

Supplementary Material

A comparative study of the chloroplast genomes of five *Lepidium* species with high medicinal value

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Supplementary Materials

Table S1. Codon-anticodon recognition patterns and codon usage of the cp genome of five *Lepidium* species.

Amino acid	Codon	tRNA	<i>L. apetalum</i>		<i>L. perfoliatum</i>		<i>L. sativum</i>		<i>L. virginicum</i>		<i>L. meyenii</i>	
			Count	RSCU	Count	RSCU	Count	RSCU	Count	RSCU	Count	RSCU
Phe	UUU		997	1.34	1096	1.37	998	1.34	1002	1.34	1020	1.34
Phe	UUC	tmF-GAA	495	0.66	508	0.63	493	0.66	499	0.66	497	0.66
Leu	UUA	tmL-UAA	864	1.85	944	2.00	836	1.81	864	1.84	871	1.85
Leu	UUG	tmL-CAA	572	1.22	534	1.13	576	1.25	570	1.22	567	1.21
Leu	CUU		605	1.29	597	1.27	614	1.33	609	1.30	599	1.27
Leu	CUC		178	0.38	186	0.39	178	0.39	180	0.38	185	0.39
Leu	CUA	tmL-UAG	394	0.84	395	0.84	378	0.82	395	0.84	401	0.85
Leu	CUG		195	0.42	171	0.36	191	0.41	196	0.42	197	0.42
Ile	AUU		1096	1.47	1155	1.51	1106	1.48	1100	1.48	1102	1.48
Ile	AUC	tmI-GAU	461	0.62	433	0.56	467	0.63	463	0.62	460	0.62
Ile	AUA	tmI-CAU	675	0.91	713	0.93	667	0.89	669	0.90	673	0.90
Met	AUG	tm(f)M-CAU	628	1.00	601	1.00	619	1.00	629	1.00	631	1.00
Val	GUU		528	1.46	528	1.48	522	1.49	529	1.46	540	1.49
Val	GUC	tmV-GAC	179	0.49	178	0.50	175	0.50	180	0.50	164	0.45
Val	GUA	tmV-UAC	549	1.52	511	1.43	517	1.47	547	1.51	558	1.54
Val	GUG		193	0.53	209	0.59	189	0.54	191	0.53	190	0.52
Tyr	UAU		596	1.72	797	1.63	604	1.70	590	1.71	598	1.75
Tyr	UAC	tmY-GUA	339	0.98	178	0.37	339	0.95	345	1.00	340	0.99
Stop	UAA		403	1.17	51	1.80	421	1.19	400	1.16	404	1.18
Stop	UAG		199	0.58	23	0.81	210	0.59	202	0.58	182	0.53
Stop	UGA		405	1.44	11	0.39	397	1.42	406	1.43	424	1.50
His	CAU		240	0.85	466	1.51	241	0.86	238	0.84	226	0.80
His	CAC	tmH-GUG	324	1.15	150	0.49	316	1.13	326	1.15	314	1.11
Gln	CAA	tmQ-UUG	159	0.56	728	1.56	162	0.58	162	0.57	169	0.60
Gln	CAG		534	1.61	206	0.44	527	1.59	541	1.62	532	1.60
Asn	AAU		249	0.75	989	1.52	250	0.76	250	0.75	250	0.75
Asn	AAC	tmN-GUU	394	1.19	312	0.48	389	1.18	390	1.17	402	1.21
Lys	AAA	tmK-UUU	146	0.44	1160	1.54	157	0.47	151	0.45	146	0.44
Lys	AAG		607	1.73	344	0.46	567	1.70	605	1.73	610	1.74
Asp	GAU		233	0.67	851	1.63	222	0.67	236	0.67	236	0.67
Asp	GAC	tmD-GUC	392	1.12	193	0.37	380	1.14	393	1.12	394	1.12
Glu	GAA	tmE-UUC	169	0.48	1058	1.53	163	0.49	167	0.48	162	0.46
Glu	GAG		773	1.63	328	0.47	774	1.60	774	1.63	763	1.62
Ser	UCU		178	0.37	583	1.71	194	0.40	175	0.37	181	0.38
Ser	UCC	tmS-GGA	49	1.63	313	0.92	68	1.46	47	1.60	48	1.66
Ser	UCA	tmS-UGA	24	0.80	410	1.20	34	0.73	22	0.75	20	0.69
Ser	UCG		483	1.54	200	0.59	471	1.52	482	1.53	473	1.52
Ser	AGU		146	0.46	410	1.20	147	0.48	148	0.47	150	0.48
Ser	AGC	tmS-GCU	724	1.54	129	0.38	710	1.54	726	1.54	722	1.54
Pro	CCU		215	0.46	428	1.60	212	0.46	217	0.46	217	0.46
Pro	CCC		964	1.54	199	0.74	970	1.54	971	1.54	962	1.52
Pro	CCA	tmP-UGG	292	0.46	306	1.14	293	0.46	290	0.46	301	0.48
Pro	CCG		1072	1.48	136	0.51	1072	1.47	1068	1.48	1086	1.49
Thr	ACU		376	0.52	554	1.62	385	0.53	375	0.52	369	0.51
Thr	ACC	tmT-GGU	861	1.60	237	0.69	853	1.60	869	1.60	866	1.61
Thr	ACA	tmT-UGU	212	0.40	430	1.26	214	0.40	217	0.40	207	0.39
Thr	ACG		1022	1.50	144	0.42	995	1.49	1018	1.50	1032	1.51
Ala	GCU		340	0.50	637	1.85	340	0.51	343	0.50	335	0.49
Ala	GCC		219	1.48	214	0.62	245	1.36	224	1.52	223	1.52
Ala	GCA	tmA-UGC	76	0.52	386	1.12	114	0.64	70	0.48	71	0.48
Ala	GCG		17	0.57	143	0.41	38	0.81	19	0.65	19	0.66
Cys	UGU		467	1.00	243	1.49	465	1.00	471	1.00	468	1.00
Cys	UGC	tmC-GCA	340	1.27	83	0.51	331	1.20	342	1.28	338	1.26
Trp	UGG	tmW-CCA	124	0.47	456	1.00	129	0.47	121	0.45	122	0.45
Arg	CGU	tmR-ACG	357	1.34	343	1.30	357	1.29	355	1.33	348	1.30
Arg	CGC		130	0.49	106	0.40	147	0.53	131	0.49	143	0.53
Arg	CGA		425	1.23	372	1.41	425	1.20	422	1.22	412	1.20
Arg	CGG		113	0.33	118	0.45	132	0.37	116	0.34	117	0.34
Arg	AGA	tmR-UCU	489	1.83	475	1.80	508	1.84	491	1.84	494	1.84
Arg	AGG		160	0.60	173	0.65	183	0.66	161	0.60	164	0.61
Gly	GGU		542	1.21	592	1.34	511	1.16	541	1.21	552	1.23
Gly	GGC	tmG-GCC	194	0.43	161	0.36	203	0.46	192	0.43	198	0.44
Gly	GGA	tmG-UCC	724	1.62	732	1.66	699	1.59	723	1.61	715	1.6

Gly	GGG	333	0.74	284	0.64	342	0.78	337	0.75	325	0.73
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Table S2. Comparison of 18 intron-containing genes among five *Lepidium* cp genomes.

	Gene	Location	<i>L. apetalum</i>	<i>L. perfoliatum</i>	<i>L. sativum</i>	<i>L. virginicum</i>	<i>L. meyenii</i>	
Exon I	<i>trnK-UUU</i>	LSC	37	37	37	37	37	
	<i>trnG-UCC</i>	LSC	38	38	23	23	23	
	<i>trnL-UAA</i>	LSC	35	35	37	35	35	
	<i>trnV-UAC</i>	LSC	39	39	39	39	39	
	<i>trnI-GAU</i>	IR	37	37	42	37	37	
	<i>trnA-UGC</i>	IR	38	38	38	38	38	
	<i>rps16</i>	LSC	40	40	40	40	40	
	<i>rpl16</i>	LSC	9	9	9	9	9	
	<i>rpl2</i>	IR	391	391	390	390	390	
	<i>rpoC1</i>	LSC	453	453	432	432	432	
	<i>ndhA</i>	SSC	552	552	553	553	553	
	<i>ndhB</i>	IR	777	777	723	723	723	
	<i>petB</i>	LSC	6	6	6	6	6	
	<i>petD</i>	LSC	8	8	8	8	8	
	<i>atpF</i>	LSC	145	145	145	145	145	
	<i>ycf3</i>	LSC	126	126	126	126	126	
	<i>clpP</i>	LSC	71	71	71	71	71	
	<i>rps12</i>	LSC	114	114	114	114	114	
	Intron I	<i>trnK-UUU</i>	LSC	2552	2533	2549	2529	2557
		<i>trnG-UCC</i>	LSC	65	65	718	717	717
<i>trnL-UAA</i>		LSC	520	522	518	526	521	
<i>trnV-UAC</i>		LSC	610	604	600	603	603	
<i>trnI-GAU</i>		IR	947	947	942	947	947	
<i>trnA-UGC</i>		IR	800	800	806	800	800	
<i>rps16</i>		LSC	879	866	877	880	888	
<i>rpl16</i>		LSC	1094	1075	1101	1103	1102	
<i>rpl2</i>		IR	682	682	682	682	682	
<i>rpoC1</i>		LSC	784	776	781	783	777	
<i>ndhA</i>		SSC	1087	1089	1086	1091	1076	
<i>ndhB</i>		IR	685	685	685	685	685	
<i>petB</i>		LSC	799	793	775	799	799	
<i>petD</i>		LSC	726	718	725	731	730	
<i>atpF</i>		LSC	718	735	718	736	717	
<i>ycf3</i>		LSC	711	719	710	711	718	
<i>clpP</i>		LSC	883	869	884	882	891	
<i>rps12</i>		LSC	—	—	—	—	—	
Exon II		<i>trnK-UUU</i>	LSC	35	35	35	35	35
		<i>trnG-UCC</i>	LSC	38	38	49	49	49
	<i>trnL-UAA</i>	LSC	50	50	50	50	50	
	<i>trnV-UAC</i>	LSC	35	35	37	35	35	
	<i>trnI-GAU</i>	IR	35	35	35	35	35	
	<i>trnA-UGC</i>	IR	35	35	35	35	35	
	<i>rps16</i>	LSC	227	227	227	227	227	
	<i>rpl16</i>	LSC	399	399	399	399	399	
	<i>rpl2</i>	IR	434	434	435	435	435	
	<i>rpoC1</i>	LSC	1611	1611	1611	1611	1611	
	<i>ndhA</i>	SSC	531	531	530	530	530	
	<i>ndhB</i>	IR	762	762	762	762	762	
	<i>petB</i>	LSC	642	642	642	642	642	
	<i>petD</i>	LSC	475	475	475	475	475	
	<i>atpF</i>	LSC	410	410	410	410	410	
	<i>ycf3</i>	SSC	228	228	228	228	228	
	<i>clpP</i>	LSC	292	292	292	292	292	
	<i>rps12</i>	LSC	232	232	232	232	232	
	Intron II	<i>ycf3</i>	LSC	792	775	790	791	792
		<i>clpP</i>	LSC	583	575	578	577	571
<i>rps12</i>		LSC	537	537	537	537	537	
Exon III	<i>ycf3</i>	LSC	153	153	153	153	153	
	<i>clpP</i>	LSC	228	228	228	228	228	
	<i>rps12</i>	LSC	26	26	26	26	26	

Table S3. RNA editing sites of the cp genomes of five *Lepidium* species.

Gene	Nucleotide position					Condon (amino acid) change	Score
	<i>L. apetalum</i>	<i>L. perfoliatum</i>	<i>L. sativum</i>	<i>L. virginicum</i>	<i>L. meyenii</i>		
<i>accD</i>	742	742	742	742	742	CAT (H) => TAT (Y)	0.8
	782	782	782	782	782	TCG (S) => TTG (L)	0.8
	1391	1391	1391	1391	1391	CCT (P) => CTT (L)	1
<i>atpF</i>	92	92	92	92	92	CCA (P) => CTA (L)	0.86
<i>clpP</i>	559	559	559	559	559	CAT (H) => TAT (Y)	1
<i>ndhA</i>	125	—	125	125	125	ACA (T) => ATA (I)	0.8
	341	341	341	341	341	TCA (S) => TTA (L)	1
<i>matK</i>	706	640	706	706	706	CAT (H) => TAT (Y)	1
	1250	1184	1250	1250	1250	TCA (S) => TTA (L)	0.86
	—	1210	—	—	—	CTT (L) => TTT (F)	1
<i>ndhB</i>	467	467	413	413	413	CCA (P) => CTA (L)	1
	586	586	532	532	532	CAT (H) => TAT (Y)	1
	611	611	557	557	557	TCA (S) => TTA (L)	0.8
	746	746	692	692	692	TCT (S) => TTT (F)	1
	830	830	776	776	776	TCA (S) => TTA (L)	1
	836	—	782	782	782	TCA (S) => TTA (L)	1
	1255	1255	1201	1201	1201	CAT (H) => TAT (Y)	1
	1481	1481	1427	1427	1427	CCA (P) => CTA (L)	1
<i>ndhD</i>	74	131	74	5	20	ACG (T) => ATG (M)	1
	119	176	119	50	65	TCT (S) => TTT (F)	0.8
	455	1007	455	386	401	TCA (S) => TTA (L)	1
	950	—	950	881	896	TCA (S) => TTA (L)	1
	959	1016	959	890	905	CCC (P) => CTC (L)	1
	1382	1439	1382	1313	1328	TCA (S) => TTA (L)	0.8
<i>ndhF</i>	1477	1534	1477	1408	1423	CTT (L) => TTT (F)	0.8
	205	205	—	205	205	CAT (H) => TAT (Y)	0.8
	290	290	290	290	290	TCA (S) => TTA (L)	1
	586	586	586	586	586	CTT (L) => TTT (F)	0.8
	2135	2135	2135	2135	2135	ACA (T) => ATA (I)	0.8
	166	166	166	166	166	CAT (H) => TAT (Y)	0.8
<i>ndhG</i>	314	314	314	314	314	ACA (T) => ATA (I)	0.8
	214	214	214	214	214	CCT (P) => TCT (S)	1
<i>psbE</i>	77	77	77	77	77	TCT (S) => TTT (F)	1
<i>rpoB</i>	338	338	338	338	338	TCT (S) => TTT (F)	1
	551	551	551	551	551	TCA (S) => TTA (L)	1
	566	566	566	566	566	TCG (S) => TTG (L)	1
	973	973	973	973	973	CTC (L) => TTC (F)	0.86
	2432	2432	2432	2432	2432	TCA (S) => TTA (L)	0.86
	1961	1961	1940	1940	1940	ACT (T) => ATT (I)	0.86
	1628	—	1616	1616	1616	ACT (T) => ATT (I)	0.86
<i>rpoC1</i>	2305	2305	2293	2293	2293	CGG (R) => TGG (W)	1
	2354	2354	2342	2342	2342	GCC (A) => GTC (V)	0.86
	80	80	80	80	80	TCA (S) => TTA (L)	1
<i>rps14</i>	149	149	149	149	149	CCA (P) => CTA (L)	1
	212	212	212	212	212	TCA (S) => TTA (L)	0.83

Table S4. Numbers of SSRs types in five *Lepidium* cp genomes.

Type	Numbers of SSRs types				
	<i>L. apetalum</i>	<i>L. perfoliatum</i>	<i>L. sativum</i>	<i>L. virginicum</i>	<i>L. meyenii</i>
A	19	21	21	20	27
C	—	1	—	—	1
G	—	2	1	—	1
T	40	44	42	39	34
AT	7	10	7	7	8
TA	7	8	7	8	8
AAG	—	—	—	—	1
AAT	1	1	1	1	1
ATA	1	1	1	2	1
TAC	1	—	1	1	1
TAT	1	1	1	1	1
TTC	—	1	—	—	—
AATA	1	1	—	—	1
AAAT	1	—	1	2	1
TATT	—	—	1	—	—
ATAA	1	1	1	—	1
ATAG	1	1	1	1	1
CAAA	1	1	1	1	1
GATA	1	—	—	1	1
TAAA	2	—	2	1	2
TAAT	1	—	1	1	1
TTTA	—	1	—	—	—
TTTC	1	1	1	1	1
AATAG	—	1	—	—	—
TAGAC	—	1	—	—	—
AAATTC	—	—	—	—	1
TTGTAT	—	—	—	—	1

Table S5. Repeated sequences in cp genome.

