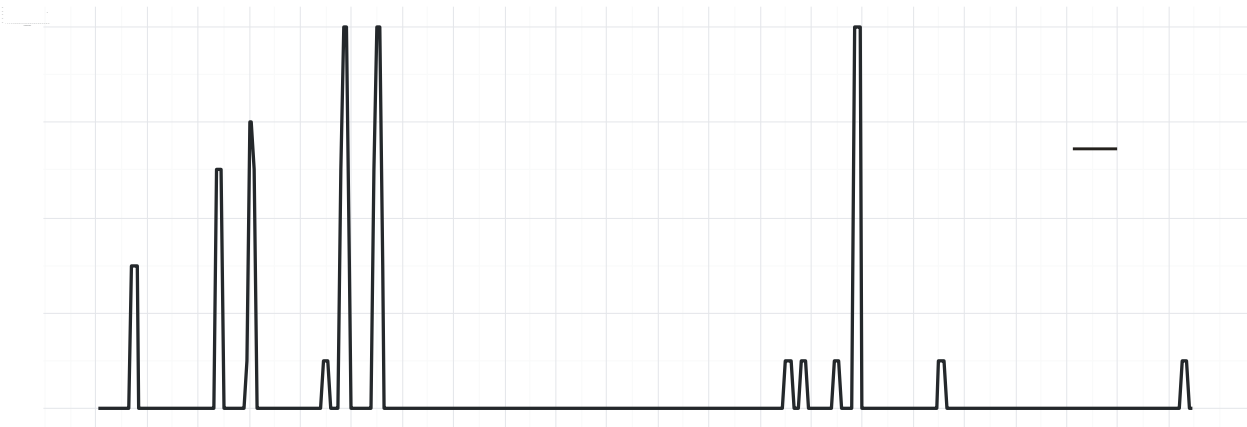


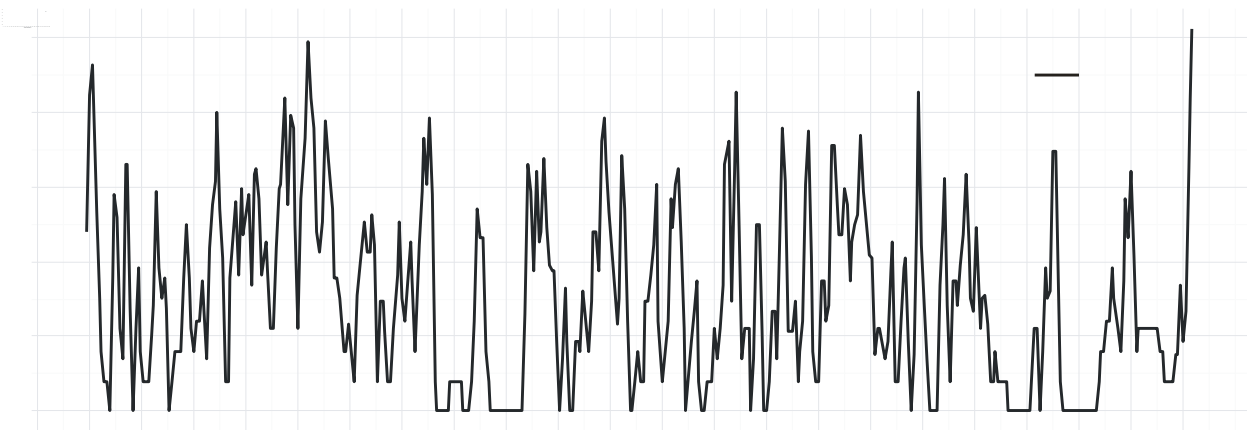
**Supplements** to the study “Structure, evolution and phylogenetic informativeness of eelpouts (Cottoidei: Zoarcales) mitochondrial control region sequences” by Turanov et al. 2018

**Supplementary Table S1.** The length and relative positions of annotated regions within full-length *CR* sequences of *S. grigorjewi*

Region	Position		Length, bp	Strain
	Beginning	End		
tRNA <sup>Pro</sup>	1	70	70	L
Control region	71	932	862	H
tRNA <sup>Phe</sup>	933	1000	78	H
12S rRNA	1001	1254	254	H



**Supplementary Figure S1.** The nucleotide diversity ( $\Pi$ ) landscape of 29 *CR* sequences of *S. grigorjewi* based on Jukes and Cantor correction.



**Supplementary Figure S2.** The landscape of *CR* nucleotide diversity ( $\Pi$ ) among eelpouts based on Jukes and Cantor correction.

