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6 **Mitogenomic phylogeny of Nassariidae (Neogastropoda: Buccinoidea)**

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8
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20 Running head: PHYLOGENY OF MUD SNAILS (BUCCINOIDEA, NASSARIIDAE)

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ABSTRACT

Mud snails (family Nassariidae) represent a highly diversified lineage within superfamily Buccinoidea. Recent molecular phylogenies contradicted in some instances the traditional nassariid classification and revealed important levels of homoplasy in phenotypic characters. In order to clarify the boundaries of family Nassariidae, as well as to inquire on the diversification of the cosmopolitan Nassariinae, a robust phylogenetic framework is needed. Here, the near-complete mitogenomes of 31 species representing almost all lineages of Nassariidae plus several buccinoid outgroups were sequenced. All mitogenomes of buccinoids shared the same gene order, which is identical to the consensus reported for caenogastropods. The monophyly of Nassariidae as previously defined was not confirmed. The reconstructed phylogeny revealed distant relationships between the genera *Cyllene*, *Anentome*, *Tomlinia*, *Engoniophos*, *Phos*, *Antillophos* and the majority of nassariids, represented by Nassariinae + *Bullia*. Within Nassariinae, a robust phylogeny, which recognized a total of seven regional groups, was reconstructed. The West Atlantic / Mediterranean genus *Tritia* was divided into three clades. The biogeographical analysis together with the inferred chronogram suggested that Nassariinae might have originated during the late Paleocene in the Indo-Pacific region. Subsequent climate change and continental drift events triggered diversification within the subfamily, leading to the worldwide distribution of current genera.

INTRODUCTION

Mud snails or dog whelks (Family Nassariidae Iredale, 1916) belong to the superfamily Buccinoidea, and consist of more than 600 extant species (MolluscaBase, 2022). Mud snails have fusiform, slender to broad ovate shells, of small to medium size, moderately sculptured from cancellate to smooth surface with a shortened siphonal canal (Cernohorsky, 1984). Distributed worldwide and with greater diversity of taxa in the Indo-Pacific region (Cernohorsky, 1984), nassariids are mostly found in shallow marine soft bottoms, except few species that live in mesohaline and even in freshwater conditions (Kantor & Kilburn, 2001; Strong *et al.*, 2008, 2017; Neiber & Glaubrecht, 2019).

In the past century, classifications of family Nassariidae were based solely on shell and radula characters. The first thorough classification based on the shape of the shell columella divided Nassariidae into three subfamilies: Dorsaniinae, Cylleninae and the cosmopolitan Nassariinae (Cossmann, 1901). This division of Nassariidae into three subfamilies was accepted for many years (Cernohorsky, 1984) until several genera previously included in Dorsaniinae were removed to establish the new subfamily Bulliinae (Allmon, 1990). However, due to the putative homoplasy of many morphological characters, the internal classification of Nassariidae and the accepted boundary between Nassariidae and Buccinidae were deemed to need a thorough revision (Haasl, 2000; Kantor, 2003).

More recently, the application of molecular markers helped clarifying the phylogenetic relationships of Nassariidae. Using the DNA sequences of three mitochondrial (*cox1*, *rrnL* and *rrnS*) and two nuclear (*28S* and *H3*) fragments, Galindo *et al.* (2016) reconstructed the most comprehensive phylogeny of Nassariidae to date (including > 200 species) and revisited nassariid

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4 64 systematics. At the family and subfamily levels, several genera (*Antillophos*, *Engoniophos*, *Phos*,
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6 65 *Nassaria*, *Tomlinia* and *Anentome*), which were previously considered as members of the closely
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9 66 related family Buccinidae, were reassigned into Nassariidae, leading to the classification of this
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11
12 67 later family into seven subfamilies (Photinae, Dorsaniinae, Cylleninae, Bulliinae, Buccinanopsinae,
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14 68 Anentominae, and Nassariinae; Bouchet *et al.*, 2017). Within the cosmopolitan Nassariinae, five
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17 69 genera were redefined corresponding to five clades in the phylogeny with distinct geographical
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20 70 distributions (Galindo *et al.* 2016), including the Indo-Pacific genera *Nassarius* (Yang *et al.*, 2019)
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22 71 and *Reticunassa* (the 'pauper-complex' *sensu* Kool and Dekker, 2006, 2007; Galindo *et al.*, 2017);
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25 72 the mostly East Atlantic-Mediterranean genus *Tritia* (Yang *et al.*, 2021); the (East and West)
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27 73 African genus *Naytia*; and the Caribbean-Panamanian genus *Phrontis*.

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30 74 Later, Strong *et al.* (2017) revised the systematics of genus *Anentome* (Anentominae) and
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32
33 75 considered that this freshwater taxon was a complex of at least four molecularly and
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35 76 morphologically distinct species. Moreover, the brackish-water genus *Nassodonta* (Anentominae)
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38 77 was found to be polyphyletic (Neiber & Glaubrecht, 2019), with *Nassodonta insignis* (H. Adams,
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40 78 1867; type species of the genus) from the southwestern coastal region of India (Jayachandran *et al.*,
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43 79 2018) clustering with *Tritia reticulata* (Linnaeus, 1758), instead of with the congeneric *Nassodonta*
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45
46 80 *dorri* (Wattebled, 1886) from Vietnam, which was hence reassigned to the new genus
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48 81 *Oligohalinophila* (Neiber & Glaubrecht, 2019) i.e., *Oligohalinophila dorri* (Wattebled, 1886).
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51 82 Furthermore, the mitogenomic phylogeny of genus *Tritia* by Yang *et al.* (2021) recovered the
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54 83 Northwest Atlantic species *Ilyanassa obsoleta* (Say, 1822) as sister to the mostly East
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56 84 Atlantic/Mediterranean species within the genus, prompting the reinstatement of the genus
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59 85 *Ilyanassa*. Finally, a phylogeny of Buccinoidea by Kantor *et al.* (2022) revealed a distant
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relationship between genera *Tomlinia* + *Nassaria* and genus *Cyllene*, and hence the former two genera were removed from Cylleninae to the new subfamily Tomliniinae. In addition, Buccinanopsinae was ranked to Buccinanopsidae, since it was not recovered within Nassariidae (Kantor *et al.*, 2022).

The above-mentioned studies revealed on the one hand that traditional nassariid taxonomy based on morphological traits was rather inconsistent with molecular phylogenies (Pastorino & Simone, 2021), but also on the other hand that mitochondrial and nuclear partial nucleotide sequences failed to resolve with strong statistical support the deeper nodes within Buccinoidea and Nassariidae phylogenies, often rendering contradicting results. For instance, Strong *et al.* (2017) recovered genus *Anentome* sister to genus *Nassodonta*, whereas according to Galindo *et al.* (2016) these two genera were two isolated offshoots within Nassariidae (but note that both alternative phylogenetic hypotheses received low support values in each study). Similarly, in the phylogeny of Buccinoidea by Kantor *et al.* (2022), the family Columbellidae clustered within the clade formed by subfamilies Cylleninae and Tomliniinae, thus rendering Nassariidae paraphyletic. In short, the various flaws found in previous molecular studies indicate that phylogenetic relationships of Nassariidae remain rather unresolved and still plagued by uncertainty.

Complete mitochondrial (mt) genomes have proven to be useful molecular markers for reconstructing relatively highly resolved phylogenies at the family and superfamily levels, and have been already applied to different buccinoid groups within Nassariidae (Yang *et al.* 2019; 2021) and Buccinidae (Vaux *et al.* 2017). At present, the complete or near-complete mitogenomes of 39 nassariid species, restricted to subfamilies Nassariinae and Anentominae, are available in GenBank. Here, we sequenced the nearly complete mt genomes of another 31 species, representing six out of

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4 108 the seven subfamilies of Nassariidae proposed by Kantor *et al.* (2022) (except for Dorsaninae, today
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6 109 restricted to the single species *Dorsanum miran* (Bruguière, 1789) from West Africa), as well as
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9 110 other buccinoid outgroups. We aimed at (1) delimiting Nassariidae within Buccinoidea and
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12 111 confirming the phylogenetic placements of major lineages within this family; (2) improving the
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14 112 resolution of phylogenetic relationships within the cosmopolitan Nassariinae; and (3) dating major
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17 113 cladogenetic events involving geographical structuring of genera within Nassariinae.
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22 115 MATERIALS AND METHODS

25 116 *Samples and DNA extraction*

27 117 The complete list of specimens analyzed in the present study, including their sampling sites and
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30 118 museum vouchers, is shown in Table 1. All samples were stored in 100% ethanol and total genomic
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33 119 DNA was isolated from about 25 mg of foot tissue using the DNeasy Blood & Tissue Kit (Qiagen,
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35 120 Germany).
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40 122 *PCR amplification and sequencing of mt genomes*

43 123 Nearly complete (without the control region) mt genomes were amplified through long PCRs using
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46 124 a combination of three/ four primer pairs (see Suppl. Mat. Table S1), which were designed in a
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48 125 previous study (Yang *et al.*, 2021). The long PCR reactions contained 2.5 µl of 10× buffer (Mg²⁺
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51 126 plus), 3 µl of dNTPs (2.5 mM), 0.5 µl of each primer (10 µM), 0.8 µl of template DNA (25-40
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53 127 ng/µl), 0.2 µl of TaKaRa LA Taq DNA polymerase (5 U/µl), 0.2 µl of BSA (10 mg/ml) and DEPC
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56 128 water up to 25 µl. The following PCR conditions were used: initial denaturing step at 94 °C for 60
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59 129 s; 45 cycles of denaturing at 98 °C for 10 s, annealing at 53-56 °C for 30 s, and extension at 68 °C
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for 60 s per kb; and a final extension step at 68 °C for 10 min. Long PCR products were purified by ethanol precipitation, and fragments from the same mitogenome were pooled together in equimolar concentrations for high-throughput sequencing. For each mitogenome, a separate indexed library was constructed using the NEXTERA XT DNA library prep Kit (Illumina, San Diego, CA, USA) and run (together with indexed libraries from other sequencing projects of unrelated species) in an Illumina MiSeq platform (2 × 150 paired-end) at AllGenetics (A Coruña, Spain) and NIMGenetics (Madrid, Spain).

Sequence gaps in some mitogenomes were filled out through standard PCRs, which were carried out in a total volume of 25 µl with 1 µl of template DNA (25-40 ng/µl), 2.5 µl of 10× buffer (Mg²⁺ plus), 0.5 µl of dNTPs (2.5 mM), 0.5 µl of each primer (10 µM), 0.2 µl of Taq DNA polymerase (5 U/µl), 0.25µl of BSA (10 mg/ml) and 19.55 µl of DEPC water. The PCR conditions were as follows: an initial denaturing step at 94 °C for 5 min; 40 cycles of denaturing at 94 °C for 60 s, annealing at 39-48°C for 60 s, and extension at 72 °C for 90 s; and a final extension step at 72°C for 10 min. Standard-PCR products were purified by ethanol precipitation, and Sanger sequenced at Macrogen (Seoul, Korea). Information on standard PCR primers is shown in Suppl. Mat. Table S1.

Mitogenome assembly and annotation

The Sanger sequences were assembled using Sequencher 5.0.1. For some of the specimens, the already reported *cox1* sequences were downloaded from Genbank (Suppl. Mat. Table S1). For Illumina sequence data, the reads corresponding to different individuals were sorted by the corresponding library indices. The reads corresponding to each mt genome were cleaned following

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4 152 Abalde *et al.* (2017) and assembled using Geneious Prime 2019.0.3 (Kearse *et al.*, 2012). The
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6 153 mitogenomes were constructed by repeatedly mapping the clean reads (setting a minimum identity
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9 154 of 99%) to contigs that elongated from the Sanger fragments of the same mitogenome.
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12 155 The newly determined mt genomes were annotated using Geneious Prime 2019.0.3.
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14 156 Annotations of the 13 protein-coding genes (PCGs) were defined by setting a limit of 75%
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17 157 nucleotide identity to previously published nassariid mitogenomes (Table 1), and further
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20 158 corroborated using the MITOS Webserver (Bernt *et al.*, 2013) with the Invertebrate Mitochondrial
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22 159 genetic code. The transfer RNA (tRNA) genes were identified using tRNA scan-SE 1.21 (Schattner
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25 160 *et al.*, 2005) and ARWEN (Laslett & Canbäck, 2008). The ribosomal RNA (rRNA) genes were
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27 161 identified by comparison with other nassariid mt genomes, and their boundaries were assumed to be
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30 162 between the adjacent genes.
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33 164 *Sequence alignment*

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38 165 The newly sequenced mitogenomes were aligned along with those of other buccinoids available in
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40 166 Genbank (Table 1). Two datasets were constructed and analyzed following Uribe *et al.* (2017). The
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42
43 167 first data set (hereafter referred to as the Nassariidae data set) was aimed at testing the monophyly
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46 168 of Nassariidae and included main lineages within the family as well as closely related members of
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48 169 buccinoid families. The species *Crassicantharus noumeensis* (Crosse, 1870; family Dolicholatiridae
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50
51 170 after Kantor *et al.*, 2022) and *Belomitra viridis* (Okutani, 1966; family Belomitridae) were used as
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53 171 outgroup, following Kantor *et al.* (2022). The Nassariidae data set was comprised of the deduced
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55
56 172 amino acid sequences of the 13 mt PCGs and the nucleotide sequences of the two rRNA genes. The
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58
59 173 second data set (hereafter referred to as the Nassariinae data set) was aimed at reconstructing the
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4 174 internal phylogenetic relationships within Nassariinae, using five species of the genus *Bullia*
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6 175 (subfamily Bulliinae) as outgroup taxa. This data set included the nucleotide sequences of the 13 mt
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9 176 PCGs and the two rRNA genes.

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12 177 For each data set, the deduced amino acid sequences of the 13 PCGs were aligned separately
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14 178 and used to guide the alignment of the corresponding nucleotide sequences with Translator X
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17 179 (Abascal *et al.*, 2010), using the Invertebrate Mitochondrial genetic code. The nucleotide sequences
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20 180 of the rRNA genes were aligned separately using MAFFT v7 (Kato & Standley, 2013) with default
21
22 181 parameters. Ambiguously aligned positions were removed using Gblocks v.0.91b (Castresana,
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24
25 182 2000) with the following settings: minimum sequence for flanking positions: 85%; maximum
26
27 183 contiguous non-conserved positions: 8; minimum block length: 10; gaps in final blocks: no. Finally,
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29
30 184 the different single gene alignments were concatenated into a single data set in Geneious Prime
31
32
33 185 2019.0.3. Sequences were converted into different formats for further analyses using DAMBE5
34
35 186 (Xia, 2013).

36 37 38 187 39 40 188 *Phylogenetic analyses*

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43 189 Phylogenetic trees were reconstructed under maximum likelihood (ML; Felsenstein, 1981) and
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45
46 190 Bayesian inference (BI; Huelsenbeck & Ronquist, 2001) using the CIPRES Science Gateway v.3.3
47
48 191 (Miller *et al.*, 2010). ML analyses were carried out using RAxML-HPC2 on XSEDE (Stamatakis,
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50
51 192 2006) with the rapid bootstrap algorithm and 1000 replicates. BI analyses were conducted with
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53 193 MrBayes on XSEDE (3.2.6; Ronquist & Huelsenbeck, 2003), running four simultaneous Monte
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56 194 Carlo Markov chains (MCMC) for 10,000,000 generations, sampling every 1,000 generations, and
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59 195 discarding the first 25% generations as burn-in. Two independent Bayesian inference runs were
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4 196 performed to increase the chance of adequate mixing of the Markov chains and of detecting failure
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6
7 197 to converge, as determined by using Tracer v1.6. The effective sample size (ESS) of all parameters
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9 198 was more than 200. The resulting phylogenetic trees were visualized in FigTree v1.4.2.
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11
12 199 The best partition schemes and best-fit substitution models for the two data sets were
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14 200 determined using PartitionFinder 2 (Lanfear *et al.*, 2017), under the Bayesian Information Criterion
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17 201 (BIC; Schwarz 1978). For PCGs of the Nassariidae data set (analyzed at the amino acid level) and
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19
20 202 of the Nassariinae data set (analyzed at the nucleotide level), the partitions tested were: all genes
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22 203 combined; all genes separated (except *atp6-atp8* and *nad4-nad4L*); and genes grouped by
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25 204 enzymatic complexes (*atp*, *cob*, *cox* and *nad*). Additionally, the three partition schemes were tested
26
27 205 considering separately the three codon positions. The rRNA genes were analyzed with two different
28
29
30 206 schemes (genes grouped or separated). The best best-fit substitution models of the two data sets are
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32
33 207 provided in Suppl. Mat. Table S2.
34

35 208 36 37 38 209 *Reconstruction of ancestral geographical distributions*

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40 210 Biogeographical inferences were performed with an ancestral character state reconstruction in
41
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43 211 Mesquite v3.6.1 (Maddison & Maddison, 2018) using the Tracing Character History option under
44
45
46 212 ML and mapping onto the topology inferred by the ML analysis. The distribution range of each
47
48 213 species was derived from previous reviews (Cernohorsky, 1975 1984; Allmon, 1990; Galindo *et al.*,
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51 214 2016; Gofas *et al.*, 2017, among others).
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53 215 54 55 56 216 *Estimation of divergence times* 57 58 59 60

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4 217 BEAST v.1.10.4 (Drummond & Rambaut, 2007) was used to perform a Bayesian estimation of
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6 218 divergence times only among genera within Nassariinae (based on the Nassariinae dataset) given
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9 219 that the other lineages previously considered as part of the Nassariidae were distantly recovered in
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11
12 220 the buccinoid tree (see results). An uncorrelated relaxed molecular clock was used to infer branch
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14 221 lengths and node ages. The tree topology was fixed using the one recovered by the BI analysis. For
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17 222 the clock model, the lognormal relaxed-clock model was selected, which allows rates to vary
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20 223 among branches without any *a priori* assumption of autocorrelation between adjacent branches. For
21
22 224 the tree prior, a Yule process of speciation was employed. The partitions selected by PartitionFinder
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25 225 2 (see above) were applied. The Markov chain was run twice for 100 million generations, sampling
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27 226 every 10,000 generations and discarding the first 10 million as burn-in, according to the
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29
30 227 convergence of chains checked with Tracer v.1.6. The effective sample size of all the parameters
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32
33 228 was above 200.

