

Supplementary Files: Tables and figures

Table S1. Statistics of the mitogenome assembly in *M. elegans*.

Statistical list	Number
Number of raw reads	1,642
Total length of raw reads (bp)	25,062,966
Average raw read length (bp)	15,264
Longest raw read (bp)	21,406
Number of assembled contigs	21
Longest contig (bp)	93,797
Number of read depth	56×
Total number(>=15 kb)	878
Total number(>=10 kb)	1,642

Table S2. Basic information of *M. elegans* mitogenome.

NCBI Accession number	Contigs	Type	Length	GC content %
OP429117 - OP429118	Molecule 1-2	Branched	416,354 bp	44.33
OP429117	Molecule 1	circular	221,573 bp	44.32
OP429118	Molecule 2	circular	194,781 bp	44.33

Table S3. Relative synonymous codon usage in *M. elegans* mitogenome.

Amino	Codon 1 RSCU	Codon 2 RSCU	Codon 3 RSCU	Codon 4 RSCU	Codon 5 RSCU	Codon 6 RSCU
Ala	GCU 1.63	GCA 0.98	GCC 0.78	GCG 0.50		
Arg	AGA 1.46	CGA 1.35	CGU 1.18	AGG 0.72	CGG 0.69	CGC 0.61
Asn	AAU 1.32	AAC 0.68				
Asp	GAU 1.41	GAC 0.59				
Cys	UGU 1.2	UGC 0.8				
End	UAA 1.61	UAG 1.07	UGA 0.32			
Gln	CAA 1.53	CAG 0.47				
Glu	GAA	GAG				

		1.39	0.61				
Gly	GGA	GGU	GGG	GGC			
		1.52	1.32	0.75	0.51		
His	CAU	CAC					
		1.54	0.46				
Ile	AUU	AUA	AUC				
		1.34	0.87	0.79			
Leu	UUA	CUU	UUG	CUA	CUC	CUG	
		1.6	1.29	1.18	0.89	0.56	0.48
Lys	AAA	AAG					
		1.29	0.71				
Met	AUG						
		1.0					
Phe	UUU	UUC					
		1.23	0.77				
Pro	CCU	CCA	CCC	CCG			
		1.59	1.09	0.73	0.58		
Ser	UCU	UCA	AGU	UCC	UCG	AGC	
		1.49	1.16	1.06	1.09	0.87	0.66
Thr	ACU	ACC	ACA	ACG			
		1.51	0.99	0.98	0.52		
Trp	UGG						
		1.0					
Tyr	UAU	UAC					
		1.48	0.52				
Val	GUU	GUA	GUG	GUC			
		1.27	1.25	0.83	0.66		

Table S4. SSRs in the mitogenome of M1.

Mitogenome	SSR nr.	SSR type	SSR	size	start	end
M1	1	p1	(T)11	11	1965	1975
M1	2	p1	(T)10	10	3984	3993
M1	3	p4	(TAAG)3	12	7554	7565
M1	4	p1	(G)10	10	12980	12989
M1	5	p5	(GGATG)3	15	15878	15892
M1	6	p2	(TC)5	10	17368	17377
M1	7	p2	(TA)5	10	24902	24911
M1	8	p1	(A)11	11	29071	29081
M1	9	p1	(T)10	10	33542	33551
M1	10	p4	(TTAA)3	12	38042	38053
M1	11	p4	(TCAA)3	12	39486	39497

M1	12	p2	(AG)6	12	41642	41653
M1	13	p3	(TTC)4	12	42166	42177
M1	14	p4	(TCTT)3	12	52401	52412
M1	15	p4	(AAGG)3	12	52953	52964
M1	16	p4	(ACTG)3	12	66144	66155
M1	17	p4	(TCGC)3	12	70539	70550
M1	18	p2	(AG)5	10	70593	70602
M1	19	p6	(TCGTCT)3	18	70667	70684
M1	20	p4	(GGCT)3	12	76673	76684
M1	21	p1	(T)10	10	78798	78807
M1	22	p1	(A)11	11	78913	78923
M1	23	p4	(AAGA)3	12	83737	83748
M1	24	p2	(AG)5	10	88567	88576
M1	25	p1	(A)10	10	97596	97605
M1	26	p1	(A)11	11	97644	97654
M1	27	p1	(A)10	10	100261	100270
M1	28	p1	(T)11	11	102816	102826
M1	29	p4	(AATG)3	12	103566	103577
M1	30	p1	(A)10	10	104403	104412
M1	31	p1	(A)10	10	105383	105392
M1	32	p1	(A)11	11	106285	106295
M1	33	p4	(AAGA)3	12	106838	106849
M1	34	p1	(A)11	11	106995	107005
M1	35	p2	(AT)17	34	108842	108875
M1	36	p2	(AT)5	10	109489	109498
M1	37	p2	(TA)5	10	119379	119388
M1	38	p4	(GAAA)3	12	124315	124326
M1	39	p4	(CTTC)3	12	125809	125820
M1	40	p4	(GAAA)4	16	127445	127460
M1	41	p4	(AAGC)3	12	127780	127791
M1	42	p4	(TTTA)3	12	143258	143269
M1	43	p3	(AAT)4	12	143785	143796
M1	44	p1	(T)10	10	144210	144219
M1	45	p3	(TTC)4	12	151681	151692
M1	46	p2	(CT)5	10	153524	153533
M1	47	p4	(AGAA)3	12	155405	155416
M1	48	p4	(TACT)3	12	161343	161354
M1	49	p4	(TTGC)3	12	167209	167220
M1	50	p1	(T)11	11	173751	173761
M1	51	p1	(A)12	12	176187	176198
M1	52	p2	(CT)5	10	177895	177904
M1	53	p3	(ATA)4	12	179997	180008

M1	54	p1	(T)10	10	180474	180483
M1	55	p5	(AAGTG)3	15	180655	180669
M1	56	p4	(GAAA)3	12	180855	180866
M1	57	p4	(ATGA)3	12	181948	181959
M1	58	p2	(CT)5	10	182672	182681
M1	59	p1	(T)11	11	183300	183310
M1	60	p4	(CGCC)3	12	210107	210118
M1	61	p2	(AG)5	10	221353	221362

Table S5. SSRs in the mitogenome of M2.

Mitogenome	SSR nr.	SSR type	SSR	size	start	end
M2	1	p4	(CGCC)3	12	8205	8216
M2	2	p2	(AG)5	10	19451	19460
M2	3	p4	(TCTT)3	12	27687	27698
M2	4	p4	(ATTC)3	12	29983	29994
M2	5	p1	(A)10	10	40961	40970
M2	6	p1	(T)15	15	42925	42939
M2	7	p4	(GAAA)3	12	45860	45871
M2	8	p1	(A)10	10	50398	50407
M2	9	p3	(ATA)4	12	53775	53786
M2	10	p2	(TA)5	10	58680	58689
M2	11	p1	(T)11	11	59655	59665
M2	12	p1	(T)10	10	63501	63510
M2	13	p4	(GGAT)3	12	63791	63802
M2	14	p4	(GAAA)3	12	64439	64450
M2	15	p3	(GAA)4	12	66734	66745
M2	16	p2	(AG)6	12	77553	77564
M2	17	p1	(T)10	10	80302	80311
M2	18	p1	(T)10	10	81853	81862
M2	19	p1	(T)11	11	83784	83794
M2	20	p1	(A)10	10	96600	96609
M2	21	p1	(A)12	12	97324	97335
M2	22	p1	(A)10	10	103178	103187
M2	23	p1	(A)10	10	103189	103198
M2	24	p1	(T)10	10	105527	105536
M2	25	p2	(CT)5	10	107946	107955
M2	26	p1	(A)10	10	120139	120148
M2	27	p1	(A)10	10	122652	122661

M2	28	p1	(A)10	10	130982	130991
M2	29	p4	(GAAA)3	12	133245	133256
M2	30	p1	(A)10	10	133502	133511
M2	31	p1	(A)10	10	136913	136922
M2	32	p4	(TTTA)3	12	146935	146946
M2	33	p1	(T)11	11	149649	149659
M2	34	p2	(AT)6	12	150112	150123
M2	35	p1	(A)11	11	151740	151750
M2	36	p2	(AG)6	12	152046	152057
M2	37	p1	(A)10	10	153466	153475
M2	38	p1	(A)11	11	153848	153858
M2	39	p3	(AGA)4	12	158209	158220
M2	40	p2	(TC)5	10	159013	159022
M2	41	p1	(A)10	10	161194	161203
M2	42	p4	(TTCC)3	12	168532	168543
M2	43	p1	(T)11	11	178567	178577
M2	44	p1	(A)10	10	183307	183316
M2	45	p1	(A)10	10	187111	187120
M2	46	p4	(GAAT)3	12	190070	190081
M2	47	p4	(AGAA)3	12	190089	190100
M2	48	p3	(TCT)4	12	192270	192281

Table S6. Tandem repeat sequences in the mitogenome of M1.

Indices	Period	Copy	Consensus	Percent	Percent	Score	A	C	G	T	Entropy
	Size	Number	Size	Matches	Indels						(0-2)
59874--59917	21	2	21	82	13	52	31	29	6	31	1.84
173619--173662	23	1.9	23	90	0	70	59	11	25	4	1.51
213145--213190	24	1.9	24	82	8	58	26	19	34	19	1.96
216813--216855	18	2.4	18	80	0	50	37	23	20	18	1.94

Table S7. Tandem repeat sequences in the mitogenome of *M. elegans*.

Indices	Period	Copy	Consensus	Percent	Percent	Score	A	C	G	T	Entropy
	Size	Number	Size	Matches	Indels						(0-2)
11243--11288	24	1.9	24	82	8	58	26	19	34	19	1.96

14911--14953 18 2.4 18 80 0 50 37 23 20 18 1.94

Table S8. Dispersed repeats sequences in M1.

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
148	186626	F	148	220497	-2	1.06E-74
115	2243	F	115	67720	0	8.00E-60
109	29132	P	109	212144	0	3.28E-56
116	102008	F	116	105076	-2	1.20E-55
110	50327	P	110	113541	-1	2.70E-54
105	80658	F	105	193388	0	8.39E-54
104	70740	F	104	88711	-2	1.62E-48
89	86947	F	89	113907	0	3.60E-44
87	70757	F	87	88728	0	5.77E-43
84	114346	P	84	210110	0	3.69E-41
82	37123	F	82	84246	0	5.90E-40
81	75362	P	81	173638	0	2.36E-39
77	80219	P	77	88268	0	6.05E-37
66	113705	P	66	158893	0	2.54E-30
76	72888	P	76	133707	-3	4.59E-30
62	70590	F	62	88564	0	6.49E-28
62	133725	P	62	182140	0	6.49E-28
65	29330	F	65	73408	-1	1.98E-27
64	29349	F	64	86998	-1	7.79E-27
63	130892	P	63	212078	-1	3.07E-26
58	86994	P	58	133729	0	1.66E-25
58	86994	F	58	182140	0	1.66E-25
59	29344	F	59	72883	-1	7.35E-24
59	29344	P	59	133729	-1	7.35E-24
54	29349	F	54	182144	0	4.25E-23
54	130901	P	54	212078	0	4.25E-23
52	29241	P	52	212084	0	6.81E-22
55	47075	P	55	180075	-1	1.76E-21

55	72888	F	55	182144	-1	1.76E-21
51	72883	F	51	73422	0	2.72E-21
51	113002	P	51	218928	0	2.72E-21
54	72888	F	54	86998	-1	6.89E-21
50	86993	P	50	97248	0	1.09E-20
53	73412	F	53	219963	-1	2.71E-20
56	84282	P	56	113905	-2	3.69E-20
49	97248	F	49	133738	0	4.36E-20
49	97248	P	49	182140	0	4.36E-20
49	183892	P	49	219975	0	4.36E-20
58	73423	P	58	97239	-3	1.38E-19
58	130740	P	58	206218	-3	1.38E-19
48	29245	F	48	130901	0	1.74E-19
51	67644	F	51	113026	-1	4.17E-19
51	72904	F	51	75388	-1	4.17E-19
51	72904	P	51	173642	-1	4.17E-19
51	75388	P	51	133716	-1	4.17E-19
51	133716	F	51	173642	-1	4.17E-19
54	84282	P	54	86947	-2	5.48E-19
53	29334	F	53	219963	-2	2.11E-18
45	29349	P	45	97248	0	1.12E-17
45	84293	P	45	113905	0	1.12E-17
48	31229	P	48	99940	-1	2.51E-17
51	73422	P	51	133737	-2	3.12E-17
44	68184	P	44	80611	0	4.46E-17
47	102077	F	47	105145	-1	9.83E-17
50	72914	P	50	133707	-2	1.20E-16
43	84293	P	43	86947	0	1.78E-16
43	97255	P	43	113953	0	1.78E-16
46	73427	F	46	86998	-1	3.85E-16
46	73427	F	46	182144	-1	3.85E-16
46	186728	F	46	220599	-1	3.85E-16
49	72884	P	49	97248	-2	4.61E-16
42	107687	F	42	133713	0	7.14E-16
42	113954	P	42	133745	0	7.14E-16
42	113954	F	42	182140	0	7.14E-16
45	113954	F	45	219974	-1	1.51E-15
41	72914	F	41	75398	0	2.86E-15
41	72914	P	41	173642	0	2.86E-15
50	80770	F	50	218905	-3	5.76E-15
44	72916	P	44	107685	-1	5.89E-15
44	113955	P	44	183897	-1	5.89E-15

40	119478	P	40	140672	0	1.14E-14
40	189565	F	40	212110	0	1.14E-14
43	72883	F	43	219973	-1	2.30E-14
43	133745	P	43	219973	-1	2.30E-14
46	37159	P	46	86955	-2	2.60E-14
46	37159	P	46	113915	-2	2.60E-14
39	75388	F	39	182160	0	4.57E-14
39	133728	F	39	173654	0	4.57E-14
39	173654	P	39	182160	0	4.57E-14
42	86994	F	42	219974	-1	8.99E-14
42	97255	P	42	219974	-1	8.99E-14
42	110986	F	42	138838	-1	8.99E-14
42	182140	F	42	219974	-1	8.99E-14
45	73494	P	45	97652	-2	9.94E-14
38	29349	F	38	113958	0	1.83E-13
38	29365	F	38	75388	0	1.83E-13
38	29365	P	38	173655	0	1.83E-13
38	72888	P	38	183900	0	1.83E-13
38	73427	P	38	183900	0	1.83E-13
38	73427	F	38	219978	0	1.83E-13
38	75388	F	38	87014	0	1.83E-13
38	87014	P	38	173655	0	1.83E-13
41	86995	P	41	183900	-1	3.51E-13
41	97255	F	41	183900	-1	3.51E-13
41	133745	F	41	183900	-1	3.51E-13
41	182141	P	41	183900	-1	3.51E-13
44	73532	P	44	97161	-2	3.80E-13
37	113475	P	37	212026	0	7.31E-13
40	90215	P	40	207259	-1	1.37E-12
40	186596	F	40	220429	-1	1.37E-12
39	75400	P	39	107690	-1	5.35E-12
39	107690	F	39	173642	-1	5.35E-12
42	32724	F	42	73299	-2	5.53E-12
42	72884	F	42	113954	-2	5.53E-12
42	73423	F	42	113954	-2	5.53E-12
35	822	P	35	47996	0	1.17E-11
35	37170	P	35	86955	0	1.17E-11
35	37170	P	35	113915	0	1.17E-11
35	64131	P	35	220315	0	1.17E-11
38	6748	F	38	68041	-1	2.08E-11
38	29349	P	38	183900	-1	2.08E-11
38	29349	F	38	219978	-1	2.08E-11

