

Complete mitochondrial genome and phylogenetic analysis of the Atrato slider, *Trachemys medemi* (Testudines: Emydidae)

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Supplementary information

Long-range PCR and primer walking. Two long-range PCR reactions were performed using DNA extractions from three *Trachemys medemi* samples to target the mitogenome. The resulting amplicons overlap by more than 1000 bp and have a length of 11,824 bp and 6797 bp, respectively. Following the methodology of Fritz et al. (2012, 2023), the following primer pairs were employed for the long-range PCR reactions: Tscripta_tPhe.for + Tscripta_tLeu_a.rev and Tscripta_tArg_b.for + DES2_rev. Each reaction was performed in a 50 µl volume containing 1 unit of TaKaRa LA Taq DNA polymerase, Hot-Start Version (Clontech Laboratories Inc.), 10 mM of dNTPs, 5 pmol of each primer, and volumes according to manufacturer's recommendation. PCR conditions included an initial denaturation at 93°C for 3 min, 35 cycles of 93°C for 20 s, 57°C for 30s, 68°C for 12 min, and a final elongation step at 68°C for 20 min. PCR products were visualized in a 2% agarose gel and purified using the ExoSAP-IT enzymatic clean-up (USB Europe, Staufeu, Germany). Cleaned long-range PCR products were then used for PCR sequencing reactions. Initially, amplification and sequencing were performed using primers specified in the Supplementary Table 1. Subsequently, specific primers designed from the *T. medemi* sequences were used to fill the remaining gaps in the assembly. The first part of the tRNA-Phe and the final of control region's 3'-end were amplified using the primers medemitRNA-Phe (5'-TGGGTAACCAATATACCCCA-3'), medemitRNA-Phe2 (5'-TTAGATTGCTAGGGC GTTTT-3'), and medemiCRend (5'-ACCCACGACAGTAATTTTCA-3') under the following thermocycling conditions: Initial denaturation at 94°C for 5 min, followed by 30 cycles of 94°C for 30s, 60°C for 45s, 72°C for 30 s, and final elongation at 72°C for 10 min. Sequencing was performed on an ABI 3730 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) using the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems) following manufacturer's instructions.

Phylogenetic analyses. Phylogenetic analyses were conducted using two datasets. The first dataset included *Trachemys* mitogenomes obtained from Russel and Beckenbach (2008), Yu et al. (2014), Park et al. (2021), Ryu et al. (2021), and Fritz et al. (2023, 2024), alongside with mitogenomes from *Pseudemys concinna* (OM935747; Park et al. 2022) and *Graptemys ouachitensis* (OP115973) as outgroups. Protein-coding genes were screened for internal stop codons in GENEIOUS R7 (<http://geneious.com>). Mitogenome alignment was performed with MUSCLE (Edgar 2004) and manually curated to correct alignment

errors. Problematic sequence features, such as internal stop codons in coding genes, genes or tRNAs overlapping regions, frame shift inducing in coding region, and non-coding spacer DNA were identified and 232 positions were removed from the alignment. For the second dataset, our dataset was concatenated with the mtDNA alignment used by Fritz et al. (2024) covering almost all continental *Trachemys* taxa, except for *T. hartwegi*. Their dataset comprised 3221 bp and included sequences of the partial 12S gene and the complete ND4L, ND4, and *cyt b* genes plus part of the adjacent tRNA-Thr gene. Missing data was coded as Ns. The best partitioning schemes and evolutionary models (Supplementary Tables S4, S5) were determined by using a greedy search and the Bayesian Information Criterion in PARTITIONFINDER 2 (Lanfear et al. 2017). For the extended mtDNA dataset, PARTITIONFINDER 2 detected a single partitioning scheme with HKY+G+I model as the best fit. This partition scheme was used for the complete mitogenome dataset.

Phylogeny was analyzed using maximum likelihood (ML) and Bayesian inference (BA). ML analyses were performed in IQ-TREE 1.6.12 (Nguyen et al. 2015) with 1000 non-parametric thorough bootstrap replicates to assess node support, plotted against the best tree obtained. Bayesian analyses were conducted in MRBAYES 3.2.6 (Ronquist et al. 2012), with two simultaneous runs and four chains each, sampling every 1000th generation for 50 million generations. After a burn-in of 25%, convergence was assessed by verifying that the average standard deviation of split frequencies was below 0.01 and the effective sample size exceeded 200 for all parameters using TRACER 1.7.1 (Rambaut et al. 2018).