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35 229 The posterior distribution of the estimated divergence times was obtained by specifying two
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38 230 calibration points, which were based on fossil records as priors for divergence times of the
39
40 231 corresponding splits. The first calibration point was set at the origin of *Tritia*. A lognormal
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43 232 distribution was applied, with the minimum of 23 Mya and a 95% upper limit of 28.4 Mya (offset:
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45
46 233 23; mean: 1.9; standard deviation: 1.9) based on the species *Nassarius (Hinia) pygmaea* (von
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48 234 Schlotheim, 1820) from Germany (Albright *et al.*, 2019) and *Nassarius (Hinia) schlotheimi*
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51 235 (Beyrich, 1854) from Hungary (Báldi, 1973), both from the Upper Oligocene (Chattian; 28.4 - 23.0
52
53 236 Mya), the oldest Nassariinae fossils in Europe. A second calibration point was set at the root of the
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56 237 tree. A lognormal distribution was applied, with the minimum of 55.8 Mya and a 95% upper limit
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59 238 of 58.7 Mya (offset: 55.8; mean: 1.0; standard deviation: 1.0) based on the oldest known
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4 239 Nassariinae fossil, which is *Buccitriton sagemum* (Conrad, 1833) from the Paleocene (Thanetian;
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6 240 58.7 - 55.8 Mya) of Louisiana (Glawe *et al.*, 2014).
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11 RESULTS

14 243 *Sequencing, assembly and genome organization*

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17 244 The number of reads, mean coverage, length, and accession number in Genbank of each newly
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19 245 sequenced mitogenome are provided in Table 1. The mt genomes of *Bullia* sp. and *Cyllene parvula*
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21
22 246 Bozzetti, 2014 (family Nassariidae) received the minimum (23,590) and maximum (2,142,544)
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24
25 247 reads, respectively. Those of *Peristernia marquesana* (A. Adams, 1855; family Fasciolaridae) and
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27 248 *Cyllene parvula* received the minimum (20 ×) and maximum (16,095 ×) coverage, respectively
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29
30 249 (Table 1).
31

32 250 All mitogenomes encoded for 13 PCGs, two rRNA and 22 tRNA genes (but note that all
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34
35 251 lacked the sequences of the *trnF* gene, the control region, and the start of the *cox3* gene because the
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37
38 252 corresponding fragment could not be PCR amplified; see annotation of each mt genome in Suppl.
39
40 253 Mat. Table S3). They all shared the same consensus genome organization described for
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43 254 Caenogastropoda (Osca *et al.*, 2015), with most genes encoded by the major strand and a cluster of
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46 255 tRNA genes (*trnM*, *trnY*, *trnC*, *trnW*, *trnQ*, *trnG*, *trnE*) and the *trnT* gene encoded by the minor
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48 256 strand.
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53 258 *Phylogenetic relationships of Nassariidae within Buccinoidea*

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56 259 The monophyly and phylogenetic relationships of Nassariidae within Buccinoidea (Fig. 1) were
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59 260 analyzed based on the Nassariidae data set using probabilistic methods and *C. noumeensis*,
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4 261 (Dolicholatiridae) sister to *B. viridis* (Belomitridae) as outgroup. The final matrix was 5,120
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7 262 positions in length. The best partition scheme for the amino acid sequences of PCGs was combining
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9 263 genes by subunits, whereas that for the nucleotide sequences of rRNA genes was combining *rrnL*
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12 264 and *rrnS* genes. Both ML ($-\ln L = 86830.23$) and BI ($-\ln L = 87375.33$ for run1; $-\ln L = 87376.87$ for
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14 265 run2) arrived at similar topologies that only differed in some internal relationships within
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17 266 Buccinidae and Nassariinae (Fig. 1). In the reconstructed phylogeny, the family Nassariidae was not
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19
20 267 monophyletic because some of the taxa previously considered as nassariids were recovered in five
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22 268 distant lineages in the tree: (1) the freshwater *Anentome* sp. was recovered sister to a clade
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25 269 including (2) *Cyllene* plus the remaining buccinoids to the exclusion of family Belomitridae (the
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27 270 earliest offshoot in the ingroup), with maximum statistical support; (3) *Tomlinia fraussenii* Thach,
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30 271 2014 was recovered as sister to *Nassaria* sp. with maximum support, and both grouped together
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33 272 with family Columbelloidea (only strongly supported by BI, Fig. 1); and (4) the highly supported
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35 273 group formed by *Engoniophos uncinatus* (Say, 1826) + (*Phos hirasei* G.B. Sowerby III, 1913 +
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38 274 (*Phos cf. roseatus* Hinds, 1844 and *Antillophos chazaliei* (Dautzenberg, 1900))) clustered with a
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41 275 clade including (5) *Buccinanops* sister to family Buccinidae (with maximum BPP value and
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43 276 moderately high BP value of 77%), and both groups with the cosmopolitan Nassariinae but this
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46 277 later node received low statistical support (Fig. 1).

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51 279 *Phylogenetic relationships of Nassariinae*

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53 280 In order to further clarify phylogenetic relationships within Nassariinae, the Nassariinae data set
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56 281 was reconstructed and analyzed with probabilistic methods using genus *Bullia* as outgroup (Fig. 2).
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59 282 The final matrix was 12,587 positions in length. The best partition schemes for the PCGs and rRNA
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4 283 genes analyzed at the nucleotide level were combining genes by subunits but analyzing each codon
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7 284 position separately and combining *rrnL* and *rrnS* genes, respectively (Suppl. Mat. Table S2). Both
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9 285 ML ($-\ln L = 175,595.22$) and BI ($-\ln L = 172,291.41$ for run1; $-\ln L = 172,295.27$ for run2) arrived at
10
11
12 286 almost identical topologies, only differing in the internal relationships within *Nassarius* (Fig. 2).
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14 287 The reconstructed phylogeny divided Nassariinae into seven lineages: (1) *Nassarius jacksonianus*
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17 288 (Quoy & Gaimard, 1833) and *Nassarius* sp.; (2) *Reticunassa*; (3) *Naytia*, (including *Tritia vaucheri*;
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20 289 (Pallary, 1906)); (4) *Phrontis*; (5) *Nassarius*; (6) *Ilyanassa*; and (7) *Tritia* (Fig. 2).
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25 291 *Biogeographical origin and divergence times*

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27 292 The main lineages (i.e., genera) within Nassariinae showed distinct geographical distributions. An
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30 293 ancestral reconstruction analysis under ML inferred and Indo-Pacific origin for the subfamily (Fig.
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33 294 3), Major cladogenetic events within Nassariinae were dated using an uncorrelated relaxed
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35 295 molecular clock, which was calibrated using two fossils. The origin of subfamily Nassariinae was
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38 296 dated in the Paleocene at a mean of 56.5 (58.2–55.8, credible interval) million years ago (Mya).
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40 297 Within Nassariinae, the first divergence was dated in the Eocene/ Oligocene transition at 37.3
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43 298 (43.0–32.8) Mya, separating the Indo-Pacific groups (*Nassarius jacksonianus* and *Nassarius* sp.) +
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46 299 *Reticunassa* from the remaining nassariids. The divergences separating the western African genus
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48 300 *Naytia*, the Caribbean-Panamic *Phrontis*, and the Indo-Pacific group *Nassarius* plus *Tritia* and
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51 301 *Ilyanassa* were dated at 32.0 (36.3–28.6), 29.8 (33.7–26.5) and 24.2 (26.8–23.2) Mya, respectively.
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53 302 Further, the divergence between the Northwest Atlantic *Ilyanassa* and the Northeast
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56 303 Atlantic/Mediterranean genus *Tritia* was dated at 22.1 (24.8–20.0) Mya. Finally, the main
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59 304 diversification events within the above-mentioned genera occurred during the Miocene (Fig. 4).
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DISCUSSION

Phylogenetic relationships of Nassariidae within Buccinoidea

The recent classification of Buccinoidea by Kantor *et al.* (2022) confirmed the monophyly of most families except for Buccinidae, which was completely revised and redefined, and for Nassariidae, which remained open to further revision. Even though some buccinid-like species were reassigned to Nassariidae following the phylogenies of Galindo *et al.* (2016) and Kantor *et al.* (2022), there is still no morphological synapomorphy to define the boundary of this family.

Among the seven subfamilies recently assigned to Nassariidae (Kantor *et al.*, 2022), all but Dorsaninae were included in our phylogeny. In contrast to the most comprehensive phylogenetic study to date based on partial gene sequences (Galindo *et al.*, 2016), the monophyly of Nassariidae as currently proposed (Kantor *et al.*, 2022; WoRMS, 2024), was not recovered here, as species of the subfamilies Photinae, Cylleninae, Anentominae and Tomliniinae fell outside the majority of nassariids, made up by subfamilies Nassariinae and Bulliinae. It should be noted that Kantor *et al.* (2022) recovered Nassariinae + Dorsaniinae with strong support. Bulliinae and Anentominae were sister to that clade but without statistical support in ML. The next sister clade included Cylleninae, Tomliniinae and Columbelloidea, but had no statistical support and rendered Nassariidae, as currently understood, paraphyletic (unless Columbelloidea are considered one more subfamily of Nassariidae). Finally, the subfamily Photinae was recovered as the earliest offshoot of the Nassariidae.

In the phylogeny here reconstructed, the freshwater species *Anentome* sp. (Anentominae) was recovered as an early offshoot of the superfamily Buccinoidea (Fig. 1), contradicting previous

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4 327 studies that supported *Anentome* to be classified into Buccinidae (Strong *et al.* 2008) or Nassariidae
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6 328 (Galindo *et al.*, 2016). The assassin snail *Anentome helena* (von dem Busch, 1847) was found to
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9 329 comprise a group of molecularly and morphologically distinct taxonomical species (including the
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12 330 *Anentome* sp. of our study) that were sister to the estuarine *O. dorri* (Strong *et al.*, 2017). The latter
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14 331 was previously classified in the genus *Nassodonta*, whereas according to Neiber & Glaubrecht
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17 332 (2019), the type species *Nassodonta insignis* H. Adams, 1867 resulted more closely related to the
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20 333 Nassariinae than to the Anentominae, despite of the low support values they obtained.

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22 334 Represented by *Cyllene parvula* Bozzetti, 2014 and *Cyllene lamarcki* Cernohorsky, 1975 in
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25 335 our phylogenetic analysis, Cylleninae showed a distant relationship with Nassariinae + *Bullia* with
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27 336 moderate support values, and was placed in a second offshoot of the superfamily Buccinoidea after
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30 337 Anemontinae. The genus *Cyllene* is distributed in Western Africa and the Indo-Pacific Ocean, and
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33 338 was considered as the only genus of Cylleninae (Allmon, 1990; Cernohorsky, 1984) until Galindo
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35 339 *et al.* (2016) included *Trajana*, *Nassaria* and *Tomlinia* into this subfamily. However, the affinity of
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38 340 *Tomlinia* and *Cyllene* was not recovered here, hence contradicting both Galindo *et al.* (2016) as
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41 341 well as Strong *et al.* (2017), who recovered *Cyllene* sister to Photinae; Kantor *et al.* (2022), in which
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43 342 *Cyllene* was sister to Columbelloidea, and both to *Tomlinia* but without support; deMaintenon &
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46 343 Strong (2022), who recovered Cylleninae sister to Columbelloidea, and both to Photinae but without
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48 344 support. Therefore, the position of Cyllenidae varies in the different molecular phylogenies (even in
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51 345 those using the same five partial gene sequences) and its systematic allocation remains uncertain.

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53 346 The brackish water species *Tomlinia fraussenii* Thach, 2014, which is only found in estuaries
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56 347 in Vietnam (Thach, 2014), was recovered as sister to a representative of *Nassaria* (Fig. 1), which is
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59 348 a diversified marine genus distributed in the Indo-Pacific region (Cernohorsky, 1981). In recent
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phylogenies (Galindo *et al.*, 2016; Strong *et al.*, 2017; Kantor *et al.*, 2022), *T. fraussenii* also clustered with *Nassaria*. However, while both genera were recovered sister to *Cyllene* by Galindo *et al.* (2016) and Strong *et al.* (2017), and hence included in Cylleninae by them, Kantor *et al.* (2022) removed *Nassaria*, *Trajana* and *Tomlinia* from Cylleninae to a newly established subfamily Tomliniinae. In our phylogenetic analysis, *Tomlinia* plus *Nassaria* were recovered sister to Columbelloidea only with strong support in BI analysis. The distant phylogenetic positions of *Anentome* sp. and *Tomlinia fraussenii* indicate that at least these freshwater invasions happened independently within Buccinoidea, and pending elucidation of the phylogenetic position of other freshwater taxa from south-east Asia (*Clea*, *Nassodonta*, and *Oligohalinophila*) that were not included here.

The subfamily Photinae, represented by the monospecific genus *Engoniophos* (from the Caribbean), *Phos* (diversified in the Indo-Pacific) and *Antillophos* (present on both sides of the Atlantic but mostly diversified in the Western side) in our phylogenetic analysis, was grouped with Buccinidae (with maximum support value of BI and moderate support value of ML). This result contradicted the affinity of Photinae to Nassariidae obtained by Galindo *et al.* (2016) and Kantor *et al.* (2022), as well as the anatomical argumentation provided by Abatte *et al.* (2018) for *Engoniophos uncinatus* (Say, 1826), despite they noted some disparities with typical nassariids. In any case, Photinae was recovered by Galindo *et al.* (2016), Strong *et al.* (2017) and Kantor *et al.* (2022) as a first offshoot, sister to the remaining taxa they considered Nassariidae. Moreover, the phylogenetic position of Photinae within Nassariidae was already questioned by other phylogenetic studies. For example, in the phylogeny of Zou *et al.* (2011) based on five partial gene sequences, the genus *Phos* was recovered in a distant position from Nassariidae (there represented by the

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371 Indo-Pacific genus *Nassarius*) with well-supported values. Likewise, Waters (2009) included
372 *Antillophos* within the subfamily Pisaninae (Buccinidae). Furthermore, most members in Photinae
373 (except for *Engoniophos*) are characterized by paucicuspid rachidian teeth, a character state shared
374 with most species of Buccinidae, what is in agreement with the close relationship of Photinae and
375 Buccinidae in our phylogeny.

376 The close sister group relationship of Nassariinae and *Bullia* (Bulliinae) was highly supported
377 in our phylogeny, and represents another inconsistency with previous studies that placed *Bullia* in a
378 more distant position with respect to Nassariinae (Haasl, 2000; Galindo *et al.*, 2016; Kantor *et al.*,
379 2022). The southern hemisphere *Bullia*, together with the South American *Buccinanops* and the
380 West African *Dorsanum*, were traditionally included in the subfamily Dorsaninae based on
381 morphological characteristics (Cernohorsky, 1984). Moreover, recently, the new genus
382 *Buccinastrum* was split from *Buccinanops* and also added to this group based on anatomical studies
383 (Pastorino & Simone, 2021). However, according to reported molecular phylogenies (Galindo *et al.*,
384 2016; Kantor *et al.*, 2022; present study), the synapomorphies that define the group should be
385 considered a case of convergence (and thus homoplastic characters for phylogenetic
386 reconstruction). Previous molecular phylogenies prompted the exclusion of *Buccinanops* and *Bullia*
387 from Dorsaninae. Galindo *et al.* (2016) supported *Buccinanops* as a monogeneric subfamily
388 (Buccinanopsinae) within Nassariidae, whereas Kantor *et al.* (2022) proposed *Buccinanops* as a
389 separate family, Buccinanopsidae, only distantly related to Nassariidae. In our phylogeny,
390 *Buccinanops* was recovered sister to Buccinidae (with moderate and maximal support in ML and
391 BI, respectively), supporting Buccinanopsidae as a separate family (Kantor *et al.* 2022).

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392 As a conclusion, we agree with Kantor et al. (2022) considering Buccinanopsidae as a
393 separate family. On the other hand, our phylogeny recovers the subfamilies Photinae, Cylleninae,
394 Anentominae and Tomliniinae as distantly related to subfamilies Nassariinae and Bulliinae.
395 Although we have not included any species of Dorsaninae in our analysis, this subfamily has been
396 always placed with strong support within this Nassariidae in previous phylogenies. Although
397 several key nodes in the phylogeny here reconstructed (node recovering Collumbellidae sister to
398 Tomliniinae; node recovering Photinae sister to Buccinanopsidae plus Buccinidae, Cominellidae,
399 Tudicidae, and Austrosiphonidae; node connecting the latter to Bullia + Nassariinae to the
400 exclusion of several families and in particular, subfamilies Cylleninae and Anentominae) received
401 relatively strong support, others did not, and the long branch of Collumbellidae may be introducing
402 serious bias in the final reconstructed topology, what prevents us for suggesting further
403 nomenclatural changes until new studies base on nuclear genomic data are performed.

405 *Phylogenetic relationships of Nassariinae*

406 The phylogenetic relationships of Nassariinae were well resolved, with seven main lineages
407 recognized. The first offshoot of the tree showed the Indo-Pacific '*Nassarius*' *jascksonianus* (Quoy
408 & Gaimard, 1833) and '*Nassarius*' sp. (incorrectly identified as *Nassarius acuticostus*
409 (Montrouzier, 1864) in Yang *et al.*, 2019; see Yang *et al.*, 2021) sister to the sympatric *Reticunassa*,
410 as previously suggested (Yang *et al.*, 2019; 2021). Both morphological and molecular differences
411 between *Reticunassa* and '*Nassarius*' *jascksonianus* + '*Nassarius*' sp. support the establishment of
412 a new genus for the latter clade, which relies on a larger taxon sampling and thorough
413 morphological revision beyond the scope of this study. *Reticunassa* was elevated to full genus rank

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4 414 by Galindo *et al.* (2017) to include the species of the so-called “*Nassarius pauper* complex”. The
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6 415 type species of the genus is *Reticunassa paupera* (A. Gould, 1850), which was recovered in the
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9 416 same clade as *Nassarius festivus* (Powys, 1835; see Galindo *et al.*, 2016; Liu & Yang, 2021), which
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12 417 prompts its inclusion in genus *Reticunassa* along with *Nassarius fraterculus* (Dunker, 1860) and
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14 418 *Nassarius hiradoensis* (Pilsbry, 1904), within the first offshoot of the Nassariinae. This genus has
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17 419 experienced high diversification in the Western Pacific (Galindo *et al.*, 2017; Zhang *et al.*, 2022).
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20 420 The next lineage branching off in the phylogeny was the African genus *Naytia* (Fig. 2), which
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22 421 is characterized by high morphological disparity (Galindo *et al.*, 2016). While the type species,
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25 422 *Naytia glabrata* (G.B. Sowerby II, 1842) exhibits a smooth shell (also *Naytia granulosa* (Lamarck,
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27 423 1822) not included here), *Naytia priscardi* Bozzetti, 2006, *Naytia vaucheri* and *Naytia johni*
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30 424 (Monterosato, 1889) (not included here) are characterized by a reticulate shell sculpture.