38	29371	P	38	97191	-1	2.08E-11
41	73504	F	41	146074	-2	2.11E-11
34	71966	F	34	73542	0	4.68E-11
34	73508	P	34	107689	0	4.68E-11
34	73508	P	34	133715	0	4.68E-11
34	108841	P	34	108841	0	4.68E-11
43	72238	P	43	101968	-3	5.95E-11
33	37133	F	33	183841	0	1.87E-10
33	84256	F	33	183841	0	1.87E-10
33	87020	P	33	97196	0	1.87E-10
33	108841	R	33	108841	0	1.87E-10
33	108841	C	33	108842	0	1.87E-10
33	108842	R	33	108842	0	1.87E-10
39	29294	F	39	113476	-2	3.05E-10
36	106681	F	36	173619	-1	3.16E-10
32	71907	F	32	73347	0	7.49E-10
32	75394	P	32	97197	0	7.49E-10
32	97197	F	32	133729	0	7.49E-10
32	97197	F	32	173655	0	7.49E-10
32	97197	P	32	182166	0	7.49E-10
32	108841	P	32	108841	0	7.49E-10
32	108841	F	32	108843	0	7.49E-10
32	108843	P	32	108843	0	7.49E-10
35	176802	F	35	178440	-1	1.23E-09
31	47099	P	31	180075	0	2.99E-09
31	108841	R	31	108841	0	2.99E-09
31	108841	C	31	108844	0	2.99E-09
31	108844	R	31	108844	0	2.99E-09
34	72922	F	34	73508	-1	4.77E-09
34	72922	F	34	146078	-1	4.77E-09
34	114447	P	34	215106	-1	4.77E-09
39	104466	P	39	116013	-3	1.13E-08
30	74452	P	30	74452	0	1.2E-08
30	107699	P	30	182172	0	1.2E-08
30	108841	P	30	108841	0	1.2E-08
30	108841	F	30	108845	0	1.2E-08
30	108845	P	30	108845	0	1.2E-08
30	133758	P	30	219973	0	1.2E-08
36	29294	P	36	212026	-2	1.66E-08
33	73508	F	33	75406	-1	1.85E-08
33	73508	P	33	173642	-1	1.85E-08
33	75406	F	33	146078	-1	1.85E-08

33	146078	P	33	173642	-1	1.85E-08
35	97652	P	35	146074	-2	6.26E-08
35	109156	F	35	191103	-2	6.26E-08
32	32655	P	32	157911	-1	7.19E-08
32	70575	P	32	182666	-1	7.19E-08
32	72910	P	32	97197	-1	7.19E-08
32	72914	F	32	182170	-1	7.19E-08
34	71966	P	34	97161	-2	2.36E-07
34	107689	P	34	146078	-2	2.36E-07
34	133715	P	34	146078	-2	2.36E-07
31	1975	F	31	48002	-1	2.78E-07
31	72922	P	31	97652	-1	2.78E-07
31	75406	P	31	97652	-1	2.78E-07
31	97652	F	31	173644	-1	2.78E-07
31	130892	P	31	189565	-1	2.78E-07
36	67635	P	36	218928	-3	5.64E-07
33	77315	F	33	144573	-2	8.89E-07
30	821	P	30	1975	-1	1.08E-06
30	73443	F	30	75388	-1	1.08E-06
30	73443	P	30	173663	-1	1.08E-06
30	75387	P	30	97248	-1	1.08E-06
30	97247	F	30	173663	-1	1.08E-06
30	97268	F	30	183913	-1	1.08E-06
30	97268	P	30	219973	-1	1.08E-06
30	107702	F	30	173654	-1	1.08E-06
30	107884	P	30	218282	-1	1.08E-06
30	108840	R	30	108841	-1	1.08E-06
30	108840	C	30	108845	-1	1.08E-06
30	108845	R	30	108846	-1	1.08E-06
30	182667	P	30	215366	-1	1.08E-06
35	123712	P	35	149985	-3	2.07E-06
35	177810	F	35	215385	-3	2.07E-06
32	106674	F	32	107683	-2	3.34E-06
34	3297	F	34	107714	-3	7.56E-06
34	50499	F	34	218957	-3	7.56E-06
31	97652	F	31	107692	-2	0.0000125
31	97652	F	31	133718	-2	0.0000125
31	122440	F	31	132550	-2	0.0000125
31	189926	F	31	212037	-2	0.0000125
33	31440	F	33	97780	-3	0.0000276
33	109164	F	33	191111	-3	0.0000276
33	115742	P	33	190039	-3	0.0000276

30	7512	P	30	31592	-2	0.0000469
30	17736	F	30	182971	-2	0.0000469
30	29374	P	30	107702	-2	0.0000469
30	29375	F	30	72914	-2	0.0000469
30	70576	F	30	215366	-2	0.0000469
30	72914	F	30	87024	-2	0.0000469
30	87023	P	30	107702	-2	0.0000469
30	89711	F	30	183840	-2	0.0000469
30	97197	F	30	107703	-2	0.0000469
30	108841	F	30	108847	-2	0.0000469
30	133758	F	30	183913	-2	0.0000469
32	8983	P	32	16263	-3	0.0001
32	41590	P	32	121519	-3	0.0001
32	60423	F	32	72016	-3	0.0001
31	16510	F	31	50620	-3	0.000363
31	107868	P	31	218297	-3	0.000363
31	113475	P	31	189921	-3	0.000363
31	186433	P	31	206151	-3	0.000363
31	187849	P	31	209317	-3	0.000363
30	27279	P	30	113016	-3	0.00131
30	27279	F	30	218935	-3	0.00131
30	29241	P	30	189561	-3	0.00131
30	29530	F	30	70887	-3	0.00131
30	37133	F	30	89712	-3	0.00131
30	50597	P	30	67472	-3	0.00131
30	70676	F	30	88640	-3	0.00131
30	72930	P	30	106676	-3	0.00131
30	73453	P	30	97237	-3	0.00131
30	73502	F	30	182172	-3	0.00131
30	84256	F	30	89712	-3	0.00131
30	104476	P	30	116012	-3	0.00131
30	106676	F	30	133711	-3	0.00131
30	106691	F	30	173629	-3	0.00131
30	108841	C	30	108848	-3	0.00131
30	152149	F	30	180044	-3	0.00131
30	160021	F	30	207404	-3	0.00131

Table S9. Dispersed repeats sequences in the mitogenome of M2.

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
197	97881	F	197	129478	-1	1.56E-106
170	79003	P	170	97832	-1	2.43E-90
121	79003	P	121	129478	-1	5.48E-61
97	48318	P	97	144057	-2	1.78E-44
88	97590	P	88	111485	0	1.11E-43
95	80302	F	95	112076	-2	2.73E-43
78	134251	P	78	149432	0	1.17E-37
74	17014	F	74	149658	0	2.99E-35
70	18061	P	70	57879	0	7.66E-33
72	38154	P	72	106541	-1	1.03E-31
75	38161	F	75	57874	-2	1.87E-31
71	16944	P	71	44186	-1	4.08E-31
69	18061	P	69	38167	-1	6.34E-30
65	57874	P	65	106541	-1	1.53E-27
59	18071	F	59	106541	0	3.21E-26
69	14043	F	69	84658	-3	4.33E-26
61	18073	P	61	142225	-1	3.67E-25
58	57879	F	58	142228	-1	2.23E-23
57	106543	P	57	142229	-1	8.79E-23
52	43983	F	52	104853	0	5.26E-22
57	38167	F	57	142229	-2	7.38E-21
56	52754	P	56	140511	-3	1.54E-18
54	48447	P	54	143972	-3	2.2E-17
54	62355	P	54	122952	-3	2.2E-17
44	44041	P	44	85943	0	3.45E-17
47	44006	P	47	183239	-1	7.6E-17
47	104875	F	47	159991	-1	7.6E-17
46	62456	F	46	142237	-1	2.97E-16
41	106574	F	41	172848	0	2.21E-15
41	130651	F	41	142245	0	2.21E-15
50	18072	P	50	62456	-3	4.45E-15
50	57888	F	50	62456	-3	4.45E-15
50	62456	P	50	106542	-3	4.45E-15
49	13870	F	49	84485	-3	1.67E-14
39	38154	P	39	172848	0	3.53E-14
39	48283	F	39	177874	0	3.53E-14

42	18072	P	42	130651	-1	6.95E-14
42	57896	F	42	130651	-1	6.95E-14
42	106542	P	42	130651	-1	6.95E-14
47	14518	F	47	85151	-3	2.36E-13
44	43984	F	44	62442	-2	2.94E-13
44	62442	F	44	104854	-2	2.94E-13
46	38175	F	46	62456	-3	8.83E-13
43	62464	F	43	130651	-2	1.12E-12
43	62505	P	43	172820	-2	1.12E-12
36	38200	F	36	57913	0	2.26E-12
42	38183	F	42	130651	-2	4.27E-12
35	134329	P	35	149396	0	9.04E-12
38	113485	F	38	179323	-1	1.61E-11
34	34512	F	34	192604	0	3.62E-11
34	44019	P	34	183239	0	3.62E-11
37	8267	F	37	89413	-1	6.27E-11
33	44005	F	33	159991	0	1.45E-10
33	48508	P	33	143933	0	1.45E-10
39	62373	P	39	136935	-2	2.35E-10
36	122952	F	36	136938	-1	2.44E-10
32	18098	P	32	38167	0	5.78E-10
32	18102	P	32	142225	0	5.78E-10
32	19021	F	32	126949	0	5.78E-10
38	8689	P	38	90334	-2	8.94E-10
35	18413	P	35	106467	-1	9.49E-10
37	111590	P	37	128176	-2	3.39E-09
37	160879	R	37	160879	-2	3.39E-09
30	18092	P	30	43998	0	9.26E-09
30	18092	P	30	104868	0	9.26E-09
30	43998	F	30	57888	0	9.26E-09
30	43998	P	30	106562	0	9.26E-09
30	57888	F	30	104868	0	9.26E-09
30	104868	P	30	106562	0	9.26E-09
33	19278	F	33	71395	-1	1.43E-08
38	51510	F	38	67105	-3	3.22E-08
35	48466	P	35	143972	-2	4.84E-08
32	57874	P	32	172848	-1	5.55E-08
32	62475	F	32	130662	-1	5.55E-08
32	159992	P	32	183254	-1	5.55E-08
31	62381	P	31	136935	-1	2.15E-07
36	106304	F	36	192913	-3	4.36E-07
33	48386	P	33	144053	-2	6.87E-07

30	8862	P	30	125742	-1	8.33E-07
30	38175	F	30	43998	-1	8.33E-07
30	38175	F	30	104868	-1	8.33E-07
30	43998	F	30	142237	-1	8.33E-07
30	57909	F	30	130664	-1	8.33E-07
30	57909	F	30	142258	-1	8.33E-07
30	62475	F	30	142256	-1	8.33E-07
30	104868	F	30	142237	-1	8.33E-07
30	172821	F	30	177028	-1	8.33E-07
35	37378	F	35	87520	-3	0.0000016
35	53027	F	35	53066	-3	0.0000016
32	104876	P	32	183254	-2	0.00000258
31	57907	F	31	62475	-2	0.00000968
31	62378	P	31	122952	-2	0.00000968
31	62475	P	31	106542	-2	0.00000968
31	82188	P	31	118017	-2	0.00000968
31	106572	P	31	142226	-2	0.00000968
31	130645	P	31	183261	-2	0.00000968
33	22185	P	33	150505	-3	0.0000213
33	169519	P	33	170034	-3	0.0000213
30	38196	F	30	130664	-2	0.0000362
30	38196	F	30	142258	-2	0.0000362
30	75343	F	30	172131	-2	0.0000362
30	82154	P	30	85969	-2	0.0000362
30	142229	P	30	172844	-2	0.0000362
30	160014	P	30	177023	-2	0.0000362
32	17058	P	32	112053	-3	0.0000775
31	18102	F	31	172846	-3	0.000281
31	18393	P	31	106496	-3	0.000281
31	38194	F	31	62475	-3	0.000281
31	44031	F	31	130671	-3	0.000281
31	82137	P	31	82184	-3	0.000281
31	143102	F	31	169389	-3	0.000281
30	44031	F	30	62484	-3	0.00101
30	60767	F	30	157240	-3	0.00101
30	62517	P	30	177028	-3	0.00101
30	85997	F	30	106588	-3	0.00101
30	85997	F	30	172862	-3	0.00101
30	94043	P	30	127630	-3	0.00101
30	104897	P	30	172817	-3	0.00101
30	112056	P	30	149701	-3	0.00101
30	134365	P	30	149376	-3	0.00101

30

171834

P

30

179160

-3

0.00101

Table S10. The homologous DNA fragment in the *M. elegans* mitogenome.

Num- ber	Mitogenome	% Identity	Alignment Length	Misma- tches	Gap Openings	Alignment start (plastome)	Alignment end (plastome)	Alignment start (mitogenome)	Alignment end (mitogenome)	E-value	Bit Score	MTPT annotation
1	Circular M1	95.768	2221	47	13	39504	41705	202592	204784	0	3537	Partial (<i>psaB,psaA</i>)
2	Circular M2	95.768	2221	47	13	39504	41705	690	2882	0	3537	Partial (<i>psaB,psaA</i>)
3	Circular M1	92.157	714	17	5	38457	39156	201903	202591	0	972	Partial (<i>psaB</i>)
4	Circular M2	92.157	714	17	5	38457	39156	1	689	0.00E+00	972	Partial (<i>psaB</i>)
5	Circular M1	81.494	616	74	26	66621	67215	8267	7671	1.00E-131	470	Complete (<i>petG,trnW-CCA,trnP-UGG</i>)
6	Circular M1	91.185	329	20	2	153302	153626	93470	93147	2.83E-122	438	Partial (<i>rpl23,rpl2</i>)
7	Circular M1	91.185	329	20	2	86466	86790	93147	93470	2.83E-122	438	Partial (<i>rpl23,rpl2</i>)
8	Circular M1	91.327	196	7	4	154697	154892	39866	39681	2.36E-68	259	Partial (<i>rpl2</i>)
9	Circular M1	91.327	196	7	4	85200	85395	39681	39866	2.36E-68	259	Partial (<i>rpl2</i>)
10	Circular M1	86.957	161	8	3	153011	153165	93688	93535	4.10E-41	169	Complete (<i>trnM-CAU</i>)
11	Circular M1	86.957	161	8	3	86927	87081	93535	93688	4.10E-41	169	Complete (<i>trnM-CAU</i>)
12	Circular M2	86.239	109	9	1	35702	35810	94711	94609	1.71E-24	113	Partial (<i>psaC</i>)
13	Circular M2	97.619	84	1	1	109298	109380	62419	62336	2.18E-33	143	Complete (<i>trnN-GUU</i>)
14	Circular M2	97.619	84	1	1	130712	130794	62336	62419	2.18E-33	143	Complete (<i>trnN-GUU</i>)
15	Circular M1	96.386	83	2	1	30680	30762	143955	143874	4.16E-31	135	Complete (<i>trnD-GUC</i>)
16	Circular M1	92.208	77	5	1	53809	53884	201653	201729	9.06E-23	108	Complete (<i>trnM-CAU</i>)
17	Circular M1	97.368	76	2	0	1	76	107175	107100	1.93E-29	130	Complete (<i>trnH-GUG</i>)
18	Circular M2	97.015	67	2	0	38390	38456	194715	194781	1.71E-24	113	Partial (<i>psaB</i>)

Table S11. The collection of long reads obtained from BLASTn results that can support different paths.