Supplementary Table S1. Primers used for PCR and sequencing. Position according to the mapping of each primer to the mitochondrial genome of *Trachemys scripta elegans* (GenBank accession number MW019443).

Primer	Sequence (5'-3')	LR-PCR	Position
Tscripta_tPhe.for	AGCACGGCACTGAAGTTGCC	1	22-41
L25195_for	AAACTGGGATTAGATACCCCACTAT	1	506-530
sulcata_cytb-12S_Rev	AGGCAAGTCGTAACAAGG	1	1001-1018
16SA_For	CGCCTGTTTATCAAAAACAT	1	1985-2004
graeca_cytb_16S_Rev	AACCGTGCAAAGGTAGCGTA	1	2078-2097
16SB_Rev	ACGTGATCTGAGTTCAGACCGG	1	2570-2591
medemi1F*	AAATGCAAAGGCCTAAACC	1	2760-2779
medemi5F*	ACTCTCAGCAGGATTCTAT	1	3643-3662
medemi5R*	ACCAATTACACCAACCCTAC	1	5022-5041
L-turtCOI_For	ACTCAGCCATCTTACCTGTGATT	1	5420-5443
medemi1R*	TTTGGTCGCTCCTAAAAGG	1	5552-5571
Jerry_For	CAACAYTTATTTTGTATTTTTGG	1	6130-6152
medemi2F*	TTTTAGGCTTCATCGTGTGA	1	6259-6278
H-turtCOIb_Rev	CGAGCCTATTTTACATCTGCAAC	1	6340-6362
medemi6F*	CATGTACAAACCCAAGAAAG	1	6966-6985
medemi2R*	TCTGAGCATTGTCCGTAATA	1	7671-7690
medemi6R*	TTTTACGGACAATGCTCAGA	1	7695-7714
nigraATP6-cytb_For	AAGCCACAAAYCCTWGGAA	1	8070-8090
graeca_12S_ATP6_Rev	ACAGCCAATTTAACAGCCGG	1	8525-8545
medemi3F*	CAGCAGCAGCACTACTATA	1	8764-8783
nebulosa_long_F_For	CCTAGAATGAGCAGAATCGA	1	9911-9931
Tscripta_tArg_b.for	CTTAGTTAATCGTGATTAACCTCCACGGC	1, 2	9963-9992
medemi3R*	TAGGTGAGTTTGGTGAACG	1, 2	10035-10054
L-ND4_For	GTAGAAGCCCCAATCGCAG	1, 2	10951-10971
Tscripta_tHis_a.for	CATTAGACTGTGGCTCTAAAAATAGGAGTT	1, 2	11692-11721
Tscripta_tHis_b.rev	GTGGCTCTAAAAATAGGAGTTCAAACCTC	1, 2	11701-11730
medemi4F*	GCTCCCTCACTTTTAAAGGA	1, 2	11777-11796
LR1-Rev_Tscripta_tLeu_a.rev	CCATTGGTTTTAGAAACCATCCACCC	1, 2	11828-11854
H-Leu_Rev	TGGTGCAAATCCAAGTAAAAGTAAT	2	11855-11880
medemi7F*	CTGCCCTATCCCAAAATGAT	2	12747-12766
medemi7R*	TTAACAACAACCCTCAACCA	2	13931-13950
nigra_ND6-12S_For	AACYAACATCCCRCCCAAAT	2	14199-14219
medemi4R*	TAGTCTTAGGAGCAGCTTCT	2	14227-14246
sulcata_cytb-12S_For	CCTACAAATCACCACCGGAA	2	14599-14618
sulcata_ATP6-cytb_Rev	AGCCCATATCACCCGAGATG	2	14671-14690
Tscripta_tThr_a.rev	AAAGCATTGTCTTGTAACCAAAGACTGA	2	15635-15664

*Primers newly designed for this study.

Supplementary Table S2. Annotation of the *Trachemys medemi* mitogenome BTBC13207.