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33 425 Geographically, *N. vaucheri* is found in the southwestern Spanish Mediterranean and the nearby
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35 426 Atlantic coasts (Gofas, 2011). Since the distribution of *N. vaucheri* is partially sympatric with
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38 427 several species of the North-east Atlantic/Mediterranean *Tritia*, and it is morphologically similar to
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40 428 *Tritia incrassata* (Strøm, 1768), it had been erroneously assigned to *Tritia* until Yang *et al.* (2021)
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43 429 recovered a distant phylogenetic relationship between them. Here, we clearly assign this species to
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46 430 genus *Naytia*. This result does not reveal any consistency between the molecular phylogeny and
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48 431 shell sculpture as pointed out by Yang *et al.* (2021). Interestingly, *N. vaucheri* is sympatric with *N.*
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51 432 *johni*. Another species that may belong to this clade is *Nassarius argenteus* (Marrat, 1877) from
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53 433 Mauritania, which is very similar, if not conspecific to *N. vaucheri*. According to Galindo *et al.*
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56 434 (2016), molecular data seem to be the only source of support to group these species within the same
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59 435 genus.
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The remaining taxa included in the phylogeny formed a clade in which *Phrontis* was recovered sister to *Nassarius* plus *Tritia* and *Ilyanassa*. According to Galindo *et al.* (2016), the genus *Phrontis*, restricted to the Caribbean-Panamic region, is the result of a re-invasion of nassariids into American coasts after the *Buccinanops* and Photinae radiations. The phylogenetic relationships of *Tritia* + *Ilyanassa* were discussed in a previous study (Yang *et al.*, 2021) that re-established the validity of the latter genus. The present results corroborate previous ones. The mostly northeast Atlantic / Mediterranean *Tritia* form a natural group divided into two main clades. The first clade includes *Tritia cuvierii* (Payraudeau, 1826), *Tritia tenuicosta* (Bucquoy, Dautzenberg & Dollfus, 1882), *Tritia unifasciata* (Kiener, 1834), *Tritia nitida* (Jeffreys, 1867), *Tritia denticulata* (A. Adams, 1852), *Tritia ephamilla* (R. B. Watson, 1882), *Tritia elata* (A. Gould, 1845) and *Tritia reticulata* (Linnaeus, 1758).. This latter is the type species of the genus, and thus the species of this clade are those that must be retained within genus *Tritia*. Other species not studied here but that should be kept in this genus are: *T. lanceolata* (Bucquoy, Dautzenberg & Dollfus, 1882) and *T. djerbaensis* Aissaoui, Galindo, Puillandre & Bouchet, 2017 (endemic to the Gulf of Gabès), close to *T. unifasciata* according to Aissaoui *et al.* (2017); *T. miga* (Bruguère, 1789) and *T. caboverdensis* (Rolán, 1984) (both from West Africa), close to *T. cuvierii* (Galindo *et al.*, 2016; Rolán, 1984), and the West African species of the group of *T. denticulata* according to Rolán & Hernández (2005), i.e., *Tritia turbinea* (A. Gould, 1845), *T. webbei* (Petit de la Saussaye, 1850), *T. clathrata* (Born, 1778), *T. desmoulioides* (G.B. Sowerby III, 1903), *T. arcadioi* Rolán & Hernández, 2005 . The second clade (that could deserve a new putative genus) is composed by two subclades, one with species characterized by smooth shell, i.e., *Tritia neritea* (Linnaeus, 1758), *Tritia pellucida* (Risso, 1826), *Tritia mutabilis* (Linnaeus, 1758), *Tritia pfeifferi* (R.A. Philippi,

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4 458 1844), *Tritia corniculum* (Olivi, 1792), *Tritia pallaryana* Aissaoui, Galindo, Puillandre & Bouchet,
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6 459 2017, and *Tritia elongata* (Bucquoy, Dautzenberg & Dollfus, 1882); the other including *T.*
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9 460 *incrassata* and *T. varicosa* (W. Turton, 1825). Other extant species not studied here that should be
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12 461 included in the first subclade is *Tritia compersa* (R.A. Philippi, 1849), which according to Segers et
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14 462 al. (2008) replaces *Tritia pfeifferi* (R. A. Philippi, 1844) in Canary Islands. The second subclade
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17 463 should also include *Tritia varicosa* (W. Turton, 1825), *Tritia goreensis* (Maltzan, 1884), and *Tritia*
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19 464 *senegalensis* (Maltzan, 1884), since Galindo *et al.* (2016) recovered these last two species within
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22 465 this clade.
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25 466 The few species included from the species-rich genus *Nassarius* in our phylogeny preclude
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27 467 further discussion, as a separate phylogenetic analysis with a richer taxon sampling is needed. In
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30 468 addition to the above mentioned genera, three species-poor genera, *Nassodonta* from India, *Caesia*
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32 469 from America, and *Demoulia* from Africa were also included within Nassariinae by Kantor *et al.*
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35 470 (2022) based on morphological evidence. In fact, none of these three genera has been included in
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38 471 previous molecular phylogenies, *Nassodonta* was represented by '*Nassodonta*' *dorri* in Galindo *et*
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40 472 *al.* (2016) and Strong *et al.* (2017), which was later removed to *Oligohalinophila* by Neiber &
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43 473 Glaubrecht (2019). Hence, their placement within Nassariinae has yet to be tested.
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45 474 46 47 48 475 *Nassariinae diversification in light of phylogeny* 49

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51 476 A robust phylogeny of Nassariinae could help understanding how the global diversification of this
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53 477 cosmopolitan group occurred. In fact, our reconstructed molecular phylogeny of Nassariinae fits
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56 478 better to biogeography than those reconstructed based on morphology, as has been pointed out by
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58 479 Oyston *et al.* (2022) in other animal groups. The result of the biogeographical reconstruction and
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4 480 the molecular clock dating supported the hypothesis that Nassariinae originated from the
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7 481 Indo-Pacific region (Galindo *et al.*, 2016), back in the Paleocene, ~56 Mya. At that time is dated
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9 482 one of the most dramatic global warming events of the Cenozoic, the Paleocene-Eocene thermal
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12 483 maximum (PETM), which might have triggered diversification processes in Nassariidae and the
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14 484 origin of Nassariinae, as has been suggested for other marine organisms (Gingerich, 2006; Speijer
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17 485 *et al.*, 2012). The PETM caused substantial increases in sea-surface temperatures over a
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20 486 considerable time scale and has been linked to the emergence of several shallow-water associated
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22 487 marine species (Zolkaply *et al.*, 2021). This environmental change could also explain the first
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25 488 diversification of the Indo-Pacific lineage formed by *N. jacksonianus* and *Nassarius* sp. +
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27 489 *Reticunassa*, extending back to the late Eocene. Another two diversifications were dated back to the
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30 490 Oligocene, leading to the successive divergences of *Naytia* and *Phrontis*. During the early
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33 491 Oligocene, there was a dramatic cooling event in the northern Pacific. This climate change event
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35 492 caused a striking turnover of certain marine species (Kelly & Eernisse, 2008), and could have been
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38 493 involved in the divergence of the assumed tropical ancestors of both *Naytia* in Africa and *Phrontis*
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40 494 in the Caribbean-Panamic region. Finally, continental drift may account for the divergence of
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43 495 Indo-Pacific *Nassarius* and North Atlantic/Mediterranean *Tritia* plus North American *Ilyanassa*
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46 496 (Yang *et al.*, 2021). Altogether, these results support a major role of vicariant events in producing
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48 497 disjunct geographical distributions, which ultimately could have led to the astonishing global
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51 498 diversification of mud snails.

52 53 499 54 55 56 500 CONCLUSIONS 57 58 59 60

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4 501 Buccinoideans are an example of group in which convergent processes likely shaped most of the
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6 502 morphological diversity observed today and thus, resolving phylogenetic relationships within this
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9 503 superfamily necessarily requires reconstructing robust molecular phylogenies. The nodes with
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12 504 strong statistical support in the phylogeny of buccinoidean families here reconstructed suggest that
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14 505 genera *Cyllene*, *Anentome*, *Tomlinia*, *Engoniophos*, *Phos*, *Antillophos*, and *Buccinanops*, are only
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17 506 distantly related to Nassariinae and Bulliinae,. However, the internal nodes connecting the different
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20 507 families are rather short and their statistical support, particularly for ML inferences, is not high
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22 508 enough to lead to definitive conclusions. This pattern of short branches indicates rapid radiation
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25 509 processes at the origin and early diversification of the Buccionidea, which will require denser taxon
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27 510 sampling and gathering phylogenomic datasets to be resolved. The robust phylogeny of Nassariinae
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30 511 clarified the placement of *N. vaucheri* within the African genus *Naytia* and allowed inferring that
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33 512 the ancestor of Nassariinae had originated from the Indo-Pacific region. The inferred divergence
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35 513 dates suggest an important role of climatic and tectonic changes during the Eocene to Oligocene in
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38 514 promoting vicariant events that promoted diversification and the origin of the different genera
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40 515 within Nassariinae. At the subfamily level, mt genomes provide high levels of resolution and could
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43 516 render similar robust results for other subfamilies such as Nassariinae provided that an appropriate
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46 517 taxon representation is gathered. Moreover, they could be highly useful in reconstructing a robust
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48 518 phylogeny of the entire family, hence providing the long-needed framework to understand
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51 519 diversification and adaptation processes underpinning the evolutionary success of this family.
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4 542 CONFLICT OF INTEREST

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6 543 The authors certify that they have NO affiliations with or involvement in any organization or entity
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9 544 with any a financial or non-financial interest in the subject matter or materials discussed in this
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17 547 DATA AVAILABILITY

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19 548 All sequence data newly generated in this study has been deposited at NCBI and the corresponding
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22 549 accession numbers are listed in Table 1.
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27 551 AUTHORS' CONTRIBUTIONS

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30 552 All authors conceptualized the study and contributed to the collection of the data, Y.Y. obtained and
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33 553 analysed the sequence data. All authors participated in writing the manuscript and approved the
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4 744 **Figure Captions**

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6 745 Figure 1. Phylogenetic relationships of Nassariidae within Buccinoidea based on the amino acid
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9 746 sequences of 13 mitochondrial PCGs and the nucleotide sequences of two rRNAs. The
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12 747 reconstructed BI phylogram using *Crassicantharus noumeensis* (Crosse, 1870; family
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14 748 Dolicholatiridae) and *Belomitra viridis* (Okutani, 1966; family Belomitridae) as outgroup
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17 749 is shown. The names of the families are indicated. Numbers at nodes are statistical
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20 750 support values for ML (bootstrap proportions)/BI (Bayesian posterior probabilities). The
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22 751 black circle indicates nodes with maximal ML and BI support. Scale bar indicates
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25 752 substitutions/site.

26
27 753 Figure 2. Phylogenetic relationships within Nassariinae based on the nucleotide sequences of 13
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30 754 mitochondrial PCGs and two rRNAs. The reconstructed BI phylogram using genus *Bullia*
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33 755 (subfamily Bulliinae) as outgroup is shown. The names of the genera are indicated.
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35 756 Numbers at nodes are statistical support values for ML (bootstrap proportions)/BI
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38 757 (Bayesian posterior probabilities). The red circle indicates nodes with maximal ML and
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40 758 BI support. Scale bar indicates substitutions/site.

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43 759 Figure 3. Biogeographic ancestral reconstruction of subfamily Nassariinae under ML. Pie charts
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46 760 represent the statistical support at every node.

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48 761 Figure 4. Chronogram with age estimates of major divergence events within Nassariinae based on
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51 762 the concatenated nucleotide sequences of 13 mitochondrial PCGs and two rRNAs using
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53 763 Bayesian relaxed dating methods. Horizontal bars represent 95% credible intervals of
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56 764 relevant nodes, and calibration constraints are indicated with an asterisk on the
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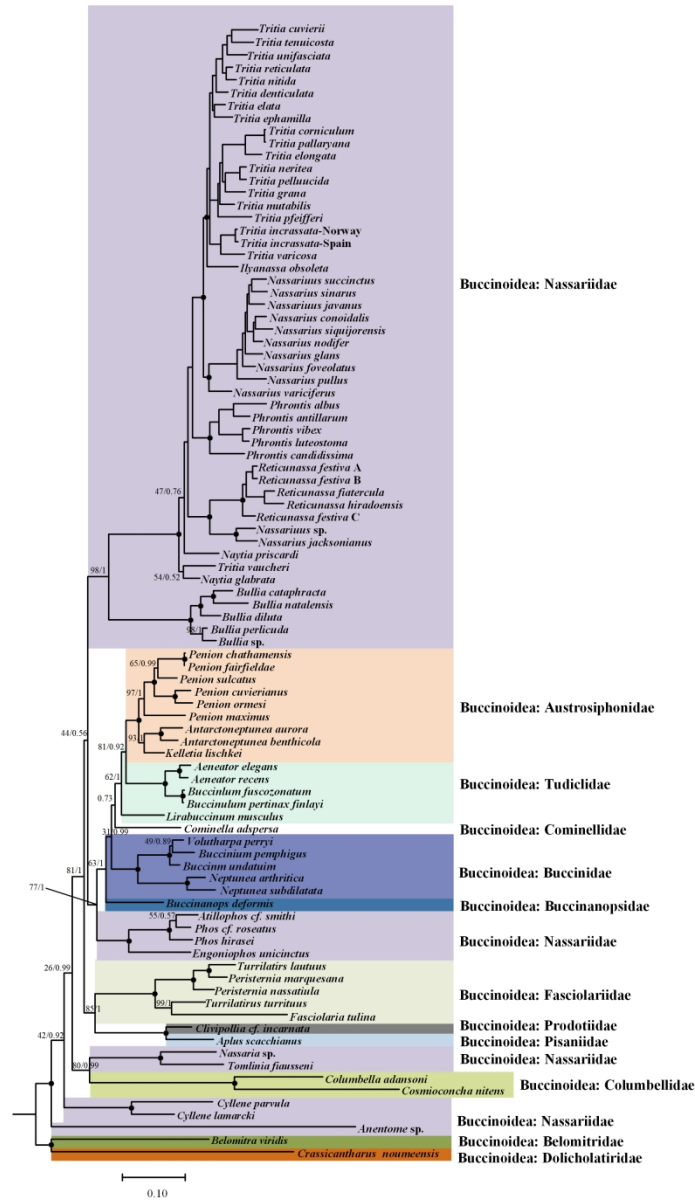
corresponding nodes. Dates (and highest posterior density intervals, HPD) are in millions

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of years. Geological ages are indicated.

For Review Only

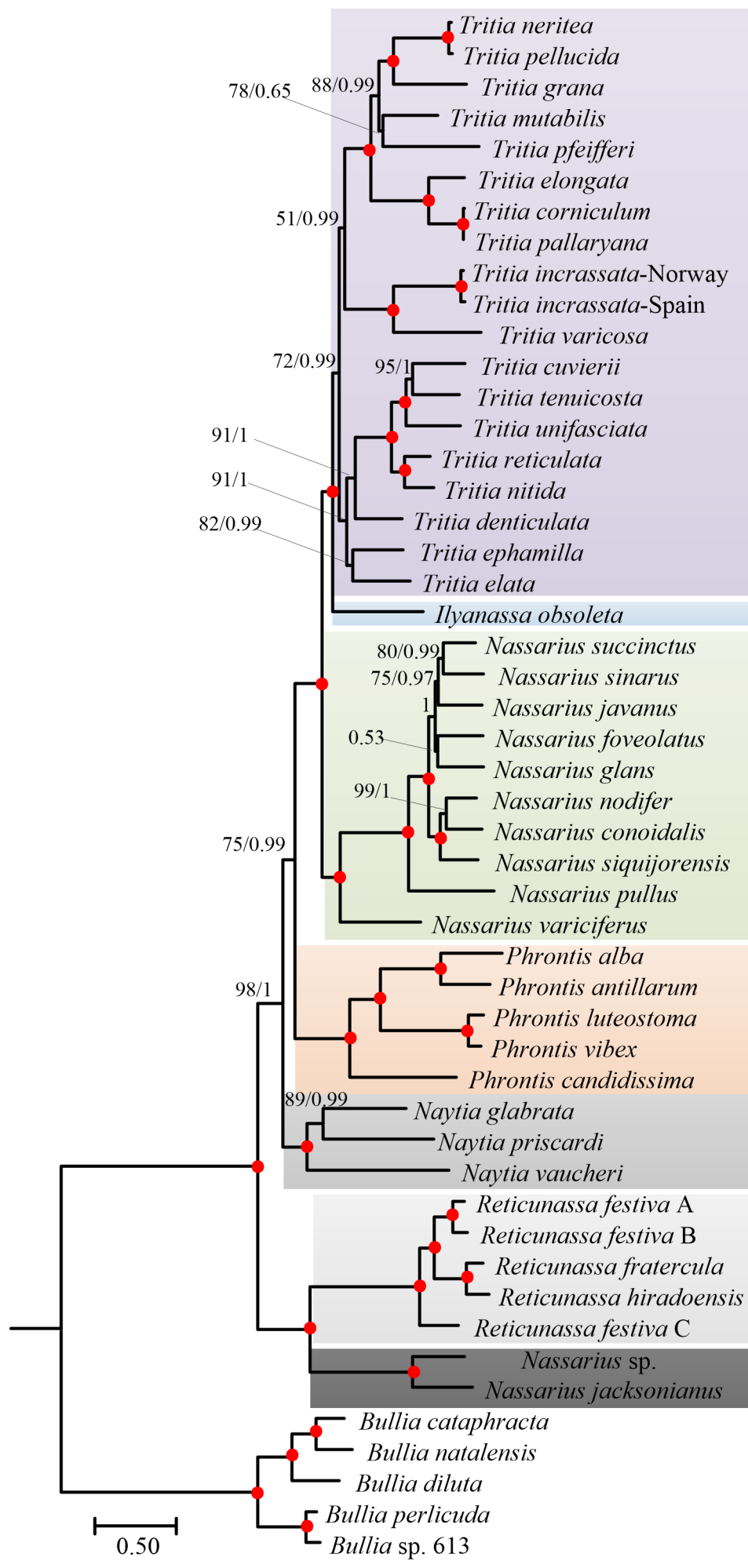
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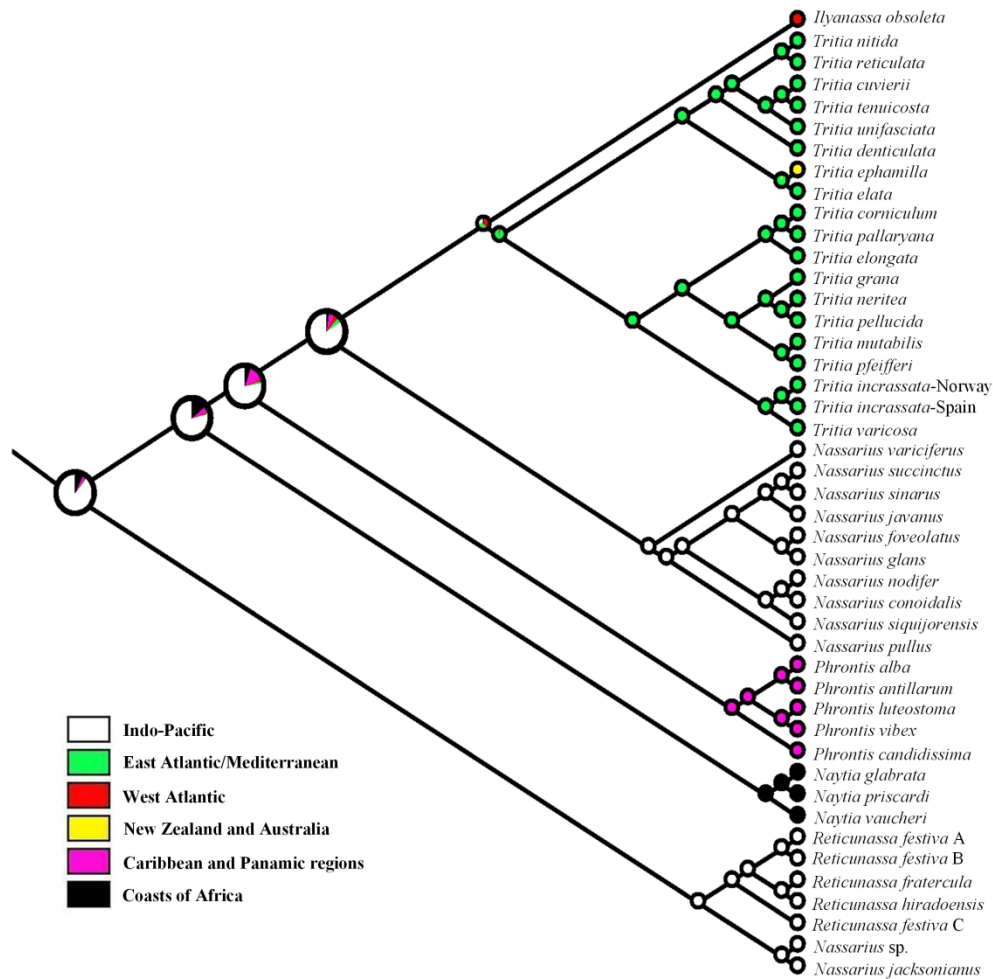


Phylogenetic relationships of Nassariidae within Buccinoidea based on the amino acid sequences of 13 mitochondrial PCGs and the nucleotide sequences of two rRNAs.

167x290mm (300 x 300 DPI)

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Biogeographic ancestral reconstruction of subfamily Nassariinae under ML. Pie charts represent the statistical support at every node.

