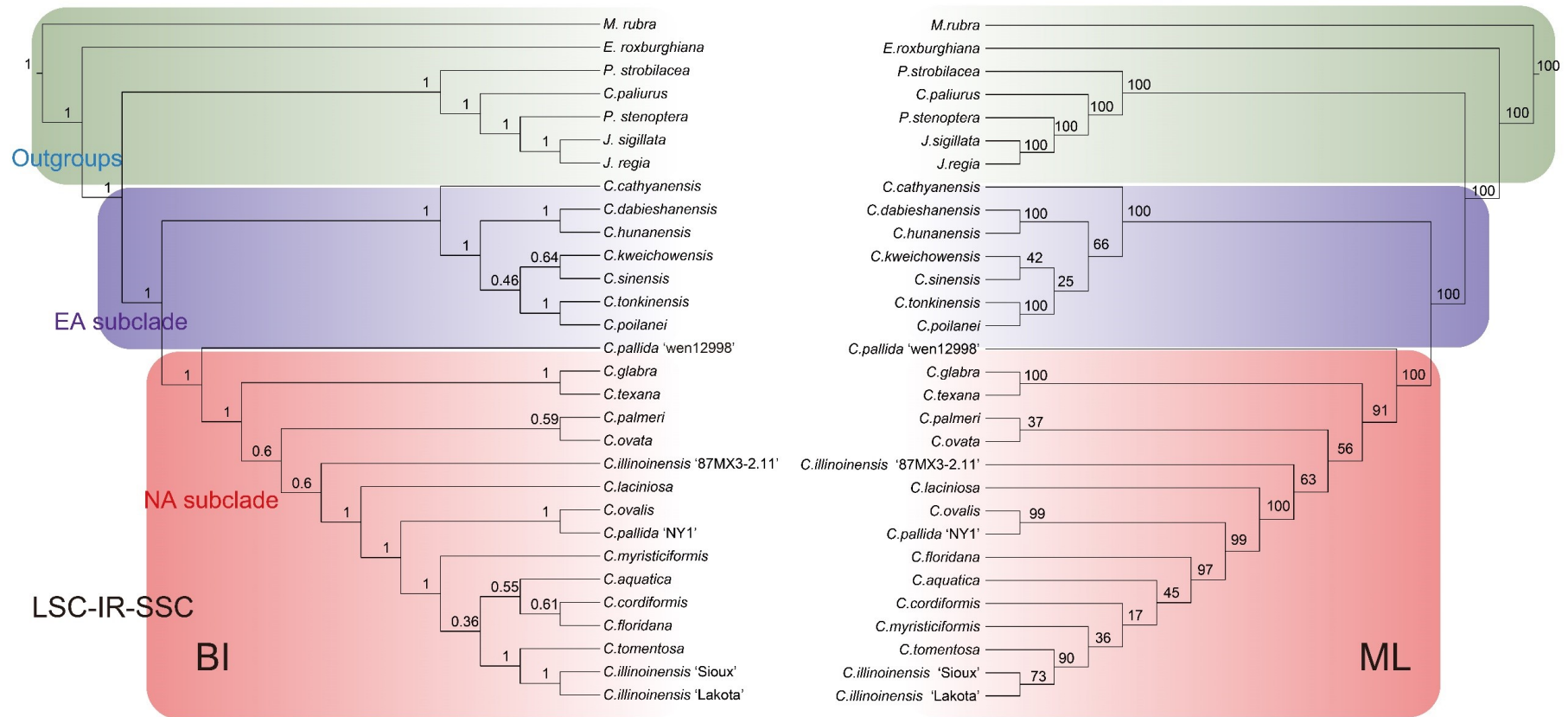
Supplementary Figure 12. Phylogenetic trees of *Carya* species and representative species in other genera of Juglandaceae inferred from the datasets of SSC regions using Bayesian Inference (BI) and Maximum likelihood methods. The posterior probability (PP) and bootstrap (BS) values that supported each node are shown above the branches. The colors in green, light purple and pink indicate the outgroups, EA and NA *Carya* species, respectively.