Paths	Reference length (bp)	Reads ID	Identity (%)	Alignment (bp)	Mis- match	Gap	Query_ start	Query_ end	Reads_sta rt	Reads_e nd	E-value	Score
10_(28)_4	1238	m64196e_210606_053615/115607092/ccs	100	1238	0	0	1	1238	4582	5819	0	2287
10_(28)_4	1238	m64196e_210606_053615/111740640/ccs	100	1238	0	0	1	1238	9444	10681	0	2287
10_(28)_4	1238	m64196e_210606_053615/88607549/ccs	100	1238	0	0	1	1238	12527	11290	0	2287
10_(28)_4	1238	m64196e_210606_053615/80611414/ccs	100	1238	0	0	1	1238	6855	5618	0	2287
10_(28)_4	1238	m64196e_210606_053615/67045760/ccs	100	1238	0	0	1	1238	1799	3036	0	2287
10_(28)_4	1238	m64196e_210606_053615/55247931/ccs	100	1238	0	0	1	1238	3651	2414	0	2287
10_(28)_4	1238	m64196e_210606_053615/47319010/ccs	100	1238	0	0	1	1238	9574	10811	0	2287
10_(28)_4	1238	m64196e_210606_053615/43778700/ccs	100	1238	0	0	1	1238	6098	7335	0	2287
10_(28)_4	1238	m64198e_210604_164159/163906079/ccs	100	1238	0	0	1	1238	3724	4961	0	2287
10_(28)_4	1238	m64198e_210604_164159/140771425/ccs	100	1238	0	0	1	1238	8468	9705	0	2287
10_(28)_4	1238	m64198e_210604_164159/134152632/ccs	100	1238	0	0	1	1238	6894	8131	0	2287
10_(28)_4	1238	m64198e_210604_164159/134021423/ccs	100	1238	0	0	1	1238	13207	11970	0	2287
10_(28)_4	1238	m64198e_210604_164159/128191321/ccs	100	1238	0	0	1	1238	3651	2414	0	2287
10_(28)_4	1238	m64198e_210604_164159/120849453/ccs	100	1238	0	0	1	1238	12113	10876	0	2287
10_(28)_4	1238	m64198e_210604_164159/118686798/ccs	100	1238	0	0	1	1238	10413	11650	0	2287
10_(28)_4	1238	m64198e_210604_164159/40110779/ccs	100	1238	0	0	1	1238	12180	13417	0	2287
10_(28)_4	1238	m64198e_210604_164159/30212381/ccs	100	1238	0	0	1	1238	13263	14500	0	2287
10_(28)_4	1238	m64196e_210606_053615/119603589/ccs	99.919	1239	0	1	1	1238	11430	12668	0	2281
10_(28)_4	1238	m64196e_210606_053615/99484063/ccs	99.919	1239	0	1	1	1238	10672	11910	0	2281
10_(28)_4	1238	m64196e_210606_053615/94896895/ccs	99.919	1239	0	1	1	1238	8494	7256	0	2281
10_(28)_4	1238	m64196e_210606_053615/51184443/ccs	99.919	1239	0	1	1	1238	2754	1516	0	2281
10_(28)_4	1238	m64196e_210606_053615/123340094/ccs	99.919	1238	0	1	1	1238	13289	12053	0	2279

10_(28)_4	1238	m64196e_210606_053615/83954403/ccs	99.919	1238	0	1	1	1238	931	2167	0	2279
10_(28)_4	1238	m64196e_210606_053615/7211414/ccs	99.919	1238	0	1	1	1238	6703	5467	0	2279
10_(28)_4	1238	m64198e_210604_164159/97386752/ccs	99.919	1238	0	1	1	1238	12217	10981	0	2279
10_(28)_4	1238	m64196e_210606_053615/163449331/ccs	99.839	1240	0	2	1	1238	1168	2407	0	2278
10_(28)_4	1238	m64196e_210606_053615/153815572/ccs	99.839	1240	0	2	1	1238	7500	8739	0	2278
10_(28)_4	1238	m64196e_210606_053615/178521686/ccs	99.839	1239	0	2	1	1238	4008	5245	0	2276
10_(28)_4	1238	m64196e_210606_053615/120391747/ccs	99.839	1239	0	2	1	1238	14303	15540	0	2276
10_(28)_4	1238	m64196e_210606_053615/18483726/ccs	99.838	1238	0	2	1	1238	8604	7369	0	2274
10_(28)_4	1238	m64198e_210604_164159/75893556/ccs	99.838	1238	0	2	1	1238	3652	4887	0	2274
10_(28)_4	1238	m64198e_210604_164159/1050151/ccs	99.838	1238	0	2	1	1238	12237	11002	0	2274
10_(28)_4	1238	m64198e_210604_164159/35390305/ccs	99.758	1241	0	3	1	1238	4324	3084	0	2272
10_(28)_4	1238	m64198e_210604_164159/158859484/ccs	99.758	1239	0	3	1	1238	14429	13193	0	2268
10_(28)_4	1238	m64198e_210604_164159/174982549/ccs	99.758	1238	0	3	1	1238	7406	6172	0	2266
10_(28)_4	1238	m64198e_210604_164159/160891337/ccs	99.678	1241	0	4	1	1238	6222	7461	0	2266
10_(28)_4	1238	m64198e_210604_164159/56886168/ccs	99.758	1238	0	3	4	1238	13730	12493	0	2266
10_(28)_4	1238	m64198e_210604_164159/55183005/ccs	99.678	1241	0	4	1	1238	15233	16472	0	2266
10_(28)_4	1238	m64198e_210604_164159/21104117/ccs	99.678	1241	0	4	1	1238	8026	9265	0	2266
10_(28)_4	1238	m64196e_210606_053615/145490090/ccs	99.677	1238	4	0	1	1238	1764	527	0	2265
10_(28)_4	1238	m64196e_210606_053615/48103573/ccs	99.677	1238	4	0	1	1238	2227	3464	0	2265
10_(28)_4	1238	m64196e_210606_053615/45155487/ccs	99.677	1238	4	0	1	1238	12654	11417	0	2265
10_(28)_4	1238	m64196e_210606_053615/40764755/ccs	99.677	1238	4	0	1	1238	7078	5841	0	2265
10_(28)_4	1238	m64196e_210606_053615/3541532/ccs	99.677	1240	0	4	1	1238	12383	11146	0	2265
10_(28)_4	1238	m64198e_210604_164159/169804790/ccs	99.677	1238	4	0	1	1238	2755	3992	0	2265
10_(28)_4	1238	m64198e_210604_164159/16122794/ccs	99.677	1238	4	0	1	1238	7666	8903	0	2265
10_(28)_4	1238	m64198e_210604_164159/2032651/ccs	99.518	1244	0	6	1	1238	10495	9252	0	2259

10_(28)_4	1238	m64196e_210606_053615/149554662/ccs	99.517	1241	2	4	1	1238	926	2165	0	2255
10_(28)_4	1238	m64198e_210604_164159/7406630/ccs	99.517	1241	0	6	1	1238	7210	5973	0	2254
10_(28)_4	1238	m64198e_210604_164159/18809994/ccs	99.436	1241	4	3	1	1238	4256	3016	0	2250
10_(28)_4	1238	m64196e_210606_053615/175770066/ccs	99.357	1244	0	8	1	1238	19203	17962	0	2246
10_(28)_4	1238	m64196e_210606_053615/152830384/ccs	99.355	1241	0	8	1	1238	12686	11451	0	2241
10_(28)_4	1238	m64198e_210604_164159/34867271/ccs	99.195	1243	0	10	1	1238	1009	2246	0	2231
10_(28)_4	1238	m64198e_210604_164159/77332750/ccs	99.034	1242	0	12	1	1238	4387	3154	0	2217
10_(28)_4	1238	m64198e_210604_164159/130875525/ccs	98.875	1244	2	12	1	1238	3500	4737	0	2209
10_(28)_4	1238	m64198e_210604_164159/125306259/ccs	99.417	1201	4	3	1	1199	1200	1	0	2176
8_(28)_11	1238	m64196e_210606_053615/114360574/ccs	100	1238	0	0	1	1238	10312	11549	0	2287
8_(28)_11	1238	m64196e_210606_053615/111412666/ccs	100	1238	0	0	1	1238	13332	12095	0	2287
8_(28)_11	1238	m64196e_210606_053615/5245742/ccs	100	1238	0	0	1	1238	13162	14399	0	2287
8_(28)_11	1238	m64198e_210604_164159/129172406/ccs	100	1238	0	0	1	1238	11006	9769	0	2287
8_(28)_11	1238	m64198e_210604_164159/121046361/ccs	100	1238	0	0	1	1238	11067	12304	0	2287
8_(28)_11	1238	m64198e_210604_164159/80938156/ccs	100	1238	0	0	1	1238	9802	11039	0	2287
8_(28)_11	1238	m64198e_210604_164159/51314779/ccs	100	1238	0	0	1	1238	9720	10957	0	2287
8_(28)_11	1238	m64198e_210604_164159/34210348/ccs	100	1238	0	0	1	1238	1691	454	0	2287
8_(28)_11	1238	m64198e_210604_164159/19989763/ccs	100	1238	0	0	1	1238	9595	8358	0	2287
8_(28)_11	1238	m64196e_210606_053615/176425804/ccs	99.919	1239	0	1	1	1238	5325	4087	0	2281
8_(28)_11	1238	m64196e_210606_053615/38537201/ccs	99.919	1239	0	1	1	1238	10782	9544	0	2281
8_(28)_11	1238	m64198e_210604_164159/150931943/ccs	99.919	1239	0	1	1	1238	8304	9542	0	2281
8_(28)_11	1238	m64198e_210604_164159/130352974/ccs	99.919	1239	0	1	1	1238	2972	1734	0	2281
8_(28)_11	1238	m64196e_210606_053615/126681693/ccs	99.919	1238	0	1	1	1238	9368	8132	0	2279
8_(28)_11	1238	m64198e_210604_164159/60883666/ccs	99.919	1238	0	1	1	1238	12943	14179	0	2279
8_(28)_11	1238	m64198e_210604_164159/146604342/ccs	99.839	1240	0	2	1	1238	6915	5676	0	2278

8_(28)_11	1238	m64198e_210604_164159/49481506/ccs	99.839	1240	0	2	1	1238	1651	412	0	2278
8_(28)_11	1238	m64198e_210604_164159/100141672/ccs	99.839	1239	0	2	1	1238	15159	16396	0	2276
8_(28)_11	1238	m64198e_210604_164159/90768547/ccs	99.839	1239	0	2	1	1238	10284	11521	0	2276
8_(28)_11	1238	m64196e_210606_053615/155912632/ccs	99.838	1238	0	2	1	1238	9214	7979	0	2274
8_(28)_11	1238	m64196e_210606_053615/2032866/ccs	99.838	1238	0	2	1	1238	17226	15991	0	2274
8_(28)_11	1238	m64198e_210604_164159/100338251/ccs	99.758	1241	0	3	1	1238	1972	3212	0	2272
8_(28)_11	1238	m64198e_210604_164159/42993204/ccs	99.758	1241	0	3	1	1238	10000	8760	0	2272
8_(28)_11	1238	m64196e_210606_053615/140837300/ccs	99.758	1240	0	3	1	1238	6324	7562	0	2270
8_(28)_11	1238	m64196e_210606_053615/70910434/ccs	99.758	1239	0	3	1	1238	4080	2844	0	2268
8_(28)_11	1238	m64196e_210606_053615/44173067/ccs	99.678	1242	0	4	1	1238	5080	6321	0	2268
8_(28)_11	1238	m64196e_210606_053615/8390684/ccs	99.758	1239	0	3	1	1238	1404	168	0	2268
8_(28)_11	1238	m64198e_210604_164159/14155787/ccs	99.758	1238	0	3	1	1238	13930	12696	0	2266
8_(28)_11	1238	m64196e_210606_053615/148113465/ccs	99.677	1240	0	4	1	1238	15829	17066	0	2265
8_(28)_11	1238	m64198e_210604_164159/75827167/ccs	99.677	1239	0	4	1	1238	12550	11315	0	2263
8_(28)_11	1238	m64198e_210604_164159/66782436/ccs	99.597	1241	0	5	1	1238	3422	2184	0	2259
8_(28)_11	1238	m64196e_210606_053615/148898338/ccs	99.597	1240	0	5	1	1238	3141	1905	0	2257
8_(28)_11	1238	m64196e_210606_053615/135464205/ccs	99.597	1240	0	5	1	1238	11943	13179	0	2257
8_(28)_11	1238	m64196e_210606_053615/112526038/ccs	99.597	1240	0	5	1	1238	2329	1093	0	2257
8_(28)_11	1238	m64196e_210606_053615/60228947/ccs	99.356	1243	2	6	1	1238	1850	609	0	2246
8_(28)_11	1238	m64196e_210606_053615/93653513/ccs	99.355	1240	0	8	1	1238	10150	8917	0	2239
8_(28)_11	1238	m64198e_210604_164159/42074419/ccs	99.275	1242	3	6	1	1238	2801	1562	0	2239
8_(28)_11	1238	m64198e_210604_164159/114362750/ccs	99.276	1243	0	9	1	1238	8879	7641	0	2237
8_(28)_11	1238	m64198e_210604_164159/50266896/ccs	99.197	1245	2	8	1	1238	8871	7628	0	2237
8_(28)_11	1238	m64196e_210606_053615/174653453/ccs	99.197	1245	0	10	1	1238	2897	1656	0	2235
8_(28)_11	1238	m64196e_210606_053615/76874045/ccs	99.036	1245	0	11	1	1238	2195	3434	0	2222