Name	Start	Stop	Length	Strand	Intergenic/overlapping nucleotides
tRNA-Phe	1	70	70	+	0
12S rRNA	71	1039	969	+	0
tRNA-Val	1040	1110	71	+	0
16S rRNA	1111	2726	1616	+	1
tRNA-Leu	2728	2802	75	+	0
ND1	2803	3773	971	+	0
tRNA-Ile	3774	3843	70	+	-1
tRNA-Gln	3843	3914	72	-	-2
tRNA-Met	3914	3982	69	+	-1
ND2	3983	5021	1039	+	0
tRNA-Trp	5022	5096	75	+	1
tRNA-Ala	5098	5166	69	-	1
tRNA-Asn	5168	5240	73	-	1
tRNA-Cys	5267	5332	66	-	-5
tRNA-Tyr	5333	5403	71	-	1
COX1	5405	6948	1544	+	-5
tRNA-Ser	6944	7015	72	-	2
tRNA-Asp	7018	7087	70	+	0
COX2	7088	7774	687	+	1
tRNA-Lys	7776	7847	72	+	-2
ATP8	7850	8038	189	+	-31
ATP6	8008	8691	684	+	-1
COX3	8691	9474	784	+	-1
tRNA-Gly	9475	9543	69	+	0
ND3	9544	9893	350	+	0
tRNA-Arg	9894	9963	70	+	0
ND4L	9964	10261	297	+	-7
ND4	10255	11635	1381	+	0
tRNA-His	11636	11705	70	+	0
tRNA-Ser	11706	11771	66	+	0
tRNA-Leu	11772	11843	72	+	-2
ND5	11842	13671	1830	+	128
ND6	13800	14324	525	-	0
tRNA-Glu	14325	14392	68	-	4
CYTB	14397	15536	1140	+	3
tRNA-Thr	15540	15613	74	+	1
tRNA-Pro	15615	15684	70	-	2
D-Loop	15687	>16711	>955	+	0

Supplementary Table S3. Composition and skewness of protein-coding genes (PCGs), tRNAs, rRNAs, and control region of *Trachemys* species and related taxa.

Taxon	Accession no.	A (%)	C (%)	G (%)	T (%)	GC (%)	AT skew	GC skew
Complete mitogenome								
<i>Graptemys ouachitensis</i>	OP115973	34.1	26.0	13.1	26.8	38.6	0.120	-0.330
<i>Pseudemys concinna</i>	OM935747	34.4	26.1	13.0	26.6	38.6	0.128	-0.340
<i>Trachemys medemi</i>	OZ183365	34.3	26.1	12.8	26.6	39.0	0.123	-0.342
<i>Trachemys scripta elegans</i>	KM216748	34.1	26.0	12.9	26.9	38.7	0.118	-0.337
<i>Trachemys scripta scripta</i>	KM216749	34.2	26.0	12.9	26.9	38.7	0.120	-0.337
<i>Trachemys scripta troostii</i>	MW122292	34.2	26.0	12.9	26.9	38.7	0.120	-0.337
<i>Trachemys decorata</i>	OX453475	34.1	26.2	12.9	26.7	38.6	0.122	-0.340
<i>Trachemys decussata angusta</i>	OX453476	34.3	26.2	12.7	26.8	38.5	0.123	-0.347
<i>Trachemys decussata decussata</i>	OX453477	34.3	26.2	12.8	26.7	38.5	0.125	-0.344
<i>Trachemys grayi emolli</i>	OX453490	34.3	26.1	12.8	26.8	38.9	0.123	-0.342
<i>Trachemys grayi panamensis</i>	OX453491	34.3	26.1	12.8	26.8	38.9	0.123	-0.342
<i>Trachemys stejnegeri vicina</i>	OX453495	34.2	26.2	12.9	26.8	38.6	0.121	-0.340
<i>Trachemys terrapen</i>	OX453498	34.3	26.2	12.8	26.6	38.5	0.126	-0.344
<i>Trachemys venusta venusta</i>	OX453499	34.0	26.0	12.9	26.8	38.5	0.118	-0.337
<i>Trachemys venusta taylori</i>	OZ038157	34.0	26.0	12.9	26.8	38.5	0.118	-0.337
<i>Trachemys venusta cataspila</i>	OZ038159	34.8	26.2	13.0	26.8	38.9	0.130	-0.337
<i>Trachemys venusta uhrigi</i>	OZ038162	34.1	26.1	12.9	26.9	38.8	0.118	-0.339
PCGs								
<i>Graptemys ouachitensis</i>	OP115973	33.2	27.6	11.8	27.3	39.4	0.098	-0.401
<i>Pseudemys concinna</i>	OM935747	33.6	27.7	11.7	27.0	39.4	0.109	-0.406
<i>Trachemys medemi</i>	OZ183365	33.4	27.9	11.7	27.1	39.5	0.104	-0.409
<i>Trachemys scripta elegans</i>	KM216748	33.4	27.5	11.6	27.4	39.1	0.099	-0.407
<i>Trachemys scripta scripta</i>	KM216749	33.4	27.5	11.6	27.4	39.1	0.099	-0.407
<i>Trachemys scripta troostii</i>	MW122292	33.5	27.5	11.6	27.4	39.1	0.100	-0.407
<i>Trachemys decorata</i>	OX453475	33.4	27.8	11.6	27.3	39.3	0.101	-0.411
<i>Trachemys decussata angusta</i>	OX453476	33.4	27.9	11.5	27.2	39.3	0.102	-0.416
<i>Trachemys decussata decussata</i>	OX453477	33.4	27.8	11.6	27.2	39.3	0.102	-0.411
<i>Trachemys grayi emolli</i>	OX453490	33.6	27.8	11.5	27.2	39.2	0.105	-0.415
<i>Trachemys grayi panamensis</i>	OX453491	33.6	27.7	11.5	27.2	39.2	0.105	-0.413
<i>Trachemys stejnegeri vicina</i>	OX453495	33.3	27.7	11.6	27.3	39.3	0.099	-0.410
<i>Trachemys terrapen</i>	OX453498	33.4	27.8	11.6	27.3	39.3	0.101	-0.411
<i>Trachemys venusta venusta</i>	OX453499	33.2	27.7	11.8	27.3	39.4	0.098	-0.403
<i>Trachemys venusta taylori</i>	OZ038157	33.1	27.7	11.9	27.3	39.5	0.096	-0.400
<i>Trachemys venusta cataspila</i>	OZ038159	33.2	27.7	11.9	27.3	39.5	0.098	-0.400
<i>Trachemys venusta uhrigi</i>	OZ038162	33.2	27.7	11.8	27.3	39.4	0.098	-0.403
tRNAs								
<i>Graptemys ouachitensis</i>	OP115973	34.3	22.5	16.0	27.2	38.2	0.116	-0.169

