forests

MDPI

Article

Integration of Illumina and PacBio HiFi Sequencing Reveals a Three-Linear-Molecule Mitogenome with RNA-Editing Sites and Phylogeny in Arrow Bamboo (*Fargesia qinlingensis*)

Hao Wu [1,†], Xue Li [1,†], Ke Qu [1], Lele Yang [1], Tao Su [1,*], Lijun Yong [2], Mei Han [1,*] and Fuliang Cao [3]

[1] State Key Laboratory of Tree Genetics and Breeding, College of Life Sciences, Co-Innovation Center for Sustainable Forestry in Southern China, Functional Genomics and Molecular Breeding Innovation Group for Bamboo, College of Life and Sciences, Nanjing Forestry University, Nanjing 210037, China
[2] Foping National Nature Reserve, Foping Country, Hanzhong 723400, China
[3] College of Forestry, Nanjing Forestry University; Nanjing, China
* Correspondence: sutao@njfu.edu.cn (T.S.); sthanmei@njfu.edu.cn (M.H.); Tel.: +86-1589-598-3381 (T.S.)
† These authors contributed equally to this work.

Abstract: Arrow bamboo (*Fargesia qinlingensis*) is endemic to the Qinling Mountains and has remarkable adaptive resilience to changing climates. However, its complete mitogenome remains unknown. Using the Illumina and PacBio HiFi sequencing platforms, we found that the mitogenome assembly of the *F. qinlingensis* has a multi-branched skeleton comprising three linear molecules (M1, M2, and M3), with a length of 442,368 bp and a GC content of 44.05%. Thirty-five unique PCGs were identified in the complete mitogenome, including twenty-four core structural genes, eleven noncore structural genes, three rRNAs, and sixteen tRNAs. The GCU for alanine and CAA for glutamine represented the most significant frequency (RSCU = 1.55) in the codon usage preference. A total of 51, 28, and 14 SSRs were determined on M1, M2, and M3, respectively. The mitogenome contained 149 pairs of dispersed repeats with lengths greater than 30 bp, the most abundant of which were 82 forward and 67 palindromic repeats. A long repeat sequence (14,342 bp) was characterized in mediating mitogenome recombination. DNA transfer analyses suggested that 44 MTPTs (30,943 bp, 6.99%) originated from the plastome. Among the 482 potential C-U/T RNA-editing sites predicted in 35 PCGs, *ccmFn* (38 times) and *ccmC* (36 times) shoed the highest frequency. Collinearity and phylogenetic trees revealed the close relationship between *F. qinlingensis* and *Bambusa oldhamii*. The primary features of the mitogenome of *F. qinlingensis* will help decipher the functional mitochondrial traits related to growth performance and climate resilience. Moreover, our findings provide insights into the evolution, environmental adaptation, and sustainable use of subalpine bamboo resources in the Qinling Mountains.

Keywords: *Fargesia qinlingensis*; mitogenome; HiFi sequencing; RNA-editing; stress resilience

Citation: Wu, H.; Li, X.; Qu, K.; Yang, L.; Su, T.; Yong, L.; Han, M.; Cao, F. Integration of Illumina and PacBio HiFi Sequencing Revealed Three-Linear-Molecule Mitogenome with RNA-Editing Sites and Phylogeny in Arrow Bamboo (*Fargesia qinlingensis*). *Forests* **2024**, *15*, 1267. https://doi.org/10.3390/f15071267

Academic Editor: Claudia Mattioni

Received: 29 June 2024
Revised: 13 July 2024
Accepted: 18 July 2024
Published: 20 July 2024

Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

Table S1. Qualimap analyses of mitogenome assembly in *F. qinlingensis*.

Statistical list	ctg1	ctg2	ctg3
Globals			
Reference length	212,356	169,782	85,920
Number of reads	161,951	143,226	76,301
Mapped reads	161,951/100%	143,226/100%	76,301/100%
Unmapped reads	0/0%	0/0%	0/0%
Mapped paired reads	161,951/100%	143,226/100%	76,301/100%
Mapped reads, first in pair	80,964/49.99%	71,621/50.01%	38,150/50%
Mapped reads, second in pair	80,987/50.01%	71,605/49.99%	38,151/50%
Mapped reads, both in pair	161,951/100%	143,226/100%	76,301/100%
Supplementary alignments	811/0.5%	996/0.7%	165/0.22%
Read min/max/mean length	30/150 /149.51	30/150/149.29	30/150/149.79
Duplicated reads	83,586/51.61%	80,931/56.51%	42,248/55.37%
Duplication rate	36.17%	38.98%	39.05%
Clipped reads	38,862/24%	35,085/24.5%	25,984/34.05%
ACGT Content			
Number/percentage of A	5,921,933/28.27%	5,558,063/29.24%	2,592,785/28.06%
Number/percentage of C	4,712,078/22.49%	4,139,449/21.78%	2,033,558/22.01%
Number/percentage of T	5,868,754/28.01%	5,363,759/28.22%	2,646,236/28.64%
Number/percentage of G	4,446,375/21.22%	3,947,972/20.77%	1,968,247/21.3%
Number/percentage of N	264/0%	235/0%	133/0%
GC percentage	43.72%	42.54%	43.31%
Coverage			
Mean	98.6971	112.1069	107.7638
Standard Deviation (SD)	127.8098	166.8374	105.4568
Mapping Quality			
Mean Mapping Quality	57.73	51.89	42.35
Insert size			
Mean	636.29	1,225.46	367.75
SD	6,278.12	9,274.26	2,903.95
P25/Median/P75	187/248/300	195/250/302	178/239/295
Mismatches and indels			
General error rate	0.93%	1.57%	2.13%
Mismatches	168,276	246,566	170,663
Insertions	5,200	12,798	6,795
Mapped reads with at least one insertion	2.59%	7.29%	7.55%
Deletions	3,781	9,722	6,288
Mapped reads with at least one deletion	2.24%	5.28%	7.53%
Homopolymer indels	0.7332	0.6146	0.5172
Chromosome stats	ctg1	ctg2	ctg3
Length	212,356	169,782	85,920
Mapped bases	20,958,914	19,033,726	9,259,064
Mean coverage	98.6971	112.1069	107.7638
SD	127.8098	166.8374	105.4568

Table S2. Potential paths and number of long reads.

Paths	Number of supported long-reads
ctg4-ctg5-ctg6	2
ctg1-ctg5-ctg2	3
ctg4-ctg5-ctg2	2
ctg1-ctg5-ctg6	4

Table S3. Collection of long reads obtained from BLASTn results supporting different paths.

Paths	Reference length (bp)	Reads ID	Identity (%)	Alignment (bp)	Mis-match	Gap	Query_start	Query_end	Reads_start	Reads_end	E-value	Score
ctg4-ctg5-ctg6	15342	m64116_210518_205908/28903839/ccs	99.356	15380	6	92	1	15342	10530	25854	0	27767
ctg4-ctg5-ctg6	15342	m64116_210518_205908/174196148/ccs	99.01	15454	14	134	1	15342	18275	2849	0	27562
ctg1-ctg5-ctg2	15342	m64116_210518_205908/127927294/ccs	99.928	15346	0	11	1	15342	3884	19222	0	28267
ctg1-ctg5-ctg2	15342	m64116_210518_205908/37685486/ccs	99.857	15359	1	20	1	15342	1814	17168	0	28221
ctg1-ctg5-ctg2	15342	m64116_210518_205908/26346536/ccs	99.642	15377	2	53	1	15342	3374	18732	0	28042
ctg4-ctg5-ctg2	15342	m64116_210518_205908/10814423/ccs	99.772	15355	1	34	1	15342	17401	2068	0	28131
ctg4-ctg5-ctg2	15342	m64116_210518_205908/62194360/ccs	99.236	15448	2	110	1	15342	1992	17429	0	27767
ctg1-ctg5-ctg6	15342	m64116_210518_205908/37749813/ccs	99.915	15348	0	13	1	15342	945	16285	0	28258
ctg1-ctg5-ctg6	15342	m64116_210518_205908/14353363/ccs	99.837	15361	0	21	1	15342	22933	7579	0	28205
ctg1-ctg5-ctg6	15342	m64116_210518_205908/98960271/ccs	99.474	15397	4	74	1	15342	19019	3645	0	27913
ctg1-ctg5-ctg6	15342	m64116_210518_205908/21891169/ccs	98.798	15468	26	151	1	15342	2831	18264	0	27386

Table S4. Basic information on the *F. qinlingensis* mitogenome.

NCBI Accession number	Contigs	Type	Length (bp)	GC content %
OP324798	M1	linear	208,716	44.21
OP324799	M2	linear	160,262	44.06
OP324800	M3	linear	73,390	43.57

Table S5. Relative synonymous codon usage in the *F. qinlingensis* mitogenome.

Amino	Codon 1	Codon 2	Codon 3	Codon 4	Codon 5	Codon 6
	RSCU	RSCU	RSCU	RSCU	RSCU	RSCU
Ala	GCU	GCA	GCC	GCG		
	1.55	0.97	0.92	0.56		
Arg	AGA	CGA	CGU	AGG	CGG	CGC
	1.42	1.28	1.23	0.81	0.69	0.56
Asn	AAU	AAC				
	1.37	0.63				
Asp	GAU	GAC				
	1.35	0.65				
Cys	UGU	UGC				
	1.09	0.91				
End	UAA	UAG	UGA			
	1.45	0.82	0.73			
Gln	CAA	CAG				
	1.55	0.45				
Glu	GAA	GAG				
	1.37	0.63				
Gly	GGA	GGU	GGG	GGC		
	1.43	1.3	0.72	0.54		
His	CAU	CAC				
	1.53	0.47				
Ile	AUU	AUA	AUC			
	1.31	0.85	0.84			
Leu	UUA	CUU	UUG	CUA	CUC	CUG
	1.41	1.25	1.19	0.88	0.65	0.6
Lys	AAA	AAG				
	1.15	0.85				
Met	AUG					
	1					
Phe	UUU	UUC				
	1.16	0.84				
Pro	CCU	CCA	CCC	CCG		
	1.38	1.18	0.86	0.58		
Ser	UCU	UCA	AGU	UCC	UCG	AGC
	1.33	1.12	1.06	1.02	0.81	0.66
Thr	ACU	ACC	ACA	ACG		
	1.43	0.99	0.95	0.62		
Trp	UGG					
	1					
Tyr	UAU	UAC				
	1.5	0.5				
Val	GUU	GUA	GUG	GUC		
	1.21	1.11	0.92	0.76		

Table S6. SSRs in the mitogenome of M1, M2, and M3.

