

## Supplementary files

### Figure legend

**Figure S1:** Mauve alignment of ten *Rorippa* plastomes. Within each of the alignment, local collinear blocks are represented by blocks of the same color connected by lines.

**Figure S2:** Sequence identity plot of the ten *Rorippa* plastomes using *R. indica* as a reference.

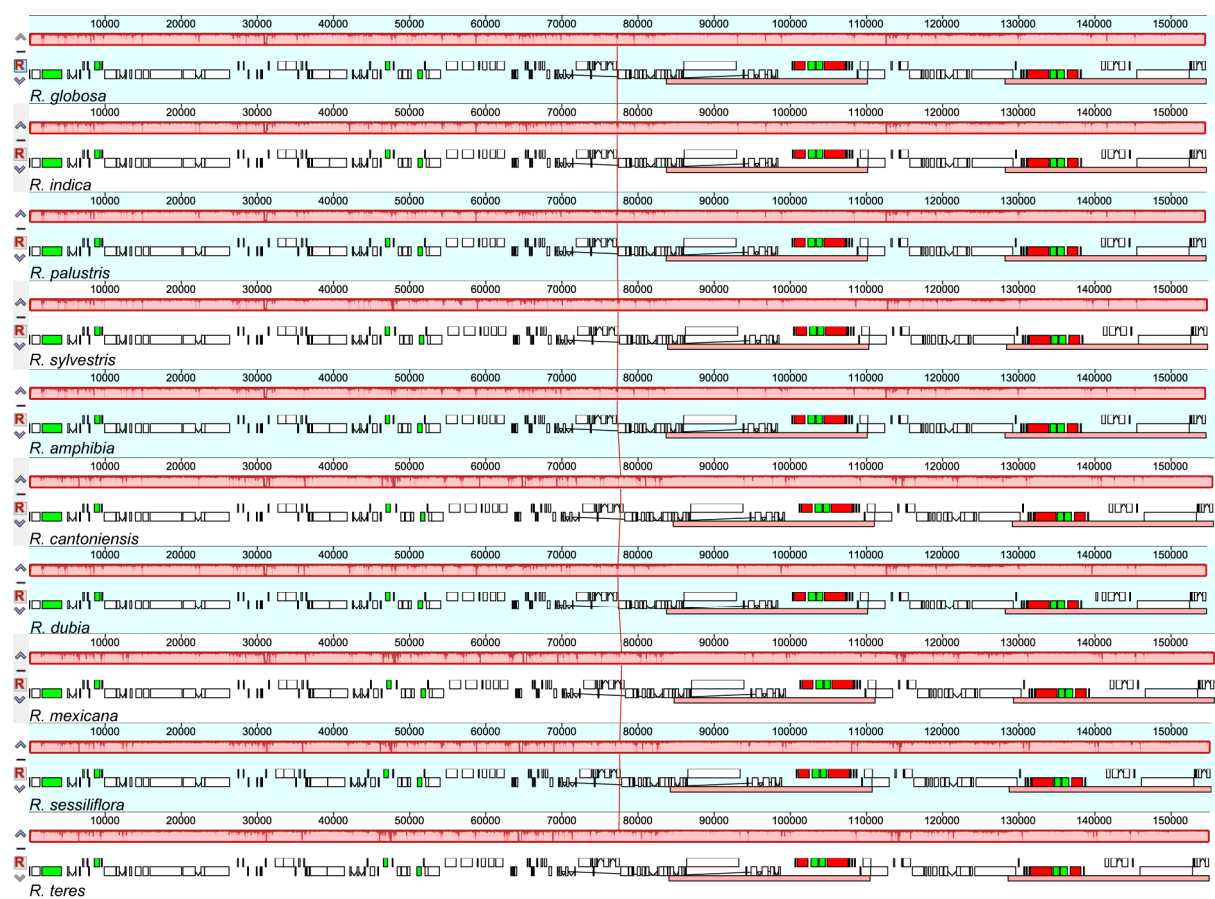


Figure S1

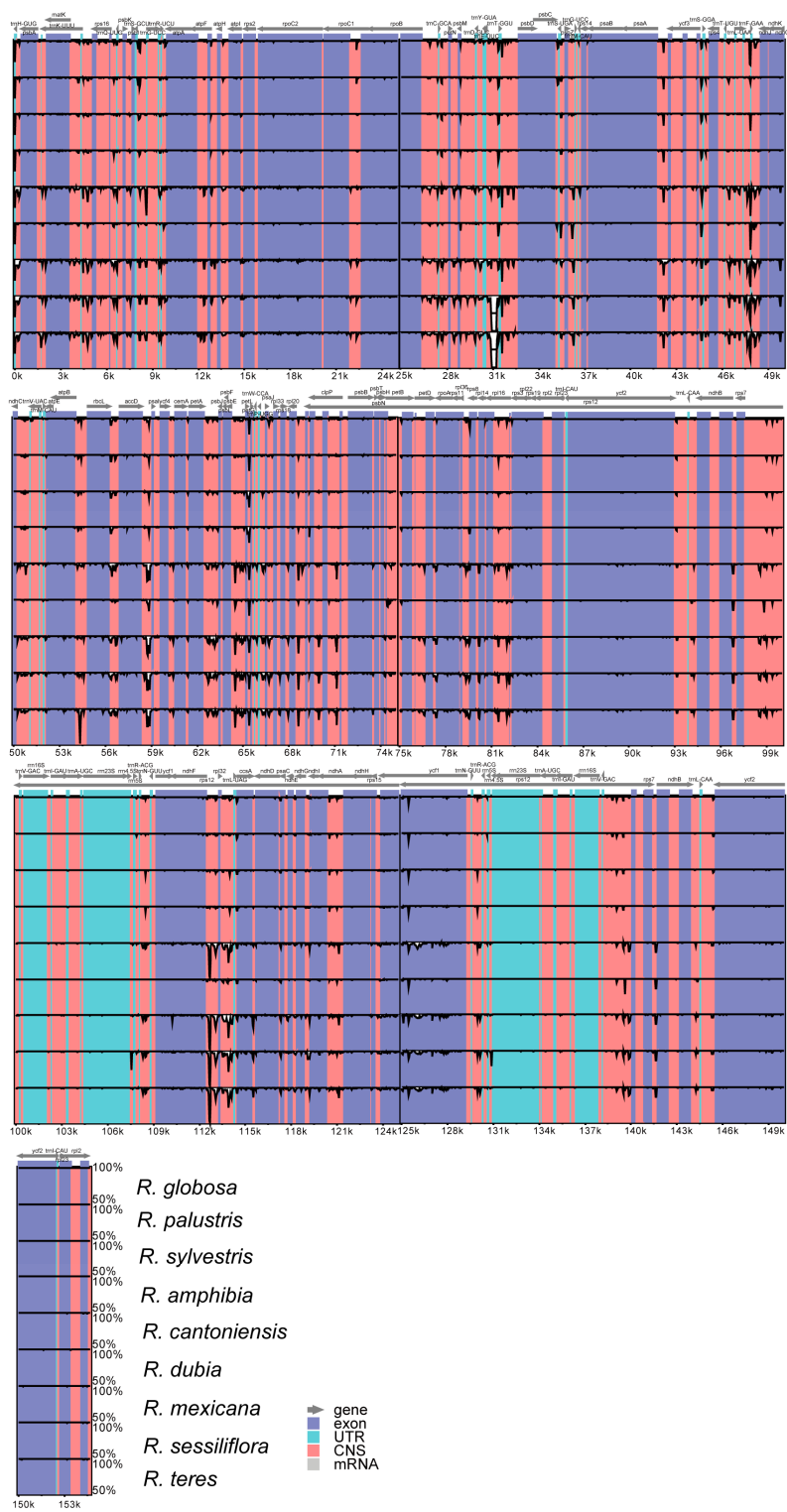


Figure S2

**Table S1 Collection locality and voucher information are provided for four newly sequenced plastomes.**

Species	Locality	Voucher information	Herbarium information
<i>R. globosa</i>	Qianyang, Shaanxi, China	1647	XBGH
<i>R. indica</i>	Xi'an, Shaanxi, China	RT2022110701	XBGH
<i>R. palustris</i>	Xi'an, Shaanxi, China	RT2023062002	XBGH
<i>R. sylvestris</i>	Taibai, Shaanxi, China	1662	XBGH

XBGH: Xi'an Botanical Garden of Shaanxi Province.

