

Table S1. List of primers.

Primer sets	Primers	Primer Sequence (5'-3')	Length	GC (%)	T _m * (°C)	Expected size (bp)
VharA	VharA-F	GTG CCC TCG TTG ACT TCA GC	20	60.0	58.7	951
	VharA-R	GCA ACA GTC GGA CAA GTG GG	20	60.0	58.8	
VharB	VharB-F	TTA GGC AGA ATA CCG TCA CCC	20	52.4	56.6	1,189
	VharB-R	GTA AGA AGC ATG ACG CAG CC	20	55.0	56.5	
VharC	VharC-F	TAA CAA GCT GGG TGG GTA TGT	21	47.6	56.1	1,035
	VharC-R	GTG CCT CTG CAT CTA GCA TTG	20	52.4	56.2	
VharD	VharD-F	GCA ACA GTC GGA CAA GTG GG	20	60.0	58.8	1,193
	VharD-R	CCC TCT AGA CCT AGC TGC TGT C	22	59.1	58.4	
VharIR1	VharIR1-F	GTC TTC CCG TTC CTT CAT CTG	21	52.4	55.7	1,039
	VharIR1-R	GGG TCG AAC TCT TCT TTG GTG	21	52.4	55.7	
VharIR2	VharIR2-F	CAG GGT TCC ACA AGC AAT CG	20	55.0	56.6	918
	VharIR2-R	ACG ATA CAT TCC GTA CCT TGC	21	47.6	54.8	
VharIR3	VharIR3-F	ACT CTA TCA ATA ACC GAG CCG	21	47.6	54.1	857
	VharIR3-R	GCC CTA TGA ATG GGG ATA TTC C	22	50.0	55.1	
VharIR4	VharIR4-F	TCC TGT TTA GCA GAA AGA CGG	21	47.6	54.7	1,056

Primer sets	Primers	Primer Sequence (5'-3')	Length	GC (%)	T _m [*] (°C)	Expected size (bp)
	VharIR4-R	TCA TGC TCG TTC CAA GTT CG	20	50.0	55.4	
VharIR5	VharIR5-F	TTG GGC TCC TAG AAT ATG GC	20	50.0	54.2	949
	VharIR5-R	AAC CAT TTC ATC CGA CAG GC	20	50.0	55.6	
VharIR6	VharIR6-F	CGG GTT CAT TGA TAT TCC TGG	21	47.6	53.3	972
	VharIR6-R	CTG ACT TGC TCC TAC GGA AC	20	55.0	55.2	
VharIR7	VharIR7-F	ACT CCA CGT ATT GCT TGA CG	20	50.0	55.1	851
	VharIR7-R	AGG AAC CCT AGA TGC TGT CG	20	55.0	56.3	
VharIR8	VharIR8-F	TCA ATG AGC GAA AGG TAC GAA	21	42.9	54.2	982
	VharIR8-R	GTT CTT ATG TGT TTC CAC GCC	21	47.6	54.3	
VharIR9	VharIR9-F	TGG TGG GGT TAC CAT TAT CC	20	50.0	54.2	938
	VharIR9-R	TCC GAC TTG CAT GTG TTA AGC	21	47.6	55.7	
VharIR10	VharIR10-F	TTG AAA GAG AGG GGT GCC TT	20	50.0	56.3	967
	VharIR10-R	AGT ACG CCA TGC TAA TGT GC	20	50.0	55.6	
VharIR11	VharIR11-F	GAC AGG CTA TTA GCT CAG TGG	21	52.4	54.9	891
	VharIR11-R	GAT TCA TCC TTC CCG AAC GC	20	55.0	56.1	
VharIR12	VharIR12-F	TGC CTG TTG AAG AAT GAG CC	20	50.0	55.5	909

Primer sets	Primers	Primer Sequence (5'-3')	Length	GC (%)	T _m [*] (°C)	Expected size (bp)
	VharIR12-R	CAC CTT GCG TCC TTG AAC C	19	57.9	56.5	
VharIR13	VharIR13-F	GAG AGG CTC GGT GAA ATA GAC	21	52.4	54.8	962
	VharIR13-R	CAC TTC CAC TTG ACA CCT ATC G	22	50.0	55.2	
VharIR14	VharIR14-F	GGG CAG AAT AGC GGA GAA AG	20	55.0	55.6	1,014
	VharIR15-R	GGT CTA CCC AAT GCT AGA TGC	21	52.4	55.2	

* Melting temperatures were calculated using OligoAnalyzer™ (Integrated DNA Technologies, USA) with 0.25 µM Oligo concentration and 50 mM Na⁺ concentration.

