

Supplementary material

Supplementary table

Table S1. Chloroplast genomes are scattered in repeat sequence characteristic values

Repeat unit one length (bp)	Repeat Type	The first point of repeat unit	Repeat unit two length (bp)	The second point of repeat unit	Repeat unit interval	E-value
38	P	165	38	165	0	8.38E-14
37	F	42832	37	96316	0	3.35E-13
37	P	42832	37	136066	0	3.35E-13
32	P	6628	32	6628	0	3.43E-10
30	P	7834	30	44273	0	5.49E-09
28	P	28811	28	28844	0	8.78E-08
25	P	206	25	235	0	5.62E-06
23	F	42832	23	117139	0	8.99E-05
23	F	96316	23	117139	0	8.99E-05
23	P	117139	23	136080	0	8.99E-05
22	F	68423	22	120797	0	3.60E-04
21	F	7840	21	34612	0	1.44E-03
21	P	34612	21	44276	0	1.44E-03
21	F	66244	21	66265	0	1.44E-03
21	F	89671	21	89689	0	1.44E-03
21	P	89671	21	142709	0	1.44E-03
21	P	89689	21	142727	0	1.44E-03
21	F	142709	21	142727	0	1.44E-03
20	P	34680	20	44215	0	5.76E-03
20	P	35391	20	35421	0	5.76E-03
20	P	42132	20	42132	0	5.76E-03
20	R	49468	20	49468	0	5.76E-03
19	F	4636	19	22294	0	2.30E-02
19	F	9319	19	35677	0	2.30E-02
19	F	34798	19	106210	0	2.30E-02
19	P	34798	19	126190	0	2.30E-02
19	R	78081	19	78081	0	2.30E-02
19	R	124094	19	124094	0	2.30E-02
18	P	2833	18	2833	0	9.21E-02
18	R	7469	18	65507	0	9.21E-02
18	F	17721	18	45666	0	9.21E-02
18	P	18192	18	18192	0	9.21E-02
18	R	30408	18	80670	0	9.21E-02
18	P	31084	18	64059	0	9.21E-02
18	C	35541	18	44113	0	9.21E-02

18	C	44122	18	109609	0	9.21E-02
18	F	47432	18	47496	0	9.21E-02
18	R	57809	18	64053	0	9.21E-02
18	R	69674	18	80669	0	9.21E-02
18	F	80801	18	110252	0	9.21E-02
18	P	99684	18	105958	0	9.21E-02
18	F	99684	18	126443	0	9.21E-02
18	F	105958	18	132717	0	9.21E-02
18	C	111866	18	122668	0	9.21E-02
18	R	124256	18	124256	0	9.21E-02
18	P	126443	18	132717	0	9.21E-02
17	R	6197	17	6197	0	3.68E-01
17	R	8304	17	8304	0	3.68E-01
17	P	8760	17	17714	0	3.68E-01

Note: P = palindromic repeat, F = forward repeat, R = reverse repeat, and C = complement repeat.

Table S2. Codon Usage in this chloroplast genome

Codon	Amino acid	Frequency	Number
GCA	A	14.191	635
GCC	A	8.135	364
GCG	A	6.66	298
GCT	A	23.645	1058
TGC	C	3.241	145
TGT	C	9.208	412
GAC	D	7.978	357
GAT	D	30.662	1372
GAA	E	38.573	1726
GAG	E	12.113	542
TTC	F	18.102	810
TTT	F	41.546	1859
GGA	G	24.896	1114
GGC	G	8.448	378
GGG	G	11.778	527
GGT	G	21.432	959
CAC	H	5.766	258
CAT	H	18.817	842
ATA	I	27.556	1233
ATC	I	15.219	681
ATT	I	40.92	1831
AAA	K	43.356	1940
AAG	K	12.359	553
CTA	L	13.565	607
CTC	L	6.995	313
CTG	L	6.928	310

CTT	L	22.773	1019
TTA	L	34.461	1542
TTG	L	21.253	951
ATG	M	22.639	1013
AAC	N	10.861	486
AAT	N	37.88	1695
CCA	P	11.398	510
CCC	P	9.297	416
CCG	P	5.699	255
CCT	P	14.661	656
CAA	Q	27.757	1242
CAG	Q	8.023	359
AGA	R	17.231	771
AGG	R	7.397	331
CGA	R	13.633	610
CGC	R	4.403	197
CGG	R	4.805	215
CGT	R	12.448	557
AGC	S	5.23	234
AGT	S	14.795	662
TCA	S	14.705	658
TCC	S	11.509	515
TCG	S	6.213	278
TCT	S	21.454	960
ACA	T	16.18	724
ACC	T	7.8	349
ACG	T	5.565	249
ACT	T	21.142	946
GTA	V	19.465	871
GTC	V	5.922	265
GTG	V	7.554	338
GTT	V	20.806	931
TGG	W	17.432	780
TAC	Y	7.487	335
TAT	Y	30.662	1372
TAA	*	3.039	136
TAG	*	2.078	93
TGA	*	2.257	101