Mitogenome	SSR nr.	SSR type	SSR	size	start	end
M1	1	p1	(T)10	10	3946	3955
M1	2	p4	(TCTT)3	12	6001	6012
M1	3	p4	(GAAA)3	12	11515	11526
M1	4	p4	(AGAA)3	12	14511	14522
M1	5	p2	(TA)6	12	19709	19720
M1	6	p4	(TTTG)3	12	19945	19956
M1	7	p2	(CT)5	10	21741	21750
M1	8	p4	(CAAG)3	12	22763	22774
M1	9	p4	(AAGT)3	12	22780	22791
M1	10	p2	(TA)5	10	31167	31176
M1	11	p1	(T)10	10	31325	31334
M1	12	p3	(ACT)4	12	38546	38557
M1	13	p4	(AAAG)3	12	46364	46375
M1	14	p5	(CAATT)3	15	48197	48211
M1	15	p1	(T)10	10	51310	51319
M1	16	p3	(TGT)4	12	53063	53074
M1	17	p4	(ATAA)3	12	53327	53338
M1	18	p4	(TTTC)3	12	54493	54504
M1	19	p4	(AATG)3	12	63303	63314
M1	20	p1	(T)10	10	68248	68257
M1	21	p2	(TA)10	20	70025	70044
M1	22	p3	(AGA)4	12	74759	74770
M1	23	p4	(GCCG)3	12	75743	75754
M1	24	p4	(CAGT)3	12	76860	76871
M1	25	p1	(T)11	11	78092	78102
M1	26	p1	(G)10	10	100787	100796
M1	27	p2	(GA)5	10	108040	108049
M1	28	p2	(TA)5	10	110082	110091
M1	29	p2	(AT)5	10	111919	111928
M1	30	p3	(ATT)4	12	113191	113202
M1	31	p1	(T)10	10	117863	117872
M1	32	p4	(ACGA)3	12	121189	121200
M1	33	p4	(CTTC)3	12	122219	122230
M1	34	p1	(A)10	10	123058	123067
M1	35	p1	(T)14	14	123245	123258
M1	36	p5	(AAATA)3	15	133140	133154
M1	37	p2	(AT)5	10	133303	133312
M1	38	p4	(GAGC)3	12	133811	133822
M1	39	p4	(CTTC)3	12	145793	145804
M1	40	p3	(TTC)4	12	147817	147828
M1	41	p2	(TA)6	12	155005	155016
M1	42	p4	(GAGC)3	12	164736	164747
M1	43	p1	(C)10	10	176646	176655
M1	44	p4	(TCAT)3	12	176699	176710
M1	45	p4	(TTCT)3	12	179070	179081
M1	46	p1	(A)10	10	182061	182070
M1	47	p4	(ATAA)3	12	194493	194504
M1	48	p4	(AAGA)3	12	203082	203093
M1	49	p2	(AG)6	12	204134	204145
M1	50	p4	(ACAG)3	12	204766	204777
M1	51	p3	(TTC)4	12	205966	205977

M2	1	p3	(TAC)4	12	13403	13414
M2	2	p2	(TC)5	10	19591	19600
M2	3	p1	(T)10	10	20038	20047
M2	4	p2	(TA)9	18	20871	20888
M2	5	p4	(TACT)3	12	24845	24856
M2	6	p1	(C)10	10	39681	39690
M2	7	p3	(CTT)4	12	45505	45516
M2	8	p2	(TA)6	12	46924	46935
M2	9	p4	(CATC)3	12	49584	49595
M2	10	p1	(A)10	10	49832	49841
M2	11	p4	(CTTG)3	12	50280	50291
M2	12	p4	(TTTC)3	12	53942	53953
M2	13	p4	(GGCC)3	12	58238	58249
M2	14	p5	(GCCCG)3	15	62615	62629
M2	15	p2	(AG)6	12	62965	62976
M2	16	p5	(TAAGA)3	15	68409	68423
M2	17	p1	(T)10	10	69826	69835
M2	18	p4	(GTAG)3	12	72181	72192
M2	19	p1	(A)10	10	87927	87936
M2	20	p4	(AAGC)3	12	87948	87959
M2	21	p3	(TAA)4	12	89613	89624
M2	22	p2	(AG)5	10	92213	92222
M2	23	p2	(TA)5	10	97602	97611
M2	24	p4	(CTTT)3	12	102664	102675
M2	25	p4	(GCTA)3	12	113394	113405
M2	26	p4	(TTTA)3	12	130608	130619
M2	27	p4	(GAAA)3	12	139325	139336
M2	28	p2	(TA)5	10	148322	148331
M3	1	p4	(CATT)3	12	21731	21742
M3	2	p1	(T)10	10	25725	25734
M3	3	p1	(G)10	10	29847	29856
M3	4	p4	(GGGC)3	12	30040	30051
M3	5	p1	(A)13	13	32046	32058
M3	6	p4	(AATA)3	12	34185	34196
M3	7	p3	(CTA)5	15	37220	37234
M3	8	p2	(CT)5	10	38072	38081
M3	9	p1	(A)10	10	38490	38499
M3	10	p3	(TAT)6	18	45234	45251
M3	11	p3	(TAA)4	12	48773	48784
M3	12	p4	(AGTC)3	12	49935	49946
M3	13	p1	(T)12	12	64857	64868
M3	14	p2	(AT)5	10	69546	69555

Table S7. Tandem repeat sequences in the mitogenome of M1, M2, and M3.

Indices	**Period Size**	**Copy Number**	**Consensus Size**	**Percent Matches**	**Percent Indels**	**Score**	**A**	**C**	**G**	**T**	**Entropy (0-2)**
M1											
68--137	33	2.1	35	91	5	119	8	30	21	40	1.83
3934--3971	20	1.9	20	83	0	55	18	13	13	55	1.69
7565--7633	33	2.1	33	100	0	138	28	5	31	33	1.81
13322--13350	15	1.9	15	100	0	58	41	17	6	34	1.76
26641--26685	21	2.1	22	87	4	69	15	37	17	28	1.91

76690--76717	11	2.5	11	100	0	56	71	0	21	7	1.09
78661--78727	33	2	34	94	2	120	40	22	28	8	1.84
78729--78799	35	2	35	100	0	142	8	32	25	33	1.86
81110--81141	12	2.7	12	85	0	50	31	21	21	25	1.98
97892--97930	15	2.6	15	79	0	50	12	25	10	51	1.71
111819--111848	15	2	15	100	0	60	20	13	33	33	1.91
123835--123862	14	2	14	100	0	56	28	21	7	42	1.79
137165--137212	24	2	24	87	0	75	14	25	29	31	1.95
142426--142470	22	2	22	95	0	83	24	0	44	31	1.54
146423--146493	22	3.2	22	77	0	93	36	23	16	22	1.94
146505--146531	14	1.9	14	100	0	54	25	29	14	29	1.95
157002--157071	33	2.1	35	91	5	119	8	30	21	40	1.83
159736--159776	20	2	20	85	0	61	21	4	12	60	1.5
159816--159858	21	2	21	100	0	86	53	18	9	18	1.7
169790--169832	22	1.9	23	80	4	58	30	30	16	23	1.96
182716--182757	21	2	21	100	0	84	14	23	4	57	1.56
193965--194002	20	2	20	84	5	55	34	15	13	36	1.87
201763--201829	21	3.2	21	78	0	85	35	22	28	13	1.92
206336--206389	27	2	27	96	0	101	33	9	27	29	1.88
M2											
1491--1552	29	2.1	30	87	3	96	35	12	16	35	1.87
4367--4412	23	2	23	95	0	85	15	32	8	43	1.77
10433--10487	18	3.1	18	100	0	110	38	10	5	45	1.63
10624--10695	35	2.1	35	94	0	130	30	22	22	25	1.99
10821--10936	41	2.8	41	100	0	232	5	38	31	25	1.77
14227--14307	27	3	27	98	0	155	33	19	18	28	1.96
14307--14360	26	2.1	26	100	0	108	29	18	22	29	1.97
30936--31005	33	2.1	35	91	5	119	8	30	21	40	1.83
46126--46193	33	2	34	94	2	122	8	29	22	39	1.84
52074--52140	33	2	34	94	2	120	8	28	22	40	1.84

70521--70556	16	2.2	16	80	0	51	13	19	5	61	1.52
99719--99785	33	2	34	94	2	120	40	22	28	8	1.84
123284--123350	21	3.2	21	78	0	85	13	28	22	35	1.92
131111--131148	20	2	20	84	5	55	36	13	15	34	1.87
137446--137514	36	1.9	36	87	0	110	27	26	23	23	2
149398--149449	27	1.9	27	96	0	97	38	11	21	28	1.88
M3											
20954--20991	18	2.1	18	90	0	62	42	21	21	15	1.89
25556--25641	35	2.5	35	88	0	130	30	9	17	43	1.8

Table S8. Dispersed repeat sequences in the mitogenome of M1, M2, and M3.

The repeat length of the first part	The starting site of the first part	Matching direction	The repeat length of the second part	The starting site of the second part	Interval distance of repeats	E-value
M1						
225	124883	F	225	154676	0	4.21E-126
219	59819	F	219	187619	0	1.73E-122
155	0	F	155	156934	0	5.87E-84
151	84226	F	151	98727	-3	2.28E-74
137	84240	F	137	98741	-2	3.38E-68
115	17	P	115	78662	0	7.10E-60
115	78662	P	115	156951	0	7.10E-60
111	3840	F	111	185775	0	1.82E-57
116	116861	P	116	199780	-3	1.21E-53
103	107779	F	103	166880	0	1.19E-52
100	107840	F	100	167485	-2	3.40E-46
92	33733	F	92	54544	0	5.00E-46
94	107898	F	94	138439	-2	1.23E-42
90	61010	F	90	189329	-1	2.16E-42
88	84289	F	88	98790	-1	3.38E-41
79	107913	F	79	138454	0	3.35E-38
74	84303	F	74	98804	0	3.43E-35
78	49966	F	78	87222	-2	3.63E-33
70	117444	F	70	166683	-1	1.85E-30
64	107876	F	64	167521	0	3.60E-29
62	56895	F	62	64692	0	5.76E-28
65	78002	F	65	101929	-2	1.69E-25

57	116920	P	57	199780	-1	1.01E-22
50	175253	F	50	185332	-1	1.45E-18
45	207	P	45	84294	0	9.90E-18
50	136718	P	50	199767	-2	1.07E-16
45	207	P	45	98795	-1	1.34E-15
44	16897	F	44	125305	-1	5.23E-15
40	107948	F	40	167584	0	1.01E-14
40	138489	F	40	167584	0	1.01E-14
46	54931	P	46	181665	-2	2.30E-14
39	70651	F	39	82784	0	4.05E-14
42	136726	P	42	199767	-1	7.98E-14
45	62029	P	45	157460	-2	8.82E-14
36	30	P	36	78763	0	2.59E-12
36	7564	F	36	7597	0	2.59E-12
36	61064	F	36	189383	0	2.59E-12
36	78728	F	36	78763	0	2.59E-12
36	78763	P	36	156964	0	2.59E-12
42	138439	F	42	167543	-2	4.91E-12
42	166941	F	42	167485	-2	4.91E-12
38	78029	F	38	101956	-1	1.85E-11
34	64213	P	34	64213	0	4.15E-11
37	98588	P	37	180857	-1	7.20E-11
37	116940	F	37	136718	-1	7.20E-11
39	36435	P	39	76715	-2	2.70E-10
36	28171	F	36	136837	-1	2.80E-10
36	58321	P	36	173139	-1	2.80E-10
40	58	P	40	157281	-3	2.70E-09
40	78696	F	40	157281	-3	2.70E-09
40	156992	P	40	157281	-3	2.70E-09
39	77989	F	39	101916	-3	1.00E-08
30	116976	P	30	199754	0	1.06E-08
31	116948	P	31	199778	-1	2.47E-07
30	70687	F	30	82822	-1	9.56E-07
30	175297	F	30	185380	-1	9.56E-07
31	72	P	31	157276	-2	1.11E-05
31	157006	P	31	157276	-2	1.11E-05
31	182981	F	31	183038	-2	1.11E-05
33	496	F	33	145299	-3	2.45E-05
33	64690	F	33	75193	-3	2.45E-05
30	124795	F	30	162578	-2	4.16E-05