8_(28)_11	1238	m64196e_210606_053615/121569345/ccs	98.799	1249	2	13	1	1238	7038	8284	0	2211
8_(28)_11	1238	m64196e_210606_053615/120785700/ccs	98.789	1239	14	1	1	1238	4212	2974	0	2204
8_(28)_11	1238	m64198e_210604_164159/84347691/ccs	98.789	1239	14	1	1	1238	4026	2788	0	2204
8_(28)_11	1238	m64198e_210604_164159/1114220/ccs	98.796	1246	0	15	1	1238	572	1810	0	2204
8_(28)_11	1238	m64196e_210606_053615/139003203/ccs	99.505	1211	0	6	29	1238	16992	15787	0	2198
8_(28)_11	1238	m64196e_210606_053615/54591560/ccs	98.639	1249	2	14	1	1238	2606	1362	0	2198
8_(28)_11	1238	m64196e_210606_053615/77859427/ccs	98.708	1238	14	2	1	1238	5145	3910	0	2196
8_(28)_11	1238	m64196e_210606_053615/80284510/ccs	98.551	1242	14	4	1	1238	7043	5802	0	2191
8_(28)_11	1238	m64196e_210606_053615/155257240/ccs	98.548	1240	14	4	1	1238	16025	14788	0	2187
8_(28)_11	1238	m64198e_210604_164159/147980954/ccs	98.547	1239	15	3	1	1238	10013	11249	0	2185
8_(28)_11	1238	m64198e_210604_164159/8651118/ccs	98.47	1242	14	5	1	1238	1573	333	0	2183
8_(28)_11	1238	m64198e_210604_164159/167642272/ccs	97.99	1244	16	9	1	1238	16983	15743	0	2150
8_(28)_11	1238	m64196e_210606_053615/47513737/ccs	97.271	1246	17	17	1	1238	1340	104	0	2097
10_(28)_11	1238	m64198e_210604_164159/147720583/ccs	99.758	1241	0	3	1	1238	11811	10571	0	2272
48_(44)_11	1139	m64196e_210606_053615/117114124/ccs	100	1139	0	0	1	1139	9966	8828	0	2104
48_(44)_11	1139	m64196e_210606_053615/67568997/ccs	100	1139	0	0	1	1139	9071	10209	0	2104
48_(44)_11	1139	m64196e_210606_053615/66127953/ccs	100	1139	0	0	1	1139	7596	8734	0	2104
48_(44)_11	1139	m64196e_210606_053615/25755652/ccs	100	1139	0	0	1	1139	10296	9158	0	2104
48_(44)_11	1139	m64196e_210606_053615/6425095/ccs	100	1139	0	0	1	1139	11085	12223	0	2104
48_(44)_11	1139	m64198e_210604_164159/163315883/ccs	100	1139	0	0	1	1139	10420	9282	0	2104
48_(44)_11	1139	m64198e_210604_164159/130025879/ccs	100	1139	0	0	1	1139	1979	841	0	2104
48_(44)_11	1139	m64198e_210604_164159/31981641/ccs	100	1139	0	0	1	1139	11018	12156	0	2104
48_(44)_11	1139	m64198e_210604_164159/984146/ccs	100	1139	0	0	1	1139	6486	7624	0	2104
48_(44)_11	1139	m64196e_210606_053615/115018540/ccs	99.912	1140	0	1	1	1139	11269	12408	0	2098
48_(44)_11	1139	m64196e_210606_053615/73007997/ccs	99.912	1140	0	1	1	1139	2542	1403	0	2098

48_(44)_11	1139	m64196e_210606_053615/21563064/ccs	99.912	1139	1	0	1	1139	3026	4164	0	2098
48_(44)_11	1139	m64198e_210604_164159/172754514/ccs	99.912	1140	0	1	1	1139	8743	9882	0	2098
48_(44)_11	1139	m64198e_210604_164159/136840791/ccs	99.912	1140	0	1	1	1139	10224	9085	0	2098
48_(44)_11	1139	m64198e_210604_164159/13043557/ccs	99.912	1140	0	1	1	1139	7661	6522	0	2098
48_(44)_11	1139	m64196e_210606_053615/143197999/ccs	99.912	1139	0	1	1	1139	7652	6515	0	2097
48_(44)_11	1139	m64198e_210604_164159/134023375/ccs	99.912	1139	0	1	1	1139	9833	8696	0	2097
48_(44)_11	1139	m64196e_210606_053615/87688399/ccs	99.825	1141	0	2	1	1139	6185	7325	0	2095
48_(44)_11	1139	m64198e_210604_164159/37488937/ccs	99.825	1141	0	2	1	1139	12447	11307	0	2095
48_(44)_11	1139	m64198e_210604_164159/133038789/ccs	99.825	1140	0	2	1	1139	13127	11989	0	2093
48_(44)_11	1139	m64196e_210606_053615/62194227/ccs	99.824	1139	0	2	1	1139	12761	13897	0	2091
48_(44)_11	1139	m64198e_210604_164159/41287975/ccs	99.824	1139	0	2	1	1139	5482	4346	0	2091
48_(44)_11	1139	m64196e_210606_053615/173606627/ccs	99.737	1142	0	3	1	1139	6715	7856	0	2089
48_(44)_11	1139	m64196e_210606_053615/61868157/ccs	99.737	1142	0	3	1	1139	11430	12571	0	2089
48_(44)_11	1139	m64196e_210606_053615/2032866/ccs	99.737	1141	0	3	1	1139	1825	2964	0	2087
48_(44)_11	1139	m64196e_210606_053615/109512519/ccs	99.737	1140	0	3	1	1139	14089	12952	0	2085
48_(44)_11	1139	m64198e_210604_164159/6029350/ccs	99.737	1140	0	3	1	1139	11894	10757	0	2085
48_(44)_11	1139	m64196e_210606_053615/111151897/ccs	99.649	1141	0	4	1	1139	2994	4132	0	2082
48_(44)_11	1139	m64198e_210604_164159/29818887/ccs	99.649	1141	1	3	1	1139	11959	13098	0	2082
48_(44)_11	1139	m64196e_210606_053615/85525462/ccs	99.389	1145	0	7	1	1139	5593	4450	0	2069
48_(44)_11	1139	m64198e_210604_164159/175571692/ccs	99.474	1140	0	6	1	1139	3993	2859	0	2067
48_(44)_11	1139	m64198e_210604_164159/176685980/ccs	99.387	1142	0	7	1	1139	10271	11408	0	2063
48_(44)_11	1139	m64198e_210604_164159/150930501/ccs	99.387	1142	0	7	1	1139	9116	10253	0	2063
48_(44)_11	1139	m64198e_210604_164159/100338251/ccs	99.213	1144	1	8	1	1139	17388	16248	0	2056
48_(44)_11	1139	m64196e_210606_053615/157024504/ccs	99.126	1144	1	9	1	1139	13439	14578	0	2049
48_(44)_11	1139	m64196e_210606_053615/32638013/ccs	99.211	1141	0	9	1	1139	1519	386	0	2049

48_(44)_11	1139	m64198e_210604_164159/106628567/ccs	99.125	1143	1	9	2	1139	225	1363	0	2047
48_(44)_11	1139	m64196e_210606_053615/139003203/ccs	98.862	1142	0	13	1	1139	1678	2809	0	2025
48_(44)_11	1139	m64198e_210604_164159/48826536/ccs	98.777	1145	1	12	1	1139	14412	15549	0	2025
8_(44)_2	1139	m64196e_210606_053615/138675925/ccs	100	1139	0	0	1	1139	2895	1757	0	2104
8_(44)_2	1139	m64196e_210606_053615/122030543/ccs	100	1139	0	0	1	1139	10163	11301	0	2104
8_(44)_2	1139	m64196e_210606_053615/55642932/ccs	100	1139	0	0	1	1139	3923	5061	0	2104
8_(44)_2	1139	m64196e_210606_053615/34537532/ccs	100	1139	0	0	1	1139	8151	9289	0	2104
8_(44)_2	1139	m64198e_210604_164159/136774654/ccs	100	1139	0	0	1	1139	3361	4499	0	2104
8_(44)_2	1139	m64198e_210604_164159/130877113/ccs	100	1139	0	0	1	1139	6576	5438	0	2104
8_(44)_2	1139	m64198e_210604_164159/116394147/ccs	100	1139	0	0	1	1139	7798	6660	0	2104
8_(44)_2	1139	m64198e_210604_164159/48955926/ccs	100	1139	0	0	1	1139	4553	5691	0	2104
8_(44)_2	1139	m64198e_210604_164159/28510449/ccs	100	1139	0	0	1	1139	10304	11442	0	2104
8_(44)_2	1139	m64198e_210604_164159/22020505/ccs	100	1139	0	0	1	1139	9720	8582	0	2104
8_(44)_2	1139	m64198e_210604_164159/3473773/ccs	100	1139	0	0	1	1139	13939	15077	0	2104
8_(44)_2	1139	m64196e_210606_053615/104597940/ccs	99.912	1140	0	1	1	1139	14373	15512	0	2098
8_(44)_2	1139	m64198e_210604_164159/176292411/ccs	99.912	1140	0	1	1	1139	7078	5939	0	2098
8_(44)_2	1139	m64196e_210606_053615/110691045/ccs	99.912	1139	0	1	1	1139	9432	8295	0	2097
8_(44)_2	1139	m64196e_210606_053615/1837441/ccs	99.912	1139	0	1	1	1139	546	1683	0	2097
8_(44)_2	1139	m64198e_210604_164159/135202299/ccs	99.912	1139	0	1	1	1139	7854	6717	0	2097
8_(44)_2	1139	m64198e_210604_164159/134941315/ccs	99.912	1139	0	1	1	1139	6961	5824	0	2097
8_(44)_2	1139	m64198e_210604_164159/108724420/ccs	99.912	1139	0	1	1	1139	15705	14568	0	2097
8_(44)_2	1139	m64198e_210604_164159/49613596/ccs	99.912	1139	0	1	1	1139	2537	3674	0	2097
8_(44)_2	1139	m64196e_210606_053615/143656352/ccs	99.825	1141	0	1	1	1139	13693	12553	0	2095
8_(44)_2	1139	m64196e_210606_053615/177932209/ccs	99.825	1140	0	2	1	1139	5389	6527	0	2093
8_(44)_2	1139	m64196e_210606_053615/37817057/ccs	99.825	1140	0	2	1	1139	5271	4133	0	2093

8_(44)_2	1139	m64198e_210604_164159/92670393/ccs	99.825	1140	0	2	1	1139	4275	5413	0	2093
8_(44)_2	1139	m64198e_210604_164159/21955917/ccs	99.825	1140	0	2	1	1139	917	2055	0	2093
8_(44)_2	1139	m64196e_210606_053615/150405860/ccs	99.824	1139	0	2	1	1139	2633	3769	0	2091
8_(44)_2	1139	m64196e_210606_053615/95619295/ccs	99.824	1139	0	2	1	1139	11794	12930	0	2091
8_(44)_2	1139	m64198e_210604_164159/136577954/ccs	99.737	1142	0	3	1	1139	3251	2110	0	2089
8_(44)_2	1139	m64198e_210604_164159/126093115/ccs	99.737	1140	0	3	1	1139	12376	13513	0	2085
8_(44)_2	1139	m64198e_210604_164159/6097730/ccs	99.65	1143	0	4	1	1139	1492	2634	0	2085
8_(44)_2	1139	m64196e_210606_053615/91031054/ccs	99.65	1142	0	4	1	1139	4976	3836	0	2084
8_(44)_2	1139	m64196e_210606_053615/46334337/ccs	99.649	1139	0	4	1	1139	5177	6311	0	2078
8_(44)_2	1139	m64196e_210606_053615/84281204/ccs	99.476	1145	0	6	1	1139	13216	14360	0	2076
8_(44)_2	1139	m64196e_210606_053615/10880136/ccs	99.389	1145	0	7	1	1139	994	2137	0	2069
8_(44)_2	1139	m64198e_210604_164159/29952601/ccs	99.474	1141	0	6	1	1139	12241	13377	0	2069
8_(44)_2	1139	m64196e_210606_053615/155254835/ccs	99.388	1143	0	7	1	1139	9109	10248	0	2065
8_(44)_2	1139	m64196e_210606_053615/171181345/ccs	99.299	1141	2	6	1	1139	4967	6103	0	2058
8_(44)_2	1139	m64198e_210604_164159/52299750/ccs	99.213	1143	0	9	1	1139	206	1343	0	2052
8_(44)_2	1139	m64196e_210606_053615/3015505/ccs	99.127	1145	1	9	1	1139	9344	10485	0	2050
8_(44)_2	1139	m64198e_210604_164159/128715562/ccs	98.607	1149	4	12	1	1139	4443	5589	0	2023
8_(44)_2	1139	m64198e_210604_164159/82117642/ccs	98.527	1154	2	15	1	1139	7087	5934	0	2023
48_(44)_2	1139	m64196e_210606_053615/63965609/ccs	99.825	1140	0	2	1	1139	9916	8778	0	2093
5_(45)_13	1135	m64198e_210604_164159/124387416/ccs	100	1135	0	0	1	1135	6829	7963	0	2097
5_(45)_13	1135	m64198e_210604_164159/120195320/ccs	100	1135	0	0	1	1135	6923	5789	0	2097
5_(45)_13	1135	m64198e_210604_164159/108136392/ccs	100	1135	0	0	1	1135	6202	7336	0	2097
5_(45)_13	1135	m64198e_210604_164159/92144897/ccs	100	1135	0	0	1	1135	1234	100	0	2097
5_(45)_13	1135	m64198e_210604_164159/20449316/ccs	100	1135	0	0	1	1135	6723	7857	0	2097
5_(45)_13	1135	m64198e_210604_164159/108920994/ccs	99.912	1136	0	1	1	1135	5251	4116	0	2091