Taxon	Accession no.	A (%)	C (%)	G (%)	T (%)	GC (%)	AT skew	GC skew
tRNAs (continued)								
<i>Pseudemys concinna</i>	OM935747	34.6	22.6	15.7	27.1	38.1	0.122	-0.180
<i>Trachemys medemi</i>	OZ183365	34.8	22.4	15.8	26.9	38.1	0.128	-0.173
<i>Trachemys scripta elegans</i>	KM216748	34.9	22.5	15.6	27.0	37.9	0.128	-0.181
<i>Trachemys scripta scripta</i>	KM216749	34.9	22.5	15.6	27.0	37.9	0.128	-0.181
<i>Trachemys scripta troostii</i>	MW122292	34.7	22.6	15.7	27.1	38.1	0.123	-0.180
<i>Trachemys decorata</i>	OX453475	34.7	22.6	15.7	27.1	38.1	0.123	-0.180
<i>Trachemys decussata angusta</i>	OX453476	34.7	22.6	15.6	27.1	38.0	0.123	-0.183
<i>Trachemys decussata decussata</i>	OX453477	34.7	22.8	15.5	27.0	38.1	0.125	-0.191
<i>Trachemys grayi emolli</i>	OX453490	34.4	22.2	15.5	27.9	37.7	0.104	-0.178
<i>Trachemys grayi panamensis</i>	OX453491	34.3	22.3	15.6	27.9	37.8	0.103	-0.177
<i>Trachemys stejnegeri vicina</i>	OX453495	34.7	22.8	15.6	26.9	38.2	0.127	-0.188
<i>Trachemys terrapen</i>	OX453498	34.9	22.8	15.4	26.9	38.0	0.130	-0.194
<i>Trachemys venusta venusta</i>	OX453499	34.6	22.7	15.7	27.0	38.2	0.123	-0.182
<i>Trachemys venusta taylori</i>	OZ038157	34.6	22.7	15.7	27.0	38.2	0.123	-0.182
<i>Trachemys venusta cataspila</i>	OZ038159	34.7	22.7	15.7	27.0	38.1	0.125	-0.182
<i>Trachemys venusta uhrigi</i>	OZ038162	34.6	22.6	15.7	27.0	38.1	0.123	-0.180
rRNAs								
<i>Graptemys ouachitensis</i>	OP115973	38.7	22.5	16.7	22.1	38.8	0.273	-0.148
<i>Pseudemys concinna</i>	OM935747	38.8	22.7	16.5	21.9	39.0	0.278	-0.158
<i>Trachemys medemi</i>	OZ183365	38.6	23.1	16.7	21.6	39.4	0.282	-0.161
<i>Trachemys scripta elegans</i>	KM216748	38.5	22.9	16.7	21.9	39.3	0.275	-0.157
<i>Trachemys scripta scripta</i>	KM216749	38.5	22.9	16.8	21.8	39.2	0.277	-0.154
<i>Trachemys scripta troostii</i>	MW122292	38.5	22.9	16.7	21.9	39.3	0.275	-0.157
<i>Trachemys decorata</i>	OX453475	38.7	23.3	16.7	21.3	39.7	0.290	-0.165
<i>Trachemys decussata angusta</i>	OX453476	38.7	23.3	16.5	21.5	39.5	0.286	-0.171
<i>Trachemys decussata decussata</i>	OX453477	38.7	23.1	16.6	21.6	39.4	0.284	-0.164
<i>Trachemys grayi emolli</i>	OX453490	38.9	22.9	16.3	21.9	39.3	0.280	-0.169
<i>Trachemys grayi panamensis</i>	OX453491	38.9	23	16.4	21.7	39.4	0.284	-0.168
<i>Trachemys stejnegeri vicina</i>	OX453495	38.8	23	16.7	21.5	39.4	0.287	-0.159
<i>Trachemys terrapen</i>	OX453498	38.8	23.2	16.6	21.3	39.5	0.291	-0.166
<i>Trachemys venusta venusta</i>	OX453499	38.6	22.9	16.5	22.0	39.0	0.274	-0.162
<i>Trachemys venusta taylori</i>	OZ038157	38.8	22.9	16.4	21.9	38.9	0.278	-0.165
<i>Trachemys venusta cataspila</i>	OZ038159	38.7	22.9	16.4	22.0	38.8	0.275	-0.165
<i>Trachemys venusta uhrigi</i>	OZ038162	38.7	22.9	16.4	22.0	38.9	0.275	-0.165
Control Region								
<i>Graptemys ouachitensis</i>	OP115973	31.5	21.9	13.3	33.4	31.2	-0.029	-0.244
<i>Pseudemys concinna</i>	OM935747	33.2	20.9	12.8	33.1	29.9	0.002	-0.240
<i>Trachemys medemi</i>	OZ183365	33.7	20.7	12.0	33.5	32.7	0.002	-0.266
<i>Trachemys scripta elegans</i>	KM216748	30.2	22.1	14.0	33.7	34.9	-0.055	-0.224