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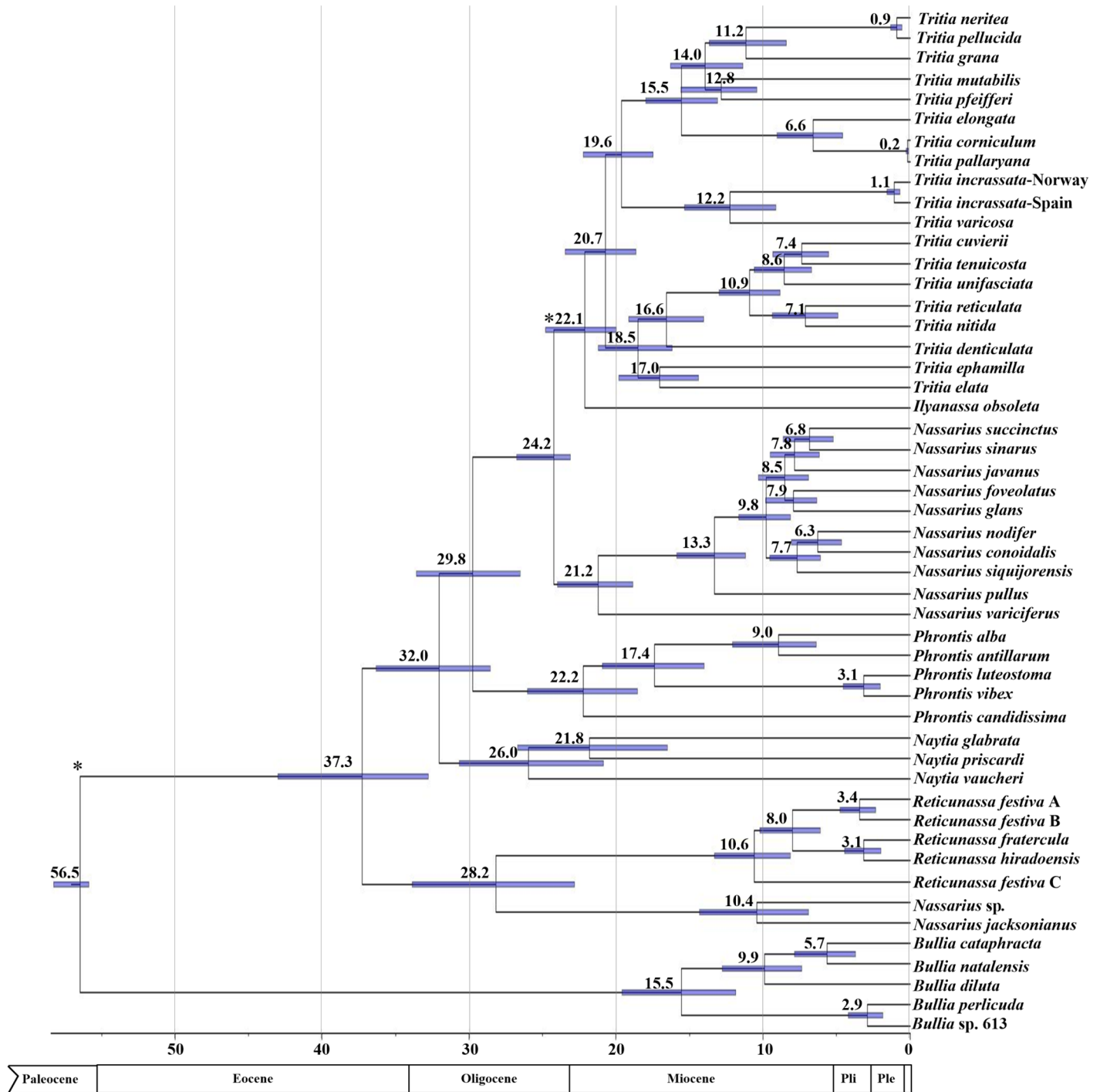


Table 1. New mitochondrial (mt) genomes analyzed in this study.

Classification	Species	Location	Coordinates	Coverage n° reads	Mean depth (mts)	Length (bp)	Genbank Acc. No*	Voucher Museum
Family Nassariidae								
Subfamily Bulliinae	<i>Bullia diluta</i>	Baie De Maputo, Inhaca, Mozambique	25°58'12"S, 32°59'24"E	30,830	103	15,084	OR085336	MNHN-IM-2009-22535
	<i>Bullia perlucida</i>	Port d'Ehoala, Sud Madagascar	25°3'44"S, 46°57'45"E	34,872	55	15,099	OR085335	MNHN-IM-2009-12299
	<i>Bullia</i> sp. 613	Port d'Ehoala, Sud Madagascar	25°3'32"S, 46°57'46"E	23,590	45	15,103	OR085333	MNHN-IM-2009-12877
	<i>Bullia natalensis</i>	Baie De Maputo, Inhaca, Mozambique	25°58'12"S, 32°59'24"E	30,630	234	15,103	OR085334	MNHN-IM-2009-22718
	<i>Bullia cataphracta</i>	Baie De Maputo, Inhaca, Mozambique	25°58'12"S, 32°59'24"E	37,980	51	15,094	OR085337	MNHN-IM-2009-22716
	Subfamily Cylleninae	<i>Cyllene lamarcki</i>	Baie de Pointe-Noire, Congo	4°43'2"S, 11°48'53"E	45,280	81	15,187	OR085330
<i>Cyllene parvula</i>		Secteur de Lavanono, Sud Madagascar	25°24'21"S, 44°54'36"E	2,142,544	16095	15,207	OR085329	MNHN-IM-2009-12838
Subfamily Tomliniinae	<i>Tomlinia frausseni</i>	Vietnam	--	33,286	101	15,269	PP147851	MNHN-IM-2013-52188
	<i>Nassaria</i> sp.	Papua New Guinea	5°11'45"S, 145°50'48"E	36,660	64	15,092	OR198153	MNHN-IM-2013-17053

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5	Subfamily Photinae	<i>Antillophos cf. smithi</i>	Grand cul de sac marin, Guadeloupe	16°23'12"N, 61°35'54"W	288,68	60	15,226	OR198150	MNHN-IM-2013-20358
6									
7		<i>Phos hirasei</i>	Jacquinet Bay, Papua New Guinea	5°33'36"S, 151°31'48"E	55,946	96	15,196	OQ979297	MNHN-IM-2009-13112
8									
9		<i>Phos cf. roseatus</i>	Récif Pétrie, Nouvelle-Caledonie	18°35'54"S, 164°23'54"E	36,080	70	15,199	OQ979298	MNHN-IM-2009-20623
10									
11		<i>Engoniophos</i>	Anse Babin, Guadeloupe	16°20'27"N, 61°31'33"W	77,028	105	15,215	OR085328	MNHN-IM-2009-24414
12		<i>unicinctus</i>							
13	Subfamily	<i>Naytia glabrata</i>	Baie de Pointe-Noire, Congo	4°43'2"S, 11°48'53" E	30,198	22	15,111	OR085326	MNHN-IM-2009-23946
14	Nassariinae								
15		<i>Naytia priscardi</i>	Secteur Ouest de Lavanono, Sud Madagascar	25°23'27"S, 44°51'39"E	34,346	111	15,178	OR085325	MNHN-IM-2009-12870
16									
17		<i>Phrontis antillarum</i>	Les 3 arches, Port- Louis, Guadeloupe	16°23'15"N, 61°31'47"W	36,660	70	15,129	OQ979295	MNHN-IM-2009-24320
18									
19		<i>Phrontis vibex</i>	Banc Frotte-ton-cul, Guadeloupe	16°17'21"N, 61°34'44"W	43,034	150	15,115	OQ979293	MNHN-IM-2009-24334
20									
21		<i>Phrontis candidissima</i>	Sud Anse Caraïbe, Guadeloupe	16°12'2"N, 61°47'20"W	45,760	95	15,124	OQ979294	MNHN-IM-2009-24297
22									
23		<i>Phrontis alba</i>	Rocroy sud, Guadeloupe	16°2'23"N, 61°45'43"W	36,862	94	15,123	OQ979296	MNHN-IM-2009-24295
24									
25		<i>Phrontis luteostoma</i>	East of Panama City, Panama	--	39,510	102	15,142	OQ939953	MNHN-IM-2009-21715
26									
27	Family	<i>Buccinanops deformis</i>	Puerto Madryn, Argentine	--	30,628	36	15,173	OR198149	MNHN-IM-2009-24004
28	Buccinanopsidae								
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5	Family Belomitridae	<i>Belomitra viridis</i>	Dongsha Islands, South China Sea	19°50'26"N, 116°27'11"E	55,946	53	15,039	OR198151	MNHN-IM-2013-44507
6									
7	Family Prodotiidae	<i>Clivipollia cf.</i> <i>incarnata</i>	Papua New Guinea	5°7'6"S, 145°49'23"E	77,028	121	15,182	OR198152	MNHN-IM-2013-17091
8									
9	Family	<i>Cosmioconcha nitens</i>	Guyane Francaise	5°13'45"N, 52°8'54"W	36,862	117	15,041	OR085332	MNHN-IM-2013-56890
10	Columbellidae								
11	Family	<i>Turritatirus lautus</i>	Papua New Guinea	5°11'55"S, 145°49'37"E	34,872	109	15,089	OQ939951	MNHN-IM-2013-15295
12	Fascioliariidae								
13		<i>Peristernia nassatula</i>	Papua New Guinea	--	36,080	86	15,106	OQ979299	MNHN-IM-2013-18061
14									
15		<i>Peristernia</i> <i>marquesana</i>	Papua New Guinea	5°12'27"S, 145°49'1"E	35,824	20	15,088	OQ979300	MNHN-IM-2013-15306
16									
17		<i>Turritatirus turritus</i>	Papua New Guinea	5°10'6"S, 145°50'15"E	58,170	86	15,076	PP147852	MNHN-IM-2013-17100
18									
19		<i>Fasciolaria tulipa</i>	platier de l'ilet à Cabrit,Guadeloupe	16°11'58"N, 61°34'17"W	43,804	54	15,042	OR085327	MNHN-IM-2013-19559
20									
21	Family	<i>Crassicantharus</i>	Papua New Guinea	5°11'55"S, 145°49'37"E	37,980	91	15,112	OR085331	MNHN-IM-2013-4032
22	Dolicholatiridae	<i>noumeensis</i>							
23									
24	Family Pisaniidae	<i>Aplus scacchianus</i>	Limnos Island, Greece	--	34,502	82	15,167	OQ939952	MNHN-IM-2013-32770
25									

Genbank mt genomes

Species	Family	Length (bp)	GenBank acc. no.	Reference
<i>Tritia corniculum</i>	Nassariidae	15,114	MT755650	Yang et al., 2021
<i>Tritia cuvierii</i>	Nassariidae	15,185	MT755651	Yang et al., 2021
<i>Tritia grana</i>	Nassariidae	15,198	MT762151	Yang et al., 2021

5	<i>Tritia incrassata</i> -SP	Nassariidae	15,159	MT762153	Yang et al., 2021
6	<i>Tritia incrassata</i> -NW	Nassariidae	15,170	MT762152	Yang et al., 2021
7	<i>Tritia mutabilis</i>	Nassariidae	15,148	MT762154	Yang et al., 2021
9	<i>Tritia neritea</i>	Nassariidae	15,179	MT762155	Yang et al., 2021
10	<i>Tritia pellucida</i>	Nassariidae	15,175	MT768039	Yang et al., 2021
11	<i>Tritia pfeifferi</i>	Nassariidae	15,142	MT768040	Yang et al., 2021
12	<i>Tritia unifasciata</i>	Nassariidae	15,168	MT768043	Yang et al., 2021
13	<i>Tritia vaucheri</i>	Nassariidae	15,153	MT768044	Yang et al., 2021
14	<i>Tritia denticulata</i>	Nassariidae	15,167	MT755652	Yang et al., 2021
15	<i>Tritia ephamilla</i>	Nassariidae	15,157	MT755654	Yang et al., 2021
16	<i>Tritia pallaryana</i>	Nassariidae	15,144	MT762157	Yang et al., 2021
17	<i>Tritia tenuicosta</i>	Nassariidae	15,169	MT768042	Yang et al., 2021
18	<i>Tritia elongata</i>	Nassariidae	15,145	MT755653	Yang et al., 2021
19	<i>Tritia nitida</i>	Nassariidae	15,157	MT762156	Yang et al., 2021
20	<i>Tritia varicosa</i>	Nassariidae	15,142	MT768041	Yang et al., 2021
21	<i>Tritie elata</i>	Nassariidae	15,167	MT768045	Yang et al., 2021
22	<i>Tritia tingitana</i>	Nassariidae	13,337	MW194096	Yang et al., 2021
23	<i>Tritia ovoidea</i>	Nassariidae	14,889	MW194095	Yang et al., 2021
24	<i>Anentome</i> sp.	Nassariidae	15,069	MT755649	Yang et al., 2021
25	<i>Tritia obsoleta</i>	Nassariidae	15,263	DQ238598	Simison, Lindberg, & Boore, 2006
26	<i>Tritia reticulata</i>	Nassariidae	15,271	EU827201	Cunha, Grande, & Zardoya, 2009
27	<i>Nassarius variciferus</i>	Nassariidae	15,269	KM603509	Yang, Li, Kong, & Yu, 2018
28	<i>Nassarius succinctus</i>	Nassariidae	15,329	KT768016	Yang, Li, Kong, & Yu, 2019
29	<i>Nassarius nodifer</i>	Nassariidae	15,337	KT818617	Yang, Li, Kong, & Yu, 2019
30	<i>Nassarius conoidalis</i>	Nassariidae	15,332	KT826694	Yang, Li, Kong, & Yu, 2019

5	<i>Nassarius pullus</i>	Nassariidae	15,278	KT900947	Yang, Li, Kong, & Yu, 2019
6	<i>Nassarius sinarus</i>	Nassariidae	15,325	MH346208	Yang, Li, Kong, & Yu, 2019
7	<i>Nassarius foveolatus</i>	Nassariidae	15,343	MH346209	Yang, Li, Kong, & Yu, 2019
9	<i>Nassarius javanus</i>	Nassariidae	15,325	MH346210	Yang, Li, Kong, & Yu, 2019
10	<i>Reticunassa festiva-A</i>	Nassariidae	15,195	KT735055	Yang, Li, Kong, & Yu, 2018
11	<i>Reticunassa festiva-B</i>	Nassariidae	15,194	MF148855	Yang, Li, Kong, & Yu, 2018
12	<i>Reticunassa festiva-C</i>	Nassariidae	15,172	MG744570	Yang, Li, Kong, & Yu, 2018
13	<i>Reticunassa fratercula</i>	Nassariidae	15,174	KT826695	Yang, Li, Kong, & Yu, 2018
14	<i>Reticunassa hiradoensis</i>	Nassariidae	15,194	MG744569	Yang, Li, Kong, & Yu, 2018
15	<i>Nassarius jacksonianus</i>	Nassariidae	15,234	MH346212	Yang, Li, Kong, & Yu, 2019
16	<i>Nassarius sp.</i>	Nassariidae	15,240	MH346211	Yang, Li, Kong, & Yu, 2019
17	<i>Penion chathamensis</i>	Austrosiphonidae	15,227	MH140428	Vaux et al., 2018
18	<i>Penion fairfieldae</i>	Austrosiphonidae	15,226	MH198165	Vaux et al., 2018
19	<i>Penion sulcatus</i>	Austrosiphonidae	15,227	MH198164	Vaux et al., 2018
20	<i>Penion cuvierianus</i>	Austrosiphonidae	15,235	MH140431	Vaux et al., 2018
21	<i>Penion ormesi</i>	Austrosiphonidae	15,234	MH198167	Vaux et al., 2018
22	<i>Penion maximus</i>	Austrosiphonidae	15,249	MG211144	—
23	<i>Antarctoneptunea aurora</i>	Austrosiphonidae	15,227	MH140430	Vaux et al., 2018
24	<i>Antarctoneptunea benthicola</i>	Austrosiphonidae	15,229	MH198173	Vaux et al., 2018
25	<i>Kelletia lischkei</i>	Austrosiphonidae	15,225	MH198160	Vaux et al., 2018
26	<i>Aeneator elegans</i>	Tudicidae	15,254	MH198157	Vaux et al., 2018
27	<i>Aeneator recens</i>	Tudicidae	15,264	MH198159	Vaux et al., 2018
28	<i>Buccinulum fuscozonatum</i>	Tudicidae	15,246	MH198158	Vaux et al., 2018
29	<i>Buccinulum pertinax finlayi</i>	Tudicidae	15,247	MH198162	Vaux et al., 2018
30	<i>Lirabuccinum musculus</i>	Tudicidae	15,292	MH931230	Tian et al., 2019

5	<i>Cominella adspersa</i>	Cominellidae	15,251	MH198163	Vaux et al., 2018
6	<i>Volutharpa perryi</i>	Buccinidae	15,255	KT382829	Bao et al., 2016
7	<i>Buccinum pemphigus</i>	Buccinidae	15,265	KT962044	—
8	<i>Buccinum undatum</i>	Buccinidae	15,265	MK035573	Jónsson et al., 2019
9	<i>Neptunea arthritica</i>	Buccinidae	15,256	KU246047	Hao et al., 2016
10	<i>Neptunea subdilata</i>	Buccinidae	15,393	MG827217	—
11	<i>Columbella adansoni</i>	Columbellidae	16,272	KP716637	Osca, Templado, & Zardoya, 2015

For Review Only

Table S1 Standard and Long PCR primers for nassariid mitogenomes.

