

S1 Table. Primer pairs used for PCR amplification of *C. crocodilus* mitogenome.

Primer	Sequences(<i>H. quoyi</i>)	Annealing temperature(°C)
1F	CGGCGTAAAGCGTGGTTA	55
1R	GTTGGCGATAAGAACTCAAAAGAG	
2F	GAAGTGAAGCAACCAGGAGC	55
2R	GCTTTCGTGGGTTTCAGTATCAT	
3F	TTTAACATTCGCGCCTGTCTC	55
3R	GGAGGGATAGGAGAAGTAGAACG	
4F	ATGATACGGACGAGCAGACG	55
4R	CCAATAACAATAAACGGGTCCTC	
5F	CTCTTTTACCGCCATCTACAGC	55
5R	CGAGACAGAGGCAAATGGTG	
6F	TCCCTAATAAACTGGGAGGTGTC	55
6R	TTGGAAAAGTTATGCGTGGG	

S2 Table. Codon number and RSCU in *C. crocodilus* mitochondrial PCGs. A total of 3,804 codons were analysed excluding the initiation and termination codons. Amino acids encoded by these codons are labelled according to the IUPAC-IUB single-letter amino acid codes.

Codon	n(RSCU)	Codon	n(RSCU)	Codon	n(RSCU)	Codon	n(RSCU)
UCU(S2)	42(1.02)	UAU(Y)	32(0.58)	UGU(C)	5(0.43)	UCU(S2)	42(1.02)
UCC(S2)	66(1.61)	UAC(Y)	78(1.42)	UGC(C)	18(1.57)	UCC(S2)	66(1.61)
UCA(S2)	74(1.8)	UAA(*)	0(0)	UGA(W)	93(1.58)	UCA(S2)	74(1.8)
UCG(S2)	6(0.15)	UAG(*)	1(2)	UGG(W)	25(0.42)	UCG(S2)	6(0.15)
CCU(P)	70(1.29)	CAU(H)	24(0.46)	CGU(R)	8(0.43)	CCU(P)	70(1.29)
CCC(P)	93(1.71)	CAC(H)	80(1.54)	CGC(R)	15(0.8)	CCC(P)	93(1.71)
CCA(P)	43(0.79)	CAA(Q)	80(1.76)	CGA(R)	43(2.29)	CCA(P)	43(0.79)
CCG(P)	11(0.2)	CAG(Q)	11(0.24)	CGG(R)	9(0.48)	CCG(P)	11(0.2)
ACU(T)	53(0.7)	AAU(N)	38(0.61)	AGU(S1)	12(0.29)	ACU(T)	53(0.7)
ACC(T)	116(1.54)	AAC(N)	86(1.39)	AGC(S1)	46(1.12)	ACC(T)	116(1.54)
ACA(T)	124(1.64)	AAA(K)	67(1.79)	AGA(S1)	0(0)	ACA(T)	124(1.64)
ACG(T)	9(0.12)	AAG(K)	8(0.21)	AGG(S1)	0(0)	ACG(T)	9(0.12)
GCU(A)	61(0.69)	GAU(D)	34(0.88)	GGU(G)	44(0.75)	GCU(A)	61(0.69)
GCC(A)	140(1.59)	GAC(D)	43(1.12)	GGC(G)	68(1.15)	GCC(A)	140(1.59)
GCA(A)	143(1.62)	GAA(E)	73(1.45)	GGA(G)	78(1.32)	GCA(A)	143(1.62)
GCG(A)	9(0.1)	GAG(E)	28(0.55)	GGG(G)	46(0.78)	GCG(A)	9(0.1)

