Supplementary Table S1. Primers used for chloroplast DNA, and cDNA amplification and sequencing

For amplification of chloroplast DNA

DNA fragment	Name	Sequence (5'→ 3')	Ref.
Fragment 1	1-1	CTGAGAAGAACCCATAGAGAAAA	This study
(702 bp)	1-2	TATTATTTCTTTTACTACTTCTTTTG	This study
Fragment 2	2-1	CCTCCAAACGAATACGATACTG	AF231894
(1223 bp)	2-2	GGTCAAAAGGTTATTATTCGTTAG	AY312947
Fragment 3	3-1	TGTGTCAATGAAAAGAGATAGAAAC	This study
(743 bp)	3-2	AACGATATTACAACTTTTTCTCTC	This study
Fragment 4	4-1	TATGCCACGACTGTACCGCC	AY312947
(2136 bp)	4-2	GAACCTATGGGAGATGCTTGG	AB086179
Fragment 5	5-1	CAATTCATTAAAACTCATAGCCC	This study
(3834 bp)	5-2	AAAAATTGCATGTTGGGTTCCTG	AB086179
Fragment 6	6-1	AGGGCTATACGGATTTGAACC	AB086179
(1566 bp)	6-2	TAGTCCCGTAGAAACAATTAAAGG	AY688826
Fragment 7	7-1	GAGCCATTACACGAAGATTTAG	This study
(1563 bp)	7-2	GACTTTTCTCGGTACAATCAG	This study
Fragment 8	8-1	ATACGAGCCCCTGGTGGTTC	AY688826
(1588 bp)	8-2	CTCCAGCAACAGACTCTATG	AY312936
Fragment 9	9-1	TTAATTGAGTTGTAGGGAGGG	This study
(844 bp)	9-2	ACCTCCTGTCGAATAGTCATGCG	AY312936
Fragment 10	10-1	TGAAGACACGATGAAAAGGGCG	AY312936
(753 bp)	10-2	TTTCTCTTCTATTCACCTCTATC	This study
Fragment 11	11-1	TTGCTCGTGAAGGTAATGAAGT	AY312936
(2037 bp)	11-2	AAGAATGGAAGGTAAGTAAGAGG	AB086179
Fragment 12	12-1	ACAGCCTCTTACTTACCTTCC	This study
(1775 bp)	12-2	ATCCAAGCTAGTTTTTTATTCATC	AP005672
Fragment 13	13-1	TAGTAGAATTTCCAAACGATATAG	This study
(1686 bp)	13-2	GATTACCTATTTTTTCTTTCATTTC	AB086179
Fragment 14	14-1	GGAATTATAAGCCGGGGGTAGC	This study
(1138 bp)	14-2	CAGCAACCATCAATAAGAGAGGAA	This study
Fragment 15	15-1	GATGCAGAAATAGTACCTCAAG	AB086179
(1477 bp)	15-2	TGAAAAGGGAGTAAGATAAATGG	This study
Fragment 16	16-1	TAAATTGTACGTGTATAGTTCCTTC	This study
(847 bp)	16-2	TTATGTCCCCCTCGCCTCTAC	This study
Fragment 17	17-1	GGAACCTCTTGTCGGCTCTC	This study
(2337 bp)	17-2	TACTATTCCAGACAGCAAAGC	AB086179
Fragment 18	18-1	AATCTAGGTAATTGCTTTACGAGGG	This study
(2943 bp)	18-2	GACTAGAGTTAAACGTGGGTATG	AP005672
Fragment 19	19-1	ATTTGTGCAAGCATTTTTCGATTT	AP005672
(2192 bp)	19-2	CAACAGAACCATAATAGTATT	AP005672