<i>Bullia diluta</i>		
Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-trnF</i> (8.8K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART T	<i>cox3-cox1</i> (2.5K)
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451224	
<i>Bullia perlucida</i>		
Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART T	<i>cox3-cox1</i> (2.5K)
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451227	
<i>Bullia</i> sp. 613		
Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART T	<i>cox3-cox1</i> (2.5K)
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451232	
<i>Bullia natalensis</i>		

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KY451226		

Bullia cataphracta

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KY451223		

Cyllene lamarcki

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KY451235		

Cyllene parvula

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)

cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
Primer Link <i>cox1</i>		
Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAAATCA	
<i>Tomlinia frausseni</i>		
Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KY451417		
<i>Nassaria</i> sp.		
Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.4K)
coblaR	GCYCCTCARAARGATATYTGACCTCARGG	
coblaF	GAYCCWGARAAYTTTATYCCTGCTAAYCC	<i>cob-trnF</i> (4.0K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
Primer Link <i>cox1</i>		
Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAAATCA	

Primer Link *cytb*

Primer	Sequence 5'-3'	Fragment (bp)
cytbF	GGWTAYGTWYTWCCWTGRGGWCARAT	<i>cytb</i> (0.5K)
cytbR	GCRTAWGCRAAWARRAARTAYCAYTCWGG	

*Antillophos cf. smithi***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

Primer Link *cox1*

Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAAATCA	

*Phos hirasei***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

cox1 Genbank Acc. No: KY451410*Phos cf. roseatus***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)

trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451409	

Engoniophos uncinatus

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
coblaF	GAYCCWGARAAYTTTATYCCTGCTAAYCC	<i>cob-trnF</i> (4.0K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451413	

Naytia glabrata

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451307	

Naytia priscardi

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.4K)
coblaR	GCYCCTCARAARGATATYTGACCTCARGG	
coblaF	GAYCCWGARAAYTTTATYCCTGCTAAYCC	<i>cob-trnF</i> (4.0K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)

T

cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
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cox1 Genbank Acc. No: KY489424

Primer Link *cytb*

Primer	Sequence 5'-3'	Fragment (bp)
cytbF	GGWTAYGTWYTWCCWTGRGGWCARAT	<i>cytb</i> (0.5K)
cytbR	GCRTAWGCRAAWARRAARTAYCAYTCWGG	

Phrontis antillarum

Long PCR

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)

T

cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
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cox1 Genbank Acc. No: KY451258

Phrontis vibex

Long PCR

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)

T

cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
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cox1 Genbank Acc. No: KY451402

Phrontis candidissima

Long PCR

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAAYATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)

trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451269	

Phrontis alba

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451256	

Phrontis luteostoma

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i>	Genbank Acc. No: KY451328	

Buccinanops deformis

Long PCR		
Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGYTTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)

	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

cox1 Genbank Acc. No: KY451220

*Belomitra viridis***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)

	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

Primer Link *cox1*

Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAAATCA	

*Clivipollia cf. incarnata***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)

	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

Primer Link *cox1*

Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAAATCA	

*Cosmioconcha nitens***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	

12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KX422209		

*Turritatirus lautus***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

Primer Link *cox1*

Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAATCA	

*Peristernia nassatula***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAATRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KT753957		

*Peristernia marquesana***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
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cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KT753914		

*Turriturris turritus***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KT753981		

*Fasciolaria tulipa***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KT753954		

*Crassicantharus noumeensis***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	

12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	
<i>cox1</i> Genbank Acc. No: KT753998		

*Aplus scacchianus***Long PCR**

Primer	Sequence 5'-3'	Fragment (bp)
cox1laF	AAyatRCGATGACGAGGRATRCARTTTGA	<i>cox1-rrnS</i> (4K)
12SlaR	ATAGGCTGCACCTTGATCTGACGTYTT	
12SlaF	CAGTTTGTATAACCGTCGTCGTCAGGT	<i>rrnS-cob</i> (4.5K)
cobla2R	GGRTTAGCWGGRATAAARTTYTCWGGRTC	
cobla2F	CCYTGAGGTCARATATCYTTYTGAGGRGC	<i>cob-trnF</i> (4.3K)
trnF-R	CACCCTAGCATCTTCAGTGCTATGCTCT	
cox3la2F	ATGGCRCGNAATCCTTTTCATTTAGTWGART	<i>cox3-cox1</i> (2.5K)
	T	
cox1laR	CGAGGAAAAGCYATRTCAGGAGC	

Primer Link *cox1*

Primer	Sequence 5'-3'	Fragment (bp)
LCO1490 F	GGTCAACAAATCATAAAGATATTGG	<i>cox1</i> (709)
HCO2198 R	TTAACTTCAGGGTGACCAAAAAATCA	

Table S2. Best fit partitions and substitution models.

Nassariidae dataset	Set Partition (Conducted by PartitionFinder 2)	Best Model for BI (Selected by PartitionFinder 2)
Best Partition CDS genes	<i>atp6-8</i>	MTMAM+I+G+F
	<i>cox1-2-3</i>	MTMAM+I+G+F
	<i>cob</i>	MTART+I+G
	<i>nad1-2-3-4-4L-5-6</i>	MTART+I+G+F
Best Partition to rRNA genes	<i>rrnS-L</i>	GTR+I+G
Nassariinae dataset	Set Partition (Conducted by PartitionFinder 2)	Best Model for BI (Selected by PartitionFinder 2)
Best Partition CDS genes	<i>atp6-8</i> 1th	TRN+I+G
	<i>atp6-8</i> 2th	HKY+I
	<i>atp6-8</i> 3th	TVM+I+G
	<i>cox1-2-3</i> 1th	TRN+I+G
	<i>cox1-2-3</i> 2th	TVM+I+G
	<i>cox1-2-3</i> 3th	TVM+I+G
	<i>cob</i> 1th	TRN+I+G
	<i>cob</i> 2th	TVM+I+G
	<i>cob</i> 3th	K81UF+I+G
	<i>nad1-2-3-4-4L-5-6</i> 1th	GTR+I+G
	<i>nad1-2-3-4-4L-5-6</i> 2th	GTR+I+G
	<i>nad1-2-3-4-4L-5-6</i> 3th	TVM+I+G
Best Partition to rRNA genes	<i>rrnS-L</i>	GTR+I+G

Table S3. Mitochondrial genome features.

Turriturris turritus 15,076 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-748	incomplete	—	TAA	18
tRNA- <i>Lys</i>	H	767-832	66			3
tRNA- <i>Ala</i>	H	836-902	67			0
tRNA- <i>Arg</i>	H	903-971	69			3
tRNA- <i>Asn</i>	H	975-1041	67			11
tRNA- <i>Ile</i>	H	1053-1120	68			3
<i>Nad3</i>	H	1124-1477	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1478-1545	68			0
<i>Nad2</i>	H	1546-2600	1055	ATG	TA	0
<i>Cox1</i>	H	2601-4136	1536	ATG	TAA	16
<i>Cox2</i>	H	4153-4839	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4838-4905	68			1
<i>Atp8</i>	H	4907-5065	159	ATG	TAA	2
<i>Atp6</i>	H	5068-5763	696	ATG	TAA	32
tRNA- <i>Met</i>	L	5796-5860	65			5
tRNA- <i>Tyr</i>	L	5866-5931	66			1
tRNA- <i>Cys</i>	L	5933-5996	64			0
tRNA- <i>Trp</i>	L	5997-6063	67			1
tRNA- <i>Gln</i>	L	6065-6126	62			1
tRNA- <i>Gly</i>	L	6127-6194	67			0
tRNA- <i>Glu</i>	L	6195-6262	68			0
12s	H	6263-7215	953			0
tRNA- <i>Val</i>	H	7216-7283	68			0
16s	H	7284-8639	1356			0
tRNA- <i>Leu</i>	H	8640-8709	70			3
tRNA- <i>Leu</i>	H	8713-8781	69			0
<i>Nad1</i>	H	8782-9723	942	ATG	TAA	5
tRNA- <i>Pro</i>	H	9729-9798	70			1
<i>Nad6</i>	H	9800-10300	501	ATG	TAA	2
<i>Cytb</i>	H	10303-11442	1140	ATG	TAA	8
tRNA- <i>Ser</i>	H	11451-11514	64			0
tRNA- <i>Thr</i>	L	11515-11580	66			16
<i>Nad4L</i>	H	11597-11893	297	ATG	TAG	11
<i>Nad4</i>	H	11905-13260	1356	CTG	TAA	0
tRNA- <i>His</i>	H	13261-13329	69			0
<i>Nad5</i>	H	13330-15048	1719	ATG	TAG	28
tRNA- <i>Phe</i>	H	incomplete	—			—

Tomlinia fraussenii 15,269 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-755	incomplete	—	TAA	47
tRNA- <i>Lys</i>	H	803-869	67			6
tRNA- <i>Ala</i>	H	876-943	68			5
tRNA- <i>Arg</i>	H	949-1017	69			1
tRNA- <i>Asn</i>	H	1019-1088	70			17
tRNA- <i>Ile</i>	H	1106-1174	69			3
<i>Nad3</i>	H	1178-1531	354	ATG	TAG	8
tRNA- <i>Ser</i>	H	1540-1607	68			0
<i>Nad2</i>	H	1608-2663	1056	ATG	TAG	10
<i>Cox1</i>	H	2674-4209	1536	ATG	TAG	19
<i>Cox2</i>	H	4229-4915	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4914-4982	69			1
<i>Atp8</i>	H	4984-5142	159	ATG	TAA	9
<i>Atp6</i>	H	5152-5847	696	ATG	TAG	47
tRNA- <i>Met</i>	L	5895-5961	67			21
tRNA- <i>Tyr</i>	L	5983-6047	65			2
tRNA- <i>Cys</i>	L	6050-6114	65			0
tRNA- <i>Trp</i>	L	6115-6182	68			1
tRNA- <i>Gln</i>	L	6184-6245	62			1
tRNA- <i>Gly</i>	L	6247-6312	66			0
tRNA- <i>Glu</i>	L	6313-6380	68			0
12s	H	6381-7356	976			0
tRNA- <i>Val</i>	H	7357-7423	67			0
16s	H	7424-8788	1365			0
tRNA- <i>Leu</i>	H	8789-8858	70			11
tRNA- <i>Leu</i>	H	8870-8938	69			0
<i>Nad1</i>	H	8939-9880	942	ATG	TAA	7
tRNA- <i>Pro</i>	H	9888-9955	68			1
<i>Nad6</i>	H	9957-10454	498	ATG	TAA	7
<i>Cytb</i>	H	10462-11601	1140	ATG	TAA	13
tRNA- <i>Ser</i>	H	11615-11680	66			0
tRNA- <i>Thr</i>	L	11681-11747	67			23
<i>Nad4L</i>	H	11771-12067	297	ATG	TAG	11
<i>Nad4</i>	H	12079-13432	1354	TTA	T	0
tRNA- <i>His</i>	H	13433-13498	66			1
<i>Nad5</i>	H	13500-15221	1722	ATG	TAA	48
tRNA- <i>Phe</i>	H	incomplete	—			—

Aplus scacchianus 15,167 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-756	incomplete	—	TAA	18
tRNA- <i>Lys</i>	H	775-843	69			5
tRNA- <i>Ala</i>	H	849-915	67			0
tRNA- <i>Arg</i>	H	916-984	69			13
tRNA- <i>Asn</i>	H	998-1066	69			15
tRNA- <i>Ile</i>	H	1082-1152	71			3
<i>Nad3</i>	H	1156-1509	354	ATG	TAA	-1
tRNA- <i>Ser</i>	H	1509-1576	68			0
<i>Nad2</i>	H	1577-2634	1058	ATG	TA	0
<i>Cox1</i>	H	2635-4170	1536	ATG	TAA	28
<i>Cox2</i>	H	4199-4885	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4884-4951	68			1
<i>Atp8</i>	H	4953-5111	159	ATG	TAA	7
<i>Atp6</i>	H	5119-5814	696	ATG	TAA	36
tRNA- <i>Met</i>	L	5851-5916	66			6
tRNA- <i>Tyr</i>	L	5923-5988	66			1
tRNA- <i>Cys</i>	L	5990-6053	64			6
tRNA- <i>Trp</i>	L	6060-6126	67			1
tRNA- <i>Gln</i>	L	6128-6189	62			1
tRNA- <i>Gly</i>	L	6191-6257	67			0
tRNA- <i>Glu</i>	L	6258-6325	68			0
12s	H	6326-7274	949			0
tRNA- <i>Val</i>	H	7275-7343	69			0
16s	H	7344-8710	1367			0
tRNA- <i>Leu</i>	H	8711-8780	70			8
tRNA- <i>Leu</i>	H	8789-8857	69			0
<i>Nad1</i>	H	8858-9799	942	ATG	TAG	10
tRNA- <i>Pro</i>	H	9810-9879	70			1
<i>Nad6</i>	H	9881-10381	501	ATG	TAA	7
<i>Cytb</i>	H	10389-11528	1140	ATG	TAA	9
tRNA- <i>Ser</i>	H	11538-11602	65			0
tRNA- <i>Thr</i>	L	11603-11671	69			13
<i>Nad4L</i>	H	11685-11981	297	ATG	TAG	11
<i>Nad4</i>	H	11993-13348	1356	CTC	TAA	5
tRNA- <i>His</i>	H	13354-13418	65			1
<i>Nad5</i>	H	13419-15140	1722	ATG	TAG	27
tRNA- <i>Phe</i>	H	incomplete	—			—

Turritalirus lautus 15,089

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	14
tRNA- <i>Lys</i>	H	765-830	66			5
tRNA- <i>Ala</i>	H	836-903	68			0
tRNA- <i>Arg</i>	H	904-972	69			8
tRNA- <i>Asn</i>	H	981-1048	68			14
tRNA- <i>Ile</i>	H	1063-1129	67			3
<i>Nad3</i>	H	1133-1486	354	ATG	TAG	0
tRNA- <i>Ser</i>	H	1487-1554	68			0
<i>Nad2</i>	H	1555-2609	1055	ATG	TA	0
<i>Cox1</i>	H	2610-4145	1536	ATG	TAA	12
<i>Cox2</i>	H	4158-4844	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4843-4910	68			1
<i>Atp8</i>	H	4912-5070	159	ATG	TAA	6
<i>Atp6</i>	H	5077-5772	696	ATG	TAG	33
tRNA- <i>Met</i>	L	5806-5871	66			6
tRNA- <i>Tyr</i>	L	5878-5943	66			2
tRNA- <i>Cys</i>	L	5946-6010	65			6
tRNA- <i>Trp</i>	L	6011-6077	67			1
tRNA- <i>Gln</i>	L	6079-6140	62			1
tRNA- <i>Gly</i>	L	6142-6208	67			0
tRNA- <i>Glu</i>	L	6209-6275	67			0
12s	H	6276-7233	958			0
tRNA- <i>Val</i>	H	7234-7300	67			0
16s	H	7301-8651	1351			0
tRNA- <i>Leu</i>	H	8652-8721	70			5
tRNA- <i>Leu</i>	H	8727-8795	69			0
<i>Nad1</i>	H	8796-9737	942	ATG	TAG	6
tRNA- <i>Pro</i>	H	9744-9813	70			1
<i>Nad6</i>	H	9815-10315	501	ATG	TAA	3
<i>Cytb</i>	H	10319-11458	1140	ATG	TAA	9
tRNA- <i>Ser</i>	H	11468-11531	64			0
tRNA- <i>Thr</i>	L	11532-11598	67			19
<i>Nad4L</i>	H	11618-11914	297	ATG	TAG	11
<i>Nad4</i>	H	11926-13279	1354	CTA	T	0
tRNA- <i>His</i>	H	13280-13348	69			0
<i>Nad5</i>	H	13349-15067	1719	ATG	TAG	22
tRNA- <i>Phe</i>	H	incomplete	—			—

Phrontis luteostoma 15,142 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-758	incomplete	—	TAA	15
tRNA- <i>Lys</i>	H	774-838	65			2
tRNA- <i>Ala</i>	H	841-907	67			4
tRNA- <i>Arg</i>	H	912-980	69			5
tRNA- <i>Asn</i>	H	986-1053	68			12
tRNA- <i>Ile</i>	H	1066-1133	68			3
<i>Nad3</i>	H	1137-1490	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1491-1558	68			0
<i>Nad2</i>	H	1559-2613	1055	ATG	TA	0
<i>Cox1</i>	H	2614-4149	1536	ATG	TAA	29
<i>Cox2</i>	H	4179-4865	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4864-4931	68			1
<i>Atp8</i>	H	4933-5091	159	ATG	TAA	13
<i>Atp6</i>	H	5105-5800	696	ATG	TAA	33
tRNA- <i>Met</i>	L	5834-5900	67			2
tRNA- <i>Tyr</i>	L	5903-5969	67			1
tRNA- <i>Cys</i>	L	5971-6035	65			0
tRNA- <i>Trp</i>	L	6036-6101	66			1
tRNA- <i>Gln</i>	L	6103-6164	62			1
tRNA- <i>Gly</i>	L	6166-6232	67			12
tRNA- <i>Glu</i>	L	6245-6309	65			0
12s	H	6310-7266	957			0
tRNA- <i>Val</i>	H	7267-7334	68			0
16s	H	7335-8692	1358			0
tRNA- <i>Leu</i>	H	8693-8761	69			0
tRNA- <i>Leu</i>	H	8762-8830	69			0
<i>Nad1</i>	H	8831-9772	942	ATG	TAG	11
tRNA- <i>Pro</i>	H	9784-9852	69			1
<i>Nad6</i>	H	9854-10354	501	ATG	TAA	4
<i>Cytb</i>	H	10359-11498	1140	ATG	TAA	6
tRNA- <i>Ser</i>	H	11505-11569	65			0
tRNA- <i>Thr</i>	L	11570-11635	66			18
<i>Nad4L</i>	H	11654-11950	297	ATG	TAG	11
<i>Nad4</i>	H	11962-13317	1356	TTG	TAA	0
tRNA- <i>His</i>	H	13318-13383	66			1
<i>Nad5</i>	H	13385-15106	1722	ATG	TAG	36
tRNA- <i>Phe</i>	H	incomplete	—			—

Phrontis vibex 15,115 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-748	incomplete	—	TAA	15
tRNA- <i>Lys</i>	H	764-828	65			2
tRNA- <i>Ala</i>	H	831-897	67			4
tRNA- <i>Arg</i>	H	902-970	69			5
tRNA- <i>Asn</i>	H	976-1043	68			12
tRNA- <i>Ile</i>	H	1056-1123	68			3
<i>Nad3</i>	H	1127-1480	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1481-1548	68			0
<i>Nad2</i>	H	1549-2603	1055	ATG	TA	0
<i>Cox1</i>	H	2604-4139	1536	ATG	TAA	29
<i>Cox2</i>	H	4169-4855	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4854-4921	68			1
<i>Atp8</i>	H	4923-5081	159	ATG	TAA	13
<i>Atp6</i>	H	5095-5790	696	ATG	TAA	33
tRNA- <i>Met</i>	L	5824-5890	67			2
tRNA- <i>Tyr</i>	L	5893-5959	67			1
tRNA- <i>Cys</i>	L	5961-6024	64			0
tRNA- <i>Trp</i>	L	6025-6090	66			1
tRNA- <i>Gln</i>	L	6092-6153	62			1
tRNA- <i>Gly</i>	L	6155-6221	67			12
tRNA- <i>Glu</i>	L	6234-6298	65			0
12s	H	6299-7255	957			0
tRNA- <i>Val</i>	H	7256-7323	68			0
16s	H	7324-8680	1357			0
tRNA- <i>Leu</i>	H	8681-8749	69			0
tRNA- <i>Leu</i>	H	8750-8818	69			0
<i>Nad1</i>	H	8819-9760	942	ATG	TAG	11
tRNA- <i>Pro</i>	H	9772-9840	69			1
<i>Nad6</i>	H	9842-10342	501	ATG	TAA	4
<i>Cytb</i>	H	10347-11486	1140	ATG	TAA	6
tRNA- <i>Ser</i>	H	11493-11557	65			0
tRNA- <i>Thr</i>	L	11558-11623	66			20
<i>Nad4L</i>	H	11644-11940	297	ATG	TAG	11
<i>Nad4</i>	H	11952-13307	1356	TTA	TAA	0
tRNA- <i>His</i>	H	13308-13374	67			1
<i>Nad5</i>	H	13376-15097	1722	ATG	TAG	18
tRNA- <i>Phe</i>	H	incomplete	—			—

Phrontis candidissima 15,124 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-747	incomplete	—	TAA	11
tRNA- <i>Lys</i>	H	759-823	65			2
tRNA- <i>Ala</i>	H	826-893	68			6
tRNA- <i>Arg</i>	H	900-968	69			3
tRNA- <i>Asn</i>	H	972-1038	67			12
tRNA- <i>Ile</i>	H	1051-1118	68			3
<i>Nad3</i>	H	1122-1475	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1476-1543	68			0
<i>Nad2</i>	H	1544-2598	1055	ATG	TA	0
<i>Cox1</i>	H	2599-4134	1536	ATG	TAG	31
<i>Cox2</i>	H	4166-4852	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4851-4918	68			1
<i>Atp8</i>	H	4920-5078	159	ATG	TAA	5
<i>Atp6</i>	H	5084-5779	696	ATG	TAA	38
tRNA- <i>Met</i>	L	5818-5884	67			2
tRNA- <i>Tyr</i>	L	5887-5953	67			1
tRNA- <i>Cys</i>	L	5955-6020	66			0
tRNA- <i>Trp</i>	L	6021-6087	67			1
tRNA- <i>Gln</i>	L	6089-6150	62			1
tRNA- <i>Gly</i>	L	6152-6218	67			8
tRNA- <i>Glu</i>	L	6227-6291	65			0
12s	H	6292-7246	955			0
tRNA- <i>Val</i>	H	7247-7314	68			0
16s	H	7315-8671	1357			0
tRNA- <i>Leu</i>	H	8672-8740	69			15
tRNA- <i>Leu</i>	H	8756-8824	69			0
<i>Nad1</i>	H	8825-9766	942	ATG	TAA	7
tRNA- <i>Pro</i>	H	9774-9841	68			1
<i>Nad6</i>	H	9843-10343	501	ATG	TAA	3
<i>Cytb</i>	H	10347-11486	1140	ATG	TAA	8
tRNA- <i>Ser</i>	H	11495-11559	65			0
tRNA- <i>Thr</i>	L	11560-11625	66			20
<i>Nad4L</i>	H	11646-11942	297	ATG	TAG	11
<i>Nad4</i>	H	11954-13309	1356	CTA	TAG	-1
tRNA- <i>His</i>	H	13309-13378	70			1
<i>Nad5</i>	H	13380-15101	1722	ATG	TAA	23
tRNA- <i>Phe</i>	H	incomplete	—			—

