

Electronic Supplementary Material

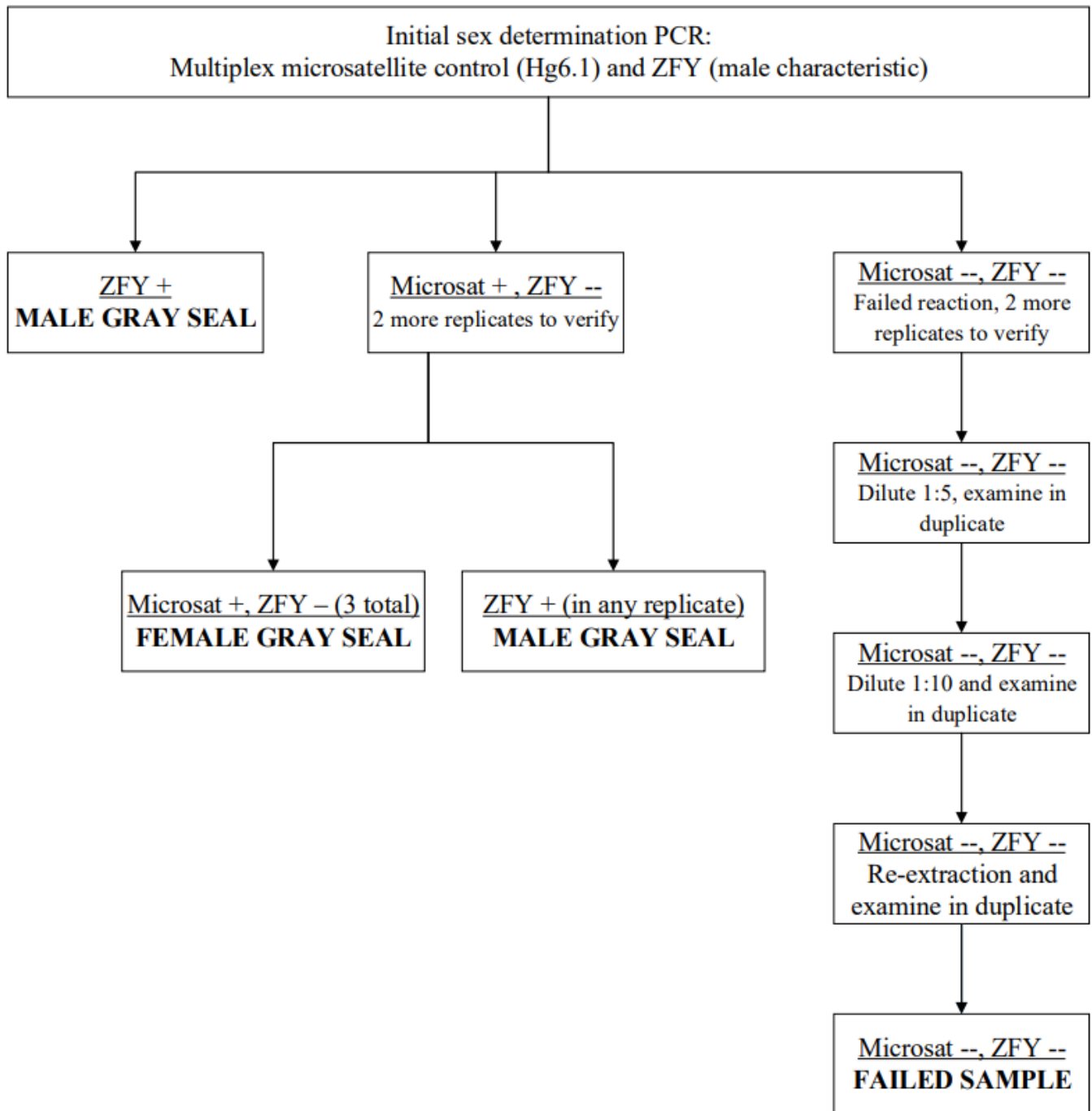


Fig. S1. A flow-chart depicting the decision process for assigning a grey seal scat sample as having originated from a male or a female seal based on a ZFY primer set (Matejusová et al. 2013) and a microsatellite internal control (Allen et al. 1995).

Table S1. Prey groups and GenBank accession numbers of representative sequences used to construct a set of haplotypes. Haplotypes were used to assess specificity of next-generation sequencing primers (Deagle et al. 2009) for Gulf of Maine species.