Species	ID	Repeat Start 1	Type	Size (bp)	Repeat Start 2	Gene	Region	Mismatch (bp)	E-value
<i>L. apetalum</i>	1	166	P	60	166	IGS(<i>trnH-GUG, psbA</i>), IGS(<i>trnH-GUG, psbA</i>)	LSC	0	5.07E-27
	2	7667	F	32	34934	<i>trnS-GCU</i> (CDS), <i>trnS-UGA</i> (CDS)	LSC	-3	4.90E-05
	3	7669	P	30	44451	<i>trnS-GCU</i> (CDS), <i>trnS-GGA</i> (CDS)	LSC	-1	5.26E-07
	4	9251	P	41	9251	IGS(<i>trnG-UCC, trnR-UCU</i>), IGS(<i>trnG-UCC, trnR-UCU</i>)	LSC	-3	4.01E-10
	5	28254	P	30	28254	IGS(<i>petN, psbM</i>), IGS(<i>petN, psbM</i>)	LSC	0	5.85E-09
	6	34936	P	30	44451	<i>trnS-UGA</i> (CDS), <i>trnS-GGA</i> (CDS)	LSC	-3	6.41E-04
	7	34996	P	30	44389	<i>trnS-UGA</i> (CDS), <i>trnS-GGA</i> (CDS)	LSC	-2	2.29E-05
	8	38271	F	73	40495	<i>psaB</i> (CDS), <i>psaA</i> (CDS)	LSC	-3	1.27E-28
	9	38289	F	55	40513	<i>psaB</i> (CDS), <i>psaA</i> (CDS)	LSC	-2	6.94E-20
	10	43359	P	39	140168	<i>ycf3</i> (intron), IGS(<i>trnV-GAC, rps7</i>)	LSC,IRB	-3	5.51E-09
	11	43359	F	39	98535	<i>ycf3</i> (intron), IGS(<i>rps7, trnV-GAC</i>)	LSC,IRA	-3	5.51E-09
	12	43371	P	30	140165	<i>ycf3</i> (intron), IGS(<i>trnV-GAC, rps7</i>)	LSC,IRB	-2	2.29E-05
	13	43371	F	30	98547	<i>ycf3</i> (intron), IGS(<i>rps7, trnV-GAC</i>)	LSC,IRA	-2	2.29E-05
	14	47580	F	31	47746	IGS(<i>trnL-UAA, trnF-GAA</i>), IGS(<i>trnL-UAA, trnF-GAA</i>)	LSC	-3	1.77E-04
	15	47601	F	51	47767	IGS(<i>trnL-UAA, trnF-GAA</i>), IGS(<i>trnL-UAA, trnF-GAA</i>)	LSC	-3	7.48E-16
	16	47604	F	63	47687	IGS(<i>trnL-UAA, trnF-GAA</i>), IGS(<i>trnL-UAA, trnF-GAA</i>)	LSC	-3	8.50E-23
	17	47612	F	50	47778	IGS(<i>trnL-UAA, trnF-GAA</i>), <i>trnF-GAA</i> (CDS)	LSC	-3	2.82E-15
	18	47613	F	62	47696	IGS(<i>trnL-UAA, trnF-GAA</i>), IGS(<i>trnL-UAA, trnF-GAA</i>)	LSC	-3	3.24E-22
	19	47625	F	37	47791	IGS(<i>trnL-UAA, trnF-GAA</i>), <i>trnF-GAA</i> (CDS)	LSC	-1	3.96E-11
	20	47631	F	48	47714	IGS(<i>trnL-UAA, trnF-GAA</i>), IGS(<i>trnL-UAA, trnF-GAA</i>)	LSC	-3	3.97E-14
	21	47699	F	36	47782	IGS(<i>trnL-UAA, trnF-GAA</i>), <i>trnF-GAA</i> (CDS)	LSC	-2	8.10E-09
	22	47708	F	37	47791	IGS(<i>trnL-UAA, trnF-GAA</i>), <i>trnF-GAA</i> (CDS)	LSC	-3	7.49E-08
	23	73970	P	44	73970	IGS(<i>psbT, psbN</i>), IGS(<i>psbT, psbN</i>)	LSC	0	2.18E-17
	24	88790	P	45	149883	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA, IRB	-3	2.09E-12
	25	88790	F	45	88814	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA	-3	2.09E-12
	26	88814	P	45	149907	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA, IRB	-3	2.09E-12
	27	88836	P	32	149853	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA, IRB	-2	1.63E-06
	28	88836	F	32	88857	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA	-2	1.63E-06
	29	88857	P	32	149874	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA, IRB	-2	1.63E-06
	30	107669	P	33	131008	IGS(<i>rrn4.5, rrn5</i>), IGS(<i>rrn5, rrn4.5</i>)	IRA, SSC	-2	4.34E-07
	31	107669	F	33	107701	IGS(<i>rrn4.5, rrn5</i>), IGS(<i>rrn4.5, rrn5</i>)	IRA	-2	4.34E-07
	32	107701	P	33	131040	IGS(<i>rrn4.5, rrn5</i>), IGS(<i>rrn5, rrn4.5</i>)	IRA, IRB	-2	4.34E-07
	33	113773	P	45	113773	IGS(<i>rpl32, trnL-UAG</i>), IGS(<i>rpl32, trnL-UAG</i>)	SSC	-3	2.09E-12
	34	131008	F	33	131040	IGS(<i>rrn5, rrn4.5</i>), IGS(<i>rrn5, rrn4.5</i>)	IRB	-2	4.34E-07
	35	149853	F	32	149874	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRB	-2	1.63E-06
	36	149883	F	45	149907	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRB	-3	2.09E-12
<i>L. perfoliatum</i>	1	253	P	55	253	IGS(<i>trnH-GUG, psbA</i>), IGS(<i>trnH-GUG, psbA</i>)	LSC	-3	3.65E-18
	2	4620	F	30	31024	IGS(<i>matK, rps16</i>), IGS(<i>trnE-UUC, trnT-GGU</i>)	LSC	-3	6.36E-04
	3	4620	F	32	31026	IGS(<i>matK, rps16</i>), IGS(<i>trnE-UUC, trnT-GGU</i>)	LSC	-3	4.86E-05
	4	4630	P	30	31026	IGS(<i>matK, rps16</i>), IGS(<i>trnE-UUC, trnT-GGU</i>)	LSC	-3	6.36E-04
	5	7763	F	32	34964	<i>trnS-GCU</i> (CDS), <i>trnS-UGA</i> (CDS)	LSC	-2	1.62E-06
	6	7765	P	30	44453	<i>trnS-GCU</i> (CDS), <i>trnS-GGA</i> (CDS)	LSC	-1	5.22E-07
	7	7962	R	31	7962	IGS(<i>trnS-GCU, trnG-UCC</i>), IGS(<i>trnS-GCU, trnG-UCC</i>)	LSC	-2	6.07E-06
	8	8009	R	30	31020	IGS(<i>trnS-GCU, trnG-UCC</i>), IGS(<i>trnE-UUC, trnT-GGU</i>)	LSC	-3	6.36E-04
	9	9333	P	41	9333	IGS(<i>trnG-UCC, trnR-UCU</i>), IGS(<i>trnG-UCC, trnR-UCU</i>)	LSC	-3	3.98E-10

10	28360	P	40	28360	IGS(<i>petN</i> , <i>psbM</i>), IGS(<i>petN</i> , <i>psbM</i>)	LSC	0	5.54E-15
11	31026	R	35	31026	IGS(<i>trnE-UUC</i> , <i>trnT-GGU</i>), IGS(<i>trnE-UUC</i> , <i>trnT-GGU</i>)	LSC	-2	3.04E-08
12	31030	P	30	31030	IGS(<i>trnE-UUC</i> , <i>trnT-GGU</i>), IGS(<i>trnE-UUC</i> , <i>trnT-GGU</i>)	LSC	-2	2.27E-05
13	34966	P	30	44453	<i>trnS-UGA</i> (CDS), <i>trnS-GGA</i> (CDS)	LSC	-3	6.36E-04
14	35025	P	30	44391	<i>trnS-UGA</i> (CDS), <i>trnS-GGA</i> (CDS)	LSC	-2	2.27E-05
15	38294	F	67	40518	<i>psaB</i> (CDS), <i>psaA</i> (CDS)	LSC	-3	3.98E-25
16	38312	F	55	40536	<i>psaB</i> (CDS), <i>psaA</i> (CDS)	LSC	-3	3.65E-18
17	43353	F	39	98006	<i>ycf3</i> (intron), IGS(<i>rps7</i> , <i>trnV-GAC</i>)	LSC, IRA	-3	5.46E-09
18	43353	P	39	139610	<i>ycf3</i> (intron), IGS(<i>trnV-GAC</i> , <i>rps7</i>)	LSC, IRB	-3	5.46E-09
19	43365	F	30	98018	<i>ycf3</i> (intron), IGS(<i>rps7</i> , <i>trnV-GAC</i>)	LSC, IRA	-2	2.27E-05
20	43365	P	30	139607	<i>ycf3</i> (intron), IGS(<i>trnV-GAC</i> , <i>rps7</i>)	LSC, IRB	-2	2.27E-05
21	47008	P	32	47008	<i>trnL-UAA</i> (intron), <i>trnL-UAA</i> (intron)	LSC	0	3.63E-10
22	47611	F	34	47802	IGS(<i>trnL-UAA</i> , <i>trnF-GAA</i>), <i>trnF-GAA</i> (CDS)	LSC	-1	2.31E-09
23	47614	F	32	47652	IGS(<i>trnL-UAA</i> , <i>trnF-GAA</i>), IGS(<i>trnL-UAA</i> , <i>trnF-GAA</i>)	LSC	0	3.63E-10
24	47647	F	46	47800	IGS(<i>trnL-UAA</i> , <i>trnF-GAA</i>), <i>trnF-GAA</i> (CDS)	LSC	-3	5.54E-13
25	47668	P	30	47717	IGS(<i>trnL-UAA</i> , <i>trnF-GAA</i>), IGS(<i>trnL-UAA</i> , <i>trnF-GAA</i>)	LSC	-3	6.36E-04
26	73420	P	44	73420	IGS(<i>psbT</i> , <i>psbN</i>), IGS(<i>psbT</i> , <i>psbN</i>)	LSC	-2	1.84E-13
27	88307	F	32	88328	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA	-2	1.62E-06
28	88307	P	32	149295	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA, IRB	-2	1.62E-06
29	88328	P	32	149316	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRA, IRB	-2	1.62E-06
30	98009	F	37	120065	IGS(<i>rps7</i> , <i>trnV-GAC</i>), <i>ndhA</i> (intron)	IRA, SSC	-3	7.43E-08
31	107141	F	33	107173	IGS(<i>rrn4.5</i> , <i>rrn5</i>), IGS(<i>rrn4.5</i> , <i>rrn5</i>)	IRA	-2	4.31E-07
32	107141	P	33	130449	IGS(<i>rrn4.5</i> , <i>rrn5</i>), IGS(<i>rrn5</i> , <i>rrn4.5</i>)	IRA, IRB	-2	4.31E-07
33	107173	P	33	130481	IGS(<i>rrn4.5</i> , <i>rrn5</i>), IGS(<i>rrn5</i> , <i>rrn4.5</i>)	IRA, IRB	-2	4.31E-07
34	112275	R	32	123852	IGS(<i>ndhF</i> , <i>rpl32</i>), <i>ycf1</i> (CDS)	SSC	-3	4.86E-05
35	113209	P	45	113209	IGS(<i>rpl32</i> , <i>trnL-UAG</i>), IGS(<i>rpl32</i> , <i>trnL-UAG</i>)	SSC	-3	2.07E-12
36	118852	P	37	118852	IGS(<i>ndhG</i> , <i>ndhI</i>), IGS(<i>ndhG</i> , <i>ndhI</i>)	SSC	-1	3.93E-11
37	120065	P	37	139609	<i>ndhA</i> (intron), IGS(<i>trnV-GAC</i> , <i>rps7</i>)	SSC, IRB	-3	7.43E-08
38	130449	F	33	130481	IGS(<i>rrn5</i> , <i>rrn4.5</i>), IGS(<i>rrn5</i> , <i>rrn4.5</i>)	IRB	-2	4.31E-07
39	149295	F	32	149316	<i>ycf2</i> (CDS), <i>ycf2</i> (CDS)	IRB	-2	1.62E-06

Table S6. Tandem repeat sequence of *L. apetalum* and *L. perfoliatum*.

Species	ID	Size (bp)	Copy number	Location	Repeat unit
<i>L. apetalum</i>	1	12	2.2	<i>ndhA</i>	TTTTTTAACTTA
	2	13	4.5	IGS(<i>psbZ</i> , <i>trnG-GCC</i>)	AATATTAATATAT
	3	14	2.2	IGS(<i>matK</i> , <i>rps16</i>)	ATATATAATTTTAT
	4	15	1.9	IGS(<i>trnT-GGU</i> , <i>psbD</i>)	AATTTTCATCTAATT
	5	15	2	IGS(<i>trnT-GGU</i> , <i>psbD</i>)	ATATATAACATTAAG
	6	15	2.3	IGS(<i>psbE</i> , <i>petL</i>)	TATTTATTTTTTATG
	7	15	2.3	IGS(<i>clpP</i> , <i>psbB</i>)	TTAAATTAATCATAT
	8	17	2	IGS(<i>psbM</i> , <i>trnD-GUC</i>)	AAAAAGAAAAATAAAAC
	9	17	1.9	IGS(<i>psbZ</i> , <i>trnG-GCC</i>)	AATTCAATATTCATAA
	10	17	2.7	IGS(<i>petA</i> , <i>psbJ</i>)	TTTAATATATATAACTG
	11	18	3.4	<i>yef2</i>	TATTGATGCTAGTAACGA
	12	18	1.9	IGS (<i>rps7</i> , <i>trnV-GAC</i>)	ATTTTCTATTATATTAGG
	13	18	1.9	IGS(<i>trnV-GAC</i> , <i>rps7</i>)	CTAATAGAATAGAAAATC
	14	18	2.6	<i>yef2</i>	ATCAATATCGTCACTAGC
	15	18	3.4	<i>yef2</i>	ATCAATATCGTTACTAGC
	16	19	2.1	IGS(<i>psbA</i> , <i>trnK-UUU</i>)	TAGAAAATATAAATAAAAT
	17	20	2	<i>rpl2</i>	TCTTATATATATCGTAGAAT
	18	20	2	<i>rpl2</i>	TTCTACCATATATAGAAGAA
	19	21	4.2	<i>yef2</i>	TTTTTGTCGAAGTTACTTCTT
	20	21	4.3	<i>yef2</i>	AAAAAGAGAAGTAACTTGGAC
	21	22	2	IGS(<i>ndhF</i> , <i>rpl32</i>)	AAATAAAAAAAAAAGTAAAAAAC
	22	24	2.3	IGS(<i>psbZ</i> , <i>trnG-GCC</i>)	AATATTAATATATAGAATAAATAT
	23	24	4.3	<i>yef2</i>	TTTGTCCTAAGTCACTTCGTTTCTT
	24	24	5.1	<i>yef2</i>	AAAAAGAAAACGAAGTGACTTAGAC
	25	24	3.7	<i>yef2</i>	GAAGTAACTTGGACAAAAAGAAAAC
	26	25	2.1	IGS(<i>accD</i> , <i>psaI</i>)	TATTTATATTAGGTTCTATTCTAGA
	27	32	1.9	IGS (<i>rrn4.5</i> , <i>rrn5</i>)	GTTCAACTCTTTGACAACACGAAAAAACCAT
	28	32	1.9	IGS (<i>rrn4.5</i> , <i>rrn5</i>)	GGTTTTTTCATGTTGTCAAAGAGTTGAACAAT
	29	42	2.6	<i>yef2</i>	TTTGTCCTAAGTCACTTCTTTTTTTTGTCGAAGTTACTTCTTCT
	30	83	3	<i>trnF-GAA</i>	TAGTACAATGAGAATGATACTTCGGTAATGGTCGGCATAGCT CACTTGGTAGAGCAGAGGACTGAAAAATCCTTGTGTCCACCAT
<i>L. perfoliatum</i>	1	2	18.5	IGS(<i>trnS-GCU</i> , <i>trnG-UCC</i>)	TA
	2	2	18.5	IGS(<i>trnE-UUC</i> , <i>trnT-GGU</i>)	TA
	3	13	7.2	IGS(<i>trnS-GCU</i> , <i>trnG-UCC</i>)	TTTATATATATAT
	4	13	3.2	IGS(<i>psbZ</i> , <i>trnG-GCC</i>)	ATATAATATTAAT
	5	13	2.8	IGS(<i>ndhC</i> , <i>trnV-UAC</i>)	TCTAGATATATCG
	6	15	2.6	IGS(<i>trnS-GCU</i> , <i>trnG-UCC</i>)	TATATATATATATAT
	7	15	2	IGS(<i>trnT-GGU</i> , <i>psbD</i>)	ATATATAACATTAAG
	8	15	2.3	IGS(<i>clpP</i> , <i>psbB</i>)	TTAATTTAATCATAT
	9	16	2	IGS(<i>trnC-GCA</i> , <i>petN</i>)	ATACAGACTAATGAAA
	10	17	3.8	IGS(<i>trnS-GCU</i> , <i>trnG-UCC</i>)	TATATATATATATTTAT
	11	17	2.1	<i>atpF</i>	TTTTTTATTAGACTACA
	12	17	2.7	IGS(<i>petA</i> , <i>psbJ</i>)	TTTAATATATATAACTG
	13	18	3.4	<i>yef1</i>	TATTGATGATAGTACGAT
	14	18	2.6	<i>yef2</i>	ATCAATATCGTCACTAGC
	15	18	3.4	<i>yef2</i>	
	16	20	2	<i>rpl2</i>	TCTTATATATATCGTAGAAT
	17	20	2	<i>rpl2</i>	TTCTACCATATATAGAAGAA
	18	21	3.2	<i>yef2</i>	TTTTTGTCGAAGTTACTTCTT
	19	21	4.1	<i>yef2</i>	AAAAAGAGAAGTAACTTAGAC
	20	32	1.9	IGS (<i>rrn4.5</i> , <i>rrn5</i>)	GTTCAACTCTTTGACAACACGAAAAAACCAT
	21	32	1.9	IGS (<i>rrn4.5</i> , <i>rrn5</i>)	GGTTTTTTCATGTTGTCAAAGAGTTGAACAAT

Table S7. SNP number in 78 genes of the cp genomes of five *Lepidium* species.