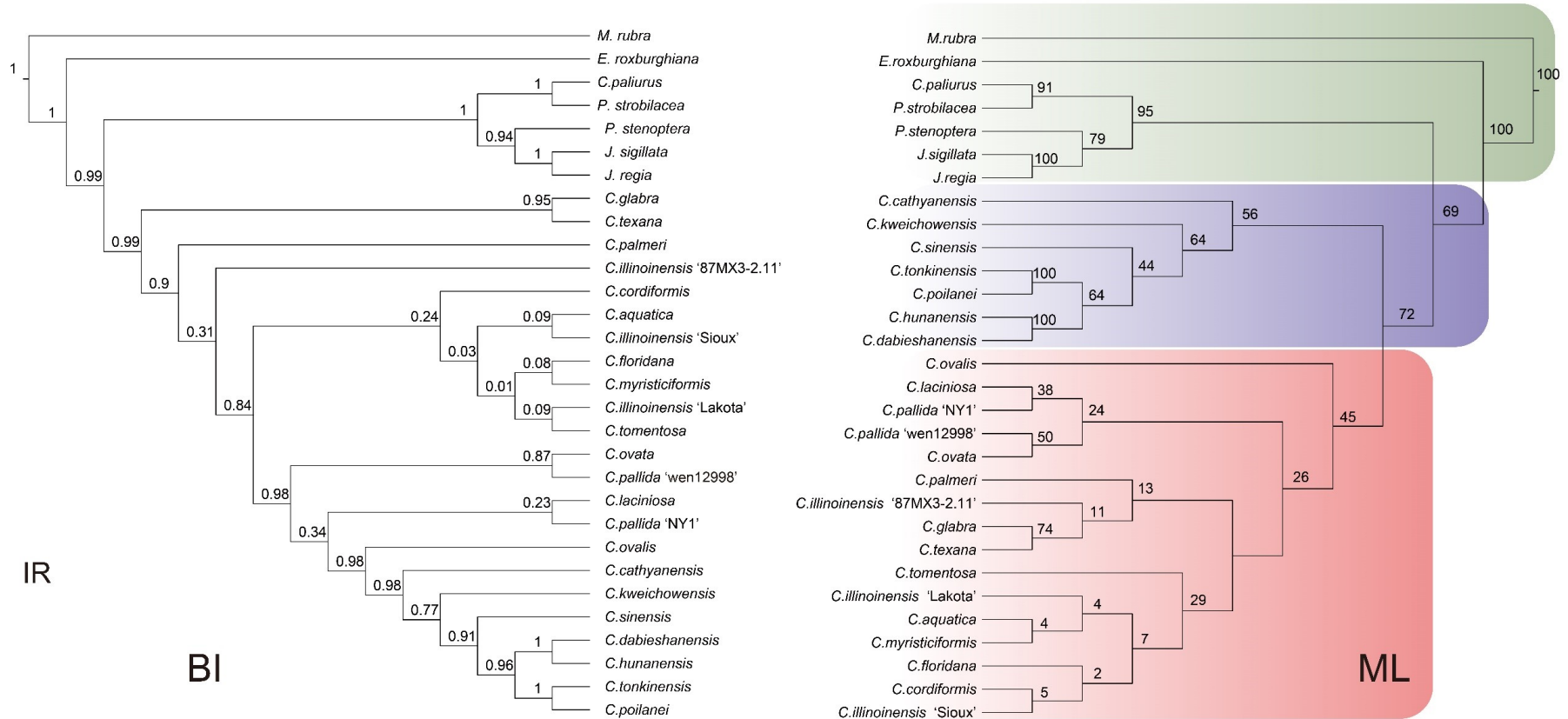
Supplementary Figure 13. Phylogenetic trees of *Carya* species and representative species in other genera of Juglandaceae inferred from the datasets of CDS regions using Bayesian Inference (BI) and Maximum likelihood methods. The posterior probability (PP) and bootstrap (BS) values that supported each node are shown above the branches. The colors in green, light purple and pink indicate the outgroups, EA and NA *Carya* species, respectively.



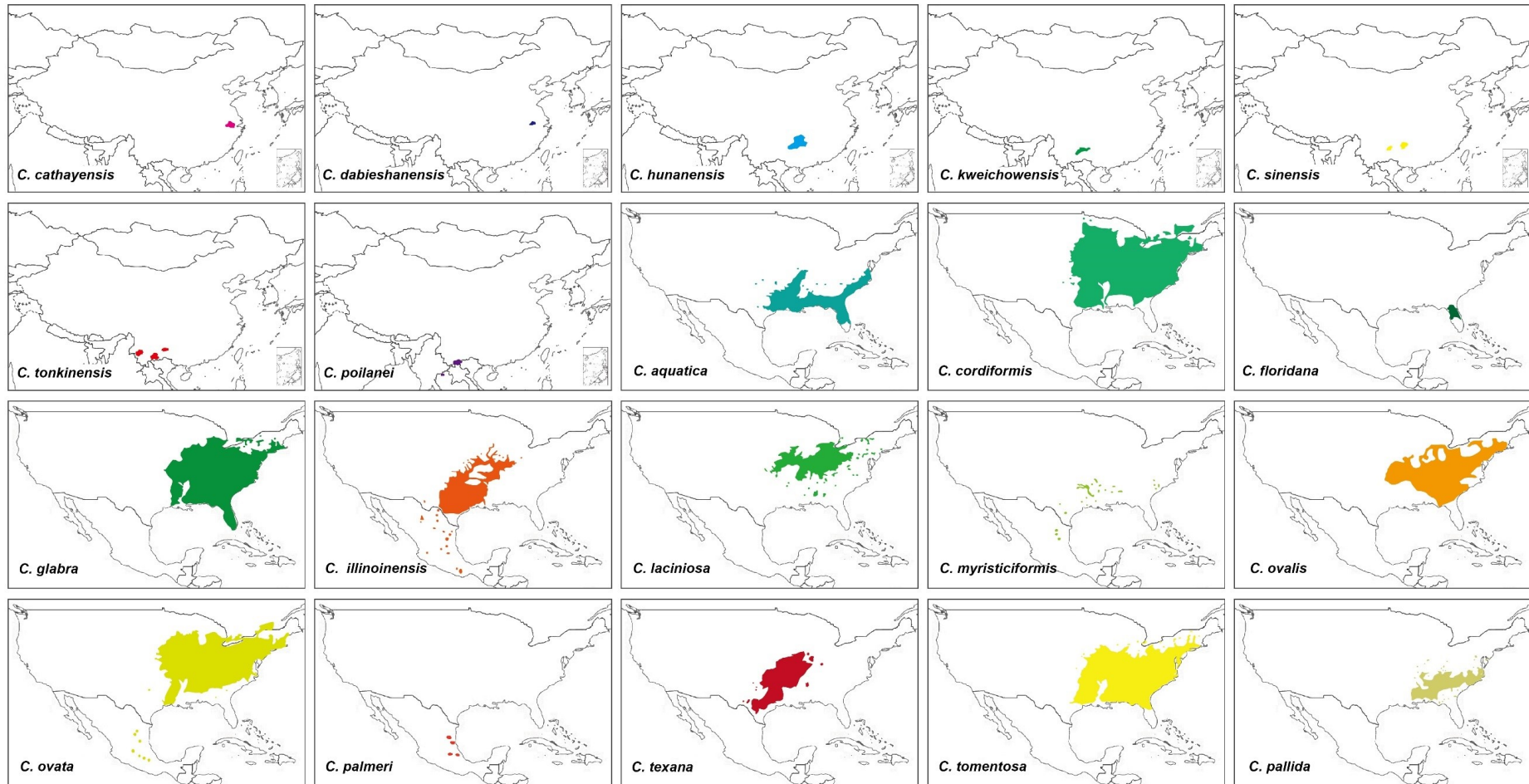
Supplementary Figure 14. Phylogenetic trees of *Carya* species and representative species in other genera of Juglandaceae inferred from the datasets of LSC-IR-SSC regions Bayesian Inference (BI) and Maximum likelihood methods. The posterior probability (PP) and bootstrap (BS) values that supported each node are shown above the branches. The colors in green, light purple and pink indicate the outgroups, EA and NA *Carya* species, respectively.



