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Table S1 a. Mitogenome features of GP1397.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	61	61				0	H	32.8	21.3	18.0	27.9	39.3	60.70	-0.08	0.08
12SrRNA	62	979	918				0	H	36.6	24.9	17.0	21.5	41.9	58.10	-0.19	0.26
tRNA-Val(V)	980	1042	63				0	H	38.1	20.6	11.1	30.2	31.7	68.30	-0.30	0.12
16SrRNA	1043	2509	1467				0	H	37.2	23.1	16.2	23.6	39.3	60.70	-0.18	0.22
ND1	2510	3473	964	321	ATA	T	0	H	30.4	30.6	11.0	28.0	41.6	58.40	-0.47	0.04
tRNA-Ile(I)	3474	3538	65				0	H	29.2	26.2	26.2	18.5	52.3	47.70	0.00	0.22
CR2	3539	5247	1709				0	H	29.8	18.0	13.3	38.9	31.2	68.80	-0.15	-0.13
tRNA-Leu2(L2)	5248	5320	73				1	H	35.6	24.7	16.4	23.3	41.1	58.90	-0.20	0.21
tRNA-Gln(Q)	5322	5391	70				-1	L	38.6	22.9	10.0	28.6	32.9	67.10	-0.39	0.15
tRNA-Met(M)	5391	5453	63				0	H	33.3	28.6	19.0	19.0	47.6	52.40	-0.20	0.27
ND2	5454	6485	1032	343	ATT	TAG	-2	H	37.3	26.8	8.8	27.0	35.7	64.30	-0.51	0.16
tRNA-Trp(W)	6484	6548	65				57	H	36.9	23.1	16.9	23.1	40	60.00	-0.16	0.23
tRNA-Asn(N)	6606	6676	71				608	L	35.2	33.8	12.7	18.3	46.5	53.50	-0.45	0.32
tRNA-Ala(A)	7285	7348	64				95	L	34.4	20.3	12.5	32.8	32.8	67.20	-0.24	0.02
tRNA-Cys(C)	7444	7502	59				0	L	23.7	28.8	22.0	25.4	50.8	49.20	-0.13	-0.03
tRNA-Tyr(Y)	7503	7563	61				-8	L	34.4	23.0	13.1	29.5	36.1	63.90	-0.27	0.08
COX1	7556	9166	1611	536	ATA	AGG	-10	H	29.7	24.8	15.6	29.9	40.4	59.60	-0.23	0.00
tRNA-Ser2(S2)	9157	9223	67				0	L	31.3	23.9	13.4	31.3	37.3	62.70	-0.28	0.00
tRNA-Asp(D)	9224	9286	63				0	H	30.2	27.0	19.0	23.8	46	54.00	-0.17	0.12
COX2	9287	9971	685	228	ATG	T	0	H	33.0	27.0	15.6	24.4	42.6	57.40	-0.27	0.15
tRNA-Lys(K)	9972	10035	64				1	H	31.3	14.1	18.8	35.9	32.8	67.20	0.14	-0.07
ATP8	10037	10198	162	53	ATG	TAG	-10	H	42.6	28.4	7.4	21.6	35.8	64.20	-0.59	0.33
ATP6	10189	10869	681	226	ATG	TAA	-1	H	35.5	24.4	9.5	30.5	33.9	66.10	-0.44	0.08
COX3	10869	11652	784	261	ATG	T	0	H	30.2	27.2	15.4	27.2	42.6	57.40	-0.28	0.05
tRNA-Gly(G)	11653	11713	61				0	H	36.1	23.0	16.4	24.6	39.3	60.70	-0.17	0.19
ND3	11714	12056	343	114	ATT	T	0	H	30.3	27.7	10.8	31.2	38.5	61.50	-0.44	-0.01
tRNA-Arg(R)	12057	12119	63				0	H	33.3	19.0	17.5	30.2	36.5	63.50	-0.04	0.05

ND4L	12120	12410	291	96	ATG	TAA	-1	H	33.0	25.1	11.3	30.6	36.4	63.60	-0.38	0.04
ND4	12410	13747	1338	445	ATG	TAG	-1	H	32.7	27.9	10.8	28.7	38.6	61.40	-0.44	0.07
tRNA-His(H)	13747	13808	62				1	H	33.9	24.2	19.4	22.6	43.5	56.50	-0.11	0.20
tRNA-Ser1(S1)	13810	13866	57				-3	H	28.1	26.3	17.5	28.1	43.9	56.10	-0.20	0.00
tRNA-Leu1(L1)	13864	13934	71				1	H	31.0	22.5	22.5	23.9	45.1	54.90	0.00	0.13
ND5	13936	15717	1782	593	ATG	TAA	535	H	34.2	25.5	10.5	29.8	36	64.00	-0.42	0.07
ND6	16253	16768	516	171	TAC	TCT	0	L	44.4	26.7	7.4	21.5	34.1	65.90	-0.57	0.35
tLNA-Glu	16769	16831	63				-2	L	36.5	22.2	14.3	27.0	36.5	63.50	-0.22	0.15
CYTB	16830	17942	1113	370	ATG	TAA	5	H	30.2	27.3	10.4	32.1	37.7	62.30	-0.45	-0.03
tRNA-Thr(T)	17948	18010	63				1	H	30.2	22.2	19.0	28.6	41.3	58.70	-0.08	0.03
tRNA-Pro(P)	18012	18072	61				0	L	31.1	27.9	11.5	29.5	39.3	60.70	-0.42	0.03
CR1	18073	19648	1576				0	H	29.4	19.1	13.0	38.5	32.1	67.90	-0.19	-0.13
Total			19648						32.9	24.7	12.9	29.5	37.6	62.4	-0.31	0.05
PCGs			11293						32.1	25.8	12.5	29.6	38.3	61.7	-0.35	0.04
rRNA			2385						36.9	23.8	16.5	22.8	40.3	59.7	-0.18	0.24
tRNAs			1410						31.0	19.6	21.0	28.4	40.6	59.4	0.03	0.04
CR			3285						29.6	18.5	13.2	38.7	31.7	68.3	-0.17	-0.13
WANCY			1081						32.3	25.0	16.8	25.9	41.8	58.2	-0.20	0.11
Intergenicspacer			535						34.0	25.2	6.2	34.6	31.4	68.6	-0.61	-0.01

Table S1 b. Mitogenome features of GP2947.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	62	62				0	H	32.3	22.6	17.7	27.4	40.3	59.7	-0.12	0.08
12SrRNA	63	979	917				0	H	36.6	24.8	17.0	21.6	41.8	58.2	-0.19	0.26
tRNA-Val(V)	980	1042	63				0	H	38.1	20.6	11.1	30.2	31.7	68.3	-0.30	0.12
16SrRNA	1043	2509	1467				0	H	37.2	23.1	16.2	23.6	39.3	60.8	-0.18	0.22
ND1	2510	3473	964	321	ATA	T	0	H	30.4	30.5	11.0	28.1	41.5	58.5	-0.47	0.04
tRNA-Ile(I)	3474	3538	65				0	H	29.2	26.2	26.2	18.5	52.3	47.7	0.00	0.22
CR2	3539	5134	1596				0	H	29.6	18.9	12.5	39.1	31.4	68.7	-0.20	-0.14
tRNA-Leu2(L2)	5135	5207	73				1	H	35.6	24.7	16.4	23.3	41.1	58.9	-0.20	0.21
tRNA-Gln(Q)	5209	5278	70				-1	L	38.6	22.9	10.0	28.6	32.9	67.2	-0.39	0.15
tRNA-Met(M)	5278	5340	63				0	H	33.3	28.6	19.0	19.0	47.6	52.3	-0.20	0.27
ND2	5341	6372	1032	343	ATT	TAG	-2	H	37.2	26.8	8.9	27.0	35.8	64.2	-0.50	0.16
tRNA-Trp	6371	6435	65				813	H	38.6	23.1	15.4	23.1	38.5	61.7	-0.20	0.25
tRNA-Ala	7249	7312	64				0	L	34.4	20.3	12.5	32.8	32.8	67.2	-0.24	0.02
tRNA-Asn	7313	7385	73				22	L	31.6	27.4	17.9	23.3	45.2	54.9	-0.21	0.15
tRNA-Cys	7408	7466	59				0	L	23.7	28.8	22.0	25.4	50.8	49.1	-0.13	-0.03
tRNA-Tyr	7467	7527	61				1	L	34.4	23.3	13.1	29.5	36.1	63.9	-0.28	0.08
COX1	7529	9130	1602	533	GTG	AGG	-10	H	29.7	24.7	15.7	29.9	40.4	59.6	-0.22	0.00
tRNA-Ser2(S2)	9121	9187	67				0	L	31.3	23.9	13.4	31.3	37.3	62.6	-0.28	0.00
tRNA-Asp(D)	9188	9250	63				0	H	30.2	27.0	19.0	23.8	46.0	54	-0.17	0.12
COX2	9251	9935	685	228	ATG	T	0	H	33.0	27.0	15.6	24.4	42.6	57.4	-0.27	0.15
tRNA-Lys(K)	9936	9999	64				1	H	31.3	14.1	18.8	35.9	32.8	67.2	0.14	-0.07
ATP8	10001	10162	162	53	ATG	TAG	-10	H	42.6	28.4	7.4	21.6	35.8	64.2	-0.59	0.33
ATP6	10153	10833	681	226	ATG	TAA	-1	H	35.4	24.4	9.6	30.6	34.0	66	-0.44	0.07
COX3	10833	11616	784	261	ATG	T	0	H	30.2	27.0	15.4	27.3	42.5	57.5	-0.27	0.05
tRNA-Gly(G)	11617	11677	61				0	H	36.1	23.0	16.4	24.6	39.3	60.7	-0.17	0.19
ND3	11678	12020	343	114	ATT	T	0	H	30.4	27.5	10.8	31.3	38.3	61.7	-0.44	-0.01
tRNA-Arg(R)	12021	12083	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	12084	12374	291	96	ATG	TAA	-1	H	33.0	25.1	11.3	30.6	36.4	63.6	-0.38	0.04
ND4	12374	13711	1338	445	ATG	TAG	-1	H	32.7	27.9	10.7	28.7	38.6	61.4	-0.45	0.07
tRNA-His(H)	13711	13772	62				1	H	33.9	24.2	19.4	22.6	43.5	56.5	-0.11	0.20
tRNA-Ser1(S1)	13774	13830	57				-3	H	28.1	26.3	17.5	28.1	43.9	56.2	-0.20	0.00
tRNA-Leu1(L1)	13828	13898	71				1	H	31.0	22.5	22.5	23.9	45.1	54.9	0.00	0.13
ND5	13900	15681	1782	593	ATG	TAA	535	H	34.2	25.5	10.4	29.8	36.0	64	-0.42	0.07
ND6	16217	16732	516	171	ATG	AGA	0	L	44.4	26.7	7.4	21.5	34.1	65.9	-0.57	0.35
tRNA-Glu(E)	16733	16795	63				-2	L	36.5	22.2	14.3	27.0	36.5	63.5	-0.22	0.15
CYTB	16794	17906	1113	370	ATG	TAA	5	H	30.2	27.3	10.4	32.1	37.7	62.3	-0.45	-0.03
tRNA-Thr(T)	17912	17974	63				1	H	30.2	22.2	19.0	28.6	41.3	58.8	-0.08	0.03
tRNA-Pro(P)	17976	18036	61				9	L	31.1	27.9	11.5	29.5	39.3	60.6	-0.42	0.03
CR1	18046	19534	1489				0	H	28.9	19.9	12.7	38.5	21.7	67.4	-0.22	-0.14
Total			19629						33.0	24.8	12.7	29.4	37.5	62.4	-0.32	0.06
PCGs			11293						33.1	26.7	11.6	28.6	38.3	61.7	-0.39	0.07
rRNA			2384						37.0	23.7	16.5	22.8	40.2	59.8	-0.18	0.24
tRNAs			1413						32.9	23.6	16.8	26.6	40.5	59.5	-0.17	0.11
CR			3085						29.2	19.4	12.6	38.8	32.0	68	-0.21	-0.14
WANCY			1158						33.4	25.5	15.7	25.4	41.2	58.8	-0.24	0.14
Intergenicspacer			534						34.2	25.2	6.0	34.6	31.2	68.8	-0.62	-0.01

