

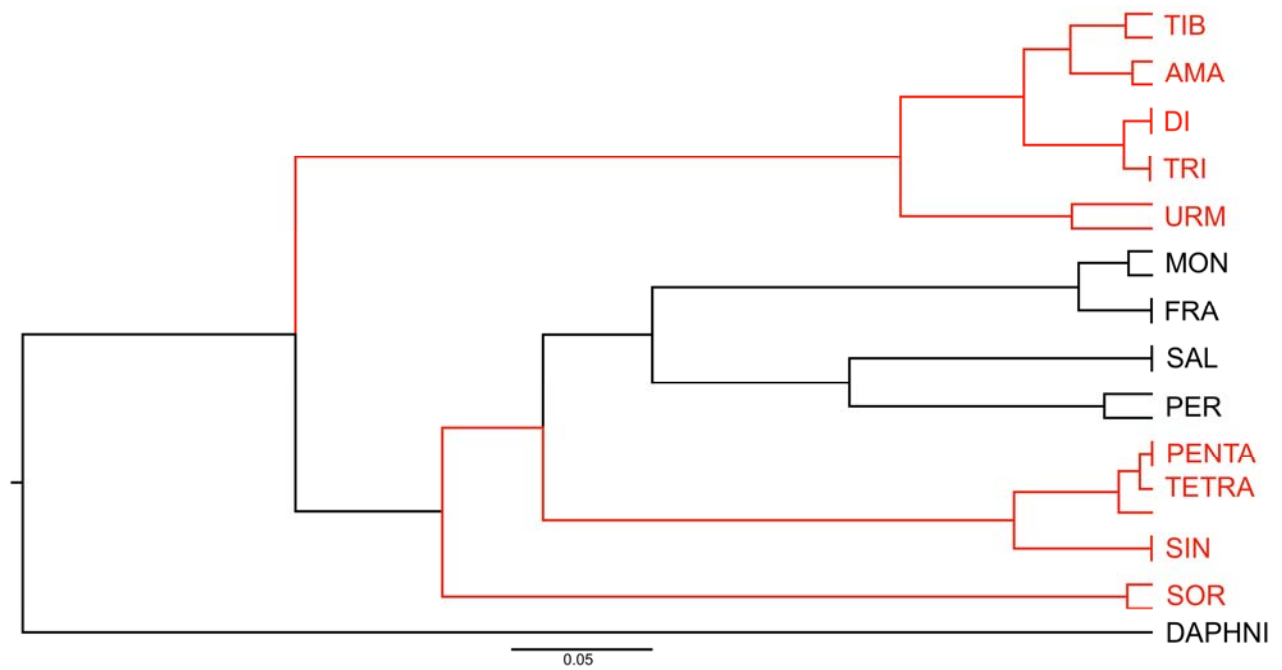


Fig. S1. A chronogram for the genus *Artemia* using the mitogenome following “relaxed clock” over 40 million generations (taking samples every 1,000 generations).

Table S1A. Gene characteristics in the mitochondrial genome assembly of *A. salina* (SAL1: OR423222).

SAL1: OR423222						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1105	1170	66	L		
tRNA-Cys	1207	1268	62	L		
tRNA-Tyr	1273	1334	62	L		
COX1	1336	2869	1534	H	ATG	T
tRNA-Leu	2869	2934	66	H		
COX2	2934	3615	682	H	GTG	T
tRNA-Lys	3616	3679	64	H		
tRNA-Asp	3682	3742	61	H		
ATP8	3743	3904	162	H	ATC	TAA
ATP6	3898	4557	660	H	ATG	TAA
COX3	4557	5342	786	H	ATG	TAA
tRNA-Gly	5343	5406	64	H		
ND3	5406	5741	336	H	ATT	TAG
tRNA-Ala	5766	5824	59	H		
tRNA-Arg	5825	5889	65	H		
tRNA-Asn	5889	5950	62	H		
tRNA-Ser	5951	6015	65	H		
tRNA-Glu	6014	6078	65	H		
tRNA-Phe	6075	6139	65	L		
ND5	6139	7759	1621	L	TTG	T
tRNA-His	7759	7821	63	L		
ND4	7821	8952	1132	L	ATA	T
ND4L	9002	9262	261	L	ATC	TAA
tRNA-Thr	9264	9325	62	H		
tRNA-Pro	9325	9387	63	L		
ND6	9389	9856	468	H	GTG	TAG
CYTB	9874	11004	1131	H	ATG	TAG
tRNA-Ser	11005	11071	67	H		
ND1	11076	11972	897	L	ATG	TAA
tRNA-Leu	11984	12047	64	L		
16S rRNA	12050	13193	1144	L		
tRNA-Val	13195	13256	62	L		
12S rRNA	13257	13966	710	L		
Control Region	13967	15433	1467			

Table S1B. Gene characteristics in the mitochondrial genome assembly of *A. salina* (SAL2: OR423223).

SAL2: OR423223						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1105	1170	66	L		
tRNA-Cys	1207	1268	62	L		
tRNA-Tyr	1273	1334	62	L		
COX1	1336	2869	1534	H	ATG	T
tRNA-Leu	2869	2934	66	H		
COX2	2934	3615	682	H	GTG	T
tRNA-Lys	3616	3679	64	H		
tRNA-Asp	3682	3742	61	H		
ATP8	3743	3904	162	H	ATC	TAA
ATP6	3898	4557	660	H	ATG	TAA
COX3	4557	5342	786	H	ATG	TAA
tRNA-Gly	5343	5406	64	H		
ND3	5406	5741	336	H	ATT	TAG
tRNA-Ala	5766	5824	59	H		
tRNA-Arg	5825	5889	65	H		
tRNA-Asn	5889	5950	62	H		
tRNA-Ser	5951	6015	65	H		
tRNA-Glu	6014	6078	65	H		
tRNA-Phe	6075	6139	65	L		
ND5	6139	7759	1621	L	TTG	T
tRNA-His	7759	7821	63	L		
ND4	7821	8952	1132	L	ATA	T
ND4L	9002	9262	261	L	ATC	TAA
tRNA-Thr	9264	9325	62	H		
tRNA-Pro	9325	9387	63	L		
ND6	9389	9856	468	H	GTG	TAG
CYTB	9874	11004	1131	H	ATG	TAG
tRNA-Ser	11005	11071	67	H		
ND1	11076	11972	897	L	ATG	TAA
tRNA-Leu	11984	12047	64	L		
16S rRNA	12050	13193	1144	L		
tRNA-Val	13195	13256	62	L		
12S rRNA	13257	13966	710	L		
Control Region	13967	15434	1468			

Table S1C. Gene characteristics in the mitochondrial genome assembly of *A. sinica* (SIN1: OP800906).

SIN1: OP800906						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1106	1171	66	L		
tRNA-Cys	1226	1286	61	L		
tRNA-Tyr	1298	1359	62	L		
COX1	1361	2894	1534	H	ATG	T
tRNA-Leu	2894	2959	66	H		
COX2	2959	3640	682	H	GTG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5368	784	H	ATG	T
tRNA-Gly	5368	5430	63	H		
ND3	5430	5765	336	H	ATT	TAA
tRNA-Ala	5790	5848	59	H		
tRNA-Arg	5849	5913	65	H		
tRNA-Asn	5913	5975	63	H		
tRNA-Ser	5976	6040	65	H		
tRNA-Glu	6039	6104	66	H		
tRNA-Phe	6101	6164	64	L		
ND5	6164	7784	1621	L	TTG	T
tRNA-His	7784	7846	63	L		
ND4	7846	8977	1132	L	ATA	T
ND4L	9027	9287	261	L	ATT	TAA
tRNA-Thr	9289	9350	62	H		
tRNA-Pro	9350	9412	63	L		
ND6	9414	9881	468	H	ATT	TAG
CYTB	9906	11036	1131	H	ATG	TAA
tRNA-Ser	11040	11106	67	H		
ND1	11113	12009	897	L	ATG	TAA
tRNA-Leu	12021	12084	64	L		
16S rRNA	12085	13234	1150	L		
tRNA-Val	13236	13296	61	L		
12S rRNA	13297	14007	711	L		
Control Region	14008	15689	1682			

Table S1D. Gene characteristics in the mitochondrial genome assembly of *A. sinica* (SIN2: OP805358).

SIN2: OP805358						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1106	1171	66	L		
tRNA-Cys	1226	1286	61	L		
tRNA-Tyr	1298	1359	62	L		
COX1	1361	2894	1534	H	ATG	T
tRNA-Leu	2894	2959	66	H		
COX2	2959	3640	682	H	GTG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5368	784	H	ATG	T
tRNA-Gly	5368	5430	63	H		
ND3	5430	5765	336	H	ATT	TAA
tRNA-Ala	5790	5848	59	H		
tRNA-Arg	5849	5913	65	H		
tRNA-Asn	5913	5975	63	H		
tRNA-Ser	5976	6040	65	H		
tRNA-Glu	6039	6104	66	H		
tRNA-Phe	6101	6164	64	L		
ND5	6164	7784	1621	L	TTG	T
tRNA-His	7784	7846	63	L		
ND4	7846	8977	1132	L	ATA	T
ND4L	9027	9287	261	L	ATT	TAA
tRNA-Thr	9289	9350	62	H		
tRNA-Pro	9350	9412	63	L		
ND6	9414	9881	468	H	ATT	TAG
CYTB	9906	11036	1131	H	ATG	TAA
tRNA-Ser	11040	11106	67	H		
ND1	11113	12009	897	L	ATG	TAA
tRNA-Leu	12021	12084	64	L		
16S rRNA	12085	13234	1150	L		
tRNA-Val	13236	13296	61	L		
12S rRNA	13297	14007	711	L		
Control Region	14008	15687	1680			

Table S1E. Gene characteristics in the mitochondrial genome assembly of *A. tibetiana* (TIB2: OR423229).

TIB2: OR423229						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	63	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1107	1172	66	L		
tRNA-Cys	1225	1285	61	L		
tRNA-Tyr	1297	1358	62	L		
COX1	1360	2893	1534	H	ATG	T
tRNA-Leu	2893	2959	67	H		
COX2	2959	3640	682	H	ATG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5370	786	H	ATG	TAA
tRNA-Gly	5372	5432	61	H		
ND3	5433	5768	336	H	ATT	TAG
tRNA-Ala	5797	5855	59	H		
tRNA-Arg	5856	5920	65	H		
tRNA-Asn	5920	5982	63	H		
tRNA-Ser	5983	6047	65	H		
tRNA-Glu	6046	6111	66	H		
tRNA-Phe	6108	6171	64	L		
ND5	6171	7791	1621	L	TTG	T
tRNA-His	7791	7852	62	L		
ND4	7852	8983	1132	L	ATA	T
ND4L	9033	9293	261	L	ATT	TAA
tRNA-Thr	9295	9356	62	H		
tRNA-Pro	9356	9418	63	L		
ND6	9420	9887	468	H	GTG	TAG
CYTB	9912	11042	1131	H	ATG	TAA
tRNA-Ser	11046	11112	67	H		
ND1	11119	12015	897	L	ATG	TAA
tRNA-Leu	12027	12090	64	L		
16S rRNA	12093	13243	1151	L		
tRNA-Val	13245	13304	60	L		
12S rRNA	13305	14015	711	L		
Control Region	14016	15638	1623			

Table S1F. Gene characteristics in the mitochondrial genome assembly of *A. sorgeloosi* (SOR2: OR423219).

SOR2: OR423219						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAG
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1109	1174	66	L		
tRNA-Cys	1223	1283	61	L		
tRNA-Tyr	1295	1356	62	L		
COX1	1358	2891	1534	H	ATG	T
tRNA-Leu	2891	2956	66	H		
COX2	2956	3637	682	H	ATG	T
tRNA-Lys	3638	3701	64	H		
tRNA-Asp	3706	3767	62	H		
ATP8	3768	3929	162	H	ATT	TAA
ATP6	3923	4582	660	H	ATG	TAA
COX3	4582	5367	786	H	ATG	TAG
tRNA-Gly	5369	5429	61	H		
ND3	5430	5765	336	H	ATT	TAA
tRNA-Ala	5794	5852	59	H		
tRNA-Arg	5853	5917	65	H		
tRNA-Asn	5917	5979	63	H		
tRNA-Ser	5980	6044	65	H		
tRNA-Glu	6043	6108	66	H		
tRNA-Phe	6105	6168	64	L		
ND5	6168	7788	1621	L	TTG	T
tRNA-His	7788	7849	62	L		
ND4	7849	8980	1132	L	ATA	T
ND4L	9030	9290	261	L	ATT	TAA
tRNA-Thr	9292	9353	62	H		
tRNA-Pro	9353	9415	63	L		
ND6	9417	9884	468	H	GTG	TAA
CYTB	9909	11039	1131	H	ATG	TAA
tRNA-Ser	11043	11109	67	H		
ND1	11116	12012	897	L	ATG	TAA
tRNA-Leu	12024	12087	64	L		
16S rRNA	12090	13240	1151	L		
tRNA-Val	13242	13302	61	L		
12S rRNA	13303	14013	711	L		
Control Region	14014	15754	1741			

Table S1G. Gene characteristics in the mitochondrial genome assembly of *A. amati* (AMA2: OR423218).

AMA2: OR423218						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1107	1172	66	L		
tRNA-Cys	1227	1287	61	L		
tRNA-Tyr	1299	1360	62	L		
COX1	1362	2895	1534	H	ATG	T
tRNA-Leu	2895	2961	67	H		
COX2	2961	3642	682	H	ATG	T
tRNA-Lys	3643	3706	64	H		
tRNA-Asp	3711	3772	62	H		
ATP8	3773	3934	162	H	ATC	TAA
ATP6	3928	4587	660	H	ATG	TAA
COX3	4587	5372	786	H	ATG	TAA
tRNA-Gly	5374	5434	61	H		
ND3	5435	5770	336	H	ATT	TAG
tRNA-Ala	5799	5857	59	H		
tRNA-Arg	5858	5922	65	H		
tRNA-Asn	5922	5984	63	H		
tRNA-Ser	5985	6049	65	H		
tRNA-Glu	6048	6113	66	H		
tRNA-Phe	6110	6173	64	L		
ND5	6173	7793	1621	L	TTG	T
tRNA-His	7793	7854	62	L		
ND4	7854	8985	1132	L	ATA	T
ND4L	9035	9295	261	L	ATT	TAA
tRNA-Thr	9297	9358	62	H		
tRNA-Pro	9358	9420	63	L		
ND6	9422	9889	468	H	GTG	TAG
CYTB	9914	11044	1131	H	ATG	TAA
tRNA-Ser	11048	11114	67	H		
ND1	11121	12017	897	L	ATG	TAA
tRNA-Leu	12029	12092	64	L		
16S rRNA	12095	13245	1151	L		
tRNA-Val	13247	13306	60	L		
12S rRNA	13307	14017	711	L		
Control Region	14018	15680	1663			

Table S1H. Gene characteristics in the mitochondrial genome assembly of *A. urmiana* (URM2: OR423228).

URM2: OR423228						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1107	1172	66	L		
tRNA-Cys	1220	1280	61	L		
tRNA-Tyr	1292	1353	62	L		
COX1	1355	2888	1534	H	ATG	T
tRNA-Leu	2888	2954	67	H		
COX2	2954	3635	682	H	ATG	T
tRNA-Lys	3636	3699	64	H		
tRNA-Asp	3704	3765	62	H		
ATP8	3766	3927	162	H	ATC	TAA
ATP6	3921	4580	660	H	GTG	TAA
COX3	4580	5365	786	H	ATG	TAA
tRNA-Gly	5367	5427	61	H		
ND3	5428	5763	336	H	ATT	TAG
tRNA-Ala	5792	5850	59	H		
tRNA-Arg	5851	5915	65	H		
tRNA-Asn	5915	5977	63	H		
tRNA-Ser	5978	6042	65	H		
tRNA-Glu	6041	6106	66	H		
tRNA-Phe	6103	6166	64	L		
ND5	6166	7786	1621	L	TTG	T
tRNA-His	7786	7847	62	L		
ND4	7847	8978	1132	L	ATA	T
ND4L	9028	9288	261	L	ATC	TAA
tRNA-Thr	9290	9351	62	H		
tRNA-Pro	9351	9413	63	L		
ND6	9415	9882	468	H	GTG	TAG
CYTB	9907	11037	1131	H	ATG	TAA
tRNA-Ser	11041	11107	67	H		
ND1	11114	12010	897	L	ATG	TAA
tRNA-Leu	12022	12085	64	L		
16S rRNA	12088	13239	1152	L		
tRNA-Val	13241	13300	60	L		
12S rRNA	13301	14011	711	L		
Control Region	14012	15675	1664			

Table S11. Gene characteristics in the mitochondrial genome assembly of *A. monica* (MON1: OR423226).

MON1: OR423226						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1033	1097	65	L		
tRNA-Gln	1105	1170	66	L		
tRNA-Cys	1209	1270	62	L		
tRNA-Tyr	1283	1344	62	L		
COX1	1346	2879	1534	H	ATG	T
tRNA-Leu	2879	2944	66	H		
COX2	2944	3625	682	H	GTG	T
tRNA-Lys	3626	3689	64	H		
tRNA-Asp	3693	3754	62	H		
ATP8	3755	3916	162	H	ATT	TAG
ATP6	3910	4569	660	H	ATG	TAA
COX3	4569	5354	786	H	ATG	TAG
tRNA-Gly	5356	5416	61	H		
ND3	5417	5752	336	H	ATT	TAA
tRNA-Ala	5783	5842	60	H		
tRNA-Arg	5843	5908	66	H		
tRNA-Asn	5908	5970	63	H		
tRNA-Ser	5971	6035	65	H		
tRNA-Glu	6034	6099	66	H		
tRNA-Phe	6096	6159	64	L		
ND5	6159	7779	1621	L	ATT	T
tRNA-His	7778	7841	64	L		
ND4	7841	8972	1132	L	ATA	T
ND4L	9022	9282	261	L	ATC	TAA
tRNA-Thr	9284	9345	62	H		
tRNA-Pro	9345	9407	63	L		
ND6	9409	9876	468	H	ATC	TAG
CYTB	9902	11032	1131	H	ATG	TAA
tRNA-Ser	11035	11103	69	H		
ND1	11109	12005	897	L	ATG	TAA
tRNA-Leu	12017	12080	64	L		
16S rRNA	12083	13233	1151	L		
tRNA-Val	13235	13297	63	L		
12S rRNA	13297	14008	712	L		
Control Region	14009	15825	1817			

Table S1J. Gene characteristics in the mitochondrial genome assembly of *A. monica* (MON2: OR423227).