**Table S2 List of genes in the plastome of ten *Rorippa* species.**

Gene group	Gene name
Ribosomal RNAs	rrn16(2), rrn23(2), rrn4.5(2), rrn5(2)
Transfer RNAs	trnA-UGC*(2), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnM-CAU, trnG-UCC*, trnG-GCC, trnH-GUG, trnI-CAU(2), trnI-GAU*(2), trnK-UUU*, trnL-CAA(2), trnL-UAA*, trnL-UAG, trnM-CAU, trnN-GUU(2), trnP-UGG, trnQ-UUG, trnR-ACG(2), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC(2), trnV-UAC*, trnW-CCA, trnY-GUA
Proteins of small ribosomal subunit	rps16*, rps2, rps14, rps15, rps4, rps7(2), rps18, rps12* (2), rps11, rps8, rps3, rps19(2)
Proteins of large ribosomal subunit	rpl33, rpl20, rpl36, rpl14, rpl16*, rpl22, rpl2* (2), rpl23(2), rpl32
Subunits of RNA polymerase	rpoC2, rpoC1*
Photosystem I	psaB, psaA, psaI, psaJ, psaC
Photosystem II	psbA, psbB, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ
Cytochrome b/f complex	petA, petB*, petD*, petG, petL, petN
Subunits of ATP synthase	atpA, atpB, atpE, atpF*, atpH, atpI
Protease	clpP**
Large subunit of rubisco	rbcL
NADH dehydrogenase	ndhA*, ndhB*(2), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK
Maturase	matK
Envelope membrane protein	cemA
Acetyl-CoA carboxylase	accD
Synthesis gene	ccsA
Open reading frames (ORF, ycf)	ycf1, ycf2(2), ycf3**, ycf4, ycf15(2)

\* indicates gene with one introns;

\*\* indicates gene with two introns;

(2) indicates gene repeated in the IRs;

The *rps16* gene in *R. dubia* and *R. mexicana* plastome was identified as pseudogene.

**Table S3 Codon usage and relative synonymous codon usage (RSCU) values of protein-coding genes of ten *Rorippa* species.**