Table S1 c. Mitogenome features of GP3009.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	62	62				0	H	32.3	22.6	17.7	27.4	40.3	59.7	-0.12	0.08
12SrRNA	63	978	916				0	H	36.6	24.8	17.0	21.6	41.8	58.2	-0.19	0.26
tRNA-Val(V)	979	1041	63				0	H	38.1	20.6	11.1	30.2	31.7	68.3	-0.30	0.12
16SrRNA	1042	2509	1468				0	H	37.2	23.1	16.2	23.6	39.3	60.8	-0.18	0.22
ND1	2510	3473	964	321	ATA	T	0	H	30.4	30.5	11.0	28.1	41.5	58.5	-0.47	0.04
tRNA-Ile(I)	3474	3538	65				0	H	29.2	26.2	26.2	18.5	52.3	47.7	0.00	0.22
CR2	3539	5359	1821				0	H	29.6	18.9	12.5	39.4	31.4	69	-0.20	-0.14
tRNA-Leu2(L2)	5360	5432	73				1	H	35.6	24.7	16.4	23.3	41.1	58.9	-0.20	0.21
tRNA-Gln(Q)	5434	5503	70				-1	L	38.6	22.9	10.0	28.6	32.9	67.2	-0.39	0.15
tRNA-Met(M)	5503	5565	63				0	H	33.3	28.6	19.0	19.0	47.6	52.3	-0.20	0.27
ND2	5566	6597	1032	343	ATT	TAG	-2	H	37.2	26.8	8.9	27.0	35.8	64.2	-0.50	0.16
tRNA-Trp	6596	6652	57				519	H	38.5	23.1	15.4	23.1	38.5	61.6	-0.20	0.25
tRNA-Ala	7172	7235	64				0	L	34.4	18.8	12.5	34.4	31.3	68.8	-0.20	0.00
tRNA-Asn	7236	7308	73				22	L	34.2	27.4	15.1	23.3	42.5	57.5	-0.29	0.19
tRNA-Cys	7331	7389	59				0	L	23.7	28.8	22.0	25.4	50.8	49.1	-0.13	-0.03
tRNA-Tyr	7390	7450	61				1	L	32.8	23.0	13.1	31.1	36.1	63.9	-0.27	0.03
COX1	7452	9053	1602	533	GTG	AGG	-10	H	29.3	25.0	15.9	29.7	40.9	59	-0.22	-0.01
tRNA-Ser2(S2)	9044	9110	67				0	L	31.3	22.4	13.4	32.8	35.8	64.1	-0.25	-0.02
tRNA-Asp(D)	9111	9173	63				0	H	30.2	27.0	19.0	23.8	46.0	54	-0.17	0.12
COX2	9174	9858	685	228	ATG	T	0	H	33.4	26.7	15.3	24.5	42.0	57.9	-0.27	0.15
tRNA-Lys(K)	9859	9922	64				1	H	31.3	14.1	18.8	35.9	32.8	67.2	0.14	-0.07
ATP8	9924	10085	162	53	ATG	TAA	-10	H	43.2	26.5	6.8	23.5	33.3	66.7	-0.59	0.30
ATP6	10076	10756	681	226	ATG	TAA	-1	H	35.1	24.2	9.8	30.8	34.1	65.9	-0.42	0.07
COX3	10756	11539	784	261	ATG	T	0	H	30.4	26.3	15.3	28.1	41.6	58.5	-0.26	0.04
tRNA-Gly(G)	11540	11600	61				0	H	36.1	23.0	16.4	24.6	39.3	60.7	-0.17	0.19
ND3	11601	11943	343	114	ATT	T	0	H	30.6	26.5	10.5	32.4	37.0	63	-0.43	-0.03
tRNA-Arg(R)	11944	12006	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	12007	12297	291	96	ATG	TAA	-1	H	32.6	25.4	11.7	30.2	37.1	62.8	-0.37	0.04
ND4	12297	13634	1338	445	ATG	TAG	-1	H	32.8	27.7	10.5	28.9	38.3	61.7	-0.45	0.06
tRNA-His(H)	13634	13695	62				1	H	33.9	24.2	19.4	22.6	43.5	56.5	-0.11	0.20
tRNA-Ser1(S1)	13697	13753	57				-3	H	28.1	26.3	17.5	28.1	43.9	56.2	-0.20	0.00
tRNA-Leu1(L1)	13751	13821	71				1	H	31.0	22.5	22.5	23.9	45.1	54.9	0.00	0.13
ND5	13823	15604	1782	593	ATG	TAA	534	H	34.1	25.6	10.6	29.7	36.2	63.8	-0.41	0.07
ND6	16139	16654	516	171	ATG	AGA	0	L	44.4	27.3	7.4	20.9	34.7	65.3	-0.57	0.36
tRNA-Glu(E)	16655	16717	63				-2	L	36.5	22.2	14.3	27.0	36.5	63.5	-0.22	0.15
CYTB	16716	17828	1113	370	ATG	TAA	5	H	30.0	27.5	10.6	31.9	38.1	61.9	-0.44	-0.03
tRNA-Thr(T)	17834	17896	63				1	H	30.2	22.2	19.0	28.6	41.3	58.8	-0.08	0.03
tRNA-Pro(P)	17898	17958	61				0	L	31.1	27.9	11.5	29.5	39.3	60.6	-0.42	0.03
CR1	17959	19441	1483				0	H	28.7	20.1	13.1	38.0	33.3	66.7	-0.21	-0.14
Total			19441						33.0	24.6	12.7	29.7	37.3	62.7	-0.32	0.05
PCGs			11293						33.0	26.6	11.6	28.7	38.3	61.7	-0.39	0.07
rRNA			2384						37.2	23.5	16.4	22.9	39.9	60.1	-0.18	0.24
tRNAs			1405						33.0	23.6	16.7	26.8	40.3	59.8	-0.17	0.10
CR			3304						29.7	18.6	13.0	38.6	31.7	68.3	-0.18	-0.13
WANCY			856						33.4	25.5	15.7	26.2	41.2	59.6	-0.24	0.12
Intergenicspacer			534						34.3	23.6	5.6	36.5	29.2	70.8	-0.62	-0.03

Table S1 d. Mitogenome features of GP6451.

gene	Position		Length	Aminoacid	Codon		intergenic	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop	region									
tRNA-Phe(F)	1	62	62				0	H	32.3	22.6	17.7	27.4	40.3	59.7	-0.12	0.08
12SrRNA	63	978	916				0	H	36.8	24.6	16.9	21.7	41.5	58.5	-0.19	0.26
tRNA-Val(V)	979	1041	63				0	H	38.1	20.6	11.1	30.2	31.7	68.3	-0.30	0.12
16SrRNA	1042	2509	1468				0	H	37.4	22.9	16.0	23.7	38.9	61.1	-0.18	0.22
ND1	2510	3473	964	321	ATA	T	0	H	30.3	30.6	11.0	28.1	41.6	58.4	-0.47	0.04
tRNA-Ile(I)	3474	3538	65				0	H	30.8	26.2	26.2	16.9	52.3	47.7	0.00	0.29
CR2	3539	5090	1552				0	H	29.1	19.3	12.9	38.9	32.2	68	-0.20	-0.14
tRNA-Leu2(L2)	5091	5163	73				1	H	35.6	21.9	16.4	26.0	38.4	61.6	-0.14	0.16
tRNA-Gln(Q)	5165	5234	70				-1	L	38.6	22.9	10.0	28.6	32.9	67.2	-0.39	0.15
tRNA-Met(M)	5234	5296	63				0	H	33.3	28.6	19.0	19.0	47.6	52.3	-0.20	0.27
ND2	5297	6328	1032	343	ATT	TAG	-2	H	37.2	26.8	8.8	27.1	35.7	64.3	-0.51	0.16
tRNA-Trp	6327	6391	65				684	H	38.5	23.1	15.4	23.1	38.5	61.6	-0.20	0.25
tRNA-Ala	7076	7139	64				0	L	34.4	18.8	12.5	34.4	31.3	68.8	-0.20	0.00
tRNA-Asn	7140	7212	73				23	L	34.2	27.4	15.1	23.3	42.5	57.5	-0.29	0.19
tRNA-Cys	7236	7294	59				0	L	23.7	28.8	22.0	25.4	50.8	49.1	-0.13	-0.03
tRNA-Tyr	7295	7355	61				1	L	32.8	23.0	13.1	31.1	36.1	63.9	-0.27	0.03
COX1	7357	8958	1602	533	GTG	AGG	-10	H	29.4	25.0	15.9	29.7	40.9	59.1	-0.22	-0.01
tRNA-Ser2(S2)	8949	9015	67				0	L	31.3	22.4	13.4	32.8	35.8	64.1	-0.25	-0.02
tRNA-Asp(D)	9016	9078	63				0	H	30.2	27.0	19.0	23.8	46.0	54	-0.17	0.12
COX2	9079	9763	685	228	ATG	T	0	H	33.4	26.6	15.3	24.7	41.9	58.1	-0.27	0.15
tRNA-Lys(K)	9764	9827	64				1	H	31.3	14.1	18.8	35.9	32.8	67.2	0.14	-0.07
ATP8	9829	9990	162	53	ATG	TAA	-10	H	43.2	26.5	6.8	23.5	33.3	66.7	-0.59	0.30
ATP6	9981	10661	681	226	ATG	TAA	-1	H	35.1	24.2	9.8	30.8	34.1	65.9	-0.42	0.07
COX3	10661	11444	784	261	ATG	T	0	H	30.4	26.3	15.3	28.1	41.6	58.5	-0.26	0.04
tRNA-Gly(G)	11445	11505	61				0	H	36.1	23.0	16.4	24.6	39.3	60.7	-0.17	0.19
ND3	11506	11848	343	114	ATT	T	0	H	30.6	26.5	10.5	32.4	37.0	63	-0.43	-0.03
tRNA-Arg(R)	11849	11911	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11912	12202	291	96	ATG	TAA	-1	H	32.6	24.7	11.7	30.9	36.4	63.5	-0.36	0.03
ND4	12202	13539	1338	445	ATG	TAG	-1	H	32.8	27.7	10.5	29.0	38.2	61.8	-0.45	0.06
tRNA-His(H)	13539	13600	62				1	H	33.9	24.2	19.4	22.6	43.5	56.5	-0.11	0.20
tRNA-Ser1(S1)	13602	13658	57				-3	H	28.1	26.3	17.5	28.1	43.9	56.2	-0.20	0.00
tRNA-Leu1(L1)	13656	13726	71				1	H	31.0	22.5	22.5	23.9	45.1	54.9	0.00	0.13
ND5	13728	15509	1782	590	ATG	TAA	535	H	34.1	25.6	10.5	29.8	36.1	63.9	-0.42	0.07
ND6	16045	16560	516	171	ATG	AGA	0	L	44.6	27.3	7.2	20.9	34.5	65.5	-0.58	0.36
tRNA-Glu(E)	16561	16623	63				-2	L	36.5	22.2	14.3	27.0	36.5	63.5	-0.22	0.15
CYTB	16622	17734	1113	370	ATG	TAA	5	H	29.6	27.5	10.7	31.9	38.2	61.5	-0.44	-0.04
tRNA-Thr(T)	17740	17802	63				1	H	30.2	22.2	19.0	28.6	41.3	58.8	-0.08	0.03
tRNA-Pro(P)	17804	17864	61				0	L	31.1	27.9	11.5	29.5	39.3	60.6	-0.42	0.03
CR1	17865	19525	1661				0	H	30.2	18.4	12.3	39.1	30.8	69.3	-0.20	-0.13
Total			19525						33.0	24.6	12.6	29.7	37.3	62.7	-0.32	0.05
PCGs			11293						33.0	26.6	11.6	28.8	38.2	61.8	-0.39	0.07
rRNA			2384						36.8	24.6	16.9	21.7	41.5	58.5	-0.19	0.26
tRNAs			1413						37.2	23.5	16.4	22.9	39.9	60.1	-0.18	0.24
CR			3213						29.7	18.9	12.6	38.9	31.5	68.6	-0.20	-0.13
WANCY			1030						33.9	25.0	15.0	26.0	40.0	59.9	-0.25	0.13
Intergenicspacer			535						34.2	23.6	5.6	36.6	29.2	70.8	-0.62	-0.03