MON2: OR423227						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1033	1097	65	L		
tRNA-Gln	1105	1170	66	L		
tRNA-Cys	1209	1270	62	L		
tRNA-Tyr	1283	1344	62	L		
COX1	1346	2879	1534	H	ATG	T
tRNA-Leu	2879	2944	66	H		
COX2	2944	3625	682	H	GTG	T
tRNA-Lys	3626	3689	64	H		
tRNA-Asp	3693	3754	62	H		
ATP8	3755	3916	162	H	ATT	TAG
ATP6	3910	4569	660	H	ATG	TAA
COX3	4569	5354	786	H	ATG	TAG
tRNA-Gly	5356	5416	61	H		
ND3	5417	5752	336	H	ATT	TAA
tRNA-Ala	5783	5842	60	H		
tRNA-Arg	5843	5908	66	H		
tRNA-Asn	5908	5970	63	H		
tRNA-Ser	5971	6035	65	H		
tRNA-Glu	6034	6099	66	H		
tRNA-Phe	6096	6159	64	L		
ND5	6159	7779	1621	L	ATT	T
tRNA-His	7778	7841	64	L		
ND4	7841	8972	1132	L	ATA	T
ND4L	9022	9282	261	L	ATC	TAA
tRNA-Thr	9284	9345	62	H		
tRNA-Pro	9345	9407	63	L		
ND6	9409	9876	468	H	ATC	TAG
CYTB	9902	11032	1131	H	ATG	TAA
tRNA-Ser	11035	11103	69	H		
ND1	11109	12005	897	L	ATG	TAA
tRNA-Leu	12017	12080	64	L		
16S rRNA	12083	13233	1151	L		
tRNA-Val	13235	13297	63	L		
12S rRNA	13297	14008	712	L		
Control Region	14009	15824	1816			

Table S1K. Gene characteristics in the mitochondrial genome assembly of *A. franciscana* (FRA1: OR423224).

FRA1: OR423224						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1033	1097	65	L		
tRNA-Gln	1105	1170	66	L		
tRNA-Cys	1209	1270	62	L		
tRNA-Tyr	1283	1344	62	L		
COX1	1346	2879	1534	H	ATG	T
tRNA-Leu	2879	2944	66	H		
COX2	2944	3625	682	H	GTG	T
tRNA-Lys	3626	3689	64	H		
tRNA-Asp	3693	3754	62	H		
ATP8	3755	3916	162	H	ATT	TAG
ATP6	3910	4569	660	H	ATG	TAA
COX3	4569	5354	786	H	ATG	TAA
tRNA-Gly	5356	5416	61	H		
ND3	5417	5752	336	H	ATT	TAA
tRNA-Ala	5783	5842	60	H		
tRNA-Arg	5843	5908	66	H		
tRNA-Asn	5908	5970	63	H		
tRNA-Ser	5971	6035	65	H		
tRNA-Glu	6034	6099	66	H		
tRNA-Phe	6096	6159	64	L		
ND5	6159	7779	1621	L	TTG	T
tRNA-His	7779	7842	64	L		
ND4	7842	8973	1132	L	ATA	T
ND4L	9023	9283	261	L	ATC	TAA
tRNA-Thr	9285	9346	62	H		
tRNA-Pro	9346	9408	63	L		
ND6	9410	9877	468	H	ATC	TAG
CYTB	9903	11033	1131	H	ATG	TAA
tRNA-Ser	11036	11104	69	H		
ND1	11110	12006	897	L	ATG	TAA
tRNA-Leu	12018	12081	64	L		
16S rRNA	12084	13234	1151	L		
tRNA-Val	13236	13298	63	L		
12S rRNA	13298	14009	712	L		
Control Region	14010	15829	1820			

Table S1L. Gene characteristics in the mitochondrial genome assembly of *A. franciscana* (FRA2: OR423225).

FRA2: OR423225						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1033	1097	65	L		
tRNA-Gln	1105	1170	66	L		
tRNA-Cys	1209	1269	61	L		
tRNA-Tyr	1282	1343	62	L		
COX1	1345	2878	1534	H	ATG	T
tRNA-Leu	2878	2943	66	H		
COX2	2943	3624	682	H	GTG	T
tRNA-Lys	3625	3688	64	H		
tRNA-Asp	3692	3753	62	H		
ATP8	3754	3915	162	H	ATT	TAG
ATP6	3909	4568	660	H	ATG	TAA
COX3	4568	5353	786	H	ATG	TAA
tRNA-Gly	5355	5415	61	H		
ND3	5416	5751	336	H	ATT	TAA
tRNA-Ala	5782	5841	60	H		
tRNA-Arg	5842	5907	66	H		
tRNA-Asn	5907	5969	63	H		
tRNA-Ser	5970	6034	65	H		
tRNA-Glu	6033	6098	66	H		
tRNA-Phe	6095	6158	64	L		
ND5	6158	7778	1621	L	TTG	T
tRNA-His	7778	7841	64	L		
ND4	7841	8972	1132	L	ATA	T
ND4L	9022	9282	261	L	ATC	TAA
tRNA-Thr	9284	9345	62	H		
tRNA-Pro	9345	9407	63	L		
ND6	9409	9876	468	H	ATC	TAG
CYTB	9902	11032	1131	H	ATG	TAA
tRNA-Ser	11035	11103	69	H		
ND1	11109	12005	897	L	ATG	TAA
tRNA-Leu	12017	12080	64	L		
16S rRNA	12083	13233	1151	L		
tRNA-Val	13235	13297	63	L		
12S rRNA	13297	14008	712	L		
Control Region	14009	15827	1819			

Table S1M. Gene characteristics in the mitochondrial genome assembly of *A. persimilis* (PER1: OR423220).

PER1: OR423220						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATC	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1029	1091	63	L		
tRNA-Gln	1107	1174	68	L		
tRNA-Cys	1196	1256	61	L		
tRNA-Tyr	1268	1329	62	L		
COX1	1331	2864	1534	H	ATG	T
tRNA-Leu	2864	2929	66	H		
COX2	2929	3610	682	H	GTG	T
tRNA-Lys	3611	3674	64	H		
tRNA-Asp	3676	3737	62	H		
ATP8	3738	3899	162	H	ATT	TAA
ATP6	3893	4552	660	H	ATG	TAA
COX3	4552	5337	786	H	ATG	TAA
tRNA-Gly	5338	5400	63	H		
ND3	5400	5735	336	H	ATT	TAA
tRNA-Ala	5756	5815	60	H		
tRNA-Arg	5816	5882	67	H		
tRNA-Asn	5882	5944	63	H		
tRNA-Ser	5945	6009	65	H		
tRNA-Glu	6008	6073	66	H		
tRNA-Phe	6070	6133	64	L		
ND5	6133	7753	1621	L	TTG	T
tRNA-His	7753	7815	63	L		
ND4	7815	8934	1120	L	ATA	T
ND4L	8996	9256	261	L	ATC	TAG
tRNA-Thr	9258	9320	63	H		
tRNA-Pro	9320	9382	63	L		
ND6	9384	9851	468	H	TTG	TAG
CYTB	9880	11010	1131	H	ATG	TAA
tRNA-Ser	11011	11079	69	H		
ND1	11083	11979	897	L	ATG	TAG
tRNA-Leu	11993	12052	60	L		
16S rRNA	12057	13196	1140	L		
tRNA-Val	13198	13259	62	L		
12S rRNA	13260	13968	709	L		
Control Region	13969	15764	1796			

Table S1N. Gene characteristics in the mitochondrial genome assembly of *A. persimilis* (PER2: OR423221).

PER2: OR423221						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATC	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1029	1091	63	L		
tRNA-Gln	1109	1176	68	L		
tRNA-Cys	1198	1258	61	L		
tRNA-Tyr	1270	1331	62	L		
COX1	1333	2866	1534	H	ATG	T
tRNA-Leu	2866	2931	66	H		
COX2	2931	3612	682	H	GTG	T
tRNA-Lys	3613	3676	64	H		
tRNA-Asp	3678	3739	62	H		
ATP8	3740	3901	162	H	ATT	TAA
ATP6	3895	4554	660	H	ATG	TAA
COX3	4554	5339	786	H	ATG	TAA
tRNA-Gly	5340	5402	63	H		
ND3	5402	5737	336	H	ATT	TAA
tRNA-Ala	5758	5817	60	H		
tRNA-Arg	5818	5884	67	H		
tRNA-Asn	5884	5946	63	H		
tRNA-Ser	5947	6011	65	H		
tRNA-Glu	6010	6075	66	H		
tRNA-Phe	6072	6135	64	L		
ND5	6135	7755	1621	L	TTG	T
tRNA-His	7755	7817	63	L		
ND4	7817	8936	1120	L	ATA	T
ND4L	8998	9258	261	L	ATC	TAG
tRNA-Thr	9260	9322	63	H		
tRNA-Pro	9322	9384	63	L		
ND6	9386	9853	468	H	TTG	TAG
CYTB	9882	11012	1131	H	ATG	TAA
tRNA-Ser	11013	11081	69	H		
ND1	11085	11981	897	L	ATG	TAG
tRNA-Leu	11995	12054	60	L		
16S rRNA	12059	13198	1140	L		
tRNA-Val	13200	13261	62	L		
12S rRNA	13262	13970	709	L		
Control Region	13971	15766	1796			

Table S10. Gene characteristics in the mitochondrial genome assembly of diploid parthenogenetic lineage (DI1: OR423214).

DI1: OR423214						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1101	1168	68	L		
tRNA-Cys	1215	1275	61	L		
tRNA-Tyr	1287	1348	62	L		
COX1	1350	2883	1534	H	ATG	T
tRNA-Leu	2883	2949	67	H		
COX2	2949	3630	682	H	ATG	T
tRNA-Lys	3631	3694	64	H		
tRNA-Asp	3699	3760	62	H		
ATP8	3761	3922	162	H	ATC	TAA
ATP6	3916	4575	660	H	ATG	TAA
COX3	4575	5360	786	H	ATG	TAA
tRNA-Gly	5362	5422	61	H		
ND3	5423	5758	336	H	ATT	TAG
tRNA-Ala	5787	5845	59	H		
tRNA-Arg	5846	5910	65	H		
tRNA-Asn	5910	5972	63	H		
tRNA-Ser	5973	6037	65	H		
tRNA-Glu	6036	6101	66	H		
tRNA-Phe	6098	6161	64	L		
ND5	6161	7781	1621	L	TTG	T
tRNA-His	7781	7842	62	L		
ND4	7842	8973	1132	L	ATA	T
ND4L	9023	9283	261	L	ATT	TAA
tRNA-Thr	9285	9346	62	H		
tRNA-Pro	9346	9408	63	L		
ND6	9410	9877	468	H	GTG	TAG
CYTB	9902	11032	1131	H	ATG	TAA
tRNA-Ser	11036	11102	67	H		
ND1	11109	12005	897	L	ATG	TAA
tRNA-Leu	12017	12080	64	L		
16S rRNA	12083	13233	1151	L		
tRNA-Val	13235	13294	60	L		
12S rRNA	13295	14005	711	L		
Control Region	14006	15666	1661			

Table S1P. Gene characteristics in the mitochondrial genome assembly of diploid parthenogenetic lineage (DI2: OR423215).

DI2: OR423215						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1101	1168	68	L		
tRNA-Cys	1215	1275	61	L		
tRNA-Tyr	1287	1348	62	L		
COX1	1350	2883	1534	H	ATG	T
tRNA-Leu	2883	2949	67	H		
COX2	2949	3630	682	H	ATG	T
tRNA-Lys	3631	3694	64	H		
tRNA-Asp	3699	3760	62	H		
ATP8	3761	3922	162	H	ATC	TAA
ATP6	3916	4575	660	H	ATG	TAA
COX3	4575	5360	786	H	ATG	TAA
tRNA-Gly	5362	5422	61	H		
ND3	5423	5758	336	H	ATT	TAG
tRNA-Ala	5787	5845	59	H		
tRNA-Arg	5846	5910	65	H		
tRNA-Asn	5910	5972	63	H		
tRNA-Ser	5973	6037	65	H		
tRNA-Glu	6036	6101	66	H		
tRNA-Phe	6098	6161	64	L		
ND5	6161	7781	1621	L	TTG	T
tRNA-His	7781	7842	62	L		
ND4	7842	8973	1132	L	ATA	T
ND4L	9023	9283	261	L	ATT	TAA
tRNA-Thr	9285	9346	62	H		
tRNA-Pro	9346	9408	63	L		
ND6	9410	9877	468	H	GTG	TAG
CYTB	9902	11032	1131	H	ATG	TAA
tRNA-Ser	11036	11102	67	H		
ND1	11109	12005	897	L	ATG	TAA
tRNA-Leu	12017	12080	64	L		
16S rRNA	12083	13233	1151	L		
tRNA-Val	13235	13294	60	L		
12S rRNA	13295	14005	711	L		
Control Region	14006	15668	1663			

Table S1Q. Gene characteristics in the mitochondrial genome assembly of triploid parthenogenetic lineage (TRI1: OR423216).

TRI1: OR423216						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1111	1176	66	L		
tRNA-Cys	1228	1288	61	L		
tRNA-Tyr	1300	1361	62	L		
COX1	1363	2896	1534	H	ATG	T
tRNA-Leu	2896	2962	67	H		
COX2	2962	3643	682	H	ATG	T
tRNA-Lys	3644	3707	64	H		
tRNA-Asp	3712	3773	62	H		
ATP8	3774	3935	162	H	ATC	TAA
ATP6	3929	4588	660	H	ATG	TAA
COX3	4588	5373	786	H	ATG	TAA
tRNA-Gly	5375	5435	61	H		
ND3	5436	5771	336	H	ATT	TAG
tRNA-Ala	5800	5858	59	H		
tRNA-Arg	5859	5923	65	H		
tRNA-Asn	5923	5985	63	H		
tRNA-Ser	5986	6050	65	H		
tRNA-Glu	6049	6114	66	H		
tRNA-Phe	6111	6174	64	L		
ND5	6174	7794	1621	L	TTG	T
tRNA-His	7794	7855	62	L		
ND4	7855	8986	1132	L	ATA	T
ND4L	9036	9296	261	L	ATT	TAA
tRNA-Thr	9298	9359	62	H		
tRNA-Pro	9359	9421	63	L		
ND6	9423	9890	468	H	GTG	TAG
CYTB	9915	11045	1131	H	ATG	TAA
tRNA-Ser	11049	11115	67	H		
ND1	11122	12018	897	L	ATG	TAA
tRNA-Leu	12030	12093	64	L		
16S rRNA	12095	13245	1151	L		
tRNA-Val	13247	13306	60	L		
12S rRNA	13307	14017	711	L		
Control Region	14018	15679	1662			

Table S1R. Gene characteristics in the mitochondrial genome assembly of triploid parthenogenetic lineage (TRI2: OR423217).

TRI2: OR423217						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1098	63	L		
tRNA-Gln	1111	1176	66	L		
tRNA-Cys	1228	1288	61	L		
tRNA-Tyr	1300	1361	62	L		
COX1	1363	2896	1534	H	ATG	T
tRNA-Leu	2896	2962	67	H		
COX2	2962	3643	682	H	ATG	T
tRNA-Lys	3644	3707	64	H		
tRNA-Asp	3712	3773	62	H		
ATP8	3774	3935	162	H	ATC	TAA
ATP6	3929	4588	660	H	ATG	TAA
COX3	4588	5373	786	H	ATG	TAA
tRNA-Gly	5375	5435	61	H		
ND3	5436	5771	336	H	ATT	TAG
tRNA-Ala	5800	5858	59	H		
tRNA-Arg	5859	5923	65	H		
tRNA-Asn	5923	5985	63	H		
tRNA-Ser	5986	6050	65	H		
tRNA-Glu	6049	6114	66	H		
tRNA-Phe	6111	6174	64	L		
ND5	6174	7794	1621	L	TTG	T
tRNA-His	7794	7855	62	L		
ND4	7855	8986	1132	L	ATA	T
ND4L	9036	9296	261	L	ATT	TAA
tRNA-Thr	9298	9359	62	H		
tRNA-Pro	9359	9421	63	L		
ND6	9423	9890	468	H	GTG	TAG
CYTB	9915	11045	1131	H	ATG	TAA
tRNA-Ser	11049	11115	67	H		
ND1	11122	12018	897	L	ATG	TAA
tRNA-Leu	12030	12093	64	L		
16S rRNA	12095	13245	1151	L		
tRNA-Val	13247	13306	60	L		
12S rRNA	13307	14017	711	L		
Control Region	14018	15680	1663			

Table S1S. Gene characteristics in the mitochondrial genome assembly of tetraploid parthenogenetic lineage (TETRA1: OR423213).