Taxon	Accession no.	A (%)	C (%)	G (%)	T (%)	GC (%)	AT skew	GC skew
Control Region (continued)								
<i>Trachemys scripta scripta</i>	KM216749	30.4	22.1	13.9	33.5	34.7	-0.049	-0.228
<i>Trachemys scripta troostii</i>	MW122292	30.4	22.2	14	33.4	34.9	-0.047	-0.227
<i>Trachemys decorata</i>	OX453475	30.3	21.1	13.8	34.8	30.5	-0.069	-0.209
<i>Trachemys decussata angusta</i>	OX453476	31.5	20.6	12.9	35.0	29.5	-0.053	-0.230
<i>Trachemys decussata decussata</i>	OX453477	31.5	21.2	13.1	34.2	30.0	-0.041	-0.236
<i>Trachemys grayi emolli</i>	OX453490	30.4	21.3	14.0	34.3	30.9	-0.060	-0.207
<i>Trachemys grayi panamensis</i>	OX453491	30.1	20.9	14.2	34.7	30.8	-0.071	-0.191
<i>Trachemys stejnegeri vicina</i>	OX453495	30.2	21.2	13.7	35.0	30.5	-0.074	-0.215
<i>Trachemys terrapen</i>	OX453498	32.5	21.1	12.5	33.8	33.7	-0.020	-0.256
<i>Trachemys venusta venusta</i>	OX453499	32.2	21.2	12.8	33.8	30.3	-0.024	-0.247
<i>Trachemys venusta taylori</i>	OZ038157	32.4	21.4	12.6	33.6	30.3	-0.018	-0.259
<i>Trachemys venusta cataspila</i>	OZ038159	31.6	22.2	12.9	33.3	34.2	-0.026	-0.265
<i>Trachemys venusta uhrigi</i>	OZ038162	31.8	22.2	12.7	33.3	34.1	-0.023	-0.272

