

Supplementary:

C. meridianus

TAAGGTAAATÄÄÄÄÄTCTAAGGAACACTACATTTTTTAACAACGAAATAAATACÄÄ
 ÄÄÄÄÄCAAGAAAAATGCAACTAAGATAATCAAATTAATCCCTCTATTATAAATA
AAATTTTTCTTGCCCACTAAATAGÄÄÄÄÄÄCTTTCCAAAAACAAATCCGAAAA
 TAAAACTATTACAAACAAATAAAATTCTAACTTTAATAAACAACCCAACCCGCA
 TCAAATAAAGTTTCTATAAATAA

C. relictus

[illegible]

C. kye bangensis

TAAAGTAAACAAAAATTTTCAGGATCACTACCCCAAATAAAGAAACAAATÄÄÄÄ
 ÄÄÄÄÄTÄÄÄÄÄÄÄÄÄGCAACTAATTAAAAATCAAAC TTTCAGCACAAATATAAAT
TTTTCTTGCCCAACTAAATAGATATAAAACTTTTCAAAAATAAACTAAAAATAAA
 ACTATTATAAAGTAAAACAAAAATTTTCAGGATCACTACCCCAAATAAAGAAACA
 AATÄÄÄÄÄÄÄÄÄTÄÄÄÄÄÄÄÄÄGCAACTAATTAAAAATCAAAC TTTCAGCACAA
 ATAAATTTTTCTTGCCCAACTAAATAGATAAAACTTTTCAAAAATAAACTAAA
 AATAAACTATTATAAAGTAAAACAAAAATTTTCAGGATCACTACCCCAAATAAA

GAAACAAATĀĀĀĀĀĀĀĀTĀĀĀĀĀĀĀĀGCAACTAATTAAAAATCAAACCTTCCA
GCACAAATAAAATTTTTCTTGCCCAACTAAATAGATAAAACTTTTCAAAAATAAA
ACTAAAAATAAACTATTATAAAGTAAACAAAAACCCACGGATCAAACCCTTA
ATAATAGTTCCATTGAATATAAGGAGTAATAACACTTTCCTAGATCTCAĀĀĀĀĀĀĀĀ
ATTTTATATAAATGAGATCTAGGAAAGTGTTATTACTCTTTATAGTTTACTATAAG
AATTTAAGTTGACATACTCATTATTGGAACATATTTATTATTATAATATAAGAATT
AAATTACAAGATAATTATTATTGGATAGTATAATATAATATATTTATCTAATATGA
ATAATACCATTATATTCATAAATAAAAAATATATTTAAATAAGATTCAATATGTTTA
ACTAAATTCCTTATATATGTATAATCTATTTCTCTCTATATAGAGCTATATGATATA
TAAGTTCAAAGTGTATATACATAAGACTTTATATTAATATGGCĀĀĀĀĀĀĀĀĀĀTĀ
TTATATAAAGACAAATAAAACATAAACĀĀĀĀĀĀĀĀTGAACCCAAGCCATATCAT
TAAAAAGTTACATAAAATAT

Figure S1. The D-loop regions sequence of the three *Cryptocercus* species' mitochondrial genomes. Bold and underlined segments indicate the 31bp relatively conserved sequence in the three *Cryptocercus* species. Framed segment indicates TA repeats. Dotted segments indicate A/T single copy sequences.