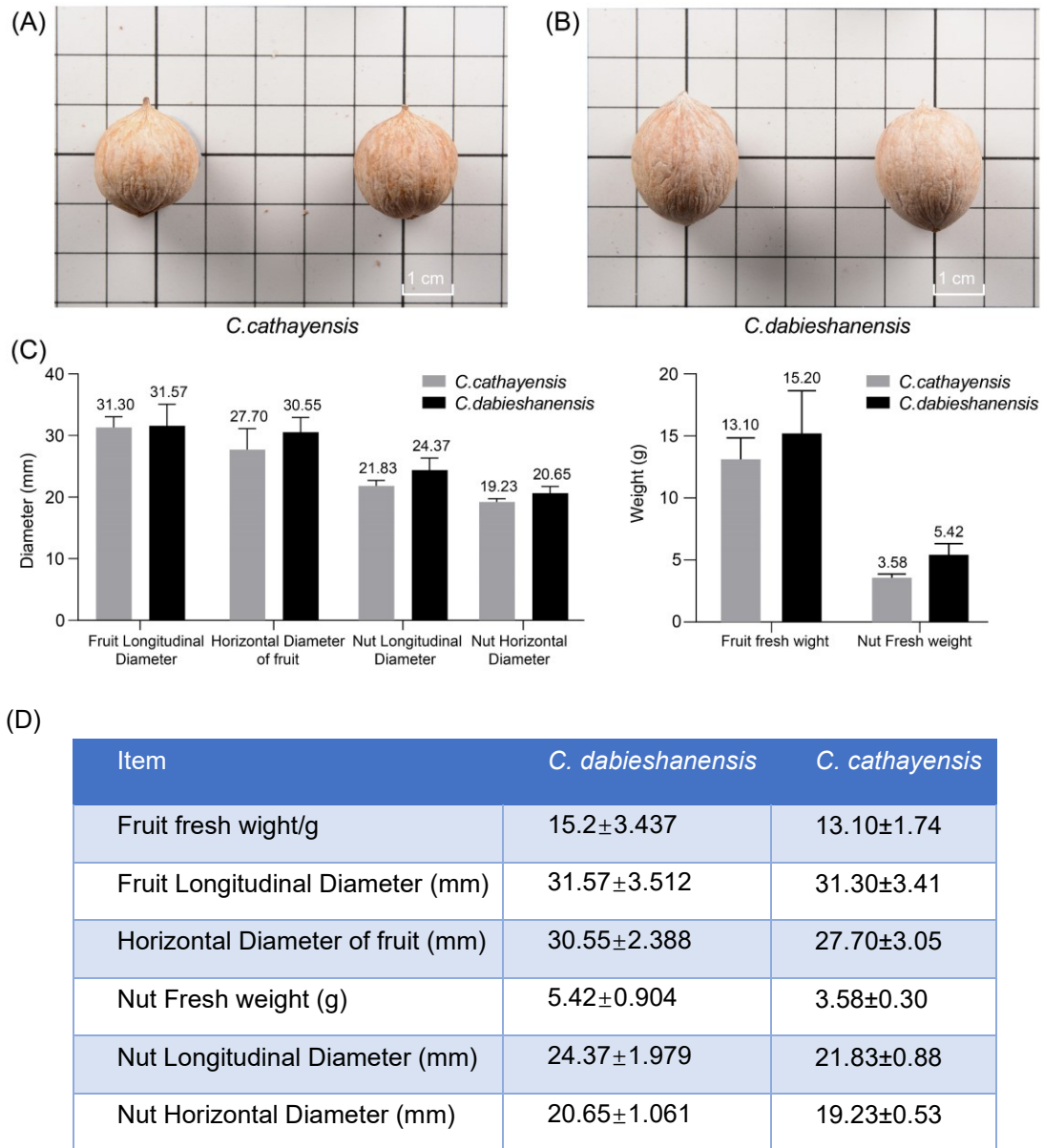
Supplementary Figure 15. Phylogenetic trees of *Carya* species and representative species in other genera of Juglandaceae inferred from the datasets of IR regions using Bayesian Inference (BI) and Maximum likelihood methods. The posterior probability (PP) and bootstrap (BS) values that supported each node are shown above the branches. The colors in green, light purple and pink indicate the outgroups, EA and NA *Carya* species, respectively.