Phrontis antillarum 15,129 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	10
tRNA- <i>Lys</i>	H	761-825	65			2
tRNA- <i>Ala</i>	H	828-894	67			4
tRNA- <i>Arg</i>	H	899-967	69			5
tRNA- <i>Asn</i>	H	973-1040	68			16
tRNA- <i>Ile</i>	H	1057-1124	68			3
<i>Nad3</i>	H	1128-1481	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1482-1549	68			0
<i>Nad2</i>	H	1550-2604	1055	ATG	TA	0
<i>Cox1</i>	H	2605-4140	1536	ATG	TAA	24
<i>Cox2</i>	H	4165-4851	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4850-4917	68			1
<i>Atp8</i>	H	4919-5077	159	ATG	TAA	9
<i>Atp6</i>	H	5087-5782	696	ATG	TAA	39
tRNA- <i>Met</i>	L	5822-5888	67			3
tRNA- <i>Tyr</i>	L	5892-5958	67			1
tRNA- <i>Cys</i>	L	5960-6024	65			0
tRNA- <i>Trp</i>	L	6025-6091	67			1
tRNA- <i>Gln</i>	L	6093-6154	62			1
tRNA- <i>Gly</i>	L	6156-6222	67			10
tRNA- <i>Glu</i>	L	6233-6297	65			0
12s	H	6298-7256	959			0
tRNA- <i>Val</i>	H	7257-7324	68			0
16s	H	7325-8683	1359			0
tRNA- <i>Leu</i>	H	8684-8752	69			1
tRNA- <i>Leu</i>	H	8754-8822	69			0
<i>Nad1</i>	H	8823-9764	942	ATG	TAA	7
tRNA- <i>Pro</i>	H	9772-9840	69			1
<i>Nad6</i>	H	9842-10342	501	ATG	TAA	3
<i>Cytb</i>	H	10346-11485	1140	ATG	TAA	12
tRNA- <i>Ser</i>	H	11498-11562	65			0
tRNA- <i>Thr</i>	L	11563-11629	67			22
<i>Nad4L</i>	H	11652-11948	297	ATG	TAG	11
<i>Nad4</i>	H	11960-13315	1356	CTT	TAG	-1
tRNA- <i>His</i>	H	13315-13379	65			1
<i>Nad5</i>	H	13381-15102	1722	ATG	TAG	27
tRNA- <i>Phe</i>	H	incomplete	—			—

Phrontis alba 15,123 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	9
tRNA- <i>Lys</i>	H	760-824	65			1
tRNA- <i>Ala</i>	H	826-892	67			5
tRNA- <i>Arg</i>	H	898-966	69			5
tRNA- <i>Asn</i>	H	972-1036	65			17
tRNA- <i>Ile</i>	H	1054-1121	68			3
<i>Nad3</i>	H	1125-1478	354	ATG	TAG	0
tRNA- <i>Ser</i>	H	1479-1546	68			0
<i>Nad2</i>	H	1547-2601	1055	ATG	TA	0
<i>Cox1</i>	H	2602-4137	1536	ATG	TAA	26
<i>Cox2</i>	H	4164-4850	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4849-4916	68			1
<i>Atp8</i>	H	4918-5076	159	ATG	TAA	13
<i>Atp6</i>	H	5090-5785	696	ATG	TAA	39
tRNA- <i>Met</i>	L	5825-5891	67			3
tRNA- <i>Tyr</i>	L	5895-5961	67			1
tRNA- <i>Cys</i>	L	5963-6027	65			0
tRNA- <i>Trp</i>	L	6028-6093	66			1
tRNA- <i>Gln</i>	L	6095-6156	62			1
tRNA- <i>Gly</i>	L	6158-6224	67			9
tRNA- <i>Glu</i>	L	6234-6298	65			0
12s	H	6299-7255	957			0
tRNA- <i>Val</i>	H	7256-7323	68			0
16s	H	7324-8679	1356			0
tRNA- <i>Leu</i>	H	8680-8748	69			4
tRNA- <i>Leu</i>	H	8753-8821	69			0
<i>Nad1</i>	H	8822-9763	942	ATG	TAA	7
tRNA- <i>Pro</i>	H	9771-9839	69			1
<i>Nad6</i>	H	9841-10341	501	ATG	TAG	3
<i>Cytb</i>	H	10345-11484	1140	ATG	TAA	12
tRNA- <i>Ser</i>	H	11497-11561	65			0
tRNA- <i>Thr</i>	L	11562-11629	68			21
<i>Nad4L</i>	H	11651-11947	297	ATG	TAG	11
<i>Nad4</i>	H	11959-13314	1356	CTG	TAG	-1
tRNA- <i>His</i>	H	13314-13378	65			1
<i>Nad5</i>	H	13380-15101	1722	ATG	TAG	22
tRNA- <i>Phe</i>	H	incomplete	—			—

Phos hirasei 15,196 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-747	incomplete	—	TAA	18
tRNA- <i>Lys</i>	H	766-833	68			8
tRNA- <i>Ala</i>	H	842-908	67			1
tRNA- <i>Arg</i>	H	910-978	69			10
tRNA- <i>Asn</i>	H	989-1057	69			5
tRNA- <i>Ile</i>	H	1063-1131	69			3
<i>Nad3</i>	H	1135-1488	354	ATG	TAG	-2
tRNA- <i>Ser</i>	H	1487-1554	68			0
<i>Nad2</i>	H	1555-2610	1056	ATG	TAG	3
<i>Cox1</i>	H	2614-4149	1536	ATG	TAA	23
<i>Cox2</i>	H	4173-4859	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4858-4925	68			1
<i>Atp8</i>	H	4927-5085	159	ATG	TAA	15
<i>Atp6</i>	H	5101-5796	696	ATG	TAA	45
tRNA- <i>Met</i>	L	5842-5907	66			9
tRNA- <i>Tyr</i>	L	5917-5983	67			4
tRNA- <i>Cys</i>	L	5988-6053	66			0
tRNA- <i>Trp</i>	L	6054-6119	66			1
tRNA- <i>Gln</i>	L	6121-6182	62			1
tRNA- <i>Gly</i>	L	6184-6250	67			0
tRNA- <i>Glu</i>	L	6251-6315	65			0
12s	H	6316-7293	978			0
tRNA- <i>Val</i>	H	7294-7362	69			0
16s	H	7363-8721	1359			0
tRNA- <i>Leu</i>	H	8722-8791	70			8
tRNA- <i>Leu</i>	H	8800-8868	69			0
<i>Nad1</i>	H	8869-9810	942	ATG	TAA	11
tRNA- <i>Pro</i>	H	9822-9893	72			1
<i>Nad6</i>	H	9895-10395	501	ATG	TAA	17
<i>Cytb</i>	H	10413-11552	1140	ATG	TAA	7
tRNA- <i>Ser</i>	H	11560-11624	65			0
tRNA- <i>Thr</i>	L	11625-11692	68			20
<i>Nad4L</i>	H	11713-12009	297	ATG	TAG	11
<i>Nad4</i>	H	12021-13376	1356	CTT	TAA	4
tRNA- <i>His</i>	H	13381-13445	65			1
<i>Nad5</i>	H	13447-15168	1722	ATG	TAA	28
tRNA- <i>Phe</i>	H	incomplete	—			—

Phos cf. roseatus 15,199 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	19
tRNA- <i>Lys</i>	H	770-837	68			9
tRNA- <i>Ala</i>	H	847-913	67			2
tRNA- <i>Arg</i>	H	916-984	69			10
tRNA- <i>Asn</i>	H	995-1063	69			4
tRNA- <i>Ile</i>	H	1068-1136	69			1
<i>Nad3</i>	H	1138-1491	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1492-1559	68			0
<i>Nad2</i>	H	1560-2615	1056	ATG	TAA	2
<i>Cox1</i>	H	2618-4153	1536	ATG	TAA	20
<i>Cox2</i>	H	4174-4860	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4859-4926	68			1
<i>Atp8</i>	H	4928-5086	159	ATG	TAA	14
<i>Atp6</i>	H	5101-5796	696	ATG	TAA	45
tRNA- <i>Met</i>	L	5842-5907	66			13
tRNA- <i>Tyr</i>	L	5921-5988	68			4
tRNA- <i>Cys</i>	L	5993-6058	66			0
tRNA- <i>Trp</i>	L	6059-6124	66			1
tRNA- <i>Gln</i>	L	6126-6187	62			1
tRNA- <i>Gly</i>	L	6189-6255	67			0
tRNA- <i>Glu</i>	L	6256-6321	66			0
12s	H	6322-7298	977			0
tRNA- <i>Val</i>	H	7299-7367	69			0
16s	H	7368-8734	1367			0
tRNA- <i>Leu</i>	H	8735-8804	70			4
tRNA- <i>Leu</i>	H	8809-8877	69			0
<i>Nad1</i>	H	8878-9819	942	ATG	TAG	10
tRNA- <i>Pro</i>	H	9830-9900	71			1
<i>Nad6</i>	H	9902-10402	501	ATG	TAA	17
<i>Cytb</i>	H	10420-11559	1140	ATG	TAA	9
tRNA- <i>Ser</i>	H	11569-11633	65			0
tRNA- <i>Thr</i>	L	11634-11701	68			23
<i>Nad4L</i>	H	11725-12021	297	ATG	TAG	11
<i>Nad4</i>	H	12033-13388	1356	CTA	TAA	3
tRNA- <i>His</i>	H	13392-13456	65			1
<i>Nad5</i>	H	13458-15179	1722	ATG	TAG	20
tRNA- <i>Phe</i>	H	incomplete	—			—

Peristernia nassatula 15,106 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-747	incomplete	—	TAA	15
tRNA- <i>Lys</i>	H	763-830	68			4
tRNA- <i>Ala</i>	H	835-902	68			2
tRNA- <i>Arg</i>	H	903-971	69			2
tRNA- <i>Asn</i>	H	974-1040	67			16
tRNA- <i>Ile</i>	H	1057-1123	67			3
<i>Nad3</i>	H	1127-1480	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1481-1548	68			0
<i>Nad2</i>	H	1549-2603	1055	ATG	TA	0
<i>Cox1</i>	H	2604-4139	1536	ATG	TAG	23
<i>Cox2</i>	H	4163-4849	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4848-4915	68			1
<i>Atp8</i>	H	4917-5075	159	ATG	TAA	6
<i>Atp6</i>	H	5082-5777	696	ATG	TAA	31
tRNA- <i>Met</i>	L	5809-5874	66			8
tRNA- <i>Tyr</i>	L	5883-5947	65			1
tRNA- <i>Cys</i>	L	5949-6013	65			0
tRNA- <i>Trp</i>	L	6014-6080	67			1
tRNA- <i>Gln</i>	L	6082-6143	62			1
tRNA- <i>Gly</i>	L	6145-6211	67			0
tRNA- <i>Glu</i>	L	6212-6277	66			0
12s	H	6278-7240	963			0
tRNA- <i>Val</i>	H	7241-7307	67			0
16s	H	7308-8660	1353			0
tRNA- <i>Leu</i>	H	8661-8730	70			6
tRNA- <i>Leu</i>	H	8737-8805	69			0
<i>Nad1</i>	H	8806-9747	942	ATG	TAA	6
tRNA- <i>Pro</i>	H	9754-9823	70			1
<i>Nad6</i>	H	9825-10325	501	ATG	TAG	2
<i>Cytb</i>	H	10328-11467	1140	ATG	TAA	9
tRNA- <i>Ser</i>	H	11477-11540	64			0
tRNA- <i>Thr</i>	L	11541-11608	68			17
<i>Nad4L</i>	H	11626-11922	297	ATG	TAG	11
<i>Nad4</i>	H	11934-13287	1354	ATA	T	0
tRNA- <i>His</i>	H	13288-13356	69			0
<i>Nad5</i>	H	13357-15075	1719	ATG	TAG	31
tRNA- <i>Phe</i>	H	incomplete	—			—

Peristernia marquesana 15,088 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-738	incomplete	—	TAG	16
tRNA- <i>Lys</i>	H	755-824	70			5
tRNA- <i>Ala</i>	H	830-897	68			0
tRNA- <i>Arg</i>	H	898-966	69			2
tRNA- <i>Asn</i>	H	969-1035	67			17
tRNA- <i>Ile</i>	H	1053-1119	67			3
<i>Nad3</i>	H	1123-1476	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1477-1544	68			0
<i>Nad2</i>	H	1545-2599	1055	ATG	TA	0
<i>Cox1</i>	H	2600-4135	1536	ATG	TAA	12
<i>Cox2</i>	H	4148-4834	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4833-4900	68			1
<i>Atp8</i>	H	4902-5060	159	ATG	TAA	6
<i>Atp6</i>	H	5067-5762	696	ATG	TAA	33
tRNA- <i>Met</i>	L	5796-5861	66			9
tRNA- <i>Tyr</i>	L	5871-5936	66			1
tRNA- <i>Cys</i>	L	5938-6002	65			0
tRNA- <i>Trp</i>	L	6003-6069	67			1
tRNA- <i>Gln</i>	L	6071-6133	63			1
tRNA- <i>Gly</i>	L	6135-6201	67			0
tRNA- <i>Glu</i>	L	6202-6268	67			0
12s	H	6269-7229	961			0
tRNA- <i>Val</i>	H	7230-7296	67			0
16s	H	7297-8647	1351			0
tRNA- <i>Leu</i>	H	8648-8716	69			5
tRNA- <i>Leu</i>	H	8722-8790	69			0
<i>Nad1</i>	H	8791-9732	942	ATG	TAA	6
tRNA- <i>Pro</i>	H	9739-9808	70			1
<i>Nad6</i>	H	9810-10310	501	ATG	TAA	3
<i>Cytb</i>	H	10314-11453	1140	ATG	TAA	9
tRNA- <i>Ser</i>	H	11463-11526	64			0
tRNA- <i>Thr</i>	L	11527-11593	67			19
<i>Nad4L</i>	H	11613-11909	297	ATG	TAG	11
<i>Nad4</i>	H	11921-13274	1354	ATA	T	0
tRNA- <i>His</i>	H	13275-13344	70			0
<i>Nad5</i>	H	13345-15063	1719	ATG	TAG	25
tRNA- <i>Phe</i>	H	incomplete	—			—

Naytia priscardi 15,178bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	15
tRNA- <i>Lys</i>	H	766-832	67			3
tRNA- <i>Ala</i>	H	836-903	68			6
tRNA- <i>Arg</i>	H	910-978	69			5
tRNA- <i>Asn</i>	H	984-1050	67			17
tRNA- <i>Ile</i>	H	1068-1135	68			3
<i>Nad3</i>	H	1139-1492	354	ATG	TAG	0
tRNA- <i>Ser</i>	H	1493-1560	68			0
<i>Nad2</i>	H	1561-2616	1056	ATG	TAA	0
<i>Cox1</i>	H	2617-4152	1536	ATG	TAA	30
<i>Cox2</i>	H	4183-4869	687	ATG	TAA	1
tRNA- <i>Asp</i>	H	4871-4938	68			1
<i>Atp8</i>	H	4940-5098	159	ATG	TAA	6
<i>Atp6</i>	H	5105-5800	696	ATG	TAA	43
tRNA- <i>Met</i>	L	5844-5911	68			8
tRNA- <i>Tyr</i>	L	5920-5986	67			1
tRNA- <i>Cys</i>	L	5988-6052	65			0
tRNA- <i>Trp</i>	L	6053-6118	66			1
tRNA- <i>Gln</i>	L	6120-6181	62			1
tRNA- <i>Gly</i>	L	6183-6249	67			15
tRNA- <i>Glu</i>	L	6265-6329	65			0
12s	H	6330-7285	956			0
tRNA- <i>Val</i>	H	7286-7353	68			0
16s	H	7354-8711	1358			0
tRNA- <i>Leu</i>	H	8712-8780	69			2
tRNA- <i>Leu</i>	H	8783-8851	69			0
<i>Nad1</i>	H	8852-9793	942	ATG	TAA	8
tRNA- <i>Pro</i>	H	9802-9869	68			1
<i>Nad6</i>	H	9871-10371	501	ATG	TAA	13
<i>Cytb</i>	H	10385-11524	1140	ATG	TAA	16
tRNA- <i>Ser</i>	H	11541-11605	65			0
tRNA- <i>Thr</i>	L	11606-11673	68			31
<i>Nad4L</i>	H	11705-12001	297	ATG	TAG	11
<i>Nad4</i>	H	12013-13368	1356	TTA	TAG	-1
tRNA- <i>His</i>	H	13368-13432	65			1
<i>Nad5</i>	H	13434-15158	1725	ATG	TAG	20
tRNA- <i>Phe</i>	H	incomplete	—			—

Naytia glabrata 15,111 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-747	incomplete	—	TAA	15
tRNA- <i>Lys</i>	H	763-828	66			1
tRNA- <i>Ala</i>	H	830-897	68			6
tRNA- <i>Arg</i>	H	904-972	69			3
tRNA- <i>Asn</i>	H	976-1042	67			17
tRNA- <i>Ile</i>	H	1060-1127	68			3
<i>Nad3</i>	H	1131-1484	354	ATG	TAA	1
tRNA- <i>Ser</i>	H	1486-1553	68			0
<i>Nad2</i>	H	1554-2608	1055	ATG	TA	0
<i>Cox1</i>	H	2609-4144	1536	ATG	TAG	29
<i>Cox2</i>	H	4174-4860	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4859-4926	68			1
<i>Atp8</i>	H	4928-5086	159	ATG	TAA	7
<i>Atp6</i>	H	5094-5789	696	ATG	TAA	36
tRNA- <i>Met</i>	L	5826-5892	67			6
tRNA- <i>Tyr</i>	L	5899-5964	66			1
tRNA- <i>Cys</i>	L	5966-6030	65			0
tRNA- <i>Trp</i>	L	6031-6096	66			1
tRNA- <i>Gln</i>	L	6098-6159	62			1
tRNA- <i>Gly</i>	L	6161-6227	67			13
tRNA- <i>Glu</i>	L	6241-6305	65			0
12s	H	6306-7259	954			0
tRNA- <i>Val</i>	H	7260-7327	68			0
16s	H	7328-8677	1350			0
tRNA- <i>Leu</i>	H	8678-8746	69			6
tRNA- <i>Leu</i>	H	8753-8821	69			0
<i>Nad1</i>	H	8822-9763	942	ATG	TAA	7
tRNA- <i>Pro</i>	H	9771-9838	68			1
<i>Nad6</i>	H	9840-10340	501	ATG	TAA	5
<i>Cytb</i>	H	10346-11485	1140	ATG	TAG	11
tRNA- <i>Ser</i>	H	11497-11561	65			0
tRNA- <i>Thr</i>	L	11562-11628	67			19
<i>Nad4L</i>	H	11648-11944	297	ATG	TAG	11
<i>Nad4</i>	H	11956-13311	1356	CTA	TAG	-1
tRNA- <i>His</i>	H	13311-13376	66			1
<i>Nad5</i>	H	13378-15099	1722	ATG	TAG	12
tRNA- <i>Phe</i>	H	incomplete	—			—

