

## ANNEX

Supplementary Table SI. Alignment of *lsrDNA* and *nad1*

*lsrDNA* = 1-1424

*nad1* = 1425-1934 [beginning on codon position 1]

exclusion set for phylogenetic analysis = 1-73 171 202 244-247 390 490 510 511 552 599-606 735-766 841 858-860 902 916 960-964 1134 1200-1211 1422-1472 1914-1934; see Table II for full details on taxa and updated accessions

<i>Lepidapedon_ arlenae</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ beveridgei</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ desclersae</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ discoveryi</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ elongatum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ gaevskayae</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ rachion_1_AJ405260_AJ405274</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ rachion_2_AJ405261_AJ405275</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ sommervillae</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedon_ zubchenkoi</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Neolepidapedon_ smithi</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Prodistomum_ priedei</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Profundivermis_ intercalarius</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Myzoxenus_ insolens</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Intusatrium_ robustum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Postlepidapedon_ sp.</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Prodistomum_ keyam</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepidapedoides_ angustus</i>	CGGCGAGTGAACAGGGATAAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Clavogalea_ trachinoti</i>	CGGCGAGTGAACAGGGATAAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Echeneidocoelium_ indicum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Hypocreadium_ toombo</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTCTGTTGGC
<i>Neomultitestis_ aspidogastriformis</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Nechypocreadium_ dorsoporum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Lobatocreadium_ exiguum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Diploproctodaeum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Bianium_ spongiosum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Diplocreadium_ tsontso</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Diploproctodaeum_ mamoaafata</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Multitestis_ magnacetabulum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Lepotrema_ clavatum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Hypocreadium_ sp. (nonotch)</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Hypocreadium_ toombo</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Holorchis_ castex</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTCAATTTGAT
<i>Holorchis_ gigas</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTCAATTTGAT
<i>Tetracerasta_ blepta</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTCAATTTGGT
<i>Neopreptetos_ arusettae</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Neolepocreadium_ caballeroi</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTCAATTTGAT
<i>Bulbocirrus_ aulostomi</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Aephnidiogenes_ major</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTATTTGAT
<i>Paragyliachen_ arusettae</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Robphildollfusium_ fractum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Paragyliachen_ atractus</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCGTTGGT
<i>Petalocotyle_ adenometra</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGTCAATTTGGC
<i>Affecauda_ annulata</i>	CGGCGAGTGAACAGGGAAAGCCCAGCACCGAAGCCTGTGGCCGTTGGT
<i>Koseiria_ xishaenesis</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Enenterum_ aureum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Proenenterum_ isocotylum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Proenenterum_ ericotylum</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGC
<i>Gorgocephalus_ kyphosi</i>	CGGCGAGTGAACAGGGATTAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Stephanostomum_ adlardi</i>	CGGCGAGTGAACAGGGAAAAGCCCAGCACCGAAGCCTGTGGTGTTTGGT
<i>Neopocreadium_ splendens</i>	CGGCGAGTGAACAGGGAAAAGCCCAGCACCGAAGCCTGTGTCCATTTGGG
<i>Callohelminis_ pichelinae</i>	CGGCGAGTGAACAGGGAAAAGCCCAGCACCGAAGCCTATGTCCATTTGGG
<i>Cadenatella_ pacifica</i>	TGGCGAATGAACAGGGAAAAGCCCAGCACCGAAGCCTGTGGCCGTTGGT
<i>Cadenatella_ isuzumi</i>	TGGCGAATGAACAGGGAAAAGCCCAGCACCGAAGCCTGTGGCCGTTGGT
<i>Pycnadenoides_ tendu</i>	CGGCGAGTGAAGAGGGATAAGCCCAGCACCGAAGCCTGCGGTTCGTTGGC
<i>Mitotrema_ anthostomatum</i>	CTGCGAGTGAACAAGGAATAGCCCAGCACCGAAGCCTGTGGTCAATTTGGC
<i>Siphodera_ vinaledwardsii</i>	CTGCGAGTGAACAGGGAAAAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Caecincola_ parvulus</i>	CTGCGAGTGAACAGGGAAAAGCCCAGCACCGAAGCCTGTGGCCATTTGGT
<i>Paracryptogonimus_ elongatus</i>	CTGCGAGTGAACAGGGAGAAGCCCAGCACCGAAGCCTGTGGTCAATTTGGC









































```

-----
-----
-----
GGTTTGAGGCTTGTTTTATGTGTGTTGTTATAAATGGTGGCGGTAGTGGTT
GATTTGAGGCTTGTTTTATGTGTGTTGTTATTTATGGTAGCCATGGTTATG
GGTTTGAGGCTTGTTTTATGTGATTGTTGTTTGGTTGCATTGGTTTGG