Supplementary Figure 16. The native geographical distributions of extant *Carya* species.



Supplementary Figure 17. Morphological features of *C. cathayensis* and *C. dabieshanensis*. (A), Nuts of *C. cathayensis*. (B), Nuts of *C. dabieshanensis*. (C) - (D), Statistics of fruit and nut indexes of *C. cathayensis* and *C. dabieshanensis*. The nut size was calculated from 10 trees with n = 20 fruits or nuts per three.



Supplementary Tables

Supplementary Table 1. Information on sample collection and data sources for plastome assemblies of *Carya*.

species	Sampling site	longitude	latitude	altitude (m)	NCBI ID number	String length
<i>C. cathyanensis</i>	Orchard in Zhejiang A&F University in Linan District, Zhejiang Province	119°43'42"	30°15'16"	38.0	NA	29
<i>C. dabieshanensis</i>	Yanzihe Village Jinzhai District, Anhui Province	115°49'24"	31°16'22"	712.5	NA	49
<i>C. hunanensis</i>	Orchard in Zhejiang A&F University in Linan District, Zhejiang Province	119°43'42"	30°15'16"	38.0	NA	19
<i>C. kweichowensis</i>	Qiannan Buyi and Miao Autonomous Prefecture, Guizhou Province	107°53'47"	25°11'53"	820.0	NA	39
<i>C. sinensis</i>	Qiannan Buyi and Miao Autonomous Prefecture, Guizhou Province	106°44'4"	25°37'40"	1000.6	NA	19
<i>C. tonkinensis</i>	Conservatory in Zhejiang A&F University in Linan District, Zhejiang Province	119°43'15"	30°15'55"	38.0	NA	29
<i>C. illinoensis</i> 'Sioux'	Orchard in Zhejiang A&F University in Linan District, Zhejiang Province	119°43'42"	30°15'16"	38.0	NA	40
<i>C. poilanei</i>	Jianshui County, Yunnan Province	102°51'36"	23°23'42"	1895.0	SRX13427070	39
<i>C. aquatica</i>	—	—	—	—	SRR6804841	29
<i>C. cordiformis</i>	—	—	—	—	SRR6804840	39
<i>C. floridana</i>	—	—	—	—	SRR6804844	49
<i>C. glabra</i>	—	—	—	—	SRR6804848	29
<i>C. laciniosa</i>	—	—	—	—	SRR6804855	29
<i>C. myristiciformis</i>	—	—	—	—	SRR6804845	39
<i>C. ovalis</i>	—	—	—	—	SRR6804843	19
<i>C. ovata</i>	—	—	—	—	SRR6804846	39
<i>C. palmeri</i>	—	—	—	—	SRR6804847	39
<i>C. texana</i>	—	—	—	—	SRR6804850	49
<i>C. tomentosa</i>	—	—	—	—	SRR6804842	39

Supplementary Table 2. Primers for validation of IR-SC boundaries and *Carya* plastome assemblies.

IR-SC boundary	Forward primer sequence (5'-3')	Forward primer sequence (5'-3')
<i>ycf1~ndhF</i>	AATCGAGAAGAAAGTATCAGCAA	TGGATTGGTATGAATTTGTGAC
<i>rrn23S~ndhF</i>	AAAAGTTACTCTAGGGATAACAGG	TGGATTGGTATGAATTTGTGAC
IRa-LSC	CACGGCCATACATAACATAGAAATC	GTTCTTTACATTTCTTCCTAGCGG
LSC-IRb	GCTCGGGACCAAGTTATTATTATTC	CACGGCCATACATAACATAGAAATC
IRb-SSC	CTCCGAGCTCGGATTATAGAAGAAG	TGGATTGGTATGAATTTGTGAC
SSC-IRa	GTAATTGGTAGTAAGAAGGATGCC	CTCCGAGCTCGGATTATAGAAGAAG

Supplementary Table 3. Species information used for phylogeny analysis.