Table S3. Predicted RNA editing site in *L.bubifera* chloroplast genome

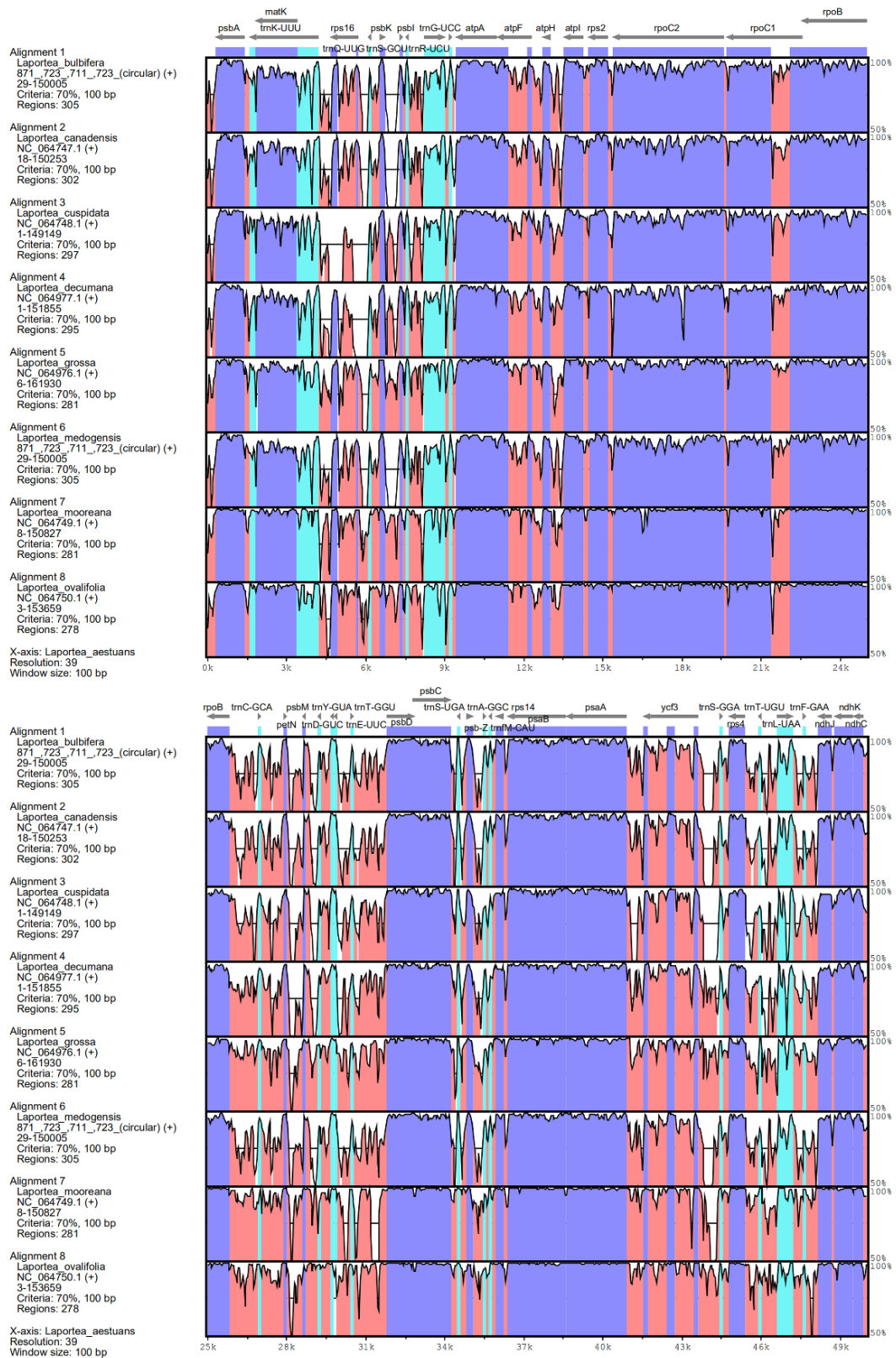
Gene	Nt Pos	AA Pos	Align Col	Effect	Score
<i>accD</i> (C = 0.8)	821	274	303	GCC (A) => GTC (V)	0.8
	1388	463	504	CCT (P) => CTT (L)	1
	1460	487	528	ACC (T) => ATC (I)	1
<i>atpA</i> (C = 0.8)	791	264	264	CCC (P) => CTC (L)	1