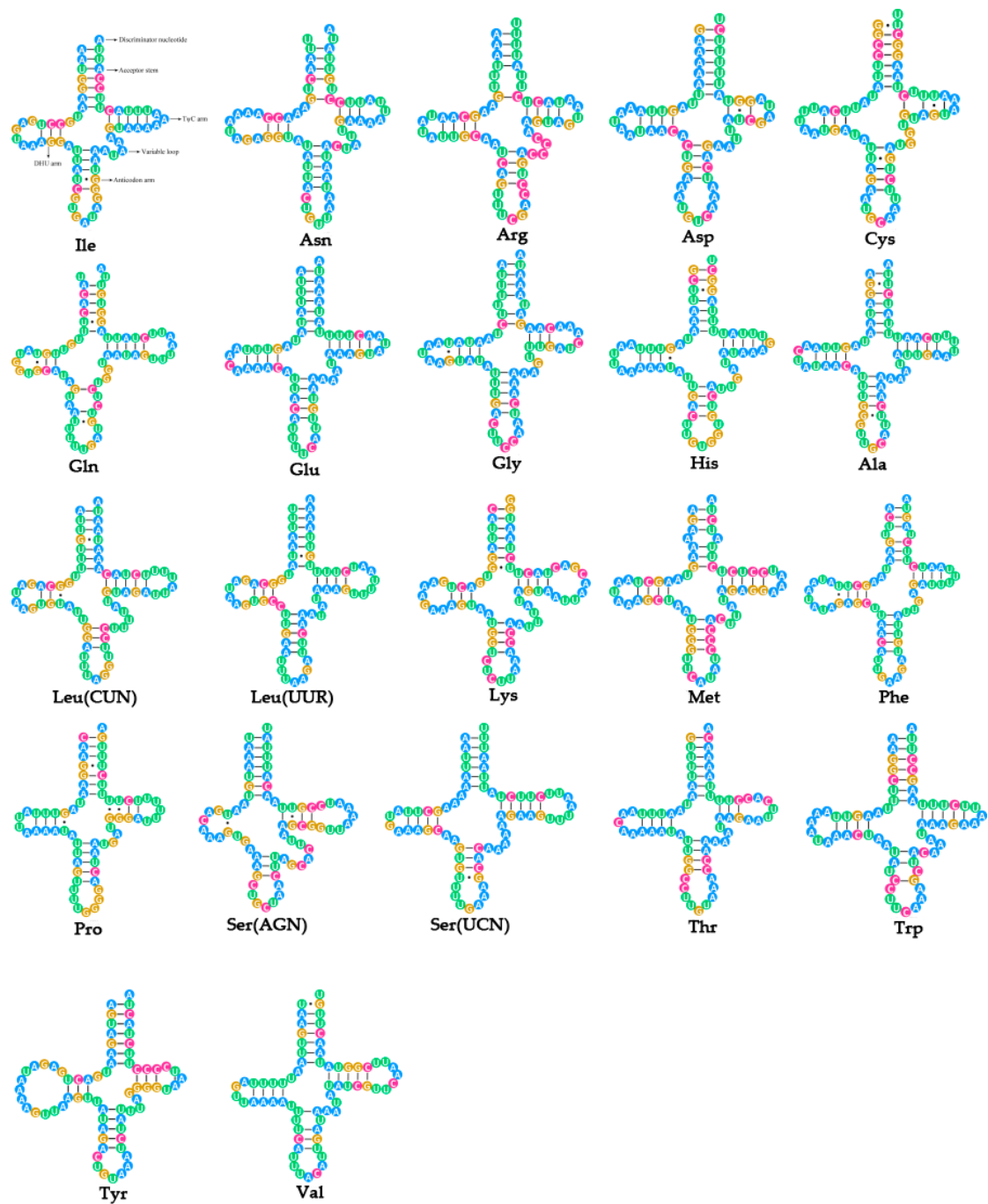


Figure S2. Inferred secondary structure of 22 tRNA genes for *C. meridianus*.

