

Table S1. Length, A + T content (%), AT skew, and GC skew for *T. auricollis* and *T. troglodytiformis*.

Region	<i>Trachys Auricollis</i>				<i>Trachys Troglodytiformis</i>			
	Length (bp)	A + T (%)	AT Skew	GC Skew	Length (bp)	A + T (%)	AT Skew	GC Skew
genome	16429	71.1	0.10	-0.20	16316	74.6	0.10	-0.19
PCGs	11097	69.4	-0.14	-0.02	11134	73.0	-0.14	-0.02
rrnl	1294	76.8	-0.15	0.31	1260	79.2	-0.13	0.32
rrns	758	75.2	-0.07	0.27	757	77.3	-0.10	0.27
CR	1847	73.4	0.04	-0.22	1728	78.9	0.16	-0.26
tRNA	1444	73.4	0.02	0.11	1450	76.0	0.01	0.12

AT skew = (A - T)/(A + T), GC skew = (G - C)/(G + C); CR = control region, also called the A + T-rich region.

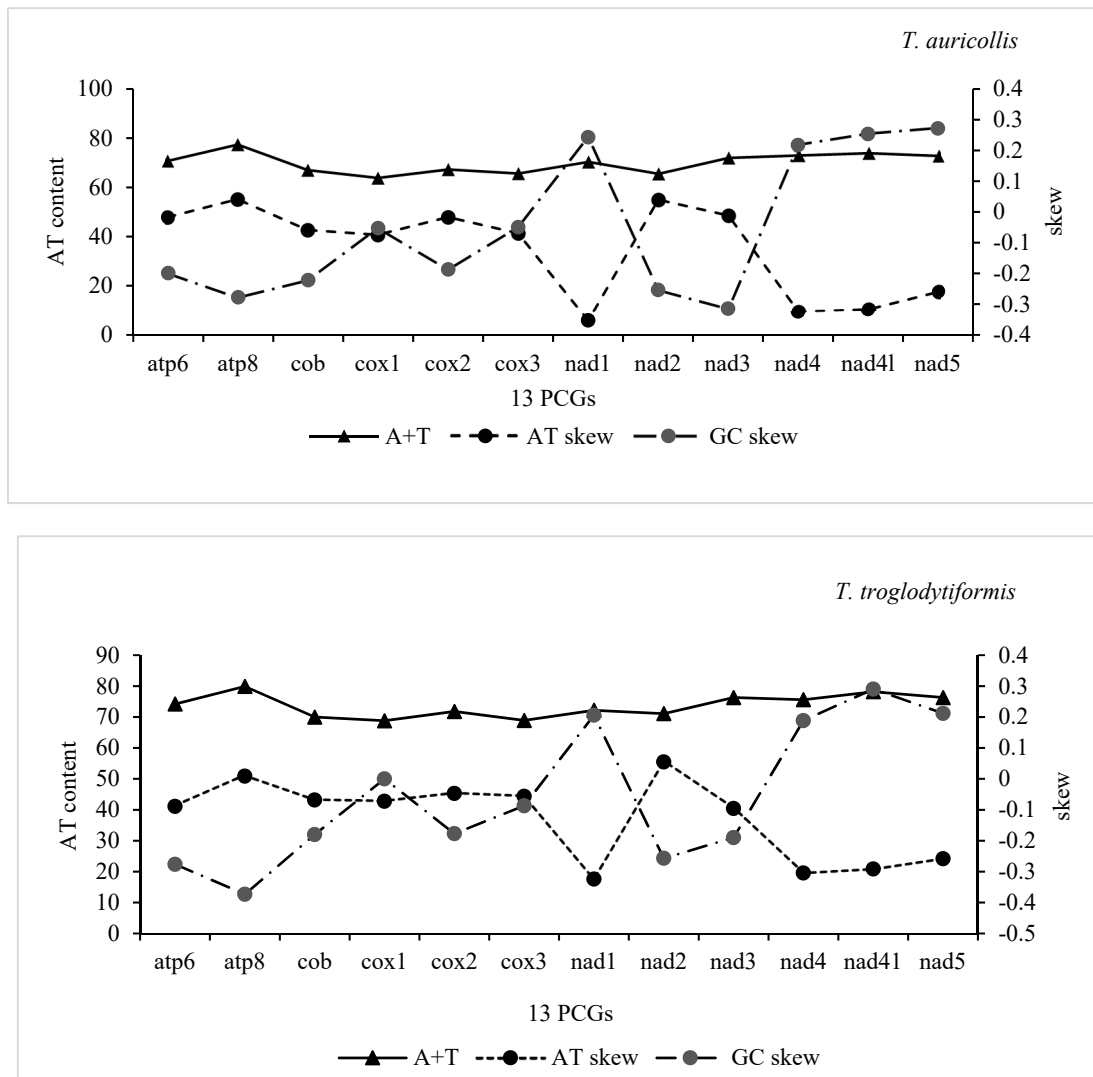


Figure S1. The base composition of protein-coding genes and two rRNAs in the mitochondrial genomes of *T. auricollis* and *T. troglodytiformis*.

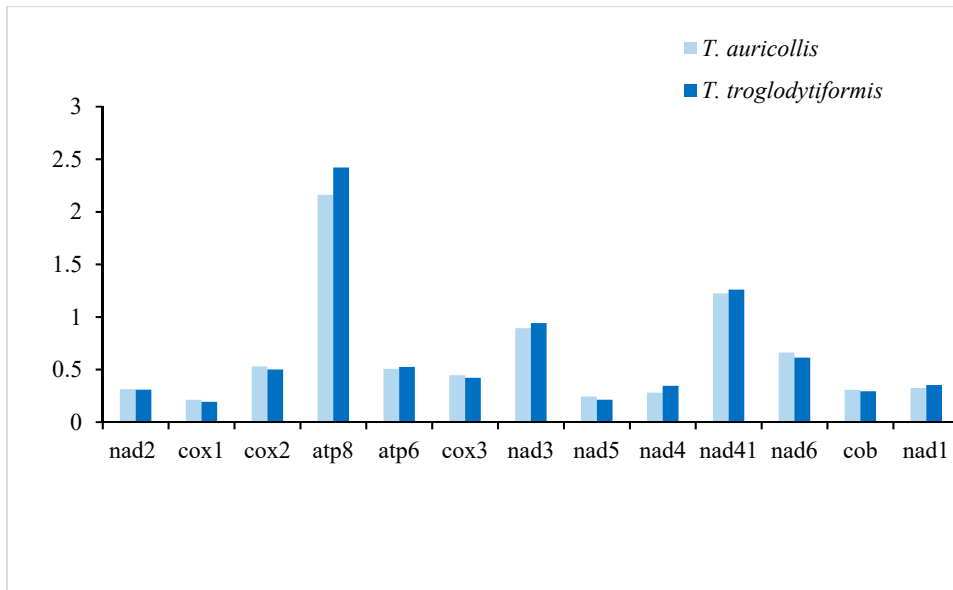
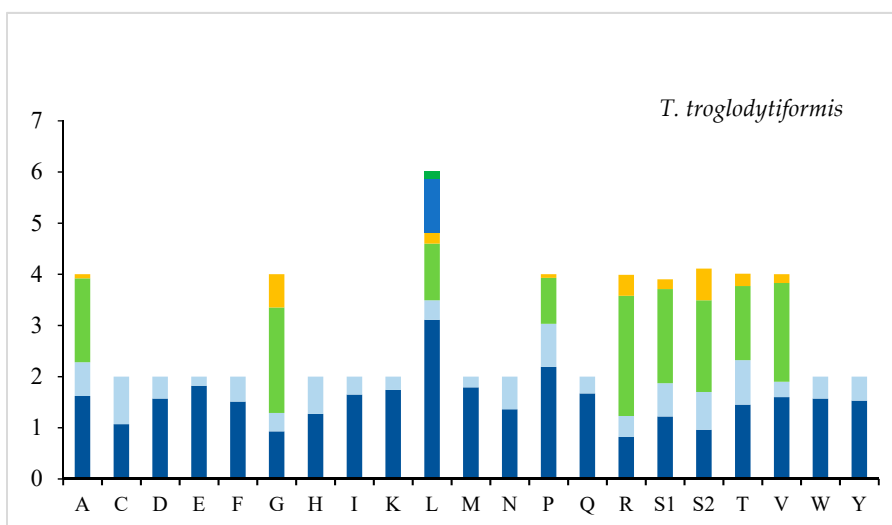
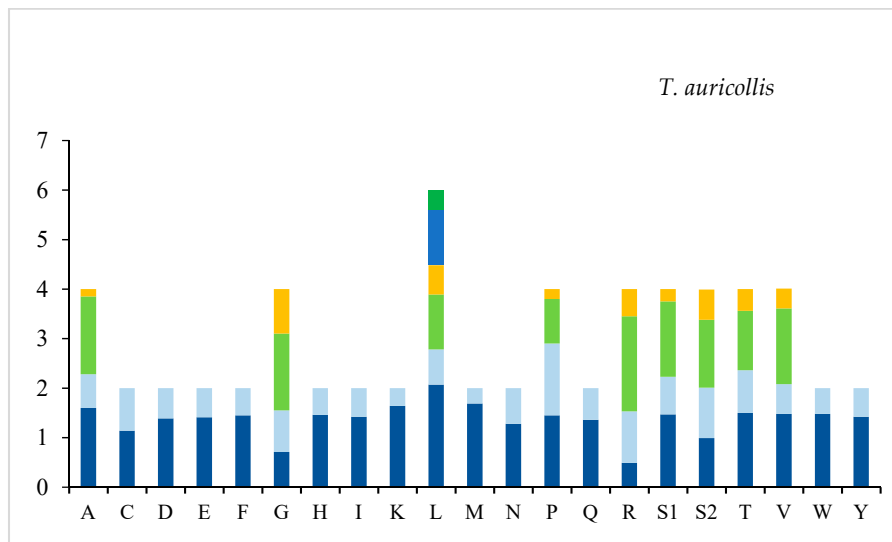