5_(45)_13	1135	m64196e_210606_053615/139987330/ccs	99.912	1135	0	1	1	1135	9165	8032	0	2089
5_(45)_13	1135	m64196e_210606_053615/111216493/ccs	99.912	1135	0	1	1	1135	1997	3130	0	2089
5_(45)_13	1135	m64196e_210606_053615/77925144/ccs	99.912	1135	0	1	1	1135	2547	3680	0	2089
5_(45)_13	1135	m64198e_210604_164159/111083966/ccs	99.912	1135	0	1	1	1135	4628	5761	0	2089
5_(45)_13	1135	m64198e_210604_164159/66848592/ccs	99.912	1135	0	1	1	1135	1193	60	0	2089
5_(45)_13	1135	m64196e_210606_053615/118686645/ccs	99.824	1137	0	2	1	1135	2099	3235	0	2087
5_(45)_13	1135	m64196e_210606_053615/68814786/ccs	99.824	1137	0	2	1	1135	11730	12866	0	2087
5_(45)_13	1135	m64196e_210606_053615/33949089/ccs	99.824	1137	0	2	1	1135	13599	12463	0	2087
5_(45)_13	1135	m64198e_210604_164159/62457697/ccs	99.824	1137	0	2	1	1135	5471	4335	0	2087
5_(45)_13	1135	m64196e_210606_053615/168298694/ccs	99.824	1136	0	2	1	1135	7402	6268	0	2085
5_(45)_13	1135	m64198e_210604_164159/112986436/ccs	99.824	1136	0	2	1	1135	725	1859	0	2085
5_(45)_13	1135	m64196e_210606_053615/25691686/ccs	99.736	1137	1	2	1	1135	11101	9965	0	2082
5_(45)_13	1135	m64198e_210604_164159/113904392/ccs	99.649	1139	0	2	1	1135	8920	10058	0	2078
5_(45)_13	1135	m64196e_210606_053615/5900086/ccs	99.648	1137	0	4	1	1135	2231	1097	0	2074
5_(45)_13	1135	m64196e_210606_053615/158335852/ccs	99.561	1138	0	5	1	1135	8092	9227	0	2069
5_(45)_13	1135	m64196e_210606_053615/107547197/ccs	99.561	1138	0	5	1	1135	14324	13189	0	2069
5_(45)_13	1135	m64196e_210606_053615/7080317/ccs	99.386	1140	0	7	1	1135	13799	14936	0	2060
5_(45)_13	1135	m64196e_210606_053615/125043167/ccs	99.212	1142	0	7	1	1135	153	1292	0	2050
5_(45)_13	1135	m64198e_210604_164159/135858999/ccs	99.296	1137	0	8	1	1135	8218	7088	0	2049
5_(45)_13	1135	m64198e_210604_164159/133693958/ccs	99.211	1140	1	8	1	1135	1622	486	0	2049
5_(45)_13	1135	m64196e_210606_053615/32244296/ccs	99.034	1139	2	8	1	1135	2772	3905	0	2034
5_(45)_13	1135	m64198e_210604_164159/37094240/ccs	99.033	1138	0	11	1	1135	9152	8023	0	2030
12_(45)_3	1135	m64196e_210606_053615/105317927/ccs	100	1135	0	0	1	1135	10574	9440	0	2097
12_(45)_3	1135	m64196e_210606_053615/100993819/ccs	100	1135	0	0	1	1135	7172	8306	0	2097
12_(45)_3	1135	m64196e_210606_053615/65800053/ccs	100	1135	0	0	1	1135	4603	5737	0	2097

12_(45)_3	1135	m64196e_210606_053615/37749245/ccs	100	1135	0	0	1	1135	11184	10050	0	2097
12_(45)_3	1135	m64196e_210606_053615/26608950/ccs	100	1135	0	0	1	1135	11505	12639	0	2097
12_(45)_3	1135	m64198e_210604_164159/176097193/ccs	100	1135	0	0	1	1135	5373	6507	0	2097
12_(45)_3	1135	m64198e_210604_164159/174392410/ccs	100	1135	0	0	1	1135	2977	4111	0	2097
12_(45)_3	1135	m64198e_210604_164159/167709143/ccs	100	1135	0	0	1	1135	9580	8446	0	2097
12_(45)_3	1135	m64198e_210604_164159/136512688/ccs	100	1135	0	0	1	1135	9010	10144	0	2097
12_(45)_3	1135	m64198e_210604_164159/127273428/ccs	100	1135	0	0	1	1135	3392	4526	0	2097
12_(45)_3	1135	m64198e_210604_164159/105709835/ccs	100	1135	0	0	1	1135	9552	8418	0	2097
12_(45)_3	1135	m64198e_210604_164159/66912495/ccs	100	1135	0	0	1	1135	12942	11808	0	2097
12_(45)_3	1135	m64198e_210604_164159/63505126/ccs	100	1135	0	0	1	1135	3728	2594	0	2097
12_(45)_3	1135	m64198e_210604_164159/35587508/ccs	100	1135	0	0	1	1135	8294	7160	0	2097
12_(45)_3	1135	m64198e_210604_164159/19202151/ccs	100	1135	0	0	1	1135	3079	1945	0	2097
12_(45)_3	1135	m64198e_210604_164159/5310040/ccs	100	1135	0	0	1	1135	15751	16885	0	2097
12_(45)_3	1135	m64196e_210606_053615/89260452/ccs	99.912	1136	0	1	1	1135	8148	9283	0	2091
12_(45)_3	1135	m64196e_210606_053615/55577215/ccs	99.912	1136	0	1	1	1135	3493	2358	0	2091
12_(45)_3	1135	m64198e_210604_164159/126354224/ccs	99.912	1136	0	1	1	1135	1351	216	0	2091
12_(45)_3	1135	m64198e_210604_164159/124518922/ccs	99.912	1136	0	1	1	1135	1277	2412	0	2091
12_(45)_3	1135	m64198e_210604_164159/72811937/ccs	99.912	1136	0	1	1	1135	13781	12646	0	2091
12_(45)_3	1135	m64198e_210604_164159/33098266/ccs	99.912	1136	0	1	1	1135	11015	9880	0	2091
12_(45)_3	1135	m64196e_210606_053615/154994113/ccs	99.912	1135	0	1	1	1135	5688	6821	0	2089
12_(45)_3	1135	m64196e_210606_053615/121176669/ccs	99.912	1135	0	1	1	1135	4383	5516	0	2089
12_(45)_3	1135	m64196e_210606_053615/52757255/ccs	99.912	1135	0	1	1	1135	3108	1975	0	2089
12_(45)_3	1135	m64196e_210606_053615/31065808/ccs	99.912	1135	0	1	1	1135	9692	10825	0	2089
12_(45)_3	1135	m64198e_210604_164159/107610992/ccs	99.912	1135	0	1	1	1135	38	1171	0	2089
12_(45)_3	1135	m64198e_210604_164159/71174602/ccs	99.912	1135	0	1	1	1135	7667	8800	0	2089

12_(45)_3	1135	m64198e_210604_164159/34801860/ccs	99.912	1135	0	1	1	1135	4629	3496	0	2089
12_(45)_3	1135	m64196e_210606_053615/103418033/ccs	99.824	1136	0	2	1	1135	6779	5645	0	2085
12_(45)_3	1135	m64198e_210604_164159/134415309/ccs	99.824	1136	0	2	1	1135	7227	8361	0	2085
12_(45)_3	1135	m64196e_210606_053615/170068722/ccs	99.736	1138	0	3	1	1135	12382	13519	0	2082
12_(45)_3	1135	m64198e_210604_164159/125962367/ccs	99.736	1138	0	3	1	1135	2557	3694	0	2082
12_(45)_3	1135	m64198e_210604_164159/64421965/ccs	99.736	1138	0	3	1	1135	11881	10744	0	2082
12_(45)_3	1135	m64196e_210606_053615/168233130/ccs	99.736	1137	0	3	1	1135	9932	11067	0	2080
12_(45)_3	1135	m64196e_210606_053615/121766818/ccs	99.736	1137	0	3	1	1135	5952	4817	0	2080
12_(45)_3	1135	m64196e_210606_053615/112198063/ccs	99.736	1137	0	3	1	1135	7908	6773	0	2080
12_(45)_3	1135	m64198e_210604_164159/112525828/ccs	99.649	1139	0	4	1	1135	699	1837	0	2078
12_(45)_3	1135	m64198e_210604_164159/71239895/ccs	99.649	1138	0	4	1	1135	5650	4514	0	2076
12_(45)_3	1135	m64196e_210606_053615/45679615/ccs	99.648	1137	0	3	1	1135	11628	12762	0	2074
12_(45)_3	1135	m64196e_210606_053615/149029009/ccs	99.383	1135	0	6	1	1135	3457	2330	0	2050
12_(45)_3	1135	m64196e_210606_053615/68682829/ccs	98.954	1147	0	12	1	1135	7133	5987	0	2041
12_(45)_3	1135	m64196e_210606_053615/33489160/ccs	99.91	1109	0	1	27	1135	1	1108	0	2041
12_(45)_13	1135	m64198e_210604_164159/114690884/ccs	99.824	1135	0	2	1	1135	12111	10979	0	2084
4_(47)_5	1132	m64196e_210606_053615/157549741/ccs	100	1132	0	0	1	1132	4452	3321	0	2091
4_(47)_5	1132	m64196e_210606_053615/147260399/ccs	100	1132	0	0	1	1132	12393	13524	0	2091
4_(47)_5	1132	m64196e_210606_053615/137560256/ccs	100	1132	0	0	1	1132	10552	9421	0	2091
4_(47)_5	1132	m64196e_210606_053615/135987378/ccs	100	1132	0	0	1	1132	9756	10887	0	2091
4_(47)_5	1132	m64196e_210606_053615/115935396/ccs	100	1132	0	0	1	1132	10833	9702	0	2091
4_(47)_5	1132	m64196e_210606_053615/99354429/ccs	100	1132	0	0	1	1132	2145	1014	0	2091
4_(47)_5	1132	m64196e_210606_053615/96141790/ccs	100	1132	0	0	1	1132	9367	8236	0	2091
4_(47)_5	1132	m64196e_210606_053615/90704164/ccs	100	1132	0	0	1	1132	13900	12769	0	2091
4_(47)_5	1132	m64196e_210606_053615/77138567/ccs	100	1132	0	0	1	1132	4808	5939	0	2091

4_(47)_5	1132	m64196e_210606_053615/76219851/ccs	100	1132	0	0	1	1132	13666	12535	0	2091
4_(47)_5	1132	m64196e_210606_053615/17564529/ccs	100	1132	0	0	1	1132	8918	10049	0	2091
4_(47)_5	1132	m64196e_210606_053615/459770/ccs	100	1132	0	0	1	1132	9041	10172	0	2091
4_(47)_5	1132	m64198e_210604_164159/165086145/ccs	100	1132	0	0	1	1132	7306	6175	0	2091
4_(47)_5	1132	m64198e_210604_164159/161743238/ccs	100	1132	0	0	1	1132	1676	545	0	2091
4_(47)_5	1132	m64198e_210604_164159/135268945/ccs	100	1132	0	0	1	1132	5202	6333	0	2091
4_(47)_5	1132	m64198e_210604_164159/77203111/ccs	100	1132	0	0	1	1132	11110	9979	0	2091
4_(47)_5	1132	m64198e_210604_164159/69471048/ccs	100	1132	0	0	1	1132	3824	2693	0	2091
4_(47)_5	1132	m64198e_210604_164159/56295987/ccs	100	1132	0	0	1	1132	7808	8939	0	2091
4_(47)_5	1132	m64198e_210604_164159/43189199/ccs	100	1132	0	0	1	1132	4261	3130	0	2091
4_(47)_5	1132	m64198e_210604_164159/9437630/ccs	100	1132	0	0	1	1132	7004	8135	0	2091
4_(47)_5	1132	m64196e_210606_053615/109970499/ccs	99.912	1133	0	1	1	1132	14450	13318	0	2085
4_(47)_5	1132	m64196e_210606_053615/70649219/ccs	99.912	1133	0	1	1	1132	10955	9823	0	2085
4_(47)_5	1132	m64196e_210606_053615/57476323/ccs	99.912	1133	0	1	1	1132	4167	3035	0	2085
4_(47)_5	1132	m64196e_210606_053615/29557122/ccs	99.912	1133	0	1	1	1132	3213	2081	0	2085
4_(47)_5	1132	m64198e_210604_164159/162201940/ccs	99.912	1133	0	1	1	1132	6062	7194	0	2085
4_(47)_5	1132	m64198e_210604_164159/93783397/ccs	99.912	1133	0	1	1	1132	8760	7628	0	2085
4_(47)_5	1132	m64198e_210604_164159/50659414/ccs	99.912	1133	0	1	1	1132	14276	13144	0	2085
4_(47)_5	1132	m64198e_210604_164159/43125026/ccs	99.912	1133	0	1	1	1132	8235	9367	0	2085
4_(47)_5	1132	m64198e_210604_164159/32769550/ccs	99.912	1133	0	1	1	1132	5372	6504	0	2085
4_(47)_5	1132	m64196e_210606_053615/49219513/ccs	99.912	1132	0	1	1	1132	12779	11649	0	2084
4_(47)_5	1132	m64196e_210606_053615/12192123/ccs	99.912	1132	0	1	1	1132	2846	3976	0	2084
4_(47)_5	1132	m64198e_210604_164159/160890992/ccs	99.912	1132	0	1	1	1132	19031	17901	0	2084
4_(47)_5	1132	m64198e_210604_164159/23135579/ccs	99.912	1132	0	1	1	1132	8906	7776	0	2084
4_(47)_5	1132	m64196e_210606_053615/160500546/ccs	99.824	1134	0	2	1	1132	12780	11647	0	2082

4_(47)_5	1132	m64196e_210606_053615/2688251/ccs	99.824	1134	0	2	1	1132	9263	8130	0	2082
4_(47)_5	1132	m64198e_210604_164159/86312640/ccs	99.824	1134	0	2	1	1132	9988	8855	0	2082
4_(47)_5	1132	m64198e_210604_164159/28967841/ccs	99.824	1134	0	2	1	1132	9645	10778	0	2082
4_(47)_5	1132	m64196e_210606_053615/173146218/ccs	99.823	1133	0	2	1	1132	6991	8122	0	2080
4_(47)_5	1132	m64196e_210606_053615/144640565/ccs	99.823	1132	2	0	1	1132	10517	11648	0	2080
4_(47)_5	1132	m64196e_210606_053615/139003365/ccs	99.823	1133	0	2	1	1132	1318	2449	0	2080
4_(47)_5	1132	m64196e_210606_053615/48958105/ccs	99.823	1132	2	0	1	1132	10938	12069	0	2080
4_(47)_5	1132	m64198e_210604_164159/157354289/ccs	99.823	1132	2	0	1	1132	14373	13242	0	2080
4_(47)_5	1132	m64196e_210606_053615/92080280/ccs	99.823	1132	0	2	1	1132	10835	11964	0	2078
4_(47)_5	1132	m64196e_210606_053615/43582480/ccs	99.823	1132	0	2	1	1132	4509	3380	0	2078
4_(47)_5	1132	m64196e_210606_053615/101254517/ccs	99.736	1135	0	3	1	1132	4719	5853	0	2076
4_(47)_5	1132	m64196e_210606_053615/37356865/ccs	99.911	1128	0	1	5	1132	1	1127	0	2076
4_(47)_5	1132	m64196e_210606_053615/156696682/ccs	99.735	1133	2	1	1	1132	9376	8244	0	2074
4_(47)_5	1132	m64196e_210606_053615/146539901/ccs	99.735	1133	2	1	1	1132	14996	13864	0	2074
4_(47)_5	1132	m64196e_210606_053615/64815883/ccs	99.735	1134	0	3	1	1132	7085	5953	0	2074
4_(47)_5	1132	m64196e_210606_053615/8587174/ccs	99.735	1133	2	1	1	1132	12589	11457	0	2074
4_(47)_5	1132	m64196e_210606_053615/177997593/ccs	99.735	1133	0	3	1	1132	11697	12827	0	2073
4_(47)_5	1132	m64196e_210606_053615/90112787/ccs	99.648	1135	0	4	1	1132	12171	13304	0	2071
4_(47)_5	1132	m64198e_210604_164159/176293865/ccs	99.735	1132	0	3	1	1132	13455	14583	0	2071
4_(47)_5	1132	m64198e_210604_164159/99878747/ccs	99.648	1135	1	3	1	1132	6555	5421	0	2071
4_(47)_5	1132	m64196e_210606_053615/68878824/ccs	99.647	1134	0	4	1	1131	12978	14110	0	2069
4_(47)_5	1132	m64198e_210604_164159/125108470/ccs	99.647	1134	0	4	1	1132	15843	14712	0	2069
4_(47)_5	1132	m64198e_210604_164159/175702403/ccs	99.559	1135	2	3	1	1132	8204	7070	0	2065
4_(47)_5	1132	m64198e_210604_164159/110495382/ccs	99.559	1135	0	5	1	1132	4516	3384	0	2063
4_(47)_5	1132	m64196e_210606_053615/16384663/ccs	99.472	1137	0	6	1	1132	15080	16215	0	2061