```

```

GGGGGATATTCTCAGTCTCTTGTAGGGGTACCGGGTACTTCTTTGGTT
GGCGGATACTCTTCTGTTTCTTGTAAAGGAGGCCAGGTGGCTCCTGTGGGT
GGGGGTTATTCTTCTGTGGCCTGCGGGGAGAGAGGATGATTATATAGGTT
GGGGGTTACTTCTGTGGCTTGTGGTGAGAGAGGGTGGTTATTATGATT
GGGGGTTATTCCTCTGTGGCTTGTAAACGAAAGGGTTGATTGGCTTTGACT
GGAGGGTATTCTCGGTTTCTTGTAGTGATACCGGGTACTTCTTTGGTT
GGGGGTTATTCTTCTGTGGCTTGTGGTGAGAGAGGGTGGTTATTATGATT
GGGGGTTACTTCTGTGGCTTGTGGTGAGAGAGGGTGGTTATTATGATT
GGAGGCTATTCTTCTGTTTCTTGTAAAGAGAGTGGGTGACTTCTTTGATT
GGCGGTTATTCTTCTGTCTCTTGCAAGGAGGCCAGATGGCTCCTGTGGGT
GGTGGTTATTCTTCTGTCTTCTTGTGTTGGAGGCCAGGTGGCTCCTGTGGGT
GGAGGGTATTCTCAGTTTCTTGTAGTGATACCGGGTACTTCTTTGGTT
GGTGGTTATTCTTCTGTCTTCTTGTGTTGGAGGCCAGGTGGCTCCTGTGGGT
GGGGGCTATTCTTTGGTTTACAGCGGTGGAGAGAGGGTATTTTGTGAAT
GGGGGTTATTCTTCTGTGTTTGTAGTAGAGCTGAGTATTCTTTTATT
GGCGGTTACTTCTCTGTTTCTATGGTGGAGGGGGTGGATTATATGAGTT
GGCGGTTATTCTAGTGTCTTGTGGCTTAGATTATCGTGGCTTGTGACT
GGTGGTTATTCTCCCTTCCAGGGCCTTGAATTCGCTTGGATGGTTTGTCT
GGGGGTTATTCTCGAGAGTGGTTTATCTAGTCTTGGCTTGTGTCCT
GGGGGTTATTCTGCTCTTTTCAAGGTTGGGAACGTGTGGTGATGTGGCT
GGGGGTTATTCTGCCACGCAGGTCTGGAATGACAGTGGGGGCTGTGACT
GGAAGATATTCTTGTATCATGGGGTCATGGGTGCTTGGTTTTTATGATT
GGGGGTTATACTTCTTTTGTCTGTTGATAGGGTTGGTGGATGCTGT
GGAGGGTATTCTCTTTTCCGGGGTATCAAGAGTGTGGATGATGTGGTT
GGTGGTTATTCTATTCTGGGGTGTGCAAGTATTGATTGATGTGATT
GGAGGCTATTCTGTCTTCTCTGGGGTGTGAGTGTGGTGGACTTGGTT
GGTGGTTACTCGTCTTTTCTGGTGTATCGGGAATTTGGTTGATGTGTTT
GGCAGTTATTCTGCTTTTCTGGGATTTCAAGTGCCTGGATGATGTCCT
GGGGGTTATGCACTCTTTTCCGGACTTTGGAGGGTTTGATTAAATGTGTTT
GGGGGTTATTATGTTTCCCGGTTCTAGTAGGGAGTGGGTTATGTTGGTT

```

```

GGGGGTTACTCTCGGCTTCCGGCCTCAGTGGGAGTGGTTGGTTTTATT
GGGGGTTATTATCTTTTCCGGGGTGGACTTCTTGAATGTTGCTGTT
GGGGGTTATTATCTTATCCTGCTGTGGAATCRAGGTGGGTTATGGTGT
GGGGGTTATTCTTCT--GGAGGGTGGTGATGTTGGTTGGTTGAGT

