

Table S1. Primers for amplifying 23 overlapping fragments to assemble mitogenomes of *Dipturus intermedius*. SKATEMG01F starts in the 12S rRNA. Primers were designed in Geneious V. 11.1.5 (Kearse et al. 2012) using Primer3 V. 2.3.7 (Untergasser et al., 2012) based on accessible mitogenomes (Jeong et al. 2015, Vargas-Caro et al. 2016). PCR included initial denaturation of 5 min at 95°C, 40 cycles of 95°C for 30 s, annealing with primer-specific temperatures (AT) for 30 s, extension at 72°C for 1.5 min, and a final extension at 72°C for 10 min

Primer Name	Sequence 5'-3'	Length (bp)	AT
SKATEMG01F	ACTGAAGGTTTGGTCCTGGC	20	60
SKATEMG01R	CGGTGTAAGGGAGGTGCTTT	20	60
SKATEMG02F	CCGTCACTCTCCTCAACTTACAT	23	60
SKATEMG02R	ATGACCTCAGGTTGGTGTGCG	20	60
SKATEMG03F	TTTCTCCAAACCCCTAACCAA	22	60
SKATEMG03R	TGGGGCATTGGCTTCATTCT	20	60
SKATEMG04F	CAGGACATCCTAATGGTGCA	20	57
SKATEMG04R	ATTATGGCTAGTGGTCAGGC	20	57
SKATEMG05F	CCCCACTCCATCTTAAACCT	20	57
SKATEMG05R	TTTTGATCTCTAGGGGCGAG	20	57
SKATEMG06F	TTCCTATGAATTCGTGCCTCCT	22	56
SKATEMG06R	CCTAGGTGGGCAATTGAGGA	20	56
SKATEMG07F	TTTGCCATCCTCTTCCAACCT	20	57
SKATEMG07R	CAACGATTAATTGCCACAGGT	21	57
SKATEMG08F	AAGCGTTCAATCCAGCGAAC	20	60
SKATEMG08R	CCAAATCCGGGTAGAATCAAATGT	25	60
SKATEMG09F	CTCCAGTTCTAGCAGCCG	19	56
SKATEMG09R	TAGGTGTGGTAAGGAGGGGG	20	56
SKATEMG10F	GGCATACCCGACGTTACTC	20	60
SKATEMG10R	CGGGAGATAATAAAGGCGGCT	21	60
SKATEMG11F	CGACTTCTAGAGACAGACCATCG	23	60
SKATEMG11R	GTCAGAGGGGAAGGGCAAAA	20	60
SKATEMG12F	GCCTGCCCTTAATTGCCCTA	20	60
SKATEMG12R	GTGTGATGGCCTTGGGAATGTTC	22	60
SKATEMG13F	AGTTGACCCAAGCCCATGAC	20	58
SKATEMG13R	GGGTAAAGAGCTGGCAGTCA	20	58
SKATEMG14F	TGATGAGGCTCATAATACTTTTCTAGT	27	58
SKATEMG14R	GGCTGAAAGAGGGTCAATACC	21	58
SKATEMG15F	CTGACCATCTTAATAACCTCAACCT	25	56
SKATEMG15R	GAAGCTTCAGGGGTTTGAA	20	56
SKATEMG16F	CCCCCTACAAAAGAAATAGCCT	23	60
SKATEMG16R	AACGGCTGTTTAAACGTGAGTG	22	60
SKATEMG17F	AAACTCTTGGTGCAACTCCA	20	57
SKATEMG17R	CCTAATTGGCTGGATGTGGA	20	57
SKATEMG18F	TCAGCACAAATTTGGCCTCCA	20	60
SKATEMG18R	TGGGTGGAGATGGTTTGAGC	20	60
SKATEMG19F	TCGGCCTCCTCTTAGCATTAG	21	59
SKATEMG19R	AGGAGTGAGCCGTAGTTTCAT	21	59
SKATEMG20F	AGAAGGATTTGAAGCCACTGC	21	59
SKATEMG20R	GGGATAAAGTTTCTGTGTCTCCT	24	59
SKATEMG21F	GGGCTCCAATAACCCCACT	19	59
SKATEMG21R	ATTGGAAGATCATAAATATGGGGGTT	26	59
SKATEMG22F	GAACCTCCATCCTTGGCTCC	20	60
SKATEMG22R	ACCAGCGAATGATATAAGTAGCGA	24	60
SKATEMG23F	GCTCACATTTGGCACCCTTG	20	60
SKATEMG23R	TCACCCTTTACGCCGTGAAG	20	60