For internal sequencing of chloroplast DNA

DNA fragment	Name	Sequence (5'→ 3')	Ref.
Fragment 2	2-3	CCCTTTCTTTTTTCATCAGTAATC	This study
Fragment 4	4-3	AGACTATACGAACAAATGCCTGA	This study
	4-4	TCTAAATTCCATAGCAAATCCTG	This study
Fragment 5	5-3	GAGGGGTCCAATACTATCTA	This study
	5-4	CTTGAAATAGAGAAAATAATGTTG	This study
Fragment 6	6-3	TTTGTCATGCTACTGTTCCCTC	This study
Fragment 7	7-3	AAAGCTCATGGCGGTGTATC	This study
Fragment 8	8-3	CCCCAAGCATTGACCTGATAAC	This study
Fragment 11	11-3	AGTATGGGTTTTGTAGTAGGAG	AB086179
	11-4	GTCTCCCAACATACCAAAACT	AB086179
	11-5	ATTTCTTCTTTTGTTTCCATTGTC	This study
Fragment 12	12-3	TTCGTCCCATCAAAATTAACAAA	This study
	12-4	TATCAATCGAAGGACTCTAAAC	This study
Fragment 13	13-3	TTGGGTTAAGATTTGGTGGAA	This study
	13-4	AGTAACAATAATGGTGAGAAATC	This study
Fragment 14	14-3	CCCTTCCTCTATTACCACCCAC	This study
Fragment 15	15-3	TATTATTTCATCTTTCCTTTATTA	This study
	15-4	ATTCAATTCTATAAAAGCTAAGTT	This study
Fragment 16	16-3	CCTTTCGCTGACATTATTACC	AB086179
	16-4	GACCCTAATCCAGAATGTGAG	AB086179
Fragment 17	17-3	CCAGTATATCTAGCGTTCTTTTG	This study
	17-4	TTATCTCATCTCAAAATCAATATCG	This study
	17-5	GTATCGTAAGCTGATGGACCTATG	This study
	17-6	AGGAGAAGCCGTAGAAGTAGTTG	This study
	17-7	TGATTCGATCTTACCAGTTACGTTG	This study
Fragment 18	18-3	ACCTTATACTTTTATTTTTTCCAAG	This study
	18-4	ACTTCCTTATTTGAACTTAAAAAAC	This study
	18-5	CACGCTCTGTAGGATTTGAAC	AB086179
	18-6	AGGGATGTAGCGCAGTTTGG	AB086179
Fragment 19	18-2	GACTAGAGTTAAACGTGGGTATG	AP005672
	19-3	TTTCGAGCTACATACCCACGT	AP005672
	19-4	GGTCTTATGGTTCCTATGGTCAG	This study
	19-5	AATTAACCCTCACTAAAGAAAACCTATGGCATTGTTGAT	AP005672

For amplification of cDNA

Gene	Name	Sequence (5'→ 3')	Ref.
rps4	1-1	CTGAGAAGAACCCATAGAGAAAA	This study
	1-2	TATTATTTCTTTTACTACTTCTTTTG	This study
ndhJ	ndhJ-1	AATGAGCGAAAAATATAATAAGAAA	This study
	ndhJ-2	CGGGAGGATGAATAGATATGAT	This study
ndhK	ndhK-1	GTTCGGTTTATGCGTGGCGG	This study
	ndhK-2	TATTATATTTTTCGCTCATTTCTCC	This study
ndhC	ndhC-1	AACCATTCTTTTTATTTCACAGGAG	This study
	ndhC-2	TTCTCGATTTTATTTTCACAATTTA	This study