VharA–D primers are for validation of the IR boundaries and VharIR1–14 primers are for correction of mismatched nucleotide bases between IRs

Table S2. List of 25 Rhamnaceae complete chloroplast genomes and the outgroup for the phylogenetic analysis.

Species	GenBank accession number	Size (bp)	Number of genes	Protein coding gene	tRNA	rRNA	GC (%)	LSC (bp)	IR (bp)	SSC (bp)	Reference
<i>Berchemia berchemiifolia</i> (<i>Berchemiella berchemiifolia</i>)	NC_037477	160410	127 (133)	82 (88)	37	8	37.2	88627	26514	18755	(1)
<i>Berchemia flavescent</i>	MK460212	160872	129 (133)	84 (88)	37	8	37.2	89066	26526	18754	(2)
<i>Berchemiella wilsonii</i>	NC_043912	160076	127 (133)	83 (88)	36 (37)	8	37.2	88331	26514	18717	(3)
<i>Berchemiella wilsonii</i> var. <i>wilsonii</i>	KY926621	160333	129 (133)	84 (88)	37	8	37.2	88582	26510	18731	(4)
<i>Hovenia acerba</i>	MN794429	161651	121 (133)	78 (88)	35 (37)	8	36.7	89443	26569	19070	(5)
<i>Hovenia acerba</i>	MN782301	161668	130 (133)	85 (88)	37	8	36.7	89452	26618	18980	(6)
<i>Hovenia dulcis</i>	NC_050971	162962	130 (133)	85 (88)	37	8	36.6	90900	26571	18920	(7)
<i>Hovenia dulcis</i>	MT225403	161667	121 (133)	78 (88)	35 (37)	8	36.7	89455	26616	18980	(8)
<i>Hovenia dulcis</i> voucher lpssy0298	MN723868	161636	131 (133)	86 (88)	37	8	36.6	89839	26316	19165	(7)
<i>Hovenia trichocarpa</i>	MT225404	161668	121 (133)	78 (88)	35 (37)	8	36.7	89455	26617	18979	(8)

Species	GenBank accession number	Size (bp)	Number of genes	Protein coding gene	tRNA	rRNA	GC (%)	LSC (bp)	IR (bp)	SSC (bp)	Reference
<i>Rhamnus crenata</i> Rhcr	LC635131	160454	126 (132)	84 (87)	34 (37)	8	37.0	88885	26418	1873 3	(9)
<i>Rhamnus globosa</i> voucher HCY2019012	MT360052	160642	129 (133)	84 (88)	37	8	37.1	88889	26428	1889 7	(10)
<i>Rhamnus heterophylla</i>	MT211599	156514	129 (133)	84 (88)	37	8	37.3	86024	25305	1988 0	(11)
<i>Rhamnus taquetii</i>	NC_045855	161205	129 (133)	84 (88)	37	8	37.1	89373	26448	1893 6	(12)
<i>Spyridium parvifolium</i> var. parvifolium isolate CC211	MH234313	161012	130 (133)	86 (88)	36 (37)	8	36.9	88814	26515	1916 8	(13)
<i>Ventilago harmandiana</i> Pierre	MZ325585	162904	134	89	37	8	36.6	90807	26401	1929 5	This study
<i>Ventilago leiocarpa</i>	MT974496	161880	127 (134)	82 (89)	37	8	37.0	90241	26255	1912 9	(14)
<i>Ziziphus incurva</i>	NC_050251	160920	129 (133)	84 (88)	37	8	36.8	88778	26477	1918 8	(15)
<i>Ziziphus jujuba</i>	NC_030299	161466	129 (134)	85 (89)	36 (37)	8	36.8	89120	26499	1934 8	(16)
<i>Ziziphus jujuba</i> cultivar Dongzao voucher BZG2016009	MF781071	161493	130 (134)	85 (89)	37	8	36.8	89178	26479	1935 7	(17)
<i>Ziziphus jujuba</i> var. <i>spinosa</i>	MW160433	161606	130 (134)	85 (89)	37	8	36.8	89292	26479	1935 6	(18)