```

```

GGCGGTTACTCTTGTCTCCTGGGTTGGAGAGTGGGTGGTTTTTGTGGAG
GGGAGGTATTCTGTGTTTCTCTGTAAGAGGTGGTTGATTGTTGTGGTT
-----
AAGAGTTATAGGTTATTTTTTGTTTAGAGGAGAGTTGGTTGTTGTTTTT

```

```

AAAAGGTATAGGATGTTTTTCTCGGAGGAGAGTTGATTATTGTGATT
GGTAGCTATGGTGATCTTCTGCTTGGAGAGGGGGTGGTTTTTATTTTTT
GGTGGTTATAGGTTGATGTGTCCTTTTGGGGTAGGTTGGTTATGTTT
GGTGGTTATTCGGTTAGGTCTAGTATTGAGACCAGCTGATTATATTTCT
GGAGGTATTCTGCAATGCTGTGTGGAGACACTGATTATTTGATTTTTT
GGCGGCTACTCTATGAGTTCTTGTGTTGAGTTCGAGCTGCTAGTGTGTTT
GGTGGTTATTCTATGCACTCCTGTGTGGATAGTAGCTGGCTTGTATGCCT
GGGGGTTATTCAATTGTTCCATCGTTGGAGGACGCTTGGTTCTTATTTTTT
GGTAGTTATTCTGTTTTTGTAGTTTAGTGGGAGACAGTTGATTCTTTTTTT
GGCAGTTACGGCGTTCAGCCACTTGTGAGGCGGGCTGGTTTCTGCCAG

```

```

GGAGGTTATTCTGTGCGCGCATGATGTCGGAGAAGTGGTTGATGCTGTT
GGGGGTTACTCTTTACCGGGTTTGTGGCTGAAAAGTGGTTGACCGCGTT
GGTGGTTACTCTTTGAGGTTGTGGTGGTAGTATTTGGGGGGTGTGGC
-----

```

```

GGAAGATATTCTCAGGGCTTTATATCGAGAAAGGTGATATCTTCTTT
-----

```

```

-----
-----
-----
GGTGCTATTCTACTGTTTCCGGGCTTAGATCTGCTTGGCTATTTGTTT
GGTCTTATTCTTGTGAAGGGGGCTGCAGTCTGTGTGATTTTTAGCTAG
-----
-----
-----

```

```

GGAAGGTACGGTGTAGGTAGTTTGGTTTACAGGTGTGTGGTTGATTGGTTT
GGTTGTATAGTGTACCAGGTATGTTTTATAATCCTTGATTTTTTTCTAT
GGGAGTTATGGTGTCTTGTGTTTGGTGAATTTGGTGGTATGTGAAT