atpE	atpE-1	ATTGATGAAGCTACTGCGAAGGC	This study
	atpE-2	TCTTGAATCGAAAAATCTCTCTT	This study
atpB	7-1	GAGCCATTACACGAAGATTTAG	This study
	7-2	GACTTTTCTCGGTACAATCAG	This study
accD	accD-1	TAGTCAGCCGTAAGAGAAAAAG	This study
	accD-2	AAGATTGATTTGATTCGACGGGTG	This study
psaI	psaI-1	TTATTAAAGGTAATTTTTTATG	This study
	psaI-2	CGATCCAACAATAAAAATATAC	This study
ycf4	ycf4-1	TATTTCGGCTCTTTCGTCCCATC	This study
	ycf4-2	ACTGAAAGAAACAGAAAAAACATC	This study
ycf10	ycf10-1	CTCCGTTCTGGCAAAGTATAAG	This study
	ycf10-2	ACAGTAACAATAATGGTGAGAAATC	This study
petA	14-1	GGAATTATAAGCCGGGGGTAGC	This study
	14-2	CAGCAACCATCAATAAGAGAGGAA	This study
psbJ-L-F-E	16-1	TAAATTGTACGTGTATAGTTCCTTC	This study
	16-2	TTATGTCCCCCTCGCCTCTAC	This study
petL-G	18-1	AATCTAGGTAATTGCTTTACGAGGG	This study
	petG-1	ATTAGACCTCCCTATCTTTTTTAG	This study
psaJ	psaJ-1	TACCTTTTTGTTATATGAACCTTTG	This study
	18-4	ACTTCCTTATTTGAACTTAAAAAAC	This study
rpl33-rps18	18-3	ACCTTATACTTTTATTTTTTCCAAG	This study
	rps18-1	TTTTCTTCTCCCTCCAACTCTTAG	This study
rpl20	rpl20-1	CTCATTCTTTATCAAAATTATTTAG	This study
	rpl20-2	TTTGTTCCGATCTGTTTTTACTTCC	This study
5'rps12	19-4	GGTCTTATGGTTCCTATGGTCAG	This study
	rps12-1	ACCGATCCCTAATACTTAAAGTTCC	This study
clpP	clpP-1	TAATTGATTGGGTTGTTACGCTTTC	This study
	clpP-2	ATCTGATGGATTCCTTATCTCATAG	This study

For internal sequencing of cDNA

Gene	Name	Sequence (5'→ 3')	Ref.
petA	14-3	CCCTTCCTCTATTACCACCCAC	This study
psbJ-L-F-E	16-3	CCTTTCGCTGACATTATTACC	AB086179
	16-4	GACCCTAATCCAGAATGTGAG	AB086179

Supplementary Table S2. List of Newly Identified RNA editing Sites in *T. lepidozioides*

Number in parentheses indicates nucleotide position, given with respect to the first base of the initiation codon(*), or the next base to the stop codon(**) as 1. Editing sites that did not alter the coded amino acid coding are indicated as "silent", and double editing sites are indicated as double.