30	138454	F	30	167558	-2	4.16E-05
31	424	P	31	138528	-3	3.22E-04
31	56895	F	31	75195	-3	3.22E-04
31	136077	P	31	199673	-3	3.22E-04
30	28180	F	30	136846	-3	1.16E-03
30	106819	F	30	124767	-3	1.16E-03
30	107121	F	30	206372	-3	1.16E-03
30	158028	P	30	176411	-3	1.16E-03
30	206332	F	30	206359	-3	1.16E-03
M2						
1777	99725	P	1777	158485	0	#######
148	31189	F	148	80841	0	#######
135	46057	P	135	99718	0	#######
128	46057	F	128	160134	0	#######
106	30894	F	106	46084	0	#######
106	30894	P	106	99720	0	#######
103	46089	F	103	52037	0	#######
103	52037	P	103	99718	0	#######
101	30894	F	101	160161	0	#######
101	30899	F	101	52037	0	1.1E-51
96	52037	F	96	160166	0	1.2E-48
75	10820	F	75	10861	0	5.1E-36
73	95312	F	73	95754	0	8.1E-35
70	30899	P	70	100836	0	5.2E-33
70	30899	F	70	159081	0	5.2E-33
70	46089	P	70	100836	0	5.2E-33
70	46089	F	70	159081	0	5.2E-33
70	52037	P	70	100836	0	5.2E-33
70	52037	F	70	159081	0	5.2E-33
70	99751	F	70	100836	0	5.2E-33
70	99751	P	70	159081	0	5.2E-33
70	100836	P	70	160166	0	5.2E-33
70	159081	F	70	160166	0	5.2E-33
59	91897	F	59	142940	0	2.2E-26
54	14226	F	54	14253	-1	3.6E-21
45	94581	P	45	114134	0	5.8E-18
49	92293	P	49	149110	-2	2.4E-16
47	66452	F	47	144233	-3	1.6E-13
37	10432	F	37	10450	0	3.8E-13
34	10820	F	34	10902	0	2.5E-11

43	31198	F	43	100822	-3	3.1E-11
43	31198	P	43	159122	-3	3.1E-11
43	80850	F	43	100822	-3	3.1E-11
43	80850	P	43	159122	-3	3.1E-11
40	30926	P	40	31215	-3	1.6E-09
40	30926	P	40	80867	-3	1.6E-09
40	31215	P	40	46116	-3	1.6E-09
40	31215	P	40	52064	-3	1.6E-09
40	31215	F	40	99754	-3	1.6E-09
40	31215	F	40	100839	-3	1.6E-09
40	31215	P	40	159108	-3	1.6E-09
40	31215	P	40	160193	-3	1.6E-09
40	46116	P	40	80867	-3	1.6E-09
40	52064	P	40	80867	-3	1.6E-09
40	80867	F	40	99754	-3	1.6E-09
40	80867	F	40	100839	-3	1.6E-09
40	80867	P	40	159108	-3	1.6E-09
40	80867	P	40	160193	-3	1.6E-09
37	10623	F	37	10658	-2	2.3E-09
38	27778	F	38	30002	-3	2.2E-08
31	14303	F	31	14329	-1	1.5E-07
30	23574	P	30	64585	-1	5.6E-07
35	94176	P	35	95751	-3	1.1E-06
35	102930	F	35	126567	-3	1.1E-06
31	30781	P	31	134469	-2	6.6E-06
31	30940	P	31	31210	-2	6.6E-06
31	30940	P	31	80862	-2	6.6E-06
31	32663	P	31	148342	-2	6.6E-06
31	46130	P	31	80862	-2	6.6E-06
31	52078	P	31	80862	-2	6.6E-06
31	83995	P	31	110098	-2	6.6E-06
31	92313	P	31	149108	-2	6.6E-06
32	14226	F	32	14280	-3	5.2E-05
32	31255	F	32	100897	-3	5.2E-05
32	31255	P	32	159058	-3	5.2E-05
32	66470	F	32	72769	-3	5.2E-05
32	80907	F	32	100897	-3	5.2E-05
32	80907	P	32	159058	-3	5.2E-05
32	94176	P	32	95312	-3	5.2E-05
31	43389	P	31	88481	-3	0.00019

30	5327	F	30	51176	-3	0.00069
30	70671	P	30	71086	-3	0.00069
M3						
125	16888	P	125	31837	0	8.37E-67
32	9860	F	32	17914	0	8.21E-11
30	34189	P	30	34189	0	1.31E-09
31	28246	P	31	67888	-2	1.37E-06
31	11359	P	31	57531	-3	3.99E-05
30	25576	F	30	25611	-3	1.44E-04
30	160021	F	30	207404	-3	0.00131

Table S9. Homologous migrated DNA fragments in the *F. qinlingensis* mitogenome.

Number	Mitogenome	% Identity	Alignment Length	Mismatches	Gap Openings	Alignment start (plastome)	Alignment end (plastome)	Alignment start (mitogenome)	Alignment end (mitogenome)	E-value	Bit Score	MTPT annotation
1	**M1**	98.811	5131	36	4	23168	28298	116817	111712	0	9114	Partial (*rpo*B，*rpo*C2)，Complete (*rpo*C1)
2	**M2**	99.951	4116	1	1	39338	43452	26309	30424	0.00E+00	7589	Partial (*psa*A), Complete (*psa*B)
3	**M3**	90.805	3143	167	45	73205	76303	4315	7379	0.00E+00	4091	Partial (*psb*T，*pet*D), Complete (*psb*N，*psb*H, *pet*B)
4	**M2**	91.045	2602	143	47	49669	52241	69352	66812	0.00E+00	3432	Partial (*trn*L-UAA, *ndh*K)，Complete (*trn*F-GAA, *ndh*J)
5	**M2**	93.695	1697	79	9	53185	54874	71094	72769	0.00E+00	2516	Complete (*trn*V-UAC, *trn*M-CAU，*atp*E), Partial (*atp*B)
6	**M2**	91.283	1629	89	22	114210	115826	97676	99263	0.00E+00	2172	Complete (*ndh*I), Partial (*ndh*A)
7	**M1**	98.277	1103	16	3	10884	11985	50051	48951	0	1929	Partial (*psb*C)
8	**M2**	85.701	1098	107	24	47066	48151	70500	69441	0.00E+00	1112	Complete (*trn*S-GGA, *rps*4)
9	M3	97.053	984	25	2	71439	72418	4325	3342	0.00E+00	1653	Partial (*psb*B)
10	M1	88.981	962	54	18	46073	47023	124772	123852	0	1142	Partial (*ycf*3)
11	M3	73.566	889	180	41	95344	96207	67654	66796	8.99E-78	289	Partial (*rrn*16S)
12	M3	73.566	889	180	41	127160	128023	66796	67654	8.99E-78	289	Partial (*rrn*16S)
13	M1	98.308	591	10	0	10380	10970	87813	87223	0.00E+00	1037	Partial (*psb*D, *psb*C)
14	M2	92.802	514	17	7	139255	139761	89444	88944	0.00E+00	726	Complete (*trn*H-GUG), Partial (*rpl*2, *rps*19)
15	M2	92.802	514	17	7	83606	84112	88944	89444	0.00E+00	726	Complete (*trn*H-GUG), Partial (*rpl*2, *rps*19)
16	M1	78.708	418	44	18	18489	18873	70538	70133	9.39E-62	237	Complete (*psb*M)
17	M3	83.838	396	40	14	79923	80307	42172	41790	8.74E-98	355	Partial (*rpl*14)
18	M2	92.157	357	17	5	52830	53185	70703	71049	3.88E-139	494	IGS (*ndh*C, *trn*V-UAC)
19	M2	82.857	350	26	22	66779	67124	20249	20568	9.13E-76	283	Complete (*trn*P-GGG)
20	M1	100	293	0	0	120349	120641	194450	194158	1.78E-153	542	Complete (*trn*R-ACG)
21	M1	100	293	0	0	102726	103018	194158	194450	1.78E-153	542	Complete (*trn*R-ACG)
22	M2	100	293	0	0	102726	103018	130955	130663	1.36E-153	542	Complete (*trn*R-ACG)
23	M2	100	293	0	0	120349	120641	130663	130955	1.36E-153	542	Complete (*trn*R-ACG)

24	M1	84.646	254	25	8	20450	20699	69045	68802	7.26E-63	241	Complete (*trn*C-GCA)
25	M1	94.301	193	10	1	47022	47213	123799	123607	5.50E-79	294	Partial (*trn*S-GGA)
26	M1	96.753	154	5	0	33540	33693	191545	191698	7.21E-68	257	Partial (*atp*I)
27	M2	96.753	154	5	0	33540	33693	133568	133415	5.54E-68	257	Partial (*atp*I)
28	M2	87.919	149	17	1	114048	114196	97455	97602	5.74E-43	174	Partial (*ndh*G)
29	M2	87.5	136	11	5	66564	66698	20019	20149	2.69E-36	152	Complete (*trn*W-CCA)
30	M3	98.462	130	2	0	135680	135809	794	665	5.53E-60	230	IGS (*trn*L-CAA, *trn*I-CAU)
31	M3	98.462	130	2	0	87558	87687	665	794	5.53E-60	230	IGS (*trn*I-CAU, *trn*L-CAA)
32	M2	92.373	118	3	4	135579	135691	153009	152893	1.24E-39	163	IGS (*trn*L-CAA, *trn*I-CAU)
33	M2	92.373	118	3	4	87676	87788	152893	153009	1.24E-39	163	IGS (*trn*I-CAU, *trn*L-CAA)
34	M1	98.246	114	2	0	99144	99257	138635	138522	1.23E-50	200	Partial (*rrn*23S)
35	M1	98.246	114	2	0	124110	124223	138522	138635	1.23E-50	200	Partial (*rrn*23S)
36	M1	82.474	97	17	0	123801	123897	924	828	3.6E-16	86.1	Partial (*rrn*23S)
37	M1	82.474	97	17	0	99470	99566	828	924	3.6E-16	86.1	Partial (*rrn*23S)
38	M2	100	86	0	0	120232	120317	49981	49896	1.61E-38	159	Complete (*trn*N-GUU)
39	M2	100	86	0	0	103050	103135	49896	49981	1.61E-38	159	Complete (*trn*N-GUU)
40	M1	93.421	76	4	1	54212	54286	35531	35456	5.94E-24	111	Complete (*trn*M-CAU)
41	M3	95.312	64	2	1	43779	43841	35601	35538	4.52E-21	100	Partial (*psa*A)
42	M3	97.917	48	1	0	40825	40872	349	302	4.55E-16	84.2	Partial (*psa*B*)*
43	M2	94.595	37	1	1	8498	8534	70341	70376	2.17E-07	56.5	Partial (*trn*S-GCU)
44	M2	96.97	33	1	0	52797	52829	70525	70557	2.17E-07	56.5	IGS (*ndh*C，*trn*V-UAC)

Table S10. RNA-editing prediction in the *F. qinlingensis* mitogenome.