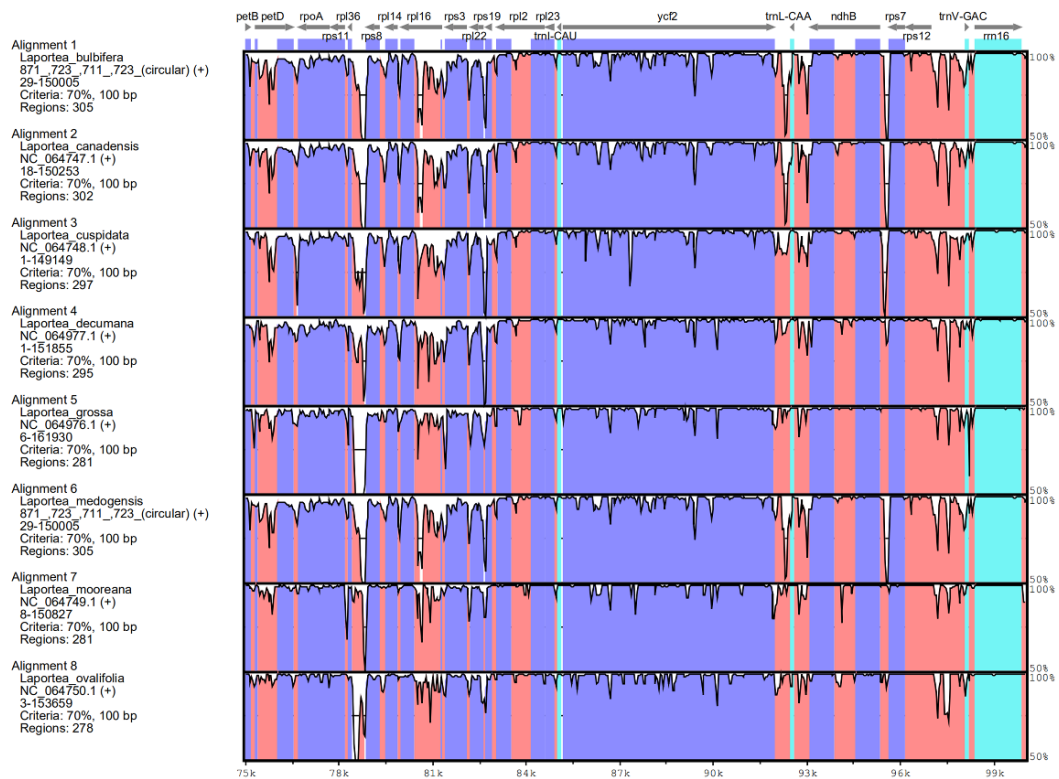
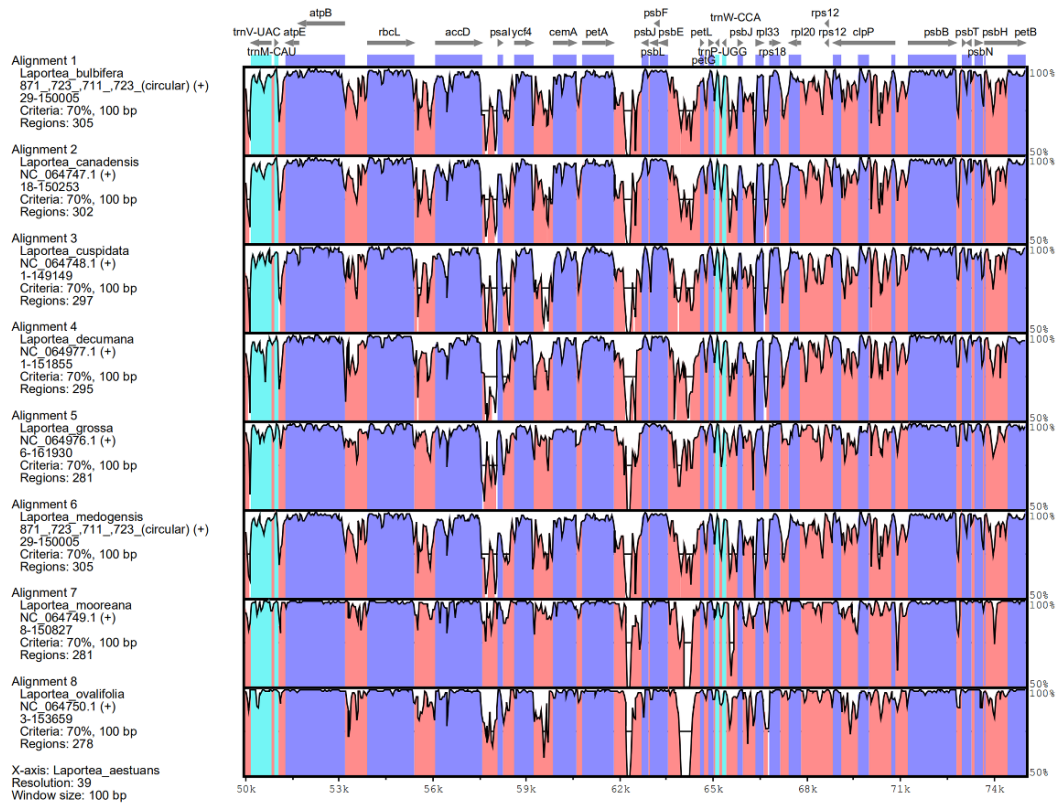
<i>atpB</i> (C = 0.8)	29	10	12	GCT (A) => GTT (V)	0.86
	31	11	13	CCC (P) => TCC (S)	1
<i>atpF</i> (C = 0.8)	92	31	31	CCA (P) => CTA (L)	0.86
<i>clpP</i> (C = 0.8)	559	187	187	CAC (H) => TAC (Y)	1
<i>matK</i> (C = 0.8)	52	18	18	CTC (L) => TTC (F)	1
<i>ndhA</i> (C = 0.8)	658	220	233	CAT (H) => TAT (Y)	1
	853	285	298	CAT (H) => TAT (Y)	1
	1205	402	415	TCA (S) => TTA (L)	0.86
	68	23	23	GCT (A) => GTT (V)	0.8
	107	36	36	CCT (P) => CTT (L)	1
	566	189	189	TCA (S) => TTA (L)	1
	853	285	285	CAC (H) => TAC (Y)	1
	1079	360	360	TCT (S) => TTT (F)	1
	149	50	50	TCA (S) => TTA (L)	1
	467	156	156	CCA (P) => CTA (L)	1
<i>ndhB</i> (C = 0.8)	542	181	181	ACG (T) => ATG (M)	1
	586	196	196	CAT (H) => TAT (Y)	1
	611	204	204	TCA (S) => TTA (L)	0.8
	737	246	246	CCA (P) => CTA (L)	1
	746	249	249	TCT (S) => TTT (F)	1
	830	277	277	TCA (S) => TTA (L)	1
	836	279	279	TCA (S) => TTA (L)	1
	1112	371	371	TCA (S) => TTA (L)	1
	1255	419	419	CAT (H) => TAT (Y)	1
	1481	494	494	CCA (P) => CTA (L)	1
<i>ndhD</i> (C = 0.8)	29	10	10	ACG (T) => ATG (M)	1
	340	114	114	CGG (R) => TGG (W)	0.8
	410	137	137	CCA (P) => CTA (L)	1
	626	209	209	TCA (S) => TTA (L)	1
	701	234	234	TCA (S) => TTA (L)	1
	905	302	302	TCA (S) => TTA (L)	1
	914	305	305	CCT (P) => CTT (L)	1
	1325	442	442	TCA (S) => TTA (L)	0.8
	1432	478	478	CTT (L) => TTT (F)	0.8
	196	66	66	CCT (P) => TCT (S)	1
<i>ndhF</i> (C = 0.8)	1427	476	476	ACA (T) => ATA (I)	0.8
<i>ndhG</i> (C = 0.8)	314	105	105	ACA (T) => ATA (I)	0.8
	494	165	165	GCC (A) => GTC (V)	0.8
<i>psbE</i> (C = 0.8)	214	72	72	CCT (P) => TCT (S)	1
<i>psbF</i> (C = 0.8)	77	26	26	TCT (S) => TTT (F)	1
<i>rpl2</i> (C = 0.8)	547	183	186	CCC (P) => TCC (S)	1
<i>rpoA</i> (C = 0.8)	830	277	279	TCA (S) => TTA (L)	1
<i>rpoC1</i> (C = 0.8)	41	14	14	TCG (S) => TTG (L)	1
	191	64	64	ACA (T) => ATA (I)	1