Fasciolaria tulipa 15,042 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-747	incomplete	—	TAA	12
tRNA- <i>Lys</i>	H	760-822	63			0
tRNA- <i>Ala</i>	H	823-889	67			0
tRNA- <i>Arg</i>	H	890-958	69			3
tRNA- <i>Asn</i>	H	962-1027	66			9
tRNA- <i>Ile</i>	H	1037-1102	66			3
<i>Nad3</i>	H	1106-1459	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1460-1527	68			0
<i>Nad2</i>	H	1528-2582	1055	ATG	TA	0
<i>Cox1</i>	H	2583-4118	1536	ATG	TAA	25
<i>Cox2</i>	H	4144-4830	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4829-4896	68			1
<i>Atp8</i>	H	4898-5056	159	ATG	TAA	2
<i>Atp6</i>	H	5059-5751	693	ATG		40
tRNA- <i>Met</i>	L	5792-5856	65			5
tRNA- <i>Tyr</i>	L	5862-5927	66			1
tRNA- <i>Cys</i>	L	5929-5991	63			0
tRNA- <i>Trp</i>	L	5992-6058	67			1
tRNA- <i>Gln</i>	L	6060-6121	62			1
tRNA- <i>Gly</i>	L	6123-6188	66			0
tRNA- <i>Glu</i>	L	6189-6254	66			0
12s	H	6255-7208	954			0
tRNA- <i>Val</i>	H	7209-7275	67			0
16s	H	7276-8608	1333			0
tRNA- <i>Leu</i>	H	8609-8678	70			4
tRNA- <i>Leu</i>	H	8683-8751	69			0
<i>Nad1</i>	H	8752-9693	942	ATG	TAG	6
tRNA- <i>Pro</i>	H	9700-9767	68			1
<i>Nad6</i>	H	9769-10269	501	ATG	TAA	2
<i>Cytb</i>	H	10272-11411	1140	ATG	TAG	11
tRNA- <i>Ser</i>	H	11423-11486	64			0
tRNA- <i>Thr</i>	L	11487-11551	65			16
<i>Nad4L</i>	H	11568-11864	297	ATG	TAG	11
<i>Nad4</i>	H	11876-13231	1356	CTT	TAA	0
tRNA- <i>His</i>	H	13232-13296	65			0
<i>Nad5</i>	H	13297-15012	1716	ATG	TAG	30
tRNA- <i>Phe</i>	H	incomplete	—			—

Engoniophos uncinatus 15,215 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-757	incomplete	—	TAA	16
tRNA- <i>Lys</i>	H	774-841	68			5
tRNA- <i>Ala</i>	H	847-913	67			0
tRNA- <i>Arg</i>	H	914-982	69			5
tRNA- <i>Asn</i>	H	988-1055	68			23
tRNA- <i>Ile</i>	H	1079-1146	68			3
<i>Nad3</i>	H	1150-1503	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1504-1571	68			0
<i>Nad2</i>	H	1572-2625	1054	ATG	T	0
<i>Cox1</i>	H	2626-4161	1536	ATG	TAA	27
<i>Cox2</i>	H	4189-4875	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4874-4941	68			1
<i>Atp8</i>	H	4943-5101	159	ATG	TAA	11
<i>Atp6</i>	H	5113-5808	696	ATG	TAA	65
tRNA- <i>Met</i>	L	5874-5939	66			9
tRNA- <i>Tyr</i>	L	5949-6016	68			2
tRNA- <i>Cys</i>	L	6019-6083	65			0
tRNA- <i>Trp</i>	L	6084-6149	66			1
tRNA- <i>Gln</i>	L	6151-6212	62			1
tRNA- <i>Gly</i>	L	6214-6280	67			0
tRNA- <i>Glu</i>	L	6281-6347	67			0
12s	H	6348-7321	974			0
tRNA- <i>Val</i>	H	7322-7390	69			0
16s	H	7391-8759	1369			0
tRNA- <i>Leu</i>	H	8760-8829	70			7
tRNA- <i>Leu</i>	H	8837-8905	69			0
<i>Nad1</i>	H	8906-9847	942	ATG	TAA	11
tRNA- <i>Pro</i>	H	9859-9929	71			1
<i>Nad6</i>	H	9931-10431	501	ATG	TAA	12
<i>Cytb</i>	H	10444-11583	1140	ATG	TAA	10
tRNA- <i>Ser</i>	H	11594-11658	65			0
tRNA- <i>Thr</i>	L	11659-11726	68			19
<i>Nad4L</i>	H	11746-12042	297	ATG	TAG	11
<i>Nad4</i>	H	12054-13409	1356	TTA	TAA	0
tRNA- <i>His</i>	H	13410-13475	66			1
<i>Nad5</i>	H	13477-15198	1722	ATG	TAG	17
tRNA- <i>Phe</i>	H	incomplete	—			—

Cyellene parvula 15,207 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-771	incomplete	—	TAA	6
tRNA- <i>Lys</i>	H	778-846	69			4
tRNA- <i>Ala</i>	H	851-918	68			0
tRNA- <i>Arg</i>	H	919-987	69			18
tRNA- <i>Asn</i>	H	1006-1074	69			9
tRNA- <i>Ile</i>	H	1084-1154	71			3
<i>Nad3</i>	H	1158-1511	354	ATG	TAA	-1
tRNA- <i>Ser</i>	H	1511-1580	70			-1
<i>Nad2</i>	H	1580-2638	1059	ATG	TAA	0
<i>Cox1</i>	H	2639-4174	1536	ATG	TAA	22
<i>Cox2</i>	H	4197-4883	687	ATG	TAA	-3
tRNA- <i>Asp</i>	H	4881-4950	70			0
<i>Atp8</i>	H	4951-5109	159	ATG	TAG	7
<i>Atp6</i>	H	5117-5812	696	ATG	TAA	36
tRNA- <i>Met</i>	L	5849-5915	67			2
tRNA- <i>Tyr</i>	L	5918-5988	71			0
tRNA- <i>Cys</i>	L	5989-6053	65			0
tRNA- <i>Trp</i>	L	6054-6121	68			0
tRNA- <i>Gln</i>	L	6122-6185	64			1
tRNA- <i>Gly</i>	L	6187-6253	67			0
tRNA- <i>Glu</i>	L	6254-6322	69			0
12s	H	6323-7283	961			0
tRNA- <i>Val</i>	H	7284-7351	68			0
16s	H	7352-8714	1363			0
tRNA- <i>Leu</i>	H	8715-8783	69			7
tRNA- <i>Leu</i>	H	8791-8860	70			0
<i>Nad1</i>	H	8861-9802	942	ATG	TAA	13
tRNA- <i>Pro</i>	H	9816-9885	70			1
<i>Nad6</i>	H	9887-10387	501	ATG	TAA	9
<i>Cytb</i>	H	10397-11536	1140	ATG	TAA	14
tRNA- <i>Ser</i>	H	11551-11614	64			0
tRNA- <i>Thr</i>	L	11615-11681	67			16
<i>Nad4L</i>	H	11698-11994	297	ATG	TAG	11
<i>Nad4</i>	H	12006-13361	1356	CTA	TAA	1
tRNA- <i>His</i>	H	13363-13429	67			0
<i>Nad5</i>	H	13430-15154	1725	ATG	TAG	53
tRNA- <i>Phe</i>	H	incomplete	—			—

Cyellene lamarcki 15,187 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	16
tRNA- <i>Lys</i>	H	767-835	69			5
tRNA- <i>Ala</i>	H	841-907	67			0
tRNA- <i>Arg</i>	H	908-976	69			20
tRNA- <i>Asn</i>	H	997-1062	66			4
tRNA- <i>Ile</i>	H	1067-1135	69			3
<i>Nad3</i>	H	1139-1492	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1493-1560	68			0
<i>Nad2</i>	H	1561-2619	1059	ATG	TAA	0
<i>Cox1</i>	H	2620-4155	1536	ATG	TAA	20
<i>Cox2</i>	H	4176-4862	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4861-4928	68			1
<i>Atp8</i>	H	4930-5088	159	ATG	TAA	7
<i>Atp6</i>	H	5096-5791	696	ATG	TAG	36
tRNA- <i>Met</i>	L	5828-5893	66			6
tRNA- <i>Tyr</i>	L	5900-5964	65			3
tRNA- <i>Cys</i>	L	5968-6032	65			0
tRNA- <i>Trp</i>	L	6033-6100	68			1
tRNA- <i>Gln</i>	L	6102-6163	62			1
tRNA- <i>Gly</i>	L	6165-6231	67			0
tRNA- <i>Glu</i>	L	6232-6297	66			0
12s	H	6298-7276	979			0
tRNA- <i>Val</i>	H	7277-7344	68			0
16s	H	7345-8709	1365			0
tRNA- <i>Leu</i>	H	8710-8778	69			7
tRNA- <i>Leu</i>	H	8786-8854	69			0
<i>Nad1</i>	H	8855-9796	942	ATG	TAA	8
tRNA- <i>Pro</i>	H	9805-9875	71			1
<i>Nad6</i>	H	9877-10377	501	ATG	TAA	5
<i>Cytb</i>	H	10383-11522	1140	ATG	TAA	9
tRNA- <i>Ser</i>	H	11532-11597	66			0
tRNA- <i>Thr</i>	L	11598-11665	68			15
<i>Nad4L</i>	H	11681-11977	297	ATG	TAG	11
<i>Nad4</i>	H	11989-13344	1356	CTA	TAA	30
tRNA- <i>His</i>	H	13375-13440	66			0
<i>Nad5</i>	H	13441-15165	1725	ATG	TAG	22
tRNA- <i>Phe</i>	H	incomplete	—			—

Crassicantharus noumeensis 15,112 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-758	incomplete	—	TAA	17
tRNA- <i>Lys</i>	H	776-841	66			1
tRNA- <i>Ala</i>	H	843-909	67			6
tRNA- <i>Arg</i>	H	916-984	69			5
tRNA- <i>Asn</i>	H	990-1057	68			3
tRNA- <i>Ile</i>	H	1061-1127	67			3
<i>Nad3</i>	H	1131-1484	354	ATG	TAA	-1
tRNA- <i>Ser</i>	H	1484-1551	68			0
<i>Nad2</i>	H	1552-2603	1052	ATG	TA	0
<i>Cox1</i>	H	2604-4136	1533	ATG	TAA	21
<i>Cox2</i>	H	4158-4844	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4843-4911	69			0
<i>Atp8</i>	H	4912-5070	159	ATG	TAG	19
<i>Atp6</i>	H	5090-5785	696	ATG	TAA	35
tRNA- <i>Met</i>	L	5821-5885	65			2
tRNA- <i>Tyr</i>	L	5888-5953	66			1
tRNA- <i>Cys</i>	L	5955-6018	64			0
tRNA- <i>Trp</i>	L	6019-6086	68			1
tRNA- <i>Gln</i>	L	6088-6150	63			1
tRNA- <i>Gly</i>	L	6152-6219	68			0
tRNA- <i>Glu</i>	L	6220-6285	66			0
12s	H	6286-7239	954			0
tRNA- <i>Val</i>	H	7240-7305	66			0
16s	H	7306-8674	1369			0
tRNA- <i>Leu</i>	H	8675-8743	69			5
tRNA- <i>Leu</i>	H	8749-8817	69			0
<i>Nad1</i>	H	8818-9759	942	ATG	TAA	2
tRNA- <i>Pro</i>	H	9762-9829	68			1
<i>Nad6</i>	H	9831-10337	507	ATG	TAA	6
<i>Cytb</i>	H	10344-11483	1140	ATG	TAA	7
tRNA- <i>Ser</i>	H	11491-11555	65			1
tRNA- <i>Thr</i>	L	11557-11621	65			13
<i>Nad4L</i>	H	11635-11931	297	ATG	TAA	11
<i>Nad4</i>	H	11943-13298	1356	GTT	TAA	2
tRNA- <i>His</i>	H	13301-13366	66			0
<i>Nad5</i>	H	13367-15088	1722	ATG	TAG	24
tRNA- <i>Phe</i>	H	incomplete	—			—

Cosmioconcha nitens 15,041 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAG	14
tRNA- <i>Lys</i>	H	765-829	65			5
tRNA- <i>Ala</i>	H	835-901	67			2
tRNA- <i>Arg</i>	H	904-972	69			0
tRNA- <i>Asn</i>	H	973-1041	69			1
tRNA- <i>Ile</i>	H	1043-1110	68			2
<i>Nad3</i>	H	1113-1466	354	ATG	TAA	7
tRNA- <i>Ser</i>	H	1474-1541	68			0
<i>Nad2</i>	H	1542-2594	1053	ATG	TAA	0
<i>Cox1</i>	H	2595-4127	1533	ATG	TAA	20
<i>Cox2</i>	H	4148-4834	687	ATG	TAA	2
tRNA- <i>Asp</i>	H	4837-4905	69			0
<i>Atp8</i>	H	4906-5064	159	ATG	TAA	8
<i>Atp6</i>	H	5073-5768	696	ATG	TAA	38
tRNA- <i>Met</i>	L	5807-5873	67			5
tRNA- <i>Tyr</i>	L	5879-5944	66			2
tRNA- <i>Cys</i>	L	5947-6010	64			0
tRNA- <i>Trp</i>	L	6011-6077	67			1
tRNA- <i>Gln</i>	L	6079-6140	62			2
tRNA- <i>Gly</i>	L	6143-6209	67			0
tRNA- <i>Glu</i>	L	6210-6274	65			0
12s	H	6275-7232	958			0
tRNA- <i>Val</i>	H	7233-7302	70			0
16s	H	7303-8651	1349			0
tRNA- <i>Leu</i>	H	8652-8720	69			3
tRNA- <i>Leu</i>	H	8724-8793	70			0
<i>Nad1</i>	H	8794-9733	940	ATG	T	0
tRNA- <i>Pro</i>	H	9734-9801	68			1
<i>Nad6</i>	H	9803-10301	499	ATG	T	0
<i>Cytb</i>	H	10302-11441	1140	ATG	TAA	2
tRNA- <i>Ser</i>	H	11444-11512	69			0
tRNA- <i>Thr</i>	L	11513-11580	68			7
<i>Nad4L</i>	H	11588-11884	297	ATG	TAG	11
<i>Nad4</i>	H	11896-13251	1356	AGT	TAG	-1
tRNA- <i>His</i>	H	13251-13315	65			1
<i>Nad5</i>	H	13317-15038	1722	ATG	TAA	3
tRNA- <i>Phe</i>	H	incomplete	—			—

Bullia sp. 15,103 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	12
tRNA- <i>Lys</i>	H	763-832	70			2
tRNA- <i>Ala</i>	H	835-902	68			0
tRNA- <i>Arg</i>	H	903-971	69			4
tRNA- <i>Asn</i>	H	976-1043	68			4
tRNA- <i>Ile</i>	H	1048-1116	69			3
<i>Nad3</i>	H	1120-1473	354	ATG	TAG	10
tRNA- <i>Ser</i>	H	1484-1551	68			0
<i>Nad2</i>	H	1552-2606	1055	ATG	TA	0
<i>Cox1</i>	H	2607-4142	1536	ATG	TAG	20
<i>Cox2</i>	H	4163-4849	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4848-4915	68			1
<i>Atp8</i>	H	4917-5075	159	ATG	TAA	7
<i>Atp6</i>	H	5083-5778	696	ATG	TAG	38
tRNA- <i>Met</i>	L	5817-5882	66			3
tRNA- <i>Tyr</i>	L	5886-5952	67			6
tRNA- <i>Cys</i>	L	5959-6022	64			5
tRNA- <i>Trp</i>	L	6028-6093	66			1
tRNA- <i>Gln</i>	L	6095-6157	63			1
tRNA- <i>Gly</i>	L	6159-6226	68			0
tRNA- <i>Glu</i>	L	6227-6293	67			0
12s	H	6294-7239	946			0
tRNA- <i>Val</i>	H	7240-7307	68			0
16s	H	7308-8653	1346			0
tRNA- <i>Leu</i>	H	8654-8724	71			5
tRNA- <i>Leu</i>	H	8730-8798	69			0
<i>Nad1</i>	H	8799-9740	942	ATG	TAA	4
tRNA- <i>Pro</i>	H	9745-9814	70			1
<i>Nad6</i>	H	9816-10316	501	ATG	TAA	1
<i>Cytb</i>	H	10318-11457	1140	ATG	TAA	13
tRNA- <i>Ser</i>	H	11471-11535	65			0
tRNA- <i>Thr</i>	L	11536-11603	68			12
<i>Nad4L</i>	H	11616-11912	297	ATG	TAG	11
<i>Nad4</i>	H	11924-13279	1356	CTT	TAA	-1
tRNA- <i>His</i>	H	13279-13344	66			0
<i>Nad5</i>	H	13345-15061	1717	ATG	T	42
tRNA- <i>Phe</i>	H	incomplete	—			—

Bullia natalensis 15,103 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-749	incomplete	—	TAA	13
tRNA- <i>Lys</i>	H	763-831	69			2
tRNA- <i>Ala</i>	H	834-901	68			0
tRNA- <i>Arg</i>	H	902-970	69			6
tRNA- <i>Asn</i>	H	977-1044	68			3
tRNA- <i>Ile</i>	H	1048-1116	69			3
<i>Nad3</i>	H	1120-1473	354	ATG	TAA	1
tRNA- <i>Ser</i>	H	1475-1542	68			0
<i>Nad2</i>	H	1543-2597	1055	ATG	TA	0
<i>Cox1</i>	H	2598-4133	1536	ATG	TAG	23
<i>Cox2</i>	H	4157-4843	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4842-4909	68			1
<i>Atp8</i>	H	4911-5069	159	ATG	TAA	7
<i>Atp6</i>	H	5077-5772	696	ATG	TAG	38
tRNA- <i>Met</i>	L	5811-5876	66			9
tRNA- <i>Tyr</i>	L	5886-5951	66			5
tRNA- <i>Cys</i>	L	5957-6023	67			7
tRNA- <i>Trp</i>	L	6031-6097	67			1
tRNA- <i>Gln</i>	L	6099-6160	62			1
tRNA- <i>Gly</i>	L	6162-6228	67			0
tRNA- <i>Glu</i>	L	6229-6294	66			0
12s	H	6295-7248	954			0
tRNA- <i>Val</i>	H	7249-7317	69			0
16s	H	7318-8671	1354			0
tRNA- <i>Leu</i>	H	8672-8742	71			5
tRNA- <i>Leu</i>	H	8748-8816	69			0
<i>Nad1</i>	H	8817-9758	942	ATG	TAA	4
tRNA- <i>Pro</i>	H	9763-9832	70			1
<i>Nad6</i>	H	9834-10334	501	ATG	TAG	1
<i>Cytb</i>	H	10336-11475	1140	ATG	TAG	15
tRNA- <i>Ser</i>	H	11491-11555	65			0
tRNA- <i>Thr</i>	L	11556-11623	68			11
<i>Nad4L</i>	H	11635-11931	297	ATG	TAG	11
<i>Nad4</i>	H	11943-13298	1356	TTT	TAA	-1
tRNA- <i>His</i>	H	13298-13364	67			0
<i>Nad5</i>	H	13365-15081	1717	ATG	T	22
tRNA- <i>Phe</i>	H	incomplete	—			—