Table S1 e. Mitogenome features of NC_060420.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	62	62				0	H	32.3	22.6	177	27.4	40.3	59.7	0.77	0.08
12SrRNA	63	978	916				0	H	36.8	24.6	16.9	21.7	41.5	58.5	-0.19	0.26
tRNA-Val(V)	979	1041	63				0	H	38.1	20.6	11.1	30.2	31.7	68.3	-0.30	0.12
16SrRNA	1042	2509	1468				0	H	37.4	22.9	16.0	23.7	38.9	61.1	-0.18	0.22
ND1	2510	3473	964	321	ATA	T	0	H	30.3	30.7	10.9	28.1	41.6	58.4	-0.48	0.04
tRNA-Ile(I)	3474	3538	65				-8	H	30.8	26.2	26.2	16.9	52.3	47.7	0.00	0.29
CR2	3531	5018	1488				5	H	28.5	20.2	13.2	38.0	33.5	66.5	-0.21	-0.14
tRNA-Leu2(L2)	5024	5096	73				1	H	35.6	24.7	16.4	23.3	41.1	58.9	-0.20	0.21
tRNA-Gln(Q)	5098	5167	70				-1	L	38.6	22.9	10.0	28.6	32.9	67.2	-0.39	0.15
tRNA-Met(M)	5167	5229	63				0	H	33.3	28.6	19.0	19.0	47.6	52.3	-0.20	0.27
ND2	5230	6261	1032	343	ATT	TAG	-2	H	37.2	26.7	8.9	27.1	35.7	64.3	-0.50	0.16
tRNA-Trp	6260	6324	65				1069	H	38.5	23.1	15.4	23.1	38.5	61.6	-0.20	0.25
tRNA-Ala	7394	7457	64				0	L	34.4	18.8	12.5	34.4	31.3	68.8	-0.20	0.00
tRNA-Asn	7458	7530	73				22	L	34.2	27.4	15.1	23.3	42.5	57.5	-0.29	0.19
tRNA-Cys	7553	7611	59				0	L	23.7	28.8	22.0	25.4	50.8	49.1	-0.13	-0.03
tRNA-Tyr	7612	7672	61				1	L	32.8	23.0	13.1	31.1	36.1	63.9	-0.27	0.03
COX1	7674	9275	1602	533	GTG	AGG	-10	H	29.3	25.0	15.9	29.7	40.9	59	-0.22	-0.01
tRNA-Ser2(S2)	9266	9332	67				0	L	31.3	22.4	13.4	32.8	35.8	64.1	-0.25	-0.02
tRNA-Asp(D)	9333	9395	63				0	H	30.2	27.0	19.0	23.8	46.0	54	-0.17	0.12
COX2	9396	10080	685	228	ATG	T	0	H	33.4	26.7	15.3	24.5	42.0	57.9	-0.27	0.15
tRNA-Lys(K)	10081	10144	64				1	H	31.3	14.1	18.8	35.9	32.8	67.2	0.14	-0.07
ATP8	10146	10307	162	53	ATG	TAA	-10	H	43.2	26.5	6.8	23.5	33.3	66.7	-0.59	0.30
ATP6	10298	10978	681	226	ATG	TAA	-1	H	35.1	24.2	9.8	30.8	34.1	65.9	-0.42	0.07
COX3	10978	11761	784	261	ATG	T	0	H	30.4	26.3	15.3	28.1	41.6	58.5	-0.26	0.04
tRNA-Gly(G)	11762	11822	61				0	H	36.1	23.0	16.4	24.6	39.3	60.7	-0.17	0.19
ND3	11823	12165	343	114	ATT	T	0	H	30.6	26.5	10.5	32.4	37.0	63	-0.43	-0.03
tRNA-Arg(R)	12166	12228	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	12229	12519	291	96	ATG	TAA	-1	H	32.6	25.4	11.7	30.2	37.1	62.8	-0.37	0.04
ND4	12519	13856	1338	445	ATG	TAG	-1	H	32.8	27.7	10.5	28.9	38.3	61.7	-0.45	0.06
tRNA-His(H)	13856	13917	62				1	H	33.9	24.2	19.4	22.6	43.5	56.5	-0.11	0.20
tRNA-Ser1(S1)	13919	13975	57				-3	H	28.1	26.3	17.5	28.1	43.9	56.2	-0.20	0.00
tRNA-Leu1(L1)	13973	14043	71				1	H	31.0	22.5	22.5	23.9	45.1	54.9	0.00	0.13
ND5	14045	15826	1782	593	ATG	TAA	534	H	34.1	25.6	10.6	29.7	36.2	63.8	-0.41	0.07
ND6	16361	16876	516	171	ATG	AGA	0	L	44.4	27.3	7.4	20.9	34.7	65.3	-0.57	0.36
tRNA-Glu(E)	16877	16939	63				-2	L	36.5	22.2	14.3	27.0	36.5	63.5	-0.22	0.15
CYTB	16938	18050	1113	370	ATG	TAA	5	H	30.0	27.5	10.6	31.9	38.1	61.9	-0.44	-0.03
tRNA-Thr(T)	18056	18118	63				1	H	30.2	22.2	19.0	28.6	41.3	58.8	-0.08	0.03
tRNA-Pro(P)	18180	18120	61				0	L	31.1	27.9	11.5	29.5	39.3	60.6	-0.42	0.03
CR1	18181	19669	1489				0	H	28.9	19.9	13.0	38.1	33.0	67	-0.21	-0.14
Total			19669						33.0	24.9	12.8	29.3	37.7	62.3	-0.32	0.06
PCGs			11293						33.0	26.6	11.6	28.7	38.3	61.7	-0.39	0.07
rRNA			2384						37.2	23.5	16.4	22.9	39.9	60.1	-0.18	0.24
tRNAs			1413						33.1	23.5	16.7	26.8	40.2	59.9	-0.17	0.11
CR			2977						28.7	20.1	13.1	38.1	33.2	66.8	-0.21	-0.14
WANCY			1414						33.7	25.5	15.6	25.2	14.0	58.9	-0.24	0.14
Intergenicspacer			534						34.3	23.6	5.6	36.5	29.2	70.8	-0.62	-0.03

Table S1 f. Mitogenome features of GP13328.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe	1	61	61				0	H	34.4	23.0	16.4	26.2	39.3	60.70	-0.17	0.14
12SrRNA	62	981	920				0	H	37.1	24.9	17	21.1	41.8	58.20	-0.19	0.27
tRNA-Val	982	1044	63				0	H	38.1	20.6	11.1	30.2	31.7	68.30	-0.30	0.12
16SrRNA	1045	2515	1471				0	H	37.5	22.2	16.1	24.2	38.3	61.70	-0.16	0.22
ND1	2516	3476	961	320	ATA	T	0	H	30.8	27.8	11.1	30.3	38.9	61.10	-0.43	0.01
tRNA-Ile	3477	3541	65				0	H	29.2	29.2	26.2	15.4	55.4	44.60	-0.05	0.31
CR2	3542	5196	1655				0	H	29.8	20.7	11.1	38.4	31.8	68.20	-0.30	-0.13
tRNA-Leu2	5197	5269	73				1	H	28.8	26.0	17.8	27.4	43.8	56.20	-0.19	0.02
tRNA-Gln	5271	5340	70				-1	L	40.0	20.0	10.0	30.0	30.0	70.00	-0.33	0.14
tRNA-Met	5340	5401	62				0	H	33.9	27.4	17.7	21.0	45.2	54.80	-0.22	0.23
ND2	5402	6433	1032	343	ATC	TAG	19	H	35.4	28.0	9.1	27.5	37.1	62.90	-0.51	0.13
tRNA-Ala	6453	6518	66				0	L	33.3	21.2	10.6	34.8	31.8	68.20	-0.33	-0.02
tRNA-Asn	6519	6591	73				255	L	32.9	24.7	16.4	26	41.1	58.90	-0.20	0.12
tRNA-Trp	6847	6911	65				110	H	36.9	18.5	15.4	29.2	33.8	66.20	-0.09	0.12
tRNA-Cys	7022	7082	61				0	L	21.3	27.9	21.3	29.5	49.2	50.80	-0.13	-0.16
tRNA-Tyr	7083	7145	63				-8	L	27.0	22.2	17.5	33.3	39.7	60.30	-0.12	-0.10
COX1	7138	8748	1611	536	ATA	AGG	-10	H	28.6	23.3	16.6	31.5	39.9	60.10	-0.17	-0.05
tRNA-Ser2	8739	8805	67				1	L	28.4	20.9	13.4	37.3	34.3	65.70	-0.22	-0.14
tRNA-Asp	8807	8867	61				0	H	34.4	19.7	18	27.9	37.7	62.30	-0.05	0.10
COX2	8868	9552	685	228	ATG	T	0	H	32.1	26.9	15.6	25.4	42.5	57.50	-0.27	0.12
tRNA-Lys	9553	9615	63				1	H	31.7	14.3	19.0	34.9	33.3	66.70	0.14	-0.05
ATP8	9617	9778	162	53	ATG	TAA	-10	H	37.0	24.7	7.4	30.9	32.1	67.90	-0.54	0.09
ATP6	9769	10449	681	226	GTG	TAA	-1	H	33.9	26.7	10.1	29.2	36.9	63.10	-0.45	0.07
COX3	10449	11232	784	261	ATG	T	0	H	29.1	26.0	16.2	28.7	42.2	57.80	-0.23	0.01
tRNA-Gly	11233	11293	61				0	H	36.1	21.3	16.4	26.2	37.7	62.30	-0.13	0.16
ND3	11294	11636	343	114	ATT	T	0	H	31.8	26.2	10.2	31.8	36.4	63.60	-0.44	0.00
tRNA-Arg	11637	11698	62				0	H	33.9	17.7	16.1	32.3	33.9	66.10	-0.05	0.02