Codon	<i>R. globosa</i>		<i>R. indica</i>		<i>R. palustris</i>		<i>R. sylvestris</i>		<i>R. amphibia</i>		<i>R. cantoniensis</i>		<i>R. dubia</i>		<i>R. mexicana</i>		<i>R. sessiliflora</i>		<i>R. teres</i>	
	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU	Number	RSCU
UUU(F)	888	1.4	886	1.4	889	1.4	887	1.4	888	1.4	889	1.4	886	1.4	895	1.41	889	1.4	890	1.4
UUC(F)	380	0.6	380	0.6	380	0.6	382	0.6	382	0.6	383	0.6	382	0.6	379	0.59	385	0.6	383	0.6
UUA(L)	807	2.16	811	2.17	807	2.16	808	2.16	807	2.16	801	2.14	808	2.16	807	2.16	805	2.15	804	2.15
UUG(L)	406	1.09	407	1.09	406	1.09	408	1.09	408	1.09	411	1.1	408	1.09	407	1.09	409	1.09	408	1.09
CUU(L)	474	1.27	473	1.26	474	1.27	474	1.27	476	1.27	473	1.26	474	1.27	473	1.27	472	1.26	475	1.27
CUC(L)	123	0.33	123	0.33	123	0.33	124	0.33	124	0.33	123	0.33	123	0.33	122	0.33	122	0.33	124	0.33
CUA(L)	309	0.83	306	0.82	309	0.83	306	0.82	305	0.82	307	0.82	306	0.82	304	0.81	304	0.81	308	0.82
CUG(L)	125	0.33	127	0.34	125	0.33	125	0.33	125	0.33	129	0.34	128	0.34	130	0.35	130	0.35	126	0.34
AUU(I)	933	1.51	931	1.51	933	1.51	932	1.51	935	1.51	940	1.52	932	1.51	945	1.52	943	1.52	942	1.52
AUC(I)	326	0.53	326	0.53	326	0.53	325	0.53	325	0.53	330	0.53	326	0.53	323	0.52	330	0.53	325	0.52
AUA(I)	594	0.96	594	0.96	594	0.96	594	0.96	594	0.96	589	0.95	594	0.96	592	0.95	586	0.95	592	0.96
AUG(M)	472	1	471	1	472	1	472	1	475	1	472	1	470	1	471	1	472	1	472	1
GUU(V)	431	1.49	432	1.49	431	1.49	433	1.5	433	1.49	432	1.5	434	1.5	432	1.5	432	1.5	432	1.5
GUC(V)	145	0.5	146	0.5	145	0.5	146	0.5	145	0.5	145	0.5	145	0.5	143	0.5	143	0.5	143	0.5
GUA(V)	422	1.46	421	1.45	422	1.46	421	1.45	423	1.46	415	1.44	419	1.45	414	1.44	416	1.44	417	1.45
GUG(V)	159	0.55	159	0.55	159	0.55	158	0.55	158	0.55	160	0.56	160	0.55	162	0.56	161	0.56	158	0.55
UCU(S)	471	1.77	471	1.78	471	1.77	470	1.77	470	1.77	462	1.75	468	1.77	465	1.76	463	1.76	465	1.76
UCC(S)	232	0.87	233	0.88	232	0.87	230	0.87	232	0.87	237	0.9	234	0.88	234	0.89	236	0.9	236	0.9
UCA(S)	312	1.17	311	1.17	312	1.17	311	1.17	311	1.17	308	1.17	309	1.17	307	1.16	307	1.17	307	1.17
UCG(S)	153	0.58	153	0.58	153	0.58	156	0.59	156	0.59	154	0.58	156	0.59	155	0.59	153	0.58	153	0.58
CCU(P)	346	1.63	343	1.61	346	1.63	346	1.63	346	1.63	349	1.64	345	1.62	347	1.63	347	1.62	349	1.63
CCC(P)	156	0.73	159	0.75	156	0.73	155	0.73	155	0.73	149	0.7	156	0.73	154	0.72	154	0.72	152	0.71
CCA(P)	245	1.15	245	1.15	245	1.15	245	1.15	245	1.15	249	1.17	245	1.15	248	1.16	249	1.16	250	1.17
CCG(P)	102	0.48	103	0.48	102	0.48	103	0.49	103	0.49	105	0.49	104	0.49	105	0.49	105	0.49	103	0.48
ACU(T)	442	1.63	441	1.63	442	1.63	442	1.63	443	1.63	441	1.63	442	1.63	443	1.63	446	1.65	445	1.64
ACC(T)	186	0.69	185	0.68	186	0.69	186	0.69	186	0.69	186	0.69	185	0.68	186	0.69	184	0.68	185	0.68
ACA(T)	345	1.27	343	1.27	345	1.27	345	1.27	346	1.28	342	1.27	343	1.27	342	1.26	341	1.26	341	1.26