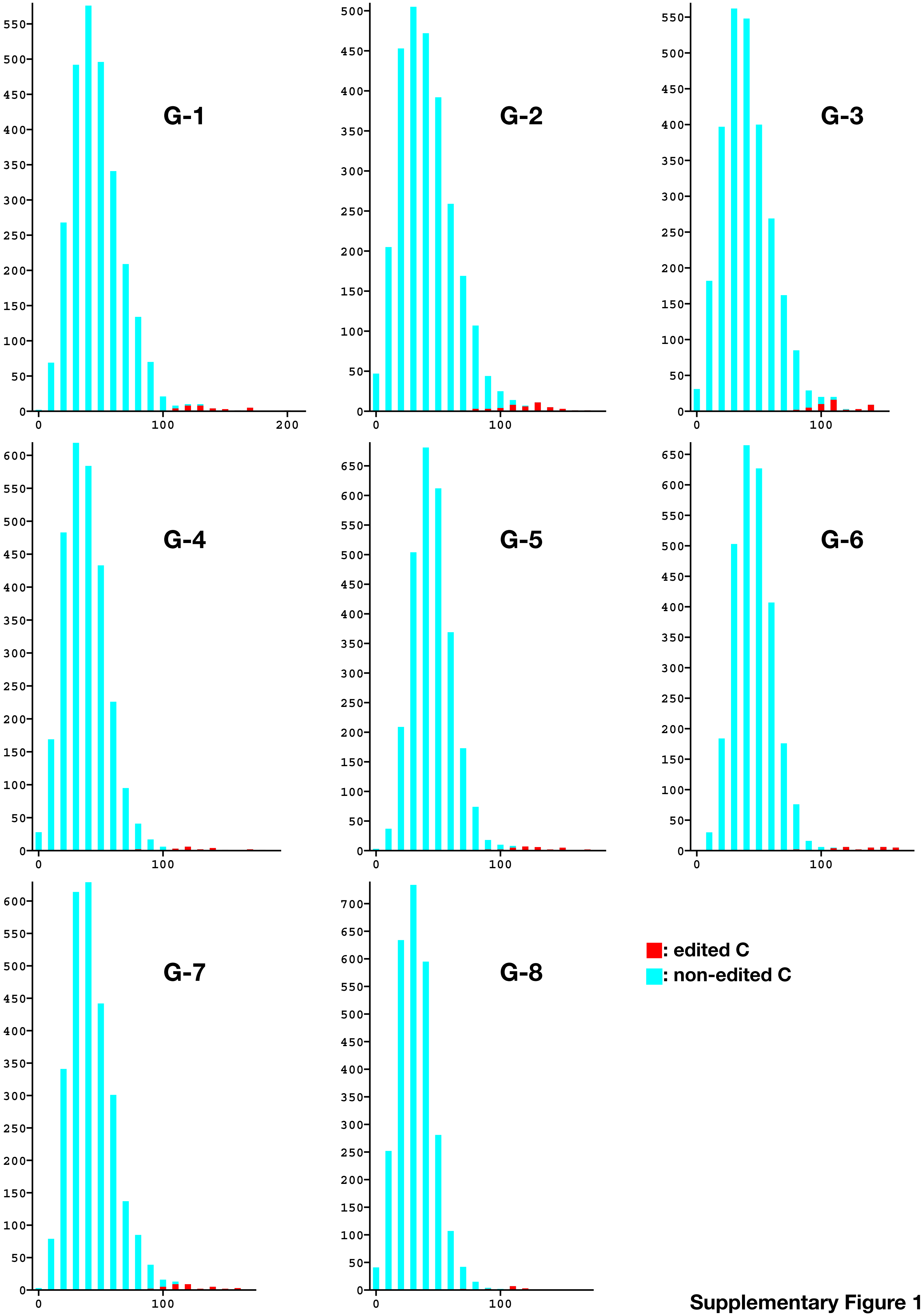
Gene	Codon Position	Genomic DNA		cDNA	Remarks
rps4	1	Thr(aCg)	→	Met(aTg)	
rps4	18	Ser(tCa)	→	Leu(tTa)	
rps4	59	His(Cat)	→	Tyr(Tat)	
rps4	84	Ser(tCg)	→	Leu(tTg)	
rps4	133	Pro(ccC)	→	Pro(ccT)	silent
ndhJ	49	Ser(tcC)	→	Ser(tcT)	silent
ndhJ	58	Gly(ggC)	→	Gly(ggT)	silent
ndhJ	59	Ser(tCt)	→	Phe(tTt)	
ndhJ	62	Leu(ctC)	→	Leu(ctT)	silent
ndhJ	64	Ser(tcC)	→	Ser(tcT)	silent
ndhK	34	Thr(aCt)	→	Ile(aTt)	
ndhK	60	His(Cac)	→	Tyr(Tac)	
ndhK	64	Arg(Cgt)	→	Cys(Tgt)	
ndhK	95	Pro(cCc)	→	Leu(cTc)	
ndhK	97	Thr(aCa)	→	Ile(aTa)	
ndhK	104	Thr(aCg)	→	Met(aTg)	
ndhK	126	Thr(aCg)	→	Met(aTg)	
ndhC	2	Phe(ttC)	→	Phe(ttT)	silent
ndhC	67	Ser(tCa)	→	Leu(tTa)	
ndhC	71	Thr(aCt)	→	Ile(aTt)	
ndhC	72	Phe(ttC)	→	Phe(ttT)	silent
ndhC	78	Ser(tCt)	→	Phe(tTt)	
ndhC	98	Ser(tCg)	→	Leu(tTg)	
ndhC	104	Ser(tCa)	→	Leu(tTa)	
ndhC	108	Ser(tCg)	→	Leu(tTg)	
ndhC	117	Ser(tCg)	→	Leu(tTg)	
atpE	24	Pro(cCa)	→	Leu(cTa)	
atpE	40	Pro(cCt)	→	Leu(cTt)	
atpE	44	Pro(cCg)	→	Leu(cTg)	
atpE	119	Ser(tCt)	→	Phe(tTt)	
atpE	134	Ser(tCt)	→	Phe(tTt)	
atpB	(-12)*	C	→	T	5'-untranslated region of *atpB*
atpB	(-10)*	C	→	T	5'-untranslated region of *atpB*
atpB	(-4)*	C	→	T	5'-untranslated region of *atpB*
atpB	13	Pro(cCc)	→	Leu(cTc)	
atpB	33	Ser(tCc)	→	Phe(tTc)	
atpB	44	Pro(Cct)	→	Ser(Tct)	
atpB	75	Ala(gCg)	→	Val(gTg)	
atpB	77	Thr(aCg)	→	Met(aTg)	
atpB	96	Ser(tCa)	→	Leu(tTa)	
atpB	105	Pro(cCt)	→	Leu(cTt)	
atpB	119	Ser(tCa)	→	Leu(tTa)	
atpB	137	Ser(tCt)	→	Phe(tTt)	
atpB	157	Ser(tCa)	→	Leu(tTa)	