Gene name	SNP number	Gene name	SNP number	Gene name	SNP number	Gene name	SNP number
<i>accD</i>	31	<i>ndhJ</i>	7	<i>psbI</i>	2	<i>rpoC1</i>	16
<i>atpA</i>	23	<i>ndhK</i>	5	<i>psbJ</i>	2	<i>rpoC2</i>	73
<i>atpB</i>	16	<i>petA</i>	10	<i>psbK</i>	2	<i>rps11</i>	10
<i>atpE</i>	2	<i>petB</i>	2	<i>psbL</i>	0	<i>rps12</i>	1
<i>atpF</i>	12	<i>petD</i>	5	<i>psbM</i>	2	<i>rps14</i>	6
<i>atpH</i>	0	<i>petG</i>	1	<i>psbN</i>	0	<i>rps15</i>	4
<i>atpI</i>	9	<i>petL</i>	4	<i>psbT</i>	1	<i>rps16</i>	8
<i>ccsA</i>	37	<i>petN</i>	0	<i>psbZ</i>	1	<i>rps18</i>	1
<i>cemA</i>	6	<i>psaA</i>	13	<i>rbcL</i>	29	<i>rps19</i>	5
<i>clpP</i>	7	<i>psaB</i>	28	<i>rpl14</i>	3	<i>rps2</i>	7
<i>matK</i>	56	<i>psaC</i>	5	<i>rpl16</i>	5	<i>rps3</i>	16
<i>ndhA</i>	16	<i>psaI</i>	1	<i>rpl2</i>	3	<i>rps4</i>	7
<i>ndhB</i>	4	<i>psaJ</i>	2	<i>rpl20</i>	5	<i>rps7</i>	0
<i>ndhC</i>	7	<i>psbA</i>	5	<i>rpl22</i>	9	<i>rps8</i>	7
<i>ndhD</i>	29	<i>psbB</i>	29	<i>rpl23</i>	1	<i>ycf1</i>	303
<i>ndhE</i>	4	<i>psbC</i>	14	<i>rpl32</i>	4	<i>ycf2</i>	29
<i>ndhF</i>	57	<i>psbD</i>	8	<i>rpl33</i>	3	<i>ycf3</i>	2
<i>ndhG</i>	6	<i>psbE</i>	2	<i>rpl36</i>	1	<i>ycf4</i>	6
<i>ndhH</i>	14	<i>psbF</i>	1	<i>rpoA</i>	14		
<i>ndhI</i>	9	<i>psbH</i>	4	<i>rpoB</i>	40		

Table S8. Table S8 Nucleotide diversity in five *Lepidium* chloroplast genomes, annotated based on *L. apetalum* regions.

Midpoint	Pi	Region	Midpoint	Pi	Region	Midpoint	Pi	Region
505	0.01125	LSC	52857	0.00675	LSC	105035	0	IR
705	0.00525	LSC	53057	0.00575	LSC	105235	0.0005	IR
905	0.0015	LSC	53257	0.00525	LSC	105435	0.001	IR
1105	0.002	LSC	53457	0.0025	LSC	105641	0.0015	IR
1305	0.00525	LSC	53657	0.0025	LSC	105841	0.0015	IR
1505	0.00725	LSC	53857	0.00225	LSC	106041	0.002	IR
1765	0.01013	LSC	54057	0.00275	LSC	106241	0.0015	IR
1999	0.014	LSC	54257	0.00425	LSC	106441	0.001	IR
2199	0.01625	LSC	54457	0.00625	LSC	106641	0.0015	IR
2399	0.016	LSC	54657	0.0105	LSC	106841	0.0005	IR
2599	0.01663	LSC	54864	0.01613	LSC	107041	0.0005	IR
2799	0.01525	LSC	55085	0.01713	LSC	107241	0.0005	IR
2999	0.01475	LSC	55299	0.01463	LSC	107441	0	IR
3199	0.016	LSC	55502	0.00962	LSC	107641	0	IR
3399	0.017	LSC	55702	0.0045	LSC	107841	0.0005	IR
3599	0.0145	LSC	55902	0.005	LSC	108041	0.0005	IR
3799	0.01325	LSC	56102	0.0055	LSC	108241	0.0005	IR
4001	0.01125	LSC	56302	0.0075	LSC	108441	0.001	IR
4209	0.01513	LSC	56502	0.00925	LSC	108641	0.0005	IR
4410	0.02313	LSC	56702	0.0085	LSC	108841	0.0005	IR
4629	0.02338	LSC	56902	0.0125	LSC	109047	0.001	IR
4909	0.02538	LSC	57125	0.0135	LSC	109252	0.0005	IR
5109	0.0205	LSC	57343	0.01225	LSC	109456	0.00375	IR
5309	0.0165	LSC	57554	0.012	LSC	109675	0.00425	IR
5512	0.0155	LSC	57754	0.0105	LSC	109891	0.00375	IR
5716	0.019	LSC	57954	0.008	LSC	110102	0.00475	IR
5927	0.0175	LSC	58154	0.008	LSC	110303	0.0015	IR
6133	0.017	LSC	58354	0.008	LSC	110503	0.001	SSR
6344	0.01925	LSC	58554	0.0075	LSC	110709	0.0015	SSR
6557	0.01713	LSC	58754	0.0085	LSC	110909	0.0005	SSR
6758	0.017	LSC	58954	0.01288	LSC	111109	0.0015	SSR
6958	0.015	LSC	59154	0.02063	LSC	111309	0.002	SSR
7158	0.01425	LSC	59364	0.02163	LSC	111509	0.0045	SSR
7358	0.01438	LSC	59682	0.02063	LSC	111841	0.00975	SSR
7563	0.01875	LSC	59888	0.01625	LSC	112041	0.01275	SSR
7789	0.02475	LSC	60093	0.008	LSC	112241	0.01575	SSR
7990	0.02425	LSC	60304	0.00538	LSC	112441	0.01475	SSR
8229	0.02375	LSC	60533	0.00688	LSC	112641	0.012	SSR
8442	0.02113	LSC	60733	0.00837	LSC	112841	0.0105	SSR
8654	0.01613	LSC	60933	0.01075	LSC	113041	0.00875	SSR
8854	0.01463	LSC	61140	0.01088	LSC	113241	0.00775	SSR
9054	0.01363	LSC	61387	0.01075	LSC	113441	0.00725	SSR
9254	0.01838	LSC	61587	0.00725	LSC	113641	0.00725	SSR
9456	0.02613	LSC	61787	0.00488	LSC	113841	0.0165	SSR
9688	0.02513	LSC	61987	0.00588	LSC	114048	0.02538	SSR
9900	0.02438	LSC	62187	0.00538	LSC	114260	0.03113	SSR

10119	0.017	LSC	62389	0.00675	LSC	114478	0.03013	SSR
10319	0.00775	LSC	62589	0.00575	LSC	114695	0.02613	SSR
10519	0.00925	LSC	62789	0.00525	LSC	114900	0.0255	SSR
10719	0.0065	LSC	62989	0.00588	LSC	115130	0.02513	SSR
10919	0.0055	LSC	63189	0.008	LSC	115349	0.03538	SSR
11119	0.0065	LSC	63389	0.01338	LSC	115552	0.03463	SSR
11319	0.0055	LSC	63599	0.01475	LSC	115760	0.02775	SSR
11519	0.0085	LSC	63815	0.01888	LSC	115981	0.02338	SSR
11720	0.0105	LSC	64038	0.01688	LSC	116187	0.01463	SSR
11920	0.011	LSC	64238	0.011	LSC	116387	0.01363	SSR
12120	0.01338	LSC	64438	0.00862	LSC	116587	0.01575	SSR
12321	0.01138	LSC	64638	0.0035	LSC	116787	0.01863	SSR
12541	0.00937	LSC	64838	0.00475	LSC	116987	0.01863	SSR
12741	0.00738	LSC	65038	0.00625	LSC	117216	0.01588	SSR
12941	0.005	LSC	65238	0.011	LSC	117430	0.01275	SSR
13151	0.00725	LSC	65446	0.012	LSC	117630	0.00838	SSR
13353	0.00825	LSC	65655	0.0125	LSC	117830	0.00688	SSR
13559	0.01225	LSC	66395	0.016	LSC	118030	0.00787	SSR
13764	0.0145	LSC	66595	0.01375	LSC	118230	0.008	SSR
13979	0.01175	LSC	66801	0.01588	LSC	118430	0.008	SSR
14186	0.01125	LSC	67001	0.01563	LSC	118630	0.008	SSR
14386	0.00825	LSC	67201	0.01413	LSC	118830	0.0065	SSR
14586	0.0045	LSC	67403	0.01213	LSC	119033	0.0065	SSR
14786	0.0075	LSC	67613	0.01625	LSC	119233	0.00888	SSR
14986	0.008	LSC	67826	0.01475	LSC	119433	0.00788	SSR
15191	0.0065	LSC	68039	0.01275	LSC	119633	0.01038	SSR
15391	0.007	LSC	68240	0.01838	LSC	119833	0.01238	SSR
15591	0.005	LSC	68440	0.01063	LSC	120033	0.00925	SSR
15791	0.007	LSC	68645	0.00912	LSC	120233	0.01025	SSR
15991	0.0065	LSC	68851	0.01463	LSC	120433	0.01125	SSR
16196	0.0065	LSC	69051	0.011	LSC	120633	0.01275	SSR
16396	0.0075	LSC	69265	0.012	LSC	120839	0.014	SSR
16596	0.0055	LSC	69465	0.0135	LSC	121057	0.0145	SSR
16796	0.0075	LSC	69665	0.01088	LSC	121257	0.009	SSR
16996	0.01	LSC	69866	0.00987	LSC	121457	0.0055	SSR
17196	0.009	LSC	70067	0.00838	LSC	121657	0.005	SSR
17396	0.0095	LSC	70267	0.00887	LSC	121857	0.0075	SSR
17596	0.0075	LSC	70477	0.005	LSC	122057	0.01213	SSR
17796	0.0055	LSC	70679	0.005	LSC	122257	0.01563	SSR
17996	0.0045	LSC	70879	0.00975	LSC	122457	0.01613	SSR
18196	0.0055	LSC	71086	0.00925	LSC	122668	0.01363	SSR
18396	0.009	LSC	71297	0.01025	LSC	122869	0.01275	SSR
18596	0.0085	LSC	71499	0.00925	LSC	123075	0.00925	SSR
18796	0.00925	LSC	71701	0.01113	LSC	123285	0.00925	SSR
18996	0.00775	LSC	71901	0.01263	LSC	123485	0.00875	SSR
19196	0.00525	LSC	72131	0.01413	LSC	123685	0.006	SSR
19396	0.00713	LSC	72333	0.01463	LSC	123885	0.0055	SSR
19596	0.00638	LSC	72542	0.0095	LSC	124085	0.0045	SSR

19796	0.00763	LSC	72742	0.008	LSC	124285	0.00425	SSR
19996	0.00763	LSC	72943	0.007	LSC	124485	0.00475	SSR
20196	0.00575	LSC	73165	0.007	LSC	124685	0.00625	SSR
20396	0.00625	LSC	73366	0.00725	LSC	124885	0.00675	SSR
20596	0.005	LSC	73566	0.00775	LSC	125086	0.0105	SSR
20796	0.0035	LSC	73766	0.00775	LSC	125286	0.0115	SSR
20996	0.004	LSC	73966	0.00825	LSC	125545	0.013	SSR
21196	0.003	LSC	74166	0.01	LSC	125745	0.0195	SSR
21396	0.0025	LSC	74366	0.008	LSC	125945	0.02288	SSR
21596	0.004	LSC	74566	0.00975	LSC	126145	0.037	SSR
21796	0.0045	LSC	74766	0.00875	LSC	126345	0.038	SSR
21996	0.007	LSC	74967	0.00575	LSC	126545	0.03438	SSR
22202	0.0105	LSC	75167	0.00675	LSC	126745	0.03138	SSR
22403	0.01075	LSC	75367	0.00525	LSC	126945	0.0185	SSR
22611	0.00975	LSC	75568	0.0065	LSC	127145	0.01725	SSR
22814	0.00725	LSC	75773	0.0085	LSC	127345	0.01975	SSR
23014	0.00375	LSC	75974	0.0085	LSC	127545	0.02063	SSR
23214	0.003	LSC	76199	0.01125	LSC	127751	0.0245	SSR
23414	0.003	LSC	76405	0.009	LSC	127951	0.03275	SSR
23614	0.005	LSC	76605	0.007	LSC	128151	0.03088	SSR
23814	0.0055	LSC	76805	0.006	LSC	128351	0.03188	SSR
24014	0.006	LSC	77005	0.0025	LSC	128551	0.03175	IR
24214	0.008	LSC	77205	0.0035	LSC	128751	0.03213	IR
24414	0.008	LSC	77406	0.009	LSC	128957	0.04062	IR
24614	0.0075	LSC	77606	0.0115	LSC	129157	0.042	IR
24814	0.007	LSC	77820	0.014	LSC	129375	0.03987	IR
25014	0.005	LSC	78020	0.0145	LSC	129575	0.029	IR
25214	0.004	LSC	78220	0.0095	LSC	129787	0.0165	IR
25414	0.0035	LSC	78420	0.01	LSC	130119	0.00787	IR
25614	0.0025	LSC	78620	0.01025	LSC	130319	0.003	IR
25814	0.0025	LSC	78820	0.00975	LSC	130519	0.0015	IR
26014	0.0025	LSC	79027	0.00925	LSC	130719	0.0005	IR
26214	0.003	LSC	79227	0.00875	LSC	130919	0.0015	IR
26414	0.00525	LSC	79427	0.0055	LSC	131125	0.001	IR
26623	0.0075	LSC	79627	0.0055	LSC	131325	0.001	IR
26840	0.01	LSC	79827	0.0095	LSC	131525	0.00425	IR
27047	0.0135	LSC	80032	0.0085	LSC	131737	0.00325	IR
27255	0.01275	LSC	80232	0.01	LSC	131953	0.00375	IR
27458	0.0125	LSC	80435	0.01625	LSC	132153	0.00375	IR
27672	0.013	LSC	80635	0.01613	LSC	132376	0.0005	IR
27892	0.00975	LSC	80843	0.01663	LSC	132581	0.0005	IR
28096	0.012	LSC	81060	0.01513	LSC	132787	0.0005	IR
28302	0.0125	LSC	81260	0.01238	LSC	132987	0.0005	IR
28532	0.01138	LSC	81460	0.0095	LSC	133187	0.001	IR
28733	0.01163	LSC	81691	0.0075	LSC	133387	0.001	IR
28973	0.01288	LSC	81891	0.0085	LSC	133587	0.0005	IR
29177	0.01338	LSC	82091	0.005	LSC	133787	0.0005	IR
29377	0.01575	LSC	82292	0.00825	LSC	133987	0	IR