4_(47)_5	1132	m64198e_210604_164159/22021958/ccs	99.382	1133	4	3	1	1132	2370	1240	0	2050
4_(47)_5	1132	m64196e_210606_053615/137954358/ccs	99.296	1137	0	8	1	1132	12882	11749	0	2049
4_(47)_5	1132	m64198e_210604_164159/97127016/ccs	99.382	1132	2	5	1	1132	8625	9751	0	2047
4_(47)_5	1132	m64198e_210604_164159/27855579/ccs	99.295	1135	2	6	1	1132	7992	9123	0	2047
4_(47)_5	1132	m64196e_210606_053615/101580999/ccs	99.208	1137	1	8	1	1132	313	1446	0	2043
4_(47)_5	1132	m64198e_210604_164159/146997272/ccs	98.946	1139	2	9	1	1132	7824	8959	0	2028
4_(47)_5	1132	m64198e_210604_164159/122356559/ccs	98.858	1138	1	12	1	1132	1636	2767	0	2019
4_(47)_5	1132	m64198e_210604_164159/82512092/ccs	98.368	1103	2	14	1	1087	17019	18121	0	1923
4_(47)_5	1132	m64196e_210606_053615/24905569/ccs	96.752	1170	0	37	1	1132	14380	13211	0	1916
2_(47)_9	1132	m64196e_210606_053615/158335768/ccs	100	1132	0	0	1	1132	4231	5362	0	2091
2_(47)_9	1132	m64196e_210606_053615/128911629/ccs	100	1132	0	0	1	1132	1854	723	0	2091
2_(47)_9	1132	m64196e_210606_053615/92014713/ccs	100	1132	0	0	1	1132	1449	318	0	2091
2_(47)_9	1132	m64196e_210606_053615/88605097/ccs	100	1132	0	0	1	1132	9781	10912	0	2091
2_(47)_9	1132	m64196e_210606_053615/82903987/ccs	100	1132	0	0	1	1132	4357	3226	0	2091
2_(47)_9	1132	m64196e_210606_053615/16516866/ccs	100	1132	0	0	1	1132	7932	9063	0	2091
2_(47)_9	1132	m64196e_210606_053615/3410771/ccs	100	1132	0	0	1	1132	1354	223	0	2091
2_(47)_9	1132	m64198e_210604_164159/175506471/ccs	100	1132	0	0	1	1132	10064	11195	0	2091
2_(47)_9	1132	m64198e_210604_164159/163447787/ccs	100	1132	0	0	1	1132	12057	13188	0	2091
2_(47)_9	1132	m64198e_210604_164159/156306188/ccs	100	1132	0	0	1	1132	10752	11883	0	2091
2_(47)_9	1132	m64198e_210604_164159/137037961/ccs	100	1132	0	0	1	1132	9857	8726	0	2091
2_(47)_9	1132	m64198e_210604_164159/135528947/ccs	100	1132	0	0	1	1132	4521	5652	0	2091
2_(47)_9	1132	m64198e_210604_164159/131467056/ccs	100	1132	0	0	1	1132	10877	9746	0	2091
2_(47)_9	1132	m64198e_210604_164159/86575291/ccs	100	1132	0	0	1	1132	12515	13646	0	2091
2_(47)_9	1132	m64198e_210604_164159/68815528/ccs	100	1132	0	0	1	1132	11220	10089	0	2091
2_(47)_9	1132	m64198e_210604_164159/68616777/ccs	100	1132	0	0	1	1132	10706	11837	0	2091

2_(47)_9	1132	m64198e_210604_164159/54984913/ccs	100	1132	0	0	1	1132	3447	4578	0	2091
2_(47)_9	1132	m64198e_210604_164159/50465061/ccs	100	1132	0	0	1	1132	8798	9929	0	2091
2_(47)_9	1132	m64196e_210606_053615/34998204/ccs	99.912	1133	0	1	1	1132	7946	6814	0	2085
2_(47)_9	1132	m64198e_210604_164159/133170230/ccs	99.912	1133	0	1	1	1132	1521	389	0	2085
2_(47)_9	1132	m64196e_210606_053615/162792196/ccs	99.912	1132	0	1	1	1132	2079	949	0	2084
2_(47)_9	1132	m64198e_210604_164159/68288647/ccs	99.912	1132	0	1	1	1132	14439	15569	0	2084
2_(47)_9	1132	m64198e_210604_164159/19137941/ccs	99.912	1132	0	1	1	1132	8234	9364	0	2084
2_(47)_9	1132	m64198e_210604_164159/25692451/ccs	99.824	1134	0	2	1	1132	2815	1682	0	2082
2_(47)_9	1132	m64198e_210604_164159/44499725/ccs	99.823	1133	0	2	1	1132	10736	9605	0	2080
2_(47)_9	1132	m64198e_210604_164159/21497295/ccs	99.823	1133	0	2	1	1132	6200	5069	0	2080
2_(47)_9	1132	m64196e_210606_053615/17500201/ccs	99.823	1132	0	2	1	1132	13321	12192	0	2078
2_(47)_9	1132	m64196e_210606_053615/124715100/ccs	99.735	1133	0	3	1	1132	11703	12833	0	2073
2_(47)_9	1132	m64196e_210606_053615/65340591/ccs	99.648	1136	0	4	1	1132	12207	11072	0	2073
2_(47)_9	1132	m64196e_210606_053615/50857515/ccs	99.648	1135	0	4	1	1132	7819	6686	0	2071
2_(47)_9	1132	m64198e_210604_164159/148243803/ccs	99.648	1135	0	4	1	1132	8865	7732	0	2071
2_(47)_9	1132	m64198e_210604_164159/79364413/ccs	99.647	1134	0	4	1	1132	1360	229	0	2069
2_(47)_9	1132	m64196e_210606_053615/141557796/ccs	99.384	1136	0	6	1	1132	4528	5660	0	2052
2_(47)_9	1132	m64198e_210604_164159/37421888/ccs	99.119	1135	0	10	1	1132	7058	8185	0	2032
2_(47)_9	1132	m64198e_210604_164159/144638676/ccs	96.643	1132	38	0	1	1132	5895	7026	0	1881
2_(47)_9	1132	m64198e_210604_164159/144574405/ccs	96.643	1132	38	0	1	1132	6743	7874	0	1881
12_(48)_(-6)	1100	m64196e_210606_053615/155976263/ccs	100	1100	0	0	1	1100	6257	7356	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/143066932/ccs	100	1100	0	0	1	1100	300	1399	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/138545139/ccs	100	1100	0	0	1	1100	13406	12307	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/123799387/ccs	100	1100	0	0	1	1100	7977	6878	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/104925586/ccs	100	1100	0	0	1	1100	322	1421	0	2032

12_(48)_(-6)	1100	m64196e_210606_053615/87753232/ccs	100	1100	0	0	1	1100	2948	4047	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/50135155/ccs	100	1100	0	0	1	1100	9171	10270	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/31786098/ccs	100	1100	0	0	1	1100	7981	9080	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/10095092/ccs	100	1100	0	0	1	1100	9638	10737	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/124520572/ccs	100	1100	0	0	1	1100	13369	12270	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/124387751/ccs	100	1100	0	0	1	1100	7535	6436	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/106759293/ccs	100	1100	0	0	1	1100	5960	4861	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/89260464/ccs	100	1100	0	0	1	1100	11210	12309	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/86901158/ccs	100	1100	0	0	1	1100	6913	8012	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/78973503/ccs	100	1100	0	0	1	1100	11746	10647	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/63505126/ccs	100	1100	0	0	1	1100	15104	16203	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/56033281/ccs	100	1100	0	0	1	1100	8667	7568	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/47579872/ccs	100	1100	0	0	1	1100	2866	3965	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/43714468/ccs	100	1100	0	0	1	1100	5929	4830	0	2032
12_(48)_(-6)	1100	m64198e_210604_164159/15794803/ccs	100	1100	0	0	1	1100	4295	5394	0	2032
12_(48)_(-6)	1100	m64196e_210606_053615/155913026/ccs	99.909	1100	1	0	1	1100	13835	12736	0	2026
12_(48)_(-6)	1100	m64198e_210604_164159/81003454/ccs	99.909	1101	0	1	1	1100	9295	10395	0	2026
12_(48)_(-6)	1100	m64196e_210606_053615/17500578/ccs	99.909	1100	0	1	1	1100	5026	3928	0	2025
12_(48)_(-6)	1100	m64196e_210606_053615/17433037/ccs	99.909	1100	0	1	1	1100	2753	3851	0	2025
12_(48)_(-6)	1100	m64198e_210604_164159/18547866/ccs	99.909	1100	0	1	1	1100	11922	10824	0	2025
12_(48)_(-6)	1100	m64196e_210606_053615/78971663/ccs	99.819	1102	0	2	1	1100	2003	902	0	2023
12_(48)_(-6)	1100	m64198e_210604_164159/126354224/ccs	99.819	1102	0	2	1	1100	12726	13827	0	2023
12_(48)_(-6)	1100	m64198e_210604_164159/173999752/ccs	99.818	1101	0	2	1	1100	3042	4141	0	2021
12_(48)_(-6)	1100	m64198e_210604_164159/125503977/ccs	99.818	1101	0	2	1	1100	11182	12281	0	2021
12_(48)_(-6)	1100	m64198e_210604_164159/5310040/ccs	99.818	1101	0	2	1	1100	4373	3274	0	2021

12_(48)_(-6)	1100	m64198e_210604_164159/115474503/ccs	99.818	1100	0	2	1	1100	7818	8915	0	2019
12_(48)_(-6)	1100	m64196e_210606_053615/105776281/ccs	99.728	1103	0	2	1	1100	10669	11771	0	2017
12_(48)_(-6)	1100	m64196e_210606_053615/172427839/ccs	99.728	1101	0	3	1	1100	5091	6189	0	2013
12_(48)_(-6)	1100	m64196e_210606_053615/143720551/ccs	99.728	1101	0	3	1	1100	8153	9251	0	2013
12_(48)_(-6)	1100	m64198e_210604_164159/94898360/ccs	99.728	1101	0	3	1	1100	551	1649	0	2013
12_(48)_(-6)	1100	m64198e_210604_164159/114294804/ccs	99.637	1103	0	2	1	1100	4661	5762	0	2012
12_(48)_(-6)	1100	m64196e_210606_053615/149029009/ccs	99.637	1102	0	4	1	1100	14812	15911	0	2010
12_(48)_(-6)	1100	m64198e_210604_164159/71893183/ccs	99.637	1101	0	4	1	1100	13405	12308	0	2008
12_(48)_(-6)	1100	m64198e_210604_164159/78252806/ccs	99.546	1101	0	5	1	1100	12154	11058	0	2001
12_(48)_(-6)	1100	m64196e_210606_053615/161481232/ccs	99.188	1108	0	9	1	1100	2681	1575	0	1988
12_(48)_(-6)	1100	m64198e_210604_164159/113445713/ccs	99.187	1107	2	6	1	1100	4281	3175	0	1988
12_(48)_(-6)	1100	m64198e_210604_164159/46137822/ccs	99.097	1108	1	9	1	1100	10088	8982	0	1982
12_(48)_(-6)	1100	m64198e_210604_164159/61670922/ccs	99.095	1105	0	10	1	1100	3315	4414	0	1977
12_(48)_(-6)	1100	m64198e_210604_164159/147393168/ccs	99.093	1103	2	8	1	1100	8973	7876	0	1975
12_(48)_(-6)	1100	m64198e_210604_164159/114819579/ccs	99.094	1104	1	9	1	1100	6660	5562	0	1975
12_(48)_(-6)	1100	m64198e_210604_164159/153094652/ccs	98.914	1105	1	11	1	1100	4273	3175	0	1964
44_(48)_(+6)	1100	m64196e_210606_053615/117114124/ccs	100	1100	0	0	1	1100	8967	10066	0	2032
44_(48)_(+6)	1100	m64196e_210606_053615/67568997/ccs	100	1100	0	0	1	1100	10070	8971	0	2032
44_(48)_(+6)	1100	m64196e_210606_053615/66127953/ccs	100	1100	0	0	1	1100	8595	7496	0	2032
44_(48)_(+6)	1100	m64196e_210606_053615/25755652/ccs	100	1100	0	0	1	1100	9297	10396	0	2032
44_(48)_(+6)	1100	m64196e_210606_053615/21563064/ccs	100	1100	0	0	1	1100	4025	2926	0	2032
44_(48)_(+6)	1100	m64196e_210606_053615/6425095/ccs	100	1100	0	0	1	1100	12084	10985	0	2032
44_(48)_(+6)	1100	m64198e_210604_164159/130025879/ccs	100	1100	0	0	1	1100	980	2079	0	2032
44_(48)_(+6)	1100	m64198e_210604_164159/31981641/ccs	100	1100	0	0	1	1100	12017	10918	0	2032
44_(48)_(+6)	1100	m64198e_210604_164159/984146/ccs	100	1100	0	0	1	1100	7485	6386	0	2032