Figure S2. Ka/Ks ratios of 13 protein-coding genes. Ka is the nonsynonymous substitution rate, and Ks is the synonymous substitution rate.



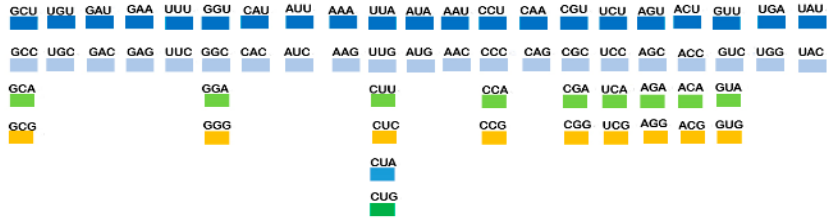


Figure s3. Relative synonymous codon usage (RSCU) for protein-coding genes of *T. auricollis* and *T. troglodytiformis* mitochondrial genomes. Codon families are provided on the x-axis.

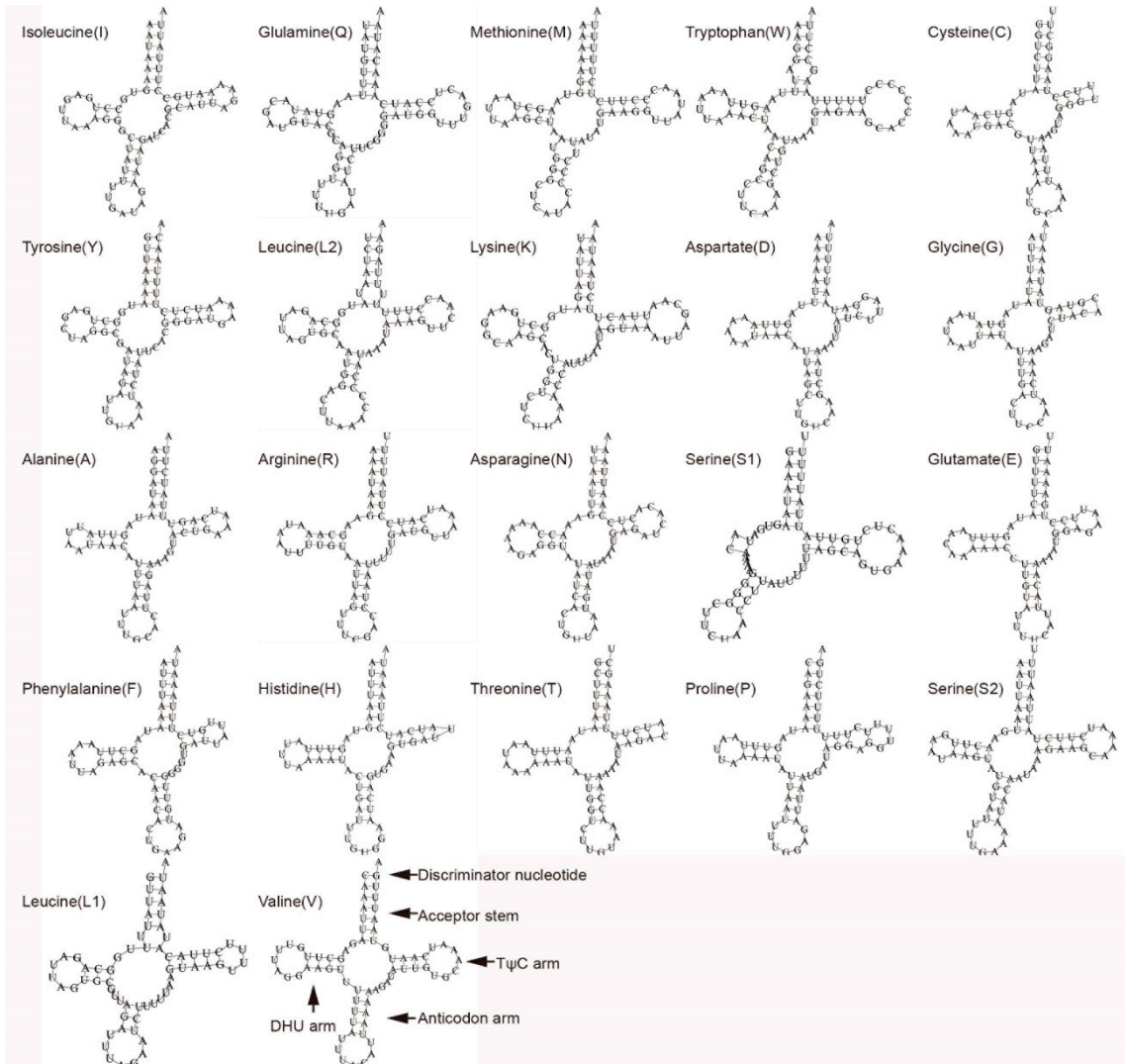


Figure S4. Predicted secondary structures of the 22 typical tRNA genes of the *T. auricollis* mitochondrial genome.