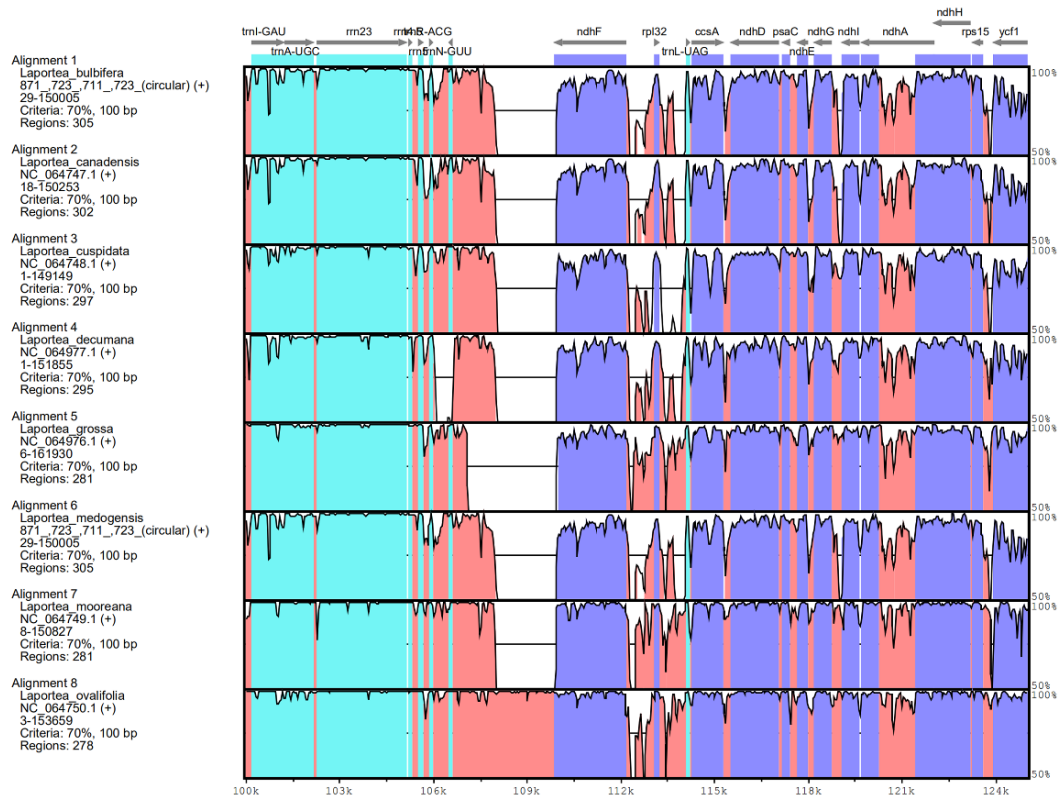
	1550	517	534	ACG (T) => ATG (M)	0.86
<i>rps2</i> (C = 0.8)	248	83	83	TCA (S) => TTA (L)	1
<i>rps14</i> (C = 0.8)	80	27	27	TCA (S) => TTA (L)	1
	149	50	53	CCA (P) => CTA (L)	1
<i>rps16</i> (C = 0.8)	212	71	71	TCA (S) => TTA (L)	0.83

Supplementary figure

Figure S1. Global alignment of eight chloroplast genomes of *Laportea* using mVISTA. Y-axis indicates the range of identity (50~100%). Alignment was performed using *L. aestuans* as a reference.