TETRA1: OR423213						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1106	1171	66	L		
tRNA-Cys	1226	1286	61	L		
tRNA-Tyr	1298	1359	62	L		
COX1	1361	2894	1534	H	ATG	T
tRNA-Leu	2894	2959	66	H		
COX2	2959	3640	682	H	GTG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5370	786	H	ATG	TAA
tRNA-Gly	5371	5431	61	H		
ND3	5432	5767	336	H	ATT	TAG
tRNA-Ala	5792	5850	59	H		
tRNA-Arg	5851	5915	65	H		
tRNA-Asn	5915	5977	63	H		
tRNA-Ser	5978	6042	65	H		
tRNA-Glu	6041	6106	66	H		
tRNA-Phe	6103	6166	64	L		
ND5	6166	7786	1621	L	TTG	T
tRNA-His	7786	7848	63	L		
ND4	7848	8979	1132	L	ATA	T
ND4L	9029	9289	261	L	ATT	TAA
tRNA-Thr	9291	9352	62	H		
tRNA-Pro	9352	9414	63	L		
ND6	9416	9883	468	H	ATT	TAG
CYTB	9908	11038	1131	H	ATG	TAA
tRNA-Ser	11042	11108	67	H		
ND1	11115	12011	897	L		TAA
tRNA-Leu	12023	12086	64	L		
16S rRNA	12087	13236	1150	L		
tRNA-Val	13238	13298	61	L		
12S rRNA	13299	14009	711	L		
Control Region	14010	15683	1674			

Table S1T. Gene characteristics in the mitochondrial genome assembly of tetraploid parthenogenetic lineage (TETRA2: OP805359).

TETRA2: OP805359						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1106	1171	66	L		
tRNA-Cys	1226	1286	61	L		
tRNA-Tyr	1298	1359	62	L		
COX1	1361	2894	1534	H	ATG	T
tRNA-Leu	2894	2959	66	H		
COX2	2959	3640	682	H	GTG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5370	786	H	ATG	TAG
tRNA-Gly	5371	5431	61	H		
ND3	5432	5767	336	H	ATT	TAG
tRNA-Ala	5792	5850	59	H		
tRNA-Arg	5851	5915	65	H		
tRNA-Asn	5915	5977	63	H		
tRNA-Ser	5978	6042	65	H		
tRNA-Glu	6041	6106	66	H		
tRNA-Phe	6103	6166	64	L		
ND5	6166	7786	1621	L	TTG	T
tRNA-His	7786	7848	63	L		
ND4	7848	8979	1132	L	ATA	T
ND4L	9029	9289	261	L	ATT	TAA
tRNA-Thr	9291	9352	62	H		
tRNA-Pro	9352	9414	63	L		
ND6	9416	9883	468	H	ATT	TAG
CYTB	9908	11038	1131	H	ATG	TAA
tRNA-Ser	11042	11108	67	H		
ND1	11115	12011	897	L	ATG	TAA
tRNA-Leu	12023	12086	64	L		
16S rRNA	12087	13236	1150	L		
tRNA-Val	13238	13298	61	L		
12S rRNA	13299	14009	711	L		
Control Region	14010	15693	1684			

Table S1U. Gene characteristics in the mitochondrial genome assembly of pentaploid parthenogenetic lineage (PENTA1: OP830835).

PENTA1: OP830835						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1106	1171	66	L		
tRNA-Cys	1226	1286	61	L		
tRNA-Tyr	1298	1359	62	L		
COX1	1361	2894	1534	H	ATG	T
tRNA-Leu	2894	2959	66	H		
COX2	2959	3640	682	H	GTG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5370	786	H	ATG	TAA
tRNA-Gly	5371	5431	61	H		
ND3	5432	5767	336	H	ATT	TAG
tRNA-Ala	5792	5850	59	H		
tRNA-Arg	5851	5915	65	H		
tRNA-Asn	5915	5977	63	H		
tRNA-Ser	5978	6042	65	H		
tRNA-Glu	6041	6106	66	H		
tRNA-Phe	6103	6166	64	L		
ND5	6166	7786	1621	L	TTG	T
tRNA-His	7786	7848	63	L		
ND4	7848	8979	1132	L	ATA	T
ND4L	9029	9289	261	L	ATT	TAA
tRNA-Thr	9291	9352	62	H		
tRNA-Pro	9352	9414	63	L		
ND6	9416	9883	468	H	ATT	TAG
CYTB	9908	11038	1131	H	ATG	TAA
tRNA-Ser	11042	11108	67	H		
ND1	11115	12011	897	L	ATG	TAA
tRNA-Leu	12023	12086	64	L		
16S rRNA	12087	13236	1150	L		
tRNA-Val	13238	13298	61	L		
12S rRNA	13299	14009	711	L		
Control Region	14010	15690	1681			

Table S1V. Gene characteristics in the mitochondrial genome assembly of pentaploid parthenogenetic lineage (PENTA2: OP830836).

PENTA2: OP830836						
Gene	5'	3'	Length (bp)	Strand	Start	Stop
tRNA-Met	1	65	65	H		
ND2	65	955	891	H	ATG	TAA
tRNA-Trp	953	1017	65	H		
tRNA-Ile	1036	1097	62	L		
tRNA-Gln	1106	1171	66	L		
tRNA-Cys	1226	1286	61	L		
tRNA-Tyr	1298	1359	62	L		
COX1	1361	2894	1534	H	ATG	T
tRNA-Leu	2894	2959	66	H		
COX2	2959	3640	682	H	GTG	T
tRNA-Lys	3641	3704	64	H		
tRNA-Asp	3709	3770	62	H		
ATP8	3771	3932	162	H	ATC	TAA
ATP6	3926	4585	660	H	ATG	TAA
COX3	4585	5370	786	H	ATG	TAA
tRNA-Gly	5371	5431	61	H		
ND3	5432	5767	336	H	ATT	TAG
tRNA-Ala	5792	5850	59	H		
tRNA-Arg	5851	5915	65	H		
tRNA-Asn	5915	5977	63	H		
tRNA-Ser	5978	6042	65	H		
tRNA-Glu	6041	6106	66	H		
tRNA-Phe	6103	6166	64	L		
ND5	6166	7786	1621	L	TTG	T
tRNA-His	7786	7848	63	L		
ND4	7848	8979	1132	L	ATA	T
ND4L	9029	9289	261	L	ATT	TAA
tRNA-Thr	9291	9352	62	H		
tRNA-Pro	9352	9414	63	L		
ND6	9416	9883	468	H	ATT	TAG
CYTB	9908	11038	1131	H	ATG	TAA
tRNA-Ser	11042	11108	67	H		
ND1	11115	12011	897	L	ATG	TAA
tRNA-Leu	12023	12086	64	L		
16S rRNA	12087	13236	1150	L		
tRNA-Val	13238	13298	61	L		
12S rRNA	13299	14009	711	L		
Control Region	14010	15693	1684			

Table S2. List of start codons of *Artemia* species and parthenogenetic lineages.

Species/Lineages	protein-coding gene												
	ND2	COX1	COX2	ATP8	ATP6	COX3	ND3	ND5	ND4	ND4L	ND6	CYTB	ND1
DI1	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
DI2	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
TRI1	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
TRI2	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
TIB1	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
TIB2	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
AMA1	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
AMA2	ATG	ATG	ATG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
URM1	ATG	ATG	ATG	ATC	GTG	ATG	ATT	TTG	ATA	ATC	GTG	ATG	ATG
URM2	ATG	ATG	ATG	ATC	GTG	ATG	ATT	TTG	ATA	ATC	GTG	ATG	ATG
SOR1	ATG	ATG	ATG	ATT	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
SOR2	ATG	ATG	ATG	ATT	ATG	ATG	ATT	TTG	ATA	ATT	GTG	ATG	ATG
SIN1	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	ATT	ATG	ATG
SIN2	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	ATT	ATG	ATG
TETRA1	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	ATT	ATG	ATG
TETRA2	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	ATT	ATG	ATG
PENTA1	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	ATT	ATG	ATG
PENTA2	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATT	ATT	ATG	ATG
FAR1	ATG	ATG	GTG	ATT	ATG	ATG	ATT	TTG	ATA	ATC	ATC	ATG	ATG
FRA2	ATG	ATG	GTG	ATT	ATG	ATG	ATT	TTG	ATA	ATC	ATC	ATG	ATG
MON1	ATG	ATG	GTG	ATT	ATG	ATG	ATT	ATT	ATA	ATC	ATC	ATG	ATG
MON2	ATG	ATG	GTG	ATT	ATG	ATG	ATT	ATT	ATA	ATC	ATC	ATG	ATG
SAL1	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATC	GTG	ATG	ATG
SAL2	ATG	ATG	GTG	ATC	ATG	ATG	ATT	TTG	ATA	ATC	GTG	ATG	ATG
PER1	ATC	ATG	GTG	ATT	ATG	ATG	ATT	TTG	ATA	ATC	TTG	ATG	ATG
PER2	ATC	ATG	GTG	ATT	ATG	ATG	ATT	TTG	ATA	ATC	TTG	ATG	ATG

Table S3. List of stop codons of *Artemia* species and parthenogenetic lineages.

Species/Lineages	protein-coding gene												
	ND2	COX1	COX2	ATP8	ATP6	COX3	ND3	ND5	ND4	ND4L	ND6	CYTB	ND1
DI1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
DI2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
TRI1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
TRI2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
TIB1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
TIB2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
AMA1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
AMA2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
URM1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
URM2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
SOR1	TAG	T-	T-	TAA	TAA	TAG	TAA	T-	T-	TAA	TAG	TAA	TAA
SOR2	TAG	T-	T-	TAA	TAA	TAG	TAA	T-	T-	TAA	TAA	TAA	TAA
SIN1	TAA	T-	T-	TAA	TAA	T-	TAA	T-	T-	TAA	TAG	TAA	TAA
SIN2	TAA	T-	T-	TAA	TAA	T-	TAA	T-	T-	TAA	TAG	TAA	TAA
TETRA1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
TETRA2	TAA	T-	T-	TAA	TAA	TAG	TAG	T-	T-	TAA	TAG	TAA	TAA
PENTA1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
PENTA2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAA	TAA
FAR1	TAA	T-	T-	TAG	TAA	TAA	TAA	T-	T-	TAA	TAG	TAA	TAA
FRA2	TAA	T-	T-	TAG	TAA	TAA	TAA	T-	T-	TAA	TAG	TAA	TAA
MON1	TAA	T-	T-	TAG	TAA	TAG	TAA	T-	T-	TAA	TAG	TAA	TAA
MON2	TAA	T-	T-	TAG	TAA	TAG	TAA	T-	T-	TAA	TAG	TAA	TAA
SAL1	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAG	TAA
SAL2	TAA	T-	T-	TAA	TAA	TAA	TAG	T-	T-	TAA	TAG	TAG	TAA
PER1	TAA	T-	T-	TAA	TAA	TAA	TAA	T-	T-	TAG	TAG	TAA	TAG
PER2	TAA	T-	T-	TAA	TAA	TAA	TAA	T-	T-	TAG	TAG	TAA	TAG

Table S4. Number of start codons and stop codons for each protein-coding gene.

	Codon	protein-coding gene												
		ND2	COX1	COX2	ATP8	ATP6	COX3	ND3	ND5	ND4	ND4L	ND6	CYTB	ND1
Start codon	ATG	24	26	12	0	24	26	0	0	0	0	0	26	26
	ATC	2	0	0	18	0	0	0	0	0	10	4	0	0
	ATT	0	0	0	8	0	0	26	2	0	16	6	0	0
	GTG	0	0	14	0	2	0	0	0	0	0	14	0	0
	ATA	0	0	0	0	0	0	0	0	26	0	0	0	0
	TTG	0	0	0	0	0	0	0	24	0	0	2	0	0
Stop codon	TAA	24	0	0	22	26	19	10	0	0	24	1	24	24
	TAG	2	0	0	4	0	5	16	0	0	2	25	2	2
	T-	0	26	26	0	0	2	0	26	26	0	0	0	0

Table S5. The values of GC% and AT% of PCGs+rRNAs of *Artemia* species and parthenogenetic lineages.

Species/Lineages	GC%	AT%
SAL 1	44.79	55.21
SAL 2	44.79	55.21
SIN 1	36.14	63.86
SIN 2	36.14	63.86
TIB 1	38.22	61.78
TIB 2	38.2	61.8
SOR 1	37.95	62.05
SOR 2	37.97	62.03
AMA 1	38.06	61.94
AMA 2	38.01	61.99
URM 1	38.08	61.92
URM 2	38.13	61.87
MON 1	36.41	63.59
MON 2	36.4	63.6
FRA 1	36.19	63.81
FRA 2	36.19	63.81
PER 1	36.09	63.91
PER 2	36.02	63.98
DI 1	37.82	62.18
DI 2	37.81	62.19
TRI 1	37.75	62.25
TRI 2	37.75	62.25
TETRA 1	36.19	63.81
TETRA 2	36.22	63.78
PENTA 1	36.20	63.80
PENTA 2	36.20	63.80

Table S6. The values of GC-Skew and AT-Skew of PCGs+rRNAs of *Artemia* species and parthenogenetic lineages.

Species/Lineages	GC-Skew	AT-Skew
SAL 1	-0.0569	-0.1885
SAL 2	-0.0569	-0.1885
SIN 1	-0.0470	-0.1713
SIN 2	-0.0470	-0.1713
TIB 1	-0.0549	-0.1657
TIB 2	-0.0555	-0.1661
SOR 1	-0.0482	-0.1651
SOR 2	-0.0482	-0.1655
AMA 1	-0.0515	-0.1669
AMA 2	-0.0502	-0.1676
URM 1	-0.0530	-0.1660
URM 2	-0.0490	-0.1695
MON 1	-0.0368	-0.1740
MON 2	-0.0390	-0.1729
FRA 1	-0.0342	-0.1753
FRA 2	-0.0342	-0.1753
PER 1	-0.0213	-0.1666
PER 2	-0.0197	-0.1678
DI 1	-0.0481	-0.1673
DI 2	-0.0478	-0.1673
TRI 1	-0.0490	-0.1665
TRI 2	-0.0490	-0.1665
TETRA 1	-0.0475	-0.1721
TETRA 2	-0.0497	-0.1715
PENTA 1	-0.0513	-0.1708
PENTA 2	-0.0513	-0.1708

Table S7. The values of Observed frequency and RSCU for each species and parthenogenetic lineages.														
	DI1					DI2					TRI1			
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
1	UAG	*	2	0.444		UAG	*	2	0.444		UAG	*	2	0.444
2	UAA	*	7	1.556		UAA	*	7	1.556		UAA	*	7	1.556
3	GCU	A	64	1.384		GCU	A	64	1.384		GCU	A	63	1.385
4	GCG	A	15	0.324		GCG	A	15	0.324		GCG	A	14	0.308
5	GCC	A	67	1.449		GCC	A	67	1.449		GCC	A	67	1.473
6	GCA	A	39	0.843		GCA	A	39	0.843		GCA	A	38	0.835
7	UGU	C	28	1.217		UGU	C	28	1.217		UGU	C	28	1.217
8	UGC	C	18	0.783		UGC	C	18	0.783		UGC	C	18	0.783
9	GAU	D	53	1.413		GAU	D	53	1.413		GAU	D	54	1.44
10	GAC	D	22	0.587		GAC	D	22	0.587		GAC	D	21	0.56
11	GAG	E	28	0.644		GAG	E	28	0.644		GAG	E	27	0.621
12	GAA	E	59	1.356		GAA	E	59	1.356		GAA	E	60	1.379
13	UUU	F	205	1.362		UUU	F	205	1.362		UUU	F	206	1.36
14	UUC	F	96	0.638		UUC	F	96	0.638		UUC	F	97	0.64
15	GGU	G	43	0.764		GGU	G	43	0.764		GGU	G	42	0.743
16	GGG	G	76	1.351		GGG	G	76	1.351		GGG	G	76	1.345
17	GGC	G	26	0.462		GGC	G	26	0.462		GGC	G	27	0.478
18	GGA	G	80	1.422		GGA	G	80	1.422		GGA	G	81	1.434
19	CAC	H	37	1.028		CAC	H	37	1.028		CAC	H	37	1.028
20	CAU	H	35	0.972		CAU	H	35	0.972		CAU	H	35	0.972
21	AUU	I	212	1.472		AUU	I	212	1.472		AUU	I	212	1.467
22	AUC	I	76	0.528		AUC	I	76	0.528		AUC	I	77	0.533
23	AAA	K	38	1.101		AAA	K	38	1.101		AAA	K	38	1.101
24	AAG	K	31	0.899		AAG	K	31	0.899		AAG	K	31	0.899
25	CUA	L	102	1.222		CUA	L	102	1.222		CUA	L	103	1.237
26	CUC	L	80	0.958		CUC	L	80	0.958		CUC	L	80	0.961
27	CUG	L	41	0.491		CUG	L	41	0.491		CUG	L	41	0.492
28	CUU	L	111	1.329		CUU	L	111	1.329		CUU	L	109	1.309
29	UUA	L	159	1.371		UUA	L	159	1.371		UUA	L	160	1.385
30	UUG	L	73	0.629		UUG	L	73	0.629		UUG	L	71	0.615
31	AUG	M	43	0.489		AUG	M	43	0.489		AUG	M	43	0.489
32	AUA	M	133	1.511		AUA	M	133	1.511		AUA	M	133	1.511
33	AAC	N	39	0.729		AAC	N	39	0.729		AAC	N	38	0.71
34	AAU	N	68	1.271		AAU	N	68	1.271		AAU	N	69	1.29
35	CCU	P	49	1.342		CCU	P	49	1.342		CCU	P	49	1.333