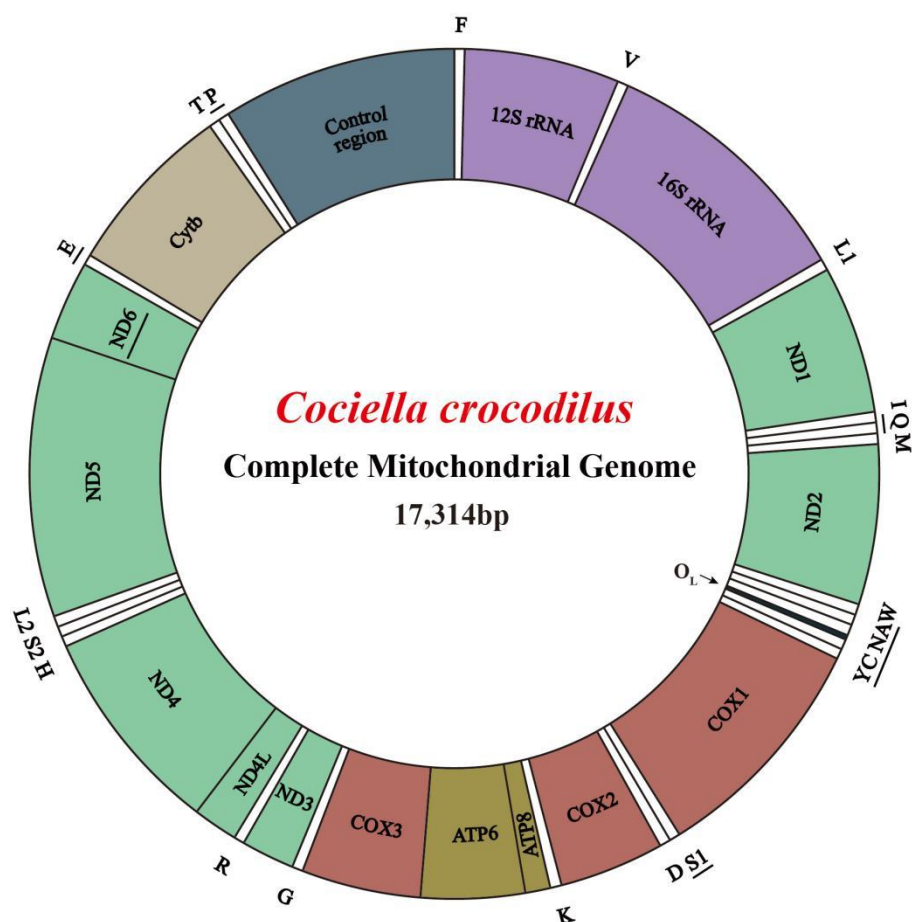


Fig. S1 Organization of the complete mitochondrial genome of *C. crocodilus*. Single letter amino acids representing tRNAs refer to IUPAC-IUB (S1:trnL^{AGN}; S2:trnL^{UCN}; L1:trnL^{CUN}; L2: trnL^{UUR}). The coding gene name on the heavy strand is not underlined, while the coding gene on the light chain is underlined.