Family	Species	GenBank accession
	<i>Carya cathayensis</i>	MW410227
	<i>Carya aquatica</i>	MW255965
	<i>Carya cordiformis</i>	MW368387
	<i>Carya dabieshanensis</i>	MW410228
	<i>Carya floridana</i>	MW410229
	<i>Carya glabra</i>	MW410230
	<i>Carya hunanensis</i>	MW298527
	<i>Carya illinoensis</i> ‘sioux’	MW410238
	<i>Carya kweichowensis</i>	MW410237
	<i>Carya laciniosa</i>	MW410231
	<i>Carya myristiciformis</i>	MW410232
	<i>Carya ovalis</i>	MW440674
	<i>Carya ovata</i>	MW410233
	<i>Carya palmeri</i>	MW410234
Juglandaceae	<i>Carya sinensis</i>	MW421595
	<i>Carya pallinda</i> ‘NY1’	MT554070
	<i>Carya pallinda</i> ‘Wen12998’	MT554071
	<i>Carya texana</i>	MW410235
	<i>Carya tomentosa</i>	MW410236
	<i>Carya tonkinensis</i>	MW368388
	<i>Carya poilanei</i>	ON568300
	<i>Juglans regia</i>	NC_028617.1
	<i>Juglans sigillata</i>	NC_031373.1
	<i>Pterocarya stenoptera</i>	MN262640.1
	<i>Platycarya strobilacea</i>	NC_035413.1
	<i>Cyclocarya paliurus</i>	NC_034315.1
	<i>Engelhardia roxburghiana</i>	NC_046434.1
	<i>Carya sinensis</i>	KX703001.1
	<i>Carya illinoensis</i> ‘87MX3-2.11’	MH909600.1
	<i>Carya illinoensis</i> ‘Lakota’	MH909599.1
Myricaceae	<i>Myrica rubra</i>	NC_035006.1

Supplementary Table 4. Summary of intron-containing genes in *Carya* plastomes.

Gene	Region	Exon I length (bp)	Intron I length (bp)	Exon II length (bp)	Intron II length (bp)	Exon III length (bp)
<i>atpF</i>	LSC	411	(759~764) ^a , (747~755) ^b	147,144 ^c	-	-
<i>clpP</i>	LSC	228	(611~615) ^a , (609~620) ^b	294	(848~851) ^a , (847~855) ^b	69
<i>ndhA</i>	SSC	537	(1186~1121) ^a , (1167~1229) ^b	555	-	-
<i>ndhB</i>	IR	792	671	762	-	-
<i>rpl2</i>	IR	434 ^a , 471 ^b	(663~692) ^a , (656~662) ^b	391 ^a , 390 ^b	-	-
<i>rpoC1</i>	LSC	1626	(819~831) ^a , (811~814) ^b	456	-	-
<i>rps12</i>	LSC- IR	114	537	231	-	30
<i>rps16</i>	LSC	234, 225 ^d	(888~897) ^a , (896~904) ^b		-	-
<i>ycf3</i>	LSC	155 ^a , 161 ^b	(792~796) ^a , (790~791) ^b	226 ^a , 223 ^b	720~721	126
<i>trnA-UGC</i>	IR	38	(805~808) ^a , 807 ^b	35	-	-
<i>trnI-GAU</i>	IR	37	955	35	-	-
<i>trnL-UAA</i>	LSC	35	526	50	-	-
<i>trnS-CGA</i>	LSC	23	(724~726) ^a , (685~725) ^b	38	-	-
<i>trnV-UAC</i>	LSC	37	617	36	-	-

Note: a, Exist in EA species; b, Exist in NA species; c, Exon II length of *atpF* is 144 bp in *C. dabieshanensis*; d, Exon I length of *rps16* is 225 bp in *C. tonkinensis*.

Supplementary Table 5. The numbers and repeat sequences of each SSR type in *Carya* plastomes.