ND4L	11699	11989	291	96	ATG	TAA	-1	H	33.7	23.0	11.7	31.6	34.7	65.30	-0.33	0.03
ND4	11989	13326	1338	445	ATG	TAG	-1	H	32.3	26.3	10.4	31	36.7	63.30	-0.43	0.02
tRNA-His	13326	13387	62				1	H	33.9	22.6	19.4	24.2	41.9	58.10	-0.08	0.17
tRNA-Ser1	13389	13444	56				-3	H	26.8	21.4	19.6	32.1	41.1	58.90	-0.04	-0.09
tRNA-Leu1	13442	13512	71				1	H	32.4	22.5	21.1	23.9	43.7	56.30	-0.03	0.15
ND5	13514	15298	1785	594	ATG	TAA	752	H	33.6	25.2	10.9	30.3	36.1	63.90	-0.40	0.05
ND6	16051	16569	519	172	TAC	TCT	0	L	45.7	27.2	5.2	22.0	32.4	67.60	-0.68	0.35
tRNA-Glu	16570	16631	62				-2	L	37.1	21.0	14.5	27.4	35.5	64.50	-0.18	0.15
CYTB	16630	17746	1117	372	ATG	T	0	H	30.6	25.0	10.5	33.9	35.5	64.50	-0.41	-0.05
tRNA-Thr	17747	17810	64				0	H	26.6	25.0	18.8	29.7	43.8	56.20	-0.14	-0.06
tRNA-Pro	17811	17871	61				0	L	32.8	27.9	9.8	29.5	37.7	62.30	-0.48	0.05
CR1	17872	19518	1647				0	H	29.9	20.6	11.0	38.5	31.6	68.40	-0.30	-0.13
Total			19518						32.7	24.4	12.4	30.5	36.8	63.2	-0.33	0.03
PCGs			11300						31.4	24.8	12.8	31.0	37.6	62.4	-0.32	0.01
rRNA			2391						37.3	23.2	16.4	23.0	39.6	60.3	-0.17	0.24
tRNAs			1412						32.0	19.2	20.0	28.8	39.2	60.8	0.02	0.05
CR			3302						29.8	20.7	11.1	38.5	31.8	68.3	-0.30	-0.13
WANCY			713						33.1	22.9	15.3	28.8	38.1	61.9	-0.20	0.07
Intergenicspacer			752						33.9	26.3	7.1	32.7	33.4	66.6	-0.57	0.02

Table S1 g. Mitogenome features of GP4299.

gene	Position		Length	Aminoacid	Codon		intergenic	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop	region									
tRNA-Phe	1	62	62				0	H	35.5	17.7	16.1	30.6	33.9	66.10	-0.05	0.07
12SrRNA	63	978	916				0	H	36.5	25.6	17.2	20.8	42.7	57.30	-0.20	0.27
tRNA-Val	979	1041	63				0	H	36.5	17.5	11.1	34.9	28.6	71.40	-0.22	0.02
16SrRNA	1042	2514	1473				0	H	37.6	22.3	15.9	24.2	38.2	61.80	-0.17	0.22
ND1	2515	3475	361	320	ATA	T	0	H	30.3	29.4	11.2	29.0	40.7	59.30	-0.45	0.02
tRNA-Ile	3476	3540	65				0	H	32.3	26.2	24.6	16.9	50.8	49.20	-0.03	0.31
CR2	3541	4854	1314				0	H	27.1	23.0	12.3	37.6	35.4	64.70	-0.30	-0.16
tRNA-Leu2	4855	4927	73				3	H	31.5	26.0	17.8	24.7	43.8	56.20	-0.19	0.12
tRNA-Gln	4931	5000	70				-1	L	37.1	24.3	11.4	27.1	35.7	64.20	-0.36	0.16
tRNA-Met	5000	5061	62				0	H	35.5	29.0	16.1	19.4	45.2	54.90	-0.29	0.29
ND2	5062	6093	1032	343	ATT	TAG	-3	H	36.3	27.7	8.7	27.2	36.4	63.50	-0.52	0.14
tRNA-Ala	6091	6156	66				0	L	34.8	22.7	10.6	31.8	33.3	66.60	-0.36	0.05
tRNA-Asn	6157	6229	73				95	L	32.9	27.4	16.4	23.3	43.8	56.20	-0.25	0.17
tRNA-Trp	6325	6387	63				217	L	31.7	22.2	12.7	33.3	34.9	65.00	-0.27	-0.02
tRNA-Cys	6605	6669	65				94	H	38.5	21.5	15.4	24.6	36.9	63.10	-0.17	0.22
tRNA-Tyr	6764	6822	59				55	L	22.0	30.5	23.7	23.7	54.2	45.70	-0.13	-0.04
COX1	6878	8488	1611	536	ATG	AGG	-10	H	29.1	24.1	16.2	30.6	40.3	59.70	-0.20	-0.03
tRNA-Ser2	8479	8545	67				1	L	34.3	20.9	11.9	32.8	32.8	67.10	-0.27	0.02
tRNA-Asp	8547	8608	62				0	H	32.3	24.2	17.7	25.8	41.9	58.10	-0.16	0.11
COX2	8609	9293	685	228	ATG	TAA	0	H	31.2	26.3	16.6	25.8	42.9	57.00	-0.23	0.09
tRNA-Lys	9294	9356	63				1	H	31.7	14.3	19.0	34.9	33.3	66.60	0.14	-0.05
ATP8	9358	9519	162	53	ATG	TAA	-10	H	40.7	28.4	7.4	23.5	35.8	64.20	-0.59	0.27
ATP6	9510	10190	681	226	ATG	TAA	-1	H	34.9	26.0	9.7	29.4	35.7	64.30	-0.46	0.09
COX3	10190	10973	784	261	ATG	T	0	H	29.5	27.6	16.3	26.7	43.9	56.20	-0.26	0.05
tRNA-Gly	10974	11034	61				0	H	36.1	24.6	14.8	24.6	39.3	60.70	-0.25	0.19
ND3	11035	11377	343	114	ATC	T	0	H	28.0	26.8	13.4	31.8	40.2	59.80	-0.33	-0.06
tRNA-Arg	11378	11439	62				0	H	35.5	19.4	16.1	29.0	35.5	64.50	-0.09	0.10

ND4L	11440	11730	291	96	ATG	TAA	-1	H	32.6	25.1	12.7	29.6	37.8	62.20	-0.33	0.05
ND4	11730	13067	1338	445	ATG	TAA	0	H	32.7	25.3	10.4	31.6	35.7	64.30	-0.42	0.02
tRNA-His	13068	13129	62				0	H	33.9	22.6	19.4	24.2	41.9	58.10	-0.08	0.17
tRNA-Ser1	13130	13185	56				-3	H	28.6	25.0	19.6	26.8	44.6	55.40	-0.12	0.03
tRNA-Leu1	13183	13253	71				1	H	31.0	23.9	21.1	23.9	45.1	54.90	-0.06	0.13
ND5	13255	15036	1782	593	ATG	TAA	926	H	32.1	25.0	12.4	30.5	37.4	62.60	-0.34	0.03
ND6	15963	16481	519	172	TCC	TAC	0	L	43.4	27.0	7.9	21.8	34.9	65.20	-0.55	0.33
tRNA-Glu	16482	16544	63				-2	L	36.5	22.2	14.3	27.0	36.5	63.50	-0.22	0.15
CYTB	16543	17659	1117	372	ATG	T	0	H	30.0	25.4	11.2	33.4	36.6	63.40	-0.39	-0.05
tRNA-Thr	17660	17722	63				1	H	30.2	27.0	19.0	23.8	46.0	54.00	-0.17	0.12
tRNA-Pro	17724	17784	61				0	L	32.8	26.2	9.8	31.1	36.1	63.90	-0.46	0.03
CR1	17785	19715	1931				0	H	31.6	18.2	10.9	39.3	29.1	70.90	-0.25	-0.11
Total			19715						32.6	24.5	12.9	30.0	37.4	62.6	-0.31	0.04
PCGs			11297						31.2	25.2	13.2	30.4	38.4	61.6	-0.31	0.01
rRNA			2389						37.1	23.6	16.4	22.9	40.0	60.0	-0.18	0.24
tRNAs			1412						31.7	19.5	20.3	28.5	39.8	60.2	0.02	0.05
CR			3245						29.8	20.2	11.5	38.6	31.7	68.4	-0.27	-0.13
WANCY			795						32.7	24.0	15.5	27.8	39.5	60.5	-0.22	0.08
Intergenicspacer			938						35.3	24.0	10.3	30.4	34.3	65.7	-0.40	0.07

