

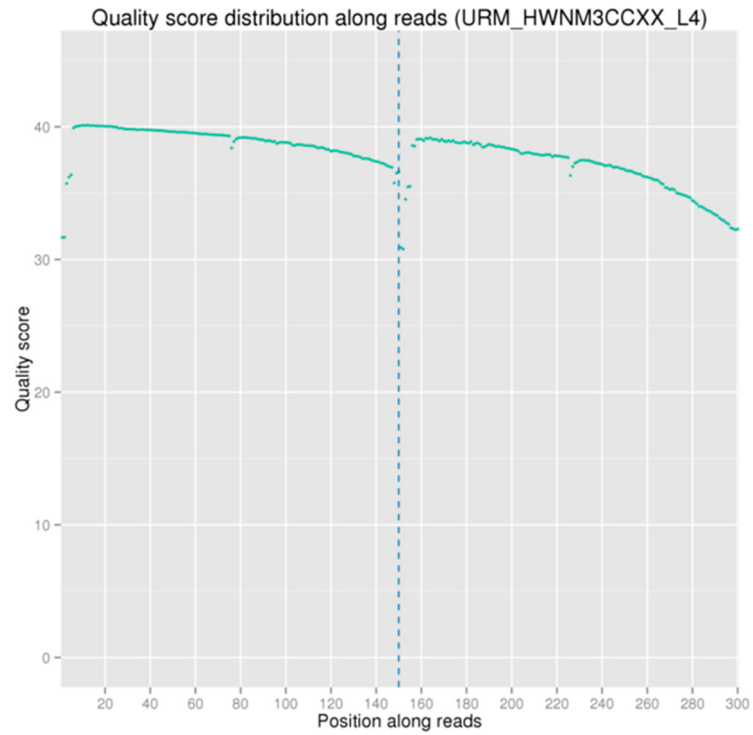


Figure S1. The quality of sequencing of *A. urmiana*

Table S1. Summary of data output quality for *A. urmiana*

Raw Reads	Clean Reads	Raw Base (G)	Clean Base (G)	Effective Rate (%)	Error Rate (%)	Q20 (%)	Q30 (%)	GC Content (%)
56,193,117	55,893,580	16.86	16.77	99.47	0.03	95.47	90.31	36.02

Table S2. The complete mitochondrial genome characteristics of *A. urmiana*

gene	Type	Position		Length (bp)	INC	Start codon	Stop codon	Anti codon	Strand
tRNA-Met	transfer RNA	1	65	65	-1			CAU	H
ND2	protein coding	65	955	891	-3	ATG	TAA		H
tRNA-Trp	transfer RNA	953	1017	65	18			UCA	H
tRNA-Ile	transfer RNA	1036	1098	63	12			GAU	L

tRNA-Gln	transfer RNA	1111	1176	66	57			UUG	L
tRNA-Cys	transfer RNA	1234	1294	61	11			GCA	L
tRNA-Tyr	transfer RNA	1306	1367	62	1			GUA	L
COX1	protein coding	1369	2902	1534	-1	ATG	T		H
tRNA-Leu	transfer RNA	2902	2968	67	-1			UAA	H
COX2	protein coding	2968	3649	682	0	ATG	T		H
tRNA-Lys	transfer RNA	3650	3713	64	4			CUU	H
tRNA-Asp	transfer RNA	3718	3779	62	0			GUC	H
ATP8	protein coding	3780	3941	162	-7	ATC	TAA		H
ATP6	protein coding	3935	4594	660	-1	GTG	TAA		H
COX3	protein coding	4594	5379	786	1	ATG	TAA		H
tRNA-Gly	transfer RNA	5381	5441	61	0			UCC	H
ND3	protein coding	5442	5777	336	28	ATT	TAG		H
tRNA-Ala	transfer RNA	5806	5864	59	0			UGC	H
tRNA-Arg	transfer RNA	5865	5929	65	-1			UCG	H
tRNA-Asn	transfer RNA	5929	5991	63	0			GUU	H
tRNA-Ser	transfer RNA	5992	6056	65	-2			GCU	H
tRNA-Glu	transfer RNA	6055	6120	66	-4			UUC	H
tRNA-Phe	transfer RNA	6117	6180	64	-1			GAA	L
ND5	protein coding	6180	7776	1597	23	ATG	T		L
tRNA-His	transfer RNA	7800	7861	62	-1			GUG	L
ND4	protein coding	7861	8992	1132	49	ATA	T		L
ND4L	protein coding	9042	9302	261	1	ATC	TAA		L
tRNA-Thr	transfer RNA	9304	9365	62	-1			UGU	H
tRNA-Pro	transfer RNA	9365	9427	63	1			UGG	L
ND6	protein coding	9429	9896	468	24	GTG	TAG		H
CYTB	protein coding	9921	11051	1131	3	ATG	TAA		H
tRNA-Ser	transfer RNA	11055	11121	67	6			UGA	H
ND1	protein coding	11128	12024	897	11	ATG	TAA		L
tRNA-Leu	transfer RNA	12036	12099	64	2			UAG	L
16S ribosomal RNA	ribosomal RNA	12102	13255	1154	1				L
tRNA-Val	transfer RNA	13257	13316	60	0			UAC	L
12S ribosomal RNA	ribosomal RNA	13317	14027	711	0				L
control region	-	14028	15699	1672					