Gene	Nt Pos	AA Pos	Align Col	Effect	Score	Editing Type
atp1	971	324	326	TCG (S) => TTG (L)	0.8	C=>T
atp1	1178	393	395	TCA (S) => TTA (L)	0.9	C=>T
atp1	1292	431	433	CCC (P) => CTC (L)	0.8	C=>T
atp1	1490	497	499	CCT (P) => CTT (L)	0.9	C=>T
atp1	1499	500	502	TCT (S) => TTT (F)	0.9	C=>T
atp4	56	19	23	CCA (P) => CTA (L)	0.86	C=>T
atp4	59	20	24	TCT (S) => TTT (F)	0.57	C=>T
atp4	71	24	28	TCA (S) => TTA (L)	1	C=>T
atp4	76	26	30	CCG (P) => TCG (S)	1	C=>T
atp4	89	30	34	TCA (S) => TTA (L)	1	C=>T
atp4	118	40	44	CGT (R) => TGT (C)	0.71	C=>T
atp4	248	83	87	CCG (P) => CTG (L)	1	C=>T
atp4	395	132	140	TCA (S) => TTA (L)	1	C=>T
atp4	416	139	147	ACT (T) => ATT (I)	0.86	C=>T
atp4	536	179	192	GCC (A) => GTC (V)	0.67	C=>T
atp4	593	198	211	GCG (A) => GTG (V)	0.67	C=>T
atp6	403	135	136	CCA (P) => TCA (S)	0.75	C=>T
atp6	413	138	139	TCT (S) => TTT (F)	1	C=>T
atp6	448	150	151	CTT (L) => TTT (F)	0.25	C=>T
atp6	482	161	162	TCA (S) => TTA (L)	1	C=>T
atp6	595	199	200	CGC (R) => TGC (C)	0.75	C=>T
atp6	602	201	202	TCG (S) => TTG (L)	0.67	C=>T
atp6	620	207	208	TCG (S) => TTG (L)	1	C=>T
atp6	628	210	211	CGT (R) => TGT (C)	1	C=>T
atp6	635	212	213	CCC (P) => CTC (L)	1	C=>T
atp6	826	276	277	CCT (P) => TCT (S)	1	C=>T
atp6	829	277	278	CAT (H) => TAT (Y)	1	C=>T
atp6	851	284	285	TCA (S) => TTA (L)	1	C=>T
atp6	893	298	299	TCA (S) => TTA (L)	1	C=>T
atp6	1022	341	342	TCA (S) => TTA (L)	1	C=>T
atp6	1030	344	345	CAT (H) => TAT (Y)	1	C=>T
atp6	1037	346	347	TCT (S) => TTT (F)	1	C=>T
atp6	1046	349	350	TCA (S) => TTA (L)	1	C=>T
atp6	1073	358	359	ACA (T) => ATA (I)	0.92	C=>T
atp6	1084	362	363	CAA (Q) => TAA (X)	1	C=>T
atp8	55	19	19	CTC (L) => TTC (F)	0.75	C=>T
atp8	58	20	20	CTC (L) => TTC (F)	1	C=>T
atp8	200	67	67	TCG (S) => TTG (L)	1	C=>T
atp8	248	83	83	TCC (S) => TTC (F)	0.75	C=>T
atp8	434	145	152	ACA (T) => ATA (I)	0.62	C=>T
atp8	443	148	155	CCA (P) => CTA (L)	0.75	C=>T

atp9	**20**	**7**	**7**	**TCA (S) => TTA (L)**	**1**	**C=>T**
atp9	**82**	**28**	**28**	**CTC (L) => TTC (F)**	**1**	**C=>T**
atp9	**92**	**31**	**31**	**TCG (S) => TTG (L)**	**1**	**C=>T**
atp9	**134**	**45**	**45**	**TCA (S) => TTA (L)**	**1**	**C=>T**
atp9	**182**	**61**	**61**	**TCG (S) => TTG (L)**	**1**	**C=>T**
atp9	**191**	**64**	**64**	**CAA (Q) => TAA (X)**	**1**	**C=>T**
atp9	**212**	**71**	**71**	**TCA (S) => TTA (L)**	**1**	**C=>T**
atp9	**223**	**75**	**75**	**CGA (R) => TGA (X)**	**1**	**C=>T**
ccmB	28	10	10	CAT (H) => TAT (Y)	0.89	C=>T
ccmB	43	15	15	CCC (P) => TCC (S)	0.67	C=>T
ccmB	80	27	29	TCG (S) => TTG (L)	1	C=>T
ccmB	128	43	45	TCA (S) => TTA (L)	1	C=>T
ccmB	137	46	48	TCC (S) => TTC (F)	1	C=>T
ccmB	149	50	52	TCG (S) => TTG (L)	1	C=>T
ccmB	154	52	54	CGG (R) => TGG (W)	1	C=>T
ccmB	160	54	56	CCT (P) => TCT (S)	0.67	C=>T
ccmB	172	58	60	CCC (P) => TCC (S)	0.89	C=>T
ccmB	179	60	62	CCT (P) => CTT (L)	1	C=>T
ccmB	181	61	63	CCC (P) => TCC (S)	0.78	C=>T
ccmB	193	65	69	CCT (P) => TTT (F)	0.89	C=>T
ccmB	194	65	69	CCT (P) => TTT (F)	0.89	C=>T
ccmB	286	96	102	CGG (R) => TGG (W)	1	C=>T
ccmB	304	102	108	CGT (R) => TGT (C)	0.78	C=>T
ccmB	338	113	119	CCG (P) => CTG (L)	1	C=>T
ccmB	367	123	129	CGG (R) => TGG (W)	0.78	C=>T
ccmB	392	131	137	CCG (P) => CTG (L)	0.89	C=>T
ccmB	424	142	148	CGT (R) => TGT (C)	0.89	C=>T
ccmB	428	143	149	TCG (S) => TTG (L)	1	C=>T
ccmB	467	156	164	TCG (S) => TTG (L)	0.89	C=>T
ccmB	476	159	167	CCA (P) => CTA (L)	0.89	C=>T
ccmB	485	162	170	TCA (S) => TTA (L)	1	C=>T
ccmB	503	168	176	CCA (P) => CTA (L)	1	C=>T
ccmB	512	171	179	TCC (S) => TTC (F)	1	C=>T
ccmB	514	172	180	CGT (R) => TGT (C)	1	C=>T
ccmB	551	184	192	TCA (S) => TTA (L)	1	C=>T
ccmB	554	185	193	TCG (S) => TTG (L)	0.89	C=>T
ccmB	566	189	197	TCC (S) => TTC (F)	0.78	C=>T
ccmB	569	190	198	TCT (S) => TTT (F)	0.78	C=>T
ccmB	572	191	199	CCT (P) => CTT (L)	1	C=>T
ccmB	596	199	207	TCG (S) => TTG (L)	0.89	C=>T
ccmB	611	204	212	TCA (S) => TTA (L)	0.89	C=>T

ccmC	76	26	32	CGG (R) => TGG (W)	0.78	C=>T
ccmC	103	35	41	CAT (H) => TAT (Y)	1	C=>T
ccmC	115	39	45	CGG (R) => TGG (W)	0.78	C=>T
ccmC	128	43	49	CCA (P) => CTA (L)	0.56	C=>T
ccmC	133	45	51	CTT (L) => TTT (F)	0.67	C=>T
ccmC	161	54	60	TCG (S) => TTG (L)	0.78	C=>T
ccmC	179	60	66	GCG (A) => GTG (V)	0.78	C=>T
ccmC	184	62	68	CGG (R) => TGG (W)	1	C=>T
ccmC	227	76	82	TCC (S) => TTC (F)	0.78	C=>T
ccmC	236	79	85	CCA (P) => CTA (L)	1	C=>T
ccmC	281	94	100	ACA (T) => ATA (I)	0.56	C=>T
ccmC	299	100	106	TCT (S) => TTT (F)	1	C=>T
ccmC	331	111	117	CGG (R) => TGG (W)	1	C=>T
ccmC	358	120	126	CGG (R) => TGG (W)	1	C=>T
ccmC	400	134	140	CTT (L) => TTT (F)	0.89	C=>T
ccmC	421	141	147	CGT (R) => TGT (C)	0.78	C=>T
ccmC	436	146	152	CCT (P) => TCT (S)	0.89	C=>T
ccmC	446	149	155	CCG (P) => CTG (L)	0.78	C=>T
ccmC	451	151	157	CCT (P) => TCT (S)	1	C=>T
ccmC	458	153	159	TCA (S) => TTA (L)	0.78	C=>T
ccmC	463	155	161	CGT (R) => TGT (C)	1	C=>T
ccmC	467	156	162	GCT (A) => GTT (V)	0.78	C=>T
ccmC	473	158	164	CCG (P) => CTG (L)	1	C=>T
ccmC	497	166	172	TCT (S) => TTT (F)	1	C=>T
ccmC	499	167	173	CCA (P) => TCA (S)	1	C=>T
ccmC	521	174	180	TCG (S) => TTG (L)	1	C=>T
ccmC	548	183	189	TCT (S) => TTT (F)	1	C=>T
ccmC	568	190	196	CCT (P) => TCT (S)	1	C=>T
ccmC	575	192	198	CCC (P) => CTC (L)	1	C=>T
ccmC	608	203	209	CCC (P) => CTC (L)	0.89	C=>T
ccmC	614	205	211	TCT (S) => TTT (F)	0.22	C=>T
ccmC	619	207	213	CGT (R) => TGT (C)	0.78	C=>T
ccmC	650	217	223	CCT (P) => CTT (L)	0.78	C=>T
ccmC	656	219	225	CCA (P) => CTA (L)	0.89	C=>T
ccmC	665	222	228	CCC (P) => CTC (L)	0.78	C=>T
ccmC	673	225	231	CCC (P) => TCC (S)	0.78	C=>T
ccmFc	38	13	13	TCC (S) => TTC (F)	0.83	C=>T
ccmFc	50	17	17	CCC (P) => CTC (L)	1	C=>T
ccmFc	52	18	18	CGT (R) => TGT (C)	1	C=>T
ccmFc	103	35	35	CCC (P) => TCC (S)	1	C=>T
ccmFc	119	40	40	TCT (S) => TTT (F)	1	C=>T
ccmFc	122	41	41	TCC (S) => TTC (F)	1	C=>T