Prey group	GenBank accession numbers
<i>Amblyraja radiata</i>	KJ128695.1 KJ128694.1 HM140433.1 NC_000893.1 AF106038.1
<i>Ammodytes</i> spp.	NC_028530.1 KT723027.1
<i>Anarhichas</i> spp.	NC_009773.1 EF427916.1 EF427918.1 EF427917.1
<i>Anguilla rostrata</i>	KJ564271.1 KJ564217.1 KJ564216.1 KJ564215.1 KJ564214.1
<i>Citharichthys arctifrons</i>	JQ939065.1
<i>Clupea harengus</i>	HQ592202.1 HQ592201.1 KJ128741.1 GU324147.1 KJ128740.1
<i>Cyclopterus lumpus</i>	KJ128759.1 KJ128758.1 EF508340.1 AY539043.2 AY368299.1
<i>Gadus morhua</i>	DQ356939.1 X99772.1 AM489716.1
<i>Halichoerus grypus</i>	X72004.1
<i>Hippoglossina oblonga</i>	AF420448.1
<i>Malacoraja senta</i>	KF561897.1 JQ034406.1

	NC_016429.1
<i>Menidia menidia</i>	AY538969.2 AY266085.1 NC_011174.1 AB370893.1 AY430243.1
<i>Merluccius bilinearis</i>	FJ215165.1 DQ274020.1 AF420456.1 DQ274021.1
<i>Morone saxatilis</i>	AY539046.2 AY254565.1 AF247441.1 HM447585.1 NC_014353.1
<i>Myoxocephalus octodecemspinosus</i>	KM057864.1 AY048304.1
Ophidiidae	KX120081.1 DQ027912.1
<i>Petromyzon marinus</i>	KJ128854.1 KJ128853.1 EU404075.1 EU404074.1 U11880.1
<i>Pleuronectes ferruginea</i>	AF420452.1
<i>Pollachius virens</i>	KJ128867.1 KJ128866.1 FJ215186.1 AF420461.1 GU581264.1
<i>Pseudopleuronectes americanus</i>	JQ939087.1 FJ870412.1 AF488428.1 AF420450.1
<i>Raja eglanteria</i>	KF317719.1
<i>Scomber scombrus</i>	KJ128898.1 AB120717.1 KJ128897.1 AF055615.1 AY048303.1
<i>Scophthalmus aquosus</i>	AF420449.1 AF488462.1 DQ532957.1

<i>Sebastes</i> spp.	KJ879081.1 KJ879063.1 KJ879040.1
<i>Squalus acanthias</i>	KP641549.1 KP641548.1 KP641547.1 KP641546.1 KP641545.1
<i>Stenotomus chrysops</i>	AF247433.1
<i>Tautoga onitis</i>	AY279751.1 AY662710.1 AF517588.1
<i>Urophycis chuss</i>	FJ215197.1 AF420455.1
<i>Urophycis tenuis</i>	FJ215199.1 AF420454.1
<i>Zoarces americanus</i>	GQ844858.1 GQ844857.1 GQ844856.1



Fig. S2. Sequence alignments illustrating the universal 16S chordate primers (Deagle et al. 2009), the grey seal blocker primer designed for this study, the grey seal sequence, and representative sequences of 27 prey taxa organized into Haplotypes by FaBox. Alignment conducted in BioEdit.

LITERATURE CITED IN SUPPLEMENT

Allen PJ, Amos W, Pomeroy PP, Twiss SD (1995) Microsatellite variation in grey seals (*Halichoerus grypus*) shows evidence of genetic differentiation between two British breeding colonies. Mol Ecol 4(6):653-62. <https://doi.org/10.1111/j.1365-294X.1995.tb00266.x>

Deagle BE, Kirkwood R, Jarman SN (2009) Analysis of Australian fur seal diet by pyrosequencing prey DNA in faeces. Mol Ecol 18(9):2022-38. <https://doi.org/10.1111/j.1365-294X.2009.04158.x>

Matejusová I, Bland F, Hall AJ, Harris RN, Snow M, Douglas A, Middlemas SJ (2013) Real-time PCR assays for the identification of harbor and gray seal species and sex: A molecular tool for ecology and management. Mar Mamm Sci 29:186–194. <https://doi.org/10.1111/j.1748-7692.2011.00543.x>