atpB	168	Ser(tCa)	→	Leu(tTa)	
atpB	181	Thr(aCg)	→	Met(aTg)	
atpB	197	Ser(tCc)	→	Phe(tTc)	
atpB	210	Pro(cCt)	→	Leu(cTt)	
atpB	214	Thr(aCg)	→	Met(aTg)	
atpB	249	Ser(tCa)	→	Leu(tTa)	
atpB	252	Pro(cCa)	→	Leu(cTa)	
atpB	258	Ser(tCt)	→	Phe(tTt)	
atpB	268	Ser(tCa)	→	Leu(tTa)	
atpB	274	Ser(tCt)	→	Phe(tTt)	
atpB	276	Ser(tCt)	→	Phe(tTt)	
atpB	286	Pro(cCa)	→	Leu(cTa)	
atpB	296	His(Cat)	→	Tyr(Tat)	
atpB	300	Pro(cCg)	→	Leu(cTg)	
atpB	307	Ser(tCg)	→	Leu(tTg)	
atpB	321	Pro(Cca)	→	Ser(Tca)	
atpB	326	His(Cat)	→	Tyr(Tat)	
atpB	350	Pro(cCa)	→	Leu(cTa)	
atpB	366	Ser(tCa)	→	Leu(tTa)	
atpB	370	Pro(Cct)	→	Ser(Tct)	
atpB	373	Pro(cCt)	→	Leu(cTt)	
atpB	411	Ser(tCa)	→	Leu(tTa)	
atpB	439	Ser(tCt)	→	Phe(tTt)	
atpB	449	Pro(cCc)	→	Leu(cTc)	
atpB	460	Pro(cCt)	→	Leu(cTt)	
atpB	472	Ser(tCt)	→	Phe(tTt)	
atpB	473	His(Cat)	→	Tyr(Tat)	
atpB	474	Pro(cCg)	→	Leu(cTg)	
atpB	488	Ser(tCa)	→	Leu(tTa)	
rbcL	24	His(Cat)	→	Tyr(Tat)	
rbcL	37	Ser(tCg)	→	Leu(tTg)	
rbcL	70	Arg(Cgg)	→	Trp(Tgg)	
rbcL	100	His(Cat)	→	Tyr(Tat)	
rbcL	104	Pro(ccC)	→	Pro(ccT)	silent
rbcL	105	Ser(tCa)	→	Leu(tTa)	
rbcL	107	Pro(cCa)	→	Leu(cTa)	
rbcL	133	Pro(cCa)	→	Leu(cTa)	
rbcL	135	Pro(cCa)	→	Leu(cTa)	
rbcL	148	Ser(tCt)	→	Phe(tTt)	
rbcL	180	Ser(tCa)	→	Leu(tTa)	
rbcL	185	His(Cat)	→	Tyr(Tat)	
rbcL	193	Pro(cCt)	→	Leu(cTt)	
rbcL	212	Thr(aCg)	→	Met(aTg)	
rbcL	218	Ser(tCc)	→	Phe(tTc)	
rbcL	240	Ser(tCg)	→	Leu(tTg)	
rbcL	250	Thr(aCg)	→	Met(aTg)	
rbcL	265	Ala(gCc)	→	Val(gTc)	
rbcL	266	Thr(aCg)	→	Met(aTg)	
rbcL	270	Ser(tCg)	→	Leu(tTg)	
rbcL	284	Arg(Cgc)	→	Cys(Tgc)	
rbcL	289	Pro(cCa)	→	Leu(cTa)	
rbcL	297	Thr(aCg)	→	Met(aTg)	