Table S3. Comparison of skewness in *Artemia* mitogenomes. (URM: *A. urmiana*, TIB: *A. tibetiana*, SIN: *A. sinica*, FRA: *A. franciscana*)

Sequence	Skew	URM ¹	TIB ²	SIN ³	FRA ⁴
CmtG	AT-	-0.014	-0.010	-0.022	-0.039
	GC-	-0.083	-0.078	-0.070	-0.005
PCGs+rRNAs	AT-	-0.166	-0.164	-0.169	-0.172
	GC-	-0.054	-0.051	-0.049	-0.028
ND2	AT-	-0.165	-0.149	-0.201	-0.218

	GC-	-0.164	-0.176	-0.074	-0.078
COX1	AT-	-0.154	-0.151	-0.179	-0.185
	GC-	-0.079	-0.078	-0.054	0.000
COX2	AT-	-0.158	-0.143	-0.164	-0.142
	GC-	-0.122	-0.129	-0.125	-0.054
ATP8	AT-	-0.091	-0.118	-0.266	-0.252
	GC-	-0.492	-0.433	-0.359	-0.200
ATP6	AT-	-0.177	-0.176	-0.168	-0.202
	GC-	-0.166	-0.130	-0.198	-0.127
COX3	AT-	-0.162	-0.183	-0.186	-0.220
	GC-	-0.030	0.013	-0.016	0.096
ND3	AT-	-0.256	-0.226	-0.277	-0.247
	GC-	-0.079	-0.126	-0.041	-0.009
ND5	AT-	-0.212	-0.224	-0.236	-0.215
	GC-	0.076	0.087	0.031	0.000
ND4	AT-	-0.284	-0.296	-0.272	-0.198
	GC-	-0.081	-0.022	-0.058	-0.172
ND4L	AT-	-0.180	-0.145	-0.184	-0.111
	GC-	-0.012	-0.091	-0.024	-0.051
ND6	AT-	-0.230	-0.212	-0.195	-0.274
	GC-	-0.279	-0.287	-0.283	-0.065
CYTB	AT-	-0.235	-0.195	-0.224	-0.263
	GC-	-0.165	-0.192	-0.166	-0.075
ND1	AT-	-0.230	-0.248	-0.191	-0.206
	GC-	0.035	-0.003	0.003	-0.038
16S	AT-	0.033	0.034	0.064	0.046
	GC-	0.108	0.093	0.080	0.055
12S	AT-	0.044	0.035	0.055	0.043
	GC-	0.115	0.125	0.129	0.113

1: this study; 2: JQ975177; 3: MK069595; 4: X69067

Table S4. RSCU information in *Artemia* mitogenomes (URM: *A. urmiana*, TIB: *A. tibetiana*, SIN: *A. sinica*, FRA:

A. franciscana).

Codon	AA	URM			TIB			SIN			FRA		
		ObsFreq	RSCU	%	ObsFreq	RSCU	%	ObsFreq	RSCU	%	ObsFreq	RSCU	%
UAG	*	2	0.444	-	3	0.667	-	1	0.25	-	5	0.833	-
UAA	*	7	1.556	-	6	1.333	-	7	1.75	-	7	1.167	-
GCU	A	66	1.451	1.89	66	1.467	1.88	69	1.586	1.97	78	1.714	2.21
GCG		16	0.352	0.46	11	0.244	0.31	15	0.345	0.43	18	0.396	0.51
GCC		62	1.363	1.77	63	1.4	1.79	44	1.011	1.25	46	1.011	1.31

GCA		38	0.835	1.09	40	0.889	1.14	46	1.057	1.31	40	0.879	1.14
UGU	C	27	1.2	0.77	30	1.333	0.85	24	1.091	0.68	33	1.435	0.94
UGC		18	0.8	0.51	15	0.667	0.43	20	0.909	0.57	13	0.565	0.37
GAU	D	55	1.447	1.57	52	1.444	1.48	50	1.333	1.43	50	1.408	1.42
GAC		21	0.553	0.60	20	0.556	0.57	25	0.667	0.71	21	0.592	0.60
GAG	E	22	0.512	0.63	26	0.591	0.74	23	0.535	0.66	33	0.75	0.94
GAA		64	1.488	1.83	62	1.409	1.77	63	1.465	1.80	55	1.25	1.56
UUU	F	200	1.342	5.71	204	1.388	5.81	223	1.477	6.36	215	1.369	6.10
UUC		98	0.658	2.80	90	0.612	2.56	79	0.523	2.25	99	0.631	2.81
GGU	G	42	0.743	1.20	38	0.664	1.08	54	0.977	1.54	58	1.074	1.65
GGG		80	1.416	2.29	86	1.502	2.45	64	1.158	1.83	75	1.389	2.13
GGC		27	0.478	0.77	23	0.402	0.66	21	0.38	0.60	20	0.37	0.57
GGA	H	77	1.363	2.20	82	1.432	2.34	82	1.484	2.34	63	1.167	1.79
CAC		38	1.013	1.09	37	0.961	1.05	32	0.853	0.91	20	0.533	0.57
CAU	I	37	0.987	1.06	40	1.039	1.14	43	1.147	1.23	55	1.467	1.56
AUU		201	1.431	5.74	201	1.411	5.72	223	1.497	6.36	203	1.44	5.76
AUC	K	80	0.569	2.29	84	0.589	2.39	75	0.503	2.14	79	0.56	2.24
AAA		35	1.029	1.00	44	1.222	1.25	42	1.151	1.20	41	1.012	1.16
AAG	L	33	0.971	0.94	28	0.778	0.80	31	0.849	0.88	40	0.988	1.14
CUA		107	1.255	3.06	113	1.291	3.22	88	1.11	2.51	100	1.286	2.84
CUC		78	0.915	2.23	90	1.029	2.56	63	0.795	1.80	50	0.643	1.42
CUG		40	0.469	1.14	39	0.446	1.11	27	0.341	0.77	34	0.437	0.97
CUU		116	1.361	3.31	108	1.234	3.08	139	1.754	3.96	127	1.633	3.61
UUA		156	1.381	4.46	165	1.46	4.70	176	1.402	5.02	185	1.48	5.25
UUG	M	70	0.619	2.00	61	0.54	1.74	75	0.598	2.14	65	0.52	1.85
AUG		47	0.55	1.34	58	0.659	1.65	46	0.487	1.31	59	0.631	1.68
AUA	N	124	1.45	3.54	118	1.341	3.36	143	1.513	4.08	128	1.369	3.63
AAC		34	0.636	0.97	30	0.577	0.85	33	0.606	0.94	31	0.5	0.88
AAU	P	73	1.364	2.09	74	1.423	2.11	76	1.394	2.17	93	1.5	2.64
CCU		47	1.297	1.34	49	1.38	1.40	57	1.606	1.63	66	1.872	1.87
CCG		18	0.497	0.51	21	0.592	0.60	17	0.479	0.48	15	0.426	0.43
CCC		52	1.434	1.49	46	1.296	1.31	38	1.07	1.08	27	0.766	0.77