ACG(T)	110	0.41	112	0.41	110	0.41	110	0.41	110	0.41	112	0.41	114	0.42	113	0.42	112	0.41	112	0.41
GCU(A)	542	1.89	542	1.88	542	1.89	543	1.89	543	1.89	544	1.89	541	1.89	541	1.87	543	1.88	545	1.89
GCC(A)	175	0.61	174	0.6	175	0.61	175	0.61	175	0.61	180	0.62	173	0.6	177	0.61	177	0.61	175	0.61
GCA(A)	318	1.11	320	1.11	318	1.11	317	1.1	317	1.1	312	1.08	318	1.11	318	1.1	316	1.09	315	1.09
GCG(A)	114	0.4	115	0.4	114	0.4	114	0.4	114	0.4	118	0.41	116	0.4	120	0.42	119	0.41	120	0.42
UAU(Y)	649	1.64	650	1.64	649	1.64	650	1.64	650	1.64	657	1.65	651	1.64	655	1.65	654	1.65	654	1.65
UAC(Y)	143	0.36	142	0.36	143	0.36	142	0.36	143	0.36	138	0.35	142	0.36	140	0.35	141	0.35	141	0.35
UAA(*)	34	1.92	35	1.98	34	1.92	34	1.92	34	1.92	34	1.92	35	1.98	34	1.92	34	1.92	35	1.98
UAG(*)	13	0.74	12	0.68	13	0.74	13	0.74	13	0.74	13	0.74	12	0.68	12	0.68	12	0.68	12	0.68
CAU(H)	367	1.5	368	1.5	367	1.5	366	1.5	367	1.5	369	1.49	368	1.51	368	1.5	368	1.5	366	1.49
CAC(H)	123	0.5	123	0.5	123	0.5	123	0.5	123	0.5	125	0.51	121	0.49	123	0.5	124	0.5	126	0.51
CAA(Q)	613	1.59	614	1.59	613	1.59	613	1.59	613	1.59	611	1.57	614	1.59	615	1.58	615	1.58	614	1.58
CAG(Q)	160	0.41	160	0.41	160	0.41	160	0.41	160	0.41	165	0.43	160	0.41	164	0.42	163	0.42	165	0.42
AAU(N)	793	1.52	790	1.53	794	1.53	794	1.53	795	1.53	789	1.53	791	1.52	793	1.53	790	1.53	790	1.53
AAC(N)	248	0.48	246	0.47	247	0.47	247	0.47	247	0.47	241	0.47	249	0.48	242	0.47	243	0.47	242	0.47
AAA(K)	927	1.58	926	1.58	927	1.58	925	1.58	926	1.58	930	1.58	927	1.58	928	1.58	925	1.58	928	1.58
AAG(K)	245	0.42	249	0.42	245	0.42	246	0.42	246	0.42	246	0.42	246	0.42	246	0.42	247	0.42	245	0.42
GAU(D)	675	1.61	676	1.61	675	1.61	674	1.61	674	1.61	674	1.61	674	1.61	674	1.61	676	1.61	673	1.61
GAC(D)	162	0.39	163	0.39	162	0.39	164	0.39	163	0.39	164	0.39	164	0.39	165	0.39	164	0.39	165	0.39
GAA(E)	876	1.54	876	1.55	876	1.54	876	1.54	877	1.54	881	1.54	876	1.55	877	1.54	878	1.54	880	1.54
GAG(E)	260	0.46	257	0.45	260	0.46	260	0.46	262	0.46	261	0.46	257	0.45	263	0.46	263	0.46	261	0.46
UGU(C)	185	1.51	187	1.52	185	1.51	185	1.51	186	1.51	181	1.48	187	1.51	183	1.5	181	1.49	181	1.49
UGC(C)	60	0.49	59	0.48	60	0.49	60	0.49	60	0.49	63	0.52	60	0.49	61	0.5	62	0.51	62	0.51
UGA(*)	6	0.34	6	0.34	6	0.34	6	0.34	6	0.34	6	0.34	6	0.34	7	0.4	7	0.4	6	0.34
UGG(W)	379	1	378	1	379	1	378	1	377	1	379	1	378	1	379	1	379	1	379	1
CGU(R)	279	1.36	283	1.38	279	1.36	281	1.36	281	1.36	284	1.38	285	1.38	278	1.36	283	1.38	284	1.39
CGC(R)	91	0.44	91	0.44	91	0.44	91	0.44	91	0.44	86	0.42	89	0.43	89	0.44	89	0.43	88	0.43
CGA(R)	282	1.37	278	1.35	281	1.37	281	1.36	281	1.36	286	1.39	280	1.36	284	1.39	285	1.39	282	1.38
CGG(R)	101	0.49	100	0.49	102	0.5	101	0.49	101	0.49	96	0.47	99	0.48	97	0.47	96	0.47	96	0.47
AGU(S)	335	1.26	334	1.26	335	1.26	334	1.26	334	1.26	332	1.26	333	1.26	333	1.26	332	1.26	330	1.25
AGC(S)	91	0.34	90	0.34	91	0.34	90	0.34	90	0.34	90	0.34	90	0.34	88	0.33	88	0.33	90	0.34