rbcL	343	Pro(cCa)	→	Leu(cTa)	
rbcL	348	Pro(cCa)	→	Leu(cTa)	
rbcL	371	Ser(tCg)	→	Leu(tTg)	
rbcL	385	Arg(Cgg)	→	Trp(Tgg)	
rbcL	390	Ser(tCg)	→	Leu(tTg)	
rbcL	394	Ser(tCt)	→	Phe(tTt)	
rbcL	407	Ser(tCg)	→	Leu(tTg)	
rbcL	411	Arg(Cgg)	→	Trp(Tgg)	
rbcL	424	Ser(tCa)	→	Leu(tTa)	
accD	6	Arg(Cgg)	→	Trp(Tgg)	
accD	31	Ser(agC)	→	Ser(agT)	silent
accD	51	Arg(Cgt)	→	Cys(Tgt)	
accD	88	Ser(tCa)	→	L (tTa)	
accD	94	Arg(Cgg)	→	Trp(Tgg)	
accD	149	Thr(aCg)	→	Met(aTg)	
accD	151	Ser(tCt)	→	Phe(tTt)	
accD	153	Ser(tCt)	→	Phe(tTt)	
accD	169	Pro(cCt)	→	Leu(cTt)	
accD	170	Ile(atC)	→	Ile(atT)	silent
accD	198	Pro(cCa)	→	Leu(cTa)	
accD	206	Pro(Ccc)	→	Ser(Tcc)	
accD	208	Ser(tCa)	→	L (tTa)	
accD	223	Pro(cCC)	→	Leu(cTT)	double, silent
accD	237	Thr(aCg)	→	Met(aTg)	
accD	252	Ser(tCt)	→	Phe(tTt)	
accD	284	Ser(tCg)	→	L (tTg)	
psaI	3	Ala(gcC)	→	Ala(gcT)	silent
psaI	10	Ser(tCt)	→	Phe(tTt)	
ycf4	1	Thr(aCg)	→	Met(aTg)	
ycf4	43	His(Cac)	→	Tyr(Tac)	
ycf4	82	Arg(Cgt)	→	Cys(Tgt)	
ycf4	86	Arg(Cgg)	→	Trp(Tgg)	
ycf4	95	Ser(tCc)	→	Phe(tTc)	
ycf4	120	Ser(tCt)	→	Phe(tTt)	
ycf4	163	Pro(cCg)	→	Leu(cTg)	
ycf4	176	Ser(tCc)	→	Phe(tTc)	
ycf4	177	Ser(tCg)	→	Leu(tTg)	
ycf10	83	Ser(tCa)	→	Leu(tTa)	
ycf10	306	Ser(tCt)	→	Phe(tTt)	
ycf10	399	Ala(gcC)	→	Ala(gcT)	silent
ycf10	407	Pro(cCa)	→	Leu(cTa)	
ycf10	415	Ser(tCa)	→	Leu(tTa)	
ycf10	433	Ser(tCt)	→	Phe(tTt)	
ycf10	436	Pro(cCc)	→	Leu(cTc)	
ycf10	437	Pro(cCa)	→	Leu(cTa)	
ycf10	441	Pro(cCa)	→	Leu(cTa)	
ycf10	442	Arg(Cgt)	→	Cys(Tgt)	
ycf10	489	Arg(Cgg)	→	Trp(Tgg)	
ycf10	508	Thr(aCg)	→	Met(aTg)	
petA	60	Arg(Cgt)	→	Cys(Tgt)	
petA	81	Pro(CCt)	→	Phe(TTt)	double
petA	111	Pro(cCt)	→	Leu(cTt)	

