

**Single copies of the 5S rRNA gene inserted into 45S rDNA intergenic spacers
in the genomes of Nototheniidae (Perciformes, Actinopterygii)**

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Supplementary material

Table S1. rDNA elements found in genome sequences of Nototheniidae representatives

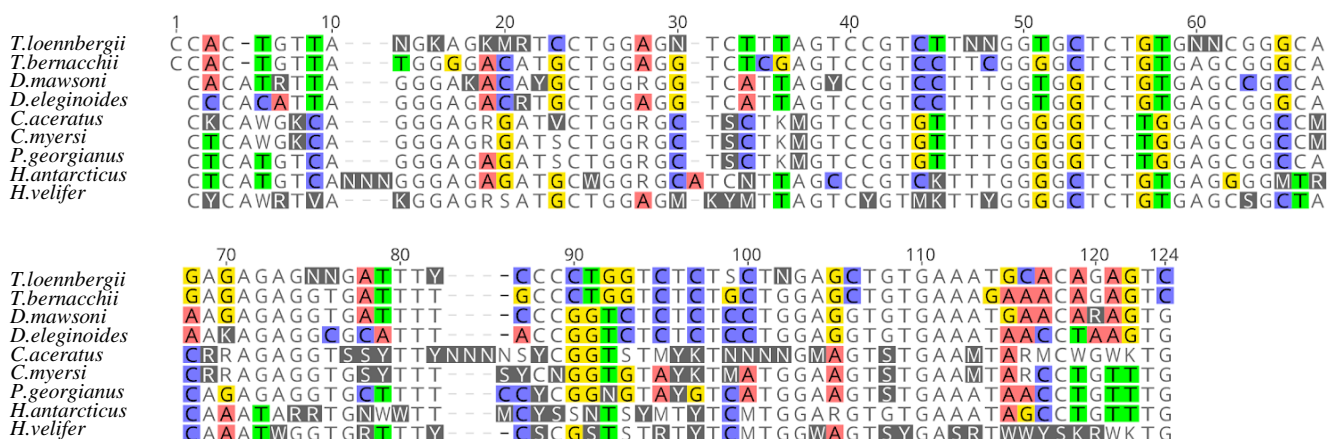
Species	NCBI whole genome shotgun sequence accession number	rDNA elements found in the genome sequence
Artedidraconinae		
<i>Histiodraco velifer</i>	CALSCB010033685	rDNA repeat partial
Bathydraconinae		
<i>Gymnodraco acuticeps</i>	CADEHQ010011037	rDNA repeat partial
Channichthyinae		
<i>Chaenocephalus aceratus</i>	JAMFTG010002228	2 Full rDNA repeats
<i>Chionodraco myersi</i>	RQJG01056976	rDNA repeat partial
<i>Pseudochaenichthys georgianus</i>	CADEHP020001122	rDNA repeat partial
Harpagiferinae		
<i>Harpagifer antarcticus</i>	CADEHR010007419	rDNA repeat partial
Dissostichinae		
<i>Dissostichus mawsoni</i>	JAAKFY010000885	1 full rDNA repeats
<i>Dissostichus eleginoides</i>	JAOVFM010000209	1 full rDNA repeats, 2 IGS
Trematominae		
<i>Trematomus loennbergii</i>	JAAOOA010003522	1 full rDNA repeats, 1 partial rDNA repeats
<i>Trematomus bernacchii</i>	CADEHO010005942	rDNA repeat partial

Figure S1. IGS repeats in Nototheniidae. The alignment of consensus repeat sequences found for each species is presented.

