

Supplementary material

Table S1: Notothenioid species sequences downloaded from GenBank and their accession numbers.

Species	GenBank accession numbers
Pseudaphritidae	
<i>Pseudaphritis urvillii</i>	JN186885
Bovichtidae	
<i>Bovichtus variegatus</i>	JN186882
Artedidraconidae	
<i>Dolloidraco longedorsalis</i>	FJ647587
<i>Pogonophryne barsukovi</i>	FJ973337
<i>Pogonophryne marmorata</i>	FJ973350
<i>Pogonophryne scotti</i>	JN186994
Bathydraconidae	
<i>Akarotaxis nudiceps</i>	HQ170108
<i>Bathydraco antarcticus</i>	HQ170113
<i>Bathydraco macrolepis</i>	HQ170110
<i>Bathydraco marri</i>	HQ170111
<i>Cygnodraco mawsoni</i>	HQ170116
<i>Gerlachea australis</i>	HQ170118
<i>Gymnodraco acuticeps</i>	HQ170120
<i>Parachaenichthys charcoti</i>	HQ170122
<i>Parachaenichthys georgianus</i>	HQ170123
<i>Psilodraco breviceps</i>	HQ170128
<i>Racovitzia glacialis</i>	HQ170130
Channichthyidae	
<i>Chaenocephalus aceratus</i>	AY249493
<i>Chaenodraco wilsoni</i>	AY249504
<i>Channichthys rhinoceratus</i>	AY249503
<i>Chionodraco hamatus</i>	HQ170101
<i>Chionodraco myersi</i>	HQ170103
<i>Chionodraco rastrospinosus</i>	AY249502
<i>Cryodraco antarcticus</i>	AY249494
<i>Dacodraco hunteri</i>	AY249479
<i>Nepagetopsis ionah</i>	HM165731

<i>Pagetopsis macropterus</i>	AY249511
<i>Pagetopsis maculatus</i>	AY249512
Harpagiferidae	
<i>Harpagifer antarcticus</i>	JN186896
Nototheniidae	
<i>Aethotaxis mitopteryx</i>	JN186895
<i>Dissostichus mawsoni</i>	AY517753
<i>Notothenia angustata</i>	AY256562
<i>Notothenia microlepidota</i>	AY256565
<i>Pagothenia borchgrevinki</i>	FJ647716
<i>Pleuragramma antarctica</i>	JN186912
<i>Trematomus bernacchii</i>	AY256569
<i>Trematomus eulepidotus</i>	FJ647718
<i>Trematomus hansonii</i>	FJ647748
<i>Trematomus lepidorhinus</i>	JN186913
<i>Trematomus loennbergii</i>	FJ647725
<i>Trematomus newnesi</i>	FJ647729
<i>Trematomus nicolai</i>	FJ647731
<i>Trematomus pennellii</i>	FJ647742

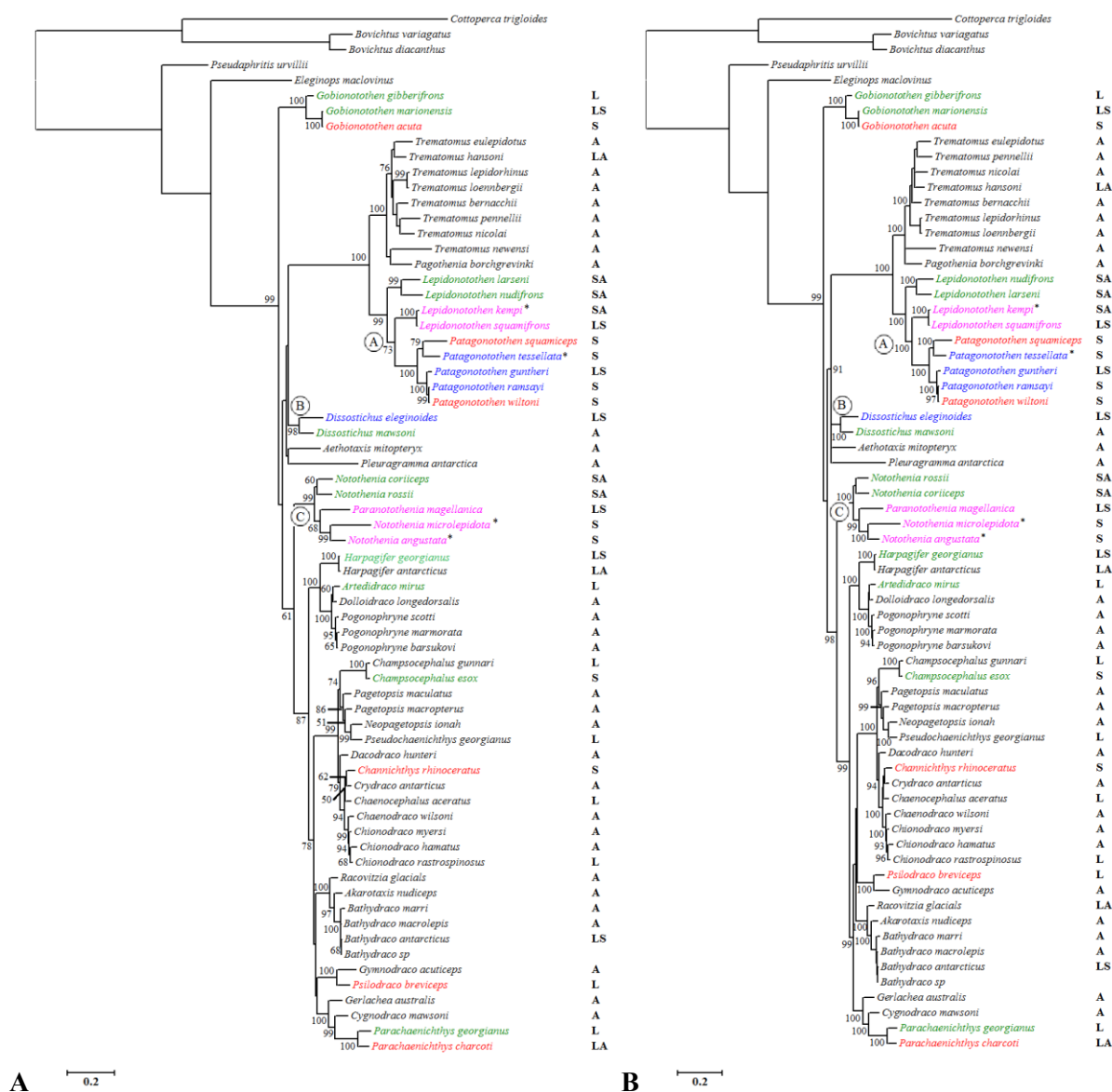


Fig. S1: ML (A) and BI (B) phylogenetic trees resulted from mtDNA ND2 gene analyses (for colour coding see Fig. 4). Trees were rooted with Bovichtidae. Nodes support for the ML tree (boot strap scores ≥ 50) and for the BI tree (posterior probabilities ≥ 90) are given.