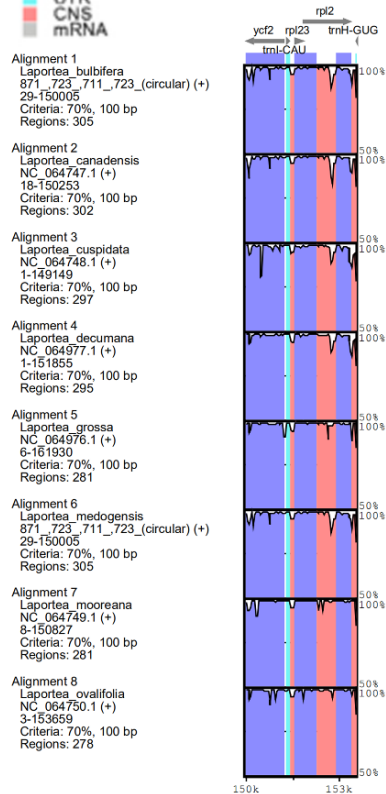
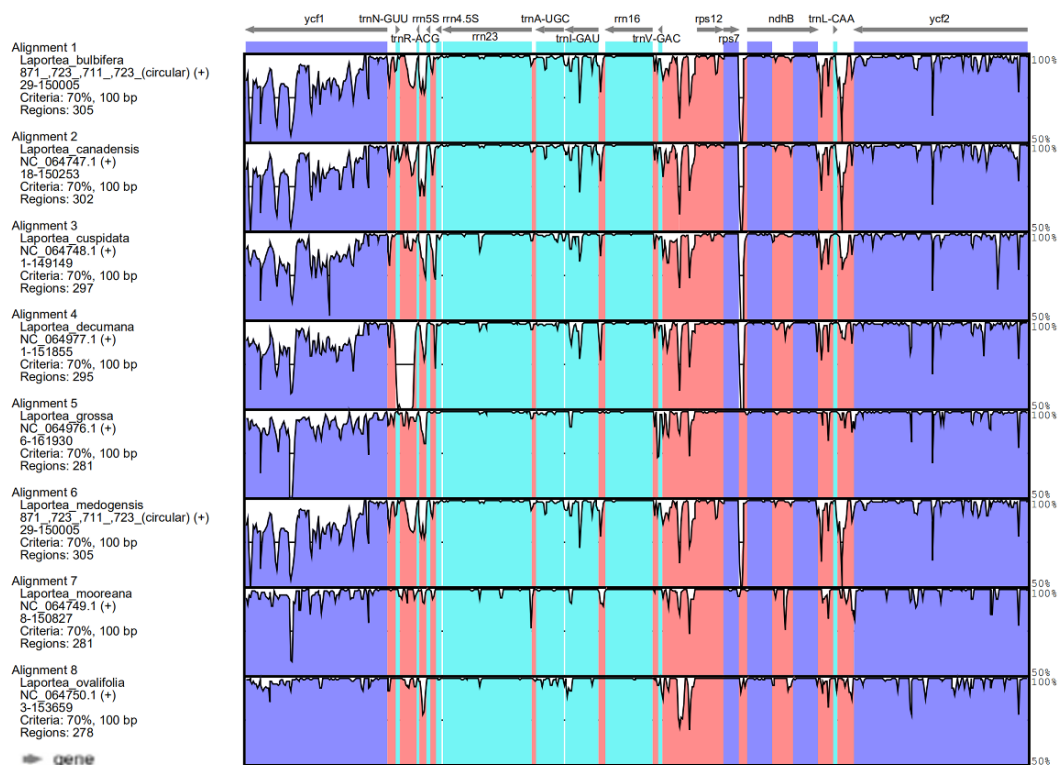
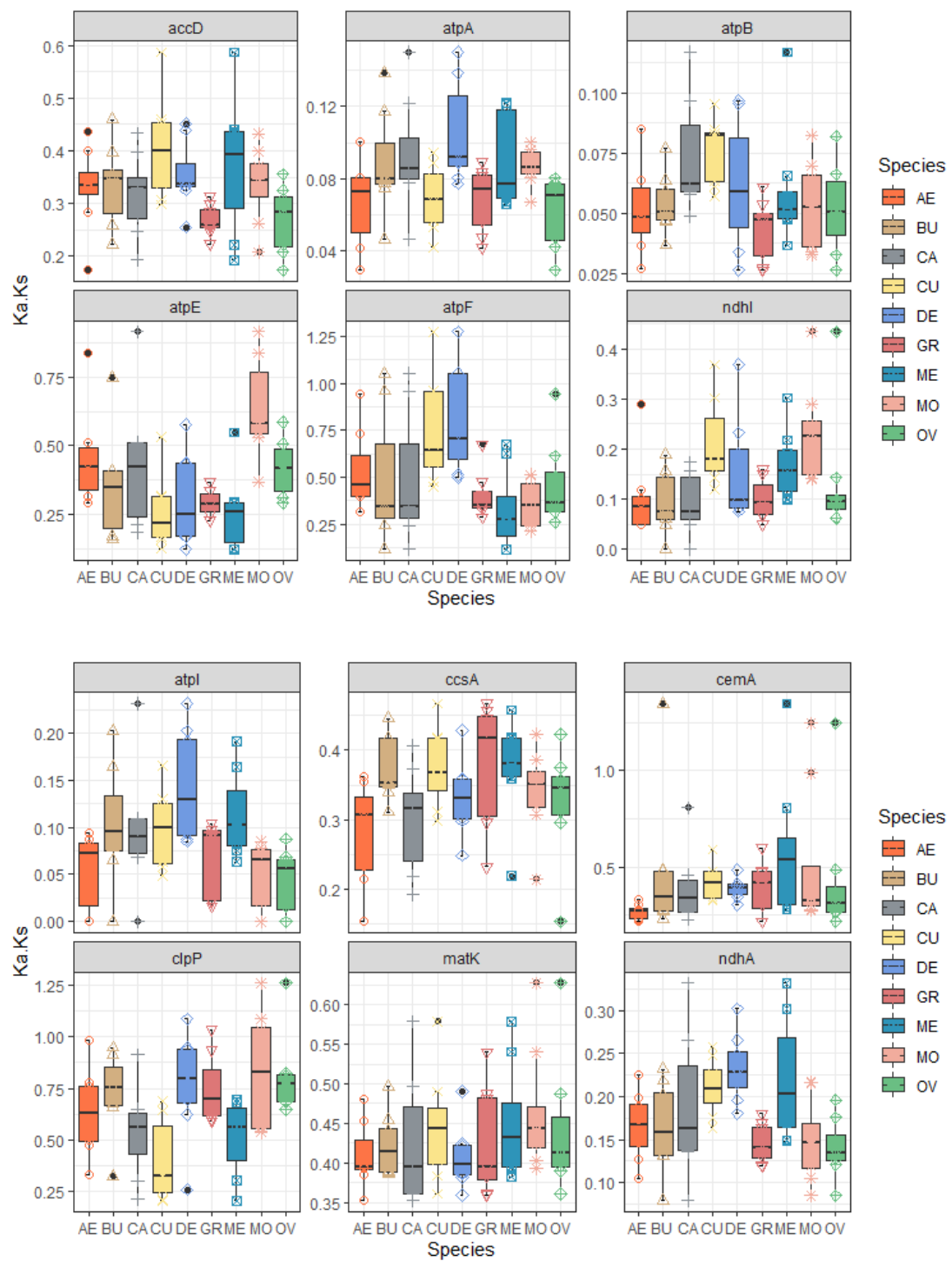