Repeat NR1 found in Trematominae (*Trematomus loennbergii*, *T. bernacchii*), Dissostichinae (*Dissostichus mawsoni*, *D. eleginoides*), Channichthyinae (*Chionodraco myersi*, *Chaenocephalus aceratus*, *Pseudochaenichthys georgianus*), Bathydraconinae (*Gymnodraco acuticeps*), Harpagiferinae (*Harpagifer antarcticus*), Artedraconinae (*Histiodraco velifer*)



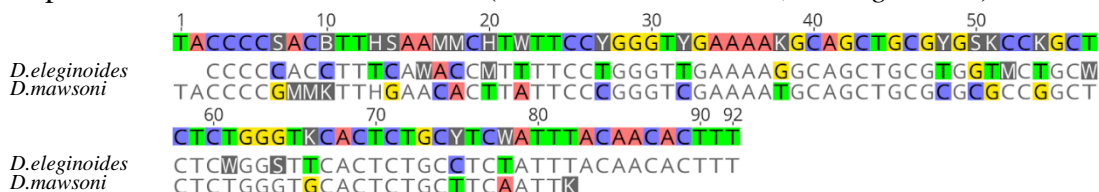
Repeat NR2 found in Trematominae (*Trematomus loennbergii*, *T. bernacchii*), Dissostichinae (*Dissostichus mawsoni*, *D. eleginoides*), Channichthyinae (*Chaenocephalus aceratus*, *Chionodraco myersi*, *Pseudochaenichthys georgianus*), Harpagiferinae (*Harpagifer antarcticus*), Artedraconinae (*Histiodraco velifer*)



Repeat GR2 found in Bathydraconinae (*Gymnodraco acuticeps*)



Repeat DR3 found in Dissostichinae (*Dissostichus mawsoni*, *D. eleginoides*)



Repeat TR3 found in Trematodinae (*Trematomus loennbergii*, *T. bernacchii*)

1 10 20 30 40 50 60
T.loennbergii AAACATGTTMCCCCACWGTAAACACAGTTTACCTGTGTTTIGARGACTCTTCCGGG
T.bernacchii AAACATGTTCCYCCACASTKTRACMCWGYTKTASCYRKSTTTYGAGSMYTCCTTTCCTGGG
 70 80 90 100 110 120
T.loennbergii TCAATGTGTCTCTCTTNNCCCCCTGGGTGTGTGTNNGAGACMAGTGAAGTGAGTCAG
T.bernacchii TCAATGTGTCTCTTCTC-CCCCCTGGGTGTGTGT--GAGACAAGTCAAGTGAGTCAG
 130 140 152
T.loennbergii SCTGCCAACAAAGCAGCAGTGTGTGTGTCATTTT
T.bernacchii SCTGCCAACAAAGCAGCAGTGTGTGTGTCATTTT

Repeat CR3 found in Channichthyinae (*Chionodraco myersi*, *Chaenocephalus aceratus*, *Pseudochaenichthys georgianus*)

1 10 20 30 40 50 60
C.myersi TTTTACCTTAA--AAACAGCTTTCTGCCCTGTAAATGATTTTAAT---CATT
C.aceratus TTTTACCTTAA--AAACAGCTTTCTGCCCTGTAAATGATTTTAAT---CATT
P.georgianus TATCTCCCTTAATTACAGCAAATCCATCTTTTNNACACTATTTATGGGTAAATNNNNNCATN
 70 80 90 100 110 120 130
C.myersi AY--ACCGTCATGGAGGAGCTGCAGGGACACTTTACCCGCTTTTAAACACCTTTTCATGGGT-AAAC
C.aceratus AY--ACCGTCATGGAGGAGCTGCAGGGACACTTTACCCGCTTTTAAACACCTTTTCATGGGT-AAAC
P.georgianus NNNWYACYGTMTKRAARGCTGCAGGACACTTTACCCGCTTTTAAACACCTTTTCATGGGTAAAC
 140 150 160 170 180 190 200 205
C.myersi AATCAATGATTTTCCGCCTGCTTTCCATCAGCACCCGCCAGTCATTTCAAACGGTTTCAAATCGTTT
C.aceratus AATCAATGATTTTCCGCCTGCTTTCCATCAGCACCCGCCAGTCATTTCAAACGGTTTCAAATCGTTT
P.georgianus AATCATKTATTTCCGCCTGCTTTCCATCAGCACCCGCCAGTCATTTCAAACGGTTTCAAATCGTTT

Repeat DR4 found in Dissostichinae (*Dissostichus mawsoni*, *D. eleginoides*)