ccmFc	146	49	49	CCT (P) => CTT (L)	1	C=>T
ccmFc	151	51	51	CCT (P) => TCT (S)	0.83	C=>T
ccmFc	160	54	54	CCT (P) => TCT (S)	0.67	C=>T
ccmFc	301	101	104	CGT (R) => TGT (C)	0.5	C=>T
ccmFc	397	133	136	CGT (R) => TGT (C)	0.83	C=>T
ccmFc	403	135	138	CTC (L) => TTC (F)	0.67	C=>T
ccmFc	572	191	197	GCC (A) => GTC (V)	0.67	C=>T
ccmFc	799	267	275	CCC (P) => TCC (S)	0.83	C=>T
ccmFc	866	289	297	TCT (S) => TTT (F)	0.83	C=>T
ccmFc	908	303	311	CCA (P) => CTA (L)	0.67	C=>T
ccmFc	1136	379	387	CCA (P) => CTA (L)	1	C=>T
ccmFc	1157	386	394	CCG (P) => CTG (L)	1	C=>T
ccmFc	1231	411	419	CGG (R) => TGG (W)	1	C=>T
ccmFc	1256	419	427	TCG (S) => TTG (L)	1	C=>T
ccmFc	1312	438	446	CGA (R) => TGA (X)	1	C=>T
ccmFn	20	7	9	TCT (S) => TTT (F)	0.67	C=>T
ccmFn	38	13	15	CCG (P) => CTG (L)	1	C=>T
ccmFn	98	33	35	CCT (P) => CTT (L)	1	C=>T
ccmFn	121	41	43	CCT (P) => TCT (S)	1	C=>T
ccmFn	137	46	48	TCG (S) => TTG (L)	1	C=>T
ccmFn	142	48	50	CGT (R) => TGT (C)	1	C=>T
ccmFn	151	51	53	CCA (P) => TCA (S)	0.83	C=>T
ccmFn	248	83	85	TCA (S) => TTA (L)	1	C=>T
ccmFn	263	88	90	CCA (P) => CTA (L)	0.83	C=>T
ccmFn	349	117	119	CTT (L) => TTT (F)	0.5	C=>T
ccmFn	356	119	121	TCC (S) => TTC (F)	0.67	C=>T
ccmFn	365	122	124	TCG (S) => TTG (L)	0.67	C=>T
ccmFn	469	157	164	CGT (R) => TGT (C)	0.83	C=>T
ccmFn	550	184	191	CTT (L) => TTT (F)	0.5	C=>T
ccmFn	697	233	240	CCT (P) => TTT (F)	0.67	C=>T
ccmFn	698	233	240	CCT (P) => TTT (F)	0.67	C=>T
ccmFn	707	236	243	TCA (S) => TTA (L)	0.83	C=>T
ccmFn	745	249	256	CGT (R) => TGT (C)	1	C=>T
ccmFn	767	256	263	TCA (S) => TTA (L)	1	C=>T
ccmFn	779	260	267	CCA (P) => CTA (L)	1	C=>T
ccmFn	794	265	272	TCA (S) => TTA (L)	1	C=>T
ccmFn	943	315	322	CGC (R) => TGC (C)	1	C=>T
ccmFn	1258	420	448	CGG (R) => TGG (W)	1	C=>T
ccmFn	1283	428	456	TCG (S) => TTG (L)	0.67	C=>T
ccmFn	1286	429	457	CCA (P) => CTA (L)	1	C=>T
ccmFn	1303	435	463	CAT (H) => TAT (Y)	1	C=>T

ccmFn	1318	440	468	CGG (R) => TGG (W)	1	C=>T
ccmFn	1336	446	474	CGG (R) => TGG (W)	1	C=>T
ccmFn	1369	457	485	CGG (R) => TGG (W)	1	C=>T
ccmFn	1387	463	491	CGT (R) => TGT (C)	1	C=>T
ccmFn	1430	477	505	TCG (S) => TTG (L)	1	C=>T
ccmFn	1450	484	512	CTT (L) => TTT (F)	1	C=>T
ccmFn	1454	485	513	CCA (P) => CTA (L)	1	C=>T
ccmFn	1466	489	517	TCA (S) => TTA (L)	1	C=>T
ccmFn	1501	501	529	CCC (P) => TCC (S)	1	C=>T
ccmFn	1514	505	533	TCT (S) => TTT (F)	1	C=>T
ccmFn	1549	517	545	CGG (R) => TGG (W)	0.67	C=>T
ccmFn	1583	528	556	ACT (T) => ATT (I)	0.67	C=>T
cob	178	60	61	CAC (H) => TAC (Y)	1	C=>T
cob	286	96	97	CTC (L) => TTC (F)	1	C=>T
cob	298	100	101	CAC (H) => TAC (Y)	1	C=>T
cob	325	109	110	CAT (H) => TAT (Y)	1	C=>T
cob	358	120	121	CGG (R) => TGG (W)	1	C=>T
cob	419	140	141	CCA (P) => CTA (L)	1	C=>T
cob	568	190	191	CAT (H) => TAT (Y)	0.92	C=>T
cob	580	194	195	CTT (L) => TTT (F)	1	C=>T
cob	680	227	228	TCT (S) => TTT (F)	1	C=>T
cob	715	239	240	CGG (R) => TGG (W)	1	C=>T
cob	725	242	243	TCT (S) => TTT (F)	1	C=>T
cob	737	246	247	TCT (S) => TTT (F)	0.92	C=>T
cob	808	270	271	CCC (P) => TCC (S)	1	C=>T
cob	853	285	286	CAT (H) => TAT (Y)	1	C=>T
cob	908	303	304	CCA (P) => CTA (L)	1	C=>T
cob	982	328	329	CAC (H) => TAC (Y)	0.85	C=>T
cob	1081	361	362	CCT (P) => TCT (S)	0.77	C=>T
cob	1124	375	376	CCG (P) => CTG (L)	1	C=>T
cox1	1402	468	469	CGT (R) => TGT (C)	0.67	C=>T
cox1	1405	469	470	CGT (R) => TGT (C)	0.78	C=>T
cox1	1433	478	479	TCA (S) => TTA (L)	1	C=>T
cox1	1489	497	498	CCA (P) => TCA (S)	1	C=>T
cox2	**71**	**24**	**56**	**TCA (S) => TTA (L)**	**0.95**	**C=>T**
cox2	**73**	**25**	**57**	**CGG (R) => TGG (W)**	**1**	**C=>T**
cox2	**163**	**55**	**87**	**CGG (R) => TGG (W)**	**1**	**C=>T**

cox2	**289**	**97**	**129**	**CGG (R) => TGG (W)**	**1**	**C=>T**
cox2	**353**	**118**	**150**	**ACG (T) => ATG (M)**	**1**	**C=>T**
cox2	**371**	**124**	**156**	**CCA (P) => CTA (L)**	**1**	**C=>T**
cox2	**386**	**129**	**161**	**TCA (S) => TTA (L)**	**1**	**C=>T**
cox2	**454**	**152**	**184**	**CCC (P) => TCC (S)**	**1**	**C=>T**
cox2	**467**	**156**	**188**	**CCT (P) => CTT (L)**	**1**	**C=>T**
cox2	**491**	**164**	**196**	**TCA (S) => TTA (L)**	**1**	**C=>T**
cox2	**524**	**175**	**207**	**TCA (S) => TTA (L)**	**1**	**C=>T**
cox2	**542**	**181**	**213**	**TCG (S) => TTG (L)**	**0.84**	**C=>T**
cox2	**586**	**196**	**228**	**CGT (R) => TGT (C)**	**1**	**C=>T**
cox2	**608**	**203**	**235**	**ACG (T) => ATG (M)**	**1**	**C=>T**
cox3	230	77	78	GCT (A) => GTT (V)	0.75	C=>T
cox3	245	82	83	CCT (P) => CTT (L)	0.92	C=>T
cox3	257	86	87	TCT (S) => TTT (F)	0.67	C=>T
cox3	289	97	98	CTT (L) => TTT (F)	0.92	C=>T
cox3	311	104	105	TCT (S) => TTT (F)	0.92	C=>T
cox3	314	105	106	TCT (S) => TTT (F)	0.92	C=>T
cox3	400	134	135	CTT (L) => TTT (F)	0.75	C=>T
cox3	413	138	139	CCT (P) => CTT (L)	0.83	C=>T
cox3	422	141	142	CCT (P) => CTT (L)	0.92	C=>T
cox3	512	171	172	TCA (S) => TTA (L)	0.75	C=>T
cox3	527	176	177	TCC (S) => TTC (F)	0.92	C=>T
cox3	566	189	190	TCC (S) => TTC (F)	0.92	C=>T
cox3	754	252	253	CGG (R) => TGG (W)	0.92	C=>T
cox3	764	255	256	CCA (P) => CTA (L)	0.92	C=>T
matR	26	9	29	CCC (P) => CTC (L)	1	C=>T
matR	32	11	31	TCC (S) => TTC (F)	0.62	C=>T
matR	235	79	99	CCC (P) => TTC (F)	0.62	C=>T
matR	236	79	99	CCC (P) => TTC (F)	0.62	C=>T
matR	239	80	100	ACT (T) => ATT (I)	0.75	C=>T
matR	382	128	148	CAC (H) => TAC (Y)	0.75	C=>T
matR	1070	357	380	CCC (P) => CTC (L)	1	C=>T
matR	1685	562	586	TCC (S) => TTC (F)	1	C=>T
matR	1706	569	593	CCT (P) => CTT (L)	1	C=>T
matR	1832	611	635	CCA (P) => CTA (L)	0.88	C=>T
matR	1840	614	638	CCC (P) => TCC (S)	1	C=>T
matR	1850	617	641	TCA (S) => TTA (L)	0.88	C=>T
mttB	44	15	15	CCG (P) => CTG (L)	0.88	C=>T
mttB	82	28	28	CGG (R) => TGG (W)	0.88	C=>T
mttB	118	40	40	CGT (R) => TGT (C)	0.88	C=>T