**Supplementary Table S2.** The relative position and sequences of conserved domains of eelpouts' *CR* sequences.

	Position of CSB-I	CSB-II	Position of CSB-II	CSB-III	Position of CSB-III
AL	609-627	TAAAACCCCCCTACCCCCC	700-718	TGAAAACCCCCGGAACA	745-762
A					
M	611-629	TAAAACCCCCCTACCCCCC	702-720	TGAAAACCCCCGGAACA	747-764
AD	612-630	TAAAACCCCCCTACCCCCC	703-721	TGAAAACCCCCGGAACA	748-765
LT	632-650	TAAAACCCCCCTACCCCCC	723-741	TGAAAACCCCCGGAACA	768-785
PC	633-651	TAAAACCCCCCTACCCCCC	724-742	TGAAAACCCCCGGAACA	769-786
PF	633-651	TAAAACCCCCCTACCCCCC	724-742	TGAAAACCCCCGGAACA	769-786
SG	643-661	TAAAACCCCCCTACCCCCC	733-751	TGAAAACCCCCGGAACA	778-795
HD	614-632	TAAAACCCCCCTACCCCCC	705-723	TGAAAACCCCCGGAACA	750-767
	Position of CSB-A	CSB-B	Position of CSB-B	CSB-C	Position of CSB-C
AL	483-505	CGAGATAACCCAGCATGCCGG	450-470	CTTTCATCGACGCTTACATATGTGA	408-432
A					
M	485-507	CGAGATAACCCAGCATGCCGA	452-472	CTTTCATCGACGCTTACATACGTGA	410-434
AD	486-508	CGAGATAACTCAGCATGCCGG	453-473	CTTTCATCGACGCTTACATATGTGA	411-435
LT	506-526	CGAGATGACTCAGCATGCCGG	474-494	CTTTCATCGACGCTTACATAGATTA	432-456
PC	507-529	CGAGATGACCCAGCATGCCGG	475-495	CTTTCATCGACGCTTGCATAAGTTA	433-457
PF	507-529	CGAGATGACCCAGCATGCCGG	475-495	CTTTCATCGACGCTTGCATAAGTTA	433-457
SG	517-539	CGAGATGACTCAGCATGCCGG	485-505	CTTTCATCGACGCTTACATAAGTTA	443-467
HD	489-511	TCCGAGAACCGACCATGCCGG	457-477	CTTTCATCGACGCTTACATAAGTTA	417-441
	Position of CSB-D	CSB-E	Position of CSB-E	CSB-F	Position of CSB-F
AL	353-374	AGGGACAAGTATTTGAAGAGTT	318-339	ATGTAGTAAGAACCGACCA	262-280
A					
M	355-376	AGGGACAAGTATTTGAAGAGTT	320-341	ATGTAGTAAGAACCGACCA	264-282
AD	356-377	AGGGACAAGTATTTGAAGAGTT	321-342	ATGTAGTAAGAACCGACCA	265-283
LT	377-398	AGGGACAAGTATTTGTGGGGGT	341-362	ATGTAGTAAGAACCGACCA	285-303
PC	378-399	AGGGACAAGTATTCGTGGGGGT	342-363	ATGTAGTAAGAACCGACCA	285-303
PF	378-399	AGGGACAAGTATTCGTGGGGGT	342-363	ATGTAGTAAGAACCGACCA	285-303
SG	388-409	AGGGACAAGTATTAGTGGGGGT	352-373	ATGTAGTAAGAACCGACCA	295-313
HD	362-383	AGGGACAAGTATTCGTGGGGGT	326-347	ATGTAGTAAGAACCTACCA	269-287

**Supplementary Table S3.** The relative position and sequences of TAS domains within eelpouts' *CR*. Dashes signs indicate the absence of the respective TAS region.

TAS1		Position of TAS1	TAS2	Position of TAS2
AL	-	-	GCATGTATGT	11-20
AM	-	-	GCATATATGT	13-22
AD	-	-	GCATATATGT	14-23
LT	TCATATATGT	17-26	GCATATATGT	34-43
PC	-	-	GCATATATGT	34-43
PF	-	-	GCATATATGT	34-43
SG	ACARTATATGT	27-37	GCATATATGT	46-55
HD	ACATATATGT	5-14	GCATATATGT	23-32
TAS3		Position of TAS3	TAS4	Position of TAS4
AL	ACATATATATGT	66-77	ACATATATAGT	85-95
AM	ACATATATATGT	68-79	ACATATATAGT	87-97
AD	ACATATATATGT	69-80	ACATATATAGT	88-98
LT	ACATATATATGT	89-100	ACATATATAGT	108-118
PC	ACATATACATGT	89-100	ACATATCTAGT	108-118
PF	ACATATATATGT	89-100	ACACATCTAGT	108-118
SG	GACATAT--ATGT	100-110	ACAYRTATAGT	118-128
HD	ACACAT--ATGA	78-87	ACGTAAATAGT	95-105