29583	0.02013	LSC	82492	0.01375	LSC	134187	0	IR
29783	0.01813	LSC	82692	0.01725	LSC	134387	0.0005	IR
30004	0.02325	LSC	82914	0.02225	LSC	134587	0.0005	IR
30204	0.0245	LSC	83119	0.02	LSC	134787	0.0005	IR
30414	0.01913	LSC	83320	0.0155	LSC	134987	0.001	IR
30620	0.02213	LSC	83530	0.01738	LSC	135187	0.001	IR
30820	0.0195	LSC	83752	0.01288	LSC	135387	0.001	IR
31034	0.01875	LSC	83965	0.01338	IR	135587	0.002	IR
31313	0.02275	LSC	84165	0.01375	IR	135787	0.002	IR
31522	0.02325	LSC	84365	0.01013	IR	135987	0.0015	IR
31728	0.021	LSC	84565	0.00862	IR	136193	0.0015	IR
31935	0.01675	LSC	84765	0.00813	IR	136393	0.0005	IR
32145	0.01725	LSC	84965	0.00725	IR	136593	0	IR
32358	0.015	LSC	85165	0.0035	IR	136793	0.0005	IR
32578	0.01125	LSC	85365	0.004	IR	136993	0.0005	IR
32778	0.011	LSC	85565	0.0025	IR	137193	0.0015	IR
32978	0.00838	LSC	85765	0.0015	IR	137393	0.002	IR
33178	0.00463	LSC	85965	0.0015	IR	137593	0.0015	IR
33378	0.00413	LSC	86165	0.0015	IR	137793	0.002	IR
33578	0.00338	LSC	86365	0.0005	IR	137993	0.001	IR
33778	0.0015	LSC	86565	0.0015	IR	138193	0.0005	IR
33978	0.0025	LSC	86765	0.002	IR	138393	0.0005	IR
34178	0.0035	LSC	86965	0.0015	IR	138593	0	IR
34378	0.004	LSC	87165	0.0015	IR	138793	0	IR
34578	0.005	LSC	87365	0.0005	IR	138993	0	IR
34778	0.0035	LSC	87565	0.0005	IR	139193	0	IR
34978	0.0045	LSC	87765	0.001	IR	139393	0	IR
35178	0.0085	LSC	87965	0.0015	IR	139593	0.0005	IR
35387	0.00987	LSC	88165	0.0015	IR	139793	0.003	IR
35588	0.01038	LSC	88365	0.0015	IR	139993	0.003	IR
35788	0.01063	LSC	88565	0.001	IR	140193	0.0045	IR
36000	0.00937	LSC	88771	0.0005	IR	140393	0.0045	IR
36200	0.01175	LSC	88971	0.001	IR	140602	0.003	IR
36411	0.01575	LSC	89171	0.0015	IR	140802	0.003	IR
36641	0.015	LSC	89371	0.0015	IR	141008	0.0035	IR
36862	0.01275	LSC	89571	0.002	IR	141208	0.004	IR
37065	0.00925	LSC	89777	0.0025	IR	141409	0.003	IR
37268	0.00825	LSC	89983	0.0015	IR	141609	0.003	IR
37468	0.00675	LSC	90207	0.002	IR	141809	0.001	IR
37671	0.00575	LSC	90407	0.002	IR	142009	0.0005	IR
37871	0.0045	LSC	90607	0.001	IR	142209	0.0005	IR
38071	0.0035	LSC	90813	0.001	IR	142409	0.0005	IR
38271	0.004	LSC	91013	0.001	IR	142609	0.0005	IR
38471	0.00625	LSC	91213	0.003	IR	142809	0	IR
38671	0.00675	LSC	91413	0.003	IR	143009	0	IR
38871	0.00613	LSC	91613	0.00475	IR	143209	0	IR
39071	0.00713	LSC	91813	0.00475	IR	143409	0	IR
39271	0.00638	LSC	92013	0.00225	IR	143609	0.0005	IR

39471	0.00588	LSC	92213	0.00225	IR	143809	0.001	IR
39671	0.0045	LSC	92413	0.0005	IR	144009	0.001	IR
39871	0.003	LSC	92613	0	IR	144209	0.001	IR
40071	0.0015	LSC	92813	0.0005	IR	144409	0.0015	IR
40271	0.003	LSC	93013	0.0015	IR	144609	0.0015	IR
40471	0.003	LSC	93213	0.0025	IR	144809	0.002	IR
40671	0.0035	LSC	93413	0.003	IR	145009	0.002	IR
40871	0.0035	LSC	93613	0.0025	IR	145209	0.001	IR
41071	0.002	LSC	93813	0.002	IR	145409	0.0005	IR
41271	0.00325	LSC	94013	0.001	IR	145609	0	IR
41471	0.00275	LSC	94213	0.003	IR	145809	0	IR
41671	0.00225	LSC	94413	0.0035	IR	146009	0.0005	IR
41871	0.00375	LSC	94613	0.003	IR	146215	0.0005	IR
42071	0.00525	LSC	94813	0.003	IR	146415	0.0005	IR
42281	0.00875	LSC	95013	0.001	IR	146615	0.001	IR
42484	0.00975	LSC	95213	0.0005	IR	146815	0.003	IR
42722	0.01075	LSC	95413	0.0005	IR	147015	0.003	IR
42927	0.01	LSC	95619	0.0005	IR	147215	0.0035	IR
43142	0.0075	LSC	95819	0	IR	147415	0.003	IR
43344	0.0085	LSC	96019	0	IR	147615	0.001	IR
43545	0.0065	LSC	96219	0.0005	IR	147815	0.002	IR
43745	0.0045	LSC	96419	0.001	IR	148015	0.0025	IR
43945	0.0055	LSC	96619	0.002	IR	148215	0.003	IR
44145	0.004	LSC	96819	0.002	IR	148415	0.0025	IR
44345	0.004	LSC	97019	0.0015	IR	148615	0.0015	IR
44551	0.007	LSC	97219	0.0015	IR	148815	0.0005	IR
44755	0.00725	LSC	97419	0.001	IR	149015	0	IR
44956	0.01025	LSC	97619	0.001	IR	149215	0.0005	IR
45157	0.01075	LSC	97819	0.001	IR	149415	0.00225	IR
45357	0.00925	LSC	98019	0.0005	IR	149615	0.00225	IR
45558	0.008	LSC	98219	0	IR	149815	0.00325	IR
45758	0.005	LSC	98419	0	IR	150015	0.00475	IR
45958	0.0055	LSC	98619	0	IR	150215	0.003	IR
46163	0.0075	LSC	98819	0	IR	150415	0.003	IR
46372	0.01275	LSC	99019	0	IR	150615	0.002	IR
46579	0.01963	LSC	99219	0.0005	IR	150815	0.001	IR
46808	0.02338	LSC	99419	0.0005	IR	151021	0.001	IR
47034	0.02188	LSC	99619	0.0005	IR	151221	0.002	IR
47239	0.01763	LSC	99819	0.0015	IR	151421	0.0025	IR
47439	0.01525	LSC	100019	0.0025	IR	151645	0.0015	IR
47645	0.015	LSC	100219	0.003	IR	151851	0.0025	IR
47847	0.0165	LSC	100419	0.004	IR	152057	0.002	IR
48051	0.016	LSC	100620	0.0035	IR	152257	0.0015	IR
48251	0.02025	LSC	100820	0.0025	IR	152457	0.0015	IR
48716	0.0325	LSC	101026	0.0025	IR	152657	0.001	IR
48952	0.0305	LSC	101229	0.0035	IR	152857	0.0005	IR
49158	0.0305	LSC	101435	0.004	IR	153063	0.001	IR
49378	0.02275	LSC	101635	0.0035	IR	153263	0.0015	IR

49578	0.007	LSC	101835	0.003	IR	153463	0.001	IR
49778	0.006	LSC	102035	0.001	IR	153663	0.0015	IR
49978	0.005	LSC	102235	0	IR	153863	0.001	IR
50178	0.005	LSC	102435	0	IR	154063	0.0005	IR
50378	0.005	LSC	102635	0	IR	154263	0.0005	IR
50583	0.00575	LSC	102835	0	IR	154463	0.001	IR
50783	0.00925	LSC	103035	0	IR	154663	0.0015	IR
50983	0.015	LSC	103235	0.0005	IR	154863	0.002	IR
51198	0.015	LSC	103435	0.0005	IR	155063	0.002	IR
51426	0.01975	LSC	103635	0.001	IR	155263	0.001	IR
51639	0.01625	LSC	103835	0.0015	IR	155463	0.0015	IR
51847	0.0115	LSC	104035	0.0015	IR	155663	0.0015	IR
52050	0.0125	LSC	104235	0.002	IR	155863	0.0015	IR
52250	0.008	LSC	104435	0.0015	IR	156053	0.00205	IR
52456	0.009	LSC	104635	0.001	IR			
52656	0.00925	LSC	104835	0.0005	IR			

We considered a slide window of 800 bp and a step size of 200 bp.

Table S9. Codon usage of the five species.

title	gene name	GC	GC1	GC2	GC3	ENC	T3s	C3s	A3s	G3s	CAI	GC3s
MT4309831_accD	<i>accD</i>	0.3408	0.4	0.3627	0.3	45.0930	0.5959	0.1458	0.3565	0.1993	0.1970	0.2480
MT4309831_atpA	<i>atpA</i>	0.4016	0.5	0.3976	0.3	45.3800	0.4675	0.1675	0.4302	0.1484	0.1980	0.2500
MT4309831_atpB	<i>atpB</i>	0.4268	0.6	0.3976	0.3	49.3760	0.4289	0.1887	0.4194	0.1774	0.2050	0.2940
MT4309831_atpE	<i>atpE</i>	0.3935	0.5	0.3910	0.3	50.9600	0.4623	0.1509	0.434	0.1739	0.1680	0.2520
MT4309831_atpF	<i>atpF</i>	0.3935	0.5	0.3910	0.3	43.7540	0.4384	0.1781	0.4779	0.2033	0.1570	0.2830
MT4309831_atpH	<i>atpH</i>	0.4431	0.6	0.4878	0.2	43.8020	0.5634	0.0423	0.3151	0.1940	0.1910	0.2030
MT4309831_atpI	<i>atpI</i>	0.3787	0.5	0.3600	0.3	48.0530	0.4502	0.1991	0.4337	0.1111	0.1700	0.2530
MT4309831_ccsA	<i>ccsA</i>	0.3009	0.3	0.3465	0.2	42.1180	0.5107	0.1286	0.4693	0.1230	0.1460	0.1910
MT4309831_cemA	<i>cemA</i>	0.3145	0.4	0.2826	0.3	46.3310	0.5304	0.1878	0.4351	0.1667	0.2010	0.2520
MT4309831_clpP	<i>clpP</i>	0.4078	0.5	0.3807	0.3	51.2850	0.4268	0.1911	0.4533	0.1527	0.1570	0.2700
MT4309831_matK	<i>matK</i>	0.3106	0.4	0.2922	0.3	51.3610	0.4931	0.1429	0.4831	0.2095	0.1460	0.2490
MT4309831_ndhA	<i>ndhA</i>	0.3343	0.4	0.3850	0.2	42.2090	0.4776	0.1154	0.4826	0.0992	0.1290	0.1720
MT4309831_ndhB	<i>ndhB</i>	0.3717	0.4	0.3899	0.3	46.0460	0.4369	0.2056	0.4313	0.1205	0.1590	0.2670
MT4309831_ndhB-2	<i>ndhB</i>	0.3717	0.4	0.3899	0.3	46.0460	0.4369	0.2056	0.4313	0.1205	0.1590	0.2670
MT4309831_ndhC	<i>ndhC</i>	0.3609	0.5	0.3471	0.3	50.1540	0.5248	0.0891	0.4045	0.1842	0.2010	0.2050
MT4309831_ndhD	<i>ndhD</i>	0.3399	0.4	0.3649	0.3	47.5030	0.4795	0.1621	0.4321	0.1173	0.1430	0.2250
MT4309831_ndhE	<i>ndhE</i>	0.3301	0.4	0.3235	0.3	58.8050	0.5281	0.1573	0.3836	0.1311	0.1500	0.2270
MT4309831_ndhF	<i>ndhF</i>	0.3039	0.4	0.3494	0.2	42.4930	0.5381	0.1026	0.4759	0.1176	0.1390	0.1660
MT4309831_ndhG	<i>ndhG</i>	0.3427	0.4	0.3446	0.2	47.1770	0.4907	0.1056	0.4167	0.1712	0.1230	0.2120
MT4309831_ndhH	<i>ndhH</i>	0.3706	0.5	0.3655	0.2	46.2990	0.5115	0.1148	0.5017	0.1230	0.1580	0.1800
MT4309831_ndhI	<i>ndhI</i>	0.3292	0.4	0.3665	0.2	38.9940	0.5746	0.1418	0.463	0.0879	0.1900	0.1750
MT4309831_ndhJ	<i>ndhJ</i>	0.4046	0.5	0.3899	0.3	54.0620	0.4724	0.2047	0.4018	0.1800	0.1680	0.2950
MT4309831_ndhK	<i>ndhK</i>	0.3776	0.4	0.4513	0.2	47.7390	0.5079	0.1152	0.4379	0.1548	0.1620	0.2120
MT4309831_petA	<i>petA</i>	0.3842	0.5	0.3551	0.3	52.8500	0.502	0.1451	0.4071	0.2027	0.1560	0.2620
MT4309831_petB	<i>petB</i>	0.3873	0.5	0.4120	0.3	41.6640	0.55	0.1278	0.3789	0.1088	0.2290	0.1960
MT4309831_petD	<i>petD</i>	0.3830	0.5	0.3913	0.2	39.9060	0.4565	0.1232	0.4677	0.1304	0.1760	0.2090
MT4309831_petG	<i>petG</i>	0.3421	0.4	0.3158	0.3	37.9230	0.5152	0.1818	0.3571	0.1250	0.1990	0.2500
MT4309831_petL	<i>petL</i>	0.3021	0.3	0.4375	0.1	49.4170	0.5172	0.1034	0.4615	0.0000	0.1130	0.1000
MT4309831_petN	<i>petN</i>	0.4333	0.5	0.4333	0.4	29.3050	0.36	0.2000	0.4545	0.0476	0.1210	0.2400
MT4309831_psaA	<i>psaA</i>	0.4177	0.5	0.4301	0.3	47.5740	0.4727	0.1732	0.4137	0.1446	0.1930	0.2560