CCA	Q	28	0.772	0.80	26	0.732	0.74	30	0.845	0.86	33	0.936	0.94
CAG		17	0.459	0.49	16	0.451	0.46	16	0.478	0.46	20	0.58	0.57
CAA	R	57	1.541	1.63	55	1.549	1.57	51	1.522	1.45	49	1.42	1.39
CGA		23	1.508	0.66	24	1.6	0.68	24	1.6	0.68	20	1.25	0.57
CGC		11	0.721	0.31	9	0.6	0.26	9	0.6	0.26	7	0.438	0.20
CGG		10	0.656	0.29	8	0.533	0.23	13	0.867	0.37	13	0.813	0.37
CGU	S	17	1.115	0.49	19	1.267	0.54	14	0.933	0.40	24	1.5	0.68
AGC		20	0.423	0.57	23	0.475	0.66	21	0.434	0.60	20	0.408	0.57
AGA		73	1.545	2.09	67	1.385	1.91	75	1.55	2.14	68	1.388	1.93
UCA		66	1.397	1.89	71	1.468	2.02	67	1.385	1.91	73	1.49	2.07
UCC		50	1.058	1.43	54	1.116	1.54	51	1.054	1.45	56	1.143	1.59
UCG		21	0.444	0.60	20	0.413	0.57	21	0.434	0.60	21	0.429	0.60
UCU		114	2.413	3.26	114	2.357	3.25	124	2.563	3.54	117	2.388	3.32
AGG		7	0.148	0.20	6	0.124	0.17	6	0.124	0.17	7	0.143	0.20
AGU	T	27	0.571	0.77	32	0.661	0.91	22	0.455	0.63	30	0.612	0.85
ACA		43	1.036	1.23	44	1.06	1.25	42	1.031	1.20	45	1.184	1.28
ACC		41	0.988	1.17	38	0.916	1.08	30	0.736	0.86	24	0.632	0.68
ACG		12	0.289	0.34	13	0.313	0.37	9	0.221	0.26	12	0.316	0.34
ACU	V	70	1.687	2.00	71	1.711	2.02	82	2.012	2.34	71	1.868	2.02
GUC		51	0.797	1.46	43	0.694	1.22	45	0.776	1.28	40	0.675	1.14
GUG		44	0.688	1.26	44	0.71	1.25	31	0.534	0.88	44	0.743	1.25
GUU		85	1.328	2.43	80	1.29	2.28	82	1.414	2.34	70	1.181	1.99
GUA	W	76	1.188	2.17	81	1.306	2.31	74	1.276	2.11	83	1.401	2.36
UGA		58	1.261	1.66	58	1.275	1.65	62	1.363	1.77	69	1.516	1.96
UGG	Y	34	0.739	0.97	33	0.725	0.94	29	0.637	0.83	22	0.484	0.62
UAC		60	0.816	1.71	47	0.635	1.34	49	0.653	1.40	45	0.604	1.28
UAU		87	1.184	2.49	101	1.365	2.88	101	1.347	2.88	104	1.396	2.95

Table S5. AT content (%) of whole mitochondrial genome, protein-coding and ribosomal RNA genes in *Artemia* mitogenomes (URM: *A. urmiana*, TIB: *A. tibetiana*, SIN: *A. sinica*, FRA: *A. franciscana*).

Sequence	URM	TIB	SIN	FRA
CmtG	62.54	62.73	64.51	64.44
PCGs+rRNAs	61.89	62.06	63.90	63.84
ND2	65.1	66.22	68.01	68.35
COX1	59.52	59.71	61.8	62.31
COX2	60.26	61.29	62.46	62.45
ATP8	61.11	62.96	67.28	66.05
ATP6	58.94	60.3	63.33	65.3
COX3	61.96	61.32	61.1	62.27
ND3	66.37	64.58	70.83	66.37
ND5	63.12	63.93	65.37	64.85
ND4	62.72	64.69	65.28	64.43
ND4L	68.2	66.28	68.58	69.77
ND6	63.25	63.46	69.02	67.09
CYTB	58.27	58.18	59.5	60.38
ND1	61.65	60.2	62.88	61.76
16S	63.96	63.07	63.88	64.01
12S	60.9	59.61	61.88	61.48