AGA(R)	365	1.77	367	1.78	364	1.77	367	1.78	367	1.78	368	1.79	366	1.78	369	1.8	368	1.8	367	1.8
AGG(R)	116	0.56	115	0.56	116	0.56	116	0.56	118	0.57	111	0.54	116	0.56	110	0.54	109	0.53	109	0.53
GGU(G)	493	1.35	490	1.34	493	1.35	494	1.35	496	1.36	497	1.37	492	1.35	501	1.38	499	1.37	497	1.37
GGC(G)	139	0.38	143	0.39	139	0.38	138	0.38	138	0.38	140	0.39	142	0.39	137	0.38	139	0.38	141	0.39
GGA(G)	596	1.63	593	1.63	596	1.63	596	1.63	598	1.64	588	1.62	595	1.63	593	1.63	596	1.64	594	1.63
GGG(G)	231	0.63	232	0.64	231	0.63	232	0.64	230	0.63	227	0.63	231	0.63	223	0.61	223	0.61	224	0.62
Total	21280		21276		21280		21280		21302		21279		21280		21285		21284		21279	



**Table S4 Long repeat sequences comparison of ten *Rorippa* species.**

	F	P	R	C	Total
<i>R. globosa</i>	16	14	2	1	33
<i>R. indica</i>	18	13	2	1	34
<i>R. palustris</i>	17	14	3	2	36
<i>R. sylvestris</i>	29	15	1	0	45
<i>R. amphibia</i>	18	17	1	0	36
<i>R. cantoniensis</i>	26	12	0	0	38
<i>R. dubia</i>	18	13	1	2	34
<i>R. mexicana</i>	26	13	1	1	41
<i>R. sessiliflora</i>	22	17	1	1	41
<i>R. teres</i>	17	13	0	2	32

F: forward repeats, P: palindromic repeats, R: reverse repeats, C: complementary repeat.

**Table S5 Simple sequence repeats (SSRs) comparison of ten *Rorippa* species.**

	Mononucleotide	Dinucleotide	Trinucleotide	Tetranucleotide	Pentanucleotide	Hexanucleotide	Total
<i>R. globosa</i>	77	19	3	8			107
<i>R. indica</i>	73	18	3	8	2		104
<i>R. palustris</i>	77	19	3	8		1	108
<i>R. sylvestris</i>	75	19	4	8			106
<i>R. amphibia</i>	74	19	3	8			104
<i>R. cantoniensis</i>	75	17	4	7	1		104
<i>R. dubia</i>	75	18	3	8			104
<i>R. mexicana</i>	74	20	3	5			102
<i>R. sessiliflora</i>	76	20	3	9	1	2	111
<i>R. teres</i>	72	19	3	7		2	103