```

```

AGCGGCTCCCCTTTGTTATGTTTTATGGTTGATTGGGATTTTATGTGAGT
GGCGGCCCCACTGTGTAYGTTTTGTGGCTGGTGGTATCTTGTGTGAAT
GGCAGCTCCTTTATGTTATATCTTGTGGTTGGTGGGCATTTTATGTGAGT
GGCGGCCCCATATGTTATATTTTGTGGCTGGTGGGATTTTGTGTGAGT
TGCGGCCCCCTTGTGTTATGTTTTGTGGCTGGTGGGATTTTGTGTGAAT
AGCGGCCCCCTTTTGTATGTTTTATGGTTGATTGGGATTTTATGTGAGT
GGCGGCTCCGTATGTTATATTTTATGGTTGGTGGGATTTCTGTGTGAGT
GGCGGCCCCATATGTTATATTTTGTGGTTGGTGGGATTTTGTGTGAGT
GGCGGCCCCGTTGTGTACGTTTTATGGTTGGTGGGATTTTATGTGAGT
GGCGGCCCCACTGTGTTATGGTCTGTGGCTGGTGGTATATTGTGTGAAT
TGTGGTCCCAGTGTGTTATGTTTTGTGGCTGGTGGTATCTTGTGTGAAT
AGCGGCCCCATTTTGTATGTTATATGGGAGATTGGGATTTTATGTGACT
TGTGGTCCCAGTGTGTTATGTTTTGTGGCTGGTGGTATCTTGTGTGAAT
GGCTGCTCCTATGTGCTATGTTTTATGATTGGTGGGATTTTGTGTGAGT
GGTAGCCCCCTTTGTTATGTTTTGTGGTTGGTGGTATTTCTGTGCGAGT
GGGGGCTCCGCTTGTGTTATGTTCTGTGGTTGATAGGATTTTGTGTGAGT
GGTTGCCCTCTGTGTTATTTTTTGTGACTTGTGGTATTTTGTGTGAGT
TGTGTTCCGATGTGTTATGCTTTGTGGTTGGTGGGATTTTGTGTGAGT
GTGTGTTCCGCTGTGTTATGTTTTGTGGTTGGTGGGATTTCTGTGTGAGT
TTCAGTGCCACTGTGTTATAGTATTTGGTTGATTGGGATATTGTGTGAGT
AGTTTCTCCGTTGTGTTATTTTCTTGGTTGGTGGTATTTTGTGTGAGT
GGTATTCCATTGTGTTATATGGTTTGGTTGGTAGGATAATTATGTGAGT
TGTATCCTTTCCTTGTGTTATTTACTTTGGCTTGTGGTATTTTGTGTGAGT
GATTGCTCCGTTGTGTTATGTTTTGTGGCTTGGCGGATTTTGTGTGAGT
AATTTCTCCTCTGTTATTTTCTTGGCTTGGCGGATTTTGTGTGAGT
AATTGCTCCCCTGTGTTATGTTCTTGGCTGGTGGTATTTTGTGTGAGT
AATGCTCCCCTGTGTTATATATATTAGGCTTGTGGGATTTTGTGTGAGT
TGTGCTCCACTGTGCTATTTTTTATGGCTTGTGGTATATTGTGTGAGT
GGTTGCCCCCCCTTTGTTATATGGTGTGATTAGTAGGGATTTTGTGTGAGT
GGTTACACCTCTATGCTATTTTTTATGGTTGGTGGGCATATTGTGTGAGT

```

```

AGTCTCTCCTGTGTGCTATTTGTTGTGGTTGGTGGGATACTGTGTGAGT
GGTTTACCAGCTGTGTGATGCTGTTGGCTTGTAGGTAATACTTTGTGAGT
TAGCTCGCCTTTGATGATAATTAGTGTGACTTGTGGTATTTTATGTGAGT
TGTGGCACCTCTGTGTTACTTTGTTTGAATGGTGGGATTTTATGTGAGT

```

```

GGTTTCTCCTCTATGCTATTTTATTTGATTGGTGGGATTTTGTGTGAGT
GATAGCTCCGTTGTGTTATATCTTGTGGCTTGTGGGATTTTGTGTGAGT
-----
GGTGGTTCCCTCTGTGTTATAGTCTTTGGCTAGTGGGAATCCTTTGTGAGT

```

```

GGTTATTCCTATGTGTTATATTTTTGTTAGTGGGATTTCTTTGTGAGT
AGTGGCTCCTTTWGTGTACRCTTTGTGGCTATRRRGATCTTGTGTGAGT
GTTGATGCCTTTGTGTTNCTTTCTTTGGTTGGTGGGAT  -----
TACTGCCCCCTTGTGTTATGTTTTGTGACTAGTGGGATTTTATGTGAGT
GAGTGTCCCTTATGTTACATCTTGGTTGGCGGGGATATTGTGTGAGT
ATCCGCCCCCTTATGCTATTTCTTGTGGTTGGTGGGATATTGTGTGAGT
CTCAGCGCCCCCTCTGTTATTTTTTGTGGCTGGTGGTATTTTATGTGAAT
GATTTCCCCCTTTGCTATTTCTTGTGGCTTATTTGGAATACTTTGCGAG-
AGTTGTTTTGCCATGTATAGTCTTTGGTTGATTGGTATCTTGTGTGAGT
CTTAGTGCCTTATGTTATATTTTTATGGTTAGCGGGGATTTTATGTGAGT