MT4309831_psaB	<i>psaB</i>	0.4036	0.5	0.4286	0.3	47.8370	0.4904	0.1635	0.4051	0.1577	0.1770	0.2540
MT4309831_psaC	<i>psaC</i>	0.4146	0.5	0.5366	0.3	47.5950	0.4697	0.1515	0.5179	0.1154	0.1900	0.2110
MT4309831_psaI	<i>psaI</i>	0.3158	0.4	0.2895	0.3	41.9010	0.5313	0.1563	0.3846	0.1364	0.1900	0.2290
MT4309831_psaJ	<i>psaJ</i>	0.3411	0.4	0.3953	0.2	29.6800	0.3947	0.0789	0.6129	0.1034	0.1320	0.1500
MT4309831_psbA	<i>psbA</i>	0.4143	0.5	0.4350	0.3	40.0020	0.5691	0.2237	0.2857	0.0811	0.3310	0.2600
MT4309831_psbB	<i>psbB</i>	0.4303	0.6	0.4597	0.3	46.8300	0.5196	0.1455	0.3854	0.1449	0.1850	0.2350
MT4309831_psbC	<i>psbC</i>	0.4339	0.5	0.4599	0.3	44.5600	0.4617	0.1877	0.3909	0.1424	0.1930	0.2750
MT4309831_psbD	<i>psbD</i>	0.4190	0.5	0.4322	0.3	44.3970	0.5284	0.1839	0.3592	0.1299	0.2490	0.2570
MT4309831_psbE	<i>psbE</i>	0.4246	0.4	0.4762	0.4	48.5660	0.4521	0.2740	0.3333	0.1111	0.1860	0.3250
MT4309831_psbF	<i>psbF</i>	0.4250	0.5	0.4500	0.4	61.0000	0.3824	0.1765	0.3667	0.2308	0.1590	0.3330
MT4309831_psbH	<i>psbH</i>	0.3919	0.4	0.4595	0.3	36.9290	0.5246	0.0492	0.3559	0.2182	0.1780	0.2210
MT4309831_psbI	<i>psbI</i>	0.3333	0.5	0.2973	0.2	24.4650	0.5313	0.1563	0.48	0.0435	0.1880	0.1710
MT4309831_psbJ	<i>psbJ</i>	0.3740	0.4	0.4878	0.2	28.6000	0.5789	0.0526	0.3333	0.1111	0.1740	0.1320
MT4309831_psbK	<i>psbK</i>	0.3817	0.4	0.3387	0.4	42.8870	0.4909	0.2545	0.2683	0.1622	0.1310	0.3450
MT4309831_psbL	<i>psbL</i>	0.2906	0.4	0.2564	0.3	39.0150	0.5313	0.1875	0.4583	0.0870	0.1700	0.2220
MT4309831_psbM	<i>psbM</i>	0.3048	0.5	0.2571	0.2	47.1670	0.6333	0.1333	0.3077	0.0952	0.2150	0.1820
MT4309831_psbN	<i>psbN</i>	0.4470	0.6	0.4091	0.4	37.1650	0.3611	0.2500	0.4545	0.1613	0.1360	0.3330
MT4309831_psbT	<i>psbT</i>	0.2941	0.3	0.3529	0.2	47.3850	0.4815	0.1111	0.5	0.1364	0.1900	0.1880
MT4309831_psbZ	<i>psbZ</i>	0.3492	0.4	0.4127	0.3	57.4430	0.5439	0.1404	0.28	0.1429	0.2290	0.2370
MT4309831_rbcL	<i>rbcL</i>	0.4419	0.6	0.4384	0.3	49.2180	0.4923	0.1913	0.3883	0.1622	0.2600	0.2810
MT4309831_rpl14	<i>rpl14</i>	0.3930	0.5	0.3902	0.3	45.9360	0.4078	0.1553	0.5	0.1548	0.1640	0.2420
MT4309831_rpl16	<i>rpl16</i>	0.4142	0.5	0.5147	0.2	40.2020	0.4286	0.1238	0.5351	0.0792	0.1500	0.1650
MT4309831_rpl2	<i>rpl2</i>	0.4327	0.5	0.4836	0.3	54.2790	0.3966	0.1853	0.448	0.1709	0.1350	0.2870
MT4309831_rpl2-2	<i>rpl2</i>	0.4327	0.5	0.4836	0.3	54.2790	0.3966	0.1853	0.448	0.1709	0.1350	0.2870
MT4309831_rpl20	<i>rpl20</i>	0.3672	0.4	0.4322	0.3	51.435	0.42	0.12	0.4889	0.2025	0.091	0.246
MT4309831_rpl22	<i>rpl22</i>	0.3395	0.4	0.3789	0.2	47.986	0.4634	0.1789	0.5508	0.0935	0.171	0.208
MT4309831_rpl23	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
MT4309831_rpl23-2	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
MT4309831_rpl32	<i>rpl32</i>	0.3082	0.3	0.434	0.2	39.62	0.5429	0.0857	0.4884	0.15	0.24	0.184
MT4309831_rpl33	<i>rpl33</i>	0.3632	0.4	0.3881	0.3	39.995	0.4902	0.2157	0.3878	0.2381	0.194	0.323
MT4309831_rpl36	<i>rpl36</i>	0.3947	0.4	0.4737	0.3	21.459	0.3793	0.1379	0.4516	0.28	0.103	0.306
MT4309831_rpoA	<i>rpoA</i>	0.3354	0.5	0.2988	0.3	48.469	0.4669	0.1634	0.5165	0.1546	0.15	0.232
MT4309831_rpoB	<i>rpoB</i>	0.3849	0.5	0.3765	0.3	48.876	0.4636	0.1303	0.4528	0.2117	0.149	0.256
MT4309831_rpoC1	<i>rpoC1</i>	0.3764	0.5	0.3759	0.3	47.434	0.4852	0.1439	0.4717	0.1678	0.155	0.234
MT4309831_rpoC2	<i>rpoC2</i>	0.3675	0.5	0.3675	0.3	49.463	0.4556	0.1652	0.4514	0.1909	0.15	0.267

MT4309831_rps11	<i>rps11</i>	0.4317	0.5	0.5683	0.2	40.862	0.4426	0.1148	0.5	0.0755	0.135	0.164
MT4309831_rps12	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
MT4309831_rps12-2	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
MT4309831_rps14	<i>rps14</i>	0.4158	0.4	0.4752	0.3	45.815	0.3733	0.12	0.4512	0.2895	0.137	0.323
MT4309831_rps15	<i>rps15</i>	0.3071	0.4	0.3034	0.2	42.408	0.4688	0.0625	0.5493	0.2154	0.156	0.207
MT4309831_rps16	<i>rps16</i>	0.3558	0.5	0.382	0.2	46.847	0.5417	0.0833	0.4429	0.1719	0.14	0.195
MT4309831_rps18	<i>rps18</i>	0.3366	0.3	0.4314	0.2	36.373	0.5063	0.1013	0.4302	0.1818	0.111	0.222
MT4309831_rps19	<i>rps19</i>	0.3477	0.4	0.3763	0.2	51.797	0.4267	0.1333	0.5211	0.1695	0.126	0.225
MT4309831_rps2	<i>rps2</i>	0.3755	0.4	0.4219	0.3	47.956	0.487	0.1347	0.4294	0.1948	0.173	0.248
MT4309831_rps3	<i>rps3</i>	0.3212	0.5	0.3242	0.2	39.303	0.5096	0.1529	0.56	0.0556	0.185	0.152
MT4309831_rps4	<i>rps4</i>	0.3828	0.5	0.3663	0.3	48.522	0.475	0.1625	0.4479	0.1533	0.151	0.247
MT4309831_rps7	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
MT4309831_rps7-2	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
MT4309831_rps8	<i>rps8</i>	0.3531	0.4	0.3926	0.3	40.168	0.3636	0.1909	0.5093	0.1628	0.112	0.269
MT4309831_ycf1	<i>ycf1</i>	0.3477	0.4	0.2997	0.3	45.862	0.4348	0.221	0.4557	0.1896	0.17	0.307
MT4309831_ycf1-2	<i>ycf1</i>	0.2884	0.3	0.2822	0.2	56.324	0.4985	0.1662	0.5662	0.1222	0.18	0.204
MT4309831_ycf2	<i>ycf2</i>	0.3732	0.4	0.3437	0.4	52.858	0.4464	0.2062	0.3976	0.2642	0.155	0.341
MT4309831_ycf2-2	<i>ycf2</i>	0.3732	0.4	0.3437	0.4	52.858	0.4464	0.2062	0.3976	0.2642	0.155	0.341
MT4309831_ycf3	<i>ycf3</i>	0.3886	0.5	0.3905	0.3	56.1	0.4924	0.1667	0.4492	0.1923	0.17	0.263
MT4309831_ycf4	<i>ycf4</i>	0.3766	0.4	0.4162	0.3	45.674	0.5232	0.1457	0.3741	0.1795	0.171	0.247
MT880913_accD	<i>accD</i>	0.3388	0.4	0.3608	0.3	45.173	0.5964	0.1542	0.3547	0.1918	0.201	0.25
MT880913_atpA	<i>atpA</i>	0.4009	0.5	0.3976	0.3	45.763	0.47	0.16	0.4302	0.1536	0.195	0.248
MT880913_atpB	<i>atpB</i>	0.4281	0.6	0.4016	0.3	48.403	0.4363	0.1838	0.4134	0.1791	0.21	0.292
MT880913_atpE	<i>atpE</i>	0.3935	0.5	0.391	0.3	50.96	0.4623	0.1509	0.434	0.1739	0.168	0.252
MT880913_atpF	<i>atpF</i>	0.3514	0.4	0.3189	0.3	46.642	0.449	0.1565	0.4745	0.2114	0.155	0.272
MT880913_atpH	<i>atpH</i>	0.4431	0.6	0.4878	0.2	43.802	0.5634	0.0423	0.3151	0.194	0.191	0.203
MT880913_atpI	<i>atpI</i>	0.3787	0.5	0.36	0.3	47.944	0.4597	0.1848	0.4235	0.1287	0.173	0.253
MT880913_ccsA	<i>ccsA</i>	0.2898	0.3	0.3435	0.2	40.924	0.5161	0.1039	0.5022	0.1053	0.145	0.159
MT880913_cemA	<i>cemA</i>	0.3072	0.4	0.2739	0.3	46.125	0.5389	0.1778	0.4444	0.168	0.197	0.243
MT880913_clpP	<i>clpP</i>	0.4027	0.5	0.3807	0.3	51.113	0.4268	0.1975	0.4733	0.1221	0.162	0.254
MT880913_matK	<i>matK</i>	0.3142	0.4	0.2931	0.3	52.427	0.4833	0.1459	0.4797	0.2124	0.146	0.256
MT880913_ndhA	<i>ndhA</i>	0.3352	0.4	0.3795	0.2	43.04	0.4727	0.1158	0.4826	0.1074	0.13	0.178

MT880913_ndhB	<i>ndhB</i>	0.3697	0.4	0.3821	0.3	46.111	0.4412	0.2081	0.4251	0.1242	0.161	0.27
MT880913_ndhB-2	<i>ndhB</i>	0.3697	0.4	0.3821	0.3	46.111	0.4412	0.2081	0.4251	0.1242	0.161	0.27
MT880913_ndhC	<i>ndhC</i>	0.3636	0.5	0.3471	0.3	51.467	0.5347	0.1089	0.3977	0.16	0.197	0.205
MT880913_ndhD	<i>ndhD</i>	0.3315	0.4	0.3585	0.3	48.005	0.4841	0.148	0.4307	0.1329	0.137	0.222
MT880913_ndhE	<i>ndhE</i>	0.3333	0.4	0.3235	0.3	54.298	0.5056	0.1573	0.3973	0.1475	0.142	0.237
MT880913_ndhF	<i>ndhF</i>	0.2999	0.4	0.3481	0.2	41.563	0.546	0.1045	0.474	0.1088	0.144	0.162
MT880913_ndhG	<i>ndhG</i>	0.3427	0.4	0.3446	0.2	47.036	0.4907	0.1118	0.4167	0.1622	0.122	0.212
MT880913_ndhH	<i>ndhH</i>	0.3723	0.5	0.3655	0.2	47.392	0.5132	0.1118	0.4931	0.1344	0.157	0.185
MT880913_ndhI	<i>ndhI</i>	0.3313	0.4	0.375	0.2	37.133	0.5652	0.1232	0.4867	0.1031	0.187	0.169
MT880913_ndhJ	<i>ndhJ</i>	0.4067	0.5	0.3899	0.3	55.122	0.4724	0.1969	0.3929	0.2	0.163	0.302
MT880913_ndhK	<i>ndhK</i>	0.3728	0.4	0.4495	0.3	50.451	0.5021	0.1328	0.4245	0.1623	0.166	0.23
MT880913_petA	<i>petA</i>	0.3842	0.5	0.3551	0.3	52.514	0.5059	0.149	0.4032	0.1982	0.158	0.262
MT880913_petB	<i>petB</i>	0.3873	0.5	0.412	0.3	41.964	0.55	0.1222	0.3789	0.1156	0.236	0.196
MT880913_petD	<i>petD</i>	0.381	0.5	0.3851	0.2	40.467	0.4565	0.1159	0.4677	0.1391	0.177	0.209
MT880913_petG	<i>petG</i>	0.3333	0.4	0.3158	0.2	37.429	0.5152	0.1515	0.3929	0.125	0.177	0.222
MT880913_petL	<i>petL</i>	0.3021	0.4	0.4062	0.1	49.1	0.5172	0.1034	0.4615	0	0.104	0.1
MT880913_petN	<i>petN</i>	0.4333	0.5	0.4333	0.4	29.305	0.36	0.2	0.4545	0.0476	0.121	0.24
MT880913_psaA	<i>psaA</i>	0.4172	0.5	0.4301	0.3	47.55	0.4743	0.1716	0.4137	0.1449	0.196	0.255
MT880913_psaB	<i>psaB</i>	0.4063	0.5	0.4327	0.3	47.717	0.492	0.1635	0.3969	0.1606	0.177	0.257
MT880913_psaC	<i>psaC</i>	0.4065	0.4	0.5366	0.2	46.706	0.4697	0.1364	0.5263	0.1132	0.177	0.197
MT880913_psaI	<i>psaI</i>	0.3158	0.4	0.2895	0.3	41.901	0.5313	0.1563	0.3846	0.1364	0.19	0.229
MT880913_psaJ	<i>psaJ</i>	0.3566	0.4	0.3953	0.2	29.68	0.3947	0.1053	0.5484	0.1379	0.147	0.2
MT880913_psbA	<i>psbA</i>	0.4134	0.5	0.435	0.3	40.078	0.5724	0.2171	0.2857	0.0856	0.327	0.257
MT880913_psbB	<i>psbB</i>	0.427	0.6	0.4597	0.3	45.898	0.5266	0.1409	0.3935	0.1333	0.191	0.222
MT880913_psbC	<i>psbC</i>	0.4325	0.5	0.4599	0.3	44.386	0.4691	0.1827	0.3853	0.1455	0.195	0.272
MT880913_psbD	<i>psbD</i>	0.42	0.5	0.4322	0.3	45.251	0.5251	0.1839	0.3592	0.1342	0.253	0.26
MT880913_psbE	<i>psbE</i>	0.4246	0.4	0.4762	0.4	46.662	0.4384	0.274	0.3492	0.1111	0.18	0.325
MT880913_psbF	<i>psbF</i>	0.4167	0.5	0.45	0.4	61	0.3824	0.1471	0.4	0.2308	0.141	0.306
MT880913_psbH	<i>psbH</i>	0.4009	0.4	0.4595	0.3	38.154	0.5	0.0484	0.35	0.25	0.174	0.246
MT880913_psbI	<i>psbI</i>	0.3423	0.5	0.2973	0.2	24.769	0.5	0.1875	0.48	0.0435	0.195	0.2
MT880913_psbJ	<i>psbJ</i>	0.3821	0.4	0.4878	0.2	29.589	0.5526	0.0526	0.3333	0.1481	0.17	0.158
MT880913_psbK	<i>psbK</i>	0.371	0.4	0.3387	0.4	45.009	0.5091	0.2545	0.2683	0.1389	0.132	0.328