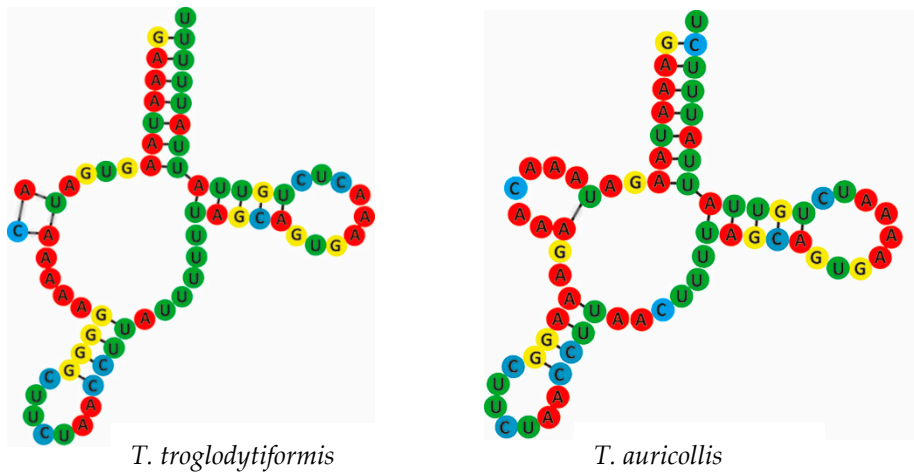


Figure S5. Predicted secondary cloverleaf structure for the *trnS1* genes of *T. auricollis* and *T. troglodytiformis*. Nucleotide sequences from 5' to 3' are indicated for *trnS1*, Watson-Crick base-pairing, and G-U base-pairing. The arms of tRNAs (clockwise from top) are the amino acid acceptor (AA) arm, TΨC (T) arm, the anticodon (AC) arm, and the dihydrouridine (DHU) arm.

T. auricollis - G T T A A G T T A G A C T T A T T A A C A A - - - T T T G
T. troglodytiformis A A A C A A G T T T A A A A T A A C A A C A A A G A T T T A

T. auricollis T C T A T T T T T T G T T A C T A A A A T T T A T T A A C G A
T. troglodytiformis A A T A T T T A T A T T A C T A A A T T T T A T T A A C G A

T. auricollis T A A A G A T A T T G T G T T A A T G A C T A A T A A A C A
T. troglodytiformis T A A T T A A A A G G T T A A A C C A A A T A A T A A A - G

T. auricollis T A G C C C T G A C A G C T A A A G T A A G A T T T T C G A
T. troglodytiformis T G A C C C T C C C T G G T A A A A C A A - - - C C T A G A

T. auricollis T G A C A G C T A A A G T A A G A T T T T C G A C T C T A G
T. troglodytiformis - A A C A A C C A G G G A A - - - - C C T G A C - C T C C

T. auricollis C T A A A G T A A G A T T T T C G A C T C T A G C T A G C T
T. troglodytiformis C C C T G G T A A A A A - - - - - C A A C C T A G A A

T. auricollis T A A G A T T T T C G A C T C T A G C T A G C T A A T C C C
T. troglodytiformis T A A - - - C C T A G A A A C - A A C T A G G G A A - - C C

T. auricollis T T T C G A C T C T A G C T A G C T A A T C C C T G A T A G
T. troglodytiformis G T C A G A A T G A A C C T T A A A A A C C C C T T - T A A

T. auricollis C T C T A G C T A G C T A A T C C C T A A T A G A T T A A C
T. troglodytiformis C - - - - - - - - - - A T C C C T C T T C A A A A C C A A

T. auricollis C C C A A A C T C G C A G G T T T C A C C C C C C A A A A A
T. troglodytiformis T T A A A A A T T - - - - - T T T T T T T T T G C A A A A A

T. auricollis A A T T T T T G A T T T T T A A A A A T A A C G A T A A T C
T. troglodytiformis A A C C A A A T A A A A A A A A A A A A C A A - A A T T

T. auricollis T T T T T T C C T C C A A A G A A T T T A T T C G G A A A A
T. troglodytiformis T T T T T T T T T A T A A A A A A A T - - A A T T A A A A A

T. auricollis A A A G C C C T A C C T T A C T A G G G C T T T C T C G T T
T. troglodytiformis A A T T A C C A A A A T A A C T G A A G A A A A A C C G T T

T. auricollis T A G T C G C A A T T C T A T A C A A A A A G A A G A T T
T. troglodytiformis T A A C G A C T T T C G T T C T C A C A C T A A A A A A T A

T. auricollis G T C T G A T T T A A G T T C A A A A A A A A T T T T T T A
T. troglodytiformis T C T T G T T T C A A G T T T G G G A A A A T A T T T T T T

T. auricollis T T A A T A A T T T G T T T A C T A A A T T T A G T T A A C
T. troglodytiformis A T A - T C T T T T A T T T A C T A A A A T T A G T T A A C

T. auricollis A T A C A T A T T T T T T T T T T T T T T T - - - - C T
T. troglodytiformis A G A C A T A T C T

T. auricollis A A T T A T A A A C A A A T T A G A A G G A T A A A T T T
T. troglodytiformis A A T T A T A T A T T A A T T A A A A G A A T A A A T T T