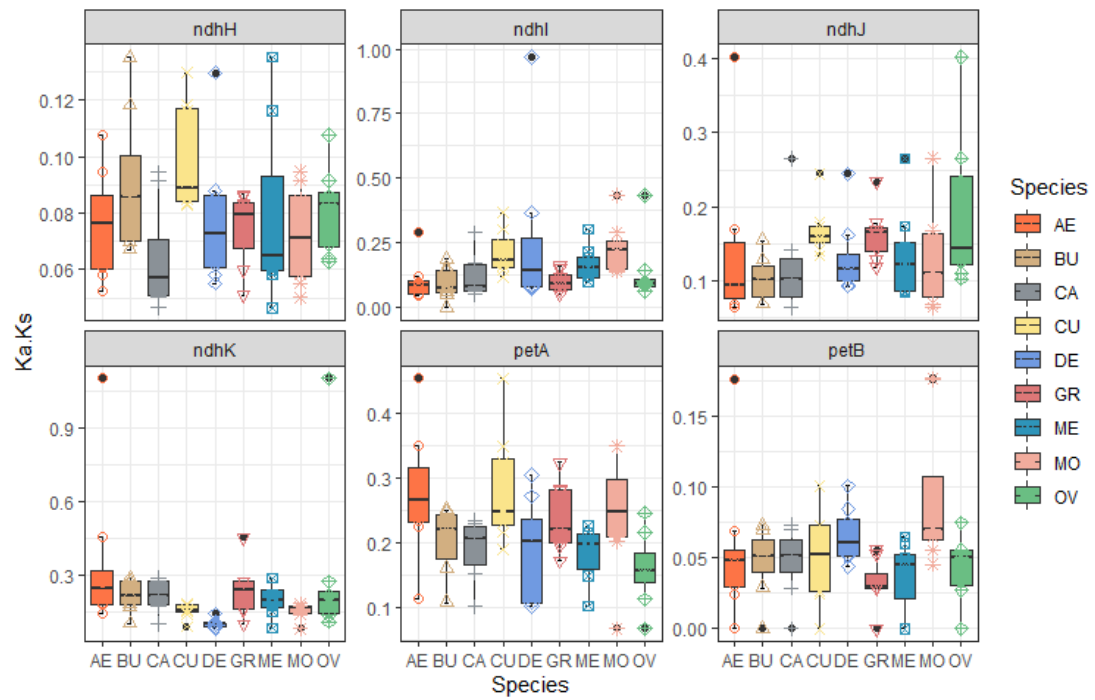
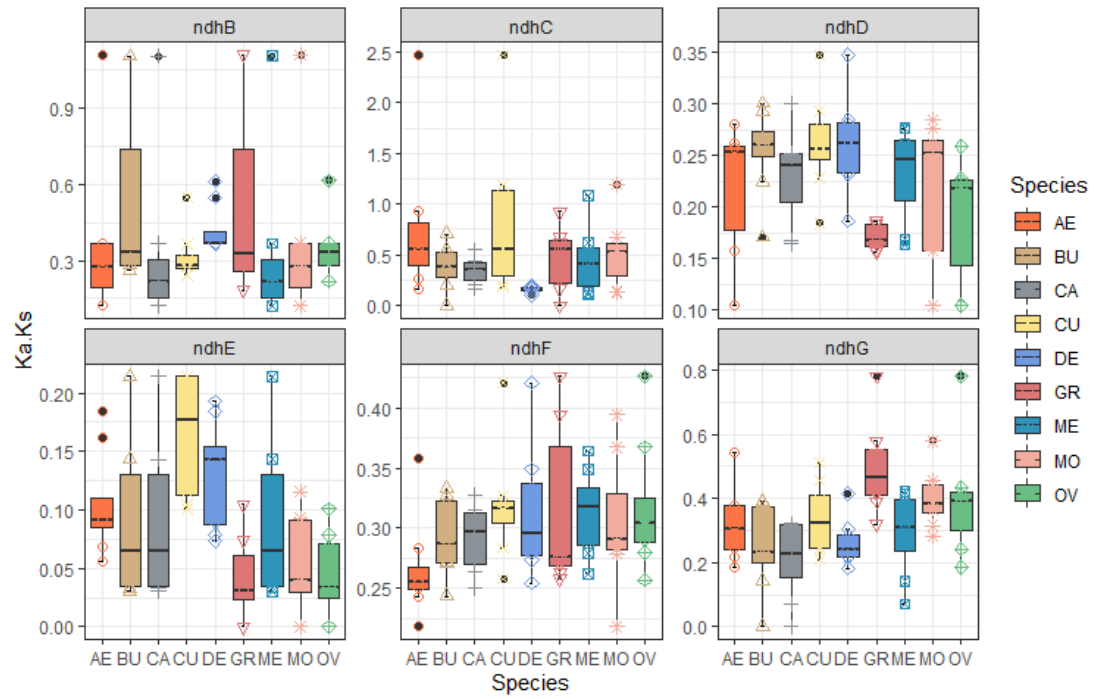
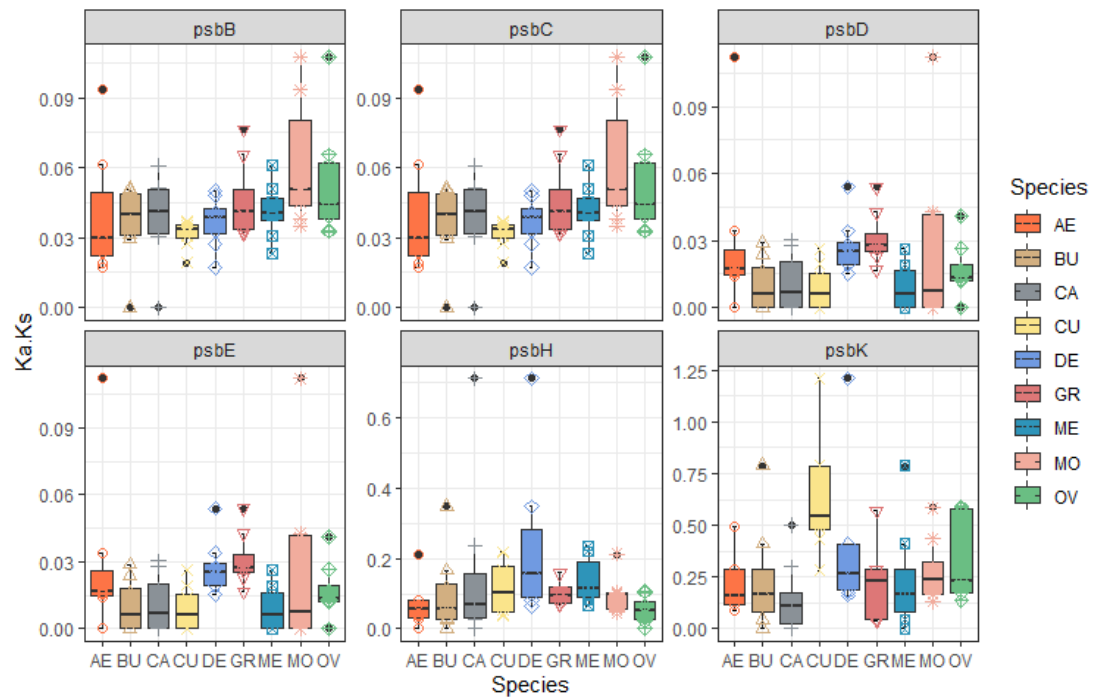