Species	GenBank accession number	Size (bp)	Number of genes	Protein coding gene	tRNA	rRNA	GC (%)	LSC (bp)	IR (bp)	SSC (bp)	Reference
<i>Ziziphus jujuba</i> var. <i>spinosa</i> voucher Suanzao-007	KX266830	161211	130 (134)	85 (89)	37	8	36.8	88898	26478	19357	(19)
<i>Ziziphus jujuba</i> voucher Junzao-001	KX266829	161215	130 (134)	85 (89)	37	8	36.8	88975	26435	19370	(19)
<i>Ziziphus mauritiana</i> voucher ZMAU20161128	NC_037151	161543	129 (134)	84 (89)	37	8	36.8	89081	26558	19346	(19)
<i>Ziziphus spina-christi</i> voucher ZSC20161128	KY628305	161615	129 (134)	84 (89)	37	8	36.8	89161	26558	19338	(19)
<i>Cannabis sativa</i> cultivar Yoruba Nigeria*	NC_027223	153854	131 (133)	86 (88)	37	8	36.7	84028	26009	17808	(20)
<i>Ficus religiosa</i> voucher Ronsted86*	NC_033979	160627	130 (133)	85 (88)	37	8	35.9	88815	25853	20106	(21)

* Outgroups in the phylogeny

Numbers in parentheses indicate the number of genes after re-annotation.

References

1. Cheon KS, Kim KA, Yoo KO. The complete chloroplast genome sequence of *Berchemia berchemiifolia* (Rhamnaceae). *Mitochondrial DNA B Resour.* 2018;3(1):133-4.
2. Zhu X-F, Li Y, Lu Z. The complete chloroplast genome sequence of *Berchemia flavescent* (Rhamnaceae). *Mitochondrial DNA Part B.* 2019;4(1):1302-3.
3. Li Y, Wang J, Li P, Cheng S, Wang F. The complete chloroplast genome sequence of *Berchemiella wilsonii* (Rhamnaceae), an endangered endemic species. *Mitochondrial DNA Part B.* 2019;4(1):452-4.
4. Wang Y-H, Chen S-Y, Zhang S-D. Characterization of the complete chloroplast genome of *Berchemiella wilsonii* var. *wilsonii* (Rhamnaceae), an endangered species endemic to China. *Conservation Genetics Resources.* 2018;10(1):39-41.
5. Zhang L, Mao R, Bi H, Shen J, Wang Y, Li M. Characterization of the complete chloroplast genome of *Hovenia acerba* (Rhamnaceae). *Mitochondrial DNA B Resour.* 2020;5(1):934-5.

6. Yin Y, Tao J, Yang X, Jiao Q, Li Y, Feng L. The first complete chloroplast genome of *Hovenia acerba* Lindl. *Mitochondrial DNA B Resour.* 2020;5(1):658-9.
7. Ling L-Z, Zhang S-D. The complete chloroplast genome of *Hovenia dulcis* (Rhamnaceae). *Mitochondrial DNA Part B.* 2020;5(1):665-6.
8. Li M, Ye X, Bi H. Characterization of the complete chloroplast genome of two *Hovenia* species (Rhamnaceae). *Mitochondrial DNA Part B.* 2020;5(2):1731-2.
9. Wang J, Yang S. The complete chloroplast genome of *Rhamnus crenata* Siebold & Zuccarini (Rhamnaceae). *Mitochondrial DNA Part B, Resources.* 2021;6(9):2489-90.
10. Xie Y, Wang Z, Jiang X, Zhang X. The complete chloroplast genome of *Rhamnus globosa* (Rhamnaceae). *Mitochondrial DNA B Resour.* 2020;5(3):2830-1.
11. Li B, Chen H, Chen J. The complete chloroplast genome of plant *Rhamnus heterophylla* (Rhamnaceae). *Mitochondrial DNA Part B.* 2020;5(2):1850-1.
12. Jin D-P, Park J-W, Park J-S, Choi B-H. The complete plastid genome of *Rhamnus taquetii*, an endemic shrub on the Jeju Island of Korea. *Mitochondrial DNA Part B.* 2020;5(1):924-6.
13. Clowes C, Fowler RM, Brown GK, Bayly MJ. The complete chloroplast genome sequence of *Spyridium parvifolium* var. *parvifolium* (family Rhamnaceae; tribe Pomaderreae). *Mitochondrial DNA Part B.* 2018;3(2):807-9.
14. Lu X, Luo Q, Qin Y, Yan Q, Guo S. The complete chloroplast genome sequence of *Ventilago leiocarpa* Benth. *Mitochondrial DNA Part B.* 2021;6(3):736-7.
15. Wang Y, Hao J, Yuan X, Lu B. The complete chloroplast genome sequence of *Ziziphus incurva*. *Mitochondrial DNA Part B, Resources.* 2019;4(2):3465-6.
16. Ma Q, Li S, Bi C, Hao Z, Sun C, Ye N. Complete chloroplast genome sequence of a major economic species, *Ziziphus jujuba* (Rhamnaceae). *Curr Genet.* 2017;63(1):117-29.
17. Gao C-M, Gao Y-C, Liu X-H. The complete genome of *Ziziphus jujuba* cv. *dongzao*, an economic crop in Yellow River Delta of China. *Mitochondrial DNA Part B.* 2017;2(2):692-3.
18. Zhang Y, Hu G, Mao W, Dong N, Chen B, Pan Q. Chloroplast genome sequence of the wild *Ziziphus jujuba* Mill. var. *spinosa* from North China. *Mitochondrial DNA B Resour.* 2021;6(2):666-7.
19. Huang J, Chen R, Li X. Comparative Analysis of the Complete Chloroplast Genome of Four Known *Ziziphus* Species. *Genes (Basel).* 2017;8(12).
20. Oh H, Seo B, Lee S, Ahn DH, Jo E, Park JK, et al. Two complete chloroplast genome sequences of *Cannabis sativa* varieties. *Mitochondrial DNA A DNA Mapp Seq Anal.* 2016;27(4):2835-7.
21. Bruun-Lund S, Clement WL, Kjellberg F, Rønsted N. First plastid phylogenomic study reveals potential cyto-nuclear discordance in the evolutionary history of *Ficus* L. (Moraceae). *Molecular Phylogenetics and Evolution.* 2017;109:93-104.