Table S1 h. Mitogenome features of GP3307.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				1	H	34.4	17.2	17.2	31.3	34.4	65.7	0.00	0.05
12SrRNA	66	985	920				0	H	36.3	25.9	17.1	20.8	42.9	57.1	-0.20	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.0	22.2	15.9	23.38	38.2	61.38	-0.17	0.24
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.4	11.0	29.3	40.4	59.7	-0.46	0.02
tRNA-Ile(I)	3483	3547	65				4	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3552	4935	1384				1	H	28.1	21.4	12.0	38.5	33.4	66.6	-0.28	-0.16
tRNA-Leu2(L2)	4937	5009	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5011	5080	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5080	5142	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5143	6174	1032	343	ATT	TAG	-2	H	37.1	28.6	7.9	26.4	36.5	63.5	-0.57	0.17
tRNA-Trp	6173	6236	64				549	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	6786	6850	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	6849	6921	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	6958	7018	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7019	7082	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7084	8685	1602	533	GTG	AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8676	8742	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8744	8805	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	8806	9489	684	227	ATG	TAA	1	H	32.9	25.7	16.1	25.3	41.8	58.2	-0.23	0.13
tRNA-Lys(K)	9491	9553	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9555	9716	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9707	10387	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.3	63.7	-0.43	0.08
COX3	10387	11170	784	261	ATG	T	0	H	30.6	26.7	15.9	26.8	52.6	57.4	-0.25	0.07
tRNA-Gly(G)	11171	11231	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11232	11574	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11575	11637	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11638	11928	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	11928	13265	1338	445	ATG	TAG	-1	H	33.4	27.1	10.0	29.4	37.1	62.8	-0.46	0.06
tRNA-His(H)	13265	13326	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13329	13385	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13383	13453	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13455	15227	1773	590	ATG	TAA	822	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16050	16565	516	171	ATG	AGA	0	L	25.5	26.4	6.2	21.9	32.6	47.4	-0.62	0.08
tRNA-Glu(E)	16566	16628	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16627	17739	1113	370	ATG	TAA	5	H	31.3	25.8	10.0	33.0	35.8	64.3	-0.44	-0.03
tRNA-Thr(T)	17745	17808	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17810	17870	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	17871	19397	1527				0	H	29.2	19.3	11.3	40.2	30.5	69.4	-0.26	-0.16
Total			19397						33.2	24.8	12.5	29.6	37.3	62.8	-0.33	0.06
PCGs			11283						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2390						37.4	23.6	16.4	22.6	40.0	60	-0.18	0.25
tRNAs			1419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			2911						28.7	20.3	11.6	39.4	31.9	68.1	-0.27	-0.16
WANCY			911						32.8	24.5	15.1	27.6	39.6	60.4	-0.24	0.09
Intergenicspacer			822						37.7	24.5	8.8	28.9	33.3	66.6	-0.47	0.13

Table S1 i. Mitogenome features of GP3318.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				1	H	34.4	17.2	17.2	31.3	34.4	65.7	0.00	0.05
12SrRNA	66	985	920				0	H	36.3	25.9	17.2	20.8	42.9	57.1	-0.20	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.0	22.2	15.9	23.8	38.2	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.5	11.0	29.1	40.5	59.5	-0.46	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	5144	1597				0	H	28.9	19.6	10.9	40.5	30.5	69.4	-0.29	-0.17
tRNA-Leu2(L2)	5145	5217	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5219	5288	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5288	5350	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5351	6382	1032	343	ATT	TAG	-2	H	37.1	28.6	7.9	26.4	36.5	63.5	-0.57	0.17
tRNA-Trp	6381	6444	64				548	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	6993	7057	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	7056	7128	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7165	7225	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7226	7289	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7291	8892	1602	533	GTG	AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8883	8949	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8951	9012	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9013	9696	684	227	ATG	TAA	1	H	32.9	25.7	16.1	25.3	41.8	58.2	-0.23	0.13
tRNA-Lys(K)	9698	9760	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9762	9923	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9914	10594	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.3	63.7	-0.43	0.08
COX3	10594	11377	784	261	ATG	T	0	H	30.6	26.7	15.9	26.8	42.6	57.4	-0.25	0.07
tRNA-Gly(G)	11378	11438	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11439	11781	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11782	11844	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11845	12135	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12135	13472	1338	445	ATG	TAG	-1	H	33.4	27.2	10.0	29.4	37.2	62.8	-0.46	0.06
tRNA-His(H)	13472	13533	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13536	13592	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13590	13660	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13662	15434	1773	590	ATG	TAA	543	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	15978	16493	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16494	16556	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16555	17667	1113	370	ATG	TAA	5	H	31.3	25.8	10.0	33.0	35.8	64.3	-0.44	-0.03
tRNA-Thr(T)	17673	17736	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17738	17798	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	17799	19096	1298				0	H	30.4	18.9	10.5	40.2	29.4	70.6	-0.29	-0.14
Total			19,096						33.3	24.7	12.4	29.6	37.1	62.9	-0.33	0.06
PCGs			11,283						33.2	26.4	11.5	28.9	37.9	62.1	-0.39	0.07
rRNA			2,390						37.4	23.6	16.4	22.6	40.0	60	-0.18	0.25
tRNAs			1,419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			2,895						29.6	19.3	10.7	40.4	30.0	70	-0.29	-0.15
WANCY			910						32.9	24.5	15.1	27.6	39.6	60.5	-0.24	0.09
Intergenicspacer			543						40.7	24.6	10.5	24.2	35.1	64.9	-0.40	0.25

Table S1 j. Mitogenome features of GP3320.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				1	H	34.4	17.2	17.2	31.3	34.4	65.7	0.00	0.05
12SrRNA	66	985	920				0	H	36.3	25.9	17.1	20.8	42.9	57.1	-0.20	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.0	22.2	15.9	23.8	38.2	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				1	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3549	5075	1527				0	H	28.7	20.1	11.3	39.9	31.4	68.6	-0.28	-0.16
tRNA-Leu2(L2)	5076	5148	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5150	5219	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5219	5281	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5282	6313	1032	343	ATT	TAG	-2	H	37.1	28.6	7.9	26.4	36.5	63.5	-0.57	0.17
tRNA-Trp	6312	6375	64				549	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	6925	6989	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	6988	7060	73				36	L	32.5	27.4	16.4	23.3	43.8	55.8	-0.25	0.16
tRNA-Cys	7097	7157	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7158	7221	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7223	8824	1602	533		AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8815	8881	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8883	8944	62				0	H	32.3	24.4	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	8945	9628	684	227	ATG	TAA	1	H	32.9	25.7	16.1	25.3	41.8	58.2	-0.23	0.13
tRNA-Lys(K)	9630	9692	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9694	9855	162	53	ATG	TAA	-10	H	40.7	30.0	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9846	10526	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.3	63.7	-0.43	0.08
COX3	10526	11309	784	261	ATG	T	0	H	30.6	26.7	15.9	26.8	42.6	57.4	-0.25	0.07
tRNA-Gly(G)	11310	11370	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11371	11713	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11714	11776	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11777	12067	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12067	13404	1338	445	ATG	TAG	-1	H	33.4	27.2	10.0	29.4	37.2	62.8	-0.46	0.06
tRNA-His(H)	13404	13465	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13468	13524	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13522	13592	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13594	15366	1773	590	ATG	TAA	830	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16197	16712	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16713	16775	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16774	17886	1113	370	ATG	TAA	5	H	31.3	25.8	10.0	33.0	35.8	64.3	-0.44	-0.03
tRNA-Thr(T)	17892	17955	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17957	18017	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	18018	19223	1206				0	H	30.1	19.4	10.7	39.8	30.1	69.9	-0.29	-0.14
Total			19223						33.3	24.8	12.4	29.5	37.2	62.8	-0.33	0.06
PCGs			11283						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2390						37.4	23.6	16.4	22.6	40.0	60	-0.18	0.25
tRNAs			1419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			2733						29.3	19.8	11.0	39.8	30.8	69.1	-0.29	-0.15
WANCY			911						32.8	24.5	15.1	27.6	39.6	60.4	-0.24	0.09
Intergenicspacer			830						38.2	24.3	9.1	28.5	33.3	66.7	-0.46	0.15

Table S1 k. Mitogenome features of GP3554.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				1	H	34.4	17.2	17.2	31.3	34.4	65.7	0.00	0.05
12SrRNA	66	985	920				0	H	36.3	25.9	17.1	20.8	42.9	57.1	-0.20	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.1	22.2	15.9	23.8	38.1	61.9	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	4814	1267				0	H	27.3	22.6	11.9	38.2	34.5	65.5	-0.31	-0.17
tRNA-Leu2(L2)	4815	4887	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	4889	4958	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	4958	5020	63				0	H	33.2	30.2	19.0	17.5	49.2	50.7	-0.23	0.31
ND2	5021	6052	1032	343	ATT	TAG	-2	H	31.7	28.5	7.9	26.5	36.4	58.2	-0.57	0.09
tRNA-Trp	6051	6114	64				461	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	6576	6640	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	6639	6711	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	6748	6808	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	6809	6872	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	6874	8475	1602	533		AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8466	8532	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8534	8595	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	8596	9279	684	227	ATG	TAA	1	H	32.9	25.7	16.1	25.3	41.8	58.2	-0.23	0.13
tRNA-Lys(K)	9281	9343	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9345	9506	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	39.3	61.7	-0.58	0.32
ATP6	9497	10177	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.6	63.7	-0.43	0.08
COX3	10177	10960	784	261	ATG	T	0	H	30.5	26.5	16.1	26.9	42.6	57.4	-0.24	0.06
tRNA-Gly(G)	10961	11021	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11022	11364	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11365	11427	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11428	11718	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	11718	13055	1338	445	ATG	TAG	-1	H	33.4	27.2	10.0	29.4	37.2	62.8	-0.46	0.06
tRNA-His(H)	13055	13116	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13119	13175	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13173	13243	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13245	15017	1773	590	ATG	TAA	799	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	15817	16332	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16333	16395	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16394	17506	1113	370	ATG	TAA	5	H	31.4	25.8	9.9	33.0	35.7	64.4	-0.45	-0.02
tRNA-Thr(T)	17512	17575	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17577	17637	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	17638	18877	1240				0	H	27.3	21.4	11.7	39.7	33.1	67	-0.29	-0.19
Total			19223						33.1	25.1	12.5	29.3	37.6	62.4	-0.34	0.06
PCGs			11283						33.2	26.3	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2390						37.4	23.6	16.3	22.6	40.0	60	-0.18	0.25
tRNAs			1419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			2733						27.3	22.0	11.8	38.9	33.8	66.2	-0.30	-0.18
WANCY			911						33.0	24.9	14.8	27.2	39.7	60.2	-0.25	0.10
Intergenicspacer			830						38.3	24.0	8.9	28.8	32.9	67.1	-0.46	0.14