1 10 20 30 40 50 60
D.mawsoni TACCCAGGWTCCARGCTMYYNCCYSGCTTTAATAGCTGTYYGYYGCCCTGGGAGTTS
D.eleginoides TACCCAGGATCCAGCTATTTTCCCTGGCTTTTAAATAGCTGTGTGGCCCTGGGAGTCT
 70 80 90 100 110 120 130 140 150
D.mawsoni TACCCAGGATCCAGGCTTTTCCCTGGCTTTTAAATAGCTGTGTGGCCCTGGGAGTCT
D.eleginoides TACCCAGGATCCAGGCTTTTCCCTGGCTTTTAAATAGCTGTGTGGCCCTGGGAGTCT
 160 170 180 190 200 210 220 230
D.mawsoni CCAYNNAASRCTGTTCACACAKWTSWTYCATCCRGGGGTGTATTTCAACCAWCTT
D.eleginoides CCA--AAGCTSTGCACACGTTT

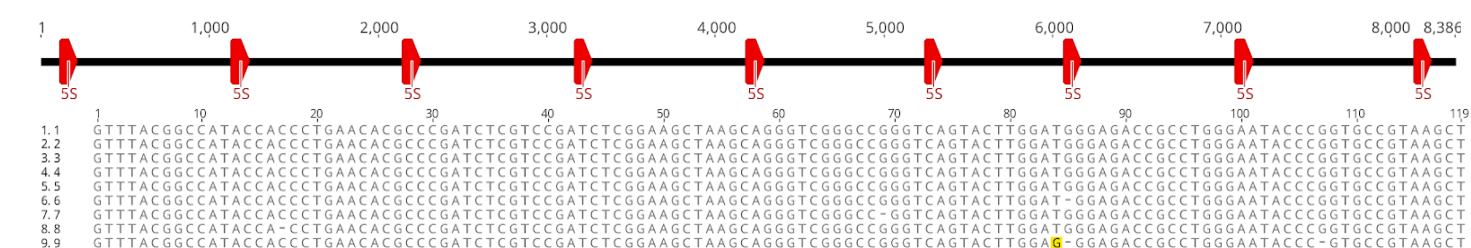
Repeat CR4 found in Channichthyinae (*Chionodraco myersi*, *Chaenocephalus aceratus*, *Pseudochaenichthys georgianus*)

1 10 20 30 40 50 60 70
C.myersi ATGAAATGGCCATATCTTCTTAAATTCACATCAMAATACCCAAGCTTTTACACACTAATTGGTGGGTAATGAGCC
C.aceratus ATGAAATGGCCATATCTTCTTAAATTCACATCAMAATACCCAAGCTTTTACACACTAATTGGTGGGTAATGAGCC
P.georgianus ATGAAATGGCCATATCTTCTTAAATTCACATCAMAATACCCAAGCTTTTACACACTAATTGGTGGGTAATGAGCC
 80 90 100 110 120 130 140 150
C.myersi ATGTGTACCTGTCTTTAAAGTAATTTTACCAGCTTTTACAGACCTAATTCCTGGGTAACAAAGTCACCCCTGGACCG
C.aceratus ATGTGTACCTGTCTTTAAAGTAATTTTACCAGCTTTTACAGACCTAATTCCTGGGTAACAAAGTCACCCCTGGACCG
P.georgianus ATGTGTACCTGTCTTTAAAGTAATTTTACCAGCTTTTACAGACCTAATTCCTGGGTAACAAAGTCACCCCTGGACCG
 160 170 180 190 200 210 220 229
C.myersi GTCATCAAAATGTGATTGAAATGGACAGATTCCTGTACATTTTCAATGCAATTTTAAATGGG-GTGGTGGTGG
C.aceratus GTCATCAAAATGTGATTGAAATGGACAGATTCCTGTACATTTTCAATGCAATTTTAAATGGG-GTGGTGGTGG
P.georgianus GTCATCAAAATGTGATTGAAATGGACAGATTCCTGTACATTTTCAATGCAATTTTAAATGGG-GTGGTGGTGG