Supplementary Table S4. Data blocks of the mtDNA alignment used for phylogenetic analyses.

tRNA-Phe	1-72
12S	73-1049
tRNA-Val	1050-1121
16S	1122-2757
tRNA-Leu	2758-2833
ND1_pos1	2834-3799\3
ND1_pos2	2835-3799\3
ND1_pos3	2836-3799\3
tRNA-Ile-Gln	3800-4006
ND2_pos1	4007-5044\3
ND2_pos2	4008-5044\3
ND2_pos3	4009-5044\3
tRNA-Trp-Tyr	5045-5400
CO1_pos1	5401-6942\3
CO1_pos2	5402-6942\3
CO1_pos3	5403-6942\3
tRNA-Ser-Asp	6943-7078
CO2_pos1	7079-7762\3
CO2_pos2	7080-7762\3
CO2_pos3	7081-7762\3
tRNA-Lys	7763-7836
ATP8_pos1	7837-7992\3
ATP8_pos2	7838-7992\3
ATP8_pos3	7839-7992\3
ATP6_pos1	7993-8640\3
ATP6_pos2	7994-8640\3
ATP6_pos3	7995-8640\3

CO3_pos1	8641-9420\3
CO3_pos2	8642-9420\3
CO3_pos3	8643-9420\3
tRNA-Gly	9421-9489
ND3_pos1	9490-9838\3
ND3_pos2	9491-9838\3
ND3_pos3	9492-9838\3
tRNA-Arg	9839-9908
ND4L_pos1	9909-10197\3
ND4L_pos2	9910-10197\3
ND4L_pos3	9911-10197\3
ND4_pos1	10198-11568\3
ND4_pos2	10199-11568\3
ND4_pos3	10200-11568\3
tRNA-His-Leu	11569-11776
ND5_pos1	11777-13615\3
ND5_pos2	11778-13615\3
ND5_pos3	11779-13615\3
ND6_pos1	13616-14137\3
ND6_pos2	13617-14137\3
ND6_pos3	13618-14137\3
tRNA-Glu	14138-14205
CYTB-pos1	14206-15342\3
CYTB-pos2	14207-15342\3
CYTB-pos3	14208-15342\3
tRNA-Thr-Pro	15343-15486
Control	15487-16562

Supplementary Table S5. Best evolutionary models and partitioning schemes determined by PartitionFinder 2 for the complete mitogenome dataset. Estimated with the greedy search scheme and the Bayesian Information Criterion.

Subset		
1	HKY+I+G	Control, tRNA-Glu, ND5_pos1, ND5_pos2, ND4L_pos1, ND2_pos2, ND4_pos1, ATP6_pos2, CYTB_pos2, CO1_pos2, ND1_pos2, CO3_pos1, tRNA-Lys, CO3_pos2, tRNA-Val, tRNA-Phe, tRNA-Leu, ND3_pos2, CO1_pos1, ND1_pos1, ND6_pos1_tRNA-Thr-Pro, ND4L_pos2, ATP8_pos1, ND3_pos1, CYTB_pos1, 16S, ATP6_pos1, ND4_pos2, ND2_pos1, ATP8_pos2, ATP8_pos3, CO2_pos2, tRNA-Arg, tRNA-Gly, tRNA-His-Leu, tRNA-Trp-Tyr, tRNA-Arg, tRNA-Ile-Gln, CO2_pos1, tRNA-Thr-Pro, 12S, ND6_pos2
2	GTR+G	CYTB_pos3, ND2_pos3, ND5_pos3, ND6_pos3, ND4L_pos3, CO1_pos3, ND3_pos3, ND1_pos3, ATP6_pos3, ND4_pos3, CO2_pos3, CO3_pos3

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