Species	Number							Repeat sequence type
	P1	P2	P3	P4	P5	P6	Total	
<i>C. cathayensis</i>	85	3	2	2	1	0	93	A/T/C/G/AT/TA/ATT/AATA/AAATA
<i>C. dabieshanensis</i>	89	6	4	2	2	2	105	A/T/G/AT/TA/AAT/ATT/TTA/AATA/TATAT/TCATATAATTC/TATTAG
<i>C. hunanensis</i>	87	6	4	2	2	2	103	A/T/AT/TA/AAT/ATT/TTA/AATA/TATAT/TCATA/TAATTC/TATTAG
<i>C. kweichowensis</i>	82	5	3	2	0	0	92	A/T/C/AT/TA/AAT/ATT/AATA
<i>C. sinensis</i>	89	6	2	2	2	0	101	A/T/C/G/AT/TA/ATT/AATA/ATATA/TCATA
<i>C. tonkinensis</i>	91	8	3	2	2	0	106	A/T/C/G/AT/TA/AAT/ATT/AATA/TATAT
<i>C. poilanei</i>	91	8	3	2	2	0	106	A/T/C/G/AT/TA/AAT/ATT/AATA/TATAT
<i>C. aquatica</i>	64	6	3	2	1	0	76	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT
<i>C. cordiformis</i>	66	6	3	2	1	1	79	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT/ATTAAT
<i>C. floridana</i>	67	6	3	2	1	0	79	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT
<i>C. glabra</i>	66	6	3	2	0	0	77	A/T/AT/TA/AAT/ATT/AAGA/AATA
<i>C. illinoensis</i> ‘Sioux’	66	5	3	2	1	1	78	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT/TAGATA
<i>C. laciniosa</i>	65	7	3	3	1	0	79	A/T/G/AT/TA/AAT/ATT/AAGA/AATA/TTAT/TATTT
<i>C. myristiciformis</i>	66	6	3	2	1	0	78	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT
<i>C. ovalis</i>	70	6	3	2	1	0	82	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT
<i>C. ovata</i>	68	5	3	3	0	2	81	A/T/AT/TA/AAT/ATT/AAGA/AATA/ATTAAT/ATTATA
<i>C. palmeri</i>	69	6	3	2	1	1	82	A/T/C/AT/TA/AAT/ATT/AAGA/TAAAATATA/AATATA
<i>C. texana</i>	65	6	3	2	0	0	76	A/T/AT/TA/AAT/ATT/AAGA/AATA
<i>C. tomentosa</i>	66	6	3	2	1	1	79	A/T/AT/TA/AAT/ATT/AAGA/AATA/TATTT/TAGATA

Supplementary Table 6. Codon usage in plastomes of assemblies and *J. regia*.

Species	Codon number	ENC	Codon GC content (%)			
			Total	1 st position	2 nd position	3 rd position
<i>C. cathayensis</i>	21,190	48.88	37.33	45.76	37.62	28.60
<i>C. dabieshanensis</i>	21,196	48.96	37.34	45.78	37.60	28.64
<i>C. hunanensis</i>	21,196	48.95	37.34	45.77	37.61	28.64
<i>C. kweichowensis</i>	21,204	48.93	37.35	45.80	37.63	28.62
<i>C. sinensis</i>	21,207	48.96	37.35	45.75	37.62	28.67
<i>C. tonkinensis</i>	21,206	56.51	37.32	39.59	31.12	41.26
<i>C. poilanei</i>	21,206	56.52	37.32	39.59	31.18	41.20
<i>C. aquatica</i>	21,210	48.98	37.37	45.82	37.59	28.70
<i>C. cordiformis</i>	21,210	48.97	37.37	45.82	37.60	28.70
<i>C. floridana</i>	21,210	48.98	37.38	45.83	37.60	28.70
<i>C. glabra</i>	21,210	48.97	37.38	45.82	37.61	28.70
<i>C. illinoensis</i> ‘Sioux’	21,210	48.98	37.38	45.82	37.60	28.70
<i>C. laciniosa</i>	21,210	48.93	37.35	45.80	37.63	28.62
<i>C. myristiciformis</i>	21,210	48.98	37.37	45.82	37.60	28.70
<i>C. ovalis</i>	21,208	48.98	37.38	45.83	37.59	28.71
<i>C. ovata</i>	21,210	49.00	37.39	45.81	37.61	28.74
<i>C. palmeri</i>	21,210	48.99	37.38	45.82	37.60	28.72
<i>C. texana</i>	21,210	48.96	37.35	45.75	37.62	28.67
<i>C. tomentosa</i>	21,210	48.98	37.38	45.82	37.60	28.71
<i>J. regia</i>	21,265	48.78	37.20	45.77	37.49	28.33

Note: ENC, Effective Number of Codon.

Supplementary Table 7. Predicted RNA-editing sites in the protein-coding genes of *Carya* plastomes.

No.	Gene	Nucleotide position	Amino acid position	Codon change	Amino acid change	value	Note
1	<i>accD</i>	154	52	CGG→UGG	R→W	1	19 species
2	<i>accD</i>	775	259	CAU→UAU	H→Y	0.8	19 species
3	<i>accD</i>	815	272	UCG→UUG	S→L	0.8	19 species
4	<i>atpA</i>	914	305	UCA→UUA	S→L	1	19 species
5	<i>atpF</i>	92	31	CCA→CUA	P→L	0.86	19 species
6	<i>atpI</i>	211	71	CUC→UUC	L→F	1	only in <i>C. poilanei</i>
7	<i>atpI</i>	629	210	UCA→UUA	S→L	1	19 species
8	<i>ccsA</i>	494	165	UCU→UUU	S→F	0.86	Not found in <i>C. tonkenensis</i> and <i>C. poilanei</i>
9	<i>ccsA</i>	500	167	UCU→UUU	S→F	0.86	Only in <i>C. tonkenensis</i> and <i>C. poilanei</i>
10	<i>clpP</i>	559	187	CAU→UAU	H→Y	1	19 species
11	<i>matK</i>	640	214	CAU→UAU	H→Y	1	19 species
12	<i>matK</i>	1177	393	CGG→UGG	R→W	1	Not found in <i>C. cathayensis</i>
13	<i>matK</i>	1183	395	CGG→UGG	R→W	1	Only in <i>C. sinensis</i>
14	<i>ndhA</i>	1028	343	UCU→UUU	S→F	1	Only in <i>C. tonkenensis</i> and <i>C. poilanei</i>
15	<i>ndhB</i>	149	50	UCA→UUA	S→L	1	19 species
16	<i>ndhB</i>	467	156	CCA→CUA	P→L	1	19 species
17	<i>ndhB</i>	586	196	CAU→UAU	H→Y	1	19 species
18	<i>ndhB</i>	611	204	UCA→UUA	S→L	0.8	19 species
19	<i>ndhB</i>	737	246	CCA→CUA	P→L	1	19 species
20	<i>ndhB</i>	746	249	UCU→UUU	S→F	1	19 species
21	<i>ndhB</i>	845	282	UCA→UUA	S→L	1	19 species
22	<i>ndhB</i>	851	284	UCA→UUA	S→L	1	19 species