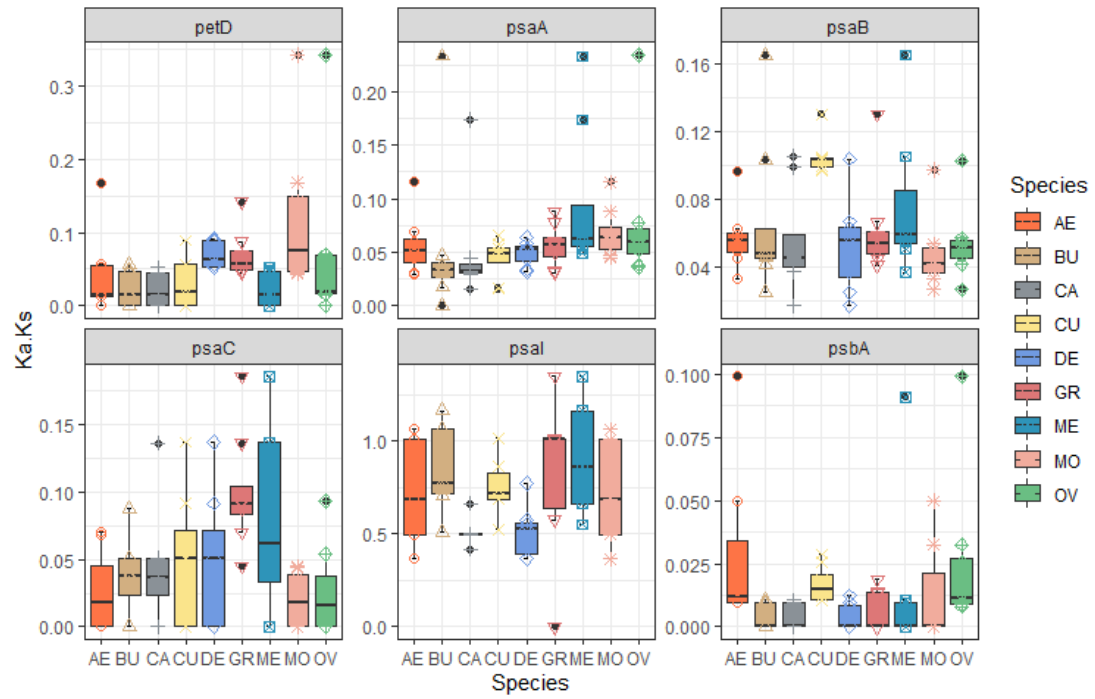
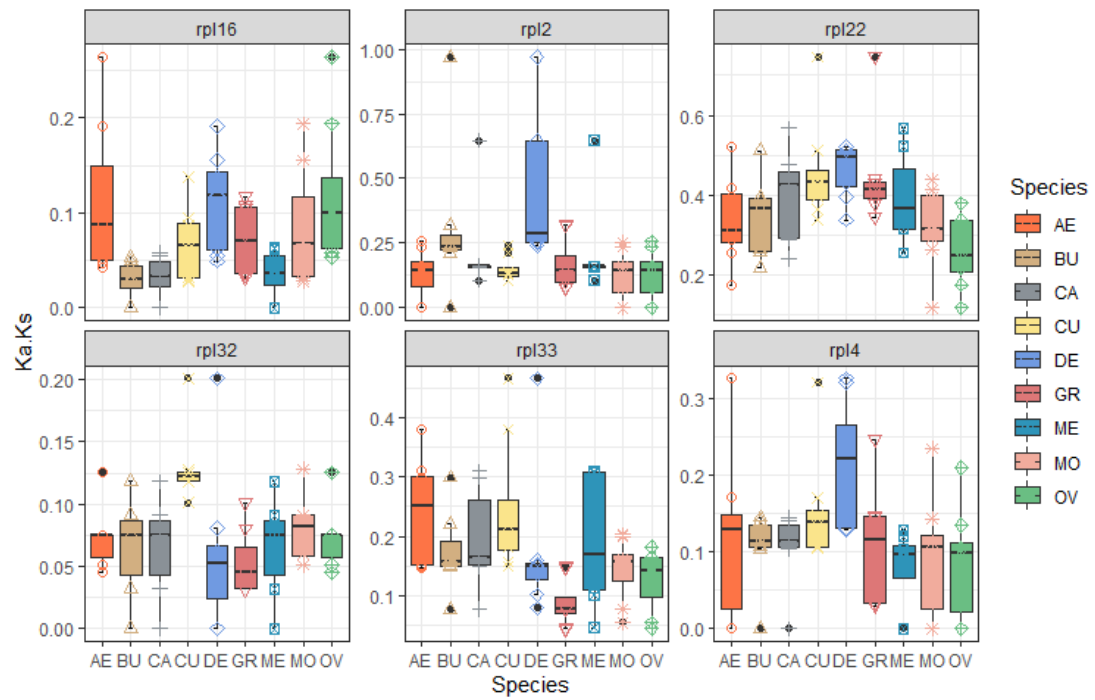
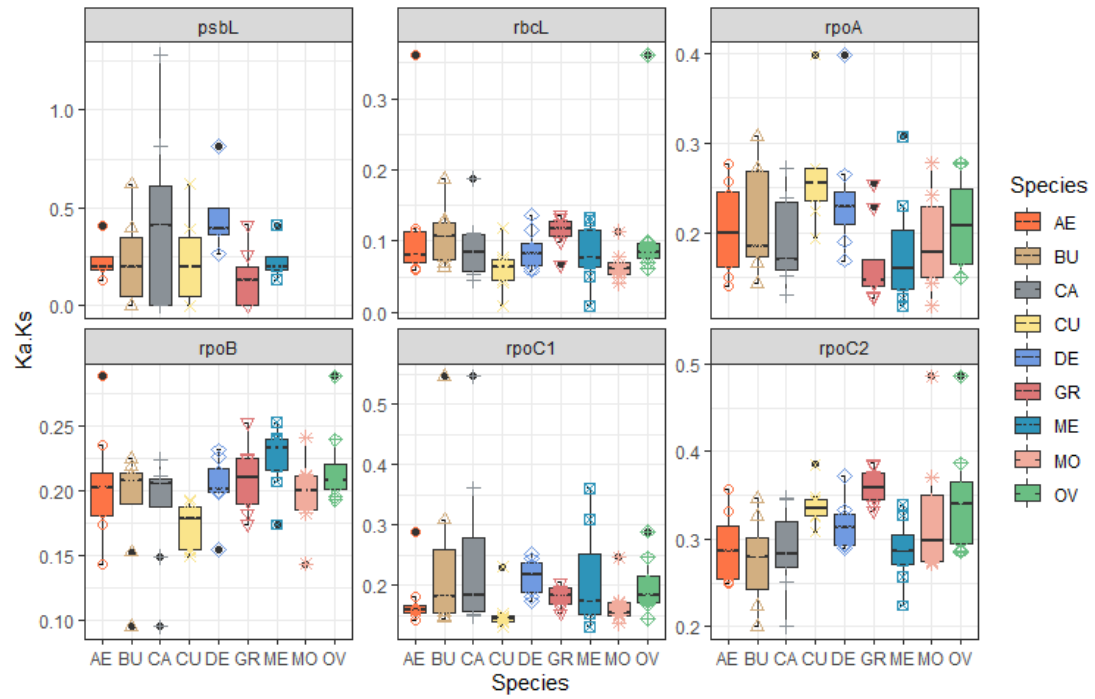