Table S1 l. Mitogenome features of GP3555.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				1	H	34.4	17.2	17.2	31.3	24.4	65.7	0.00	0.05
12SrRNA	66	985	920				0	H	36.4	25.9	17.0	20.8	42.8	57.2	-0.21	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.1	22.2	15.9	23.8	38.1	61.9	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				1	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3549	5189	1641				0	H	29.2	19.3	11.1	40.5	30.3	69.7	-0.27	-0.16
tRNA-Leu2(L2)	5190	5262	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5264	5333	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5333	5395	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5396	6427	1032	343	ATT	TAG	-2	H	37.1	28.7	7.9	26.3	36.6	63.4	-0.57	0.17
tRNA-Trp	6426	6489	64				549	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	7039	7103	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	7102	7174	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7211	7271	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7272	7335	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7337	8938	1602	536		AGG	-10	H	28.7	24.0	16.1	31.2	40.1	59.9	-0.20	-0.04
tRNA-Ser2(S2)	8929	8995	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8997	9058	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9059	9742	684	227	ATG	TAA	1	H	32.9	25.6	16.1	25.4	41.7	58.3	-0.23	0.13
tRNA-Lys(K)	9744	9806	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9808	9969	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9960	10640	681	226	ATG	TAA	-1	H	34.4	26.0	10.4	29.2	36.4	63.6	-0.43	0.08
COX3	10640	11423	784	261	ATG	T	0	H	30.5	26.5	16.1	26.9	42.6	57.4	-0.24	0.06
tRNA-Gly(G)	11424	11484	61				0	H	39.3	19.7	13.1	27.9	32.9	67.2	-0.20	0.17
ND3	11485	11827	343	114	ATT	T	0	H	30.9	28.0	11.1	30.0	39.1	60.9	-0.43	0.01
tRNA-Arg(R)	11828	11890	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11891	12181	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12181	13518	1338	445	ATG	TAG	-1	H	34.6	23.1	15.4	26.9	38.5	61.5	-0.20	0.13
tRNA-His(H)	13518	13579	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13582	13638	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13636	13706	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13708	15480	1773	590	ATG	TAA	598	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16079	16594	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16595	16657	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16656	17768	1113	370	ATG	TAA	5	H	31.3	25.7	10.1	33.0	35.9	64.3	-0.44	-0.03
tRNA-Thr(T)	17774	17837	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17839	17899	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	17900	19586	1687				0	H	29.7	17.6	10.3	42.3	28.0	72	-0.26	-0.18
Total			19586						33.1	24.4	12.3	30.2	36.7	63.3	-0.33	0.05
PCGs			11283						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2390						37.4	23.6	16.3	22.6	39.9	60	-0.18	0.25
tRNAs			1419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			3328						29.4	18.4	10.7	41.4	29.1	70.8	-0.26	-0.17
WANCY			911						32.5	24.5	15.5	27.6	40.0	60.1	-0.23	0.08
Intergenicspacer			598						37.3	23.6	8.2	30.9	31.8	68.2	-0.48	0.09

Table S1 m. Mitogenome features of GP3556.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	62	62				0	H	34.9	17.5	17.5	30.2	34.9	65.1	0.00	0.07
12SrRNA	63	986	924				-1	H	36.3	26.0	17	20.8	43	57.1	-0.21	0.27
tRNA-Val(V)	986	1048	63				-1	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1048	2489	1442				29	H	38.2	22.3	15.7	23.8	38	62	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.3	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	5852	2305				0	H	31.1	16.1	10.0	42.7	26.2	73.8	-0.23	-0.16
tRNA-Leu2(L2)	5853	5925	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5927	5996	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5996	6058	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	6059	7090	1032	343	ATT	TAG	-3	H	37.1	28.5	7.9	26.5	36.4	63.6	-0.57	0.17
tRNA-Trp	7088	7152	65				548	H	38.5	23.1	13.8	24.6	36.9	63.1	-0.25	0.22
tRNA-Ala	7701	7766	66				-2	L	30.3	22.7	15.2	31.8	37.9	62.1	-0.20	-0.02
tRNA-Asn	7765	7837	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7874	7935	62				-1	L	22.6	30.6	19.4	27.4	50.0	50	-0.22	-0.10
tRNA-Tyr	7935	7998	64				-8	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7991	9601	1611	533	GTG	AGG	-10	H	28.6	24.1	16.1	31.2	40.2	59.8	-0.20	-0.04
tRNA-Ser2(S2)	9592	9658	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	9660	9721	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9722	10405	684	227	ATG	TAA	1	H	32.9	25.8	16.1	25.2	41.9	58.1	-0.23	0.13
tRNA-Lys(K)	10407	10469	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	10471	10632	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	10623	11303	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.3	63.7	-0.43	0.08
COX3	11303	12086	784	261	ATG	T	0	H	30.5	26.5	16.1	26.9	42.6	57.4	-0.24	0.06
tRNA-Gly(G)	12087	12147	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	12148	12490	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	12491	12553	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	12554	12844	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12844	14181	1338	445	ATG	TAG	-1	H	33.4	27.2	10.0	29.4	37.2	62.8	-0.46	0.06
tRNA-His(H)	14181	14242	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	14245	14301	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	14299	14369	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	14371	16143	1773	590	ATG	TAA	534	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16678	17193	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	17194	17256	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	17255	18367	1113	370	ATG	TAA	6	H	31.3	25.9	10.0	32.9	35.8	64.2	-0.44	-0.02
tRNA-Thr(T)	18374	18436	63				1	H	27.0	28.6	20.6	23.8	49.2	50.8	-0.16	0.06
tRNA-Pro(P)	18438	18498	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	18499	19335	837				0	H	26.8	24.5	12.8	36.0	37.3	62.8	-0.31	-0.15
Total			19335						33.2	24.4	12.4	30.0	36.8	63.2	-0.33	0.05
PCGs			11292						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2366						37.4	23.7	16.2	22.6	39.9	60	-0.19	0.25
tRNAs			1420						32.4	23.9	16.8	26.9	40.7	59.3	-0.17	0.09
CR			3142						30.0	18.4	10.8	40.9	29.1	70.9	-0.26	-0.15
WANCY			911						32.5	26.4	15.4	27.5	40	60	-0.26	0.08
Intergenicspacer			534						36.7	23.8	8.2	31.3	32.0	68	-0.49	0.08

Table S1 n. Mitogenome features of GP3557.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	62	62				0	H	34.9	17.5	17.5	30.2	34.9	65.1	0.00	0.07
12SrRNA	63	986	924				-1	H	36.3	26.0	17.0	20.8	43.0	57.1	-0.21	0.27
tRNA-Val(V)	986	1048	63				-1	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1048	2489	1442				29	H	38.2	22.3	15.7	23.8	38	62	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	4909	1362				0	H	27.5	21.1	11.6	39.8	32.7	67.3	-0.29	-0.18
tRNA-Leu2(L2)	4910	4982	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	4984	5053	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5053	5115	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5116	6147	1032	343	ATT	TAG	-3	H	37.1	28.7	7.9	26.3	36.6	63.4	-0.57	0.17
tRNA-Trp	6145	6209	65				548	H	38.5	23.1	13.8	24.6	36.9	63.1	-0.25	0.22
tRNA-Ala	6758	6823	66				-2	L	30.3	22.7	15.2	31.8	37.9	62.1	-0.20	-0.02
tRNA-Asn	6822	6894	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	6931	6992	62				-1	L	22.6	30.6	19.4	27.4	50.0	50	-0.22	-0.10
tRNA-Tyr	6992	7055	64				-8	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7048	8658	1611	536	GTG	AGG	-10	H	28.6	24.1	16.1	31.2	40.2	59.8	-0.20	-0.04
tRNA-Ser2(S2)	8649	8715	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8717	8778	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	8779	9462	684	227	ATG	TAA	1	H	32.9	25.6	16.1	25.4	41.7	58.3	-0.23	0.13
tRNA-Lys(K)	9464	9526	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9528	9689	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9680	10360	681	226	ATG	TAA	-1	H	34.4	26.0	10.4	29.2	36.4	63.6	-0.43	0.08
COX3	10360	11143	784	261	ATG	T	0	H	30.5	26.5	16.1	26.9	42.6	57.4	-0.24	0.06
tRNA-Gly(G)	11144	11204	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11205	11547	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11548	11610	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11611	11901	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	11901	13238	1338	445	ATG	TAG	-1	H	33.3	27.3	10.1	29.3	37.4	62.6	-0.46	0.06
tRNA-His(H)	13238	13299	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13302	13358	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13356	13426	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13428	15200	1773	590	ATG	TAA	1003	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16204	16719	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16720	16782	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16781	17893	1113	370	ATG	TAA	6	H	31.3	25.8	10.0	33.0	35.8	64.3	-0.44	-0.03
tRNA-Thr(T)	17900	17962	63				1	H	27.0	28.6	20.6	23.8	49.2	50.8	-0.16	0.06
tRNA-Pro(P)	17964	18024	61				20	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	18045	19745	1701				0	H	29.6	17.6	10.3	42.4	27.9	72	-0.26	-0.18
Total			19335						33.2	24.6	12.3	29.9	36.9	63.1	-0.33	0.05
PCGs			11292						33.1	26.4	11.5	29.0	37.9	62.1	-0.39	0.07
rRNA			2366						37.4	23.7	16.2	22.6	39.9	60	-0.19	0.25
tRNAs			1420						32.4	23.9	16.8	26.9	40.7	59.3	-0.17	0.09
CR			3142						28.6	19.2	10.9	41.3	30.1	69.9	-0.28	-0.18
WANCY			911						32.7	24.5	15.2	27.6	39.7	60.3	-0.23	0.08
Intergenicspacer			534						39.1	23.7	9.2	28.0	32.9	67.1	-0.44	0.17

Table S1 o. Mitogenome features of GP3558.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				1	H	34.4	17.2	17.2	31.3	34.4	65.7	0.00	0.05
12SrRNA	66	985	920				0	H	36.3	25.9	17.0	20.8	42.9	57.1	-0.21	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.1	22.2	15.9	23.8	38.1	61.9	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				1	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3549	5291	1743				0	H	29.2	18.5	10.7	41.6	29.2	70.8	-0.27	-0.18
tRNA-Leu2(L2)	5292	5364	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5366	5435	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5435	5497	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5498	6529	1032	343	ATT	TAG	-2	H	37.1	28.7	7.9	26.3	36.6	63.4	-0.57	0.17
tRNA-Trp	6528	6591	64				739	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	7331	7395	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	7394	7466	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7503	7563	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7564	7627	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7629	9230	1602	533	GTG	AGG	-10	H	28.7	24.0	16.1	31.2	40.1	59.9	-0.20	-0.04
tRNA-Ser2(S2)	9221	9287	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	9289	9350	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9351	10034	684	227	ATG	TAA	1	H	32.9	25.6	16.1	25.4	41.7	58.3	-0.23	0.13
tRNA-Lys(K)	10036	10098	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	10100	10261	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	10252	10932	681	226	ATG	TAA	-1	H	34.4	26.0	10.4	29.2	36.4	63.6	-0.43	0.08
COX3	10932	11715	784	261	ATG	T	0	H	30.5	26.5	16.1	26.9	42.6	57.4	-0.24	0.06
tRNA-Gly(G)	11716	11776	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11777	12119	343	114	ATT	T	0	H	30.9	28.0	11.1	30.0	39.1	60.9	-0.43	0.01
tRNA-Arg(R)	12120	12182	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	12183	12473	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12473	13810	1338	445	ATG	TAG	-1	H	33.3	27.4	10.1	29.3	37.4	62.6	-0.46	0.06
tRNA-His(H)	13810	13871	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13874	13930	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13928	13998	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	14000	15772	1773	590	ATG	TAA	991	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16764	17279	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	17280	17342	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	17341	18453	1113	370	ATG	TAA	5	H	31.4	25.8	9.9	33.0	35.7	64.4	-0.45	-0.02
tRNA-Thr(T)	18459	18522	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	18524	18584	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	18585	20094	1510				0	H	29.1	28.6	10.7	41.5	29.4	70.6	-0.46	-0.18
Total			20094						33.2	24.4	12.3	30.0	36.8	63.2	-0.33	0.05
PCGs			11283						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2390						37.4	23.6	16.3	22.6	39.9	60	-0.18	0.25
tRNAs			1419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			3253						29.1	18.5	10.7	41.6	29.3	70.7	-0.27	-0.18
WANCY			1101						31.8	24.4	16.2	27.5	40.6	59.3	-0.20	0.07
Intergenicspacer			991						39.0	23.7	8.7	28.5	32.5	67.5	-0.46	0.16