Table S3. List of re-annotated genes.

Species	Gene	Updated position	Detail
<i>Berchemia berchemiifolia</i> NC_037477	<i>rps19</i>	complement(88822..88544)	Re-annotate a missing gene in IRb
	<i>rps19</i>	join(160216..160410,1..33)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	complement(134970..129272)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114068..115147	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(97981..98134,98411..98515)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(150523..150627,150904..151057))	Re-annotate a missing gene in IRa
<i>Berchemia flavescens</i> MK460212	<i>ndhB</i>	complement(join(99945..100700,101381..102157))	Correct gene location
	<i>ndhB</i>	join(147781..148557,149238..149993)	Correct gene location
	<i>ndhF</i>	complement(115617..117857)	Correct gene location
	<i>psbJ</i>	complement(68137..68259)	Correct gene location
	<i>psbK</i>	7782..7967	Correct gene location
	<i>rpoC1</i>	complement(join(22420..24030,24811..25242))	Correct gene location
	<i>rpoC2</i>	complement(18085..22242)	Correct gene location
	<i>rps19</i>	join(160678..160872,1..24)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114510..115598	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98441..98594,98871..98975)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(150964..151068,151345..151498))	Re-annotate a missing gene in IRa
	<i>ycf4</i>	64488..65042	Correct gene location

Species	Gene	Updated position	Detail
<i>Berchemiella wilsonii</i> KY926621	<i>rps19</i>	join(160139..160333,1..24)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114027..115097	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(97936..98089,98366..98470)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(150446..150550,150827..150980))	Re-annotate a missing gene in IRa
<i>Berchemiella wilsonii</i> NC_043912	<i>atpF</i>	complement(join(14287..14142,13353..12943))	Re-annotate a missing gene in LSC
	<i>ndhD</i>	complement(120550..122061)	Correct gene location
	<i>ndhK</i>	complement(53244..53924)	Correct gene location
	<i>petB</i>	join(79057..79062,79850..80491)	Correct gene location
	<i>petD</i>	join(80684..80690,81411..81886)	Re-annotate a missing gene in LSC
	<i>petN</i>	30714..30803	Correct gene location
	<i>psbC</i>	36619..38040	Correct gene location
	<i>psbI</i>	8491..8601	Correct gene location
	<i>psbK</i>	7856..8041	Correct gene location
	<i>psbL</i>	complement(67927..67811)	Re-annotate a missing gene in LSC
	<i>psbN</i>	complement(78152..78593)	Correct gene location
	<i>rbcL</i>	58808..60235	Correct gene location
	<i>rpl36</i>	complement(83821..83708)	Correct sequence
	<i>rpoC1</i>	complement(24770..25204)	Correct gene location
	<i>rpoC2</i>	complement(18037..22209)	Correct gene location