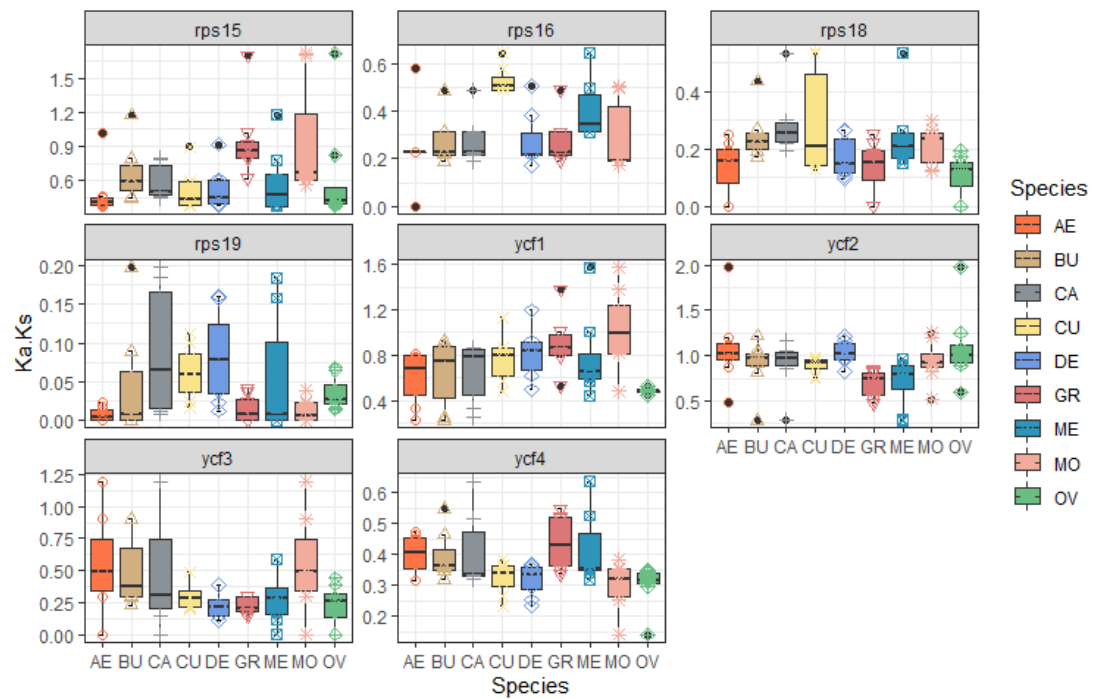
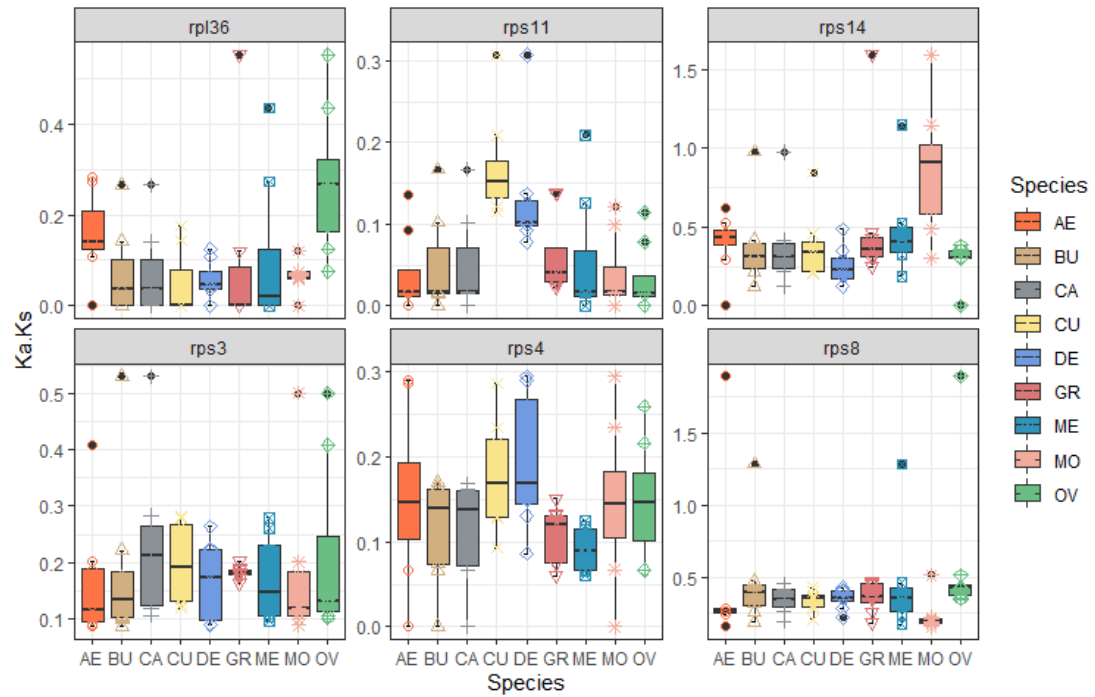
Figure S2. The dN/dS values between each plastid gene in the *Laportera* species are shown as box plots.











Tree scale: 0.01

Laportea grossa NC 064976
Laportea mooreana NC 064749
Laportea ovalifolia NC 064750
Laportea aestuans NC 064746
Laportea decumana NC 064977
Laportea cuspidata NC 064748
Laportea medogensis NC 064975
Laportea canadensis NC 064747
Laportea bulbifera
Boehmeria umbrosa NC 036990
Debregeasia orientalis NC 041413

(a) Phylogenetic tree showing relationships between various species. The tree is rooted at the bottom left and branches outwards. Species names and accession numbers are listed along the branches. Some branches are highlighted in red, and some are labeled 'Outgroup'.

(b) Phylogenetic tree showing relationships between various species. The tree is rooted at the bottom left and branches outwards. Species names and accession numbers are listed along the branches. Some branches are highlighted in red, and some are labeled 'Outgroup'.

(c) Phylogenetic tree showing relationships between various species. The tree is rooted at the bottom left and branches outwards. Species names and accession numbers are listed along the branches. Some branches are highlighted in red, and some are labeled 'Outgroup'.