```

```

-----
GGTTCTGTTCCCGTGCTATGGGCTTTGACTTGTGGTATTTTGTGTGAGT
AGTTTTATTACCTTGTTATGGTTATGGTTGGTGGGTATATTTGTGTGAGT
GGTGTTCCTGTTTGTTCCTTCTTGTGGTTGGTGGGATGCTTTGTGAGG
-----
-----
TATAGTACCTTTATGTTATTCTTCTTGGTTGGTGGTGTTTTTTGTGAGT
-----
-----
AGTGGCACCCTATGTTATGCTTTGTGGTTGGTGGTATTTTATGTGAGT
TGTGTTCCTCTGCTATATTATATGATGCGTGGGTATTTTATGTGAGT
-----
-----
-----
-----
GATTATGCCTCTCGTTTACGGTTTATGGTTAGTGGGTATATTGTGCGAGT
AGTTTTACCACCTGGTGTATGGTCTGTGGTTGGTGGTATTTTATGTGAGT
GGTGTTCCTGTAGTTTATGGTTTGTGGCTGGTGGGTATATTATGTGAAT
-----
-----
GTAACCGTACCCCC
GTAACCGGACTCCT
GTAACGTAAGTCCG
GTAATCGCACTCCG
GCAACCGTACGCGG
GTAACCGTACCCCT
GTAATCGCACTCCG
GTAATCGCACTCCG
GTAACCGTACTCCC
GTAACCGGACTCCT
GTAACCGGACTCCT
GTAACCGAACCCT
GTAACCGGACTCCT
GTAACNNNNNNNNN
GTAACCGCACTCCT
GTAATCGTACTCCA
GTAMCCKWWRCCC
GTAATCGTACGCCT
GTAATCGCACTCCT
GCAATCGTACCCCT
GCAAACGCACTCCT
GCAATCGTACTCCC
GWAATCKTACTCCG
GCAACCTAACTCCT
GTAATCGCACTCCT
-----
-----
GTAATCGAACCCT
GTAATCGGACTCCT
GTAATCGTACTCCT
GTAATCKWACACCG
SYAMTYKRACACSM
-----
-----
GTAATCGTACTCCC
GCAACCGAACTCCA
GTAATCGGACCCCC
GTAATCGTACGCCT
-----
-----
GCAACCGTACCCCT
GTAATCGTACTCCG
-----
-----
GTAACCGTACTCCG
-----
-----
GTAATCGTACTCCT
GCAATCGTACTCCT
-----
-----
GTAATCCAACCCT
GTAATCGGACACCC
GTAATCGAACCCT
GTAATCGTACTCCC
-----
-----
GTAAYCGNACYCCN
GTAACCGTACCCCG
-----
-----
GTAATCGAACTCCT
GTAACCGTACTCCC
-----
-----
-----
-----
GTAATCGTACACCT
-----
-----
-----
-----
GTAATCGAACTCCG
GTAACCGTACTCCC
-----
-----
-----
-----
GTAATCGTACTCCT
GTAATCGTACTCCT
GTAACCGTACTCCA

```

**Supplementary Table SII.** Results of tests to detect positive selection in *nad1*

Model	Np <sup>e</sup>	log likelihood	ts/tv rate ratio (k)	LRT <sup>f</sup>	<i>dN/dS</i> ( $\omega$ ) <sup>g</sup>			
a. M0 <sup>a</sup>	106	-10333.48	2.19		proportion $\omega$	1.00000 0.01210		
b. Branch-site null <sup>b</sup>	108	-10233.72	2.11		proportion background foreground	$\omega$ 0.96603 $\omega$ 0.00944 $\omega$ 0.00944	0.02398 1.00000 1.00000	0.00974 0.00024 1.00000
c. Branch model <sup>c</sup>	107	-10329.15	2.22	2(c-a) = 8.65**	proportion background foreground	1.00000 $\omega$ 0.00940 $\omega$ 0.01960		
d. Branch-site <sup>d</sup>	109	-10233.72	2.11	2(d-a) = 199.50*** 2(d-b) = 0	proportion background foreground	0.96603 $\omega$ 0.00945 $\omega$ 0.00945	0.02398 1.00000 1.00000	0.00974 0.00024 1.00000

<sup>a</sup>*dN/dS* averaged across all sites and lineages; <sup>b</sup>foreground lineages are deep-sea lineages in Table I; class of sites  $\omega$  fixed at 1; <sup>c</sup>foreground lineages are deep-sea lineages in Table I; <sup>d</sup>foreground lineages are deep-sea lineages in Table I; class of sites  $\omega$  can be >1; <sup>e</sup>number of free parameters; <sup>f</sup>likelihood ratios test (see Materials and methods) models compared are indicated by letters; \*\*<0.01, \*\*\*<0.001; <sup>g</sup>proportion of codons in site classes of different  $\omega$  values, averaged across foreground, background or all lineages.