36	CCG	P	25	0.685		CCG	P	25	0.685		CCG	P	25	0.68
37	CCC	P	50	1.37		CCC	P	50	1.37		CCC	P	51	1.388
38	CCA	P	22	0.603		CCA	P	22	0.603		CCA	P	22	0.599
39	CAG	Q	18	0.486		CAG	Q	18	0.486		CAG	Q	18	0.486
40	CAA	Q	56	1.514		CAA	Q	56	1.514		CAA	Q	56	1.514
41	CGA	R	25	1.639		CGA	R	25	1.639		CGA	R	25	1.639
42	CGC	R	9	0.59		CGC	R	9	0.59		CGC	R	9	0.59
43	CGG	R	8	0.525		CGG	R	8	0.525		CGG	R	8	0.525
44	CGU	R	19	1.246		CGU	R	19	1.246		CGU	R	19	1.246
45	AGC	S	15	0.317		AGC	S	15	0.317		AGC	S	16	0.338
46	AGA	S	72	1.52		AGA	S	72	1.52		AGA	S	72	1.52
47	UCA	S	69	1.456		UCA	S	69	1.456		UCA	S	69	1.456
48	UCC	S	47	0.992		UCC	S	46	0.971		UCC	S	47	0.992
49	UCG	S	18	0.38		UCG	S	18	0.38		UCG	S	18	0.38
50	UCU	S	117	2.47		UCU	S	118	2.491		UCU	S	117	2.47
51	AGG	S	6	0.127		AGG	S	6	0.127		AGG	S	6	0.127
52	AGU	S	35	0.739		AGU	S	35	0.739		AGU	S	34	0.718
53	ACA	T	43	1.042		ACA	T	43	1.042		ACA	T	43	1.055
54	ACC	T	38	0.921		ACC	T	38	0.921		ACC	T	37	0.908
55	ACG	T	15	0.364		ACG	T	15	0.364		ACG	T	15	0.368
56	ACU	T	69	1.673		ACU	T	69	1.673		ACU	T	68	1.669
57	GUC	V	50	0.816		GUC	V	50	0.816		GUC	V	51	0.826
58	GUG	V	38	0.62		GUG	V	38	0.62		GUG	V	39	0.632
59	GUU	V	79	1.29		GUU	V	79	1.29		GUU	V	79	1.279
60	GUA	V	78	1.273		GUA	V	78	1.273		GUA	V	78	1.263
61	UGA	W	59	1.283		UGA	W	59	1.283		UGA	W	61	1.326
62	UGG	W	33	0.717		UGG	W	33	0.717		UGG	W	31	0.674
63	UAC	Y	55	0.728		UAC	Y	55	0.728		UAC	Y	54	0.715
64	UAU	Y	96	1.272		UAU	Y	96	1.272		UAU	Y	97	1.285

	TRI2					TIB1					TIB2			
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
	UAG	*	2	0.444		UAG	*	2	0.444		UAG	*	2	0.444
	UAA	*	7	1.556		UAA	*	7	1.556		UAA	*	7	1.556
	GCU	A	63	1.385		GCU	A	64	1.369		GCU	A	63	1.348
	GCG	A	14	0.308		GCG	A	16	0.342		GCG	A	16	0.342
	GCC	A	67	1.473		GCC	A	69	1.476		GCC	A	70	1.497
	GCA	A	38	0.835		GCA	A	38	0.813		GCA	A	38	0.813
	UGU	C	28	1.217		UGU	C	28	1.217		UGU	C	27	1.174
	UGC	C	18	0.783		UGC	C	18	0.783		UGC	C	19	0.826
	GAU	D	54	1.44		GAU	D	51	1.36		GAU	D	53	1.395
	GAC	D	21	0.56		GAC	D	24	0.64		GAC	D	23	0.605
	GAG	E	27	0.621		GAG	E	26	0.598		GAG	E	25	0.581
	GAA	E	60	1.379		GAA	E	61	1.402		GAA	E	61	1.419
	UUU	F	205	1.358		UUU	F	203	1.353		UUU	F	202	1.347
	UUC	F	97	0.642		UUC	F	97	0.647		UUC	F	98	0.653
	GGU	G	42	0.743		GGU	G	40	0.711		GGU	G	41	0.729
	GGG	G	76	1.345		GGG	G	78	1.387		GGG	G	78	1.387
	GGC	G	27	0.478		GGC	G	30	0.533		GGC	G	29	0.516
	GGA	G	81	1.434		GGA	G	77	1.369		GGA	G	77	1.369
	CAC	H	37	1.028		CAC	H	37	1.014		CAC	H	38	1.041
	CAU	H	35	0.972		CAU	H	36	0.986		CAU	H	35	0.959
	AUU	I	212	1.467		AUU	I	207	1.433		AUU	I	208	1.439
	AUC	I	77	0.533		AUC	I	82	0.567		AUC	I	81	0.561
	AAA	K	38	1.101		AAA	K	38	1.118		AAA	K	38	1.118
	AAG	K	31	0.899		AAG	K	30	0.882		AAG	K	30	0.882
	CUA	L	103	1.234		CUA	L	110	1.283		CUA	L	111	1.287
	CUC	L	80	0.958		CUC	L	80	0.933		CUC	L	80	0.928
	CUG	L	41	0.491		CUG	L	40	0.466		CUG	L	39	0.452
	CUU	L	110	1.317		CUU	L	113	1.318		CUU	L	115	1.333
	UUA	L	160	1.385		UUA	L	153	1.348		UUA	L	153	1.354
	UUG	L	71	0.615		UUG	L	74	0.652		UUG	L	73	0.646
	AUG	M	43	0.489		AUG	M	45	0.529		AUG	M	45	0.529
	AUA	M	133	1.511		AUA	M	125	1.471		AUA	M	125	1.471
	AAC	N	38	0.71		AAC	N	37	0.692		AAC	N	38	0.71
	AAU	N	69	1.29		AAU	N	70	1.308		AAU	N	69	1.29
	CCU	P	49	1.333		CCU	P	47	1.297		CCU	P	47	1.306

	CCG	P	25	0.68		CCG	P	25	0.69		CCG	P	25	0.694
	CCC	P	51	1.388		CCC	P	51	1.407		CCC	P	50	1.389
	CCA	P	22	0.599		CCA	P	22	0.607		CCA	P	22	0.611
	CAG	Q	18	0.486		CAG	Q	18	0.486		CAG	Q	18	0.486
	CAA	Q	56	1.514		CAA	Q	56	1.514		CAA	Q	56	1.514
	CGA	R	25	1.639		CGA	R	25	1.667		CGA	R	25	1.639
	CGC	R	9	0.59		CGC	R	9	0.6		CGC	R	9	0.59
	CGG	R	8	0.525		CGG	R	8	0.533		CGG	R	8	0.525
	CGU	R	19	1.246		CGU	R	18	1.2		CGU	R	19	1.246
	AGC	S	16	0.338		AGC	S	20	0.422		AGC	S	20	0.422
	AGA	S	72	1.52		AGA	S	71	1.499		AGA	S	71	1.499
	UCA	S	69	1.456		UCA	S	70	1.478		UCA	S	70	1.478
	UCC	S	47	0.992		UCC	S	48	1.013		UCC	S	48	1.013
	UCG	S	18	0.38		UCG	S	17	0.359		UCG	S	17	0.359
	UCU	S	117	2.47		UCU	S	116	2.449		UCU	S	116	2.449
	AGG	S	6	0.127		AGG	S	7	0.148		AGG	S	7	0.148
	AGU	S	34	0.718		AGU	S	30	0.633		AGU	S	30	0.633
	ACA	T	43	1.055		ACA	T	45	1.091		ACA	T	45	1.091
	ACC	T	36	0.883		ACC	T	40	0.97		ACC	T	39	0.945
	ACG	T	15	0.368		ACG	T	13	0.315		ACG	T	13	0.315
	ACU	T	69	1.693		ACU	T	67	1.624		ACU	T	68	1.648
	GUC	V	51	0.826		GUC	V	51	0.823		GUC	V	51	0.826
	GUG	V	39	0.632		GUG	V	42	0.677		GUG	V	42	0.68
	GUU	V	79	1.279		GUU	V	77	1.242		GUU	V	76	1.231
	GUA	V	78	1.263		GUA	V	78	1.258		GUA	V	78	1.263
	UGA	W	61	1.326		UGA	W	58	1.261		UGA	W	57	1.239
	UGG	W	31	0.674		UGG	W	34	0.739		UGG	W	35	0.761
	UAC	Y	54	0.715		UAC	Y	58	0.773		UAC	Y	56	0.747
	UAU	Y	97	1.285		UAU	Y	92	1.227		UAU	Y	94	1.253

	AMA1					AMA2					URM1			
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
	UAG	*	2	0.444		UAG	*	2	0.444		UAG	*	2	0.444
	UAA	*	7	1.556		UAA	*	7	1.556		UAA	*	7	1.556
	GCU	A	60	1.311		GCU	A	62	1.348		GCU	A	66	1.451
	GCG	A	15	0.328		GCG	A	15	0.326		GCG	A	16	0.352
	GCC	A	70	1.53		GCC	A	69	1.5		GCC	A	62	1.363
	GCA	A	38	0.831		GCA	A	38	0.826		GCA	A	38	0.835
	UGU	C	30	1.333		UGU	C	30	1.333		UGU	C	27	1.2
	UGC	C	15	0.667		UGC	C	15	0.667		UGC	C	18	0.8
	GAU	D	51	1.36		GAU	D	52	1.387		GAU	D	55	1.447
	GAC	D	24	0.64		GAC	D	23	0.613		GAC	D	21	0.553
	GAG	E	26	0.598		GAG	E	27	0.614		GAG	E	22	0.512
	GAA	E	61	1.402		GAA	E	61	1.386		GAA	E	64	1.488
	UUU	F	206	1.369		UUU	F	206	1.369		UUU	F	201	1.344
	UUC	F	95	0.631		UUC	F	95	0.631		UUC	F	98	0.656
	GGU	G	39	0.69		GGU	G	40	0.708		GGU	G	43	0.758
	GGG	G	79	1.398		GGG	G	78	1.381		GGG	G	80	1.41
	GGC	G	30	0.531		GGC	G	29	0.513		GGC	G	27	0.476
	GGA	G	78	1.381		GGA	G	79	1.398		GGA	G	77	1.357
	CAC	H	37	1.014		CAC	H	37	1.014		CAC	H	38	1.013
	CAU	H	36	0.986		CAU	H	36	0.986		CAU	H	37	0.987
	AUU	I	206	1.431		AUU	I	206	1.436		AUU	I	201	1.431
	AUC	I	82	0.569		AUC	I	81	0.564		AUC	I	80	0.569
	AAA	K	38	1.134		AAA	K	38	1.152		AAA	K	35	1.029
	AAG	K	29	0.866		AAG	K	28	0.848		AAG	K	33	0.971
	CUA	L	107	1.255		CUA	L	106	1.247		CUA	L	107	1.255
	CUC	L	79	0.927		CUC	L	78	0.918		CUC	L	78	0.915
	CUG	L	42	0.493		CUG	L	41	0.482		CUG	L	40	0.469
	CUU	L	113	1.326		CUU	L	115	1.353		CUU	L	116	1.361
	UUA	L	156	1.368		UUA	L	157	1.371		UUA	L	158	1.38
	UUG	L	72	0.632		UUG	L	72	0.629		UUG	L	71	0.62
	AUG	M	44	0.518		AUG	M	44	0.518		AUG	M	47	0.547
	AUA	M	126	1.482		AUA	M	126	1.482		AUA	M	125	1.453
	AAC	N	36	0.679		AAC	N	37	0.692		AAC	N	34	0.636
	AAU	N	70	1.321		AAU	N	70	1.308		AAU	N	73	1.364
	CCU	P	48	1.324		CCU	P	48	1.324		CCU	P	47	1.297

	CCG	P	25	0.69		CCG	P	25	0.69		CCG	P	18	0.497
	CCC	P	50	1.379		CCC	P	50	1.379		CCC	P	52	1.434
	CCA	P	22	0.607		CCA	P	22	0.607		CCA	P	28	0.772
	CAG	Q	18	0.486		CAG	Q	18	0.486		CAG	Q	17	0.459
	CAA	Q	56	1.514		CAA	Q	56	1.514		CAA	Q	57	1.541
	CGA	R	25	1.639		CGA	R	25	1.639		CGA	R	23	1.508
	CGC	R	9	0.59		CGC	R	9	0.59		CGC	R	11	0.721
	CGG	R	8	0.525		CGG	R	8	0.525		CGG	R	10	0.656
	CGU	R	19	1.246		CGU	R	19	1.246		CGU	R	17	1.115
	AGC	S	19	0.399		AGC	S	19	0.399		AGC	S	20	0.423
	AGA	S	71	1.491		AGA	S	71	1.491		AGA	S	73	1.545
	UCA	S	71	1.491		UCA	S	71	1.491		UCA	S	66	1.397
	UCC	S	47	0.987		UCC	S	47	0.987		UCC	S	50	1.058
	UCG	S	17	0.357		UCG	S	17	0.357		UCG	S	21	0.444
	UCU	S	117	2.457		UCU	S	117	2.457		UCU	S	114	2.413
	AGG	S	8	0.168		AGG	S	8	0.168		AGG	S	7	0.148
	AGU	S	31	0.651		AGU	S	31	0.651		AGU	S	27	0.571
	ACA	T	45	1.091		ACA	T	45	1.091		ACA	T	43	1.036
	ACC	T	39	0.945		ACC	T	38	0.921		ACC	T	41	0.988
	ACG	T	12	0.291		ACG	T	12	0.291		ACG	T	12	0.289
	ACU	T	69	1.673		ACU	T	70	1.697		ACU	T	70	1.687
	GUC	V	51	0.81		GUC	V	49	0.781		GUC	V	51	0.794
	GUG	V	42	0.667		GUG	V	42	0.669		GUG	V	44	0.685
	GUU	V	80	1.27		GUU	V	81	1.291		GUU	V	85	1.323
	GUA	V	79	1.254		GUA	V	79	1.259		GUA	V	77	1.198
	UGA	W	59	1.283		UGA	W	59	1.283		UGA	W	58	1.261
	UGG	W	33	0.717		UGG	W	33	0.717		UGG	W	34	0.739
	UAC	Y	57	0.76		UAC	Y	56	0.747		UAC	Y	61	0.819
	UAU	Y	93	1.24		UAU	Y	94	1.253		UAU	Y	88	1.181

	URM2					SOR1					SOR2			
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
	UAG	*	2	0.444		UAG	*	3	0.667		UAG	*	2	0.444
	UAA	*	7	1.556		UAA	*	6	1.333		UAA	*	7	1.556
	GCU	A	65	1.413		GCU	A	66	1.467		GCU	A	66	1.475
	GCG	A	17	0.37		GCG	A	11	0.244		GCG	A	11	0.246
	GCC	A	65	1.413		GCC	A	63	1.4		GCC	A	62	1.385
	GCA	A	37	0.804		GCA	A	40	0.889		GCA	A	40	0.894
	UGU	C	26	1.156		UGU	C	30	1.333		UGU	C	31	1.378
	UGC	C	19	0.844		UGC	C	15	0.667		UGC	C	14	0.622
	GAU	D	54	1.421		GAU	D	52	1.444		GAU	D	52	1.425
	GAC	D	22	0.579		GAC	D	20	0.556		GAC	D	21	0.575
	GAG	E	23	0.535		GAG	E	26	0.591		GAG	E	26	0.591
	GAA	E	63	1.465		GAA	E	62	1.409		GAA	E	62	1.409
	UUU	F	200	1.338		UUU	F	205	1.385		UUU	F	206	1.392
	UUC	F	99	0.662		UUC	F	91	0.615		UUC	F	90	0.608
	GGU	G	41	0.722		GGU	G	39	0.678		GGU	G	39	0.678
	GGG	G	81	1.427		GGG	G	86	1.496		GGG	G	86	1.496
	GGC	G	29	0.511		GGC	G	23	0.4		GGC	G	23	0.4
	GGA	G	76	1.339		GGA	G	82	1.426		GGA	G	82	1.426
	CAC	H	35	0.933		CAC	H	37	0.974		CAC	H	37	0.961
	CAU	H	40	1.067		CAU	H	39	1.026		CAU	H	40	1.039
	AUU	I	199	1.421		AUU	I	202	1.418		AUU	I	201	1.411
	AUC	I	81	0.579		AUC	I	83	0.582		AUC	I	84	0.589
	AAA	K	34	1		AAA	K	44	1.222		AAA	K	44	1.222
	AAG	K	34	1		AAG	K	28	0.778		AAG	K	28	0.778
	CUA	L	109	1.282		CUA	L	112	1.291		CUA	L	112	1.287
	CUC	L	75	0.882		CUC	L	90	1.037		CUC	L	90	1.034
	CUG	L	36	0.424		CUG	L	38	0.438		CUG	L	39	0.448
	CUU	L	120	1.412		CUU	L	107	1.233		CUU	L	107	1.23
	UUA	L	159	1.371		UUA	L	168	1.467		UUA	L	168	1.467
	UUG	L	73	0.629		UUG	L	61	0.533		UUG	L	61	0.533
	AUG	M	48	0.555		AUG	M	58	0.663		AUG	M	56	0.644
	AUA	M	125	1.445		AUA	M	117	1.337		AUA	M	118	1.356
	AAC	N	36	0.673		AAC	N	30	0.577		AAC	N	33	0.635
	AAU	N	71	1.327		AAU	N	74	1.423		AAU	N	71	1.365
	CCU	P	48	1.324		CCU	P	49	1.38		CCU	P	50	1.408