23	<i>ndhB</i>	1127	376	UCA→UUA	S→L	1	19 species
24	<i>ndhB</i>	1270	424	CAU→UAU	H→Y	1	19 species
25	<i>ndhB</i>	1502	501	CCA→CUA	P→L	1	19 species
26	<i>ndhD</i>	2	1	ACG→AUG	U→M	1	19 species
27	<i>ndhD</i>	305	102	UCA→UUA	S→L	1	19 species
28	<i>ndhD</i>	313	105	CGG→UGG	R→W	0.8	19 species
29	<i>ndhD</i>	383	128	UCA→UUA	S→L	1	19 species
30	<i>ndhD</i>	599	200	UCA→UUA	S→L	1	19 species
31	<i>ndhD</i>	674	225	UCA→UUA	S→L	1	19 species
32	<i>ndhD</i>	878	293	UCA→UUA	S→L	1	19 species
33	<i>ndhD</i>	887	296	CCC→CUC	P→L	1	19 species
34	<i>ndhD</i>	1298	433	UCA→UUA	S→L	0.8	19 species
35	<i>ndhD</i>	1405	469	CUU→UUU	L→F	0.8	19 species
36	<i>ndhF</i>	586	196	CUU→UUU	L→F	0.8	19 species
37	<i>ndhF</i>	1780	594	CCA→UCA	P→S	1	Only in <i>C. floridana</i>
38	<i>ndhG</i>	166	56	CAU→UAU	H→Y	0.8	19 species
39	<i>ndhG</i>	314	105	ACA→AUA	U→I	0.8	19 species
40	<i>ndhG</i>	494	165	GCU→GUU	A→V	0.8	19 species
41	<i>petB</i>	373	125	CCC→UCC	P→S	1	Only in <i>C. dabieshanensis</i> and <i>C. hunanensis</i>
42	<i>petB</i>	452	151	CCA→CUA	P→L	1	19 species
43	<i>psbE</i>	214	72	CCU→UCU	P→S	1	19 species
44	<i>psbF</i>	77	26	UCU→UUU	S→F	1	19 species
45	<i>rpoA</i>	830	277	UCA→UUA	S→L	1	19 species
46	<i>rpoB</i>	314	105	UCU→UUU	S→F	1	19 species
47	<i>rpoB</i>	527	176	UCA→UUA	S→L	1	19 species

48	<i>rpoB</i>	542	181	UCG→UUG	S→L	1	19 species
49	<i>rpoB</i>	586	196	CUU→UUU	L→F	1	Not found in <i>C. sinensis</i> and <i>C. kweichowensis</i>
50	<i>rpoB</i>	1976	659	UCU→UUU	S→F	1	19 species
51	<i>rpoB</i>	2402	801	UCA→UUA	S→L	0.86	19 species
52	<i>rpoC1</i>	62	21	UCA→UUA	S→L	1	19 species
53	<i>rpoC1</i>	278	93	UCU→UUU	S→F	1	19 species
54	<i>rpoC2</i>	1456	486	CGC→UGC	R→C	0.86	19 species
55	<i>rpoC2</i>	1597	533	CUU→UUU	L→F	1	19 species
56	<i>rpoC2</i>	2345	782	GCU→GUU	A→V	1	19 species
57	<i>rpoC2</i>	3146	1049	ACC→AUC	U→I	0.86	19 species
58	<i>rpoC2</i>	3764	1255	UCA→UUA	S→L	0.86	19 species
59	<i>rps14</i>	80	27	CCC→CUC	P→L	1	19 species
60	<i>rps14</i>	149	50	CCA→CUA	P→L	1	19 species
61	<i>rps16</i>	218	73	UCA→UUA	S→L	0.83	19 species
62	<i>rps8</i>	172	58	CUU→UUU	L→F	1	only in <i>C. laciniosa</i>
63	<i>rps2</i>	248	83	UCA→UUA	S→L	1	19 species

Supplementary Table 8. Ka/Ks (ω) and nucleotide polymorphisms of protein-coding Gene in *Carya* plastomes.