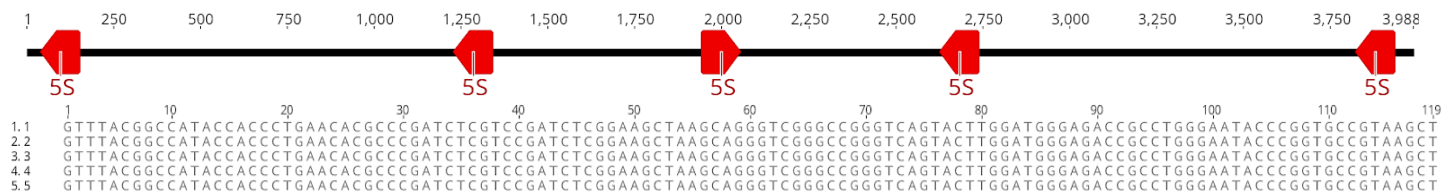
Repeat NR5 found in Dissostichinae (*Dissostichus mawsoni*, *D. eleginoides*), Trematodinae (*Trematomus loennbergii*), Channichthyinae (*Chaenocephalus aceratus*, *Chionodraco myersi*)

1 10 20 30 40 50 60 70
D.mawsoni ACACCTCTTCTGCTGTTTCTCAA
D.eleginoides AACACCCCTTTTGGCCYGGTTCTCAA
T.loennbergii GACCCCTTTTCCCGRTTCTCAC
C.aceratus CACCCCTTTTCTGGTTCTTCC
C.myersi CACCCCTTTTCTGGTTCTTCCNAAAGNNANABACCTTTCTYDAAAAGTTAACTAGACCTTTCTGACTCT
 80 90 100 110 120 130 140 150 158
D.mawsoni GGAGGAAATGAGGGGAGTTGACAGGGGACTCTABCCGCTSYATGAGCACTATTTTGGGACCTTTTATCATTTT
D.eleginoides GGAGGAAATGAGGGGAGTTGACAGGGGACTCTABCCGCTSYATGAGCACTATTTTGGGACCTTTTATCATTTT
T.loennbergii GGAGGAAATGAGGGGAGTTGACAGGGGACTCTABCCGCTSYATGAGCACTATTTTGGGACCTTTTATCATTTT
C.aceratus GGAGGAAATGAGGGGAGTTGACAGGGGACTCTABCCGCTSYATGAGCACTATTTTGGGACCTTTTATCATTTT
C.myersi GGAGGAAATGAGGGGAGTTGACAGGGGACTCTABCCGCTSYATGAGCACTATTTTGGGACCTTTTATCATTTT