petA	113	Ser(tCa)	→	Leu(tTa)	
petA	164	Ser(tCt)	→	Phe(tTt)	
petA	242	Ile(atC)	→	Ile(atT)	silent
psbL-psbJ	(-95)*	C	→	T	intergenic spacer
psbL-psbJ	(-54)*	C	→	T	intergenic spacer
psbJ	20	Pro(cCc)	→	Leu(cTc)	
psbJ	24	Ser(tCa)	→	Leu(tTa)	
psbJ	34	Ser(tcC)	→	Ser(tcT)	silent
psbJ	36	Ser(tCa)	→	Leu(tTa)	
psbJ	39	Pro(Ccc)	→	Ser(Tcc)	
psbJ	40	Leu(Cta)	→	Leu(Tta)	silent
psbL	31	Pro(cCa)	→	Leu(cTa)	
psbL	33	Pro(Cct)	→	Ser(Tct)	
psbL	39	Gln(Caa)	→	Stop(Taa)	
psbF	26	Leu(Ctt)	→	Phe(Ttt)	
psbF	28	Ser(tCa)	→	Leu(tTa)	
psbE	20	Arg(Cgg)	→	Trp(Tgg)	
psbE	30	Ser(tCg)	→	Leu(tTg)	
psbE	35	Arg(Cgg)	→	Trp(Tgg)	
petL	1	Thr(aCg)	→	Met(aTg)	
petL	8	Phe(ttC)	→	Phe(ttT)	silent
petL	11	Leu(Cta)	→	Leu(Tta)	silent
petL	21	Ser(tCa)	→	Leu(tTa)	
petL	32	Gln(Cag)	→	Stop(Tag)	
petL-petG	(-30)*	C	→	T	intergenic spacer
petL-petG	(-25)*	C	→	T	intergenic spacer
petG	11	Ser(tCg)	→	Leu(tTg)	
petG	15	Pro(Cca)	→	Ser(Tca)	
petG	22	Phe(ttC)	→	Phe(ttT)	silent
petG	38	Arg(Cga)	→	Stop(Tga)	
petG	(+2)**	C	→	T	3'-untranslated region of *petG*
petG	(+22)**	C	→	T	3'-untranslated region of *petG*
rpl33	(-20)*	C	→	T	5'-untranslated region of *rpl33*
rpl33	1	Thr(aCg)	→	Met(aTg)	
rpl33	20	Gln(Caa)	→	Stop(Taa)	
rpl33	42	Pro(ccC)	→	Pro(ccT)	silent
rpl33	44	Arg(Cga)	→	Stop(Tga)	
rpl33	60	His(caC)	→	His(caT)	silent
rps18	30	Arg(Cgc)	→	Cys(Tgc)	
rps18	67	Ser(tCa)	→	Leu(tTa)	
rps18	69	Pro(Cct)	→	Ser(Tct)	
rpl20	33	Arg(Cga)	→	Stop(Tga)	
rpl20	44	Ala(gCt)	→	Val(gTt)	
rpl20	47	His(Cat)	→	Tyr(Tat)	
rpl20	81	Gln(Caa)	→	Stop(Taa)	
5'-*rps12*	7	Leu(Ctg)	→	Leu(Ttg)	silent
clpP	(-19)*	C	→	T	5'-untranslated region of *clpP*
clpP	20	Arg(Cgg)	→	Trp(Tgg)	
clpP	27	Leu(ctC)	→	Leu(ctT)	silent
clpP	28	His(Cat)	→	Tyr(Tat)	
clpP	35	Pro(cCa)	→	Leu(cTa)	
clpP	45	Asn(aaC)	→	Asn(aaT)	silent

clpP	47	Pro(cCC)	→	Leu(cTT)	double, silent
clpP	88	Ala(gCa)	→	Val(gTa)	
clpP	106	Thr(aCc)	→	Ile(aTc)	
clpP	107	Ser(tCa)	→	Leu(tTa)	
clpP	142	Thr(aCg)	→	Met(aTg)	
clpP	192	Phe(ttC)	→	Phe(ttT)	silent
clpP	195	Thr(aCa)	→	Ile(aTa)	
clpP	199	Ser(tCa)	→	Leu(tTa)	



Supplementary Figure 1