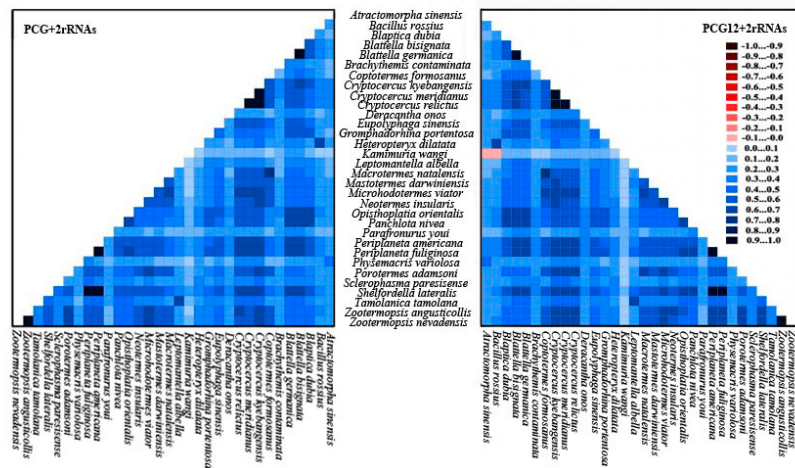


Figure S3. AliGROOVE result of concatenated gene analyses on two datasets. The mean similarity score between sequences is showed by a colored square, based on AliGROOVE scores from -1, indicating a great difference in rates from the other sequences of the data set, that is, heterogeneity (red coloring), to +1 indicating that rates match all other comparisons (blue coloring).

Table S1. Primers used in this study.

Region	Primers (F & R)	Sequence (5' →3')
<i>cox1</i> → <i>cox2</i>	C1-J-1718 ¹	GGAGGATTGGA AAT TGATTAGTTCC
	R Lys ³	GAGACCAGTACTTGCTTTCAGTCATC
<i>cox2</i> → <i>nadh4</i>	CRYs6 ²	AGCAGATGCTACACCAGGACG
	CRYs7 ²	AGATCTTGTAATATAGCCGCTCCC
subPCR <i>cox2</i> → <i>nad5</i>	CRYs6 ²	AGCAGATGCTACACCAGGACG
	CRYs25 ²	ATTGACTGTTTGTTATTCATTTCCG
subPCR <i>nad5</i> → <i>nad4</i>	CRYs24 ²	TATATCTCAATCTACTGATGAGG
	CRYs13 ²	TCCTTCTTTAGTGCTGTTTATACAC
<i>nad4</i> → <i>rrnL</i>	CRYs8 ²	AGTAGGAATCAA GCTACCCCTC
	CRYs2 ²	ACTAAATTACCTTAGGGATAACAGCG
<i>rrnL</i> → <i>cox1</i>	CRYs1 ²	ATT ATG CTA CCT TTG CAC GGT C
	CRYs3 ²	ACT AAT CAG TTA CCA AAT CCT CCG

Table S2. The best-fit model for each partition in BI analyse.

Dataset	Best partitioning scheme for Mrbayes (PCGR)		Best partitioning scheme for Mrbayes (PCG12R)	
	Best model	Partitions	Best model	Partitions
1	GTR+I+G	12S, 16S, atp6_P1, atp6_P2, atp8_P1, atp8_P2, cox1_P1, cox1_P3, cox2_P1, cox2_P2, cox3_P1, cox3_P2, cytb_P1, cytb_P2, nad2_P1, nad3_P1, nad3_P2, nad4_P1, nad4_P3, nad4L_P2, nad4L_P3, nad5_P2, nad5_P3, nad6_P1	GTR+I+G	12S, 16S, atp6_P1, atp6_P2, atp8_P1, atp8_P2, cox1_P1, cox2_P1, cox2_P2, cox3_P1, cox3_P2, cytb_P1, cytb_P2, nad1_P2, nad2_P1, nad3_P1, nad3_P2, nad5_P1, nad5_P2, nad6_P1
2	HKY+I+G	atp6_P3, atp8_P3, cox3_P3, cytb_P3, nad2_P3, nad3_P3, nad6_P3	TrN+I+G	nad4_P1
3	TVM+I+G	cox1_P2, cox2_P3, nad1_P1, nad2_P2, nad4_P2, nad4L_P1, nad6_P2	TVM+I+G	cox1_P2, nad2_P2, nad6_P2
4	GTR+G	nad1_P2	K81uf+G	nad1_P1, nad4_P2, nad4L_P1, nad4L_P2
5	K81uf+G	nad1_P3		
6	TIM+I+G	nad5_P1		