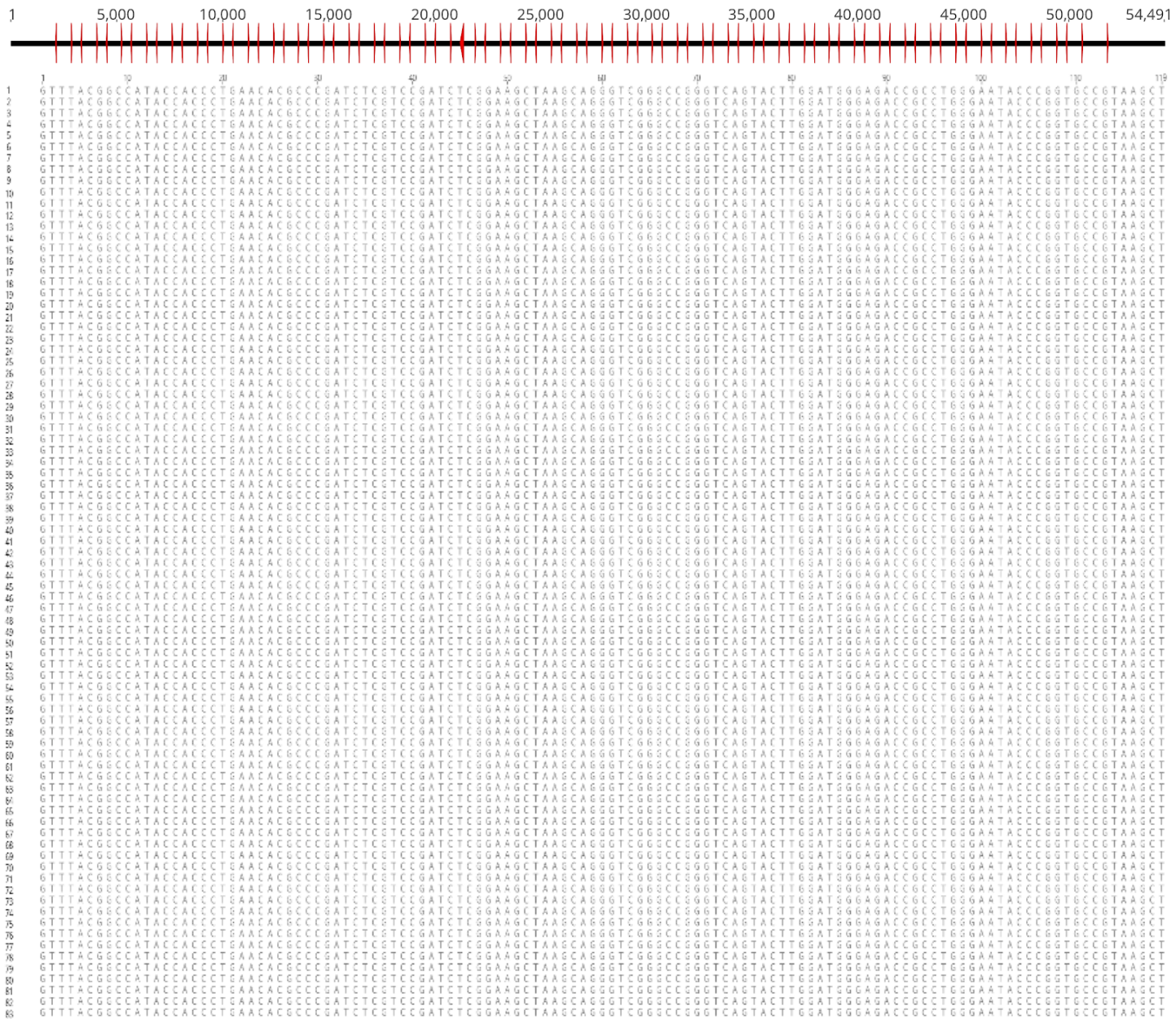
Pseudochaenichthys georgianus NCBI WGS CADEHK010005965



Trematomus bernacchii NCBI WGS CADEHO010006468



Dissostichus eleginoides NCBI WGS JAOVFM010000358



Dissostichus mawsoni NCBI WGS JAAKFY010000822

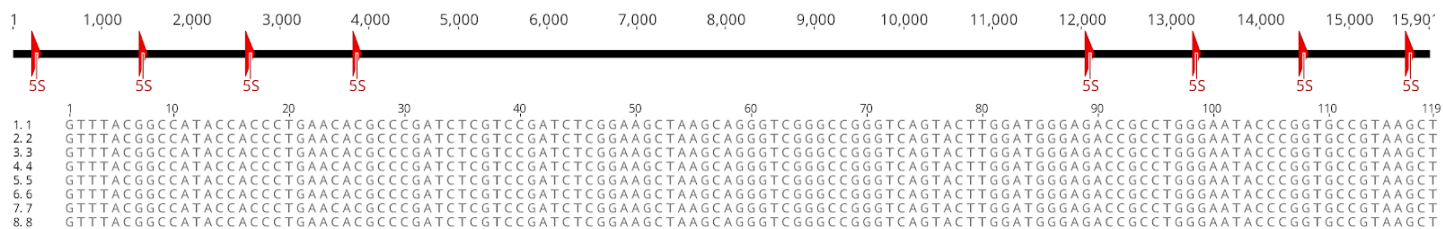


Figure S4. Different representation of the NOR-5S and NTS-5S rRNA sequencing reads in different tissue transcriptomes of *Dissostichus eleginoides* (Dissostichinae). Percentage of total 5S rRNA sequencing reads was calculated from NCBI BioProjects PRJNA864592 data.