**Table S6 Pi values in coding and non-coding regions of ten *Rorippa* plastomes.**

Coding region	Pi	Region	Non-coding region	Pi	Region
psbA	0.002469	LSC	trnH-GUG-psbA	0.026496	LSC
matK	0.010414	LSC	psbA-trnK-UUU	0.010569	LSC
rps16	0.003496	LSC	trnK-UUU-matK	0.013699	LSC
atpA	0.004885	LSC	matK-trnK-UUU	0.007438	LSC
atpF	0.005646	LSC	trnK-UUU-rps16	0.021995	LSC
atpH	0	LSC	rps16 intron	0.011035	LSC
atpI	0.004148	LSC	rps16-trnQ-UUG	0.024129	LSC
rps2	0.005157	LSC	trnQ-UUG-psbK	0.011537	LSC
rpoC2	0.005813	LSC	psbK-psbI	0.024374	LSC
rpoC1	0.003013	LSC	trnS-GCU-trnG-UCC	0.012747	LSC
rpoB	0.003445	LSC	trnG-UCC intron	0.004622	LSC
psbD	0.002699	LSC	trnR-UCU-atpA	0.014183	LSC
psbC	0.003688	LSC	atpF intron	0.005991	LSC
rps14	0	LSC	atpF-atpH	0.011014	LSC
psaB	0.001592	LSC	atpH-atpI	0.009505	LSC
psaA	0.002426	LSC	atpI-rps2	0.008908	LSC
ycf3	0.004602	LSC	rps2-rpoC2	0.009259	LSC
rps4	0.000917	LSC	rpoC1 intron	0.007322	LSC
ndhJ	0.003075	LSC	rpoB-trnC-GCA	0.01563	LSC
ndhK	0.00413	LSC	trnC-GCA-petN	0.018601	LSC
ndhC	0.00202	LSC	petN-psbM	0.017336	LSC
atpE	0.003676	LSC	psbM-trnD-GUC	0.018456	LSC
atpB	0.004973	LSC	trnD-GUC-trnY-GUA	0.021847	LSC
rbcL	0.007747	LSC	trnE-UUC-trnT-GGU	0.020734	LSC
accD	0.004276	LSC	trnT-GGU-psbD	0.011525	LSC
ycf4	0.002402	LSC	trnS-UGA-psbZ	0.00994	LSC
cemA	0.004992	LSC	psbZ-trnG-GCC	0.021574	LSC
petA	0.004477	LSC	psaA-ycf3	0.011873	LSC
psbE	0.002116	LSC	ycf3 intron1	0.005274	LSC
rpl33	0.006302	LSC	ycf3 intron2	0.002899	LSC
rps18	0.004793	LSC	ycf3-trnS-GGA	0.008011	LSC
rpl20	0.008726	LSC	trnS-GGA-rps4	0.011752	LSC
rps12	0	LSC	rps4-trnT-UGU	0.009928	LSC
clpP	0.000338	LSC	trnT-UGU-trnL-UAA	0.01137	LSC
psbB	0.004846	LSC	trnL-UAA intron	0.0092	LSC
psbH	0.002402	LSC	trnL-UAA-trnF-GAA	0.01464	LSC
petB	0.002058	LSC	trnF-GAA-ndhJ	0.024892	LSC
petD	0.001104	LSC	ndhC-trnV-UAC	0.015975	LSC
rpoA	0.004991	LSC	trnV-UAC intron	0.003085	LSC
rps11	0.00405	LSC	atpB-rbcL	0.009471	LSC
rps8	0.005761	LSC	rbcL-accD	0.015377	LSC
rpl14	0.003433	LSC	accD-psaI	0.01471	LSC

rpl16	0.007898	LSC	psaI-ycf4	0.007998	LSC
rps3	0.00345	LSC	ycf4-cemA	0.019551	LSC
rpl22	0.007315	LSC	cemA-petA	0.013471	LSC
rps19	0.001434	LSC/IR	petA-psbJ	0.017332	LSC
rpl2	0.002667	IR	psbE-petL	0.020838	LSC
rpl23	0	IR	petL-petG	0.022719	LSC
ycf2	0.001167	IR	trnP-UGG-psaJ	0.01723	LSC
ndhB	0.000866	IR	psaJ-rpl33	0.017619	LSC
rps7	0.001567	IR	rpl33-rps18	0.015307	LSC
rrna16	0	IR	rps18-rpl20	0.010733	LSC
rrna23	0.00038	IR	rpl20-rps12	0.00855	LSC
ycf1a	0.002289	IR	clpP intron1	0.007553	LSC
ndhF	0.005369	SSC	clpP intron2	0.009127	LSC
ccsA	0.008083	SSC	clpP-psbB	0.008333	LSC
ndhD	0.003356	SSC	petB intron	0.009285	LSC
psaC	0.005149	SSC	petD intron	0.010448	LSC
ndhE	0.009877	SSC	petD-rpoA	0.019127	LSC
ndhG	0.005524	SSC	rpl36-rps8	0.012922	LSC
ndhI	0.003263	SSC	rps8-rpl14	0.012391	LSC
ndhA	0.004104	SSC	rpl16 intron	0.017544	LSC
ndhH	0.001184	SSC	rpl2 intron	0	IR
rps15	0.000749	SSC	ycf2-trnL-CAA	0.000221	IR
ycf1b	0.01146	SSC	trnL-CAA-ndhB	0.000344	IR
			ndhB intron	0.001071	IR
			ndhB-rps7	0.003468	IR
			rps12 intron	0	IR
			rps12-trnV-GAC	0.002509	IR
			trnV-GAC-rrn16	0	IR
			rrn16-trnI-GAU	0.001796	IR
			trnI-GAU intron	0.001336	IR
			trnA-UGC intron	0.000667	IR
			rrn4.5-rrn5	0.007287	IR
			rrn5-trnR-ACG	0.003613	IR
			trnR-ACG-trnN-GUU	0.004528	IR
			trnN-GUU-ycf1	0.000619	IR
			ndhF-rpl32	0.017113	SSC
			rpl32-trnL-UAG	0.036942	SSC
			ccsA-ndhD	0.015764	SSC
			psaC-ndhE	0.010689	SSC
			ndhE-ndhG	0.020178	SSC
			ndhG-ndhI	0.012815	SSC
			ndhA intron	0.010472	SSC
			rps15-ycf1	0.015893	SSC