Species	Gene	Updated position	Detail
	<i>rps16</i>	complement(join(6674..6713,5794..5558))	Re-annotate a missing gene in LSC
	<i>rps19</i>	join(159882..160076,1..24)	Correct gene location
	<i>trnG-UCC</i>	join(9954..9975,10693..10739)	Re-annotate a missing gene in LSC
	<i>ycf15</i>	join(97684..97837,98114..98218)	Correct gene location
	<i>ycf15</i>	complement(join(150190..150294,150571..150724))	Correct gene location
<i>Hovenia acerba</i> MN782301	<i>ndhD</i>	complement(122015..123526)	Correct gene location
	<i>psbL</i>	complement(68666..68550)	Re-annotate a missing gene in LSC
	<i>psbN</i>	complement(79339..79470)	Correct gene location
	<i>rpoC1</i>	complement(join(22540..24165,24924..25353))	Correct gene location
	<i>rps19</i>	join(161535..161668,1..10)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114855..116090	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98787..98940,99233..99337)	Correct gene location
	<i>ycf15</i>	complement(join(151783..151887,152180..152333))	Correct gene location
<i>Hovenia acerba</i> MN794429	<i>atpF</i>	complement(join(41094..40949,40213..39803))	Re-annotate a missing gene in LSC
	<i>ndhD</i>	complement(150078..148567)	Re-annotate a missing gene in SSC
	<i>petD</i>	join(108190..108196,108934..109409)	Re-annotate a missing gene in LSC
	<i>psbC</i>	63230..64650	Re-annotate a missing gene in LSC
	<i>psbL</i>	complement(95227..95111)	Re-annotate a missing gene in LSC

Species	Gene	Updated position	Detail
	<i>rpoC2</i>	complement(44768..48931)	Correct gene location
	<i>rps19</i>	complement(116146..115868)	Re-annotate a missing gene in IRb
	<i>rps19</i>	join(26436..26569,1..10)	Re-annotate a missing gene in IRa
	<i>trnM-CAU</i>	66343..66416	Re-annotate a missing gene in LSC
	<i>trnG-UCC</i>	join(36504..36526,37230..37278)	Re-annotate a missing gene in LSC
	<i>ycf1</i>	141416..142651	Re-annotate a missing gene in IRb
	<i>ycf1</i>	complement(join(157061..161651,1..1166))	Correct gene location
	<i>ycf15</i>	join(16684..16788,17081..17234)	Re-annotate a missing gene in IRa
	<i>ycf15</i>	complement(join(125348..125501,125794..125898))	Re-annotate a missing gene in IRb
<i>Hovenia dulcis</i> MN723868	<i>ndhE</i>	complement(124050..124355)	Correct gene location
	<i>psbJ</i>	complement(68344..68466)	Correct gene location
	<i>rpoA</i>	complement(82931..83926)	Correct gene location
	<i>rpoC1</i>	complement(join(22437..24047,24811..25242))	Correct gene location
	<i>rpoC2</i>	complement(18105..22259)	Correct gene location
	<i>rps19</i>	161458..161505	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114776..116023	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98706..98859,99152..99256)	Correct gene location
	<i>ycf15</i>	complement(join(151689..151793,152086..152239))	Correct gene location

Species	Gene	Updated position	Detail
<i>Hovenia dulcis</i> MT225403	<i>atpF</i>	complement(join(14382..14527,13647..13237))	Re-annotate a missing gene in LSC
	<i>ndhD</i>	complement(123527..122016)	Re-annotate a missing gene in SSC
	<i>petD</i>	(81630..81636),(82374..82849)	Re-annotate a missing gene in LSC
	<i>psbC</i>	36669..38089	Re-annotate a missing gene in LSC
	<i>psbL</i>	complement(68668..68552)	Re-annotate a missing gene in LSC
	<i>rpoC2</i>	complement(18201..22364)	Correct gene location
	<i>rps19</i>	complement(89586..89308)	Re-annotate a missing gene in IRb
	<i>rps19</i>	join(161536..161667,1..12)	Re-annotate a missing gene in IRa
	<i>trnfM-CAU</i>	39782..39855	Re-annotate a missing gene in LSC
	<i>trnG-UCC</i>	join(9937..9959,10665..10712)	Re-annotate a missing gene in LSC
	<i>ycfI</i>	complement(join(130510..132533,132567..136266))	Correct gene location
	<i>ycfI</i>	114856..116091	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98788..98941,99234..99338)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151784..151888,152181..152334))	Re-annotate a missing gene in IRa
<i>Hovenia dulcis</i> NC_050971	<i>ndhB</i>	complement(join(101700..102455,103136..103912))	Correct gene location
	<i>ndhB</i>	join(149951..150727,151408..152163)	Correct gene location
	<i>ndhD</i>	complement(123381..124892)	Correct gene location
	<i>ndhE</i>	complement(125509..125814)	Correct gene location