Table S1 p. Mitogenome features of GP3587.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	63	63				1	H	34.9	17.5	17.5	30.2	34.9	65.1	0.00	0.07
12SrRNA	65	984	920				0	H	36.2	26.0	17.2	20.7	43.2	56.9	-0.20	0.27
tRNA-Val(V)	985	1047	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1048	2518	1471				0	H	38.0	22.3	15.9	23.8	38.2	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				1	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3549	5096	1548				0	H	28.6	19.8	11.3	40.3	31.1	68.9	-0.27	-0.17
tRNA-Leu2(L2)	5097	5169	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5171	5240	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5240	5302	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5303	6334	1032	343	ATT	TAG	-2	H	37.1	28.6	7.9	26.4	36.5	63.5	-0.57	0.17
tRNA-Trp	6333	6396	64				723	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	7120	7184	65				-2	L	32.3	24.6	13.8	29.2	38.5	61.5	-0.28	0.05
tRNA-Asn	7183	7255	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7292	7352	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7353	7416	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7418	9019	1602	533	GTG	AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	9010	9076	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	9078	9139	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9140	9823	684	227	ATG	TAA	1	H	32.7	26.0	16.2	25.0	42.3	57.7	-0.23	0.13
tRNA-Lys(K)	9825	9887	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9889	10050	162	53	ATG	TAA	-10	H	40.7	29.6	8.0	21.6	37.7	62.3	-0.57	0.31
ATP6	10041	10721	681	226	ATG	TAA	-1	H	34.4	26.0	10.1	29.5	36.1	63.9	-0.44	0.08
COX3	10721	11504	784	261	ATG	T	0	H	30.4	26.3	16.2	27.2	42.5	57.6	-0.24	0.06
tRNA-Gly(G)	11505	11565	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11566	11908	343	114	ATT	T	0	H	30.3	28.3	11.7	29.7	39.9	60	-0.42	0.01
tRNA-Arg(R)	11909	11971	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11972	12262	291	96	ATG	TAA	-1	H	35.4	25.1	10.7	28.9	35.7	64.3	-0.40	0.10
ND4	12262	13599	1338	445	ATG	TAG	-1	H	33.6	27.1	9.9	29.4	37.0	63	-0.46	0.07
tRNA-His(H)	13599	13660	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13663	13719	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13717	13787	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13789	15561	1773	590	ATG	TAA	717	H	34.2	25.4	10.3	30.1	35.7	64.3	-0.42	0.06
ND6	16279	16794	516	171	ATG	AGA	0	L	45.3	26.4	6.4	21.9	32.8	67.2	-0.61	0.35
tRNA-Glu(E)	16795	16857	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16856	17968	1113	370	ATG	TAA	5	H	31.1	25.7	10.2	33.1	35.8	64.2	-0.43	-0.03
tRNA-Thr(T)	17974	18037	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	18039	18099	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	18100	19981	1882				0	H	31.1	15.0	9.6	44.3	24.7	75.4	-0.22	-0.18
Total			19,981						33.3	24.2	12.2	30.3	36.4	63.6	-0.33	0.05
PCGs			11,283						33.1	26.4	11.5	29.0	37.9	62.1	-0.39	0.07
rRNA			2,391						37.3	23.7	16.4	22.6	40.1	59.9	-0.18	0.25
tRNAs			1,418						32.5	24.0	16.9	26.7	40.8	59.2	-0.17	0.10
CR			3,430						30.0	17.2	10.4	42.5	27.6	72.5	-0.25	-0.17
WANCY			1,085						34.1	24.8	13.9	27.1	38.7	61.2	-0.28	0.11
Intergenicspacer			717						38.1	23.2	8.9	29.7	32.1	67.8	-0.45	0.12

Table S1 q. Mitogenome features of GP3938.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	63	63				0	H	34.9	17.5	17.5	30.2	34.9	65.1	0.00	0.07
12SrRNA	64	985	922				0	H	36.2	25.9	17.0	20.8	43	57	-0.21	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.0	22.2	15.9	23.8	38.2	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.4	11.0	29.3	40.4	59.7	-0.46	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	5117	1570				0	H	29.3	20.1	11.5	39.1	31.6	68.4	-0.27	-0.14
tRNA-Leu2(L2)	5118	5190	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5192	5261	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5261	5323	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5324	6355	1032	343	ATT	TAG	-2	H	37.1	28.6	7.9	26.4	36.5	63.5	-0.57	0.17
tRNA-Trp	6354	6417	64				548	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	6966	7031	66				-2	L	30.3	22.7	15.2	31.8	37.9	62.1	-0.20	-0.02
tRNA-Asn	7030	7102	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7139	7199	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7200	7263	64				-8	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7256	8866	1611	536	GTG	AGG	-10	H	28.6	24.1	16.1	31.2	40.2	59.8	-0.20	-0.04
tRNA-Ser2(S2)	8857	8923	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8925	8986	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	8987	9670	684	227	ATG	TAA	1	H	32.9	25.7	16.1	25.3	41.8	58.2	-0.23	0.13
tRNA-Lys(K)	9672	9734	63				1	H	31.7	14.3	19.0	34.5	33.3	66.2	0.14	-0.04
ATP8	9736	9897	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9888	10568	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.3	63.7	-0.43	0.08
COX3	10568	11351	784	261	ATG	T	0	H	30.6	26.7	15.9	26.8	42.6	57.4	-0.25	0.07
tRNA-Gly(G)	11352	11412	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11413	11755	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11756	11818	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11819	12109	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12109	13446	1338	445	ATG	TAG	-1	H	33.4	27.2	10.0	29.4	37.2	62.8	-0.46	0.06
tRNA-His(H)	13446	13507	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13510	13566	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13564	13634	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13636	15408	1773	590	ATG	TAA	1002	H	34.1	25.3	10.4	30.2	35.7	64.3	-0.42	0.06
ND6	16411	16926	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16927	16989	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16988	18100	1113	370	ATG	TAA	5	H	31.3	25.8	10.0	33.0	35.8	64.3	-0.44	-0.03
tRNA-Thr(T)	18106	18169	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	18171	18231	61				0	L	31.1	31.1	26.2	26.2	42.6	57.3	-0.09	0.09
CR1	18232	19900	1669				0	H	31.9	16.4	9.7	42.0	26.1	73.9	-0.26	-0.14
Total			19,900						33.5	24.4	12.3	29.8	36.7	63.3	-0.33	0.06
PCGs			11,292						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2,392						37.3	23.7	16.3	22.7	40.0	60	-0.19	0.24
tRNAs			1,419						32.4	23.9	16.9	26.8	40.8	59.2	-0.17	0.09
CR			3,239						30.7	18.2	10.6	40.6	28.8	71.3	-0.26	-0.14
WANCY			910						32.9	24.5	15.2	27.5	39.7	60.4	-0.23	0.09
Intergenicspacer			1,002						38.7	24.1	9.3	27.8	33.4	66.5	-0.44	0.16

Table S1 r. Mitogenome features of GP3987.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	63	63				0	H	34.9	17.5	17.5	30.2	34.9	65.1	0.00	0.07
12SrRNA	64	984	921				0	H	36.2	26.0	17.2	20.7	43.2	56.9	-0.20	0.27
tRNA-Val(V)	985	1047	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1048	2518	1471				0	H	38.0	22.3	15.9	23.8	38.2	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.7	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				1	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3549	5096	1548				0	H	28.6	19.8	11.2	40.3	31.0	68.9	-0.28	-0.17
tRNA-Leu2(L2)	5097	5169	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5171	5240	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5240	5302	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5303	6334	1032	343	ATT	TAG	-2	H	37.2	28.7	7.8	26.3	36.5	63.5	-0.57	0.17
tRNA-Trp	6333	6396	64				1	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	6398	6462	65				191	L	36.9	20.0	10.8	32.3	30.8	69.2	-0.30	0.07
tRNA-Asn	6654	6726	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	6763	6823	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	6824	6887	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	6889	8490	1602	533	GTG	AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8481	8547	67				1	L	31.2	19.4	14.9	34.3	34.3	65.5	-0.13	-0.05
tRNA-Asp(D)	8549	8610	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	8611	9294	684	227	ATG	TAA	1	H	32.9	26.0	16.1	25.0	42.1	57.9	-0.24	0.14
tRNA-Lys(K)	9296	9358	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9360	9521	162	53	ATG	TAA	-10	H	40.7	29.6	8.0	21.6	37.7	62.3	-0.57	0.31
ATP6	9512	10192	681	226	ATG	TAA	-1	H	34.4	26.0	10.1	29.5	36.1	63.9	-0.44	0.08
COX3	10192	10975	784	261	ATG	T	0	H	30.4	26.4	16.1	27.2	42.5	57.6	-0.24	0.06
tRNA-Gly(G)	10976	11036	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11037	11379	343	114	ATT	T	0	H	30.3	28.3	11.7	29.7	39.9	60	-0.42	0.01
tRNA-Arg(R)	11380	11442	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11443	11733	291	96	ATG	TAA	-1	H	35.4	25.1	10.7	28.9	35.7	64.3	-0.40	0.10
ND4	11733	13070	1338	445	ATG	TAG	-1	H	33.6	27.1	9.9	29.5	36.9	63.1	-0.46	0.06
tRNA-His(H)	13070	13131	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13134	13190	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13188	13258	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13260	15032	1773	590	ATG	TAA	844	H	34.2	25.4	10.3	30.1	35.7	64.3	-0.42	0.06
ND6	15877	16392	516	171	ATG	AGA	0	L	45.3	26.3	6.4	21.9	32.8	67.2	-0.61	0.35
tRNA-Glu(E)	16393	16455	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16454	17566	1113	370	ATG	TAA	5	H	31.1	25.8	10.1	33.1	35.8	64.2	-0.44	-0.03
tRNA-Thr(T)	17572	17635	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17637	17697	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	17698	19579	1882				0	H	31.1	15.1	9.6	44.2	24.8	75.3	-0.22	-0.17
Total			19,579						33.2	24.2	122	30.4	36.4	63.6	0.67	0.04
PCGs			11,283						33.2	26.4	11.5	29.0	37.9	62.2	-0.39	0.07
rRNA			2,391						37.3	23.7	16.4	22.6	40.1	59.9	-0.18	0.25
tRNAs			1,418						32.7	23.8	16.7	26.8	40.5	59.5	-0.18	0.10
CR			3,430						30.0	17.2	10.3	42.4	27.6	72.4	-0.25	-0.17
WANCY			556						30.6	24.5	17.3	27.6	41.8	58.2	-0.17	0.05
Intergenicspacer			844						38.4	23.8	9.1	28.7	32.9	67.1	-0.45	0.14

Table S1 s. Mitogenome features of GP4125.