mttB	130	44	44	CCG (P) => TCG (S)	1	C=>T
mttB	140	47	47	TCA (S) => TTA (L)	0.5	C=>T
mttB	146	49	49	TCT (S) => TTT (F)	0.88	C=>T
mttB	149	50	50	CCA (P) => CTA (L)	1	C=>T
mttB	196	66	68	CGT (R) => TGT (C)	1	C=>T
mttB	206	69	71	TCA (S) => TTA (L)	0.75	C=>T
mttB	217	73	75	CCC (P) => TTC (F)	0.62	C=>T
mttB	218	73	75	CCC (P) => TTC (F)	0.62	C=>T
mttB	220	74	76	CCG (P) => TCG (S)	0.88	C=>T
mttB	280	94	96	CAT (H) => TAT (Y)	1	C=>T
mttB	299	100	102	TCG (S) => TTG (L)	0.75	C=>T
mttB	346	116	118	CTC (L) => TTC (F)	0.88	C=>T
mttB	349	117	119	CAT (H) => TAT (Y)	0.62	C=>T
mttB	362	121	123	TCT (S) => TTT (F)	0.75	C=>T
mttB	364	122	124	CGC (R) => TGC (C)	0.88	C=>T
mttB	371	124	126	TCC (S) => TTC (F)	0.5	C=>T
mttB	392	131	133	CCT (P) => CTT (L)	0.38	C=>T
mttB	394	132	134	CCC (P) => TCC (S)	0.5	C=>T
mttB	397	133	135	CGG (R) => TGG (W)	0.62	C=>T
mttB	425	142	144	CCA (P) => CTA (L)	0.75	C=>T
mttB	455	152	154	TCG (S) => TTG (L)	0.57	C=>T
mttB	523	175	177	CCA (P) => TCA (S)	1	C=>T
mttB	566	189	191	CCA (P) => CTA (L)	0.62	C=>T
mttB	572	191	193	CCA (P) => CTA (L)	0.5	C=>T
mttB	628	210	212	CCG (P) => TCG (S)	1	C=>T
mttB	701	234	236	TCG (S) => TTG (L)	0.5	C=>T
nad1	**2**	**1**	**4**	**ACG (T) => ATG (M)**	**0.8**	**C=>T**
nad1	**216**	**72**	**75**	**TCC (S) => TTC (F)**	**0.9**	**C=>T**
nad1	**308**	**103**	**106**	**CCG (P) => CTG (L)**	**1**	**C=>T**
nad1	**436**	**146**	**149**	**CCT (P) => TCT (S)**	**0.9**	**C=>T**
nad1	**490**	**164**	**167**	**CCC (P) => TCC (S)**	**1**	**C=>T**
nad1	**500**	**167**	**170**	**TCG (S) => TTG (L)**	**0.7**	**C=>T**
nad1	**536**	**179**	**182**	**TCC (S) => TTC (F)**	**1**	**C=>T**
nad1	**571**	**191**	**194**	**CTT (L) => TTT (F)**	**1**	**C=>T**
nad1	**577**	**193**	**196**	**CCT (P) => TCT (S)**	**1**	**C=>T**
nad1	**580**	**194**	**197**	**CGT (R) => TGT (C)**	**1**	**C=>T**

nad1	**608**	**203**	**206**	**TCT (S) => TTT (F)**	**1**	**C=>T**
nad1	**674**	**225**	**228**	**TCT (S) => TTT (F)**	**0.9**	**C=>T**
nad1	**734**	**245**	**248**	**TCG (S) => TTG (L)**	**0.9**	**C=>T**
nad1	**743**	**248**	**251**	**CCA (P) => CTA (L)**	**1**	**C=>T**
nad1	**755**	**252**	**255**	**CCG (P) => CTG (L)**	**1**	**C=>T**
nad1	**779**	**260**	**263**	**TCC (S) => TTC (F)**	**0.9**	**C=>T**
nad1	**823**	**275**	**278**	**CTT (L) => TTT (F)**	**0.7**	**C=>T**
nad1	**898**	**300**	**303**	**CGG (R) => TGG (W)**	**1**	**C=>T**
nad1	**928**	**310**	**313**	**CGG (R) => TGG (W)**	**1**	**C=>T**
nad1	**937**	**313**	**316**	**CCC (P) => TCC (S)**	**0.6**	**C=>T**
nad1	**953**	**318**	**321**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad2	26	9	10	TCC (S) => TTC (F)	0.89	C=>T
nad2	262	88	89	CTT (L) => TTT (F)	0.56	C=>T
nad2	308	103	104	TCT (S) => TTT (F)	0.67	C=>T
nad2	335	112	113	TCT (S) => TTT (F)	1	C=>T
nad2	356	119	120	CCA (P) => CTA (L)	1	C=>T
nad2	361	121	122	CCT (P) => TCT (S)	1	C=>T
nad2	367	123	124	CGC (R) => TGC (C)	1	C=>T
nad2	388	130	131	CCG (P) => TCG (S)	1	C=>T
nad2	394	132	133	CAT (H) => TAT (Y)	1	C=>T
nad2	497	166	167	TCA (S) => TTA (L)	1	C=>T
nad2	523	175	176	CCC (P) => TCC (S)	1	C=>T
nad2	677	226	230	TCC (S) => TTC (F)	1	C=>T
nad2	788	263	267	TCT (S) => TTT (F)	0.67	C=>T
nad2	800	267	271	TCA (S) => TTA (L)	1	C=>T
nad2	809	270	274	TCT (S) => TTT (F)	1	C=>T
nad2	920	307	311	CCT (P) => CTT (L)	1	C=>T
nad2	928	310	314	CAT (H) => TAT (Y)	1	C=>T
nad2	958	320	324	CGT (R) => TGT (C)	0.78	C=>T
nad2	962	321	325	ACT (T) => ATT (I)	1	C=>T
nad2	1028	343	347	TCA (S) => TTA (L)	0.78	C=>T
nad2	1058	353	357	CCA (P) => CTA (L)	1	C=>T
nad2	1127	376	380	TCG (S) => TTG (L)	1	C=>T
nad2	1247	416	420	CCA (P) => CTA (L)	0.67	C=>T
nad2	1276	426	430	CGT (R) => TGT (C)	1	C=>T
nad2	1298	433	437	GCG (A) => GTG (V)	1	C=>T
nad2	1400	467	471	TCA (S) => TTA (L)	0.67	C=>T
nad2	1403	468	472	TCC (S) => TTC (F)	1	C=>T

nad2	1409	470	474	CCA (P) => CTA (L)	1	C=>T
nad2	1457	486	490	TCA (S) => TTA (L)	1	C=>T
nad3	5	2	2	TCG (S) => TTG (L)	0.79	C=>T
nad3	44	15	15	CCG (P) => CTG (L)	1	C=>T
nad3	62	21	21	CCA (P) => CTA (L)	0.95	C=>T
nad3	80	27	27	CCA (P) => CTA (L)	1	C=>T
nad3	137	46	47	TCC (S) => TTC (F)	1	C=>T
nad3	146	49	50	TCC (S) => TTC (F)	1	C=>T
nad3	185	62	63	CCG (P) => CTG (L)	0.95	C=>T
nad3	190	64	65	CCT (P) => TCT (S)	1	C=>T
nad3	208	70	71	CCT (P) => TTT (F)	0.95	C=>T
nad3	209	70	71	CCT (P) => TTT (F)	0.95	C=>T
nad3	215	72	73	CCG (P) => CTG (L)	1	C=>T
nad3	230	77	78	TCT (S) => TTT (F)	0.86	C=>T
nad3	247	83	84	CCT (P) => TCT (S)	1	C=>T
nad3	251	84	85	CCT (P) => CTT (L)	0.91	C=>T
nad3	275	92	93	TCT (S) => TTT (F)	1	C=>T
nad3	317	106	107	TCT (S) => TTT (F)	0.95	C=>T
nad3	344	115	116	TCG (S) => TTG (L)	1	C=>T
nad3	349	117	118	CGG (R) => TGG (W)	1	C=>T
nad4	44	15	15	CCT (P) => CTT (L)	1	C=>T
nad4	74	25	25	ACT (T) => ATT (I)	0.89	C=>T
nad4	77	26	26	CCT (P) => CTT (L)	0.78	C=>T
nad4	107	36	36	CCG (P) => CTG (L)	1	C=>T
nad4	154	52	52	CCC (P) => TCC (S)	1	C=>T
nad4	158	53	53	CCT (P) => CTT (L)	1	C=>T
nad4	164	55	55	CCT (P) => CTT (L)	0.67	C=>T
nad4	166	56	56	CGG (R) => TGG (W)	1	C=>T
nad4	197	66	66	TCT (S) => TTT (F)	1	C=>T
nad4	317	106	106	TCA (S) => TTA (L)	1	C=>T
nad4	362	121	121	ACT (T) => ATT (I)	0.89	C=>T
nad4	376	126	126	CGT (R) => TGT (C)	0.78	C=>T
nad4	401	134	134	TCC (S) => TTC (F)	1	C=>T
nad4	416	139	139	CCT (P) => CTT (L)	0.89	C=>T
nad4	433	145	145	CTT (L) => TTT (F)	1	C=>T
nad4	437	146	146	TCC (S) => TTC (F)	0.89	C=>T
nad4	449	150	150	CCA (P) => CTA (L)	1	C=>T
nad4	577	193	193	CTC (L) => TTC (F)	0.67	C=>T
nad4	977	326	326	CCG (P) => CTG (L)	0.78	C=>T
nad4	1373	458	458	TCC (S) => TTC (F)	0.78	C=>T
nad4	1405	469	469	CGG (R) => TGG (W)	1	C=>T
nad4	1417	473	473	CAC (H) => TAC (Y)	1	C=>T
nad4	1433	478	478	CCG (P) => CTG (L)	1	C=>T
nad4L	11	4	14	TCT (S) => TTT (F)	1	C=>T

nad4L	25	9	19	CGG (R) => TGG (W)	1	C=>T
nad4L	65	22	32	TCA (S) => TTA (L)	1	C=>T
nad4L	70	24	34	CCA (P) => TCA (S)	1	C=>T
nad4L	80	27	37	TCA (S) => TTA (L)	1	C=>T
nad4L	149	50	60	TCA (S) => TTA (L)	0.75	C=>T
nad4L	158	53	63	TCA (S) => TTA (L)	0.88	C=>T
nad4L	167	56	66	CCA (P) => CTA (L)	0.88	C=>T
nad4L	251	84	94	TCT (S) => TTT (F)	0.88	C=>T
nad5	1490	497	501	CCC (P) => CTC (L)	0.8	C=>T
nad5	1550	517	521	ACA (T) => ATA (I)	0.9	C=>T
nad5	1580	527	531	TCA (S) => TTA (L)	0.8	C=>T
nad5	1589	530	534	TCT (S) => TTT (F)	0.9	C=>T
nad5	1859	620	624	TCT (S) => TTT (F)	0.8	C=>T
nad5	1895	632	636	TCA (S) => TTA (L)	1	C=>T
nad5	1901	634	638	CCA (P) => CTA (L)	0.7	C=>T
nad5	1916	639	643	TCT (S) => TTT (F)	0.7	C=>T
nad5	1918	640	644	CGT (R) => TGT (C)	0.7	C=>T
nad5	1958	653	657	TCG (S) => TTG (L)	0.9	C=>T
nad6	7	3	5	CTT (L) => TTT (F)	1	C=>T
nad6	26	9	11	CCT (P) => CTT (L)	0.4	C=>T
nad6	88	30	32	CCC (P) => TTC (F)	0.7	C=>T
nad6	89	30	32	CCC (P) => TTC (F)	0.7	C=>T
nad6	146	49	51	TCC (S) => TTC (F)	1	C=>T
nad6	158	53	55	TCC (S) => TTC (F)	1	C=>T
nad6	161	54	56	CCA (P) => CTA (L)	1	C=>T
nad6	169	57	59	CAT (H) => TAT (Y)	1	C=>T
nad6	191	64	66	TCA (S) => TTA (L)	1	C=>T
nad6	446	149	151	TCC (S) => TTC (F)	1	C=>T
nad6	569	190	192	TCT (S) => TTT (F)	1	C=>T
nad7	**38**	**13**	**13**	**TCG (S) => TTG (L)**	**0.75**	**C=>T**
nad7	**44**	**15**	**15**	**TCC (S) => TTC (F)**	**1**	**C=>T**
nad7	**77**	**26**	**26**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**83**	**28**	**28**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**137**	**46**	**46**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**209**	**70**	**70**	**TCA (S) => TTA (L)**	**0.88**	**C=>T**
nad7	**224**	**75**	**75**	**ACG (T) => ATG (M)**	**1**	**C=>T**
nad7	**244**	**82**	**82**	**CAT (H) => TAT (Y)**	**1**	**C=>T**
nad7	**251**	**84**	**84**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**335**	**112**	**112**	**TCA (S) => TTA (L)**	**0.88**	**C=>T**
nad7	**344**	**115**	**115**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**353**	**118**	**118**	**TCA (S) => TTA (L)**	**1**	**C=>T**