Species	Gene	Updated position	Detail
	<i>psbJ</i>	complement(69803..69925)	Correct gene location
	<i>psbZ</i>	38961..39149	Correct gene location
	<i>rpoA</i>	complement(84390..85385)	Correct gene location
	<i>rpoC1</i>	complement(join(22631..24253,25005..25436))	Correct gene location
	<i>rpoC2</i>	complement(18299..22453)	Correct gene location
	<i>rps19</i>	join(162917..162962,1..3)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	116235..117482	Correct gene location
	<i>ycf15</i>	join(100165..100318,100611..100715)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(153148..153252,153545..153698))	Re-annotate a missing gene in IRa
<i>Hovenia trichocarpa</i> MT225404	<i>atpF</i>	complement(14382..14527),complement(13647..13237)	Re-annotate a missing gene in LSC
	<i>ndhD</i>	complement(123528..122017)	Re-annotate a missing gene in SSC
	<i>petD</i>	join(81631..81637,82375..82850)	Re-annotate a missing gene in LSC
	<i>psbC</i>	36669..38090	Re-annotate a missing gene in LSC
	<i>psbL</i>	complement(68668..68552)	Re-annotate a missing gene in LSC
	<i>rpoC2</i>	complement(18201..22364)	Correct gene location
	<i>rps19</i>	complement(89587..89309)	Re-annotate a missing gene in IRb
	<i>rps19</i>	join(161537..161668,1..12)	Re-annotate a missing gene in IRa
	<i>trnfM-CAU</i>	39783..39856	Re-annotate a missing gene in LSC

Species	Gene	Updated position	Detail
	<i>trnG-UCC</i>	join(9937..9959,10664..10712)	Re-annotate a missing gene in LSC
	<i>ycfI</i>	complement(130511..136267)	Correct gene location
	<i>ycfI</i>	114857..116092	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98789..98942,99235..99339)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151785..151889,152182..152335))	Re-annotate a missing gene in IRa
<i>Rhamnus crenata</i> LC635131	<i>psbC</i>	35926..37347	Correct gene location
	<i>rpoC1</i>	complement(join(21728..23338,24122..24553))	Correct gene location
	<i>trnL-UAG</i>	129617..129696	Re-annotate a missing gene in SSC
	<i>trnN-GUU</i>	113774..113844	Re-annotate a missing gene in IRb
	<i>trnN-GUU</i>	135495..135565	Re-annotate a missing gene in IRa
	<i>ycfI</i>	complement(134037..135165)	Re-annotate a missing gene in IRa
	<i>ycf15</i>	join(98082..98235,98512..98616)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(150723..150827,151104..151257))	Re-annotate a missing gene in IRa
<i>Rhamnus globosa</i> MT360052	<i>ndhD</i>	complement(121205..122716)	Correct gene location
	<i>ndhF</i>	complement(115291..117543)	Correct gene location
	<i>psbL</i>	complement(68312..68196)	Re-annotate a missing gene in LSC
	<i>rps19</i>	join(160543..160642,1..2)	Re-annotate a missing gene in IRa

Species	Gene	Updated position	Detail
	<i>ycf15</i>	join(98175..98328,98605..98709)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(150823..150927,151204..151357))	Re-annotate a missing gene in IRa
<i>Rhamnus heterophylla</i> MT211599	<i>ndhD</i>	complement(117369..118880)	Correct gene location
	<i>psbL</i>	complement(64386..64502)	Correct gene location
	<i>rps19</i>	join(156415..156514,1..2)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	111037..111336	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(95304..95457,95886..95990)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(146548..146652,147081..147234))	Re-annotate a missing gene in IRa
<i>Rhamnus taquetii</i> NC_045855	<i>ndhD</i>	complement(121710..123221)	Correct gene location
	<i>psbL</i>	complement(68653..68769)	Correct gene location
	<i>rps19</i>	join(161106..161205,1..2)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114737..115825	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98654..98807,99084..99188)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151391..151495,151772..151925))	Re-annotate a missing gene in IRa
<i>Spyridium parvifolium</i> MH234313	<i>ndhD</i>	complement(121535..123046)	Correct gene location
	<i>psbL</i>	complement(67924..68090)	Correct gene location
	<i>rpoC2</i>	complement(17998..22161)	Correct gene location
	<i>rps19</i>	160786..160911	Re-annotate a missing gene in IRa