	CCG	P	20	0.552		CCG	P	22	0.62		CCG	P	23	0.648
	CCC	P	51	1.407		CCC	P	46	1.296		CCC	P	45	1.268
	CCA	P	26	0.717		CCA	P	25	0.704		CCA	P	24	0.676
	CAG	Q	18	0.486		CAG	Q	16	0.451		CAG	Q	16	0.451
	CAA	Q	56	1.514		CAA	Q	55	1.549		CAA	Q	55	1.549
	CGA	R	24	1.574		CGA	R	24	1.6		CGA	R	23	1.533
	CGC	R	10	0.656		CGC	R	9	0.6		CGC	R	9	0.6
	CGG	R	9	0.59		CGG	R	8	0.533		CGG	R	9	0.6
	CGU	R	18	1.18		CGU	R	19	1.267		CGU	R	19	1.267
	AGC	S	19	0.403		AGC	S	22	0.46		AGC	S	22	0.46
	AGA	S	72	1.528		AGA	S	66	1.379		AGA	S	66	1.379
	UCA	S	67	1.422		UCA	S	72	1.504		UCA	S	71	1.483
	UCC	S	49	1.04		UCC	S	54	1.128		UCC	S	53	1.107
	UCG	S	19	0.403		UCG	S	18	0.376		UCG	S	19	0.397
	UCU	S	116	2.462		UCU	S	113	2.36		UCU	S	114	2.381
	AGG	S	7	0.149		AGG	S	6	0.125		AGG	S	6	0.125
	AGU	S	28	0.594		AGU	S	32	0.668		AGU	S	32	0.668
	ACA	T	43	1.055		ACA	T	44	1.067		ACA	T	43	1.049
	ACC	T	38	0.933		ACC	T	39	0.945		ACC	T	39	0.951
	ACG	T	12	0.294		ACG	T	14	0.339		ACG	T	14	0.341
	ACU	T	70	1.718		ACU	T	68	1.648		ACU	T	68	1.659
	GUC	V	49	0.763		GUC	V	43	0.688		GUC	V	43	0.685
	GUG	V	48	0.747		GUG	V	45	0.72		GUG	V	45	0.717
	GUU	V	86	1.339		GUU	V	80	1.28		GUU	V	81	1.291
	GUA	V	74	1.152		GUA	V	82	1.312		GUA	V	82	1.307
	UGA	W	58	1.261		UGA	W	58	1.261		UGA	W	58	1.261
	UGG	W	34	0.739		UGG	W	34	0.739		UGG	W	34	0.739
	UAC	Y	60	0.805		UAC	Y	48	0.649		UAC	Y	48	0.653
	UAU	Y	89	1.195		UAU	Y	100	1.351		UAU	Y	99	1.347

	SIN1					SIN2					TETRA1			
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
	UAG	*	1	0.25		UAG	*	1	0.25		UAG	*	3	0.667
	UAA	*	7	1.75		UAA	*	7	1.75		UAA	*	6	1.333
	GCU	A	69	1.586		GCU	A	69	1.586		GCU	A	65	1.557
	GCG	A	15	0.345		GCG	A	15	0.345		GCG	A	14	0.335
	GCC	A	44	1.011		GCC	A	44	1.011		GCC	A	43	1.03
	GCA	A	46	1.057		GCA	A	46	1.057		GCA	A	45	1.078
	UGU	C	24	1.091		UGU	C	24	1.091		UGU	C	23	1.045
	UGC	C	20	0.909		UGC	C	20	0.909		UGC	C	21	0.955
	GAU	D	50	1.333		GAU	D	50	1.333		GAU	D	49	1.273
	GAC	D	25	0.667		GAC	D	25	0.667		GAC	D	28	0.727
	GAG	E	24	0.558		GAG	E	24	0.558		GAG	E	26	0.612
	GAA	E	62	1.442		GAA	E	62	1.442		GAA	E	59	1.388
	UUU	F	224	1.479		UUU	F	224	1.479		UUU	F	222	1.475
	UUC	F	79	0.521		UUC	F	79	0.521		UUC	F	79	0.525
	GGU	G	55	0.991		GGU	G	55	0.991		GGU	G	54	0.973
	GGG	G	65	1.171		GGG	G	65	1.171		GGG	G	65	1.171
	GGC	G	21	0.378		GGC	G	21	0.378		GGC	G	23	0.414
	GGA	G	81	1.459		GGA	G	81	1.459		GGA	G	80	1.441
	CAC	H	33	0.88		CAC	H	33	0.88		CAC	H	33	0.868
	CAU	H	42	1.12		CAU	H	42	1.12		CAU	H	43	1.132
	AUU	I	223	1.497		AUU	I	223	1.497		AUU	I	222	1.5
	AUC	I	75	0.503		AUC	I	75	0.503		AUC	I	74	0.5
	AAA	K	41	1.155		AAA	K	41	1.155		AAA	K	41	1.155
	AAG	K	30	0.845		AAG	K	30	0.845		AAG	K	30	0.845
	CUA	L	89	1.119		CUA	L	89	1.119		CUA	L	83	1.047
	CUC	L	63	0.792		CUC	L	63	0.792		CUC	L	63	0.795
	CUG	L	27	0.34		CUG	L	27	0.34		CUG	L	27	0.341
	CUU	L	139	1.748		CUU	L	139	1.748		CUU	L	144	1.817
	UUA	L	176	1.397		UUA	L	176	1.397		UUA	L	187	1.472
	UUG	L	76	0.603		UUG	L	76	0.603		UUG	L	67	0.528
	AUG	M	47	0.5		AUG	M	47	0.5		AUG	M	51	0.54
	AUA	M	141	1.5		AUA	M	141	1.5		AUA	M	138	1.46
	AAC	N	34	0.624		AAC	N	34	0.624		AAC	N	33	0.623
	AAU	N	75	1.376		AAU	N	75	1.376		AAU	N	73	1.377
	CCU	P	57	1.606		CCU	P	57	1.606		CCU	P	54	1.521

	CCG	P	17	0.479		CCG	P	17	0.479		CCG	P	17	0.479
	CCC	P	38	1.07		CCC	P	38	1.07		CCC	P	41	1.155
	CCA	P	30	0.845		CCA	P	30	0.845		CCA	P	30	0.845
	CAG	Q	16	0.478		CAG	Q	16	0.478		CAG	Q	16	0.485
	CAA	Q	51	1.522		CAA	Q	51	1.522		CAA	Q	50	1.515
	CGA	R	24	1.6		CGA	R	24	1.6		CGA	R	25	1.639
	CGC	R	9	0.6		CGC	R	9	0.6		CGC	R	9	0.59
	CGG	R	13	0.867		CGG	R	13	0.867		CGG	R	13	0.852
	CGU	R	14	0.933		CGU	R	14	0.933		CGU	R	14	0.918
	AGC	S	21	0.433		AGC	S	21	0.433		AGC	S	21	0.432
	AGA	S	75	1.546		AGA	S	75	1.546		AGA	S	76	1.563
	UCA	S	67	1.381		UCA	S	67	1.381		UCA	S	68	1.398
	UCC	S	53	1.093		UCC	S	53	1.093		UCC	S	55	1.131
	UCG	S	20	0.412		UCG	S	20	0.412		UCG	S	17	0.35
	UCU	S	123	2.536		UCU	S	123	2.536		UCU	S	122	2.509
	AGG	S	7	0.144		AGG	S	7	0.144		AGG	S	8	0.165
	AGU	S	22	0.454		AGU	S	22	0.454		AGU	S	22	0.452
	ACA	T	42	1.031		ACA	T	42	1.031		ACA	T	42	1
	ACC	T	30	0.736		ACC	T	30	0.736		ACC	T	36	0.857
	ACG	T	9	0.221		ACG	T	9	0.221		ACG	T	10	0.238
	ACU	T	82	2.012		ACU	T	82	2.012		ACU	T	80	1.905
	GUC	V	45	0.773		GUC	V	45	0.773		GUC	V	45	0.763
	GUG	V	31	0.532		GUG	V	31	0.532		GUG	V	31	0.525
	GUU	V	82	1.408		GUU	V	82	1.408		GUU	V	84	1.424
	GUA	V	75	1.288		GUA	V	75	1.288		GUA	V	76	1.288
	UGA	W	61	1.341		UGA	W	61	1.341		UGA	W	59	1.297
	UGG	W	30	0.659		UGG	W	30	0.659		UGG	W	32	0.703
	UAC	Y	48	0.636		UAC	Y	48	0.636		UAC	Y	46	0.605
	UAU	Y	103	1.364		UAU	Y	103	1.364		UAU	Y	106	1.395

	TETRA2					PENTA1					PENTA2			
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
	UAG	*	2	0.444		UAG	*	2	0.444		UAG	*	2	0.444
	UAA	*	7	1.556		UAA	*	7	1.556		UAA	*	7	1.556
	GCU	A	65	1.548		GCU	A	65	1.548		GCU	A	65	1.548
	GCG	A	14	0.333		GCG	A	13	0.31		GCG	A	13	0.31
	GCC	A	44	1.048		GCC	A	43	1.024		GCC	A	43	1.024
	GCA	A	45	1.071		GCA	A	47	1.119		GCA	A	47	1.119
	UGU	C	23	1.045		UGU	C	23	1.045		UGU	C	23	1.045
	UGC	C	21	0.955		UGC	C	21	0.955		UGC	C	21	0.955
	GAU	D	49	1.273		GAU	D	49	1.273		GAU	D	49	1.273
	GAC	D	28	0.727		GAC	D	28	0.727		GAC	D	28	0.727
	GAG	E	26	0.612		GAG	E	26	0.612		GAG	E	26	0.612
	GAA	E	59	1.388		GAA	E	59	1.388		GAA	E	59	1.388
	UUU	F	221	1.468		UUU	F	221	1.468		UUU	F	221	1.468
	UUC	F	80	0.532		UUC	F	80	0.532		UUC	F	80	0.532
	GGU	G	54	0.977		GGU	G	54	0.973		GGU	G	54	0.973
	GGG	G	65	1.176		GGG	G	65	1.171		GGG	G	65	1.171
	GGC	G	22	0.398		GGC	G	23	0.414		GGC	G	23	0.414
	GGA	G	80	1.448		GGA	G	80	1.441		GGA	G	80	1.441
	CAC	H	33	0.868		CAC	H	33	0.868		CAC	H	33	0.868
	CAU	H	43	1.132		CAU	H	43	1.132		CAU	H	43	1.132
	AUU	I	222	1.495		AUU	I	222	1.495		AUU	I	222	1.495
	AUC	I	75	0.505		AUC	I	75	0.505		AUC	I	75	0.505
	AAA	K	41	1.155		AAA	K	41	1.155		AAA	K	41	1.155
	AAG	K	30	0.845		AAG	K	30	0.845		AAG	K	30	0.845
	CUA	L	82	1.038		CUA	L	83	1.044		CUA	L	83	1.044
	CUC	L	63	0.797		CUC	L	63	0.792		CUC	L	63	0.792
	CUG	L	27	0.342		CUG	L	28	0.352		CUG	L	28	0.352
	CUU	L	144	1.823		CUU	L	144	1.811		CUU	L	144	1.811
	UUA	L	185	1.462		UUA	L	187	1.478		UUA	L	187	1.478
	UUG	L	68	0.538		UUG	L	66	0.522		UUG	L	66	0.522
	AUG	M	52	0.545		AUG	M	51	0.54		AUG	M	51	0.54
	AUA	M	139	1.455		AUA	M	138	1.46		AUA	M	138	1.46
	AAC	N	33	0.623		AAC	N	32	0.61		AAC	N	32	0.61
	AAU	N	73	1.377		AAU	N	73	1.39		AAU	N	73	1.39
	CCU	P	54	1.521		CCU	P	55	1.538		CCU	P	55	1.538

	CCG	P	18	0.507		CCG	P	17	0.476		CCG	P	17	0.476
	CCC	P	41	1.155		CCC	P	41	1.147		CCC	P	41	1.147
	CCA	P	29	0.817		CCA	P	30	0.839		CCA	P	30	0.839
	CAG	Q	16	0.485		CAG	Q	16	0.485		CAG	Q	16	0.485
	CAA	Q	50	1.515		CAA	Q	50	1.515		CAA	Q	50	1.515
	CGA	R	25	1.639		CGA	R	25	1.639		CGA	R	25	1.639
	CGC	R	9	0.59		CGC	R	9	0.59		CGC	R	9	0.59
	CGG	R	13	0.852		CGG	R	13	0.852		CGG	R	13	0.852
	CGU	R	14	0.918		CGU	R	14	0.918		CGU	R	14	0.918
	AGC	S	21	0.429		AGC	S	22	0.451		AGC	S	22	0.451
	AGA	S	76	1.551		AGA	S	76	1.559		AGA	S	76	1.559
	UCA	S	67	1.367		UCA	S	68	1.395		UCA	S	68	1.395
	UCC	S	55	1.122		UCC	S	55	1.128		UCC	S	55	1.128
	UCG	S	19	0.388		UCG	S	17	0.349		UCG	S	17	0.349
	UCU	S	123	2.51		UCU	S	122	2.503		UCU	S	122	2.503
	AGG	S	8	0.163		AGG	S	8	0.164		AGG	S	8	0.164
	AGU	S	23	0.469		AGU	S	22	0.451		AGU	S	22	0.451
	ACA	T	41	0.988		ACA	T	42	1.006		ACA	T	42	1.006
	ACC	T	36	0.867		ACC	T	36	0.862		ACC	T	36	0.862
	ACG	T	10	0.241		ACG	T	10	0.24		ACG	T	10	0.24
	ACU	T	79	1.904		ACU	T	79	1.892		ACU	T	79	1.892
	GUC	V	45	0.769		GUC	V	45	0.769		GUC	V	45	0.769
	GUG	V	31	0.53		GUG	V	30	0.513		GUG	V	30	0.513
	GUU	V	83	1.419		GUU	V	83	1.419		GUU	V	83	1.419
	GUA	V	75	1.282		GUA	V	76	1.299		GUA	V	76	1.299
	UGA	W	61	1.341		UGA	W	60	1.319		UGA	W	60	1.319
	UGG	W	30	0.659		UGG	W	31	0.681		UGG	W	31	0.681
	UAC	Y	47	0.618		UAC	Y	46	0.605		UAC	Y	46	0.605
	UAU	Y	105	1.382		UAU	Y	106	1.395		UAU	Y	106	1.395

	FRA1					FRA2					MON1		
	Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq
	UAG	*	2	0.444		UAG	*	2	0.444		UAG	*	3
	UAA	*	7	1.556		UAA	*	7	1.556		UAA	*	6
	GCU	A	78	1.743		GCU	A	78	1.743		GCU	A	77
	GCG	A	19	0.425		GCG	A	19	0.425		GCG	A	19
	GCC	A	44	0.983		GCC	A	44	0.983		GCC	A	44
	GCA	A	38	0.849		GCA	A	38	0.849		GCA	A	40
	UGU	C	30	1.333		UGU	C	30	1.333		UGU	C	32
	UGC	C	15	0.667		UGC	C	15	0.667		UGC	C	12
	GAU	D	52	1.405		GAU	D	52	1.405		GAU	D	49
	GAC	D	22	0.595		GAC	D	22	0.595		GAC	D	22
	GAG	E	28	0.644		GAG	E	28	0.644		GAG	E	28
	GAA	E	59	1.356		GAA	E	59	1.356		GAA	E	59
	UUU	F	222	1.392		UUU	F	222	1.392		UUU	F	217
	UUC	F	97	0.608		UUC	F	97	0.608		UUC	F	96
	GGU	G	59	1.093		GGU	G	59	1.093		GGU	G	58
	GGG	G	72	1.333		GGG	G	72	1.333		GGG	G	70
	GGC	G	22	0.407		GGC	G	22	0.407		GGC	G	24
	GGA	G	63	1.167		GGA	G	63	1.167		GGA	G	63
	CAC	H	20	0.541		CAC	H	20	0.541		CAC	H	21
	CAU	H	54	1.459		CAU	H	54	1.459		CAU	H	54
	AUU	I	201	1.42		AUU	I	201	1.42		AUU	I	211
	AUC	I	82	0.58		AUC	I	82	0.58		AUC	I	81
	AAA	K	36	0.947		AAA	K	36	0.947		AAA	K	35
	AAG	K	40	1.053		AAG	K	40	1.053		AAG	K	41
	CUA	L	101	1.329		CUA	L	101	1.329		CUA	L	105
	CUC	L	53	0.697		CUC	L	53	0.697		CUC	L	53
	CUG	L	38	0.5		CUG	L	38	0.5		CUG	L	35
	CUU	L	112	1.474		CUU	L	112	1.474		CUU	L	121
	UUA	L	192	1.518		UUA	L	192	1.518		UUA	L	179
	UUG	L	61	0.482		UUG	L	61	0.482		UUG	L	63
	AUG	M	62	0.663		AUG	M	62	0.663		AUG	M	59
	AUA	M	125	1.337		AUA	M	125	1.337		AUA	M	126
	AAC	N	29	0.523		AAC	N	29	0.523		AAC	N	30
	AAU	N	82	1.477		AAU	N	82	1.477		AAU	N	83
	CCU	P	63	1.738		CCU	P	63	1.738		CCU	P	63

	CCG	P	16	0.441		CCG	P	16	0.441		CCG	P	16
	CCC	P	31	0.855		CCC	P	31	0.855		CCC	P	32
	CCA	P	35	0.966		CCA	P	35	0.966		CCA	P	35
	CAG	Q	17	0.493		CAG	Q	17	0.493		CAG	Q	18
	CAA	Q	52	1.507		CAA	Q	52	1.507		CAA	Q	50
	CGA	R	22	1.419		CGA	R	22	1.419		CGA	R	21
	CGC	R	8	0.516		CGC	R	8	0.516		CGC	R	7
	CGG	R	9	0.581		CGG	R	9	0.581		CGG	R	11
	CGU	R	23	1.484		CGU	R	23	1.484		CGU	R	24
	AGC	S	17	0.352		AGC	S	17	0.352		AGC	S	19
	AGA	S	69	1.43		AGA	S	69	1.43		AGA	S	69
	UCA	S	76	1.575		UCA	S	76	1.575		UCA	S	71
	UCC	S	52	1.078		UCC	S	52	1.078		UCC	S	52
	UCG	S	19	0.394		UCG	S	19	0.394		UCG	S	22
	UCU	S	120	2.487		UCU	S	120	2.487		UCU	S	119
	AGG	S	4	0.083		AGG	S	4	0.083		AGG	S	6
	AGU	S	29	0.601		AGU	S	29	0.601		AGU	S	30
	ACA	T	45	1.169		ACA	T	45	1.169		ACA	T	45
	ACC	T	24	0.623		ACC	T	24	0.623		ACC	T	25
	ACG	T	14	0.364		ACG	T	14	0.364		ACG	T	13
	ACU	T	71	1.844		ACU	T	71	1.844		ACU	T	73
	GUC	V	42	0.689		GUC	V	42	0.689		GUC	V	44
	GUG	V	42	0.689		GUG	V	42	0.689		GUG	V	46
	GUU	V	74	1.213		GUU	V	74	1.213		GUU	V	68
	GUA	V	86	1.41		GUA	V	86	1.41		GUA	V	83
	UGA	W	68	1.495		UGA	W	68	1.495		UGA	W	70
	UGG	W	23	0.505		UGG	W	23	0.505		UGG	W	22
	UAC	Y	46	0.609		UAC	Y	46	0.609		UAC	Y	47
	UAU	Y	105	1.391		UAU	Y	105	1.391		UAU	Y	102