MT880913_psbL	<i>psbL</i>	0.2906	0.4	0.2564	0.3	39.015	0.5313	0.1875	0.4583	0.087	0.17	0.222
MT880913_psbM	<i>psbM</i>	0.2952	0.5	0.2571	0.2	47.167	0.6333	0.1333	0.3462	0.0476	0.213	0.152
MT880913_psbN	<i>psbN</i>	0.447	0.6	0.4091	0.4	37.165	0.3611	0.25	0.4545	0.1613	0.136	0.333
MT880913_psbT	<i>psbT</i>	0.2843	0.3	0.3529	0.2	47.385	0.5185	0.0741	0.5	0.1364	0.191	0.156
MT880913_psbZ	<i>psbZ</i>	0.3545	0.4	0.4127	0.3	59.38	0.5263	0.1404	0.28	0.1667	0.214	0.254
MT880913_rbcL	<i>rbcL</i>	0.4422	0.6	0.4415	0.3	48.905	0.4925	0.191	0.3874	0.1633	0.259	0.281
MT880913_rpl14	<i>rpl14</i>	0.3875	0.5	0.3902	0.2	44.9	0.4175	0.1553	0.5	0.1446	0.154	0.233
MT880913_rpl16	<i>rpl16</i>	0.4142	0.5	0.5147	0.2	39.827	0.4286	0.1143	0.5351	0.0891	0.146	0.165
MT880913_rpl2	<i>rpl2</i>	0.4315	0.5	0.48	0.3	54.56	0.3966	0.1853	0.448	0.1709	0.135	0.287
MT880913_rpl2-2	<i>rpl2</i>	0.4315	0.5	0.48	0.3	54.56	0.3966	0.1853	0.448	0.1709	0.135	0.287
MT880913_rpl20	<i>rpl20</i>	0.3729	0.4	0.4237	0.3	51.485	0.4242	0.1212	0.4719	0.2179	0.091	0.257
MT880913_rpl22	<i>rpl22</i>	0.3375	0.4	0.3851	0.2	47.916	0.4516	0.1855	0.5641	0.0849	0.169	0.208
MT880913_rpl23	<i>rpl23</i>	0.3688	0.4	0.383	0.3	54.145	0.4521	0.1507	0.4571	0.1774	0.124	0.253
MT880913_rpl23-2	<i>rpl23</i>	0.3688	0.4	0.383	0.3	54.145	0.4521	0.1507	0.4571	0.1774	0.124	0.253
MT880913_rpl32	<i>rpl32</i>	0.3019	0.3	0.434	0.2	39.62	0.5714	0.0571	0.4884	0.15	0.252	0.163
MT880913_rpl33	<i>rpl33</i>	0.3532	0.4	0.3881	0.3	40.755	0.5098	0.1765	0.4082	0.2381	0.178	0.292
MT880913_rpl36	<i>rpl36</i>	0.386	0.4	0.4737	0.3	26.459	0.3793	0.1379	0.4839	0.24	0.101	0.278
MT880913_rpoA	<i>rpoA</i>	0.3384	0.5	0.3018	0.3	48.69	0.471	0.1699	0.5021	0.1553	0.149	0.238
MT880913_rpoB	<i>rpoB</i>	0.3861	0.5	0.3765	0.3	49.143	0.4613	0.1279	0.4504	0.2192	0.148	0.26
MT880913_rpoC1	<i>rpoC1</i>	0.374	0.5	0.3735	0.3	47.113	0.4881	0.1371	0.4709	0.1758	0.154	0.233
MT880913_rpoC2	<i>rpoC2</i>	0.3675	0.5	0.367	0.3	48.908	0.4588	0.1594	0.4525	0.1914	0.15	0.263
MT880913_rps11	<i>rps11</i>	0.4293	0.5	0.5683	0.2	41.91	0.4262	0.1066	0.5259	0.0755	0.14	0.157
MT880913_rps12	<i>rps12</i>	0.4328	0.5	0.4758	0.3	47.656	0.3689	0.1942	0.4667	0.1546	0.129	0.287
MT880913_rps12-2	<i>rps12</i>	0.4328	0.5	0.4758	0.3	47.656	0.3689	0.1942	0.4667	0.1546	0.129	0.287
MT880913_rps14	<i>rps14</i>	0.4224	0.4	0.4752	0.3	45.961	0.36	0.12	0.4634	0.2857	0.134	0.323
MT880913_rps15	<i>rps15</i>	0.3146	0.4	0.3034	0.2	40.908	0.4531	0.0938	0.5352	0.2154	0.166	0.23
MT880913_rps16	<i>rps16</i>	0.3521	0.5	0.3708	0.2	47.797	0.5211	0.0986	0.4714	0.1587	0.148	0.195
MT880913_rps18	<i>rps18</i>	0.3366	0.3	0.4314	0.2	36.373	0.5063	0.1013	0.4302	0.1818	0.111	0.222
MT880913_rps19	<i>rps19</i>	0.3405	0.4	0.3763	0.2	47.677	0.44	0.1333	0.5352	0.1356	0.118	0.202
MT880913_rps2	<i>rps2</i>	0.3769	0.4	0.4219	0.3	47.886	0.487	0.1399	0.4205	0.2026	0.173	0.257
MT880913_rps3	<i>rps3</i>	0.3318	0.5	0.3333	0.2	42.278	0.4969	0.1698	0.5434	0.0699	0.182	0.176
MT880913_rps4	<i>rps4</i>	0.3812	0.5	0.3663	0.3	47.907	0.475	0.1563	0.454	0.1533	0.154	0.242

MT880913_rps7	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
MT880913_rps7-2	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
MT880913_rps8	<i>rps8</i>	0.358	0.4	0.3926	0.3	40.947	0.3636	0.2	0.4907	0.1744	0.117	0.285
MT880913_ycf1	<i>ycf1</i>	0.3404	0.4	0.2979	0.3	47.076	0.4358	0.2128	0.469	0.193	0.171	0.3
MT880913_ycf1-2	<i>ycf1</i>	0.2919	0.3	0.2885	0.2	56.285	0.4911	0.174	0.5615	0.1248	0.181	0.212
MT880913_ycf2	<i>ycf2</i>	0.3738	0.4	0.3444	0.4	52.895	0.4474	0.2054	0.3981	0.2645	0.155	0.34
MT880913_ycf2-2	<i>ycf2</i>	0.3738	0.4	0.3444	0.4	52.895	0.4474	0.2054	0.3981	0.2645	0.155	0.34
MT880913_ycf3	<i>ycf3</i>	0.3905	0.5	0.3905	0.3	56.437	0.4848	0.1742	0.4492	0.1923	0.172	0.269
MT880913_ycf4	<i>ycf4</i>	0.3766	0.4	0.4162	0.3	46.465	0.5232	0.1457	0.3741	0.1795	0.167	0.247
MT880914_accD	<i>accD</i>	0.343	0.4	0.3629	0.3	45.185	0.5954	0.1521	0.3495	0.2	0.2	0.254
MT880914_atpA	<i>atpA</i>	0.4022	0.5	0.3976	0.3	45.682	0.4675	0.1675	0.4279	0.151	0.197	0.252
MT880914_atpB	<i>atpB</i>	0.4261	0.6	0.3976	0.3	48.992	0.4289	0.1863	0.4243	0.1747	0.205	0.29
MT880914_atpE	<i>atpE</i>	0.3935	0.5	0.391	0.3	50.96	0.4623	0.1509	0.434	0.1739	0.168	0.252
MT880914_atpF	<i>atpF</i>	0.355	0.4	0.3243	0.3	43.912	0.4384	0.1781	0.4745	0.2016	0.158	0.283
MT880914_atpH	<i>atpH</i>	0.4431	0.6	0.4878	0.2	43.802	0.5634	0.0423	0.3151	0.194	0.191	0.203
MT880914_atpI	<i>atpI</i>	0.3773	0.5	0.356	0.3	48.062	0.4502	0.1991	0.4337	0.1111	0.17	0.253
MT880914_ccsA	<i>ccsA</i>	0.2948	0.3	0.3435	0.2	41.209	0.5197	0.1147	0.4846	0.1176	0.15	0.175
MT880914_cemA	<i>cemA</i>	0.3101	0.4	0.2739	0.3	45.683	0.5333	0.1833	0.4387	0.1667	0.202	0.248
MT880914_clpP	<i>clpP</i>	0.4027	0.5	0.3807	0.3	50.912	0.4268	0.1911	0.4733	0.1298	0.157	0.254
MT880914_matK	<i>matK</i>	0.3112	0.4	0.2998	0.3	50.897	0.4966	0.1402	0.4818	0.2057	0.144	0.245
MT880914_ndhA	<i>ndhA</i>	0.3343	0.4	0.385	0.2	42.152	0.4712	0.1218	0.4861	0.095	0.129	0.175
MT880914_ndhB	<i>ndhB</i>	0.3697	0.4	0.384	0.3	46.149	0.4412	0.2059	0.4278	0.1242	0.161	0.268
MT880914_ndhB-2	<i>ndhB</i>	0.3697	0.4	0.384	0.3	46.149	0.4412	0.2059	0.4278	0.1242	0.161	0.268
MT880914_ndhC	<i>ndhC</i>	0.3609	0.5	0.3471	0.3	50.035	0.5248	0.0891	0.4045	0.1842	0.201	0.205
MT880914_ndhD	<i>ndhD</i>	0.3371	0.4	0.3619	0.3	48.059	0.4825	0.155	0.4215	0.1325	0.139	0.228
MT880914_ndhE	<i>ndhE</i>	0.3333	0.4	0.3235	0.3	54.17	0.5169	0.1573	0.3836	0.1475	0.143	0.237
MT880914_ndhF	<i>ndhF</i>	0.3017	0.4	0.3494	0.2	42.106	0.5443	0.0995	0.474	0.1156	0.141	0.162
MT880914_ndhG	<i>ndhG</i>	0.3427	0.4	0.3446	0.2	47.177	0.4907	0.1056	0.4167	0.1712	0.123	0.212
MT880914_ndhH	<i>ndhH</i>	0.3697	0.5	0.3623	0.2	46.877	0.5049	0.1165	0.5118	0.1197	0.157	0.179
MT880914_ndhI	<i>ndhI</i>	0.3353	0.4	0.375	0.2	38.404	0.5652	0.1377	0.469	0.1031	0.185	0.181
MT880914_ndhJ	<i>ndhJ</i>	0.4025	0.5	0.3899	0.3	53.981	0.4882	0.189	0.3929	0.19	0.164	0.289
MT880914_ndhK	<i>ndhK</i>	0.3694	0.4	0.4286	0.3	48.477	0.5142	0.1321	0.4346	0.16	0.171	0.226

MT880914_petA	<i>petA</i>	0.3832	0.5	0.3551	0.3	52.73	0.502	0.1451	0.4071	0.2027	0.156	0.262
MT880914_petB	<i>petB</i>	0.3873	0.5	0.412	0.3	41.664	0.55	0.1278	0.3789	0.1088	0.229	0.196
MT880914_petD	<i>petD</i>	0.381	0.5	0.3913	0.2	39.293	0.4638	0.1159	0.4677	0.1304	0.174	0.203
MT880914_petG	<i>petG</i>	0.3421	0.4	0.3158	0.3	37.923	0.5152	0.1818	0.3571	0.125	0.199	0.25
MT880914_petL	<i>petL</i>	0.3125	0.4	0.4375	0.1	45.667	0.5172	0.1034	0.4615	0	0.11	0.1
MT880914_petN	<i>petN</i>	0.4333	0.5	0.4333	0.4	29.305	0.36	0.2	0.4545	0.0476	0.121	0.24
MT880914_psaA	<i>psaA</i>	0.4172	0.5	0.4301	0.3	47.465	0.4758	0.1716	0.4119	0.1449	0.193	0.255
MT880914_psaB	<i>psaB</i>	0.4054	0.5	0.4299	0.3	47.752	0.4888	0.1651	0.4023	0.1591	0.176	0.257
MT880914_psaC	<i>psaC</i>	0.4146	0.5	0.5366	0.3	47.595	0.4697	0.1515	0.5179	0.1154	0.19	0.211
MT880914_psaI	<i>psaI</i>	0.3158	0.4	0.2895	0.3	41.901	0.5313	0.1563	0.3846	0.1364	0.19	0.229
MT880914_psaJ	<i>psaJ</i>	0.3488	0.4	0.3953	0.2	29.68	0.3947	0.0789	0.5806	0.1379	0.127	0.175
MT880914_psbA	<i>psbA</i>	0.4134	0.5	0.435	0.3	40.096	0.5724	0.2204	0.2857	0.0811	0.328	0.257
MT880914_psbB	<i>psbB</i>	0.4322	0.6	0.4597	0.3	46.814	0.5196	0.1478	0.3811	0.1478	0.184	0.239
MT880914_psbC	<i>psbC</i>	0.4332	0.5	0.4599	0.3	44.575	0.4593	0.1901	0.3938	0.1394	0.191	0.275
MT880914_psbD	<i>psbD</i>	0.42	0.5	0.4322	0.3	44.512	0.5251	0.1873	0.3633	0.1255	0.254	0.257
MT880914_psbE	<i>psbE</i>	0.4246	0.4	0.4762	0.4	48.566	0.4521	0.274	0.3333	0.1111	0.186	0.325
MT880914_psbF	<i>psbF</i>	0.4167	0.5	0.45	0.4	61	0.3824	0.1471	0.4	0.2308	0.141	0.306
MT880914_psbH	<i>psbH</i>	0.3919	0.4	0.4595	0.3	36.929	0.5246	0.0492	0.3559	0.2182	0.178	0.221
MT880914_psbI	<i>psbI</i>	0.3333	0.5	0.2973	0.2	24.465	0.5313	0.1563	0.48	0.0435	0.188	0.171
MT880914_psbJ	<i>psbJ</i>	0.3821	0.4	0.4878	0.2	29.051	0.5526	0.0789	0.3333	0.1111	0.172	0.158
MT880914_psbK	<i>psbK</i>	0.3817	0.4	0.3387	0.4	42.887	0.4909	0.2545	0.2683	0.1622	0.131	0.345
MT880914_psbL	<i>psbL</i>	0.2906	0.4	0.2564	0.3	39.015	0.5313	0.1875	0.4583	0.087	0.17	0.222
MT880914_psbM	<i>psbM</i>	0.2952	0.5	0.2571	0.2	41.167	0.6667	0.1333	0.3077	0.0476	0.231	0.152
MT880914_psbN	<i>psbN</i>	0.447	0.6	0.4091	0.4	37.165	0.3611	0.25	0.4545	0.1613	0.136	0.333
MT880914_psbT	<i>psbT</i>	0.2941	0.3	0.3529	0.2	47.385	0.4815	0.1111	0.5	0.1364	0.19	0.188
MT880914_psbZ	<i>psbZ</i>	0.3492	0.4	0.4127	0.3	57.443	0.5439	0.1404	0.28	0.1429	0.229	0.237
MT880914_rbcL	<i>rbcL</i>	0.4415	0.6	0.4394	0.3	48.888	0.4937	0.1914	0.3874	0.1633	0.258	0.281
MT880914_rpl14	<i>rpl14</i>	0.3875	0.5	0.3902	0.2	46.004	0.4078	0.1553	0.5102	0.1446	0.151	0.233
MT880914_rpl16	<i>rpl16</i>	0.4142	0.5	0.5147	0.2	39.193	0.4286	0.1238	0.5351	0.0792	0.149	0.165
MT880914_rpl2	<i>rpl2</i>	0.4327	0.5	0.4836	0.3	54.279	0.3966	0.1853	0.448	0.1709	0.135	0.287
MT880914_rpl2-2	<i>rpl2</i>	0.4327	0.5	0.4836	0.3	54.279	0.3966	0.1853	0.448	0.1709	0.135	0.287
MT880914_rpl20	<i>rpl20</i>	0.3701	0.4	0.4322	0.3	51.935	0.42	0.12	0.4778	0.2152	0.091	0.254

MT880914_rpl22	<i>rpl22</i>	0.3395	0.4	0.3851	0.2	48.762	0.4597	0.1774	0.5508	0.1028	0.165	0.213
MT880914_rpl23	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
MT880914_rpl23-2	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
MT880914_rpl32	<i>rpl32</i>	0.3145	0.3	0.434	0.2	39.62	0.5429	0.0857	0.4651	0.175	0.243	0.204
MT880914_rpl33	<i>rpl33</i>	0.3582	0.4	0.3881	0.3	40.649	0.4902	0.1961	0.4082	0.2381	0.187	0.308
MT880914_rpl36	<i>rpl36</i>	0.3947	0.4	0.4737	0.3	21.459	0.3793	0.1379	0.4516	0.28	0.103	0.306
MT880914_rpoA	<i>rpoA</i>	0.3354	0.5	0.2988	0.3	48.478	0.469	0.1628	0.5145	0.1553	0.149	0.232
MT880914_rpoB	<i>rpoB</i>	0.3858	0.5	0.3765	0.3	48.856	0.4642	0.1293	0.451	0.2141	0.15	0.258
MT880914_rpoC1	<i>rpoC1</i>	0.3735	0.5	0.3735	0.3	47.193	0.4899	0.1408	0.4729	0.167	0.155	0.23
MT880914_rpoC2	<i>rpoC2</i>	0.3677	0.5	0.3672	0.3	49.446	0.4566	0.1622	0.452	0.1925	0.149	0.266
MT880914_rps11	<i>rps11</i>	0.4317	0.5	0.5683	0.2	41.847	0.4344	0.1148	0.5086	0.0755	0.138	0.164
MT880914_rps12	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
MT880914_rps12-2	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
MT880914_rps14	<i>rps14</i>	0.4125	0.4	0.4752	0.3	45.923	0.3733	0.12	0.4512	0.2895	0.135	0.323
MT880914_rps15	<i>rps15</i>	0.3071	0.4	0.3034	0.2	42.408	0.4688	0.0625	0.5493	0.2154	0.156	0.207
MT880914_rps16	<i>rps16</i>	0.3521	0.5	0.382	0.2	46.813	0.5417	0.0833	0.4571	0.1563	0.142	0.184
MT880914_rps18	<i>rps18</i>	0.3366	0.3	0.4314	0.2	36.373	0.5063	0.1013	0.4302	0.1818	0.111	0.222
MT880914_rps19	<i>rps19</i>	0.3477	0.4	0.3763	0.2	51.797	0.4267	0.1333	0.5211	0.1695	0.126	0.225
MT880914_rps2	<i>rps2</i>	0.3769	0.4	0.4219	0.3	48.096	0.487	0.1347	0.4237	0.2013	0.172	0.252
MT880914_rps3	<i>rps3</i>	0.3242	0.5	0.3242	0.2	39.397	0.4937	0.1582	0.5575	0.0699	0.177	0.167
MT880914_rps4	<i>rps4</i>	0.3828	0.5	0.3663	0.3	48.522	0.475	0.1625	0.4479	0.1533	0.151	0.247
MT880914_rps7	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
MT880914_rps7-2	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
MT880914_rps8	<i>rps8</i>	0.3531	0.4	0.3926	0.3	40.168	0.3636	0.1909	0.5093	0.1628	0.112	0.269
MT880914_ycf1	<i>ycf1</i>	0.3404	0.4	0.2979	0.3	45.913	0.4358	0.2162	0.4708	0.1894	0.173	0.3
MT880914_ycf1-2	<i>ycf1</i>	0.2877	0.3	0.2804	0.2	56.204	0.5012	0.1632	0.5677	0.1227	0.178	0.202
MT880914_ycf2	<i>ycf2</i>	0.3732	0.4	0.3428	0.4	52.908	0.4471	0.2063	0.3969	0.265	0.156	0.341
MT880914_ycf2-2	<i>ycf2</i>	0.3732	0.4	0.3428	0.4	52.908	0.4471	0.2063	0.3969	0.265	0.156	0.341
MT880914_ycf3	<i>ycf3</i>	0.3886	0.5	0.3905	0.3	55.203	0.4924	0.1667	0.4492	0.1923	0.172	0.263
MT880914_ycf4	<i>ycf4</i>	0.3766	0.4	0.4162	0.3	46.436	0.5132	0.1513	0.3786	0.1795	0.172	0.251
NC_009273_accD	<i>accD</i>	0.3415	0.4	0.3586	0.3	44.554	0.5979	0.1469	0.3514	0.2047	0.201	0.253
NC_009273_atpA	<i>atpA</i>	0.4049	0.5	0.3976	0.3	45.411	0.4625	0.175	0.4256	0.151	0.197	0.258