Species	Gene	Updated position	Detail
	<i>trnV-UAC</i>	join(54583..54619,55216..55254)	Re-annotate a missing gene in LSC
	<i>ycfI</i>	113993..115210	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(97936..98089,98365..98469)	Correct gene location
	<i>ycf15</i>	complement(join(151116..151220,151496..151649))	Correct gene location
<i>Ventilago leiocarpa</i> MT974496	<i>infA</i>	complement(85540..85726)	Re-annotate a missing gene in LSC
	<i>rps19</i>	complement(90251..89973)	Re-annotate a missing gene in IRb
	<i>rps19</i>	161693..161809	Re-annotate a missing gene in IRa
	<i>ycfI</i>	complement(136527..130763)	Re-annotate a missing gene in IRa
	<i>ycfI</i>	115417..116427	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(99399..99552,99829..99933)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(152011..152115,152392..152545))	Re-annotate a missing gene in IRa
<i>Ziziphus incurva</i> NC_050251	<i>ndhD</i>	complement(121369..122880)	Correct gene location
	<i>ndhE</i>	complement(123503..123808)	Correct gene location
	<i>psbJ</i>	complement(67962..68084)	Correct gene location
	<i>psbL</i>	complement(68327..68267)	Correct sequence
	<i>rpoC1</i>	complement(join(22273..23907,24681..25112))	Correct gene location
	<i>rpoC2</i>	complement(17962..22119)	Correct gene location
	<i>rps19</i>	join(160814..160920,1..22)	Re-annotate a missing gene in IRa

Species	Gene	Updated position	Detail
	<i>ycfI</i>	114129..115274	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98073..98226,98519..98623)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151076..151180,151473..151626))	Re-annotate a missing gene in IRa
<i>Ziziphus jujuba</i> KX266829	<i>accD</i>	61291..63024	Correct gene location
	<i>ndhD</i>	complement(121720..123231)	Correct gene location
	<i>ndhE</i>	complement(124159..123854)	Re-annotate a missing gene in SSC
	<i>psbL</i>	complement(68044..68160)	Correct gene location
	<i>rpoC2</i>	complement(18047..22204)	Correct gene location
	<i>rps19</i>	join(161109..161215,1..28)	Re-annotate a missing gene in IRa
	<i>ycf15</i>	join(98227..98380,98673..98777)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151413..151517,151810..151963))	Re-annotate a missing gene in IRa
<i>Ziziphus jujuba</i> KX266830	<i>accD</i>	61290..63023	Correct gene location
	<i>ndhD</i>	complement(121677..123188)	Correct gene location
	<i>ndhE</i>	complement(124116..123811)	Re-annotate a missing gene in SSC
	<i>psbL</i>	complement(68018..68134)	Correct gene location
	<i>rpoC2</i>	complement(18018..22175)	Correct gene location
	<i>rps19</i>	join(161105..161211,1..28)	Re-annotate a missing gene in IRa
	<i>ycf15</i>	join(98192..98345,98638..98742)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151367..151471,151764..151917))	Re-annotate a missing gene in IRa

Species	Gene	Updated position	Detail
<i>Ziziphus jujuba</i> MF781071	<i>infA</i>	complement(84710..84769)	Re-annotate a missing gene in LSC
	<i>psbN</i>	complement(78973..79104)	Correct gene location
	<i>rps12</i>	complement(join(74178..74291,103076..103051,103845..103614))	Re-annotate a missing gene in IRb
	<i>rps12</i>	join(complement(74178..74291),146827..147058,147596..147621)	Correct gene location
	<i>rps19</i>	join(161387..161493,1..88)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114527..115666	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98474..98627,98920..99024)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151649..151753,152046..152199))	Re-annotate a missing gene in IRa
<i>Ziziphus jujuba</i> MW160433	<i>accD</i>	61314..63047	Correct gene location
	<i>ndhD</i>	complement(122071..123582)	Correct gene location
	<i>ndhE</i>	complement(124510..124205)	Re-annotate a missing gene in SSC
	<i>psbL</i>	complement(68413..68529)	Correct gene location
	<i>rpoC2</i>	complement(18032..22189)	Correct gene location
	<i>rps19</i>	join(161500..161606,1..28)	Re-annotate a missing gene in IRa
	<i>ycf15</i>	join(98587..98740,99033..99137)	Correct gene location
	<i>ycf15</i>	complement(join(151762..151866,152159..152312))	Correct gene location
<i>Ziziphus jujuba</i> NC_030299	<i>infA</i>	complement(84650..84709)	Re-annotate a missing gene in LSC
	<i>rpoC2</i>	complement(17849..22006)	Correct gene location