		MON2					SAL1					SAL2		
RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq
0.667		UAG	*	3	0.667		UAG	*	3	0.667		UAG	*	3
1.333		UAA	*	6	1.333		UAA	*	6	1.333		UAA	*	6
1.711		GCU	A	78	1.724		GCU	A	62	1.117		GCU	A	62
0.422		GCG	A	20	0.442		GCG	A	26	0.468		GCG	A	26
0.978		GCC	A	43	0.95		GCC	A	91	1.64		GCC	A	91
0.889		GCA	A	40	0.884		GCA	A	43	0.775		GCA	A	43
1.455		UGU	C	32	1.455		UGU	C	21	0.894		UGU	C	21
0.545		UGC	C	12	0.545		UGC	C	26	1.106		UGC	C	26
1.38		GAU	D	49	1.38		GAU	D	39	1.013		GAU	D	39
0.62		GAC	D	22	0.62		GAC	D	38	0.987		GAC	D	38
0.644		GAG	E	28	0.644		GAG	E	46	1.07		GAG	E	46
1.356		GAA	E	59	1.356		GAA	E	40	0.93		GAA	E	40
1.387		UUU	F	216	1.385		UUU	F	173	1.181		UUU	F	173
0.613		UUC	F	96	0.615		UUC	F	120	0.819		UUC	F	120
1.079		GGU	G	58	1.079		GGU	G	46	0.745		GGU	G	46
1.302		GGG	G	70	1.302		GGG	G	116	1.879		GGG	G	116
0.447		GGC	G	24	0.447		GGC	G	42	0.68		GGC	G	42
1.172		GGA	G	63	1.172		GGA	G	43	0.696		GGA	G	43
0.56		CAC	H	21	0.56		CAC	H	37	0.937		CAC	H	37
1.44		CAU	H	54	1.44		CAU	H	42	1.063		CAU	H	42
1.445		AUU	I	210	1.443		AUU	I	135	1.102		AUU	I	135
0.555		AUC	I	81	0.557		AUC	I	110	0.898		AUC	I	110
0.921		AAA	K	36	0.935		AAA	K	30	0.909		AAA	K	30
1.079		AAG	K	41	1.065		AAG	K	36	1.091		AAG	K	36
1.338		CUA	L	104	1.325		CUA	L	82	0.814		CUA	L	82
0.675		CUC	L	54	0.688		CUC	L	115	1.141		CUC	L	115
0.446		CUG	L	35	0.446		CUG	L	97	0.963		CUG	L	97
1.541		CUU	L	121	1.541		CUU	L	109	1.082		CUU	L	109
1.479		UUA	L	181	1.484		UUA	L	102	1.193		UUA	L	102
0.521		UUG	L	63	0.516		UUG	L	69	0.807		UUG	L	69
0.638		AUG	M	59	0.638		AUG	M	69	0.945		AUG	M	69
1.362		AUA	M	126	1.362		AUA	M	77	1.055		AUA	M	77
0.531		AAC	N	30	0.531		AAC	N	45	0.957		AAC	N	45
1.469		AAU	N	83	1.469		AAU	N	49	1.043		AAU	N	49
1.726		CCU	P	62	1.699		CCU	P	44	1.173		CCU	P	44

0.438		CCG	P	15	0.411		CCG	P	22	0.587		CCG	P	22
0.877		CCC	P	33	0.904		CCC	P	64	1.707		CCC	P	64
0.959		CCA	P	36	0.986		CCA	P	20	0.533		CCA	P	20
0.529		CAG	Q	18	0.529		CAG	Q	32	0.955		CAG	Q	32
1.471		CAA	Q	50	1.471		CAA	Q	35	1.045		CAA	Q	35
1.333		CGA	R	21	1.333		CGA	R	19	1.118		CGA	R	19
0.444		CGC	R	7	0.444		CGC	R	10	0.588		CGC	R	10
0.698		CGG	R	11	0.698		CGG	R	23	1.353		CGG	R	23
1.524		CGU	R	24	1.524		CGU	R	16	0.941		CGU	R	16
0.392		AGC	S	19	0.394		AGC	S	33	0.715		AGC	S	33
1.423		AGA	S	69	1.43		AGA	S	62	1.344		AGA	S	62
1.464		UCA	S	69	1.43		UCA	S	54	1.171		UCA	S	54
1.072		UCC	S	53	1.098		UCC	S	74	1.604		UCC	S	74
0.454		UCG	S	23	0.477		UCG	S	27	0.585		UCG	S	27
2.454		UCU	S	118	2.446		UCU	S	99	2.146		UCU	S	99
0.124		AGG	S	5	0.104		AGG	S	5	0.108		AGG	S	5
0.619		AGU	S	30	0.622		AGU	S	15	0.325		AGU	S	15
1.154		ACA	T	45	1.154		ACA	T	33	0.805		ACA	T	33
0.641		ACC	T	24	0.615		ACC	T	50	1.22		ACC	T	50
0.333		ACG	T	13	0.333		ACG	T	23	0.561		ACG	T	23
1.872		ACU	T	74	1.897		ACU	T	58	1.415		ACU	T	58
0.73		GUC	V	43	0.714		GUC	V	78	1.102		GUC	V	78
0.763		GUG	V	44	0.73		GUG	V	63	0.89		GUG	V	63
1.129		GUU	V	70	1.162		GUU	V	79	1.117		GUU	V	79
1.378		GUA	V	84	1.394		GUA	V	63	0.89		GUA	V	63
1.522		UGA	W	70	1.522		UGA	W	51	1.085		UGA	W	51
0.478		UGG	W	22	0.478		UGG	W	43	0.915		UGG	W	43
0.631		UAC	Y	48	0.644		UAC	Y	66	0.95		UAC	Y	66
1.369		UAU	Y	101	1.356		UAU	Y	73	1.05		UAU	Y	73

		PER1					PER2			
RSCU		Codon	AA	ObsFreq	RSCU		Codon	AA	ObsFreq	RSCU
0.667		UAG	*	3	0.667		UAG	*	3	0.667
1.333		UAA	*	6	1.333		UAA	*	6	1.333
1.117		GCU	A	57	1.31		GCU	A	57	1.31
0.468		GCG	A	24	0.552		GCG	A	23	0.529
1.64		GCC	A	46	1.057		GCC	A	46	1.057
0.775		GCA	A	47	1.08		GCA	A	48	1.103
0.894		UGU	C	33	1.5		UGU	C	34	1.545
1.106		UGC	C	11	0.5		UGC	C	10	0.455
1.013		GAU	D	48	1.297		GAU	D	48	1.297
0.987		GAC	D	26	0.703		GAC	D	26	0.703
1.07		GAG	E	27	0.635		GAG	E	26	0.619
0.93		GAA	E	58	1.365		GAA	E	58	1.381
1.181		UUU	F	228	1.495		UUU	F	228	1.485
0.819		UUC	F	77	0.505		UUC	F	79	0.515
0.745		GGU	G	46	0.811		GGU	G	47	0.832
1.879		GGG	G	77	1.357		GGG	G	78	1.381
0.68		GGC	G	33	0.581		GGC	G	31	0.549
0.696		GGA	G	71	1.251		GGA	G	70	1.239
0.937		CAC	H	20	0.526		CAC	H	21	0.553
1.063		CAU	H	56	1.474		CAU	H	55	1.447
1.102		AUU	I	210	1.433		AUU	I	213	1.449
0.898		AUC	I	83	0.567		AUC	I	81	0.551
0.909		AAA	K	44	1.158		AAA	K	44	1.173
1.091		AAG	K	32	0.842		AAG	K	31	0.827
0.814		CUA	L	81	1.106		CUA	L	82	1.119
1.141		CUC	L	62	0.846		CUC	L	59	0.805
0.963		CUG	L	41	0.56		CUG	L	41	0.56
1.082		CUU	L	109	1.488		CUU	L	111	1.515
1.193		UUA	L	207	1.495		UUA	L	208	1.496
0.807		UUG	L	70	0.505		UUG	L	70	0.504
0.945		AUG	M	55	0.595		AUG	M	58	0.624
1.055		AUA	M	130	1.405		AUA	M	128	1.376
0.957		AAC	N	26	0.433		AAC	N	28	0.467
1.043		AAU	N	94	1.567		AAU	N	92	1.533
1.173		CCU	P	64	1.778		CCU	P	63	1.762

0.587		CCG	P	15	0.417		CCG	P	14	0.392
1.707		CCC	P	40	1.111		CCC	P	41	1.147
0.533		CCA	P	25	0.694		CCA	P	25	0.699
0.955		CAG	Q	24	0.676		CAG	Q	23	0.639
1.045		CAA	Q	47	1.324		CAA	Q	49	1.361
1.118		CGA	R	24	1.6		CGA	R	24	1.6
0.588		CGC	R	6	0.4		CGC	R	6	0.4
1.353		CGG	R	13	0.867		CGG	R	13	0.867
0.941		CGU	R	17	1.133		CGU	R	17	1.133
0.715		AGC	S	14	0.298		AGC	S	12	0.255
1.344		AGA	S	71	1.511		AGA	S	71	1.507
1.171		UCA	S	74	1.574		UCA	S	70	1.485
1.604		UCC	S	32	0.681		UCC	S	32	0.679
0.585		UCG	S	15	0.319		UCG	S	18	0.382
2.146		UCU	S	141	3		UCU	S	141	2.992
0.108		AGG	S	1	0.021		AGG	S	2	0.042
0.325		AGU	S	28	0.596		AGU	S	31	0.658
0.805		ACA	T	44	1.197		ACA	T	44	1.205
1.22		ACC	T	33	0.898		ACC	T	29	0.795
0.561		ACG	T	12	0.327		ACG	T	11	0.301
1.415		ACU	T	58	1.578		ACU	T	62	1.699
1.102		GUC	V	35	0.574		GUC	V	36	0.595
0.89		GUG	V	39	0.639		GUG	V	42	0.694
1.117		GUU	V	79	1.295		GUU	V	76	1.256
0.89		GUA	V	91	1.492		GUA	V	88	1.455
1.085		UGA	W	73	1.553		UGA	W	74	1.574
0.915		UGG	W	21	0.447		UGG	W	20	0.426
0.95		UAC	Y	52	0.738		UAC	Y	52	0.738
1.05		UAU	Y	89	1.262		UAU	Y	89	1.262

Table S8. Comparison of RSCU values among <i>Artemia</i> members.									
		UAG	UAA	GCU	GCG	GCC	GCA	UGU	UGC
RSCU	DI1	0.444	1.556	1.384	0.324	1.449	0.843	1.217	0.783
RSCU	DI2	0.444	1.556	1.384	0.324	1.449	0.843	1.217	0.783
RSCU	TRI1	0.444	1.556	1.385	0.308	1.473	0.835	1.217	0.783
RSCU	TRI2	0.444	1.556	1.385	0.308	1.473	0.835	1.217	0.783
RSCU	TIB1	0.444	1.556	1.369	0.342	1.476	0.813	1.217	0.783
RSCU	TIB2	0.444	1.556	1.348	0.342	1.497	0.813	1.174	0.826
RSCU	AMA1	0.444	1.556	1.311	0.328	1.53	0.831	1.333	0.667
RSCU	AMA2	0.444	1.556	1.348	0.326	1.5	0.826	1.333	0.667
RSCU	URM1	0.444	1.556	1.451	0.352	1.363	0.835	1.2	0.8
RSCU	URM2	0.444	1.556	1.413	0.37	1.413	0.804	1.156	0.844
RSCU	SOR1	0.667	1.333	1.467	0.244	1.4	0.889	1.333	0.667
RSCU	SOR2	0.444	1.556	1.475	0.246	1.385	0.894	1.378	0.622
RSCU	SIN1	0.25	1.75	1.586	0.345	1.011	1.057	1.091	0.909
RSCU	SIN2	0.25	1.75	1.586	0.345	1.011	1.057	1.091	0.909
RSCU	TETRA1	0.667	1.333	1.557	0.335	1.03	1.078	1.045	0.955
RSCU	TETRA2	0.444	1.556	1.548	0.333	1.048	1.071	1.045	0.955
RSCU	PENTA1	0.444	1.556	1.548	0.31	1.024	1.119	1.045	0.955
RSCU	PENTA2	0.444	1.556	1.548	0.31	1.024	1.119	1.045	0.955
RSCU	FRA1	0.444	1.556	1.743	0.425	0.983	0.849	1.333	0.667
RSCU	FRA2	0.444	1.556	1.743	0.425	0.983	0.849	1.333	0.667
RSCU	MON1	0.667	1.333	1.711	0.422	0.978	0.889	1.455	0.545
RSCU	MON2	0.667	1.333	1.724	0.442	0.95	0.884	1.455	0.545
RSCU	SAL1	0.667	1.333	1.117	0.468	1.64	0.775	0.894	1.106
RSCU	SAL2	0.667	1.333	1.117	0.468	1.64	0.775	0.894	1.106
RSCU	PER1	0.667	1.333	1.31	0.552	1.057	1.08	1.5	0.5
RSCU	PER2	0.667	1.333	1.31	0.529	1.057	1.103	1.545	0.455

GAU	GAC	GAG	GAA	UUU	UUC	GGU	GGG	GGC	GGA
1.413	0.587	0.644	1.356	1.362	0.638	0.764	1.351	0.462	1.422
1.413	0.587	0.644	1.356	1.362	0.638	0.764	1.351	0.462	1.422
1.44	0.56	0.621	1.379	1.36	0.64	0.743	1.345	0.478	1.434
1.44	0.56	0.621	1.379	1.358	0.642	0.743	1.345	0.478	1.434
1.36	0.64	0.598	1.402	1.353	0.647	0.711	1.387	0.533	1.369
1.395	0.605	0.581	1.419	1.347	0.653	0.729	1.387	0.516	1.369
1.36	0.64	0.598	1.402	1.369	0.631	0.69	1.398	0.531	1.381
1.387	0.613	0.614	1.386	1.369	0.631	0.708	1.381	0.513	1.398
1.447	0.553	0.512	1.488	1.344	0.656	0.758	1.41	0.476	1.357
1.421	0.579	0.535	1.465	1.338	0.662	0.722	1.427	0.511	1.339
1.444	0.556	0.591	1.409	1.385	0.615	0.678	1.496	0.4	1.426
1.425	0.575	0.591	1.409	1.392	0.608	0.678	1.496	0.4	1.426
1.333	0.667	0.558	1.442	1.479	0.521	0.991	1.171	0.378	1.459
1.333	0.667	0.558	1.442	1.479	0.521	0.991	1.171	0.378	1.459
1.273	0.727	0.612	1.388	1.475	0.525	0.973	1.171	0.414	1.441
1.273	0.727	0.612	1.388	1.468	0.532	0.977	1.176	0.398	1.448
1.273	0.727	0.612	1.388	1.468	0.532	0.973	1.171	0.414	1.441
1.273	0.727	0.612	1.388	1.468	0.532	0.973	1.171	0.414	1.441
1.405	0.595	0.644	1.356	1.392	0.608	1.093	1.333	0.407	1.167
1.405	0.595	0.644	1.356	1.392	0.608	1.093	1.333	0.407	1.167
1.38	0.62	0.644	1.356	1.387	0.613	1.079	1.302	0.447	1.172
1.38	0.62	0.644	1.356	1.385	0.615	1.079	1.302	0.447	1.172
1.013	0.987	1.07	0.93	1.181	0.819	0.745	1.879	0.68	0.696
1.013	0.987	1.07	0.93	1.181	0.819	0.745	1.879	0.68	0.696
1.297	0.703	0.635	1.365	1.495	0.505	0.811	1.357	0.581	1.251
1.297	0.703	0.619	1.381	1.485	0.515	0.832	1.381	0.549	1.239

CAC	CAU	AUU	AUC	AAA	AAG	CUA	CUC	CUG	CUU
1.028	0.972	1.472	0.528	1.101	0.899	1.222	0.958	0.491	1.329
1.028	0.972	1.472	0.528	1.101	0.899	1.222	0.958	0.491	1.329
1.028	0.972	1.467	0.533	1.101	0.899	1.237	0.961	0.492	1.309
1.028	0.972	1.467	0.533	1.101	0.899	1.234	0.958	0.491	1.317
1.014	0.986	1.433	0.567	1.118	0.882	1.283	0.933	0.466	1.318
1.041	0.959	1.439	0.561	1.118	0.882	1.287	0.928	0.452	1.333
1.014	0.986	1.431	0.569	1.134	0.866	1.255	0.927	0.493	1.326
1.014	0.986	1.436	0.564	1.152	0.848	1.247	0.918	0.482	1.353
1.013	0.987	1.431	0.569	1.029	0.971	1.255	0.915	0.469	1.361
0.933	1.067	1.421	0.579	1	1	1.282	0.882	0.424	1.412
0.974	1.026	1.418	0.582	1.222	0.778	1.291	1.037	0.438	1.233
0.961	1.039	1.411	0.589	1.222	0.778	1.287	1.034	0.448	1.23
0.88	1.12	1.497	0.503	1.155	0.845	1.119	0.792	0.34	1.748
0.88	1.12	1.497	0.503	1.155	0.845	1.119	0.792	0.34	1.748
0.868	1.132	1.5	0.5	1.155	0.845	1.047	0.795	0.341	1.817
0.868	1.132	1.495	0.505	1.155	0.845	1.038	0.797	0.342	1.823
0.868	1.132	1.495	0.505	1.155	0.845	1.044	0.792	0.352	1.811
0.868	1.132	1.495	0.505	1.155	0.845	1.044	0.792	0.352	1.811
0.541	1.459	1.42	0.58	0.947	1.053	1.329	0.697	0.5	1.474
0.541	1.459	1.42	0.58	0.947	1.053	1.329	0.697	0.5	1.474
0.56	1.44	1.445	0.555	0.921	1.079	1.338	0.675	0.446	1.541
0.56	1.44	1.443	0.557	0.935	1.065	1.325	0.688	0.446	1.541
0.937	1.063	1.102	0.898	0.909	1.091	0.814	1.141	0.963	1.082
0.937	1.063	1.102	0.898	0.909	1.091	0.814	1.141	0.963	1.082
0.526	1.474	1.433	0.567	1.158	0.842	1.106	0.846	0.56	1.488
0.553	1.447	1.449	0.551	1.173	0.827	1.119	0.805	0.56	1.515