NC_009273_atpB	<i>atpB</i>	0.4254	0.6	0.3976	0.3	48.606	0.4314	0.1838	0.4243	0.1747	0.205	0.287
NC_009273_atpE	<i>atpE</i>	0.3935	0.5	0.391	0.3	50.96	0.4623	0.1509	0.434	0.1739	0.168	0.252
NC_009273_atpF	<i>atpF</i>	0.3532	0.4	0.3189	0.3	43.401	0.4414	0.1793	0.4745	0.2016	0.163	0.283
NC_009273_atpH	<i>atpH</i>	0.4431	0.6	0.4878	0.2	43.802	0.5634	0.0423	0.3151	0.194	0.191	0.203
NC_009273_atpI	<i>atpI</i>	0.38	0.5	0.36	0.3	48.378	0.4455	0.2038	0.4337	0.1111	0.168	0.257
NC_009273_ccsA	<i>ccsA</i>	0.2969	0.3	0.3495	0.2	41.625	0.516	0.1139	0.489	0.1123	0.149	0.172
NC_009273_cemA	<i>cemA</i>	0.313	0.4	0.2826	0.3	45.924	0.5333	0.1833	0.4387	0.1654	0.201	0.248
NC_009273_clpP	<i>clpP</i>	0.4027	0.5	0.3807	0.3	50.912	0.4268	0.1911	0.4733	0.1298	0.157	0.254
NC_009273_matK	<i>matK</i>	0.3118	0.4	0.2979	0.3	50.264	0.5023	0.1399	0.4761	0.2077	0.149	0.245
NC_009273_ndhA	<i>ndhA</i>	0.3352	0.4	0.385	0.2	42.218	0.4712	0.1218	0.4861	0.095	0.129	0.175
NC_009273_ndhB	<i>ndhB</i>	0.3717	0.4	0.3899	0.3	46.046	0.4369	0.2056	0.4313	0.1205	0.159	0.267
NC_009273_ndhB-2	<i>ndhB</i>	0.3717	0.4	0.3899	0.3	46.046	0.4369	0.2056	0.4313	0.1205	0.159	0.267
NC_009273_ndhC	<i>ndhC</i>	0.3609	0.5	0.3471	0.3	50.154	0.5248	0.0891	0.4045	0.1842	0.201	0.205
NC_009273_ndhD	<i>ndhD</i>	0.34	0.4	0.3685	0.3	47.551	0.4839	0.1567	0.4305	0.1176	0.142	0.22
NC_009273_ndhE	<i>ndhE</i>	0.3301	0.4	0.3235	0.3	56.33	0.5169	0.1573	0.3973	0.1311	0.145	0.227
NC_009273_ndhF	<i>ndhF</i>	0.3061	0.4	0.3494	0.2	43.435	0.5397	0.1026	0.4635	0.129	0.139	0.173
NC_009273_ndhG	<i>ndhG</i>	0.3446	0.4	0.3446	0.2	48.537	0.4907	0.1056	0.4091	0.1802	0.122	0.218
NC_009273_ndhH	<i>ndhH</i>	0.3697	0.5	0.3655	0.2	47.064	0.5115	0.1148	0.5052	0.119	0.158	0.177
NC_009273_ndhI	<i>ndhI</i>	0.3333	0.4	0.375	0.2	38.404	0.562	0.1314	0.4825	0.102	0.192	0.175
NC_009273_ndhJ	<i>ndhJ</i>	0.4046	0.5	0.3899	0.3	54.312	0.4803	0.1969	0.3929	0.19	0.166	0.295
NC_009273_ndhK	<i>ndhK</i>	0.3776	0.4	0.4513	0.2	47.739	0.5079	0.1152	0.4379	0.1548	0.162	0.212
NC_009273_petA	<i>petA</i>	0.3853	0.5	0.3551	0.3	52.37	0.5059	0.1451	0.3992	0.2072	0.156	0.265
NC_009273_petB	<i>petB</i>	0.3873	0.5	0.412	0.3	41.664	0.55	0.1278	0.3789	0.1088	0.229	0.196
NC_009273_petD	<i>petD</i>	0.381	0.5	0.3913	0.2	39.132	0.471	0.1159	0.4597	0.1304	0.174	0.203
NC_009273_petG	<i>petG</i>	0.3421	0.4	0.3158	0.3	37.923	0.5152	0.1818	0.3571	0.125	0.199	0.25
NC_009273_petL	<i>petL</i>	0.3125	0.4	0.4375	0.1	45.667	0.5172	0.1034	0.4615	0	0.11	0.1
NC_009273_petN	<i>petN</i>	0.4333	0.5	0.4333	0.4	29.305	0.36	0.2	0.4545	0.0476	0.121	0.24
NC_009273_psaA	<i>psaA</i>	0.4168	0.5	0.4301	0.3	47.361	0.4743	0.17	0.4156	0.1446	0.194	0.253
NC_009273_psaB	<i>psaB</i>	0.4036	0.5	0.4299	0.3	47.464	0.4904	0.1635	0.4063	0.1552	0.176	0.253
NC_009273_psaC	<i>psaC</i>	0.4146	0.5	0.5366	0.3	47.595	0.4697	0.1515	0.5179	0.1154	0.19	0.211
NC_009273_psaI	<i>psaI</i>	0.3158	0.4	0.2895	0.3	41.901	0.5313	0.1563	0.3846	0.1364	0.19	0.229
NC_009273_psaJ	<i>psaJ</i>	0.3488	0.4	0.3953	0.2	29.68	0.3947	0.0789	0.5806	0.1379	0.127	0.175

NC_009273_psbA	<i>psbA</i>	0.4134	0.5	0.435	0.3	40.096	0.5724	0.2204	0.2857	0.0811	0.328	0.257
NC_009273_psbB	<i>psbB</i>	0.4303	0.6	0.4597	0.3	46.786	0.5196	0.1432	0.3854	0.1474	0.182	0.235
NC_009273_psbC	<i>psbC</i>	0.4311	0.5	0.4599	0.3	44.151	0.4617	0.1877	0.3994	0.1333	0.191	0.268
NC_009273_psbD	<i>psbD</i>	0.419	0.5	0.4322	0.3	44.317	0.5284	0.1873	0.3592	0.1255	0.254	0.257
NC_009273_psbE	<i>psbE</i>	0.4286	0.4	0.4762	0.4	51.396	0.4384	0.2877	0.3333	0.1111	0.183	0.338
NC_009273_psbF	<i>psbF</i>	0.4167	0.5	0.45	0.4	61	0.3824	0.1471	0.4	0.2308	0.141	0.306
NC_009273_psbH	<i>psbH</i>	0.3919	0.4	0.4595	0.3	36.929	0.5246	0.0492	0.3559	0.2182	0.178	0.221
NC_009273_psbI	<i>psbI</i>	0.3333	0.5	0.2973	0.2	24.12	0.5484	0.1613	0.48	0.0417	0.222	0.171
NC_009273_psbJ	<i>psbJ</i>	0.374	0.4	0.4878	0.2	28.6	0.5789	0.0526	0.3333	0.1111	0.174	0.132
NC_009273_psbK	<i>psbK</i>	0.3817	0.4	0.3387	0.4	42.887	0.4909	0.2545	0.2683	0.1622	0.131	0.345
NC_009273_psbL	<i>psbL</i>	0.2906	0.4	0.2564	0.3	39.015	0.5313	0.1875	0.4583	0.087	0.17	0.222
NC_009273_psbM	<i>psbM</i>	0.3048	0.5	0.2571	0.2	47.167	0.6333	0.1333	0.3077	0.0952	0.215	0.182
NC_009273_psbN	<i>psbN</i>	0.447	0.6	0.4091	0.4	37.165	0.3611	0.25	0.4545	0.1613	0.136	0.333
NC_009273_psbT	<i>psbT</i>	0.2941	0.3	0.3529	0.2	47.385	0.4815	0.1111	0.5	0.1364	0.19	0.188
NC_009273_psbZ	<i>psbZ</i>	0.3492	0.4	0.4127	0.3	57.443	0.5439	0.1404	0.28	0.1429	0.229	0.237
NC_009273_rbcL	<i>rbcL</i>	0.4405	0.6	0.4384	0.3	47.843	0.4936	0.1934	0.3922	0.1543	0.264	0.277
NC_009273_rpl14	<i>rpl14</i>	0.3875	0.5	0.3902	0.2	46.004	0.4078	0.1553	0.5102	0.1446	0.151	0.233
NC_009273_rpl16	<i>rpl16</i>	0.4142	0.5	0.5147	0.2	40.74	0.4286	0.1143	0.5351	0.0891	0.146	0.165
NC_009273_rpl2	<i>rpl2</i>	0.4339	0.5	0.4836	0.3	54.292	0.3966	0.1853	0.448	0.1709	0.136	0.287
NC_009273_rpl2-2	<i>rpl2</i>	0.4339	0.5	0.4836	0.3	54.292	0.3966	0.1853	0.448	0.1709	0.136	0.287
NC_009273_rpl20	<i>rpl20</i>	0.3672	0.4	0.4322	0.3	53.163	0.43	0.12	0.4778	0.2025	0.095	0.246
NC_009273_rpl22	<i>rpl22</i>	0.3437	0.4	0.3913	0.2	48.533	0.456	0.184	0.547	0.1038	0.168	0.219
NC_009273_rpl23	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
NC_009273_rpl23-2	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
NC_009273_rpl32	<i>rpl32</i>	0.3145	0.3	0.434	0.2	39.62	0.5429	0.0857	0.4651	0.175	0.243	0.204
NC_009273_rpl33	<i>rpl33</i>	0.3582	0.4	0.3881	0.3	40.649	0.4902	0.1961	0.4082	0.2381	0.187	0.308
NC_009273_rpl36	<i>rpl36</i>	0.3947	0.4	0.4737	0.3	21.459	0.3793	0.1379	0.4516	0.28	0.103	0.306
NC_009273_rpoA	<i>rpoA</i>	0.3364	0.5	0.2957	0.3	48.588	0.4669	0.1634	0.5125	0.161	0.15	0.236
NC_009273_rpoB	<i>rpoB</i>	0.3868	0.5	0.3765	0.3	49.304	0.4613	0.1303	0.4492	0.2182	0.149	0.261
NC_009273_rpoC1	<i>rpoC1</i>	0.3759	0.5	0.3759	0.3	47.54	0.4852	0.1421	0.4728	0.1674	0.153	0.232
NC_009273_rpoC2	<i>rpoC2</i>	0.3675	0.5	0.3683	0.3	49.217	0.4583	0.1634	0.4495	0.192	0.149	0.266
NC_009273_rps11	<i>rps11</i>	0.4293	0.5	0.5683	0.2	41.349	0.4426	0.1066	0.5086	0.0755	0.138	0.157

NC_009273_rps12	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
NC_009273_rps12-2	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
NC_009273_rps14	<i>rps14</i>	0.3875	0.5	0.3902	0.2	45.815	0.3733	0.12	0.4512	0.2895	0.137	0.323
NC_009273_rps15	<i>rps15</i>	0.3034	0.4	0.2921	0.2	39.869	0.4688	0.0625	0.5493	0.2188	0.157	0.207
NC_009273_rps16	<i>rps16</i>	0.3521	0.5	0.382	0.2	46.813	0.5417	0.0833	0.4571	0.1563	0.142	0.184
NC_009273_rps18	<i>rps18</i>	0.3399	0.3	0.4314	0.3	36.881	0.5	0.1125	0.4235	0.1842	0.111	0.232
NC_009273_rps19	<i>rps19</i>	0.3477	0.4	0.3763	0.2	51.797	0.4267	0.1333	0.5211	0.1695	0.126	0.225
NC_009273_rps2	<i>rps2</i>	0.3755	0.4	0.4219	0.3	48.119	0.487	0.1347	0.4237	0.2013	0.172	0.252
NC_009273_rps3	<i>rps3</i>	0.3242	0.5	0.3242	0.2	39.449	0.5	0.1582	0.5575	0.0629	0.177	0.162
NC_009273_rps4	<i>rps4</i>	0.3828	0.5	0.3663	0.3	48.522	0.475	0.1625	0.4479	0.1533	0.151	0.247
NC_009273_rps7	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
NC_009273_rps7-2	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
NC_009273_rps8	<i>rps8</i>	0.3556	0.4	0.3926	0.3	40.296	0.3636	0.2	0.5	0.1628	0.116	0.277
NC_009273_ycf1	<i>ycf1</i>	0.3509	0.4	0.3168	0.3	45.145	0.4268	0.2154	0.4408	0.1862	0.154	0.308
NC_009273_ycf1-2	<i>ycf1</i>	0.288	0.3	0.2865	0.2	56.84	0.5043	0.1605	0.5613	0.1207	0.175	0.2
NC_009273_ycf2	<i>ycf2</i>	0.3737	0.4	0.3427	0.4	52.979	0.4472	0.2067	0.3964	0.2654	0.156	0.342
NC_009273_ycf2-2	<i>ycf2</i>	0.3737	0.4	0.3427	0.4	52.979	0.4472	0.2067	0.3964	0.2654	0.156	0.342
NC_009273_ycf3	<i>ycf3</i>	0.3905	0.5	0.3905	0.3	56.437	0.4848	0.1742	0.4492	0.1923	0.172	0.269
NC_009273_ycf4	<i>ycf4</i>	0.3766	0.4	0.4162	0.3	46.347	0.5166	0.1391	0.3813	0.188	0.166	0.247
NC_047178_accD	<i>accD</i>	0.3422	0.4	0.3627	0.3	45.984	0.5887	0.1542	0.3584	0.1987	0.205	0.255
NC_047178_atpA	<i>atpA</i>	0.4035	0.5	0.3976	0.3	45.69	0.46	0.175	0.4302	0.1484	0.198	0.256
NC_047178_atpB	<i>atpB</i>	0.4258	0.6	0.3992	0.3	48.67	0.431	0.1872	0.4229	0.1725	0.207	0.289
NC_047178_atpE	<i>atpE</i>	0.3935	0.5	0.391	0.3	50.048	0.4667	0.1524	0.4299	0.172	0.173	0.252
NC_047178_atpF	<i>atpF</i>	0.3568	0.4	0.3243	0.3	44.416	0.4384	0.1849	0.4706	0.2033	0.16	0.289
NC_047178_atpH	<i>atpH</i>	0.4431	0.6	0.4878	0.2	43.802	0.5634	0.0423	0.3151	0.194	0.191	0.203
NC_047178_atpI	<i>atpI</i>	0.3773	0.5	0.36	0.3	47.368	0.4455	0.1991	0.4439	0.1053	0.168	0.249
NC_047178_ccsA	<i>ccsA</i>	0.2918	0.3	0.3435	0.2	40.496	0.5179	0.1143	0.5	0.1022	0.143	0.165
NC_047178_cemA	<i>cemA</i>	0.313	0.4	0.2826	0.3	45.924	0.5333	0.1833	0.4387	0.1654	0.201	0.248
NC_047178_clpP	<i>clpP</i>	0.4027	0.5	0.3807	0.3	50.912	0.4268	0.1911	0.4733	0.1298	0.157	0.254
NC_047178_matK	<i>matK</i>	0.3087	0.4	0.2979	0.3	49.844	0.5023	0.1307	0.4901	0.2038	0.144	0.235
NC_047178_ndhA	<i>ndhA</i>	0.3352	0.4	0.385	0.2	42.218	0.4712	0.1218	0.4861	0.095	0.129	0.175
NC_047178_ndhB	<i>ndhB</i>	0.3717	0.4	0.3899	0.3	46.046	0.4369	0.2056	0.4313	0.1205	0.159	0.267