nad7	**383**	**128**	**128**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**445**	**149**	**149**	**CCG (P) => TCG (S)**	**0.88**	**C=>T**
nad7	**533**	**178**	**178**	**TCC (S) => TTC (F)**	**1**	**C=>T**
nad7	**578**	**193**	**193**	**TCA (S) => TTA (L)**	**0.88**	**C=>T**
nad7	**679**	**227**	**227**	**CCT (P) => TCT (S)**	**0.88**	**C=>T**
nad7	**698**	**233**	**233**	**TCG (S) => TTG (L)**	**1**	**C=>T**
nad7	**724**	**242**	**242**	**CAT (H) => TAT (Y)**	**1**	**C=>T**
nad7	**734**	**245**	**245**	**TCG (S) => TTG (L)**	**0.88**	**C=>T**
nad7	**739**	**247**	**247**	**CTT (L) => TTT (F)**	**1**	**C=>T**
nad7	**769**	**257**	**257**	**CGC (R) => TGC (C)**	**1**	**C=>T**
nad7	**836**	**279**	**280**	**CCT (P) => CTT (L)**	**1**	**C=>T**
nad7	**926**	**309**	**310**	**TCA (S) => TTA (L)**	**0.88**	**C=>T**
nad7	**973**	**325**	**326**	**CCT (P) => TCT (S)**	**0.88**	**C=>T**
nad7	**1088**	**363**	**364**	**TCA (S) => TTA (L)**	**1**	**C=>T**
nad7	**1103**	**368**	**369**	**TCT (S) => TTT (F)**	**1**	**C=>T**
nad7	**1124**	**375**	**376**	**CCA (P) => CTA (L)**	**1**	**C=>T**
nad9	14	5	5	TCC (S) => TTC (F)	0.73	C=>T
nad9	92	31	31	TCT (S) => TTT (F)	0.75	C=>T
nad9	113	38	38	CCA (P) => CTA (L)	0.92	C=>T
nad9	190	64	64	CAT (H) => TAT (Y)	1	C=>T
nad9	223	75	75	CAT (H) => TAT (Y)	1	C=>T
nad9	298	100	100	CCG (P) => TCG (S)	0.83	C=>T
nad9	311	104	104	CCA (P) => CTA (L)	0.75	C=>T
nad9	328	110	110	CGG (R) => TGG (W)	1	C=>T
nad9	356	119	119	TCT (S) => TTT (F)	1	C=>T
nad9	368	123	123	TCC (S) => TTC (F)	1	C=>T
nad9	398	133	133	TCA (S) => TTA (L)	1	C=>T
rpl2	488	163	168	GCG (A) => GTG (V)	0.67	C=>T
rpl5	64	22	27	CAC (H) => TAC (Y)	1	C=>T
rpl5	202	68	76	CCT (P) => TCT (S)	0.78	C=>T
rpl16	37	13	27	CAG (Q) => TAG (X)	1	C=>T
rpl16	56	19	33	TCT (S) => TTT (F)	0.6	C=>T
rpl16	59	20	34	CCT (P) => CTT (L)	0.2	C=>T
rpl16	142	48	62	CGC (R) => TGC (C)	0.78	C=>T

rpl16	185	62	76	ACC (T) => ATC (I)	1	C=>T
rpl16	245	82	96	ACA (T) => ATA (I)	0.89	C=>T
rpl16	313	105	122	CTC (L) => TTC (F)	0.89	C=>T
rpl16	416	139	156	CCA (P) => CTA (L)	1	C=>T
rpl16	482	161	178	CCA (P) => CTA (L)	1	C=>T
rpl16	488	163	180	TCG (S) => TTG (L)	0.75	C=>T
rps1	335	112	177	TCA (S) => TTA (L)	0.67	C=>T
rps1	490	164	232	CAA (Q) => TAA (X)	1	C=>T
rps3	58	20	20	CCA (P) => TCA (S)	1	C=>T
rps3	64	22	22	CGG (R) => TGG (W)	1	C=>T
rps3	92	31	31	TCA (S) => TTA (L)	0.71	C=>T
rps3	503	168	176	TCA (S) => TTA (L)	0.71	C=>T
rps3	704	235	252	TCG (S) => TTG (L)	0.86	C=>T
rps3	1016	339	365	CCA (P) => CTA (L)	0.86	C=>T
rps3	1046	349	375	CCT (P) => CTT (L)	0.71	C=>T
rps3	1573	525	557	CCT (P) => TCT (S)	0.57	C=>T
rps3	1604	535	567	TCA (S) => TTA (L)	0.86	C=>T
rps3	1618	540	572	CGG (R) => TGG (W)	1	C=>T
rps4	38	13	26	CCA (P) => CTA (L)	0.5	C=>T
rps4	49	17	30	CGG (R) => TGG (W)	1	C=>T
rps4	278	93	107	TCG (S) => TTG (L)	0.67	C=>T
rps4	290	97	111	CCG (P) => CTG (L)	0.83	C=>T
rps4	335	112	126	CCG (P) => CTG (L)	1	C=>T
rps4	482	161	175	TCA (S) => TTA (L)	1	C=>T
rps4	902	301	349	TCG (S) => TTG (L)	0.83	C=>T
rps4	913	305	353	CAT (H) => TAT (Y)	0.83	C=>T
rps4	938	313	361	TCT (S) => TTT (F)	1	C=>T
rps4	989	330	378	CCA (P) => CTA (L)	0.83	C=>T
rps4	998	333	381	CCT (P) => CTT (L)	1	C=>T
rps4	1003	335	383	CGG (R) => TGG (W)	1	C=>T
rps7	332	111	134	TCA (S) => TTA (L)	0.88	C=>T
rps12	71	24	24	TCG (S) => TTG (L)	0.94	C=>T
rps12	196	66	66	CAC (H) => TAC (Y)	0.94	C=>T
rps12	221	74	74	TCG (S) => TTG (L)	0.88	C=>T
rps12	269	90	90	TCG (S) => TTG (L)	0.94	C=>T
rps12	284	95	95	TCC (S) => TTC (F)	0.76	C=>T
rps12	289	97	97	CGT (R) => TGT (C)	0.88	C=>T
rps13	5	2	6	TCA (S) => TTA (L)	0.6	C=>T
rps13	26	9	13	TCA (S) => TTA (L)	0.9	C=>T
rps13	56	19	23	TCA (S) => TTA (L)	0.9	C=>T
rps13	100	34	38	CGT (R) => TGT (C)	0.9	C=>T
rps13	256	86	90	CGT (R) => TGT (C)	1	C=>T

rps13	287	96	100	TCG (S) => TTG (L)	1	C=>T
rps19	116	39	60	TCG (S) => TTG (L)	1	C=>T
rps19	137	46	67	TCC (S) => TTC (F)	0.33	C=>T
rps19	163	55	76	CCT (P) => TTT (F)	1	C=>T
rps19	164	55	76	CCT (P) => TTT (F)	1	C=>T

Table S11. Primer sequences used for evaluating RNA-editing sites.

	Gene name-editing site	Forward primer (5'-3')	Reverse primer (5'-3')
gDNA	*atp9-191*	ccttccagagcctatctaacacag	cccaagataaggtcagggtttatt
	cox2-353,-608	cgtttgctctgttatactcaatgg	tttcaaagtcactgcttctacgac
	nad1-216	gcttagtcaagtgaggattccatt	tgttcggatctgacaataccatac
	nad7-224	cactccatagagggactgagaaat	aatatctcgacataagccaagagg
cDNA	*atp9-191*	tcatgacttttatgcgatcggaaaac	atgttagaaggtgctaaatcaataggt
	cox2-353,-608	gttccgtgcttgacttacgag	gtcgacccaaccttatgagtatt
	nad1-216	gaaaatcgaaaacgtacatagctg	tgttcggatctgacaataccatac
	nad7-224	cactaatcgttgtttccagatacg	cagagagcacttgtgtatgtgatg

Table S12. NCBI accession numbers of plant mitogenomes.

Bambusoideae	*Fargesia qinlingensis* T. P. Yi & J. X. Shao	OP324798-800
	Bambusa oldhamii mitochondrion, complete genome	MN166292.1
Pooideae	*Triticum aestivum* cultivar Chinese Yumai mitochondrion, complete genome	NC_015994.1
	Hordeum vulgare subsp. vulgare cultivar Maresi mitochondrion, complete genome	NC_015099.1
	Lolium perenne mitochondrion, complete genome	NC_056281.1
	Thinopyrum obtusiflorum	NC_057604.1
Oryzoideae	*Oryza minuta* voucher W1340 mitochondrion, complete genome	NC_056991.1
	Oryza rufipogon mitochondrion, complete genome	NC_048974.1
	Oryza coarctata mitochondrion, complete genome	NC_041093.1
	Oryza sativa Indica Group mitochondrion, complete genome	MN683736.1
Panicoideae	*Chrysopogon zizanioides* mitochondrion, complete genome	NC_014487.1
	Tripsacum dactyloides mitochondrion, complete genome	NC_035618.1
	Zea mays subsp. mays mitochondrion, complete genome	NC_060419.1

	Zea perennis mitochondrion, complete genome	MW971440.1
	Zea luxurians mitochondrion, complete genome	NC_039757.1
	Sorghum bicolor mitochondrion, complete genome	NC_037949.1
	Coix lacryma-jobi var. ma-yuen isolate ZI000L51 mitochondrion, complete genome	NC_023337.1
Chloridoideae	*Cynodon dactylon* x Cynodon transvaalensis mitochondrion, complete genome	NC_058584.1
	Eleusine indica mitochondrion, complete genome	NC_042378.1
	Sporobolus alterniflorus strain S0325 mitochondrion, complete genome	NC_042406.1
Puelieae	*Acacia ligulata* mitochondrion, complete genome	NC_035958.1