Bullia perluxida 15,099 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	12
tRNA- <i>Lys</i>	H	763-832	70			2
tRNA- <i>Ala</i>	H	835-902	68			0
tRNA- <i>Arg</i>	H	903-971	69			4
tRNA- <i>Asn</i>	H	976-1043	68			4
tRNA- <i>Ile</i>	H	1048-1116	69			3
<i>Nad3</i>	H	1120-1473	354	ATG	TAG	10
tRNA- <i>Ser</i>	H	1484-1551	68			0
<i>Nad2</i>	H	1552-2606	1055	ATG	TA	0
<i>Cox1</i>	H	2607-4142	1536	ATG	TAG	21
<i>Cox2</i>	H	4164-4850	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4849-4916	68			1
<i>Atp8</i>	H	4918-5076	159	ATG	TAA	7
<i>Atp6</i>	H	5084-5779	696	ATG	TAG	38
tRNA- <i>Met</i>	L	5818-5883	66			7
tRNA- <i>Tyr</i>	L	5891-5957	67			4
tRNA- <i>Cys</i>	L	5962-6026	65			4
tRNA- <i>Trp</i>	L	6031-6096	66			1
tRNA- <i>Gln</i>	L	6098-6159	62			1
tRNA- <i>Gly</i>	L	6161-6227	67			0
tRNA- <i>Glu</i>	L	6228-6294	67			0
12s	H	6295-7241	947			0
tRNA- <i>Val</i>	H	7242-7309	68			0
16s	H	7310-8655	1346			0
tRNA- <i>Leu</i>	H	8656-8725	70			5
tRNA- <i>Leu</i>	H	8731-8799	69			0
<i>Nad1</i>	H	8800-9741	942	ATG	TAA	4
tRNA- <i>Pro</i>	H	9746-9815	70			1
<i>Nad6</i>	H	9817-10317	501	ATG	TAA	1
<i>Cytb</i>	H	10319-11458	1140	ATG	TAA	13
tRNA- <i>Ser</i>	H	11472-11536	65			0
tRNA- <i>Thr</i>	L	11537-11604	68			12
<i>Nad4L</i>	H	11617-11913	297	ATG	TAG	11
<i>Nad4</i>	H	11925-13280	1356	CTT	TAA	-1
tRNA- <i>His</i>	H	13280-13345	66			0
<i>Nad5</i>	H	13346-15064	1717	ATG	T	37
tRNA- <i>Phe</i>	H	incomplete	—			—

Bullia diluta 15,084 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAG	12
tRNA- <i>Lys</i>	H	763-834	72			2
tRNA- <i>Ala</i>	H	837-904	68			0
tRNA- <i>Arg</i>	H	905-973	69			5
tRNA- <i>Asn</i>	H	979-1046	68			3
tRNA- <i>Ile</i>	H	1050-1118	69			3
<i>Nad3</i>	H	1122-1475	354	ATG	TAA	1
tRNA- <i>Ser</i>	H	1477-1544	68			0
<i>Nad2</i>	H	1545-2599	1055	ATG	TA	0
<i>Cox1</i>	H	2600-4135	1536	ATG	TAA	20
<i>Cox2</i>	H	4156-4842	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4841-4908	68			1
<i>Atp8</i>	H	4910-5068	159	ATG	TAG	7
<i>Atp6</i>	H	5076-5771	696	ATG	TAA	38
tRNA- <i>Met</i>	L	5810-5875	66			7
tRNA- <i>Tyr</i>	L	5883-5948	66			1
tRNA- <i>Cys</i>	L	5950-6013	64			8
tRNA- <i>Trp</i>	L	6022-6087	66			1
tRNA- <i>Gln</i>	L	6089-6150	62			1
tRNA- <i>Gly</i>	L	6152-6218	67			0
tRNA- <i>Glu</i>	L	6219-6285	67			0
12s	H	6286-7235	950			0
tRNA- <i>Val</i>	H	7236-7304	69			0
16s	H	7305-8651	1347			0
tRNA- <i>Leu</i>	H	8652-8721	70			5
tRNA- <i>Leu</i>	H	8727-8795	69			0
<i>Nad1</i>	H	8796-9737	942	ATG	TAA	4
tRNA- <i>Pro</i>	H	9742-9811	70			1
<i>Nad6</i>	H	9813-10313	501	ATG	TAA	1
<i>Cytb</i>	H	10315-11454	1140	ATG	TAA	13
tRNA- <i>Ser</i>	H	11468-11532	65			0
tRNA- <i>Thr</i>	L	11533-11600	68			12
<i>Nad4L</i>	H	11613-11909	297	ATG	TAG	11
<i>Nad4</i>	H	11921-13276	1356	TTT	TAA	-1
tRNA- <i>His</i>	H	13276-13342	67			0
<i>Nad5</i>	H	13343-15059	1717	ATG	T	25
tRNA- <i>Phe</i>	H	incomplete	—			—

Bullia cataphracta 15,094 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	12
tRNA- <i>Lys</i>	H	763-831	69			2
tRNA- <i>Ala</i>	H	834-901	68			0
tRNA- <i>Arg</i>	H	902-970	69			6
tRNA- <i>Asn</i>	H	977-1044	68			3
tRNA- <i>Ile</i>	H	1048-1115	68			3
<i>Nad3</i>	H	1119-1472	354	ATG	TAA	1
tRNA- <i>Ser</i>	H	1474-1541	68			0
<i>Nad2</i>	H	1542-2596	1055	ATG	TA	0
<i>Cox1</i>	H	2597-4132	1536	ATG	TAA	20
<i>Cox2</i>	H	4153-4839	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4838-4905	68			1
<i>Atp8</i>	H	4907-5065	159	ATG	TAA	7
<i>Atp6</i>	H	5073-5768	696	ATG	TAG	38
tRNA- <i>Met</i>	L	5807-5872	66			8
tRNA- <i>Tyr</i>	L	5881-5946	66			1
tRNA- <i>Cys</i>	L	5948-6011	64			12
tRNA- <i>Trp</i>	L	6024-6090	67			1
tRNA- <i>Gln</i>	L	6092-6153	62			1
tRNA- <i>Gly</i>	L	6155-6221	67			0
tRNA- <i>Glu</i>	L	6222-6287	66			0
12s	H	6288-7240	953			0
tRNA- <i>Val</i>	H	7241-7309	69			0
16s	H	7310-8661	1352			0
tRNA- <i>Leu</i>	H	8662-8732	71			5
tRNA- <i>Leu</i>	H	8738-8806	69			0
<i>Nad1</i>	H	8807-9748	942	ATG	TAA	4
tRNA- <i>Pro</i>	H	9753-9822	70			1
<i>Nad6</i>	H	9824-10324	501	ATG	TAA	1
<i>Cytb</i>	H	10326-11465	1140	ATG	TAA	15
tRNA- <i>Ser</i>	H	11481-11545	65			0
tRNA- <i>Thr</i>	L	11546-11613	68			11
<i>Nad4L</i>	H	11625-11921	297	ATG	TAG	11
<i>Nad4</i>	H	11933-13288	1356	CTT	TAA	-1
tRNA- <i>His</i>	H	13288-13354	67			0
<i>Nad5</i>	H	13355-15073	1717	ATG	T	23
tRNA- <i>Phe</i>	H	incomplete	—			—

Buccinanops deformis 15,173 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-775	incomplete	—	TAG	17
tRNA- <i>Lys</i>	H	793-858	66			5
tRNA- <i>Ala</i>	H	864-930	67			-1
tRNA- <i>Arg</i>	H	930-1000	71			13
tRNA- <i>Asn</i>	H	1014-1086	73			13
tRNA- <i>Ile</i>	H	1100-1168	69			3
<i>Nad3</i>	H	1172-1525	354	ATG	TAG	0
tRNA- <i>Ser</i>	H	1526-1593	68			0
<i>Nad2</i>	H	1594-2648	1055	ATG	TA	0
<i>Cox1</i>	H	2649-4184	1536	ATG	TAG	18
<i>Cox2</i>	H	4203-4889	687	ATG	TAA	-1
tRNA- <i>Asp</i>	H	4889-4957	69			0
<i>Atp8</i>	H	4958-5116	159	ATG	TAA	2
<i>Atp6</i>	H	5119-5814	696	ATG	TAG	36
tRNA- <i>Met</i>	L	5851-5917	67			6
tRNA- <i>Tyr</i>	L	5924-5994	71			-1
tRNA- <i>Cys</i>	L	5994-6060	67			-2
tRNA- <i>Trp</i>	L	6059-6125	67			-3
tRNA- <i>Gln</i>	L	6123-6189	67			2
tRNA- <i>Gly</i>	L	6192-6258	67			-1
tRNA- <i>Glu</i>	L	6258-6325	68			0
12s	H	6326-7298	973			0
tRNA- <i>Val</i>	H	7299-7368	70			0
16s	H	7369-8722	1354			0
tRNA- <i>Leu</i>	H	8723-8791	69			9
tRNA- <i>Leu</i>	H	8801-8869	69			0
<i>Nad1</i>	H	8870-9811	942	ATG	TAA	6
tRNA- <i>Pro</i>	H	9818-9886	69			1
<i>Nad6</i>	H	9888-10388	501	ATG	TAA	2
<i>Cytb</i>	H	10391-11530	1140	ATG	TAA	5
tRNA- <i>Ser</i>	H	11536-11606	71			-1
tRNA- <i>Thr</i>	L	11606-11671	66			23
<i>Nad4L</i>	H	11695-11991	297	ATG	TAG	11
<i>Nad4</i>	H	12003-13358	1356	CTT	TAA	4
tRNA- <i>His</i>	H	13363-13430	68			0
<i>Nad5</i>	H	13431-15152	1722	ATG	TAG	21
tRNA- <i>Phe</i>	H	incomplete	—			—

Antillophos cf. smithi 15,226 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-768	incomplete	—	TAG	19
tRNA- <i>Lys</i>	H	788-854	67			11
tRNA- <i>Ala</i>	H	866-932	67			2
tRNA- <i>Arg</i>	H	935-1003	69			9
tRNA- <i>Asn</i>	H	1013-1081	69			3
tRNA- <i>Ile</i>	H	1085-1153	69			3
<i>Nad3</i>	H	1157-1510	354	ATG	TAG	0
tRNA- <i>Ser</i>	H	1511-1578	68			0
<i>Nad2</i>	H	1579-2634	1056	ATG	TAA	2
<i>Cox1</i>	H	2637-4172	1536	ATG	TAG	26
<i>Cox2</i>	H	4199-4885	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4884-4951	68			1
<i>Atp8</i>	H	4953-5111	159	ATG	TAA	14
<i>Atp6</i>	H	5126-5821	696	ATG	TAA	42
tRNA- <i>Met</i>	L	5864-5929	66			10
tRNA- <i>Tyr</i>	L	5940-6007	68			4
tRNA- <i>Cys</i>	L	6012-6078	67			0
tRNA- <i>Trp</i>	L	6079-6144	66			1
tRNA- <i>Gln</i>	L	6146-6207	62			1
tRNA- <i>Gly</i>	L	6209-6276	68			0
tRNA- <i>Glu</i>	L	6277-6341	65			0
12s	H	6342-7320	979			0
tRNA- <i>Val</i>	H	7321-7389	69			0
16s	H	7390-8757	1368			0
tRNA- <i>Leu</i>	H	8758-8827	70			7
tRNA- <i>Leu</i>	H	8835-8903	69			0
<i>Nad1</i>	H	8904-9845	942	ATG	TAG	10
tRNA- <i>Pro</i>	H	9856-9926	71			1
<i>Nad6</i>	H	9928-10428	501	ATG	TAA	19
<i>Cytb</i>	H	10448-11587	1140	ATG	TAA	10
tRNA- <i>Ser</i>	H	11598-11662	65			-1
tRNA- <i>Thr</i>	L	11663-11730	68			23
<i>Nad4L</i>	H	11754-12050	297	ATG	TAG	11
<i>Nad4</i>	H	12062-13417	1356	CTA	TAG	4
tRNA- <i>His</i>	H	13422-13486	65			1
<i>Nad5</i>	H	13488-15209	1722	ATG	TAG	17
tRNA- <i>Phe</i>	H	incomplete	—			—

Belomitra viridis 15,039 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-748	incomplete	—	TAG	11
tRNA- <i>Lys</i>	H	760-827	68			9
tRNA- <i>Ala</i>	H	837-903	67			1
tRNA- <i>Arg</i>	H	905-973	69			12
tRNA- <i>Asn</i>	H	986-1054	69			7
tRNA- <i>Ile</i>	H	1062-1130	69			3
<i>Nad3</i>	H	1134-1487	354	ATG	TAA	0
tRNA- <i>Ser</i>	H	1488-1555	68			0
<i>Nad2</i>	H	1556-2607	1052	ATG	TA	0
<i>Cox1</i>	H	2608-4140	1533	ATG	TAA	21
<i>Cox2</i>	H	4162-4848	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4847-4914	68			1
<i>Atp8</i>	H	4916-5074	159	ATG	TAA	2
<i>Atp6</i>	H	5077-5772	696	ATG	TAA	31
tRNA- <i>Met</i>	L	5804-5868	65			7
tRNA- <i>Tyr</i>	L	5876-5942	67			1
tRNA- <i>Cys</i>	L	5944-6008	65			0
tRNA- <i>Trp</i>	L	6009-6074	66			1
tRNA- <i>Gln</i>	L	6076-6137	62			3
tRNA- <i>Gly</i>	L	6141-6206	66			0
tRNA- <i>Glu</i>	L	6207-6274	68			0
12s	H	6275-7245	971			0
tRNA- <i>Val</i>	H	7246-7313	68			0
16s	H	7314-8675	1362			0
tRNA- <i>Leu</i>	H	8676-8745	70			1
tRNA- <i>Leu</i>	H	8747-8815	69			0
<i>Nad1</i>	H	8816-9757	942	ATG	TAG	5
tRNA- <i>Pro</i>	H	9763-9831	69			1
<i>Nad6</i>	H	9833-10336	504	ATG	TAA	9
<i>Cytb</i>	H	10346-11485	1140	ATG	TAA	8
tRNA- <i>Ser</i>	H	11494-11559	66			0
tRNA- <i>Thr</i>	L	11560-11623	64			7
<i>Nad4L</i>	H	11631-11927	297	ATG	TAG	11
<i>Nad4</i>	H	11939-13294	1356	CTA	TAA	0
tRNA- <i>His</i>	H	13295-13360	66			0
<i>Nad5</i>	H	13361-15039	1679	ATG	—	0
tRNA- <i>Phe</i>	H	missing	—			—

Clivipollia cf. incarnata 15,182 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-750	incomplete	—	TAA	30
tRNA- <i>Lys</i>	H	781-849	69			5
tRNA- <i>Ala</i>	H	855-921	67			0
tRNA- <i>Arg</i>	H	922-990	69			12
tRNA- <i>Asn</i>	H	1003-1071	69			11
tRNA- <i>Ile</i>	H	1083-1152	70			3
<i>Nad3</i>	H	1156-1509	354	ATG	TAA	2
tRNA- <i>Ser</i>	H	1512-1579	68			0
<i>Nad2</i>	H	1580-2637	1058	ATG	TA	0
<i>Cox1</i>	H	2638-4173	1536	ATG	TAG	27
<i>Cox2</i>	H	4201-4887	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4886-4953	68			1
<i>Atp8</i>	H	4955-5113	159	ATG	TAA	6
<i>Atp6</i>	H	5120-5815	696	ATG	TAA	36
tRNA- <i>Met</i>	L	5852-5917	66			7
tRNA- <i>Tyr</i>	L	5925-5991	67			1
tRNA- <i>Cys</i>	L	5993-6057	65			5
tRNA- <i>Trp</i>	L	6063-6129	67			1
tRNA- <i>Gln</i>	L	6131-6192	62			1
tRNA- <i>Gly</i>	L	6194-6260	67			0
tRNA- <i>Glu</i>	L	6261-6328	68			0
12s	H	6329-7280	952			0
tRNA- <i>Val</i>	H	7281-7348	68			0
16s	H	7349-8719	1371			0
tRNA- <i>Leu</i>	H	8720-8790	71			22
tRNA- <i>Leu</i>	H	8813-8881	69			0
<i>Nad1</i>	H	8882-9823	942	ATG	TAA	11
tRNA- <i>Pro</i>	H	9835-9904	70			1
<i>Nad6</i>	H	9906-10406	501	ATG	TAA	6
<i>Cytb</i>	H	10413-11552	1140	ATG	TAA	7
tRNA- <i>Ser</i>	H	11560-11624	65			0
tRNA- <i>Thr</i>	L	11625-11692	68			15
<i>Nad4L</i>	H	11708-12004	297	ATG	TAG	11
<i>Nad4</i>	H	12016-13371	1356	TTG	TAA	5
tRNA- <i>His</i>	H	13377-13444	68			0
<i>Nad5</i>	H	13445-15166	1722	ATG	TAG	16
tRNA- <i>Phe</i>	H	incomplete	—			—

Nassaria sp. 15,092 bp

Gene	Strand	Location	Size (bp)	Start Codon	Stop codon	Intergenic nucleotides
<i>Cox3</i>	H	1-753	incomplete	—	TAA	19
tRNA- <i>Lys</i>	H	773-840	68			4
tRNA- <i>Ala</i>	H	845-911	67			1
tRNA- <i>Arg</i>	H	913-981	69			10
tRNA- <i>Asn</i>	H	992-1060	69			10
tRNA- <i>Ile</i>	H	1071-1139	69			3
<i>Nad3</i>	H	1143-1496	354	ATG	TAG	7
tRNA- <i>Ser</i>	H	1504-1571	68			0
<i>Nad2</i>	H	1572-2627	1056	ATG	TAG	5
<i>Cox1</i>	H	2633-4168	1536	ATG	TAG	17
<i>Cox2</i>	H	4186-4872	687	ATG	TAA	-2
tRNA- <i>Asp</i>	H	4871-4938	68			1
<i>Atp8</i>	H	4940-5098	159	ATG	TAA	6
<i>Atp6</i>	H	5105-5800	696	ATG	TAA	36
tRNA- <i>Met</i>	L	5837-5902	66			15
tRNA- <i>Tyr</i>	L	5918-5982	65			1
tRNA- <i>Cys</i>	L	5984-6048	65			0
tRNA- <i>Trp</i>	L	6049-6115	67			1
tRNA- <i>Gln</i>	L	6117-6178	62			1
tRNA- <i>Gly</i>	L	6180-6246	67			0
tRNA- <i>Glu</i>	L	6247-6313	67			0
12s	H	6314-7289	976			0
tRNA- <i>Val</i>	H	7290-7357	68			0
16s	H	7358-8729	1372			0
tRNA- <i>Leu</i>	H	8730-8800	71			8
tRNA- <i>Leu</i>	H	8809-8877	69			0
<i>Nad1</i>	H	8878-9819	942	ATG	TAA	8
tRNA- <i>Pro</i>	H	9828-9895	68			1
<i>Nad6</i>	H	9897-10397	501	ATG	TAA	3
<i>Cytb</i>	H	10401-11540	1140	ATG	TAA	14
tRNA- <i>Ser</i>	H	11555-11619	65			0
tRNA- <i>Thr</i>	L	11620-11686	67			15
<i>Nad4L</i>	H	11702-11998	297	ATG	TAG	11
<i>Nad4</i>	H	12010-13363	1354	TTA	T	0
tRNA- <i>His</i>	H	13364-13429	66			1
<i>Nad5</i>	H	13431-15092	1662	ATG		0
tRNA- <i>Phe</i>	H	missing	—			—