Gene	Ka/Ks (ω)	π	θ	Gene	Ka/Ks (ω)	π	θ
<i>accD</i>	0.206883	0.002260	0.002680	<i>psbH</i>	0.000000	0.000900	0.001290
<i>atpA</i>	0.191243	0.001340	0.002440	<i>psbI</i>	0.000000	0.001790	0.002580
<i>atpB</i>	0.299204	0.001400	0.000970	<i>psbJ</i>	0.000000	0.000000	0.000000
<i>atpE</i>	0.196416	0.001480	0.001420	<i>psbK</i>	0.000000	0.001070	0.001540
<i>atpF</i>	0.551268	0.002970	0.003110	<i>psbL</i>	0.000000	0.010100	0.007340
<i>atpH</i>	0.000000	0.000000	0.000000	<i>psbM</i>	0.000000	0.000000	0.000000
<i>atpI</i>	0.000000	0.001210	0.001540	<i>psbT</i>	0.000000	0.004550	0.002650
<i>ccsA</i>	0.969747	0.004290	0.005380	<i>psbZ</i>	0.000000	0.001610	0.003030
<i>cemA</i>	0.179279	0.001950	0.003730	<i>rbcL</i>	0.682693	0.001490	0.001800
<i>clpP</i>	0.089417	0.001350	0.001450	<i>rpl14</i>	0.000000	0.001970	0.004650
<i>matK</i>	0.530389	0.003300	0.005840	<i>rpl16</i>	0.000000	0.002220	0.002090
<i>ndhA</i>	1.160245	0.002630	0.002620	<i>rpl2</i>	0.000000	0.000000	0.000000
<i>ndhB</i>	0.000000	0.000070	0.000180	<i>rpl20</i>	0.457265	0.003800	0.004850
<i>ndhC</i>	0.000000	0.000000	0.000000	<i>rpl22</i>	0.249360	0.005990	0.008200
<i>ndhD</i>	0.362368	0.005420	0.004950	<i>rpl23</i>	0.000000	0.000000	0.000000
<i>ndhE</i>	0.000000	0.002600	0.002810	<i>rpl32</i>	0.000000	0.005410	0.005840
<i>ndhF</i>	0.466137	0.003260	0.003210	<i>rpl33</i>	0.144969	0.004350	0.005530
<i>ndhG</i>	0.169405	0.003480	0.003230	<i>rpl36</i>	0.000000	0.084950	0.223370
<i>ndhH</i>	0.302579	0.002720	0.002660	<i>rpoA</i>	0.518453	0.002330	0.002900
<i>ndhI</i>	0.213336	0.002480	0.002270	<i>rpoB</i>	0.332935	0.001760	0.002510
<i>ndhJ</i>	0.253986	0.002280	0.001800	<i>rpoC1</i>	0.278822	0.001260	0.002060
<i>ndhK</i>	0.067377	0.004210	0.003360	<i>rpoC2</i>	0.314354	0.002480	0.002870
<i>pbfl</i>	0.000000	0.004520	0.004340	<i>rpS11</i>	0.024313	0.002610	0.002060
<i>petA</i>	1.077751	0.002480	0.003260	<i>rpS12</i>	0.000000	0.000000	0.000000
<i>petB</i>	0.037075	0.001340	0.001760	<i>rpS14</i>	0.000000	0.003590	0.002830
<i>petD</i>	0.000000	0.001160	0.001090	<i>rpS15</i>	0.680318	0.002960	0.004190
<i>petG</i>	0.000000	0.000000	0.000000	<i>rpS16</i>	0.000000	0.003980	0.005180
<i>petL</i>	0.000000	0.001100	0.002980	<i>rpS18</i>	0.000000	0.002600	0.002810
<i>petN</i>	0.000000	0.001170	0.003180	<i>rpS19</i>	0.021620	0.004530	0.004030
<i>psaA</i>	0.093576	0.000890	0.001400	<i>rpS2</i>	0.241627	0.001250	0.001210
<i>psaB</i>	0.163367	0.001540	0.001820	<i>rpS3</i>	0.307191	0.002370	0.003470
<i>psaC</i>	0.000000	0.002810	0.002330	<i>rpS4</i>	0.140003	0.002470	0.002830
<i>psaI</i>	0.000000	0.000000	0.000000	<i>rpS7</i>	0.000000	0.000450	0.001220
<i>psaJ</i>	0.037774	0.006260	0.008870	<i>rpS8</i>	0.078369	0.001990	0.002830
<i>psbA</i>	0.114451	0.002200	0.002160	<i>ycf1</i>	0.584244905	0.004930	0.005980
<i>psbB</i>	0.000000	0.000660	0.000940	<i>ycf15</i>	0.000000	0.000000	0.000000
<i>psbC</i>	0.088545	0.001250	0.001560	<i>ycf2</i>	0.420059	0.001010	0.001130
<i>psbD</i>	0.000000	0.001410	0.001620	<i>ycf3</i>	0.257943	0.002150	0.001690
<i>psbE</i>	0.000000	0.001580	0.002270	<i>ycf4</i>	0.216835	0.001260	0.001550
<i>psbF</i>	0.000000	0.000000	0.000000				

Note: π , nucleotide polymorphism; θ , nucleotide polymorphism per site.