gene	Position		Length	Aminoacid	Codon		intergenic region	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop										
tRNA-Phe(F)	1	64	64				0	H	34.4	17.2	17.2	31.3	34.4	65.7	0.00	0.05
12SrRNA	65	985	920				0	H	36.3	25.9	17.1	20.8	42.9	57.1	-0.20	0.27
tRNA-Val(V)	986	1048	63				0	H	36.5	20.6	11.1	31.7	31.7	68.2	-0.30	0.07
16SrRNA	1049	2518	1470				0	H	38.0	22.2	15.9	23.8	38.1	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.4	11.0	29.3	40.4	59.7	-0.46	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	5162	1615				0	H	29.2	19.4	11.1	40.2	30.5	69.4	-0.27	-0.16
tRNA-Leu2(L2)	5163	5235	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5237	5306	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.8	-0.39	0.18
tRNA-Met(M)	5306	5368	63				0	H	33.3	30.2	19.0	17.5	48.2	50.8	-0.23	0.31
ND2	5369	6400	1032	343	ATT	TAG	-2	H	37.1	28.6	79	26.4	36.5	63.5	0.47	0.17
tRNA-Trp	6399	6462	64				549	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala	7012	7076	65				-2	L	30.8	23.1	15.4	30.8	38.5	61.6	-0.20	0.00
tRNA-Asn	7075	7147	73				36	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys	7184	7244	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr	7245	7308	64				1	L	26.6	23.4	15.6	34.4	39.1	61	-0.20	-0.13
COX1	7310	8911	1602	533	GTG	AGG	-10	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8902	8968	67				1	L	31.3	19.4	14.9	34.3	34.3	65.6	-0.13	-0.05
tRNA-Asp(D)	8970	9031	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9032	9715	684	227	ATG	TAA	1	H	33.0	25.7	15.9	25.3	41.7	58.3	-0.24	0.13
tRNA-Lys(K)	9717	9779	63				1	H	31.7	14.3	19.0	34.9	33.3	66.6	0.14	-0.05
ATP8	9781	9942	162	53	ATG	TAA	-10	H	40.7	30.2	8.0	21.0	38.3	61.7	-0.58	0.32
ATP6	9933	10613	681	226	ATG	TAA	-1	H	34.5	26.0	10.3	29.2	36.3	63.7	-0.43	0.08
COX3	10613	11396	784	261	ATG	T	0	H	30.6	26.7	15.9	26.8	42.6	57.4	-0.25	0.07
tRNA-Gly(G)	11397	11457	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11458	11800	343	114	ATT	T	0	H	30.6	28.0	11.4	30.0	39.4	60.6	-0.42	0.01
tRNA-Arg(R)	11801	11863	63				0	H	33.3	19.0	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11864	12154	291	96	ATG	TAA	-1	H	35.4	24.4	10.7	29.6	35.1	65	-0.39	0.09
ND4	12154	13491	1338	445	ATG	TAG	-1	H	33.4	27.2	10.0	29.4	37.2	62.8	-0.46	0.06
tRNA-His(H)	13491	13552	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13555	13611	57				-3	H	26.3	26.3	21.1	26.3	47.4	52.6	-0.11	0.00
tRNA-Leu1(L1)	13609	13679	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13681	15453	1773	590	ATG	TAA	449	H	34.1	25.3	10.4	30.1	35.8	64.2	-0.42	0.06
ND6	15903	16418	516	171	ATG	AGA	0	L	45.5	26.4	6.2	21.9	32.6	67.4	-0.62	0.35
tRNA-Glu(E)	16419	16481	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16480	17592	1113	370	ATG	TAA	5	H	31.3	25.8	10.0	33.0	35.8	64.3	-0.44	-0.03
tRNA-Thr(T)	17598	17661	64				1	H	26.6	28.1	21.9	23.4	50.0	50	-0.12	0.06
tRNA-Pro(P)	17663	17723	61				0	L	31.1	31.1	11.5	26.2	42.6	57.3	-0.46	0.09
CR1	17724	19118	1395				0	H	30.8	17.9	10.2	41.1	28.1	71.9	-0.27	-0.14
Total			19,118				-1		33.2	24.5	12.4	29.9	36.9	63.1	-0.33	0.05
PCGs			11,283	3750			-1		33.2	26.4	11.5	28.9	37.9	62.1	-0.39	0.07
rRNA							-1		37.4	23.6	16.4	22.6	40.0	60	-0.18	0.25
tRNAs			1,419				-1		32.4	23.9	16.9	26.9	40.8	59.3	-0.17	0.09
CR							-1		30.0	18.7	10.7	40.6	29.4	70.6	-0.27	-0.15
WANCY							-1		32.8	24.5	15.1	27.6	39.6	60.4	-0.24	0.09
Intergenicspacer							-1		35.9	23.6	8.2	32.3	31.8	68.2	-0.48	0.05

Table S1 t. Mitogenome features of GP3586.

gene	Position		Length	Aminoacid	Codon		intergenic	Strand	A%	C%	G%	T%	G+C	A+T	GCskews	ATskews
	Minimum	Maximum			Star	Stop	region									
tRNA-Phe(F)	1	63	63				0	H	34.9	17.5	17.5	30.2	34.9	65.1	0.00	0.07
12SrRNA	64	984	921				0	H	36.2	26.1	17.2	20.6	43.2	56.8	-0.21	0.27
tRNA-Val(V)	985	1047	63				0	H	36.5	20.6	11.1	31.7	31.7	68.3	-0.30	0.07
16SrRNA	1048	2518	1471				0	H	38.0	22.3	15.9	23.8	38.2	61.8	-0.17	0.23
ND1	2519	3482	964	321	ATA	T	0	H	30.4	29.3	11.1	29.3	40.4	59.6	-0.45	0.02
tRNA-Ile(I)	3483	3547	65				0	H	32.3	27.7	24.6	15.4	52.3	47.7	-0.06	0.35
CR2	3548	5289	1742				0	H	29.3	18.6	10.9	41.3	29.4	70.6	-0.26	-0.17
tRNA-Leu2(L2)	5290	5362	73				1	H	32.9	23.3	16.4	27.4	39.7	60.3	-0.17	0.09
tRNA-Gln(Q)	5364	5433	70				-1	L	37.1	25.7	11.4	25.7	37.1	62.9	-0.39	0.18
tRNA-Met(M)	5433	5495	63				0	H	33.3	30.2	19.0	17.5	49.2	50.8	-0.23	0.31
ND2	5496	6527	1032	343	ATT	TAG	-2	H	37.1	28.7	7.9	26.3	36.3	63.7	-0.57	0.17
tRNA-Trp(W)	6526	6589	64				0	H	39.1	23.4	14.1	23.4	37.5	62.5	-0.25	0.25
tRNA-Ala(A)	6590	6653	64				0	L	37.5	20.3	10.9	31.3	31.3	68.7	-0.30	0.09
tRNA-Asn(N)	6654	6726	73				492	L	32.9	27.4	16.4	23.3	43.8	56.2	-0.25	0.17
tRNA-Cys(C)	7219	7279	61				0	L	23.0	31.1	19.7	26.2	50.8	49.2	-0.22	-0.07
tRNA-Tyr(Y)	7280	7343	64				1	L	26.6	23.4	15.6	34.4	39.1	60.9	-0.20	-0.13
COX1	7345	8946	1602	533	GTG	AGG	1	H	28.6	24.0	16.2	31.2	40.2	59.8	-0.19	-0.04
tRNA-Ser2(S2)	8937	9003	67				1	L	31.3	19.4	14.9	34.3	34.3	65.7	-0.13	-0.05
tRNA-Asp(D)	9005	9066	62				0	H	32.3	24.2	17.7	25.8	41.9	58.1	-0.16	0.11
COX2	9067	9750	684	227	ATG	TAA	1	H	32.9	26.0	16.1	25.0	42.1	57.9	-0.24	0.14
tRNA-Lys(K)	9752	9814	63				1	H	31.7	14.3	19.0	34.9	33.3	66.7	0.14	-0.05
ATP8	9816	9977	162	53	ATG	TAA	-10	H	40.7	29.6	8.0	21.6	37.7	62.3	-0.57	0.31
ATP6	9968	10648	681	226	ATG	TAA	-1	H	34.4	26.0	10.1	29.5	36.1	63.9	-0.44	0.08
COX3	10648	11431	784	261	ATG	T	0	H	30.4	26.3	16.2	27.2	42.5	57.5	-0.24	0.06
tRNA-Gly(G)	11432	11492	61				0	H	39.3	19.7	13.1	27.9	32.8	67.2	-0.20	0.17
ND3	11493	11835	343	114	ATT	T	0	H	30.3	28.3	11.7	29.7	39.9	60.1	-0.42	0.01
tRNA-Arg(R)	11836	11898	63				0	H	33.3	19	17.5	30.2	36.5	63.5	-0.04	0.05

ND4L	11899	12189	291	96	ATG	TAA	-1	H	35.4	25.1	10.7	28.9	35.7	64.3	-0.40	0.10
ND4	12189	13526	1338	445	ATG	TAG	-1	H	33.6	27.1	9.9	29.4	37	63	-0.46	0.07
tRNA-His(H)	13526	13587	62				2	H	33.9	21.0	19.4	25.8	40.3	59.7	-0.04	0.14
tRNA-Ser1(S1)	13590	13646	57				-3	H	26.3	26.3	21.1	26.3	47.3	52.7	-0.11	0.00
tRNA-Leu1(L1)	13644	13714	71				1	H	31.0	23.9	21.1	23.9	45.1	54.9	-0.06	0.13
ND5	13716	15488	1773	590	ATG	TAA	661	H	34.2	25.4	10.3	30.1	35.7	64.3	-0.42	0.06
ND6	16150	16665	516	171	TAC	TCT	0	L	45.3	26.4	6.4	21.9	32.9	67.1	-0.61	0.35
tRNA-Glu(E)	16666	16728	63				-2	L	36.5	25.4	14.3	23.8	39.7	60.3	-0.28	0.21
CYTB	16727	17839	1113	370	ATG	TAA	5	H	31.1	25.6	10.2	33.1	35.8	64.2	-0.43	-0.03
tRNA-Thr(T)	17845	17908	64				1	H	26.6	28.1	21.9	23.4	50.0	50.0	-0.12	0.06
tRNA-Pro(P)	17910	17970	61				0	L	31.1	31.1	11.5	26.2	42.6	57.4	-0.46	0.09
CR1	17971	19854	1884				0	H	31.0	15.0	9.6	44.3	24.7	75.3	-0.22	-0.18
Total			19854						33.2	24.0	12.2	30.5	36.2	63.7	-0.33	0.04
PCGs			11283	3750					32.1	25.6	12.4	30.0	38.0	62.1	-0.35	0.03
rRNA			2392						37.3	23.7	16.4	22.6	40.1	59.9	-0.18	0.25
tRNAs			1417						31.3	19.7	20.8	28.2	40.5	59.5	0.03	0.05
CRs			3626						30.2	16.7	10.2	42.9	26.9	73.1	-0.24	-0.17
WANCY			819						33.5	24.8	14.5	27.1	39.4	60.6	-0.26	0.11
Intergenicspacer			661						38.1	23.3	8.9	29.7	32.2	67.8	-0.45	0.12