44_(48)_(+6)	1100	m64196e_210606_053615/115018540/ccs	99.909	1101	0	1	1	1100	12269	11169	0	2026
44_(48)_(+6)	1100	m64196e_210606_053615/73007997/ccs	99.909	1101	0	1	1	1100	1542	2642	0	2026
44_(48)_(+6)	1100	m64198e_210604_164159/172754514/ccs	99.909	1101	0	1	1	1100	9743	8643	0	2026
44_(48)_(+6)	1100	m64198e_210604_164159/136840791/ccs	99.909	1101	0	1	1	1100	9224	10324	0	2026
44_(48)_(+6)	1100	m64198e_210604_164159/37488937/ccs	99.909	1101	0	1	1	1100	11447	12547	0	2026
44_(48)_(+6)	1100	m64198e_210604_164159/163315883/ccs	99.909	1100	0	1	1	1100	9421	10519	0	2025
44_(48)_(+6)	1100	m64198e_210604_164159/134023375/ccs	99.909	1100	0	1	1	1100	8835	9933	0	2025
44_(48)_(+6)	1100	m64196e_210606_053615/173606627/ccs	99.819	1102	0	2	1	1100	7716	6615	0	2023
44_(48)_(+6)	1100	m64196e_210606_053615/87688399/ccs	99.819	1102	0	2	1	1100	7186	6085	0	2023
44_(48)_(+6)	1100	m64198e_210604_164159/45088926/ccs	99.819	1102	0	2	1	1100	48	1149	0	2023
44_(48)_(+6)	1100	m64198e_210604_164159/13043557/ccs	99.819	1102	0	2	1	1100	6661	7762	0	2023
44_(48)_(+6)	1100	m64198e_210604_164159/133038789/ccs	99.818	1101	0	2	1	1100	12128	13227	0	2021
44_(48)_(+6)	1100	m64198e_210604_164159/43977142/ccs	99.818	1101	0	2	1	1100	10	1109	0	2021
44_(48)_(+6)	1100	m64196e_210606_053615/143197999/ccs	99.818	1100	0	2	1	1100	6654	7751	0	2019
44_(48)_(+6)	1100	m64198e_210604_164159/41287975/ccs	99.818	1100	0	2	1	1100	4485	5582	0	2019
44_(48)_(+6)	1100	m64196e_210606_053615/61868157/ccs	99.728	1103	0	3	1	1100	12432	11330	0	2017
44_(48)_(+6)	1100	m64198e_210604_164159/29818887/ccs	99.728	1102	1	2	1	1100	12959	11858	0	2017
44_(48)_(+6)	1100	m64196e_210606_053615/2032866/ccs	99.728	1102	0	3	1	1100	2824	1724	0	2015
44_(48)_(+6)	1100	m64196e_210606_053615/109512519/ccs	99.728	1101	0	3	1	1100	13091	14189	0	2013
44_(48)_(+6)	1100	m64198e_210604_164159/6029350/ccs	99.728	1101	0	3	1	1100	10896	11994	0	2013
44_(48)_(+6)	1100	m64196e_210606_053615/62194227/ccs	99.636	1100	0	4	1	1100	13758	12663	0	2006
44_(48)_(+6)	1100	m64196e_210606_053615/111151897/ccs	99.546	1102	0	5	1	1100	3993	2895	0	2002
44_(48)_(+6)	1100	m64198e_210604_164159/150930501/ccs	99.546	1102	0	5	1	1100	10114	9016	0	2002
44_(48)_(+6)	1100	m64198e_210604_164159/100338251/ccs	99.456	1103	1	5	1	1100	16388	17488	0	1999
44_(48)_(+6)	1100	m64198e_210604_164159/175571692/ccs	99.455	1101	0	6	1	1100	2998	4093	0	1995

44_(48)_(+6)	1100	m64198e_210604_164159/176685980/ccs	99.275	1104	0	8	1	1100	11270	10171	0	1988
44_(48)_(+6)	1100	m64196e_210606_053615/85525462/ccs	99.187	1107	0	9	1	1100	4589	5693	0	1986
44_(48)_(+6)	1100	m64196e_210606_053615/157024504/ccs	99.185	1104	2	7	1	1100	14438	13338	0	1982
44_(48)_(+6)	1100	m64196e_210606_053615/32638013/ccs	99.183	1102	0	9	1	1100	524	1618	0	1977
44_(48)_(+6)	1100	m64198e_210604_164159/106628567/ccs	99.005	1105	1	10	1	1100	1224	125	0	1971
44_(48)_(+6)	1100	m64198e_210604_164159/48826536/ccs	98.826	1107	0	12	1	1100	15411	14311	0	1960
44_(48)_(+6)	1100	m64196e_210606_053615/139003203/ccs	98.373	1106	0	18	1	1100	2670	1577	0	1927
12_(48)_(+6)	1100	m64196e_210606_053615/106890675/ccs	98.913	1104	2	9	1	1100	10801	9704	0	1964

Table S12. Potential paths and the number of long-reads.

Paths	Number of supported long reads
1_(14_22_7)_10	0
1_(14_22_7)_3	0
9_(14_22_7)_10	0
9_(14_22_7)_3	0
10_(28)_11	1
10_(28)_4	56
8_(28)_11	54
8_(28)_4	0
48_(44)_2	1
48_(44)_11	39
8_(44)_11	0
8_(44)_2	40
12_(45)_13	1
12_(45)_3	43
5_(45)_13	28
5_(45)_3	0
2_(47)_5	0
2_(47)_9	36
4_(47)_5	68
4_(47)_9	0
12_(48)_(+6)	1
12_(48)_(−6)	46
44_(48)_(+6)	41
44_(48)_(−6)	0

Table S13. RNA-editing in *M. elegans* mitogenome.

Gene	Nt Pos	AA Pos	Align Col	Effect	Score	Editing Type
atp1	1168	390	392	CGC (R) => TGC (C)	1	C=>T
atp1	1292	431	433	CCG (P) => CTG (L)	0.8	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	89	30	34	TCA (S) => TTA (L)	1	C=>T
atp4	118	40	44	CGT (R) => TGT (C)	0.71	C=>T
atp4	215	72	76	TCG (S) => TTG (L)	1	C=>T
atp4	226	76	80	CCC (P) => TTC (F)	0.57	C=>T
atp4	227	76	80	CCC (P) => TTC (F)	0.57	C=>T
atp4	248	83	87	CCT (P) => CTT (L)	1	C=>T
atp4	251	84	88	CCG (P) => CTG (L)	0.43	C=>T
atp4	395	132	140	TCA (S) => TTA (L)	1	C=>T
atp4	407	136	144	CCA (P) => CTA (L)	0.71	C=>T
atp4	416	139	147	ACT (T) => ATT (I)	0.86	C=>T
atp4	490	164	172	CCC (P) => TCC (S)	0.57	C=>T
atp6	334	112	113	CCA (P) => TCA (S)	0.75	C=>T
atp6	379	127	128	CTT (L) => TTT (F)	0.25	C=>T
atp6	413	138	139	TCA (S) => TTA (L)	1	C=>T
atp6	470	157	158	TCG (S) => TTG (L)	1	C=>T
atp6	521	174	175	TCC (S) => TTC (F)	1	C=>T
atp6	559	187	188	CGT (R) => TGT (C)	1	C=>T
atp6	698	233	234	TCA (S) => TTA (L)	1	C=>T
atp6	757	253	254	CCT (P) => TCT (S)	1	C=>T
atp6	760	254	255	CAT (H) => TAT (Y)	1	C=>T
atp6	782	261	262	TCA (S) => TTA (L)	1	C=>T
atp6	824	275	276	TCA (S) => TTA (L)	1	C=>T
atp6	896	299	300	CCT (P) => CTT (L)	0.92	C=>T
atp6	961	321	322	CAT (H) => TAT (Y)	1	C=>T
atp6	977	326	327	TCA (S) => TTA (L)	1	C=>T
atp6	1015	339	340	CAA (Q) => TAA (X)	1	C=>T
atp8	47	16	16	TCA (S) => TTA (L)	1	C=>T
atp9	20	7	7	TCA (S) => TTA (L)	1	C=>T
atp9	82	28	28	CTT (L) => TTT (F)	1	C=>T
ccmB	28	10	10	CAT (H) => TAT (Y)	0.89	C=>T
ccmB	71	24	26	TCA (S) => TTA (L)	1	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	154	52	54	CGG (R) => TGG (W)	1	C=>T
ccmB	160	54	56	CCT (P) => TCT (S)	0.67	C=>T
ccmB	164	55	57	CCG (P) => CTG (L)	0.89	C=>T

ccmB	172	58	60	CCT (P) => TCT (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	367	123	129	CGG (R) => TGG (W)	0.78	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	485	162	170	TCA (S) => TTA (L)	1	C=>T
ccmB	494	165	173	TCA (S) => TTA (L)	1	C=>T
ccmB	503	168	176	TCA (S) => TTA (L)	1	C=>T
ccmB	512	171	179	TCT (S) => TTT (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	596	199	207	TCG (S) => TTG (L)	0.89	C=>T
ccmB	611	204	212	TCA (S) => TTA (L)	0.89	C=>T
ccmC	103	35	41	CAT (H) => TAT (Y)	1	C=>T
ccmC	184	62	68	CGG (R) => TGG (W)	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	395	132	138	TCG (S) => TTG (L)	1	C=>T
ccmC	400	134	140	CTT (L) => TTT (F)	0.89	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	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	605	202	208	TCC (S) => TTC (F)	1	C=>T
ccmC	614	205	211	TCA (S) => TTA (L)	0.78	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	CCT (P) => TCT (S)	0.78	C=>T
ccmFc	38	13	13	TCC (S) => TTC (F)	0.83	C=>T
ccmFc	50	17	17	CCT (P) => CTT (L)	1	C=>T
ccmFc	103	35	35	CCC (P) => TCC (S)	1	C=>T
ccmFc	122	41	41	TCC (S) => TTC (F)	1	C=>T
ccmFc	151	51	51	CCT (P) => TCT (S)	0.83	C=>T
ccmFc	155	52	52	TCA (S) => TTA (L)	1	C=>T
ccmFc	310	104	104	CGT (R) => TGT (C)	0.5	C=>T
ccmFc	391	131	131	CGT (R) => TGT (C)	1	C=>T
ccmFc	406	136	136	CGT (R) => TGT (C)	0.83	C=>T
ccmFc	977	326	330	TCA (S) => TTA (L)	0.33	C=>T
ccmFc	1139	380	387	CCA (P) => CTA (L)	1	C=>T
ccmFc	1160	387	394	TCG (S) => TTG (L)	1	C=>T
ccmFc	1234	412	419	CGG (R) => TGG (W)	1	C=>T
ccmFc	1315	439	446	CGA (R) => TGA (X)	1	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	151	51	53	CCT (P) => TCT (S)	0.83	C=>T
ccmFn	263	88	90	CCA (P) => CTA (L)	0.83	C=>T
ccmFn	283	95	97	CTT (L) => TTT (F)	0.83	C=>T
ccmFn	334	112	114	CAT (H) => TAT (Y)	0.67	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	565	189	191	CTT (L) => TTT (F)	0.5	C=>T
ccmFn	712	238	240	CCT (P) => TTT (F)	0.67	C=>T
ccmFn	713	238	240	CCT (P) => TTT (F)	0.67	C=>T
ccmFn	722	241	243	TCA (S) => TTA (L)	0.83	C=>T
ccmFn	760	254	256	CGT (R) => TGT (C)	1	C=>T
ccmFn	782	261	263	TCA (S) => TTA (L)	1	C=>T
ccmFn	794	265	267	CCA (P) => CTA (L)	1	C=>T
ccmFn	809	270	272	TCA (S) => TTA (L)	1	C=>T
ccmFn	1276	426	446	CGG (R) => TGG (W)	1	C=>T
ccmFn	1304	435	455	CCA (P) => CTA (L)	1	C=>T
ccmFn	1321	441	461	CAT (H) => TAT (Y)	1	C=>T
ccmFn	1336	446	466	CGG (R) => TGG (W)	1	C=>T
ccmFn	1354	452	472	CGG (R) => TGG (W)	1	C=>T
ccmFn	1387	463	483	CGG (R) => TGG (W)	1	C=>T
ccmFn	1493	498	518	TCT (S) => TTT (F)	1	C=>T
ccmFn	1519	507	527	CCC (P) => TCC (S)	1	C=>T
ccmFn	1567	523	543	CGG (R) => TGG (W)	0.67	C=>T
cob	140	47	48	GCC (A) => GTC (V)	0.92	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	568	190	191	CAT (H) => TAT (Y)	0.92	C=>T
cob	680	227	228	TCT (S) => TTT (F)	1	C=>T
cob	908	303	304	CCA (P) => CTA (L)	1	C=>T
cob	1049	350	351	GCG (A) => GTG (V)	1	C=>T
cob	1081	361	362	CCT (P) => TCT (S)	0.77	C=>T
cox2	71	24	26	TCT (S) => TTT (F)	1	C=>T
cox2	161	54	56	TCA (S) => TTA (L)	0.95	C=>T
cox2	253	85	87	CGG (R) => TGG (W)	1	C=>T
cox2	379	127	129	CGG (R) => TGG (W)	1	C=>T
cox2	443	148	150	ACG (T) => ATG (M)	1	C=>T
cox2	461	154	156	CCA (P) => CTA (L)	1	C=>T
cox2	476	159	161	TCA (S) => TTA (L)	1	C=>T
cox2	557	186	188	CCT (P) => CTT (L)	1	C=>T
cox2	581	194	196	TCA (S) => TTA (L)	1	C=>T
cox2	676	226	228	CGT (R) => TGT (C)	1	C=>T
cox2	742	248	250	CGG (R) => TGG (W)	1	C=>T
cox3	298	100	101	CTT (L) => TTT (F)	1	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
matR	26	9	29	CCC (P) => CTC (L)	1	C=>T
matR	32	11	31	TCC (S) => TTC (F)	0.62	C=>T
matR	127	43	63	CCT (P) => TCT (S)	1	C=>T
matR	326	109	129	CCA (P) => CTA (L)	1	C=>T
matR	1187	396	421	ACC (T) => ATC (I)	1	C=>T
matR	1448	483	511	GCC (A) => GTC (V)	0.62	C=>T
matR	1541	514	542	TCC (S) => TTC (F)	1	C=>T
matR	1679	560	588	TCC (S) => TTC (F)	1	C=>T
matR	1700	567	595	CCT (P) => CTT (L)	1	C=>T
matR	1756	586	614	CAC (H) => TAC (Y)	1	C=>T
mttB	37	13	18	CGG (R) => TGG (W)	0.88	C=>T
mttB	73	25	30	CGT (R) => TGT (C)	0.88	C=>T
mttB	85	29	34	CCG (P) => TCG (S)	1	C=>T
mttB	104	35	40	CCA (P) => CTA (L)	1	C=>T
mttB	151	51	58	CGT (R) => TGT (C)	1	C=>T
mttB	161	54	61	TCA (S) => TTA (L)	0.75	C=>T
mttB	235	79	86	CAT (H) => TAT (Y)	1	C=>T
mttB	304	102	109	CAT (H) => TAT (Y)	0.62	C=>T
mttB	319	107	114	CGC (R) => TGC (C)	0.88	C=>T
mttB	352	118	125	CGG (R) => TGG (W)	0.62	C=>T
mttB	380	127	134	CCA (P) => CTA (L)	0.75	C=>T