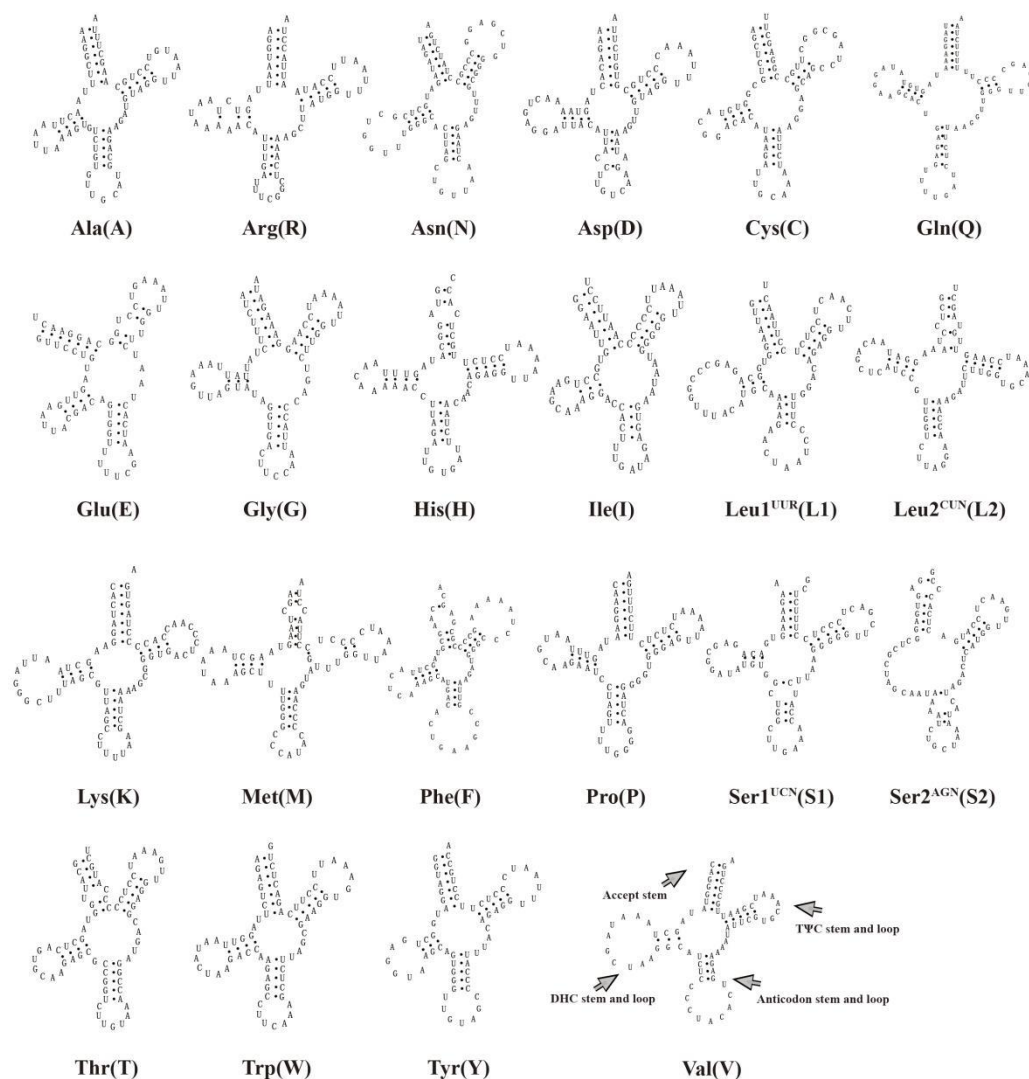


Fig. S2 Predicted secondary structures of 22 tRNA genes in the *C. crocodilus* mitogenome.

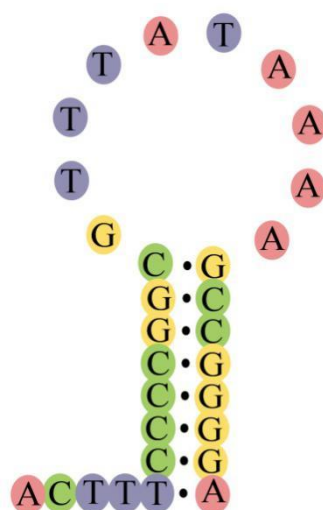


Fig. S3 The putative secondary hairpin structural features of the O_L in the mitogenome of *C. crocodilus*.

trnaP-15,868AATTCCTATATATACATATATGTATTTTCACCATAAATTTATTTAACCTTACA
 AGGAACATGTTCTGAATAAGATATACATATGATTTATTTGACATAAATTTAAAATTCCAATA
 AAGGGTCTATTAAATACTCCACAATAAGGTAGTTAAATAATTCATACCTTGTCTCACAT
 CBS-F
 TCCATTAAATAAATAATATAATTAGCAGTAAGAACCGACCATAAACTATACCTTAATGC
 CBS-E
 CAACGGTTATTGAAGGTGAGGGACAAAACTGTGGGGGTTTCACCTCATGAACTATTG
 CBS-D
CTGGCATTGGTTCCTACTTCAGGGCCATTAATTGGTATCATTCTCATACTTTTCATTGAC
 GCTTGCATAAGTTAATGGTGTACACATGTCTGGGAGCACCCAGCATCCTAATTATAGG
 TGCATAGGGTCTCTTTTTCTTTATCCTTTCACTTACATTTACAGTGCAAAGTAATATG
 ATATAACAAGGTTGAACATTTTTCTTGCTTGAAATAAATCTTACTGAATTATATTAGAAT
 CBS-1
 ATCTTTTAATAATTGCATAACTGATTTCAAGTGCATAGTTATACATACTATTCTTTATCTC
 CBS-2
 CCCC GGCTTCCGGGCGAAAACCCCCCTACCCCCCAACTACTAAAGTTTCTTAATGAT
 CBS-3
 CCTCAAAACCCCCGGAAATAGGAAAAACCTTAAATAGTTCACCTTCTACCATGT
 ATACGAACATTAGTAAAGTCGAACATGAGAATGATGGGGTATAATAAAAATTATATCTAT
 TAATATATAGTATTTATTATGCTTATATATCCTCATAAACACAACCGCCCTGATAAACCTT
 Repeat 1
 AAGTTCATAAACATATACCTTTTATATAGTATTATATATCCTCATAAACACAACCGCCCT
 Repeat 2
 GATAAACCTTAAGTTCATAAACATATACCTTTTATATAGTATTATATATCCTCATAAACAC
 Repeat 3
 AACCGCCCTGATAAACCTTAAGTTCATAAACATATACCTTTTATATAGTATTATATATCCT
 Repeat 4
 CATAAACACAACCGCCCTGATAAACCTTAAGTTCATAAACATATACCTTTTATATAGTAT
 Repeat 5
 TATATATCCTCATAAACACAACCGCCCTGATAAACCTTAAGTTCATAAACATATACCTTT
 Repeat 6
 TATATAGTATTATATATCCTCATAAACACAACCGCCCTGATAAACCTTAAGTTCATAAAC
 Repeat 7
 ATATACCTTTTATATAGTATTATATATCCTCATAAACACAACCGCCCTGATAAACCTTAAG
 Repeat 8
 TTCCATAAACATATACCTTTTATATAGTATTATATATCCTCATAAACACAACCGCCCTGATA

Fig. S4 The structure of the control region in mitogenome of *C. crocodilus*. The sequences marked gray are conserved motifs ATGTA and its complement TACAT. The green and purple background denote the eight tandem repeats.