UUA	UUG	AUG	AUA	AAC	AAU	CCU	CCG	CCC	CCA
1.371	0.629	0.489	1.511	0.729	1.271	1.342	0.685	1.37	0.603
1.371	0.629	0.489	1.511	0.729	1.271	1.342	0.685	1.37	0.603
1.385	0.615	0.489	1.511	0.71	1.29	1.333	0.68	1.388	0.599
1.385	0.615	0.489	1.511	0.71	1.29	1.333	0.68	1.388	0.599
1.348	0.652	0.529	1.471	0.692	1.308	1.297	0.69	1.407	0.607
1.354	0.646	0.529	1.471	0.71	1.29	1.306	0.694	1.389	0.611
1.368	0.632	0.518	1.482	0.679	1.321	1.324	0.69	1.379	0.607
1.371	0.629	0.518	1.482	0.692	1.308	1.324	0.69	1.379	0.607
1.38	0.62	0.547	1.453	0.636	1.364	1.297	0.497	1.434	0.772
1.371	0.629	0.555	1.445	0.673	1.327	1.324	0.552	1.407	0.717
1.467	0.533	0.663	1.337	0.577	1.423	1.38	0.62	1.296	0.704
1.467	0.533	0.644	1.356	0.635	1.365	1.408	0.648	1.268	0.676
1.397	0.603	0.5	1.5	0.624	1.376	1.606	0.479	1.07	0.845
1.397	0.603	0.5	1.5	0.624	1.376	1.606	0.479	1.07	0.845
1.472	0.528	0.54	1.46	0.623	1.377	1.521	0.479	1.155	0.845
1.462	0.538	0.545	1.455	0.623	1.377	1.521	0.507	1.155	0.817
1.478	0.522	0.54	1.46	0.61	1.39	1.538	0.476	1.147	0.839
1.478	0.522	0.54	1.46	0.61	1.39	1.538	0.476	1.147	0.839
1.518	0.482	0.663	1.337	0.523	1.477	1.738	0.441	0.855	0.966
1.518	0.482	0.663	1.337	0.523	1.477	1.738	0.441	0.855	0.966
1.479	0.521	0.638	1.362	0.531	1.469	1.726	0.438	0.877	0.959
1.484	0.516	0.638	1.362	0.531	1.469	1.699	0.411	0.904	0.986
1.193	0.807	0.945	1.055	0.957	1.043	1.173	0.587	1.707	0.533
1.193	0.807	0.945	1.055	0.957	1.043	1.173	0.587	1.707	0.533
1.495	0.505	0.595	1.405	0.433	1.567	1.778	0.417	1.111	0.694
1.496	0.504	0.624	1.376	0.467	1.533	1.762	0.392	1.147	0.699

CAG	CAA	CGA	CGC	CGG	CGU	AGC	AGA	UCA	UCC
0.486	1.514	1.639	0.59	0.525	1.246	0.317	1.52	1.456	0.992
0.486	1.514	1.639	0.59	0.525	1.246	0.317	1.52	1.456	0.971
0.486	1.514	1.639	0.59	0.525	1.246	0.338	1.52	1.456	0.992
0.486	1.514	1.639	0.59	0.525	1.246	0.338	1.52	1.456	0.992
0.486	1.514	1.667	0.6	0.533	1.2	0.422	1.499	1.478	1.013
0.486	1.514	1.639	0.59	0.525	1.246	0.422	1.499	1.478	1.013
0.486	1.514	1.639	0.59	0.525	1.246	0.399	1.491	1.491	0.987
0.486	1.514	1.639	0.59	0.525	1.246	0.399	1.491	1.491	0.987
0.459	1.541	1.508	0.721	0.656	1.115	0.423	1.545	1.397	1.058
0.486	1.514	1.574	0.656	0.59	1.18	0.403	1.528	1.422	1.04
0.451	1.549	1.6	0.6	0.533	1.267	0.46	1.379	1.504	1.128
0.451	1.549	1.533	0.6	0.6	1.267	0.46	1.379	1.483	1.107
0.478	1.522	1.6	0.6	0.867	0.933	0.433	1.546	1.381	1.093
0.478	1.522	1.6	0.6	0.867	0.933	0.433	1.546	1.381	1.093
0.485	1.515	1.639	0.59	0.852	0.918	0.432	1.563	1.398	1.131
0.485	1.515	1.639	0.59	0.852	0.918	0.429	1.551	1.367	1.122
0.485	1.515	1.639	0.59	0.852	0.918	0.451	1.559	1.395	1.128
0.485	1.515	1.639	0.59	0.852	0.918	0.451	1.559	1.395	1.128
0.493	1.507	1.419	0.516	0.581	1.484	0.352	1.43	1.575	1.078
0.493	1.507	1.419	0.516	0.581	1.484	0.352	1.43	1.575	1.078
0.529	1.471	1.333	0.444	0.698	1.524	0.392	1.423	1.464	1.072
0.529	1.471	1.333	0.444	0.698	1.524	0.394	1.43	1.43	1.098
0.955	1.045	1.118	0.588	1.353	0.941	0.715	1.344	1.171	1.604
0.955	1.045	1.118	0.588	1.353	0.941	0.715	1.344	1.171	1.604
0.676	1.324	1.6	0.4	0.867	1.133	0.298	1.511	1.574	0.681
0.639	1.361	1.6	0.4	0.867	1.133	0.255	1.507	1.485	0.679

UCG	UCU	AGG	AGU	ACA	ACC	ACG	ACU	GUC	GUG
0.38	2.47	0.127	0.739	1.042	0.921	0.364	1.673	0.816	0.62
0.38	2.491	0.127	0.739	1.042	0.921	0.364	1.673	0.816	0.62
0.38	2.47	0.127	0.718	1.055	0.908	0.368	1.669	0.826	0.632
0.38	2.47	0.127	0.718	1.055	0.883	0.368	1.693	0.826	0.632
0.359	2.449	0.148	0.633	1.091	0.97	0.315	1.624	0.823	0.677
0.359	2.449	0.148	0.633	1.091	0.945	0.315	1.648	0.826	0.68
0.357	2.457	0.168	0.651	1.091	0.945	0.291	1.673	0.81	0.667
0.357	2.457	0.168	0.651	1.091	0.921	0.291	1.697	0.781	0.669
0.444	2.413	0.148	0.571	1.036	0.988	0.289	1.687	0.794	0.685
0.403	2.462	0.149	0.594	1.055	0.933	0.294	1.718	0.763	0.747
0.376	2.36	0.125	0.668	1.067	0.945	0.339	1.648	0.688	0.72
0.397	2.381	0.125	0.668	1.049	0.951	0.341	1.659	0.685	0.717
0.412	2.536	0.144	0.454	1.031	0.736	0.221	2.012	0.773	0.532
0.412	2.536	0.144	0.454	1.031	0.736	0.221	2.012	0.773	0.532
0.35	2.509	0.165	0.452	1	0.857	0.238	1.905	0.763	0.525
0.388	2.51	0.163	0.469	0.988	0.867	0.241	1.904	0.769	0.53
0.349	2.503	0.164	0.451	1.006	0.862	0.24	1.892	0.769	0.513
0.349	2.503	0.164	0.451	1.006	0.862	0.24	1.892	0.769	0.513
0.394	2.487	0.083	0.601	1.169	0.623	0.364	1.844	0.689	0.689
0.394	2.487	0.083	0.601	1.169	0.623	0.364	1.844	0.689	0.689
0.454	2.454	0.124	0.619	1.154	0.641	0.333	1.872	0.73	0.763
0.477	2.446	0.104	0.622	1.154	0.615	0.333	1.897	0.714	0.73
0.585	2.146	0.108	0.325	0.805	1.22	0.561	1.415	1.102	0.89
0.585	2.146	0.108	0.325	0.805	1.22	0.561	1.415	1.102	0.89
0.319	3	0.021	0.596	1.197	0.898	0.327	1.578	0.574	0.639
0.382	2.992	0.042	0.658	1.205	0.795	0.301	1.699	0.595	0.694

GUU	GUA	UGA	UGG	UAC	UAU
1.29	1.273	1.283	0.717	0.728	1.272
1.29	1.273	1.283	0.717	0.728	1.272
1.279	1.263	1.326	0.674	0.715	1.285
1.279	1.263	1.326	0.674	0.715	1.285
1.242	1.258	1.261	0.739	0.773	1.227
1.231	1.263	1.239	0.761	0.747	1.253
1.27	1.254	1.283	0.717	0.76	1.24
1.291	1.259	1.283	0.717	0.747	1.253
1.323	1.198	1.261	0.739	0.819	1.181
1.339	1.152	1.261	0.739	0.805	1.195
1.28	1.312	1.261	0.739	0.649	1.351
1.291	1.307	1.261	0.739	0.653	1.347
1.408	1.288	1.341	0.659	0.636	1.364
1.408	1.288	1.341	0.659	0.636	1.364
1.424	1.288	1.297	0.703	0.605	1.395
1.419	1.282	1.341	0.659	0.618	1.382
1.419	1.299	1.319	0.681	0.605	1.395
1.419	1.299	1.319	0.681	0.605	1.395
1.213	1.41	1.495	0.505	0.609	1.391
1.213	1.41	1.495	0.505	0.609	1.391
1.129	1.378	1.522	0.478	0.631	1.369
1.162	1.394	1.522	0.478	0.644	1.356
1.117	0.89	1.085	0.915	0.95	1.05
1.117	0.89	1.085	0.915	0.95	1.05
1.295	1.492	1.553	0.447	0.738	1.262
1.256	1.455	1.574	0.426	0.738	1.262

Table S9. Comparison of Observed frequency values among <i>Artemia</i> members.												
Codon		UAG	UAA	GCU	GCG	GCC	GCA	UGU	UGC	GAU	GAC	GAG
ObsFreq	DI1	2	7	64	15	67	39	28	18	53	22	28
ObsFreq	DI2	2	7	64	15	67	39	28	18	53	22	28
ObsFreq	TRI1	2	7	63	14	67	38	28	18	54	21	27
ObsFreq	TRI2	2	7	63	14	67	38	28	18	54	21	27
ObsFreq	TIB1	2	7	64	16	69	38	28	18	51	24	26
ObsFreq	TIB2	2	7	63	16	70	38	27	19	53	23	25
ObsFreq	AMA1	2	7	60	15	70	38	30	15	51	24	26
ObsFreq	AMA2	2	7	62	15	69	38	30	15	52	23	27
ObsFreq	URM1	2	7	66	16	62	38	27	18	55	21	22
ObsFreq	URM2	2	7	65	17	65	37	26	19	54	22	23
ObsFreq	SOR1	3	6	66	11	63	40	30	15	52	20	26
ObsFreq	SIN2	2	7	66	11	62	40	31	14	52	21	26
ObsFreq	SIN1	1	7	69	15	44	46	24	20	50	25	24
ObsFreq	SON2	1	7	69	15	44	46	24	20	50	25	24
ObsFreq	TETRA1	3	6	65	14	43	45	23	21	49	28	26
ObsFreq	TETRA2	2	7	65	14	44	45	23	21	49	28	26
ObsFreq	PENTA1	2	7	65	13	43	47	23	21	49	28	26
ObsFreq	PENTA2	2	7	65	13	43	47	23	21	49	28	26
ObsFreq	FRA1	2	7	78	19	44	38	30	15	52	22	28
ObsFreq	FRA2	2	7	78	19	44	38	30	15	52	22	28
ObsFreq	MON1	3	6	77	19	44	40	32	12	49	22	28
ObsFreq	MON2	3	6	78	20	43	40	32	12	49	22	28
ObsFreq	SAL1	3	6	62	26	91	43	21	26	39	38	46
ObsFreq	SAL2	3	6	62	26	91	43	21	26	39	38	46
ObsFreq	PER1	3	6	57	24	46	47	33	11	48	26	27
ObsFreq	PER2	3	6	57	23	46	48	34	10	48	26	26

GAA	UUU	UUC	GGU	GGG	GGC	GGA	CAC	CAU	AUU	AUC	AAA	AAG	CUA	CUC
59	205	96	43	76	26	80	37	35	212	76	38	31	102	80
59	205	96	43	76	26	80	37	35	212	76	38	31	102	80
60	206	97	42	76	27	81	37	35	212	77	38	31	103	80
60	205	97	42	76	27	81	37	35	212	77	38	31	103	80
61	203	97	40	78	30	77	37	36	207	82	38	30	110	80
61	202	98	41	78	29	77	38	35	208	81	38	30	111	80
61	206	95	39	79	30	78	37	36	206	82	38	29	107	79
61	206	95	40	78	29	79	37	36	206	81	38	28	106	78
64	201	98	43	80	27	77	38	37	201	80	35	33	107	78
63	200	99	41	81	29	76	35	40	199	81	34	34	109	75
62	205	91	39	86	23	82	37	39	202	83	44	28	112	90
62	206	90	39	86	23	82	37	40	201	84	44	28	112	90
62	224	79	55	65	21	81	33	42	223	75	41	30	89	63
62	224	79	55	65	21	81	33	42	223	75	41	30	89	63
59	222	79	54	65	23	80	33	43	222	74	41	30	83	63
59	221	80	54	65	22	80	33	43	222	75	41	30	82	63
59	221	80	54	65	23	80	33	43	222	75	41	30	83	63
59	221	80	54	65	23	80	33	43	222	75	41	30	83	63
59	222	97	59	72	22	63	20	54	201	82	36	40	101	53
59	222	97	59	72	22	63	20	54	201	82	36	40	101	53
59	217	96	58	70	24	63	21	54	211	81	35	41	105	53
59	216	96	58	70	24	63	21	54	210	81	36	41	104	54
40	173	120	46	116	42	43	37	42	135	110	30	36	82	115
40	173	120	46	116	42	43	37	42	135	110	30	36	82	115
58	228	77	46	77	33	71	20	56	210	83	44	32	81	62
58	228	79	47	78	31	70	21	55	213	81	44	31	82	59

CUG	CUU	UUA	UUG	AUG	AUA	AAC	AAU	CCU	CCG	CCC	CCA	CAG	CAA	CGA
41	111	159	73	43	133	39	68	49	25	50	22	18	56	25
41	111	159	73	43	133	39	68	49	25	50	22	18	56	25
41	109	160	71	43	133	38	69	49	25	51	22	18	56	25
41	110	160	71	43	133	38	69	49	25	51	22	18	56	25
40	113	153	74	45	125	37	70	47	25	51	22	18	56	25
39	115	153	73	45	125	38	69	47	25	50	22	18	56	25
42	113	156	72	44	126	36	70	48	25	50	22	18	56	25
41	115	157	72	44	126	37	70	48	25	50	22	18	56	25
40	116	158	71	47	125	34	73	47	18	52	28	17	57	23
36	120	159	73	48	125	36	71	48	20	51	26	18	56	24
38	107	168	61	58	117	30	74	49	22	46	25	16	55	24
39	107	168	61	56	118	33	71	50	23	45	24	16	55	23
27	139	176	76	47	141	34	75	57	17	38	30	16	51	24
27	139	176	76	47	141	34	75	57	17	38	30	16	51	24
27	144	187	67	51	138	33	73	54	17	41	30	16	50	25
27	144	185	68	52	139	33	73	54	18	41	29	16	50	25
28	144	187	66	51	138	32	73	55	17	41	30	16	50	25
28	144	187	66	51	138	32	73	55	17	41	30	16	50	25
38	112	192	61	62	125	29	82	63	16	31	35	17	52	22
38	112	192	61	62	125	29	82	63	16	31	35	17	52	22
35	121	179	63	59	126	30	83	63	16	32	35	18	50	21
35	121	181	63	59	126	30	83	62	15	33	36	18	50	21
97	109	102	69	69	77	45	49	44	22	64	20	32	35	19
97	109	102	69	69	77	45	49	44	22	64	20	32	35	19
41	109	207	70	55	130	26	94	64	15	40	25	24	47	24
41	111	208	70	58	128	28	92	63	14	41	25	23	49	24

CGC	CGG	CGU	AGC	AGA	UCA	UCC	UCG	UCU	AGG	AGU	ACA	ACC	ACG	ACU
9	8	19	15	72	69	47	18	117	6	35	43	38	15	69
9	8	19	15	72	69	46	18	118	6	35	43	38	15	69
9	8	19	16	72	69	47	18	117	6	34	43	37	15	68
9	8	19	16	72	69	47	18	117	6	34	43	36	15	69
9	8	18	20	71	70	48	17	116	7	30	45	40	13	67
9	8	19	20	71	70	48	17	116	7	30	45	39	13	68
9	8	19	19	71	71	47	17	117	8	31	45	39	12	69
9	8	19	19	71	71	47	17	117	8	31	45	38	12	70
11	10	17	20	73	66	50	21	114	7	27	43	41	12	70
10	9	18	19	72	67	49	19	116	7	28	43	38	12	70
9	8	19	22	66	72	54	18	113	6	32	44	39	14	68
9	9	19	22	66	71	53	19	114	6	32	43	39	14	68
9	13	14	21	75	67	53	20	123	7	22	42	30	9	82
9	13	14	21	75	67	53	20	123	7	22	42	30	9	82
9	13	14	21	76	68	55	17	122	8	22	42	36	10	80
9	13	14	21	76	67	55	19	123	8	23	41	36	10	79
9	13	14	22	76	68	55	17	122	8	22	42	36	10	79
9	13	14	22	76	68	55	17	122	8	22	42	36	10	79
8	9	23	17	69	76	52	19	120	4	29	45	24	14	71
8	9	23	17	69	76	52	19	120	4	29	45	24	14	71
7	11	24	19	69	71	52	22	119	6	30	45	25	13	73
7	11	24	19	69	69	53	23	118	5	30	45	24	13	74
10	23	16	33	62	54	74	27	99	5	15	33	50	23	58
10	23	16	33	62	54	74	27	99	5	15	33	50	23	58
6	13	17	14	71	74	32	15	141	1	28	44	33	12	58
6	13	17	12	71	70	32	18	141	2	31	44	29	11	62

GUC	GUG	GUU	GUA	UGA	UGG	UAC	UAU
50	38	79	78	59	33	55	96
50	38	79	78	59	33	55	96
51	39	79	78	61	31	54	97
51	39	79	78	61	31	54	97
51	42	77	78	58	34	58	92
51	42	76	78	57	35	56	94
51	42	80	79	59	33	57	93
49	42	81	79	59	33	56	94
51	44	85	77	58	34	61	88
49	48	86	74	58	34	60	89
43	45	80	82	58	34	48	100
43	45	81	82	58	34	48	99
45	31	82	75	61	30	48	103
45	31	82	75	61	30	48	103
45	31	84	76	59	32	46	106
45	31	83	75	61	30	47	105
45	30	83	76	60	31	46	106
45	30	83	76	60	31	46	106
42	42	74	86	68	23	46	105
42	42	74	86	68	23	46	105
44	46	68	83	70	22	47	102
43	44	70	84	70	22	48	101
78	63	79	63	51	43	66	73
78	63	79	63	51	43	66	73
35	39	79	91	73	21	52	89
36	42	76	88	74	20	52	89

Table S10. The values of percentage of variability and nucleotide diversity for each PCG, rRNA and PCGs+rRNAs genes.