mttB	410	137	144	TCG (S) => TTG (L)	0.57	C=>T
mttB	445	149	156	CAT (H) => TAT (Y)	0.88	C=>T
mttB	470	157	164	TCG (S) => TTG (L)	0.88	C=>T
mttB	514	172	179	CGT (R) => TGT (C)	0.88	C=>T
mttB	521	174	181	CCA (P) => CTA (L)	0.62	C=>T
mttB	527	176	183	CCA (P) => CTA (L)	0.5	C=>T
mttB	583	195	202	CCG (P) => TCG (S)	1	C=>T
mttB	640	214	221	CGT (R) => TGT (C)	0.62	C=>T
mttB	686	229	236	TCG (S) => TTG (L)	0.75	C=>T
mttB	743	248	255	ACT (T) => ATT (I)	0.67	C=>T
nad1	2	1	4	ACG (T) => ATG (M)	0.8	C=>T
nad1	215	72	75	TCC (S) => TTC (F)	0.9	C=>T
nad1	265	89	92	CGG (R) => TGG (W)	1	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	CCT (P) => TCT (S)	1	C=>T
nad1	493	165	168	CGT (R) => TGT (C)	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	674	225	228	TCT (S) => TTT (F)	0.9	C=>T
nad1	734	245	248	TCG (S) => TTG (L)	0.9	C=>T
nad1	740	247	250	TCT (S) => TTT (F)	1	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	830	277	280	CCG (P) => CTG (L)	1	C=>T
nad1	898	300	303	CGG (R) => TGG (W)	1	C=>T
nad1	928	310	313	CGG (R) => TGG (W)	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	356	119	120	TCA (S) => TTA (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	394	132	133	CAT (H) => TAT (Y)	1	C=>T
nad2	401	134	135	TCA (S) => TTA (L)	1	C=>T
nad2	428	143	144	CCT (P) => CTT (L)	1	C=>T
nad2	497	166	167	TCG (S) => TTG (L)	1	C=>T
nad2	788	263	267	TCT (S) => TTT (F)	0.67	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	TCA (S) => TTA (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	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	TCA (S) => TTA (L)	1	C=>T
nad3	146	49	50	TCC (S) => TTC (F)	1	C=>T
nad3	208	70	71	CTT (L) => TTT (F)	0.95	C=>T
nad3	266	89	90	CCG (P) => CTG (L)	1	C=>T
nad3	275	92	93	TCT (S) => TTT (F)	1	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	29	10	10	TCT (S) => TTT (F)	0.67	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	107	36	36	TCG (S) => TTG (L)	1	C=>T
nad4	158	53	53	CCT (P) => CTT (L)	1	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	362	121	121	ACA (T) => ATA (I)	0.89	C=>T
nad4	368	123	123	TCT (S) => TTT (F)	1	C=>T
nad4	376	126	126	CGT (R) => TGT (C)	0.78	C=>T
nad4	433	145	145	CTT (L) => TTT (F)	1	C=>T
nad4	436	146	146	CCC (P) => TTC (F)	0.89	C=>T
nad4	437	146	146	CCC (P) => 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	608	203	203	TCA (S) => TTA (L)	1	C=>T
nad4	836	279	279	TCC (S) => TTC (F)	1	C=>T
nad4	887	296	296	TCG (S) => TTG (L)	1	C=>T
nad4	896	299	299	TCA (S) => TTA (L)	0.89	C=>T
nad4	977	326	326	CCG (P) => CTG (L)	0.78	C=>T
nad4	1010	337	337	CCG (P) => CTG (L)	1	C=>T
nad4	1016	339	339	TCA (S) => TTA (L)	1	C=>T
nad4	1129	377	377	CTC (L) => TTC (F)	1	C=>T
nad4	1148	383	383	TCT (S) => TTT (F)	0.89	C=>T
nad4	1172	391	391	TCA (S) => TTA (L)	1	C=>T
nad4	1211	404	404	TCA (S) => TTA (L)	1	C=>T
nad4	1307	436	436	GCG (A) => GTG (V)	1	C=>T
nad4	1355	452	452	CCA (P) => CTA (L)	1	C=>T
nad4	1405	469	469	CGG (R) => TGG (W)	1	C=>T
nad4	1433	478	478	CCG (P) => CTG (L)	1	C=>T

nad4	1438	480	480	CGC (R) => TGC (C)	1	C=>T
nad4L	17	6	16	TCA (S) => TTA (L)	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	80	27	37	TCA (S) => TTA (L)	1	C=>T
nad4L	101	34	44	TCG (S) => TTG (L)	0.88	C=>T
nad4L	128	43	53	TCG (S) => TTG (L)	1	C=>T
nad4L	167	56	66	TCA (S) => TTA (L)	0.88	C=>T
nad4L	251	84	94	TCT (S) => TTT (F)	0.88	C=>T
nad5	242	81	81	CCG (P) => CTG (L)	1	C=>T
nad5	358	120	120	CTT (L) => TTT (F)	1	C=>T
nad5	374	125	125	CCA (P) => CTA (L)	0.9	C=>T
nad5	398	133	133	TCT (S) => TTT (F)	0.9	C=>T
nad5	539	180	180	CCT (P) => CTT (L)	1	C=>T
nad5	548	183	183	TCG (S) => TTG (L)	0.4	C=>T
nad5	598	200	200	CGT (R) => TGT (C)	1	C=>T
nad5	629	210	214	TCT (S) => TTT (F)	0.9	C=>T
nad5	713	238	242	TCG (S) => TTG (L)	1	C=>T
nad5	835	279	283	CCA (P) => TCA (S)	0.9	C=>T
nad5	1550	517	521	ACC (T) => ATC (I)	0.9	C=>T
nad5	1580	527	531	TCA (S) => TTA (L)	0.8	C=>T
nad5	1610	537	541	CCC (P) => CTC (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	83	28	30	TCG (S) => TTG (L)	1	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	95	32	34	CCA (P) => CTA (L)	1	C=>T
nad6	103	35	37	CGC (R) => TGC (C)	1	C=>T
nad6	146	49	51	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
nad7	77	26	26	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	316	106	106	CGT (R) => TGT (C)	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	392	131	131	TCC (S) => TTC (F)	1	C=>T
nad7	404	135	135	TCT (S) => TTT (F)	1	C=>T
nad7	578	193	193	TCA (S) => TTA (L)	0.88	C=>T
nad7	679	227	227	CCA (P) => TCA (S)	0.88	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	1057	353	354	CGT (R) => TGT (C)	1	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
nad7	1166	389	390	TCT (S) => TTT (F)	1	C=>T
nad9	92	31	31	TCT (S) => TTT (F)	0.75	C=>T
nad9	298	100	100	CCG (P) => TCG (S)	0.83	C=>T
nad9	328	110	110	CGG (R) => TGG (W)	1	C=>T
nad9	398	133	133	TCA (S) => TTA (L)	1	C=>T
nad9	439	147	147	CTT (L) => TTT (F)	1	C=>T
nad9	539	180	180	TCT (S) => TTT (F)	1	C=>T
rpl5	35	12	17	TCA (S) => TTA (L)	0.78	C=>T
rpl5	47	16	21	CCG (P) => CTG (L)	1	C=>T
rpl5	64	22	27	CAC (H) => TAC (Y)	1	C=>T
rpl5	170	57	63	CCG (P) => CTG (L)	0.44	C=>T
rpl5	320	107	121	TCG (S) => TTG (L)	0.89	C=>T
rpl5	332	111	125	TCG (S) => TTG (L)	0.44	C=>T
rpl5	518	173	189	CCG (P) => CTG (L)	1	C=>T
rps3	326	109	178	TCA (S) => TTA (L)	0.71	C=>T
rps3	512	171	256	TCG (S) => TTG (L)	0.86	C=>T
rps3	817	273	367	CTT (L) => TTT (F)	1	C=>T
rps3	1160	387	486	CCG (P) => CTG (L)	1	C=>T
rps3	1187	396	495	CCG (P) => CTG (L)	0.86	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	133	45	59	CCG (P) => TCG (S)	0.67	C=>T
rps4	164	55	69	TCA (S) => TTA (L)	1	C=>T
rps4	184	62	76	CCC (P) => TCC (S)	0.83	C=>T
rps4	193	65	79	CAT (H) => TAT (Y)	1	C=>T
rps4	266	89	103	CCA (P) => CTA (L)	0.83	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	868	290	329	CCT (P) => TCT (S)	0.2	C=>T
rps4	934	312	354	CAT (H) => TAT (Y)	0.83	C=>T
rps4	959	320	362	TCT (S) => TTT (F)	1	C=>T
rps4	1010	337	379	CCA (P) => CTA (L)	0.83	C=>T
rps4	1019	340	382	CCT (P) => CTT (L)	1	C=>T
rps4	1024	342	384	CGG (R) => TGG (W)	1	C=>T
rps7	341	114	136	TCA (S) => TTA (L)	0.88	C=>T
rps10	268	90	95	CTT (L) => TTT (F)	0.8	C=>T
rps10	272	91	96	GCA (A) => GTA (V)	0.2	C=>T
rps12	71	24	24	TCG (S) => TTG (L)	0.94	C=>T
rps12	100	34	34	CGC (R) => TGC (C)	1	C=>T
rps12	104	35	35	CCG (P) => CTG (L)	1	C=>T
rps12	196	66	66	CAC (H) => TAC (Y)	0.94	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
rps13	5	2	6	TCA (S) => TTA (L)	0.6	C=>T

Table S14. Primer sequences used for RNA editing evaluation.

	Gene name-editing site	Forward primer(5'-3')	Reverse primer(5'-3')
gDNA	<i>cox2-443</i>	GAGTAGGCGTGGAGAG	GTTCGTTATCCTAACCG
	<i>nad1-2</i>	GGTAAGAGGATTCGATCTTG	GTTCGGATCTGACAATACC
	<i>nad7-224</i>	GTGAGTTCTTCGTTCCG	GTGCCACTCCACCTG
	<i>atp6-1015</i>	GCTTGGACTATGCTATGTATG	GGCTTGTGCAGTTCAG
cDNA	<i>cox2-443</i>	ATGATTGTTCTAGAATGGC	ACGACCAGGTACAGC
	<i>nad1-2</i>	GTGAGGCAGGCTAAG	GTTCGGATCTGACAATACC
	<i>nad7-224</i>	ATGACGACTAGGAACAGGC	TGTGCCACTCCACCTG
	<i>atp6-1015</i>	GTACTCCTTGAGCTAATCC	GTTGGTCCGACCAGC

Table S15. The NCBI accession numbers of all used plant mitogenomes.

Caryophyllale	<i>Myricaria elegans</i> Royle M1 and 2, complete genome	OP429118.1
		OP429117.1
	<i>Alternanthera philoxeroides</i> mitochondrion, complete genome	MN166292.1
	<i>Beta macrocarpa</i> mitochondrion, complete genome	NC_015994.1
	<i>Beta vulgaris</i> subsp. <i>maritima</i> mitochondrion, complete genome	NC_015099.1
	<i>Bougainvillea spectabilis</i> mitochondrion, complete genome	NC_056281.1
	<i>Agrostemma githago</i> mitochondrion, complete genome	NC_057604.1
	<i>Mirabilis jalapa</i> mitochondrion, complete genome	NC_056991.1
	<i>Mirabilis himalaica</i> mitochondrion, complete genome	NC_048974.1
	<i>Chenopodium quinoa</i> mitochondrion, complete genome	NC_041093.1
	<i>Sesuvium portulacastrum</i> mitochondrion, complete genome	MN683736.1
	<i>Silene latifolia</i> mitochondrion, complete genome	NC_014487.1
	<i>Spinacia oleracea</i> mitochondrion, complete genome	NC_035618.1
	<i>Suaeda glauca</i> mitochondrion, complete sequence	NC_060419.1
Asterales	<i>Tetragonia tetragonoides</i> mitochondrion, complete genome	MW971440.1
	<i>Chrysanthemum boreale</i> mitochondrion, complete genome	NC_039757.1
	<i>Codonopsis lanceolata</i> mitochondrion, complete genome	NC_037949.1
	<i>Helianthus annuus</i> mitochondrion, complete genome	NC_023337.1
	<i>Helianthus occidentalis</i> mitochondrion, complete genome	NC_058584.1
	<i>Lactuca serriola</i> mitochondrion, complete genome	NC_042378.1
	<i>Lactuca saligna</i> strain CGN5271 mitochondrion, complete geno	NC_042406.1
	<i>Platycodon grandiflorus</i> mitochondrion, complete genome	NC_035958.1
	<i>Arctium tomentosum</i> mitochondrion, complete genome	NC_058643.1
	<i>Arctium lappa</i> mitochondrion, complete genome	NC_058644.1
	<i>Ageratum conyzoides</i> mitochondrion, complete genome	NC_053927.1
	<i>Bidens tripartita</i> mitochondrion, complete genome	NC_062671.1
	<i>Saussurea costus</i> mitochondrion, complete genome	NC_059793.1
Aquifoliales	<i>Ilex pubescens</i> mitochondrion, complete genome	NC_045078.1
Santalales	<i>Malania oleifera</i> mitochondrion, complete genome	NC_053625.1
	<i>Tolypanthus maclurei</i> mitochondrion, complete genome	NC_056836.1

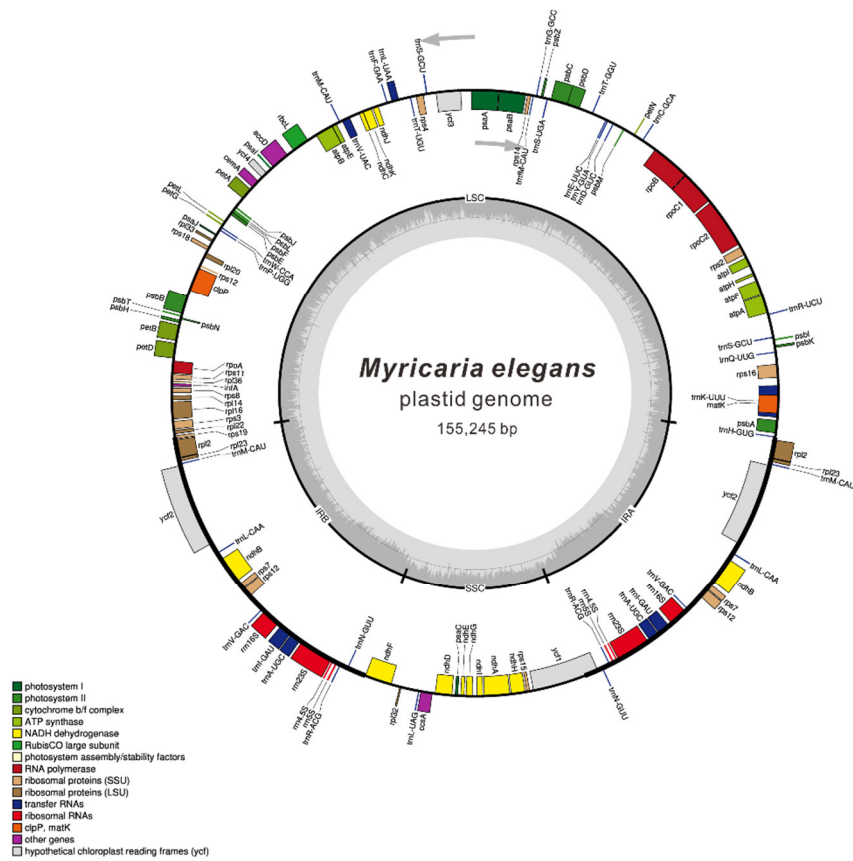


Figure S1. The plastid genome map and gene annotations of the *M. elegans*. Annotated genes showed the locations inside/outside the circle and transcribed clockwise/counterclockwise. The GC content was depicted in the inner circle, which was colored in a dark gray.