NC_047178_ndhB-2	<i>ndhB</i>	0.3717	0.4	0.3899	0.3	46.046	0.4369	0.2056	0.4313	0.1205	0.159	0.267
NC_047178_ndhC	<i>ndhC</i>	0.3609	0.5	0.3471	0.3	50.154	0.5248	0.0891	0.4045	0.1842	0.201	0.205
NC_047178_ndhD	<i>ndhD</i>	0.3359	0.4	0.36	0.3	47.771	0.4858	0.1554	0.4226	0.1297	0.141	0.226
NC_047178_ndhE	<i>ndhE</i>	0.3333	0.4	0.3235	0.3	54.17	0.5169	0.1573	0.3836	0.1475	0.143	0.237
NC_047178_ndhF	<i>ndhF</i>	0.303	0.4	0.3494	0.2	42.489	0.5412	0.1026	0.4683	0.1196	0.139	0.167
NC_047178_ndhG	<i>ndhG</i>	0.3427	0.4	0.3446	0.2	47.985	0.4907	0.1056	0.4167	0.1712	0.122	0.212
NC_047178_ndhH	<i>ndhH</i>	0.3706	0.5	0.3655	0.2	47.51	0.5115	0.1115	0.5017	0.127	0.157	0.18
NC_047178_ndhI	<i>ndhI</i>	0.3313	0.4	0.375	0.2	38.53	0.5652	0.1304	0.4867	0.0928	0.188	0.169
NC_047178_ndhJ	<i>ndhJ</i>	0.4046	0.5	0.3899	0.3	54.312	0.4882	0.1969	0.3839	0.19	0.165	0.295
NC_047178_ndhK	<i>ndhK</i>	0.3776	0.4	0.4513	0.2	47.739	0.5079	0.1152	0.4379	0.1548	0.162	0.212
NC_047178_petA	<i>petA</i>	0.3832	0.5	0.3551	0.3	52.668	0.502	0.1412	0.4111	0.2027	0.152	0.259
NC_047178_petB	<i>petB</i>	0.3873	0.5	0.412	0.3	41.664	0.55	0.1278	0.3789	0.1088	0.229	0.196
NC_047178_petD	<i>petD</i>	0.3789	0.5	0.3913	0.2	38.672	0.4638	0.1087	0.4758	0.1304	0.177	0.196
NC_047178_petG	<i>petG</i>	0.3421	0.4	0.3158	0.3	37.923	0.5152	0.1818	0.3571	0.125	0.199	0.25
NC_047178_petL	<i>petL</i>	0.3229	0.4	0.4375	0.2	46.5	0.4828	0.1379	0.4615	0	0.11	0.133
NC_047178_petN	<i>petN</i>	0.4333	0.5	0.4333	0.4	29.305	0.36	0.2	0.4545	0.0476	0.121	0.24
NC_047178_psaA	<i>psaA</i>	0.4163	0.5	0.4301	0.3	47.331	0.4743	0.17	0.4156	0.1449	0.194	0.253
NC_047178_psaB	<i>psaB</i>	0.405	0.5	0.4299	0.3	47.772	0.4888	0.1651	0.4023	0.1595	0.177	0.257
NC_047178_psaC	<i>psaC</i>	0.4146	0.5	0.5366	0.3	47.595	0.4697	0.1515	0.5179	0.1154	0.19	0.211
NC_047178_psaI	<i>psaI</i>	0.307	0.4	0.2895	0.3	41.901	0.5313	0.1563	0.3846	0.1364	0.19	0.229
NC_047178_psaJ	<i>psaJ</i>	0.3488	0.4	0.3953	0.2	29.68	0.3947	0.0789	0.5806	0.1379	0.127	0.175
NC_047178_psbA	<i>psbA</i>	0.4134	0.5	0.435	0.3	40.096	0.5724	0.2204	0.2857	0.0811	0.328	0.257
NC_047178_psbB	<i>psbB</i>	0.4316	0.6	0.4597	0.3	46.927	0.5173	0.1432	0.3827	0.1532	0.182	0.239
NC_047178_psbC	<i>psbC</i>	0.4318	0.5	0.4599	0.3	44.128	0.4642	0.1877	0.3938	0.1364	0.191	0.27
NC_047178_psbD	<i>psbD</i>	0.419	0.5	0.4322	0.3	44.45	0.5251	0.1873	0.3633	0.1255	0.254	0.257
NC_047178_psbE	<i>psbE</i>	0.4246	0.4	0.4762	0.4	48.566	0.4521	0.274	0.3333	0.1111	0.186	0.325
NC_047178_psbF	<i>psbF</i>	0.4167	0.5	0.45	0.4	61	0.3824	0.1471	0.4	0.2308	0.141	0.306
NC_047178_psbH	<i>psbH</i>	0.3919	0.4	0.4595	0.3	36.929	0.5246	0.0492	0.3559	0.2182	0.178	0.221
NC_047178_psbI	<i>psbI</i>	0.3333	0.5	0.2973	0.2	24.465	0.5313	0.1563	0.48	0.0435	0.188	0.171
NC_047178_psbK	<i>psbK</i>	0.3817	0.4	0.3387	0.4	42.887	0.4909	0.2545	0.2683	0.1622	0.131	0.345
NC_047178_psbL	<i>psbL</i>	0.2906	0.4	0.2564	0.3	39.015	0.5313	0.1875	0.4583	0.087	0.17	0.222
NC_047178_psbM	<i>psbM</i>	0.3143	0.5	0.2571	0.2	50.167	0.6333	0.1667	0.2692	0.0952	0.202	0.212

NC_047178_psbN	<i>psbN</i>	0.447	0.6	0.4091	0.4	37.165	0.3611	0.25	0.4545	0.1613	0.136	0.333
NC_047178_psbT	<i>psbT</i>	0.2941	0.3	0.3529	0.2	47.385	0.4815	0.1111	0.5	0.1364	0.19	0.188
NC_047178_psbZ	<i>psbZ</i>	0.3492	0.4	0.4127	0.3	57.443	0.5439	0.1404	0.28	0.1429	0.229	0.237
NC_047178_rbcL	<i>rbcL</i>	0.4403	0.6	0.4375	0.3	48.532	0.4898	0.1939	0.3928	0.1602	0.264	0.281
NC_047178_rpl14	<i>rpl14</i>	0.3875	0.5	0.3902	0.2	46.004	0.4078	0.1553	0.5102	0.1446	0.151	0.233
NC_047178_rpl16	<i>rpl16</i>	0.4142	0.5	0.5147	0.2	39.931	0.4286	0.1048	0.5351	0.099	0.148	0.165
NC_047178_rpl2	<i>rpl2</i>	0.4339	0.5	0.4836	0.3	54.4	0.3922	0.1853	0.448	0.1759	0.133	0.291
NC_047178_rpl2-2	<i>rpl2</i>	0.4339	0.5	0.4836	0.3	54.4	0.3922	0.1853	0.448	0.1759	0.133	0.291
NC_047178_rpl20	<i>rpl20</i>	0.3701	0.4	0.4322	0.3	51.935	0.42	0.12	0.4778	0.2152	0.091	0.254
NC_047178_rpl22	<i>rpl22</i>	0.3395	0.4	0.3851	0.2	48.762	0.4597	0.1774	0.5508	0.1028	0.165	0.213
NC_047178_rpl23	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
NC_047178_rpl23-2	<i>rpl23</i>	0.3688	0.4	0.383	0.3	53.869	0.4521	0.1507	0.4571	0.1774	0.127	0.253
NC_047178_rpl32	<i>rpl32</i>	0.3208	0.3	0.434	0.3	41.858	0.5278	0.1111	0.4524	0.1795	0.243	0.224
NC_047178_rpl33	<i>rpl33</i>	0.3582	0.4	0.3881	0.3	40.649	0.4902	0.1961	0.4082	0.2381	0.187	0.308
NC_047178_rpl36	<i>rpl36</i>	0.3947	0.4	0.4737	0.3	21.459	0.3793	0.1379	0.4516	0.28	0.103	0.306
NC_047178_rpoA	<i>rpoA</i>	0.3333	0.5	0.2988	0.2	47.828	0.4729	0.1589	0.5187	0.1505	0.148	0.226
NC_047178_rpoB	<i>rpoB</i>	0.3871	0.5	0.3765	0.3	49.282	0.4624	0.1315	0.4468	0.2182	0.15	0.262
NC_047178_rpoC1	<i>rpoC1</i>	0.3764	0.5	0.3759	0.3	47.792	0.4834	0.1439	0.4737	0.1678	0.153	0.234
NC_047178_rpoC2	<i>rpoC2</i>	0.3676	0.5	0.3681	0.3	49.395	0.4562	0.1653	0.4511	0.1916	0.15	0.267
NC_047178_rps11	<i>rps11</i>	0.4341	0.5	0.5683	0.2	42.618	0.4262	0.123	0.5086	0.0755	0.136	0.172
NC_047178_rps12	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
NC_047178_rps12-2	<i>rps12</i>	0.4355	0.5	0.4758	0.3	48.167	0.3689	0.1942	0.4571	0.1649	0.131	0.295
NC_047178_rps14	<i>rps14</i>	0.4125	0.4	0.4752	0.3	45.923	0.3733	0.12	0.4512	0.2895	0.135	0.323
NC_047178_rps15	<i>rps15</i>	0.3071	0.4	0.3034	0.2	42.765	0.4531	0.0625	0.5634	0.2154	0.148	0.207
NC_047178_rps16	<i>rps16</i>	0.3483	0.5	0.382	0.2	45.424	0.5417	0.0833	0.4783	0.1406	0.139	0.172
NC_047178_rps18	<i>rps18</i>	0.3366	0.3	0.4314	0.2	36.373	0.5063	0.1013	0.4302	0.1818	0.111	0.222
NC_047178_rps19	<i>rps19</i>	0.3477	0.4	0.3763	0.2	51.797	0.4267	0.1333	0.5211	0.1695	0.126	0.225
NC_047178_rps2	<i>rps2</i>	0.3797	0.4	0.4219	0.3	48.287	0.4767	0.1451	0.4237	0.2013	0.171	0.261
NC_047178_rps3	<i>rps3</i>	0.3242	0.5	0.3242	0.2	39.449	0.5	0.1582	0.5575	0.0629	0.177	0.162
NC_047178_rps4	<i>rps4</i>	0.3828	0.5	0.3663	0.3	48.522	0.475	0.1625	0.4479	0.1533	0.151	0.247
NC_047178_rps7	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22
NC_047178_rps7-2	<i>rps7</i>	0.4081	0.5	0.4551	0.2	45.752	0.405	0.157	0.5231	0.1176	0.187	0.22

NC_047178_rps8	<i>rps8</i>	0.3506	0.4	0.3926	0.3	37.831	0.3636	0.1909	0.5185	0.1512	0.11	0.262
NC_047178_ycf1	<i>ycf1</i>	0.2872	0.3	0.2811	0.2	45.639	0.505	0.1629	0.565	0.1227	0.182	0.202
NC_047178_ycf2	<i>ycf2</i>	0.3735	0.4	0.3432	0.4	52.86	0.4471	0.2061	0.3967	0.2654	0.156	0.341
NC_047178_ycf2-2	<i>ycf2</i>	0.3735	0.4	0.3432	0.4	52.86	0.4471	0.2061	0.3967	0.2654	0.156	0.341
NC_047178_ycf3	<i>ycf3</i>	0.3905	0.5	0.3905	0.3	56.437	0.4848	0.1742	0.4492	0.1923	0.172	0.269
NC_047178_ycf4	<i>ycf4</i>	0.3802	0.4	0.4162	0.3	46.509	0.5166	0.1457	0.3669	0.1966	0.171	0.259

GC: the total GC content; GC1:the GC content at first codon position; GC2: the GC content at second codon position; GC3: the GC content at third codon position; ENC: the effective number of codons; T3s: the thymine content at synonymous third codon position; C3s: the cytosine content at synonymous third codon position; A3s: the adenine content at synonymous third codon position; G3s: the guanine content at synonymous third codon position; CAI: the codon adaptation index; GC3s: the GC content at synonymous third codon position.

Table S10. List of chloroplast genomes used for phylogenetic analysis in this study.

Species	GenBank ID
<i>Cardamine pentaphyllos</i>	NC_049617.1
<i>Nasturtium officinale</i>	MK045962.1
<i>Rorippa islandica</i>	MK637784.1
<i>Dipoma iberideum</i>	NC_049626.1
<i>Crucihimalaya lasiocarpa</i>	NC_049612.1
<i>Erysimum cheiranthoides</i>	MN207123.1
<i>Olimarabidopsis pumila</i>	AP009368.1
<i>Turritis glabra</i>	MK637811.1
<i>Capsella bursa-pastoris</i>	MT040199.1
<i>Camelina sativa</i>	LN877386.1
<i>Stevenia cheiranthoides</i>	MK637795.1
<i>Lepidium meyenii</i>	MT430983.1
<i>Lepidium virginicum</i>	NC_009273.1
<i>Lepidium sativum</i>	NC_047178.1
<i>Lepidium apetalum</i>	MT880914
<i>Lepidium perfoliatum</i>	MT880913
<i>Yinshania furcatopilosa</i>	MK637818.1
<i>Smelowskia calycina</i>	MK637794.1
<i>Raphanus sativus</i>	KJ716483.1
<i>Leiospora exscapa</i>	NC_049661.1
<i>Dontostemon micranthus</i>	NC_049628.1

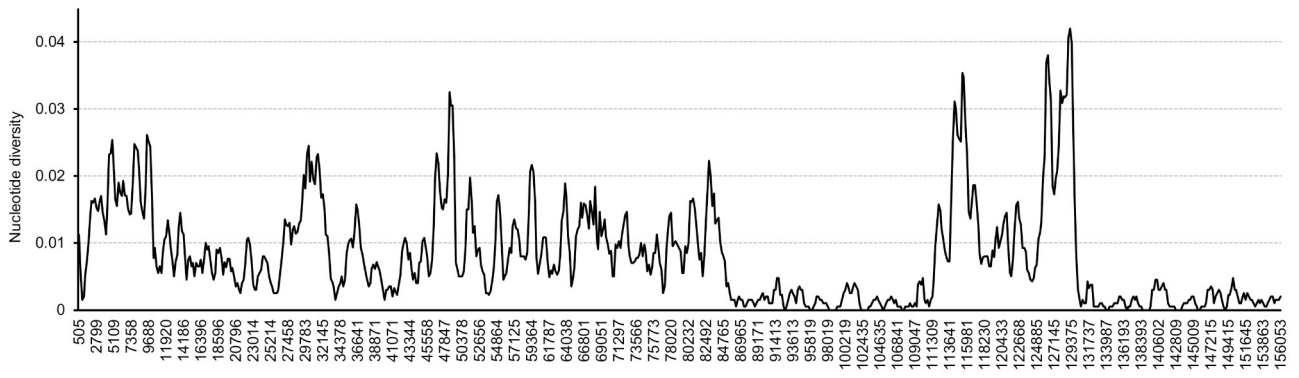


Fig. S1. Statistics of the SNPs in the five cp genomes.



Fig. S2. Analysis of relative usage of synonymous codons of CDS in five *Lepidium* species. The numbers in the figure indicate the relative synonymous codon usage (RSCU); Underlined value indicate that five *Lepidium* species gene uses this codon higher.