Gene	Variable (%)	Nucleotide diversity (SE)
ND2	50.39	0.179 (0.006)
COX1	32.20	0.121 (0.005)
COX2	33.14	0.124 (0.007)
ATP8	65.43	0.241 (0.017)
ATP6	47.88	0.184 (0.008)
COX3	38.80	0.142 (0.006)
ND3	48.51	0.176 (0.011)
ND5	51.04	0.196 (0.005)
ND4	51.06	0.197 (0.007)
ND4L	43.68	0.167 (0.013)
ND6	56.99	0.242 (0.01)
CYTB	38.37	0.157 (0.006)
ND1	45.48	0.178 (0.007)
16S	38.55	0.137 (0.006)
12S	38.71	0.141 (0.008)
PCGs+rRNAs	43.55	0.165 (0.001)

TableS11. The value of interspecific genetic distances based on 13 PCGs and rRNAs separately and concatenated sequence of PCG+rRNA genes.

ND2													
Species/Lineages	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0												
TIB	0.008	0.008											
AMA	0.009	0.009	0.008										
URM	0.026	0.026	0.025	0.025									
SOR	0.084	0.084	0.084	0.082	0.086								
SIN	0.199	0.199	0.2	0.2	0.2	0.184							
TETRA	0.196	0.196	0.198	0.198	0.198	0.182	0.022						
PENTA	0.195	0.195	0.197	0.196	0.196	0.181	0.021	0.001					
FRA	0.221	0.221	0.219	0.219	0.223	0.208	0.22	0.218	0.217				
MON	0.22	0.22	0.218	0.218	0.222	0.207	0.221	0.219	0.218	0.006			
SAL	0.29	0.29	0.29	0.288	0.282	0.279	0.285	0.291	0.291	0.283	0.281		
PER	0.276	0.276	0.271	0.272	0.27	0.272	0.292	0.29	0.289	0.253	0.256	0.324	
COX1													
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.001												
TIB	0.014	0.014											
AMA	0.014	0.015	0.006										
URM	0.023	0.024	0.016	0.015									
SOR	0.061	0.063	0.057	0.057	0.055								
SIN	0.133	0.132	0.134	0.133	0.132	0.136							
TETRA	0.139	0.138	0.14	0.14	0.138	0.143	0.013						
PENTA	0.139	0.138	0.14	0.139	0.138	0.143	0.012	0					
FRA	0.158	0.158	0.156	0.155	0.156	0.15	0.149	0.157	0.156				
MON	0.157	0.156	0.154	0.154	0.155	0.15	0.151	0.155	0.155	0.007			
SAL	0.19	0.189	0.185	0.185	0.184	0.187	0.176	0.175	0.175	0.183	0.185		
PER	0.174	0.173	0.178	0.175	0.177	0.181	0.161	0.164	0.163	0.178	0.179	0.195	
COX2													
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0												
TIB	0.007	0.007											
AMA	0.009	0.009	0.004										
URM	0.022	0.022	0.017	0.019									
SOR	0.069	0.069	0.065	0.067	0.063								
SIN	0.139	0.139	0.14	0.141	0.134	0.119							
TETRA	0.136	0.136	0.136	0.137	0.132	0.117	0.012						
PENTA	0.135	0.135	0.136	0.136	0.131	0.116	0.012	0.001					
FRA	0.163	0.163	0.162	0.164	0.166	0.161	0.157	0.159	0.158				
MON	0.161	0.161	0.161	0.163	0.164	0.163	0.158	0.158	0.157	0.004			
SAL	0.186	0.186	0.185	0.186	0.187	0.186	0.189	0.187	0.188	0.183	0.186		
PER	0.191	0.191	0.191	0.193	0.191	0.184	0.181	0.181	0.181	0.191	0.187	0.227	
ATP8													
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0												
TIB	0.025	0.025											
AMA	0.031	0.031	0.006										
URM	0.049	0.049	0.037	0.043									
SOR	0.142	0.142	0.136	0.142	0.123								
SIN	0.216	0.216	0.204	0.21	0.222	0.247							
TETRA	0.213	0.213	0.201	0.207	0.219	0.244	0.022						

PENTA	0.21	0.21	0.198	0.204	0.216	0.241	0.019	0.003					
FRA	0.333	0.333	0.333	0.327	0.333	0.327	0.272	0.256	0.259				
MON	0.333	0.333	0.333	0.327	0.321	0.315	0.278	0.262	0.265	0.012			
SAL	0.364	0.364	0.352	0.352	0.364	0.401	0.383	0.367	0.37	0.407	0.401		
PER	0.398	0.398	0.41	0.404	0.404	0.417	0.426	0.423	0.42	0.451	0.451	0.414	
	ATP6												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.003												
TIB	0.017	0.017											
AMA	0.017	0.017	0.007										
URM	0.03	0.03	0.022	0.021									
SOR	0.101	0.101	0.091	0.093	0.09								
SIN	0.226	0.229	0.223	0.219	0.226	0.226							
TETRA	0.226	0.229	0.222	0.218	0.225	0.231	0.023						
PENTA	0.226	0.229	0.222	0.218	0.225	0.231	0.023	0.002					
FRA	0.229	0.229	0.22	0.218	0.226	0.225	0.216	0.224	0.224				
MON	0.226	0.226	0.22	0.218	0.226	0.231	0.22	0.229	0.229	0.015			
SAL	0.267	0.267	0.258	0.258	0.262	0.245	0.269	0.261	0.261	0.259	0.261		
PER	0.27	0.273	0.269	0.266	0.273	0.28	0.277	0.28	0.28	0.242	0.249	0.305	
	COX3												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.001												
TIB	0.013	0.015											
AMA	0.013	0.015	0.004										
URM	0.031	0.032	0.022	0.022									
SOR	0.069	0.07	0.063	0.061	0.066								
SIN	0.14	0.142	0.137	0.138	0.135	0.143							
TETRA	0.155	0.156	0.153	0.153	0.148	0.146	0.02						
PENTA	0.154	0.155	0.153	0.154	0.148	0.146	0.022	0.003					
FRA	0.167	0.165	0.17	0.171	0.165	0.182	0.173	0.184	0.184				
MON	0.167	0.165	0.17	0.172	0.165	0.181	0.174	0.184	0.186	0.009			
SAL	0.239	0.24	0.237	0.235	0.228	0.233	0.226	0.223	0.221	0.24	0.245		
PER	0.212	0.214	0.214	0.212	0.218	0.223	0.21	0.216	0.217	0.204	0.209	0.268	
	ND3												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0												
TIB	0.016	0.016											
AMA	0.015	0.015	0.013										
URM	0.037	0.037	0.033	0.034									
SOR	0.107	0.107	0.106	0.107	0.082								
SIN	0.176	0.176	0.18	0.17	0.171	0.193							
TETRA	0.171	0.171	0.176	0.165	0.17	0.198	0.022						
PENTA	0.173	0.173	0.177	0.167	0.171	0.199	0.024	0.001					
FRA	0.223	0.223	0.231	0.226	0.251	0.265	0.214	0.213	0.214				
MON	0.229	0.229	0.237	0.232	0.257	0.271	0.22	0.219	0.22	0.006			
SAL	0.259	0.259	0.254	0.253	0.263	0.259	0.265	0.263	0.265	0.274	0.274		
PER	0.275	0.275	0.277	0.275	0.28	0.278	0.26	0.271	0.272	0.272	0.275	0.299	
	ND5												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER

TRI	0.002												
TIB	0.017	0.018											
AMA	0.020	0.022	0.008										
URM	0.045	0.045	0.035	0.036									
SOR	0.106	0.106	0.107	0.108	0.104								
SIN	0.203	0.203	0.205	0.202	0.200	0.202							
TETRA	0.201	0.202	0.202	0.200	0.199	0.199	0.027						
PENTA	0.201	0.202	0.203	0.200	0.198	0.198	0.028	0.003					
FRA	0.258	0.255	0.264	0.262	0.256	0.250	0.253	0.255	0.256				
MON	0.259	0.256	0.265	0.263	0.259	0.248	0.254	0.257	0.258	0.010			
SAL	0.293	0.294	0.293	0.294	0.295	0.300	0.299	0.296	0.296	0.305	0.302		
PER	0.290	0.289	0.296	0.296	0.296	0.301	0.293	0.295	0.295	0.302	0.304	0.332	
	ND4												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.004												
TIB	0.026	0.024											
AMA	0.024	0.022	0.008										
URM	0.045	0.044	0.034	0.034									
SOR	0.118	0.118	0.114	0.115	0.114								
SIN	0.195	0.195	0.197	0.192	0.199	0.2							
TETRA	0.205	0.203	0.204	0.201	0.208	0.201	0.032						
PENTA	0.204	0.202	0.203	0.201	0.207	0.201	0.033	0.002					
FRA	0.242	0.243	0.248	0.246	0.252	0.25	0.258	0.26	0.259				
MON	0.241	0.241	0.246	0.245	0.251	0.251	0.255	0.26	0.259	0.013			
SAL	0.292	0.291	0.292	0.292	0.292	0.29	0.31	0.31	0.309	0.296	0.294		
PER	0.297	0.297	0.302	0.307	0.3	0.296	0.308	0.308	0.308	0.305	0.307	0.33	
	ND4L												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0												
TIB	0.015	0.015											
AMA	0.017	0.017	0.002										
URM	0.048	0.048	0.033	0.034									
SOR	0.126	0.126	0.119	0.117	0.128								
SIN	0.188	0.188	0.172	0.174	0.178	0.161							
TETRA	0.192	0.192	0.176	0.178	0.178	0.157	0.019						
PENTA	0.192	0.192	0.176	0.178	0.178	0.157	0.019	0					
FRA	0.211	0.211	0.203	0.201	0.205	0.215	0.215	0.207	0.207				
MON	0.216	0.216	0.209	0.207	0.211	0.216	0.22	0.213	0.213	0.006			
SAL	0.226	0.226	0.234	0.232	0.22	0.222	0.238	0.241	0.241	0.203	0.197		
PER	0.259	0.259	0.251	0.253	0.243	0.255	0.239	0.247	0.247	0.234	0.232	0.257	
	ND6												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0												
TIB	0.017	0.017											
AMA	0.014	0.014	0.005										
URM	0.037	0.037	0.031	0.03									
SOR	0.135	0.135	0.129	0.131	0.137								
SIN	0.288	0.288	0.29	0.29	0.298	0.284							
TETRA	0.292	0.292	0.293	0.293	0.296	0.271	0.022						

PENTA	0.291	0.291	0.292	0.292	0.295	0.271	0.024	0.003					
FRA	0.31	0.31	0.31	0.311	0.314	0.337	0.301	0.299	0.301				
MON	0.312	0.312	0.316	0.313	0.318	0.341	0.306	0.303	0.306	0.006			
SAL	0.306	0.306	0.308	0.311	0.316	0.328	0.368	0.362	0.363	0.344	0.344		
PER	0.351	0.351	0.356	0.354	0.359	0.377	0.365	0.358	0.361	0.34	0.34	0.371	
	CYTB												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.005												
TIB	0.01	0.009											
AMA	0.01	0.01	0.006										
URM	0.026	0.025	0.02	0.024									
SOR	0.085	0.084	0.083	0.084	0.092								
SIN	0.191	0.194	0.191	0.19	0.195	0.182							
TETRA	0.187	0.189	0.187	0.185	0.188	0.181	0.026						
PENTA	0.187	0.19	0.187	0.186	0.189	0.182	0.027	0.002					
FRA	0.207	0.208	0.21	0.208	0.203	0.209	0.204	0.199	0.2				
MON	0.205	0.206	0.208	0.206	0.201	0.21	0.206	0.2	0.201	0.012			
SAL	0.215	0.215	0.215	0.215	0.214	0.23	0.233	0.234	0.234	0.213	0.212		
PER	0.214	0.215	0.215	0.214	0.213	0.216	0.216	0.219	0.219	0.207	0.206	0.234	
	ND1												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.004												
TIB	0.026	0.023											
AMA	0.028	0.025	0.015										
URM	0.054	0.051	0.043	0.045									
SOR	0.122	0.123	0.127	0.125	0.125								
SIN	0.187	0.189	0.193	0.192	0.19	0.195							
TETRA	0.178	0.179	0.186	0.183	0.185	0.192	0.022						
PENTA	0.177	0.179	0.185	0.183	0.185	0.192	0.021	0.001					
FRA	0.227	0.229	0.226	0.227	0.22	0.224	0.227	0.229	0.229				
MON	0.226	0.227	0.222	0.224	0.217	0.222	0.223	0.225	0.224	0.014			
SAL	0.263	0.263	0.265	0.265	0.253	0.253	0.255	0.261	0.261	0.266	0.263		
PER	0.266	0.266	0.266	0.265	0.265	0.269	0.249	0.26	0.26	0.272	0.268	0.306	
	16S												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.001												
TIB	0.012	0.011											
AMA	0.017	0.016	0.006										
URM	0.025	0.024	0.019	0.021									
SOR	0.077	0.076	0.074	0.077	0.068								
SIN	0.141	0.14	0.14	0.14	0.136	0.137							
TETRA	0.143	0.142	0.141	0.142	0.135	0.141	0.016						
PENTA	0.143	0.142	0.142	0.142	0.136	0.14	0.016	0.002					
FRA	0.162	0.163	0.164	0.165	0.163	0.17	0.17	0.173	0.171				
MON	0.156	0.157	0.158	0.159	0.159	0.166	0.165	0.168	0.167	0.011			
SAL	0.201	0.202	0.206	0.205	0.205	0.2	0.206	0.209	0.208	0.22	0.216		
PER	0.212	0.211	0.212	0.212	0.205	0.217	0.221	0.22	0.218	0.222	0.22	0.243	
	12S												
	DI	TRI	TIB	AMA	URM	SOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER

TRI	0.004												
TIB	0.013	0.014											
AMA	0.013	0.015	0.006										
URM	0.018	0.023	0.02	0.016									
SOR	0.079	0.081	0.077	0.077	0.078								
SIN	0.146	0.147	0.144	0.145	0.146	0.156							
TETRA	0.146	0.148	0.147	0.149	0.144	0.156	0.018						
PENTA	0.149	0.15	0.149	0.151	0.146	0.158	0.023	0.006					
FRA	0.171	0.17	0.167	0.163	0.169	0.177	0.175	0.183	0.185				
MON	0.17	0.169	0.168	0.167	0.171	0.18	0.175	0.182	0.185	0.019			
SAL	0.199	0.201	0.202	0.204	0.2	0.197	0.202	0.207	0.207	0.194	0.191		
PER	0.233	0.235	0.229	0.228	0.227	0.239	0.236	0.237	0.239	0.213	0.214	0.228	
	PCGs+rRNAs												
	DI	TRI	TIB	AMA	URM	DOR	SIN	TETRA	PENTA	FRA	MONO	SAL	PER
TRI	0.002												
TIB	0.015	0.015											
AMA	0.016	0.016	0.007										
URM	0.033	0.033	0.026	0.027									
SOR	0.093	0.093	0.090	0.091	0.089								
SIN	0.179	0.179	0.179	0.177	0.178	0.177							
TETRA	0.180	0.180	0.180	0.179	0.179	0.178	0.021						
PENTA	0.180	0.180	0.180	0.179	0.179	0.178	0.022	0.002					
FRA	0.210	0.210	0.211	0.210	0.210	0.211	0.208	0.210	0.211				
MON	0.209	0.208	0.210	0.209	0.209	0.211	0.208	0.211	0.211	0.010			
SAL	0.245	0.245	0.245	0.244	0.243	0.245	0.250	0.250	0.250	0.249	0.248		
PER	0.248	0.248	0.249	0.249	0.249	0.253	0.249	0.251	0.251	0.246	0.247	0.279	