Table S2. Pairwise p -values of haplotype and nucleotide diversity. Lower left matrix displays pairwise p -values of Nucleotide diversity, upper right matrix displays p -values of Haplotype diversity (Benjamini-Hochberg adjusted). MPA: Loch Sunart to the Sound of Jura Marine Protected Area, NSC: North Scotland, WS: West Scotland, CS: Celtic Sea, IRE: Ireland, HEB: the Hebrides. Values of the MPA highlighted in bold. Asterisk indicating $p < 0.05$, double asterisk indicating significant $p < 0.01$

	MPA	NSC	WS	HEB	CS	IRE
MPA		0.003**	0.005**	0.014*	0.018*	0.176
NSC	<0.001**		0.954	0.493	0.996	0.950
WS	<0.001**	0.655		0.881	0.863	0.996
HEB	0.001**	0.318	0.636		0.611	0.878
CS	<0.001**	0.176	0.051	0.015*		0.824
IRE	0.018*	0.898	0.812	0.622	0.295	

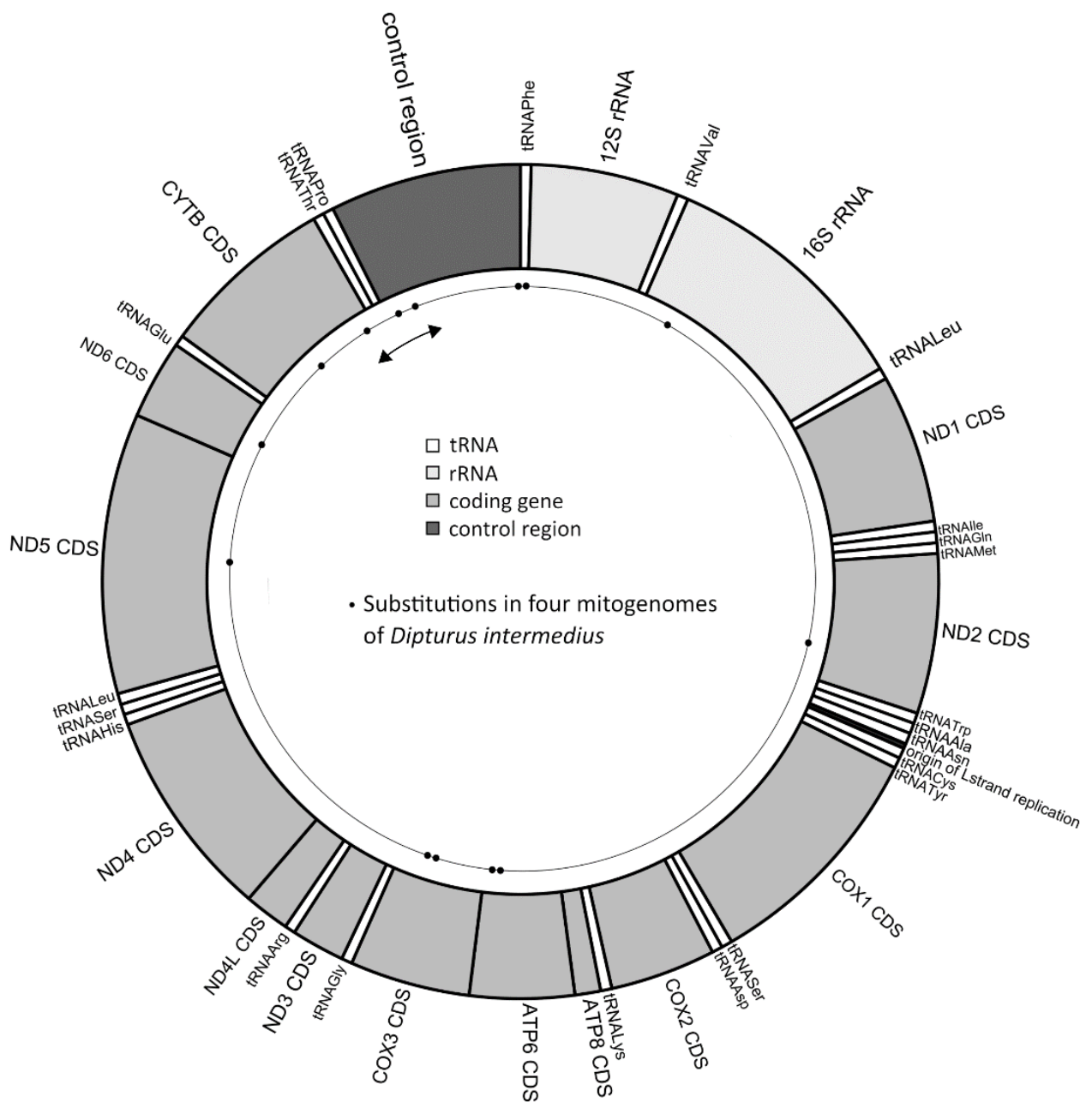


Figure S1. Mitogenome variability in *Dipturus intermedius*. Outer ring displays the mitogenomic order. Black inner ring shows substitutions found in the alignment of four mitogenomes of *D. intermedius* from the North Scotland, Ireland, the MPA and the Celtic Sea, GenBank accession numbers MT890687–MT890690. The arrows indicate the approximate region that was amplified as mitochondrial haplotype marker.

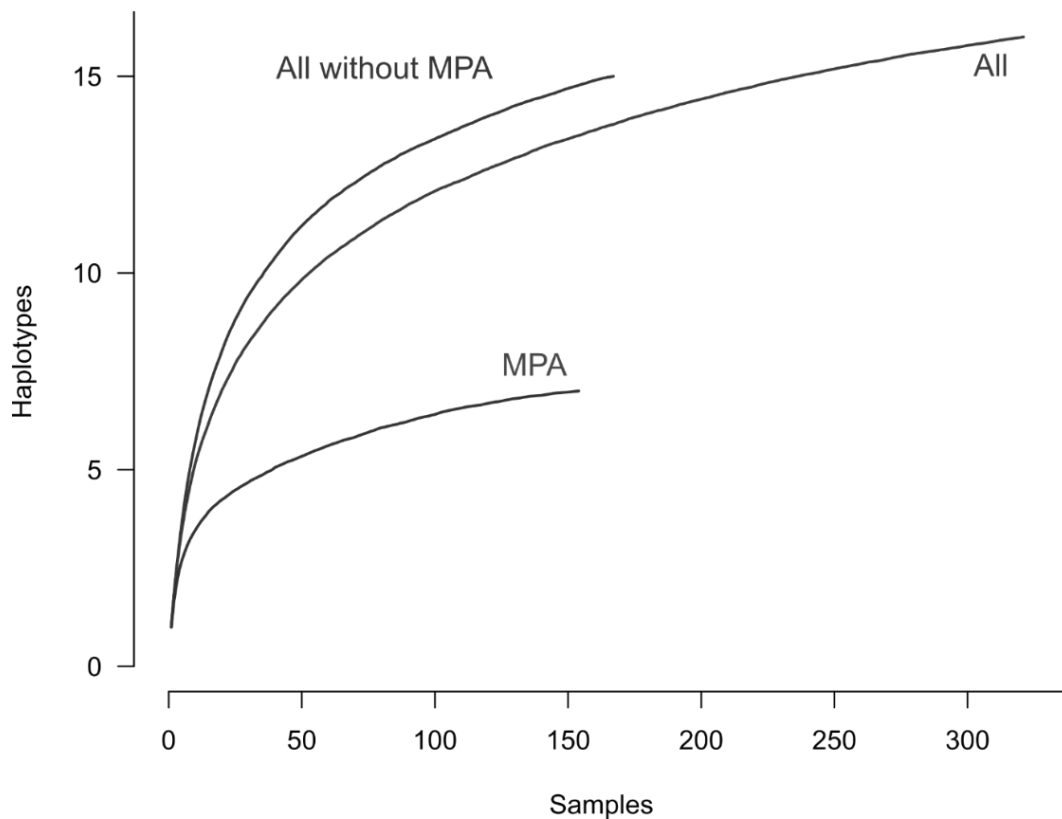


Figure S2. Haplotype accumulation curves of: all samples, all without the MPA, and the MPA, based on random subsampling of sequences, 1000 permutations.

LITERATURE CITED

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