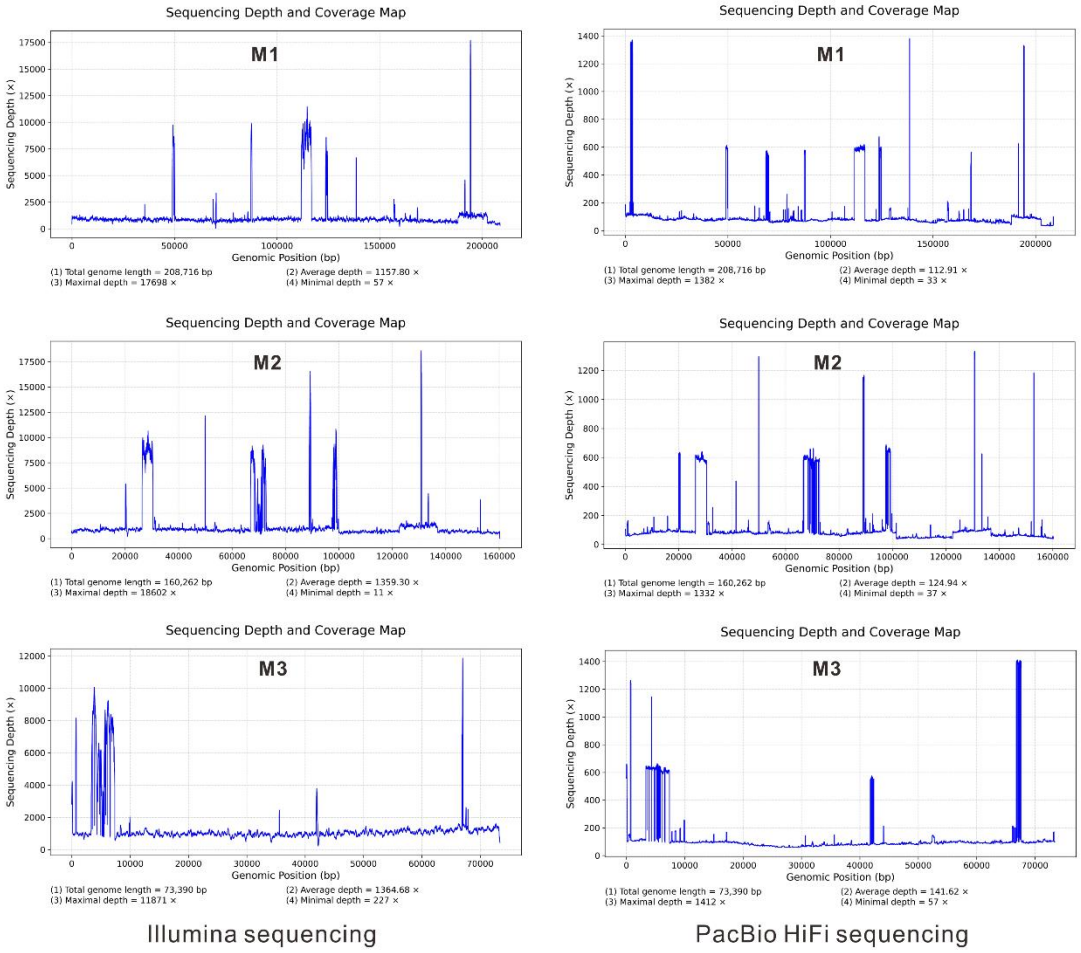


Figure S1. Sequencing depth of coverage based on Illunina short reads (left panel) and PacBio HiFi long reads (right panel). The abscissa indicates the location of the contig, and the ordinate indicates the sequencing depth between Illunina and PacBio HiFi. The average sequencing depth of the mitochondrial genome (M1, M2, and M3) was about 1293.93 × for Illunina and 126.49 × for PacBio HiFi sequencing.

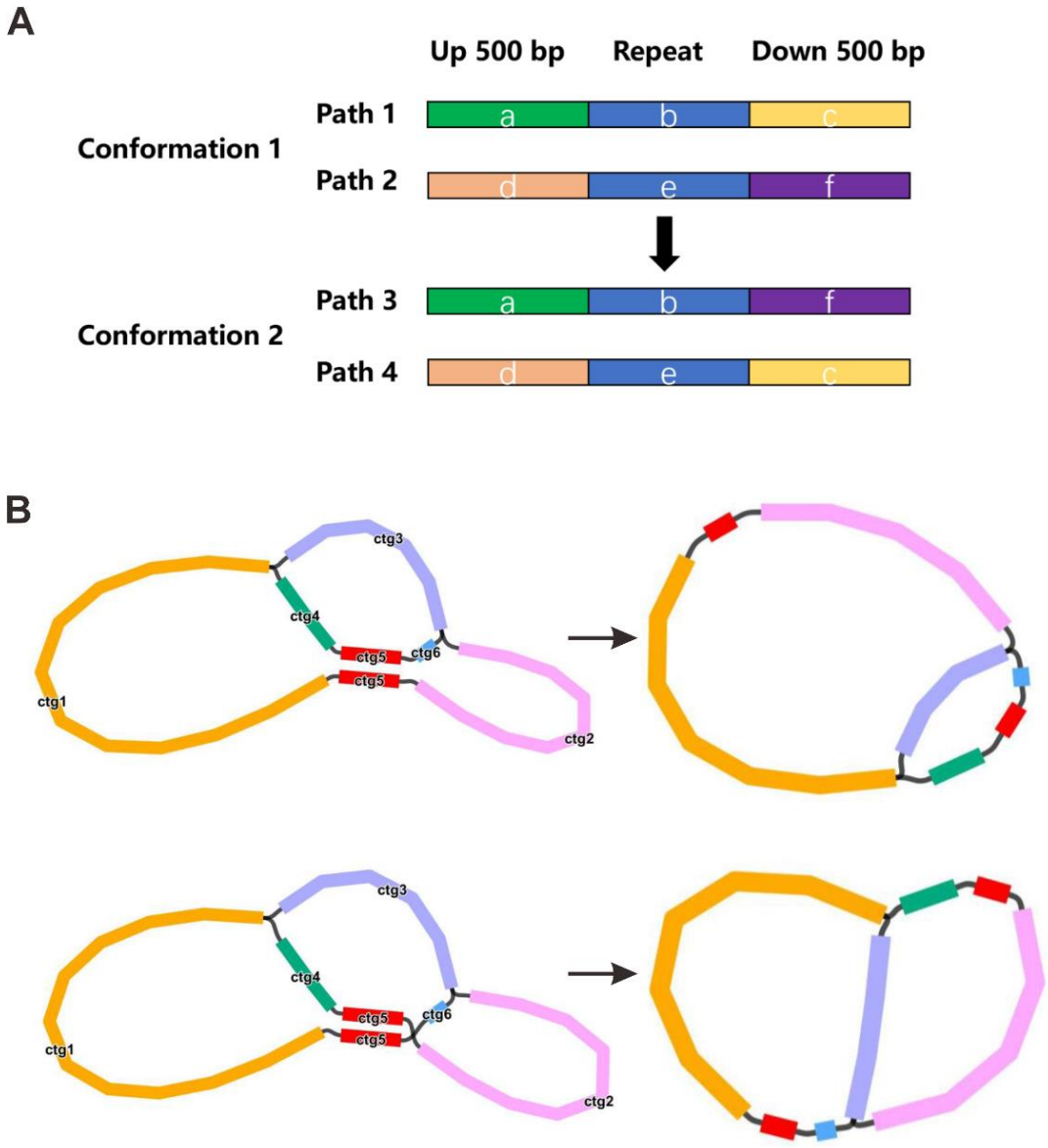


Figure S2. Mitogenome conformation changes from different path combinations. (**A**) Strategy used for evaluating the mitogenome recombination mediated by ctg5 repeat sequences. Colors represent the different paths. (**B**) Two major conformations assembled for the mitogenome draft.

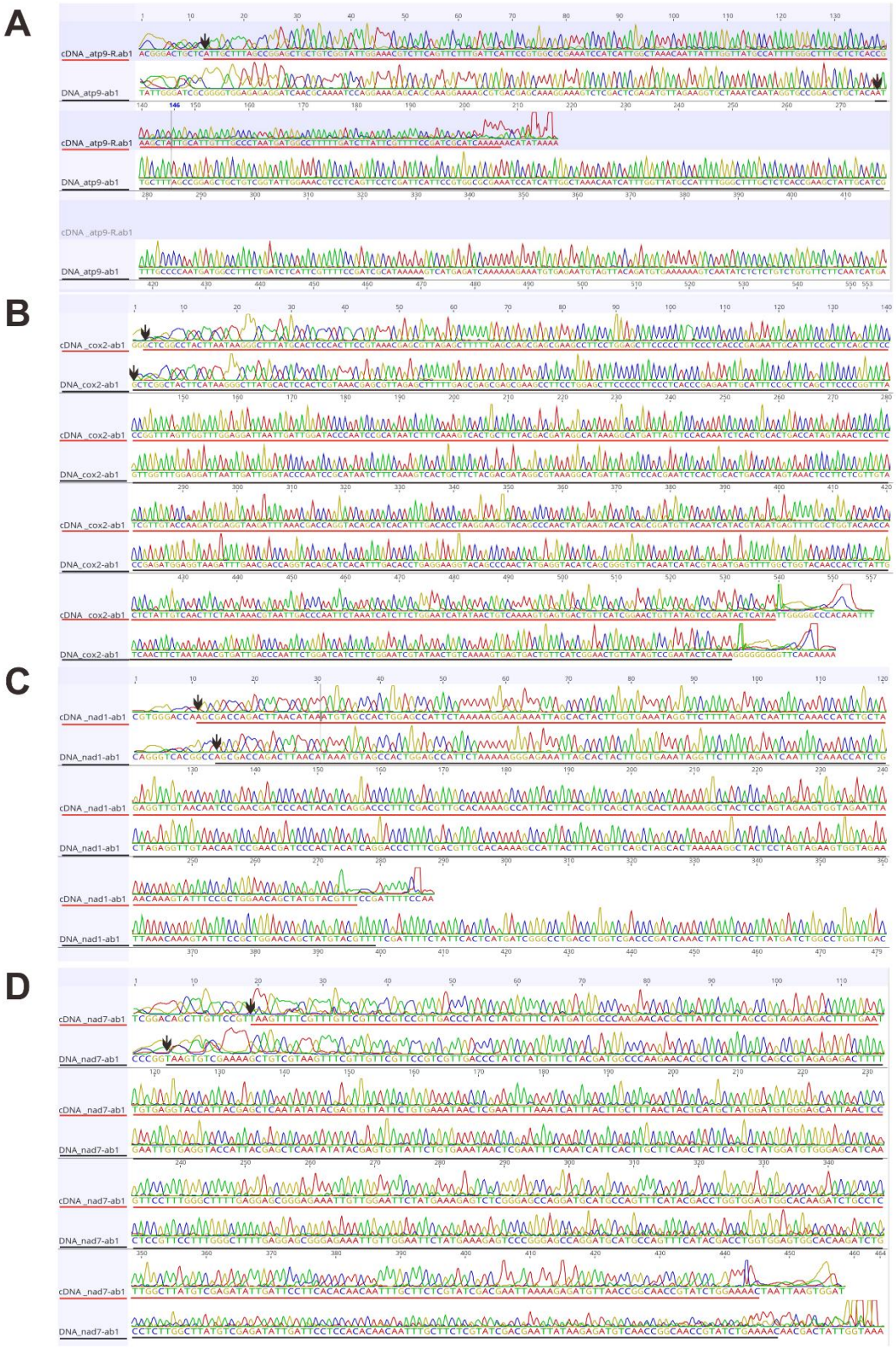


Figure S3. Validations of the RNA-editing sites in four selected PCGs using Sanger sequencing. Lined overlapping sequences between the DNA and cDNA PCR-amplified products in (**A**) *atp 9*, (**B**) *cox2*, (**C**) *nad1*, and (**D**) *nad7*. Arrows indicates the start base for the sequencing comparision.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.