T. auricollis A T A T A T T A A A A T G T T T A T A T A T A T A T T T A A
T. troglodytiformis A T G A A T T A A A A T A T C T T A T A T A T A T A T A T A A

T. auricollis A C G A T A C G G A T T T A T A A A G T A T T C T A A T A T
T. troglodytiformis A C G A T A A G G A T C C A C T A A T A T T A A G A A T A T

T. auricollis A A T A A A C G A T G T T A C A T A G A G T T A A A T A T A
T. troglodytiformis A A T A A A A T A T G T T A A A T A A G G T A A A A T A T A

T. auricollis C C C C C C C T A A A A A T T A G C T T C T C C G T T T T C
T. troglodytiformis C C C A T T T T T A A A A C T A C T A A A A G T A T T T T T

T. auricollis T G C T - C G T T T A T A A A G G G A C T T T T T A T C A G
T. troglodytiformis C C T T G C A G A T A G A A A A C G C C T T T T A A A C A G

T. auricollis T A G C T A T A T A T T C A T T T T A A A A T T G G T T A G
T. troglodytiformis T T A A T A - A C A A A A A A T A T A A C A T - A A A T A T

T. auricollis A
T. troglodytiformis -

Figure S6. Alignment of the conserved structural elements of the control regions (CRs) of *T. auricollis* and *T. troglodytiformis*. Sequence identity among species is indicated by yellow color.

T. auricollis

AAAAACCTAAAATGTAAATAACCAACAATAAATTAGCTTTAATCTTACGTAGCCCTGACAGCTAA
AGTAAGATTTTCGACTCTAGCTAGCTAATCCCTGACAGATTAGCTTTAATCATACGTAGCCCTGA
CAGCTAAAGTAAGATTTTCGACTCTAGCTAGCTAATCCCTGACAGATTAGCTTTAATCATACGTA
GCCCTGACAGCTAAAGTAAGATTTTCGACTCTAGCTAGCTAATCCCTGACAGATTAGCTTTAATC
TTACGTAGCCCTGACAGCTAAAGTAAGATTTTCGACTCTAGCTAGCTAATCCCTGACAGATTAGC
TTAATCATACGTAGCCCTGACAGCTAAAGTAAGATTTTCGACTCTAGCTAGCTAATCCCTGATA
GATTAGCTTTAATCTTACGTAGCCCTGACAACCTAAAGTAAGATTTTCGACTCTAGCTAGCTAATC
CCTAATAGATTAACCTTTAAACGAAAAATAATAGGGAGAATAAGATTCCCACTTAAAATAACC
CAAACCTCGCAGGTTTCACCCCCAAAAATCTCAAAAAAT Position(14,795-14,865)

T. troglodytiformis

ATACAGGAATTATTAACAACCAGGGAACCTGACCTCCCTGGTAAAAACAACCTAGAAACAAC
CAGGGAACCTGACCTCCCTGGTAAAAACAACCTAGAAACAACCAGGGAACCTGACCTCCCTGG
TAAAAACAACCTAGAAACAACCAGGGAACCTGACCTCCCTGGTAAAAACAACCTAGAAACAAC
CAGGGAACCTGACCTCCCTGGTAAAAATAACCTAGAAACAACCTAGGGAACCTAACTATTAATT
AAAAATATTAATAATAAATGTCAGAATGAACCTTAAAAACCCCTTTAAATCAACCAGAAATAA
AAGAAATCATAAACCAAAAAATCTGACATCCTCTTCAAACCAAAATTGAGTAAACACAAAAGA
CCTAAAAAAAAAATTTTCCAAAATTTTAAAAATTTTTTTTTTTTGCAAAAAAAAAAATTTTTTTTTTTT
AAAAATTCATTAATAAACCAATAAAAAAAAAAAAAAAAAACAAAATT Position(15,861-15,902)

Figure S7. Partial A + T-rich regions of *T. auricollis* and *T. troglodytiformis*. The underlined sequences are perfectly repeated sequences in the A + T-rich region. The position refers to the length of the first repeated sequence.