**Table S7 List of species and their accession numbers used for constructing the phylogenetic tree.**

Species	Plastome	nrDNA/ITS
<i>Rorippa sylvestris</i>	PP297068	PP329014
<i>Rorippa globosa</i>	PP297065	PP329011
<i>Rorippa indica</i>	PP297066	PP329012
<i>Rorippa palustris</i>	PP297067	PP329013
<i>Rorippa cantoniensis</i>	NC_070424	ON616575
<i>Rorippa dubia</i>	NC_070412	ON616603
<i>Rorippa amphibia</i>	ON411624	ON616548
<i>Rorippa mexicana</i>	ON892569	ON616640
<i>Rorippa sessiliflora</i>	ON892599	ON616670
<i>Rorippa teres</i>	ON892567	ON616690
<i>Barbarea verna</i>	NC_009269	MG886675
<i>Armoracia rusticana</i>	NC_060501	MG886676
<i>Cardamine impatiens</i>	NC_026445	MT922979
<i>Cardamine macrophylla</i>	MF405340	MH711273
<i>Cardamine hirsuta</i>	NC_049607	MH808258
<i>Nasturtium officinale</i>	MK045962	MW031318
<i>Pachycladon ensyii</i>	NC_018565	EF015680
<i>Arabidella trisecta</i>	OL364740	JX630158
<i>Boechera laevigata</i>	NC_049596	DQ005987
<i>Boechera puberula</i>	NC_049597	JX146949
<i>Phoenicaulis cheiranthoides</i>	MK637770	DQ399121
<i>Lepidium virginicum</i>	NC_009273	LC090012
<i>Lepidium sativum</i>	NC_047178	OM283255
<i>Smelowskia altaica</i>	MK637789	EU489519
<i>Smelowskia calycina</i>	MK637794	AY230641
<i>Yinshania acutangula</i>	MK637817	KX244387
<i>Yinshania henryi</i>	NC_061291	KX244388
<i>Descurainia sophia</i>	NC_049631	MW432488
<i>Robeschia schimperii</i>	MK637786	HQ896627
<i>Tropidocarpum gracile</i>	MK637812	GQ497883
<i>Thelypodium laciniatum</i>	MK637813	KJ953749
<i>Mostacillastrum orbignyanum</i>	NC_049673	MN836389
<i>Sisymbrium officinale</i>	MK637802	MW271765
<i>Sisymbrium altissimum</i>	NC_059802	MW271701
<i>Brassica rapa</i>	MT726210	MK424344
<i>Brassica napus</i>	NC_016734	KM975580
<i>Raphanus sativus</i>	KJ716483	KM892621
<i>Arabis hirsuta</i>	NC_009268	HQ646663
<i>Arabis verna</i>	NC_049591	GU182043
<i>Draba oreades</i>	NC_037760	DQ467410
<i>Draba nemorosa</i>	NC_009272	DQ467361
<i>Scapiarabis saxicola</i>	MK637807	JQ919855

---

<i>Pseudoturritis turrta</i>	MK637782	JQ919845
<i>Megacarpaea delavayi</i>	NC_034360	KX244385
<i>Pugionium dolabratum</i>	NC_030515	MT923159
<i>Alyssum desertorum</i>	KY498535	KF512499
<i>Alyssum alyssoides</i>	NC_049574	EF514596
<i>Clypeola jonthlaspi</i>	NC_049609	EF514644
<i>Clausia aprica</i>	NC_049602	LK021257
<i>Dontostemon micranthus</i>	NC_049628	LK021230
<i>Neotorularia torulosa</i>	NC_049683	AF137571
<i>Braya humilis</i>	NC_035515	MH808255
<i>Aethionema cordifolium</i>	NC_009265	MT799725
<i>Aethionema grandiflorum</i>	NC_009266	MT799723

---