Species	Gene	Updated position	Detail
	<i>rps19</i>	join(161360..161466,1..22)	Re-annotate a missing gene in IRa
	<i>trnV-UAC</i>	join(54936..54972,55569..55607)	Re-annotate a missing gene in LSC
	<i>ycf1</i>	complement(130377..136101)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114486..115640	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98433..98586,98879..98983)	Correct gene location
	<i>ycf15</i>	complement(join(151604..151708,152001..152154))	Correct gene location
<i>Ziziphus mauritiana</i> NC_037151	<i>accD</i>	61232..62959	Correct gene location
	<i>ndhD</i>	complement(121938..123449)	Correct gene location
	<i>ndhE</i>	complement(124378..124073)	Re-annotate a missing gene in SSC
	<i>psbL</i>	complement(68303..68419)	Correct gene location
	<i>rpoC2</i>	complement(17892..22049)	Correct gene location
	<i>rps19</i>	join(161327..161543,1..23)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114513..115658	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98468..98621,98914..99018)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151607..151711,152004..152157))	Re-annotate a missing gene in IRa
<i>Ziziphus spina-christi</i> NC_037152	<i>accD</i>	61286..63031	Correct gene location
	<i>ndhD</i>	complement(122011..123522)	Correct gene location
	<i>ndhE</i>	complement(124451..124146)	Re-annotate a missing gene in SSC

Species	Gene	Updated position	Detail
	<i>psbL</i>	complement(68359..68475)	Correct gene location
	<i>rpoC2</i>	complement(17923..22080)	Correct gene location
	<i>rps19</i>	join(161399..161615,1..23)	Re-annotate a missing gene in IRa
	<i>ycf1</i>	114593..115738	Re-annotate a missing gene in IRb
	<i>ycf15</i>	join(98548..98701,98994..99098)	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(join(151679..151783,152076..152229))	Re-annotate a missing gene in IRa
<i>Cannabis sativa</i> NC_027223*	<i>ycf15</i>	93652..93728	Re-annotate a missing gene in IRb
	<i>ycf15</i>	complement(144154..144227)	Re-annotate a missing gene in IRa
<i>Ficus religiosa</i> NC_033979*	<i>ndhD</i>	complement(121639..123150)	Correct gene location
	<i>ndhK</i>	complement(53441..54121)	Correct gene location
	<i>psbL</i>	complement(68539..68423)	Re-annotate a missing gene in LSC
	<i>rbcL</i>	58910..60337	Correct gene location
	<i>rpoC2</i>	complement(17877..22040)	Correct gene location
	<i>rps12</i>	join(146365..146596,147133..147158,complement(74189..74302))	Re-annotate a missing gene in IRa
	<i>rps19</i>	join(160535..160627,1..6)	Re-annotate a missing gene in IRa
	<i>ycf15</i>	98148..98252	Correct gene location
	<i>ycf15</i>	complement(151191..151295)	Correct gene location

* Outgroups in the phylogeny

Table S4. List of orthologous genes for phylogenetic reconstruction.

Function	Gene list
ATP-dependent protease proteolytic subunit	<i>clpP1</i>
ATP synthase	<i>atpA, atpB, atpE, atpF, atpH, atpI</i>
Cytochrome b/f complex	<i>petA, petB, petD, petG, petL, petN</i>
Cytochrome complex assembly	<i>ccsA</i>
Envelope membrane protein	<i>cemA</i>
Hypothetical chloroplast reading frames	<i>ycf1(IRA), ycf2</i>
Maturase	<i>matK</i>
NADH dehydrogenase	<i>ndhA, ndhB, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK</i>
Photosystem I	<i>psaA, psaB, psaC, psaI, psaJ, ycf3, ycf4</i>
Photosystem II	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ</i>
RubisCO large subunit	<i>rbcL</i>
Subunit of acetyl-CoA-carboxylase	<i>accD</i>
Large subunit of ribosomal proteins (LSU)	<i>rpl14, rpl16, rpl2, rpl20, rpl22, rpl23, rpl32, rpl33, rpl36</i>
Small subunit of ribosomal proteins (SSU)	<i>rps2, rps3, rps4, rps7, rps8, rps11, rps12, rps14, rps15, rps16, rps18, rps19 (IRb)</i>
RNA polymerase	<i>rpoA, rpoB, rpoC1, rpoC2</i>